

# Curriculum Vitae

Dr. Franz Herzog

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**Full name:** Franz Herzog, PhD  
**Date of birth:** October 10<sup>th</sup>, 1973  
**Place of birth:** St.Pölten, Austria  
**Nationality:** Austria

**Current address:** Institute Krems Bioanalytics  
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## Academic Positions and Education

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- 07/2021 – current **Stiftungsprofessor** and **Group Leader** of Biomedical Mass Spectrometry at the **Institute Krems Bioanalytics** of the IMC University of Applied Sciences Krems, Austria
- 07/2012 – 06/2021 **Group Leader** at the **Gene Center** of the **Ludwig-Maximilians-Universität**, Munich, Germany
- 05/2008 – 06/2012 **Postdoctoral fellow** at the **Swiss Federal Institute of Technology (ETH)**, Zurich, Switzerland. Supervisor: Ruedi Aebersold  
Topic: *“Probing the architecture of mitotic protein complexes by isotope-coded chemical cross-linking and mass spectrometry”*
- 01/2007 – 01/2008 **Postdoctoral student** at the **Research Institute of Molecular Pathology (IMP)**, Vienna, Austria. Supervisor: Jan-Michael Peters
- 12/2006 **PhD** in Molecular Biology passed with distinction. IMP, Vienna, Austria
- 01/2003 – 01/2007 **Graduate student** at the IMP within the Vienna Biocenter International PhD Program, Austria. Supervisor: Jan-Michael Peters  
Topic: *“Structure and Regulation of the Anaphase-Promoting Complex”*
- 12/2002 **Graduation in Biotechnology** passed with distinction at the **University of Natural Resources and Life Sciences**, Vienna, Austria

## **Awards**

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- 2015 ERC Young Investigator
- 2015 HFSP Grant together with Kevin Corbett (UCSD) and Attila Toth (TU Dresden)
- 2014 Member of the Graduate Program 1721
- 2013 LMU*excellent* Junior Grant
- 2012 Bavarian Research Center for Molecular Biosystems
- 2010 – 2011 Marie Curie Fellowship (FP7-PEOPLE-IEF), no.237346
- 2009 EMBO Long-term Fellowship, no.1032-2008

## **Selected Invited Talks**

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- 2019 Chromosome segregation and aneuploidy, EMBO Workshop, Cascais, Portugal  
Poster talk: The COMA complex interacts with Cse4 and positions Sli15/Ipl1 at the budding yeast inner kinetochore
- 2019 Chemical Cross-Linking and Covalent Labeling, ASMS Sanibel Conference on Mass Spectrometry. St. Petersburg, USA  
Talk: Chemical Cross-Linking and Mass Spectrometry: Insights into the Kinetochore
- 2018 Centromere Biology, Gordon Research Conference. Mount Snow, USA  
Poster talk: The architecture of the budding yeast inner kinetochore and its role in Ipl1 function.
- 2015 Dynamic Kinetochore EMBO Workshop. Copenhagen, Denmark  
Talk: Towards the Native Kinetochore Architecture using Chemical Cross-linking and Mass Spectrometry
- 2013 Structural Proteomics Symposium. Prague, Czech Republic  
Talk: Missing Links in Structural Biology and Interaction Proteomics
- 2012 Seminar Series, Max Planck Institute of Molecular Physiology, Dortmund, Germany  
Talk: Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-linking and Mass Spectrometry
- 2012 Chromosome Dynamics Symposium, Vienna, Austria  
Talk: Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-linking and Mass Spectrometry
- 2012 High Throughput Structural Biology Keystone Symposium. Keystone, USA  
Talk: Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-linking and Mass Spectrometry

## ***Lecturing and Tutoring***

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2020	Literature Seminar, Biochemistry (P4)
2019	Biochemistry 3, Ringvorlesung, Cell cycle
2018	Biochemistry 3, Ringvorlesung, Cell cycle
2018	Biochemistry 2, Practical Exercise
2014	Graduate School Lecture and Practical Exercise: Mass Spectrometry I
2013 –	Supervision of 1 undergraduate, 4 graduate and 2 postdoctoral students
2010	Supervision of 1 undergraduate student
2010 – 2011	Block course Proteomics: Structural Proteomics
2006 – 2007	Supervision of 1 graduate student

## ***Memberships of Scientific Societies***

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2010 - Member of the American Society for Mass Spectrometry

## ***Major Collaborations (past and present)***

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Andrea Musacchio, Structural proteomics of human kinetochore complexes, MPI for Molecular Physiology, Dortmund, Germany

Patrick Cramer, Structural proteomics of RNA polymerases, MPI for Biophysical Chemistry, Göttingen, Germany

Craig L. Peterson, Structural proteomics of chromatin associated complexes, University of Massachusetts, Worcester, USA

Karl-Peter Hopfner, Structural proteomics of an INO80-nucleosome complex, Gene Center, Ludwig-Maximilians-Universität-München, Munich, Germany

Eva Nogales, Structural proteomics of the PRC2 complex, Howard Hughes Medical Institute, University of California, Berkeley, USA

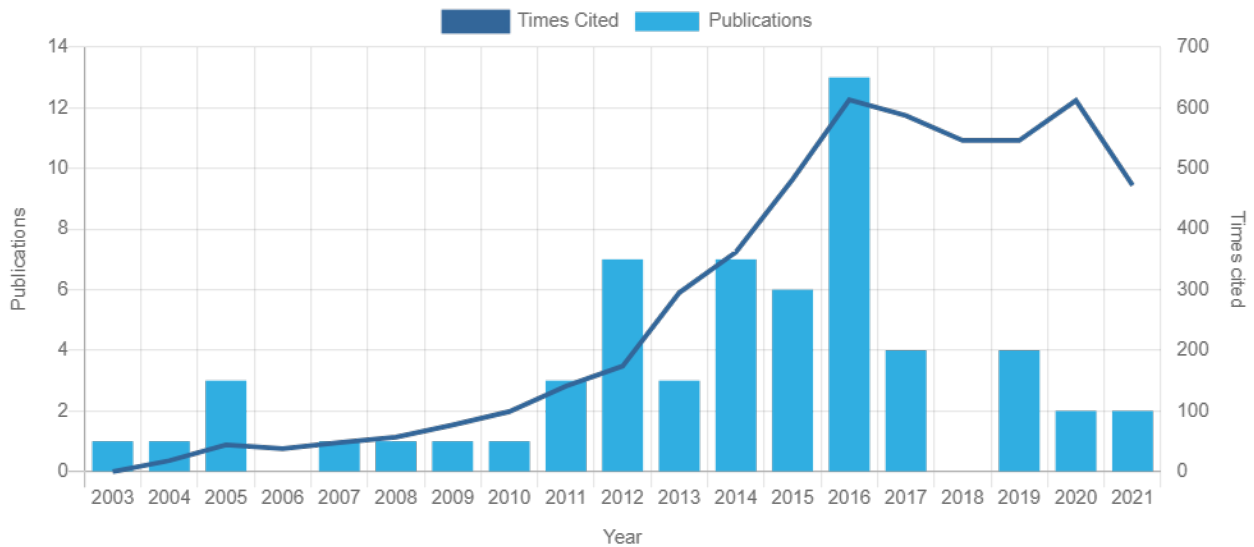
Holger Stark, 3D Electron Cryomicroscopy, Department of Cellular Biochemistry, Max Planck Institute for Biophysical Chemistry, Göttingen, Germany

Michel O. Steinmetz, Crosslinking and mass spectrometry of microtubule-binding proteins, Paul Scherrer Institute, Villigen, Switzerland

## Publications

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- Number of publications: 60
- Number of citations: 5211
- H-index: 36



Publication statistics at [publons.com](https://publons.com)

Dudziak, A., Engelhard, L., Bourque, C., Klink, B.U., Rombaut, P., Kornakov, N., Janen, K., **Herzog, F.**, Gatsogiannis, C., and Westermann, S. (2021). Phospho-regulated Bim1/EB1 interactions trigger Dam1c ring assembly at the budding yeast outer kinetochore. *EMBO J* 40, e108004.

Kratzat, H., Mackens-Kiani, T., Ameisemeier, M., Potocnjak, M., Cheng, J., Dacheux, E., Namane, A., Berninghausen, O., **Herzog, F.**, Fromont-Racine, M., Becker, T., and Beckmann, R. (2021). A structural inventory of native ribosomal ABCE1-43S pre-initiation complexes. *EMBO J* 40, e105179.

Ghodgaonkar-Steger, M., Potocnjak, M., Zimniak, T., Fischbock-Halwachs, J., Solis-Mezarino, V., Singh, S., Speljko, T., Hagemann, G., Drexler, D.J., Witte, G., and **Herzog, F.** (2020). C-Terminal Motifs of the MTW1 Complex Cooperatively Stabilize Outer Kinetochore Assembly in Budding Yeast. *Cell Rep* 32, 108190.

Killinger, K., Bohm, M., Steinbach, P., Hagemann, G., Bluggel, M., Janen, K., Hohoff, S., Bayer, P., **Herzog, F.**, and Westermann, S. (2020). Auto-inhibition of Mif2/CENP-C ensures centromere-dependent kinetochore assembly in budding yeast. *EMBO J* 39, e102938.

Fischbock-Halwachs, J., Singh, S., Potocnjak, M., Hagemann, G., Solis-Mezarino, V., Woike, S., Ghodgaonkar-Steger, M., Weissmann, F., Gallego, L.D., Rojas, J., Andreani, J., Kohler, A., and **Herzog, F.** (2019). The COMA complex interacts with Cse4 and positions Sli15/Ipl1 at the budding yeast inner kinetochore. *Elife* 8.

Iacobucci, C., Piotrowski, C., Aebersold, R., Amaral, B.C., Andrews, P., Bernfur, K., Borchers, C., Brodie, N.I., Bruce, J.E., Cao, Y., Chaignepain, S., Chavez, J.D., Claverol, S., Cox, J., Davis, T., Degliesposti, G., Dong, M.Q., Edinger, N., Emanuelsson, C., Gay, M., Gotze, M., Gomes-Neto, F., Gozzo, F.C., Gutierrez, C., Haupt, C., Heck, A.J.R., **Herzog, F.**, Huang, L., Hoopmann, M.R., Kalisman, N., Klykov, O., Kukacka, Z., Liu, F., MacCoss, M.J., Mechtler, K., Mesika, R., Moritz, R.L., Nagaraj, N., Nesati, V., Neves-Ferreira, A.G.C., Ninnis, R., Novak, P., O'Reilly, F.J., Pelzing, M., Petrotchenko, E., Piersimoni, L., Plasencia, M., Pukala, T., Rand, K.D., Rappsilber, J., Reichmann, D., Sailer, C., Sarnowski, C.P., Scheltema, R.A., Schmidt, C., Schriemer, D.C., Shi, Y., Skehel, J.M., Slavin, M., Sobott, F., Solis-Mezarino, V., Stephanowitz, H., Stengel, F., Stieger, C.E., Trabjerg, E., Trnka, M., Vilaseca, M., Viner, R., Xiang, Y., Yilmaz, S., Zelter, A., Ziemianowicz, D., Leitner, A., and Sinz, A. (2019). First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. *Anal Chem* **91**, 6953-6961.

Ivic, N., Potocnjak, M., Solis-Mezarino, V., **Herzog, F.**, Bilokapic, S., and Halic, M. (2019). Fuzzy Interactions Form and Shape the Histone Transport Complex. *Mol Cell* **73**, 1191-1203 e1196.

West, A.M., Rosenberg, S.C., Ur, S.N., Lehmer, M.K., Ye, Q., Hagemann, G., Caballero, I., Uson, I., MacQueen, A.J., **Herzog, F.**, and Corbett, K.D. (2019). A conserved filamentous assembly underlies the structure of the meiotic chromosome axis. *Elife* **8**.

Bottcher, R.T., Veelders, M., Rombaut, P., Faix, J., Theodosiou, M., Stradal, T.E., Rottner, K., Zent, R., **Herzog, F.**, and Fassler, R. (2017). Kindlin-2 recruits paxillin and Arp2/3 to promote membrane protrusions during initial cell spreading. *J Cell Biol* **216**, 3785-3798.

Mosalaganti, S., Keller, J., Altenfeld, A., Winzker, M., Rombaut, P., Saur, M., Petrovic, A., Wehenkel, A., Wohlgemuth, S., Muller, F., Maffini, S., Bange, T., **Herzog, F.**, Waldmann, H., Rauser, S., and Musacchio, A. (2017). Structure of the RZZ complex and molecular basis of its interaction with Spindly. *J Cell Biol* **216**, 961-981.

Solis-Mezarino, V., and **Herzog, F.** (2017). compleXView: a server for the interpretation of protein abundance and connectivity information to identify protein complexes. *Nucleic Acids Res* **45**, W276-W284.

Ye, Q., Kim, D.H., Dereli, I., Rosenberg, S.C., Hagemann, G., **Herzog, F.**, Toth, A., Cleveland, D.W., and Corbett, K.D. (2017). The AAA+ ATPase TRIP13 remodels HORMA domains through N-terminal engagement and unfolding. *EMBO J* **36**, 2419-2434.

Bernecky, C., **Herzog, F.**, Baumeister, W., Plitzko, J.M., and Cramer, P. (2016). Structure of transcribing mammalian RNA polymerase II. *Nature* **529**, 551-554.

Friese, A., Faesen, A.C., Huis in 't Veld, P.J., Fischbock, J., Prumbaum, D., Petrovic, A., Rauser, S., **Herzog, F.**, and Musacchio, A. (2016). Molecular requirements for the inter-subunit interaction and kinetochore recruitment of SKAP and Astrin. *Nat Commun* **7**, 11407.

Gallego, L.D., Ghodgaonkar Steger, M., Polyansky, A.A., Schubert, T., Zagrovic, B., Zheng, N., Clausen, T., **Herzog, F.**, and Kohler, A. (2016). Structural mechanism for the recognition and

ubiquitination of a single nucleosome residue by Rad6-Bre1. *Proc Natl Acad Sci U S A* 113, 10553-10558.

Heuck, A., Schitter-Sollner, S., Suskiewicz, M.J., Kurzbauer, R., Kley, J., Schleiffer, A., Rombaut, P., **Herzog, F.**, and Clausen, T. (2016). Structural basis for the disaggregase activity and regulation of Hsp104. *Elife* 5.

Petrovic, A., Keller, J., Liu, Y., Overlack, K., John, J., Dimitrova, Y.N., Jenni, S., van Gerwen, S., Stege, P., Wohlgemuth, S., Rombaut, P., **Herzog, F.**, Harrison, S.C., Vetter, I.R., and Musacchio, A. (2016). Structure of the MIS12 Complex and Molecular Basis of Its Interaction with CENP-C at Human Kinetochores. *Cell* 167, 1028-1040 e1015.

Hons, M.T., Huis In 't Veld, P.J., Kaesler, J., Rombaut, P., Schleiffer, A., **Herzog, F.**, Stark, H., and Peters, J.M. (2016). Topology and structure of an engineered human cohesin complex bound to Pds5B. *Nat Commun* 7, 12523.

Jakob, L., Treiber, T., Treiber, N., Gust, A., Kramm, K., Hansen, K., Stotz, M., Wankler, L., **Herzog, F.**, Hannus, S., Grohmann, D., and Meister, G. (2016). Structural and functional insights into the fly microRNA biogenesis factor Loquacious. *RNA* 22, 383-396.

Liu, Y., Petrovic, A., Rombaut, P., Mosalaganti, S., Keller, J., Raunser, S., **Herzog, F.**, and Musacchio, A. (2016). Insights from the reconstitution of the divergent outer kinetochore of *Drosophila melanogaster*. *Open Biol* 6, 150236.

Pekgoz Altunkaya, G., Malvezzi, F., Demianova, Z., Zimniak, T., Litos, G., Weissmann, F., Mechtler, K., **Herzog, F.**, and Westermann, S. (2016). CCAN Assembly Configures Composite Binding Interfaces to Promote Cross-Linking of Ndc80 Complexes at the Kinetochore. *Curr Biol* 26, 2370-2378.

Poli, J., Gerhold, C.B., Tosi, A., Hustedt, N., Seeber, A., Sack, R., **Herzog, F.**, Pasero, P., Shimada, K., Hopfner, K.P., and Gasser, S.M. (2016). Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. *Genes Dev* 30, 337-354.

Schmidtman, E., Anton, T., Rombaut, P., **Herzog, F.**, and Leonhardt, H. (2016). Determination of local chromatin composition by CasID. *Nucleus* 7, 476-484.

Vos, S.M., Pollmann, D., Caizzi, L., Hofmann, K.B., Rombaut, P., Zimniak, T., **Herzog, F.**, and Cramer, P. (2016). Architecture and RNA binding of the human negative elongation factor. *Elife* 5.

Weir, J.R., Faesen, A.C., Klare, K., Petrovic, A., Basilico, F., Fischbock, J., Pentakota, S., Keller, J., Pesenti, M.E., Pan, D., Vogt, D., Wohlgemuth, S., **Herzog, F.**, and Musacchio, A. (2016). Insights from biochemical reconstitution into the architecture of human kinetochores. *Nature* 537, 249-253.

Grimm, M., Zimniak, T., Kahraman, A., and **Herzog, F.** (2015). xVis: a web server for the schematic visualization and interpretation of crosslink-derived spatial restraints. *Nucleic Acids Res* **43**, W362-369.

Klare, K., Weir, J.R., Basilico, F., Zimniak, T., Massimiliano, L., Ludwigs, N., **Herzog, F.**, and Musacchio, A. (2015). CENP-C is a blueprint for constitutive centromere-associated network assembly within human kinetochores. *J Cell Biol* **210**, 11-22.

Kock, M., Nunes, M.M., Hemann, M., Kube, S., Dohmen, R.J., **Herzog, F.**, Ramos, P.C., and Wendler, P. (2015). Proteasome assembly from 15S precursors involves major conformational changes and recycling of the Pba1-Pba2 chaperone. *Nat Commun* **6**, 6123.

Martinez-Rucobo, F.W., Kohler, R., van de Waterbeemd, M., Heck, A.J., Hemann, M., **Herzog, F.**, Stark, H., and Cramer, P. (2015). Molecular Basis of Transcription-Coupled Pre-mRNA Capping. *Mol Cell* **58**, 1079-1089.

Mulholland, C.B., Smets, M., Schmidtman, E., Leidescher, S., Markaki, Y., Hofweber, M., Qin, W., Manzo, M., Kremmer, E., Thanisch, K., Bauer, C., Rombaut, P., **Herzog, F.**, Leonhardt, H., and Bultmann, S. (2015). A modular open platform for systematic functional studies under physiological conditions. *Nucleic Acids Res* **43**, e112.

Plaschka, C., Lariviere, L., Wenzek, L., Seizl, M., Hemann, M., Tegunov, D., Petrotchenko, E.V., Borchers, C.H., Baumeister, W., **Herzog, F.**, Villa, E., and Cramer, P. (2015). Architecture of the RNA polymerase II-Mediator core initiation complex. *Nature* **518**, 376-380.

Basilico, F., Maffini, S., Weir, J.R., Prumbaum, D., Rojas, A.M., Zimniak, T., De Antoni, A., Jeganathan, S., Voss, B., van Gerwen, S., Krenn, V., Massimiliano, L., Valencia, A., Vetter, I.R., **Herzog, F.**, Raunser, S., Pasqualato, S., and Musacchio, A. (2014). The pseudo GTPase CENP-M drives human kinetochore assembly. *Elife* **3**, e02978.

**Herzog, F.** (2014). Measuring spatial restraints on native protein complexes using isotope-tagged chemical cross-linking and mass spectrometry. *Methods Mol Biol* **1091**, 259-273.

Hornung, P., Troc, P., Malvezzi, F., Maier, M., Demianova, Z., Zimniak, T., Litos, G., Lampert, F., Schleiffer, A., Brunner, M., Mechtler, K., **Herzog, F.**, Marlovits, T.C., and Westermann, S. (2014). A cooperative mechanism drives budding yeast kinetochore assembly downstream of CENP-A. *J Cell Biol* **206**, 509-524.

Huis in 't Veld, P.J., **Herzog, F.**, Ladurner, R., Davidson, I.F., Piric, S., Kreidl, E., Bhaskara, V., Aebersold, R., and Peters, J.M. (2014). Characterization of a DNA exit gate in the human cohesin ring. *Science* **346**, 968-972.

Kube, S., Kapitein, N., Zimniak, T., **Herzog, F.**, Mogk, A., and Wendler, P. (2014). Structure of the VipA/B type VI secretion complex suggests a contraction-state-specific recycling mechanism. *Cell Rep* **8**, 20-30.

Maiolica, A., de Medina-Redondo, M., Schoof, E.M., Chaikuad, A., Villa, F., Gatti, M., Jeganathan, S., Lou, H.J., Novy, K., Hauri, S., Toprak, U.H., **Herzog, F.**, Meraldi, P., Penengo, L.,

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- Kahraman, A., **Herzog, F.**, Leitner, A., Rosenberger, G., Aebersold, R., and Malmstrom, L. (2013). Cross-link guided molecular modeling with ROSETTA. *PLoS One* **8**, e73411.
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- Tosi, A., Haas, C., **Herzog, F.**, Gilmozzi, A., Berninghausen, O., Ungewickell, C., Gerhold, C.B., Lakomek, K., Aebersold, R., Beckmann, R., and Hopfner, K.P. (2013). Structure and subunit topology of the INO80 chromatin remodeler and its nucleosome complex. *Cell* **154**, 1207-1219.
- Ciferri, C., Lander, G.C., Maiolica, A., **Herzog, F.**, Aebersold, R., and Nogales, E. (2012). Molecular architecture of human polycomb repressive complex 2. *Elife* **1**, e00005.
- Escher, C., Reiter, L., MacLean, B., Ossola, R., **Herzog, F.**, Chilton, J., MacCoss, M.J., and Rinner, O. (2012). Using iRT, a normalized retention time for more targeted measurement of peptides. *Proteomics* **12**, 1111-1121.
- Herzog, F.**, Kahraman, A., Boehringer, D., Mak, R., Bracher, A., Walzthoeni, T., Leitner, A., Beck, M., Hartl, F.U., Ban, N., Malmstrom, L., and Aebersold, R. (2012). Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry. *Science* **337**, 1348-1352.
- Jennebach, S., **Herzog, F.**, Aebersold, R., and Cramer, P. (2012). Crosslinking-MS analysis reveals RNA polymerase I domain architecture and basis of rRNA cleavage. *Nucleic Acids Res* **40**, 5591-5601.
- Leitner, A., Reischl, R., Walzthoeni, T., **Herzog, F.**, Bohn, S., Forster, F., and Aebersold, R. (2012). Expanding the chemical cross-linking toolbox by the use of multiple proteases and enrichment by size exclusion chromatography. *Mol Cell Proteomics* **11**, M111 014126.
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- Wu, C.C., **Herzog, F.**, Jennebach, S., Lin, Y.C., Pai, C.Y., Aebersold, R., Cramer, P., and Chen, H.T. (2012). RNA polymerase III subunit architecture and implications for open promoter complex formation. *Proc Natl Acad Sci U S A* **109**, 19232-19237.



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