Curriculum vitae Thomas Reinier Maxim Barends

Born 29 September 1975

Current position:
Research Group Leader
Department of Biomolecular Mechanisms,
Max-Planck Institute for Medical
Research, Jahnstrasse 29, D-69120 Heidelberg, Germany
(+49) 6221 486 508

Website:
http://www.mpimf-heidelberg.mpg.de/groups/structural_biology_of_elemental_cycles

---

Highlights

-Elucidation of structural biology of the anaerobic ammonium oxidation (anammox) process

-Structural enzymology of exotic biochemical processes such as lanthanide-dependent enzymes and carbon disulfide hydrolases

-Protein dynamics and energy landscapes probed by time-resolved SAXS, -crystallography, EPR and other biophysical methods

-64 publications, of which several in *Science* and *Nature*

-H-index 27

-Awarded an ERC Consolidator Grant in 2017

Formal professional history

CURRENT POSITION	
2014 – present	**Research Group Leader – permanent contract** Department of Biomolecular Mechanisms, Max Planck Institute for Medical Research, Heidelberg, Germany

PREVIOUS POSITIONS	
2010 – 2013	**Staff Scientist – permanent contract** Department of Biomolecular Mechanisms, Max Planck Institute for Medical Research, Heidelberg, Germany
2005 – 2010	**PostDoc** Department of Biomolecular Mechanisms, Max Planck Institute for Medical Research, Heidelberg, Germany
2004 – 2005	**PostDoc** Faculty of Mathematics and Natural Sciences, University of Groningen, The Netherlands

INSTITUTIONAL RESPONSIBILITIES	
2017 - present	**Faculty Member** Hartmut-Hoffmann-Berling International Graduate School of Molecular and Cellular Biology, Ruprecht—Karls-University Heidelberg
2016 - 2017	**Grant Review Committee Member** Agence Nationale de la Recherche, CES-11: Biochemistry, Biophysics, Molecular and Structural Biology
2014 - present	**Faculty Member** Max Planck Institute for Medical Research, Heidelberg, Germany
2014 – present	**Radiation Safety Officer** Max Planck Institute for Medical Research, Heidelberg, Germany

GRANTS AWARDED*	
2017	**ERC Consolidator Grant** STePLADDER: Solving the Pathway of Ladderane Biosynthesis grant: 1.7 M€ for 5 years The grant was awarded to enable the elucidation of the biosynthetic pathway of ladderane lipids, which are highly unusual bacterial lipids that contain concatenated cyclobutane rings. The investigations will combine techniques from chemical biology, biochemistry and structural biology to arrive at a comprehensive understanding of how these intriguing molecules are made.

* Researchers with permanent positions at the MPG are excluded from regular grants of the German Research Foundation (DFG)

Research interests

Structural biology of the anammox process

The discovery of anammox bacteria in the 1990's has dramatically changed our understanding of the global nitrogen cycle. These bacteria perform ANaerobic AMMonium OXidation, combining ammonium with nitrite into molecular dinitrogen (N_2) and water, yielding energy for the cell. The anammox process is responsible for up to 10% of the global nitrogen cycle, and in some ecosystems contributes up to 50% to the total N_2 production. Biochemical studies, mainly by the group of Mike Jetten and coworkers in Nijmegen, have identified the enzymes involved, and showed that the central step in the process is the combination of nitric oxide and ammonia into the extremely unusual, highly toxic and reactive intermediate hydrazine.

In collaboration with the microbiology department of Prof. Dr. Mike Jetten of the Radboud University in Nijmegen, The Netherlands, we have determined the structures of key enzymes in this process, with a view to elucidating the mechanism of anaerobic ammonium oxidation. The structure of the *Kuenenia stuttgartiensis* hydroxylamine oxidoreductase has allowed us to propose a novel mechanism for biological nitric oxide generation (Maalcke *et al.,* 2014) and identify a hitherto unknown reactivity of its heme cofactor (Dietl *et al.*, 2015a), and the structure of a 40-heme multiprotein complex containing an octaheme oxidoreductase in complex with its redox partner is now being analyzed.

Because of its unique biochemistry, and because it is the first step in producing the extremely stable triple bond in the final anammox product N_2, we have also determined the crystal structure of the enzyme combining ammonia and nitric oxide into hydrazine, the central anammox enzyme hydrazine synthase. This 225 kDa multiprotein complex has also allowed the proposal of an enzymatic mechanism for the highly unusual biochemistry performed by hydrazine synthase (Dietl *et al.*, 2015b). Moreover, the structure of the hydrazine dehydrogenase, another central anammox enzyme, is being analyzed.

Ladderane lipid biosynthesis

We have also started to investigate how the exceptional ladderane lipids found in the membranes of anammox bacteria are being produced. These lipids contain linearly concatenated cyclobutane rings and their biosynthesis is expected to involve both novel enzymes and specially evolved versions of known proteins. However, the details remain enigmatic. How do these enzymes assemble such intricate carbon skeletons? How do they control the complex stereochemistry involved? How do they deal with the typical nonreactivity of hydrocarbons? And how do they overcome the ring strain inherent in these molecules? Answering these and other questions about the molecular mechanism of ladderane biosynthesis will open up new frontiers in enzymology. An ERC Consolidator grant has been awarded to study this intriguing biosynthetic process.

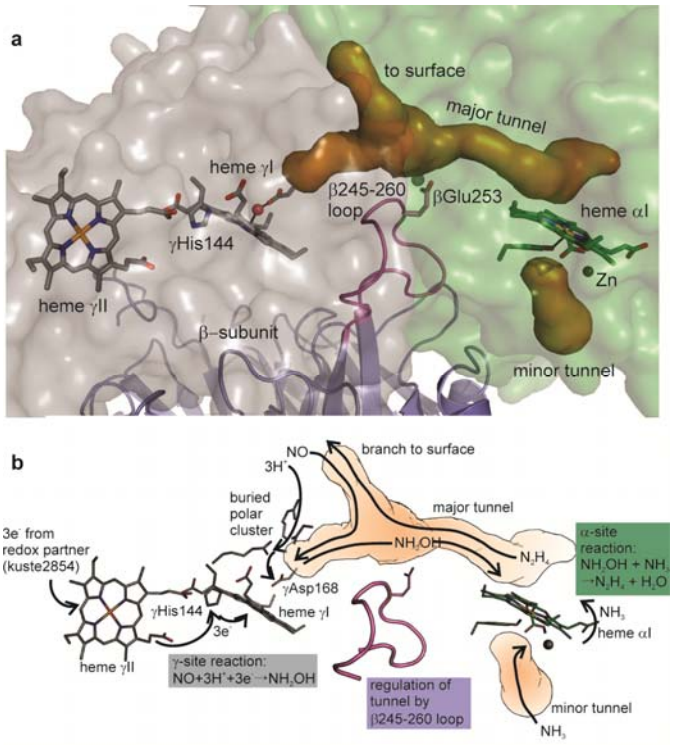
Maalcke, W. J., Dietl, A., Marrit, S. J., Butt, J. N., Jetten, M. S. M., Keltjens, J. T., **Barends, T. R. M.** and Kartal, B. (2014). Structural basis of biological NO generation by octaheme oxidoreductases. *The Journal of Biological Chemistry* **289**, 1228-1242.

Dietl, A., Maalcke, W. J., and **Barends, T. R. M.** (2015a). An unexpected reactivity of the P460 cofactor in hydroxylamine oxidoreductase. *Acta Crystallographica* **D71**, 1708-1713.

Dietl, A., Ferousi, C., Maalcke, W. J., Menzel, A., de Vries, S., Keltjens, J. T., Jetten, M. S. M., Kartal, B. and **Barends, T. R. M.** (2015b). The inner workings of the hydrazine synthase multiprotein complex. *Nature* **527**, 394-397.

Brief description of most significant publications *=as (shared) corresponding author

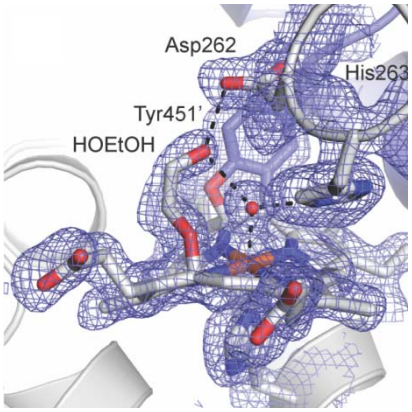
- Dietl, A., Ferousi, C., Maalcke, W. J., Menzel, A., de Vries, S., Keltjens, J. T., Jetten, M. S. M., Kartal, B. & **Barends, T. R. M.*** (2015). The inner workings of the hydrazine synthase multiprotein complex. *Nature* **527**, 394-397.



In this publication, my group and its collaborators analyze the structure of the enigmatic multiprotein complex "hydrazine synthase" (HZS) which produces the highly reactive and toxic intermediate hydrazine central to anaerobic ammonium oxidation, and find a constellation of distinct active sites connected by system of tunnels. This leads to the proposal of a mechanism for biological hydrazine synthesis in which one subunit reduces NO to NH_2OH, which travels down a tunnel to another active site where it undergoes a comproportionation reaction with NH_3 to yield hydrazine.

Figure 1. Hydrazine synthesis by HZS. **a.** Close-up of the interface between the three subunits of HZS. A heme group in the α subunit (green) is connected to one of the hemes in the γ subunit (grey) via a tunnel ("major tunnel", orange). The β subunit (blue) project a conserved loop into the interface between the α- and γ subunits which is proposed to have a regulatory function. **b.** schematic of the proposed mechanism for biological hydrazine synthesis (see text).

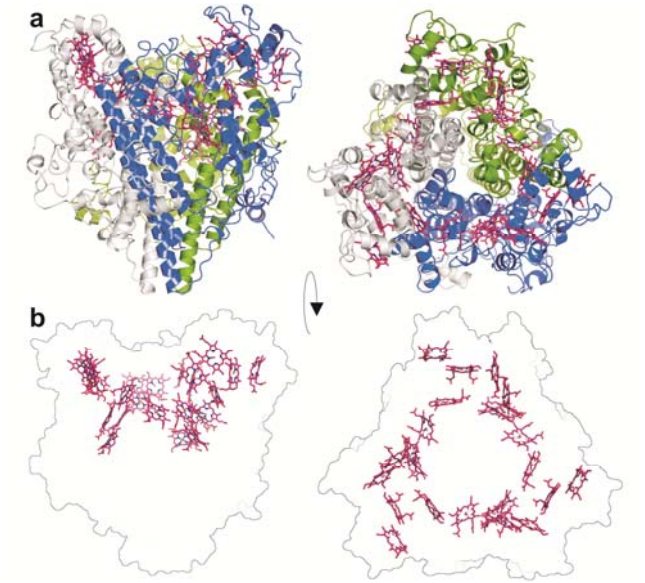
- Dietl, A., Maalcke, W. J., & **Barends, T. R. M.*** (2015). An unexpected reactivity of the P460 cofactor in hydroxylamine oxidoreductase. *Acta Crystallographica* **D71**, 1708-1713.



In this paper we describe an unexpected chemical reactivity of the cofactor in ksHAO, an unusual oxidase using a heme group that is highly distorted due to two covalent bonds to a tyrosine side chain. We found that an electrophilic centre has developed on an otherwise unreactive carbon atom of the heme's porphyrin ring, opposite the bonds to the tyrosine, which causes the heme to react with ethylene glycol, but not with other, larger molecules, probably due to restricted access to the active site. The reaction is also shown to alter the heme's spectroscopic properties.

Figure 2. Electron density of the ethylene glycol (HOEtOH) bound covalently to the distorted heme.

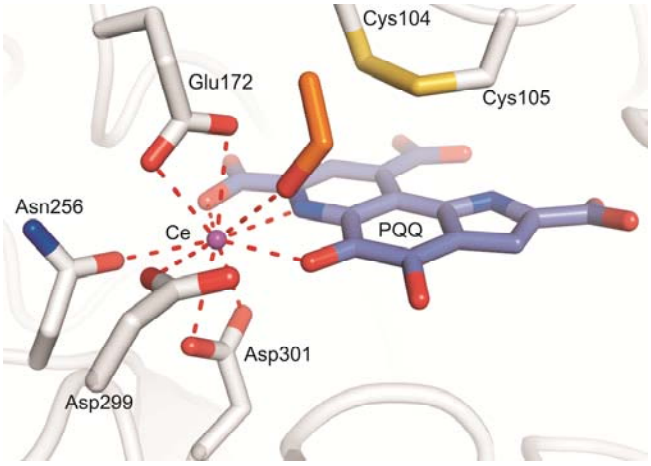
-Maalcke, W. J., Dietl, A., Marrit, S. J., Butt, J. N., Jetten, M. S. M., Keltjens, J. T., **Barends, T. R. M.*** and Kartal, B. (2014). Structural basis of biological NO generation by octaheme oxidoreductases. *The Journal of Biological Chemistry* **289**, 1228-1242.



This paper desribes the structure and mechanism of ksHAO, an unusual oxidase from anammox organisms that converts hydroxylamine into nitric oxide using an unusual heme cofactor. The high-resolution crystal structures solved by my group allowed the proposal of a mechanism that explains why this enzyme produces the anammox substrate NO, whereas homologous proteins oxidize the product further to NO_2^-.

Figure 3. a. Structure of ksHAO in two different orientations. **b**. Outline of ksHAO in the same orientations as in a, showing the "wires" of heme groups that transport electrons through the protein.

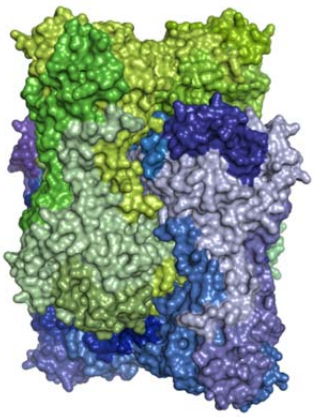
-Pol, A., **Barends, T. R. M.**, Dietl, A., Khadem, A., Eygensteyn, J., Jetten, M. S. M., Op den Camp, H. J. M. (2014). Rare earth elements are essential for methanotrophic life in volcanic mudpots. *Environmental Microbiology* **16**, 255-264.



This publication describes the discovery of a PQQ-dependent methanol dehydrogenase that uses rare-earth elements as their metal cofactor. My Ph.D. student Andreas Dietl and I solved high-resolution crystal structures of the enzyme which showed unusually high electron density at the metal binding site, as well as unusual coordination. Our collaborators, using culturing techniques and mass spectrometry showed this metal to be cerium, and that this can be replaced by a number of other lanthanides. This first-ever observation of lanthanide chemistry in biology led to the identification of a novel class of MDHs that are expected to use lanthanides as their cofactor

Figure 4. Close-up of the active site of lanthanide-dependent MDH, showing the coordination of the bound cerium atom.

- Smeulders, M. J., **Barends, T. R. M.,** Pol, A., Scherer, A., Zandvoort, Udvarhelyi, A., Khadem, A. F., Menzel, A., Hermans, J., Shoeman, R. L. Wessels, H. J. C. T., van den Heuvel, L. P., Russ, L., Schlichting, I., Jetten, M. S. M. and Op den Camp H. J. M. (2011). Evolution of a new enzyme for carbon disulfide conversion by an acidothermophilic archaeon. *Nature* **478**, 412-414.



This paper, resulting from a collaboration I initiated as a postdoc describes the structure and mechanism of CS_2 hydrolase, an enzyme that allows bacteria to use the highly toxic carbon disulfide as a source of carbon and energy. The enzyme forms octameric rings, that interlock forming hexadecamers, probably to allow high protein densities in the cell, and are closely related to carbonic anhydrases, yet do not convert CO_2. I solved the structure of the enzyme and confirmed the unusual quaternary structure observed in the crystal by analytical ultracentrifugation and solution small-angle X-ray scattering. The crystal structures revealed a tunnel that serves as a filter that lets carbon disulfide, but not CO_2, access the active site.

Figure 5. A carbon disulfide hydrolase hexadecamer, built up from two interlocking octameric rings, shown in shades of green and blue.

In addition, as a senior scientist in the department I contribute to the department's efforts in developing methods to use free electron lasers (FELs) as novel radiation sources in structural biology:

Barends, T. R. M.*, Foucar, L., Ardevol, A., Nass, K., Aquila, A., *et al.* (2015). Direct observation of ultrafast collective motions in CO myoglobin upon ligand dissociation. *Science* **350**, 445-450.

Barends, T. R. M.*, Foucar, L., Botha, S., Doak, R. B., Shoeman, R. L., *et al.* (2014). *De novo* protein crystal structure determination from X-ray free electron laser data. *Nature* **505**, 244-247.

Redecke, L., Nass, K., DePonte, D. P., White, T. A., Rehders, D., Barty, A., Stellato, F., Liang, M., **Barends, T. R. M.,** *et al.* (2013). Natively inhibited *Trypanosoma brucei* cathepsin B structure determined by using an X-ray laser. *Science* **339**, 227-230.

Boutet, S., Lomb, L., Williams, G. J., **Barends, T. R. M.,** Aquila, A., *et al.* (2012). High-resolution protein structure determination by serial femtosecond crystallography. *Science* **337**, 362-364.

Chapman, H. N., Fromme, P., Barty, A., White, T. A., Kirian, R. A., *et al.* **Barends, T. R. M.** , *et al.* (2011). Femtosecond X-ray protein crystallography. *Nature* **470**, 73-81.

PUBLICATION SUMMARY (April 2018)	
Total peer-reviewed	64, of which 10 as corresponding author (including shared corresponding author)
Total citations	3,444 (excluding self-citations)
H-index	27
No. of publications with >100 citations	8 (of which 3 with over 200 citations)

Complete List of Peer-Reviewed Publications *=as (shared) corresponding author

Jahn, B., Pol, A., Lumpe, H., **Barends, T. R. M.**, Dietl, A., Hogendoorn, C., Op den Camp, H. and Daumann, L. (2018) Similar but not the same: first kinetic and structural analyses of a methanol dehydrogenase containing a europium ion in the active site, *ChemBioChem* online publication before print, https://doi.org/10.1002/cbic.201800130

Coquelle, N., Sliwa, M., Woodhouse, J., Schiro, G., Adam, V., Aquila, A., **Barends, T. R. M.**, Boutet, S., Byrdin, M., Carbajo, S., De la Mora, E., Doak, R. B., Feliks, M., Fieschi, F., Foucar, L., Guillon, V., Hilpert, M., Hunter, M.S., Jakobs, S., Koglin, J., Kovácsová, G., Lane, T. J., Levy, B., Linag, M., Nass, K., Ridard, J., Robinson, J., Roome, C., Ruckebusch, C., Seaberg, M., Thepaut, M., Cammarata, M., Demachy, I., Field, M., Shoeman, R.L., Bourgeois, D., Colletier, J.-P. Schlichting, I., and Weik, M. (2018) Chromophore twisting in the excited state of a photoswitchable fluorescent protein captured by time-resolved serial femtosecond crystallography, *Nature Chemistry* **10**, 31-37

Gorel, A., Motomura, K., Fukuzawa, H., Doak, R. B., Grünbein, M.L., Hilpert, M., Inoue, I., Kloos, M., Kovácsová, G., Nango, E., Nass, K., Roome, C., Shoeman, R., Tanaka, R., Tono, K., Joti, Y., Yabashi, M., Iwata, S., Foucar, L., Ueda, K., **Barends, T. R. M.**, and Schlichting I. (2017) Two-colour serial femtosecond crystallography dataset from gadoteridol-derivatized lysozyme for MAD phasing, *Scientific Data* **4**, 170188

Gorel, A., Motomura, K., Fukuzawa, H., Doak, R. B., Grünbein, M. L., Hilpert, M., Inoue, I., Kloos, M., Kovácsová, G., Nango, E., Nass, K., Roome, C., Shoeman, R., Tanaka, R., Tono, K., Joti, Y., Yabashi, M., Iwata, S., Foucar, L., Ueda, K., **Barends, T. R. M.**, and Schlichting I. (2017) Multi-wavelength anomalous diffraction de novo phasing using a two-colour X-ray free-electron laser with wide tunability, *Nature Communications* **8**, 1170

Dietl, A., Kieser, C., and **Barends, T. R. M.*** (2017) A Peltier-cooled microscope stage for protein crystal post-crystallization treatment, *Journal of Applied Crystallography* **50,** 1208-1211.

Kovácsová, G., Grünbein, M. L., Kloos, M., **Barends, T. R. M.**, Schlesinger, R., Heberle, J., Kabsch, W., Shoeman, R. L., Doak, R. B., and Schlichting, I. (2017) Viscous hydrophilic injection matrices for serial crystallography, *IUCrJ* **4**, 1-11.

Maalcke, W., Reimann, J., de Vries, S., Butt, J. N., Dietl, A., Kip, N., Mersdorf, U., **Barends, T. R. M.**, Jetten, M. S. M., Keltjens, J. T., and Kartal, B. (2016) Characterization of anammox hydrazine dehydrogenase, a key N_2-producing enzyme in the global nitrogen cycle, *The Journal of Biological Chemistry* **291**, 17077-17092.

Nass, K. J., Meinhart, A., **Barends, T. R. M.**, Foucar, L., Gorel, A., Aquila, A., Botha, S., Doak, R. B., Koglin, J., Liang, M. N., Shoeman, R. L., Williams, G. W., Boutet, S., and Schlichting, I. (2016) Protein structure determination by single-wavelength anomalous diffraction phasing of X-ray free-electron laser data. *IUCrJ* **3**, 180-191.

Winkler, A., **Barends, T. R. M.**, Udvarhelyi, A., Lenherr-Frey, D., Lomb, L., Menzel, A., and Schlichting, I. (2015) Structural Details of Light Activation of the LOV2-based Photoswitch PA-Rac1, *Acs Chemical Biology 10*, 502-509.

Tarnawski, M., **Barends, T. R. M.**, and Schlichting, I. (2015) Structural analysis of an oxygen-regulated diguanylate cyclase, *Acta Crystallographica Section D-Biological Crystallography* **71**, 2158-2177.

Nass, K., Foucar, L., **Barends, T. R. M.**, Hartmann, E., Botha, S., Shoeman, R. L., Doak, R. B., Alonso-Mori, R., Aquila, A., Bajt, S., Barty, A., Bean, R., Beyerlein, K. R., Bublitz, M., Drachmann, N., Gregersen, J., Joensson, H. O., Kabsch, W., Kassemeyer, S., Koglin, J. E., Krumrey, M., Mattle, D., Messerschmidt, M., Nissen, P., Reinhard, L., Sitsel, O., Sokaras, D., Williams, G. J., Hau-Riege, S., Timneanu, N., Caleman, C., Chapman, H. N., Boutet, S., and Schlichting, I. (2015) Indications of radiation damage in ferredoxin microcrystals using high-intensity X-FEL beams, *Journal of Synchrotron Radiation* **22**, 225-238.

Galli, L., Son, S.-K., **Barends, T. R. M.**, White, T. A., Barty, A., Botha, S., Boutet, S., Caleman, C., Doak, R. B., Nanao, M. H., Nass, K., Shoeman, R. L., Timneanu, N., Santra, R., Schlichting, I., and Chapman, H. N. (2015) Towards phasing using high X-ray intensity, *IUCrJ* **2**, 627-634.

Feng, Y., Alonso-Mori, R., **Barends, T. R. M.**, Blank, V. D., Botha, S., Chollet, M., Damiani, D. S., Doak, R. B., Glownia, J. M., Koglin, J. M., Lemke, H. T., Messerschmidt, M., Nass, K., Nelson, S., Schlichting, I., Shoeman, R. L., Shvyd'ko, Y. V., Sikorski, M., Song, S., Stoupin, S., Terentyev, S., Williams, G. J., Zhu, D., Robert, A., and Boutet, S. (2015) Demonstration of simultaneous experiments using thin crystal multiplexing at the Linac Coherent Light Source, *Journal of Synchrotron Radiation* **22**, 626-633.

Dietl, A., Maalcke, W., and **Barends, T. R. M.*** (2015) An unexpected reactivity of the P-460 cofactor in hydroxylamine oxidoreductase, *Acta Crystallographica Section D-Biological Crystallography* **71**, 1708-1713.

Dietl, A., Ferousi, C., Maalcke, W. J., Menzel, A., de Vries, S., Keltjens, J. T., Jetten, M. S. M., Kartal, B., and **Barends, T. R. M.*** (2015) The inner workings of the hydrazine synthase multiprotein complex, *Nature* **527**, 404-407.

Bublitz, M., Nass, K., Drachmann, N. D., Markvardsen, A. J., Gutmann, M. J., **Barends, T. R. M.**, Mattle, D., Shoeman, R. L., Doak, R. B., Boutet, S., Messerschmidt, M., Seibert, M. M., Williams, G. J., Foucar, L., Reinhard, L., Sitsel, O., Gregersen, J. L., Clausen, J. D., Boesen, T., Gotfryd, K., Wang, K.-T., Olesen, C., Moller, J. V., Nissen, P., and Schlichting, I. (2015) Structural studies of P-type ATPase-ligand complexes using an X-ray free-electron laser, *IUCrJ* **2**, 409-420.

Boutet, S., Foucar, L., **Barends, T. R. M.**, Botha, S., Doak, R. B., Koglin, J. E., Messerschmidt, M., Nass, K., Schlichting, I., Seibert, M. M., Shoeman, R. L., and Williams, G. J. (2015) Characterization and use of the spent beam for serial operation of LCLS, *Journal of Synchrotron Radiation* **22**, 634-643.

Botha, S., Nass, K., **Barends, T. R. M.**, Kabsch, W., Latz, B., Dworkowski, F., Foucar, L., Panepucci, E., Wang, M., Shoeman, R. L., Schlichting, I., and Doak, R. B. (2015) Room-temperature serial crystallography at synchrotron X-ray sources using slowly flowing free-standing high-viscosity microstreams, *Acta Crystallographica Section D-Biological Crystallography* **71**, 387-397.

Barends, T. R. M.*, Foucar, L., Ardevol, A., Nass, K., Aquila, A., Botha, S., Doak, R. B., Falahati, K., Hartmann, E., Hilpert, M., Heinz, M., Hoffmann, M. C., Koefinger, J., Koglin, J. E., Kovácsová, G., Liang, M., Milathianaki, D., Lemke, H. T., Reinstein, J., Roome, C. M., Shoeman, R. L., Williams, G. J., Burghardt, I., Hummer, G., Boutet, S., and Schlichting, I. (2015) Direct observation of ultrafast collective motions in CO myoglobin upon ligand dissociation, *Science* **350**, 445-450.

Barends, T.*, White, T. A., Barty, A., Foucar, L., Messerschmidt, M., Alonso-Mori, R., Botha, S., Chapman, H., Doak, R. B., Galli, L., Gati, C., Gutmann, M., Koglin, J., Markvardsen, A., Nass, K., Oberthur, D., Shoeman, R. L., Schlichting, I., and Boutet, S. (2015) Effects of self-seeding and crystal post-selection on the quality of Monte Carlo-integrated SFX data, *Journal of Synchrotron Radiation* **22**, 644-652.

Zeymer, C., **Barends, T. R. M.**, Werbeck, N. D., Schlichting, I., and Reinstein, J. (2014) Elements in nucleotide sensing and hydrolysis of the AAA plus disaggregation machine ClpB: a structure-based mechanistic dissection of a molecular motor, *Acta Crystallographica Section D-Biological Crystallography* **70**, 582-595.

Pol, A., **Barends, T. R. M.**, Dietl, A., Khadem, A. F., Eygensteyn, J., Jetten, M. S. M., and Op den Camp, H. J. M. (2014) Rare earth metals are essential for methanotrophic life in volcanic mudpots, *Environmental Microbiology* **16**, 255-264.

Maalcke, W. J., Dietl, A., Marritt, S. J., Butt, J. N., Jetten, M. S. M., Keltjens, J. T., **Barends, T. R. M.***, and Kartal, B. (2014) Structural Basis of Biological NO Generation by Octaheme Oxidoreductases, *Journal of Biological Chemistry* **289**, 1228-1242.

Barends, T. R. M.*, Foucar, L., Botha, S., Doak, R. B., Shoeman, R. L., Nass, K., Koglin, J. E., Williams, G. J., Boutet, S., Messerschmidt, M., and Schlichting, I. (2014) *De novo* protein crystal structure determination from X-ray free-electron laser data, *Nature* **505**, 244-247.

Tarnawski, M., **Barends, T. R. M.**, Hartmann, E., and Schlichting, I. (2013) Structures of the catalytic EAL domain of the Escherichia coli direct oxygen sensor, *Acta Crystallographica Section D-Biological Crystallography* **69**, 1045-1053.

Smeulders, M. J., Pol, A., Venselaar, H., **Barends, T. R. M.**, Hermans, J., Jetten, M. S. M., and Op den Camp, H. J. M. (2013) Bacterial CS_2 Hydrolases from Acidithiobacillus thiooxidans Strains Are Homologous to the Archaeal Catenane CS2 Hydrolase, *Journal of Bacteriology* **195**, 4046-4056.

Redecke, L., Nass, K., DePonte, D. P., White, T. A., Rehders, D., Barty, A., Stellato, F., Liang, M., **Barends, T. R. M.**, Boutet, S., Williams, G. J., Messerschmidt, M., Seibert, M. M., Aquila, A., Arnlund, D., Bajt, S., Barth, T., Bogan, M. J., Caleman, C., Chao, T.-C., Doak, R. B., Fleckenstein, H., Frank, M., Fromme, R., Galli, L., Grotjohann, I., Hunter, M. S., Johansson, L. C., Kassemeyer, S., Katona, G., Kirian, R. A., Koopmann, R., Kupitz, C., Lomb, L., Martin, A. V., Mogk, S., Neutze, R., Shoeman, R. L., Steinbrener, J., Timneanu, N., Wang, D., Weierstall, U., Zatsepin, N. A., Spence, J. C. H., Fromme, P., Schlichting, I., Duszenko, M., Betzel, C., and Chapman, H. N. (2013) Natively Inhibited Trypanosoma brucei Cathepsin B Structure Determined by Using an X-ray Laser, *Science* **339**, 227-230.

Duhme, N., Schweizer, P. A., Thomas, D., Becker, R., Schroeter, J., **Barends, T. R. M.**, Schlichting, I., Draguhn, A., Bruehl, C., Katus, H. A., and Koenen, M. (2013) Altered HCN4 channel C-linker interaction is associated with familial tachycardia-bradycardia syndrome and atrial fibrillation, *European Heart Journal* **34**, 2768-2775.

Demirci, H., Sierra, R. G., Laksmono, H., Shoeman, R. L., Botha, S., **Barends, T. R. M.**, Nass, K., Schlichting, I., Doak, R. B., Gati, C., Williams, G. J., Boutet, S., Messerschmidt, M., Jogl, G., Dahlberg, A. E., Gregory, S. T., and Bogan, M. J. (2013) Serial femtosecond X-ray diffraction of 30S ribosomal subunit microcrystals in liquid suspension at ambient temperature using an X-ray free-electron laser, *Acta Crystallographica Section F-Structural Biology and Crystallization Communications* **69**, 1066-1069.

Barends, T. R. M.*, Foucar, L., Shoeman, R. L., Bari, S., Epp, S. W., Hartmann, R., Hauser, G., Huth, M., Kieser, C., Lomb, L., Motomura, K., Nagaya, K., Schmidt, C., Strecker, R., Anielski, D., Boll, R., Erk, B., Fukuzawa, H., Hartmann, E., Hatsui, T., Holl, P., Inubushi, Y., Ishikawa, T., Kassemeyer, S., Kaiser, C., Koeck, F., Kunishima, N., Kurka, M., Rolles, D., Rudek, B., Rudenko, A., Sato, T., Schroeter, C.-D., Soltau, H., Strueder, L., Tanaka, T., Togashi, T., Tono, K., Ullrich, J., Yase, S., Wada, S.-i., Yao, M., Yabashi, M., Ueda, K., and Schlichting, I. (2013) Anomalous signal from S atoms in protein crystallographic data from an X-ray free-electron laser, *Acta Crystallographica Section D-Biological Crystallography* **69**, 838-842.

Barends, T. R. M.*, Brosi, R. W. W., Steinmetz, A., Scherer, A., Hartmann, E., Eschenbach, J., Lorenz, T., Seidel, R., Shoeman, R. L., Zimmermann, S., Bittl, R., Schlichting, I., and Reinstein, J. (2013) Combining crystallography and EPR: crystal and solution structures of the multidomain cochaperone DnaJ, *Acta Crystallographica Section D-Biological Crystallography* **69**, 1540-1552.

Zarrine-Afsar, A., **Barends, T. R. M.**, Mueller, C., Fuchs, M. R., Lomb, L., Schlichting, I., and Miller, R. J. D. (2012) Crystallography on a chip, *Acta Crystallographica Section D-Biological Crystallography* **68**, 321-323.

Kassemeyer, S., Steinbrener, J., Lomb, L., Hartmann, E., Aquila, A., Barty, A., Martin, A. V., Hampton, C. Y., Bajt, S., Barthelmess, M., **Barends, T. R. M.**, Bostedt, C., Bott, M., Bozek, J. D., Coppola, N., Cryle, M., DePonte, D. P., Doak, R. B., Epp, S. W., Erk, B., Fleckenstein, H., Foucar, L., Graafsma, H., Gumprecht, L., Hartmann, A., Hartmann, R., Hauser, G., Hirsemann, H., Hoemke, A., Holl, P., Jonsson, O., Kimmel, N., Krasniqi, F., Liang, M., Maia, F. R. N. C., Marchesini, S., Nass, K., Reich, C., Rolles, D., Rudek, B., Rudenko, A., Schmidt, C., Schulz, J., Shoeman, R. L., Sierra, R. G., Soltau, H., Spence, J. C. H., Starodub, D., Stellato, F., Stern, S., Stier, G., Svenda, M., Weidenspointner, G., Weierstall, U., White, T. A., Wunderer, C., Frank, M., Chapman, H. N., Ullrich, J., Strueder, L., Bogan, M. J., and Schlichting, I. (2012) Femtosecond free-electron laser x-ray diffraction data sets for algorithm development, *Optics Express* **20**, 4149-4158.

Boutet, S., Lomb, L., Williams, G. J., **Barends, T. R. M.**, Aquila, A., Doak, R. B., Weierstall, U., DePonte, D. P., Steinbrener, J., Shoeman, R. L., Messerschmidt, M., Barty, A., White, T. A., Kassemeyer, S., Kirian, R. A., Seibert, M. M., Montanez, P. A., Kenney, C., Herbst, R., Hart, P., Pines, J., Haller, G., Gruner, S. M., Philipp, H. T., Tate, M. W., Hromalik, M., Koerner, L. J., van Bakel, N., Morse, J., Ghonsalves, W., Arnlund, D., Bogan, M. J., Caleman, C., Fromme, R., Hampton, C. Y., Hunter, M. S., Johansson, L. C., Katona, G., Kupitz, C., Liang, M., Martin, A. V., Nass, K., Redecke, L., Stellato, F., Timneanu, N., Wang, D., Zatsepin, N. A., Schafer, D., Defever, J., Neutze, R., Fromme, P., Spence, J. C. H., Chapman, H. N., and Schlichting, I. (2012) High-Resolution Protein Structure Determination by Serial Femtosecond Crystallography, *Science* **337**, 362-364.

Benz, J., Sendlmeier, C., **Barends, T. R. M.**, and Meinhart, A. (2012) Structural Insights into the Effector - Immunity System Tse1/Tsi1 from Pseudomonas aeruginosa, *Plos One 7*.

Benjdia, A., Heil, K., **Barends, T. R. M.**, Carell, T., and Schlichting, I. (2012) Structural insights into recognition and repair of UV-DNA damage by Spore Photoproduct Lyase, a radical SAM enzyme, *Nucleic Acids Research* **40**, 9308-9318.

Barty, A., Caleman, C., Aquila, A., Timneanu, N., Lomb, L., White, T. A., Andreasson, J., Arnlund, D., Bajt, S., **Barends, T. R. M.**, Barthelmess, M., Bogan, M. J., Bostedt, C., Bozek, J. D., Coffee, R., Coppola, N., Davidsson, J., DePonte, D. P., Doak, R. B., Ekeberg, T., Elser, V., Epp, S. W., Erk, B., Fleckenstein, H., Foucar, L., Fromme, P., Graafsma, H., Gumprecht, L., Hajdu, J., Hampton, C. Y., Hartmann, R., Hartmann, A., Hauser, G., Hirsemann, H., Holl, P., Hunter, M. S., Johansson, L., Kassemeyer, S., Kimmel, N., Kirian, R. A., Liang, M., Maia, F. R. N. C., Malmerberg, E., Marchesini, S., Martin, A. V., Nass, K., Neutze, R., Reich, C., Rolles, D., Rudek, B., Rudenko, A., Scott, H., Schlichting, I., Schulz, J., Seibert, M. M., Shoeman, R. L., Sierra, R. G., Soltau, H., Spence, J. C. H., Stellato, F., Stern, S., Strueder, L., Ullrich, J., Wang, X., Weidenspointner, G., Weierstall, U., Wunderer, C. B., and Chapman, H. N. (2012) Self-terminating diffraction gates femtosecond X-ray nanocrystallography measurements, *Nature Photonics* **6**, 35-40.

Aquila, A., Hunter, M. S., Doak, R. B., Kirian, R. A., Fromme, P., White, T. A., Andreasson, J., Arnlund, D., Bajt, S., **Barends, T. R. M.**, Barthelmess, M., Bogan, M. J., Bostedt, C., Bottin, H., Bozek, J. D., Caleman, C., Coppola, N., Davidsson, J., DePonte, D. P., Elser, V., Epp, S. W., Erk, B., Fleckenstein, H., Foucar, L., Frank, M., Fromme, R., Graafsma, H., Grotjohann, I., Gumprecht, L., Hajdu, J., Hampton, C. Y., Hartmann, A., Hartmann, R., Hauriege, S., Hauser, G., Hirsemann, H., Holl, P., Holton, J. M., Hoemke, A., Johansson, L., Kimmel, N., Kassemeyer, S., Krasniqi, F., Kuehnel, K., Liang, M., Lomb, L., Malmerberg, E., Marchesini, S., Martin, A. V., Maia, F. R. N. C., Messerschmidt, M., Nass, K., Reich, C., Neutze, R., Rolles, D., Rudek, B., Rudenko, A., Schlichting, I., Schmidt, C., Schmidt, K. E., Schulz, J., Seibert, M. M., Shoeman, R. L., Sierra, R., Soltau, H., Starodub, D., Stellato, F., Stern, S., Strueder, L., Timneanu, N., Ullrich, J., Wang, X., Williams, G. J., Weidenspointner, G., Weierstall, U., Wunderer, C., Barty, A., Spence, J. C. H., and Chapman, H. N. (2012) Time-resolved protein nanocrystallography using an X-ray free-electron laser, *Optics Express* **20**, 2706-2716.

Smeulders, M. J., **Barends, T. R. M.**, Pol, A., Scherer, A., Zandvoort, M. H., Udvarhelyi, A., Khadem, A. F., Menzel, A., Hermans, J., Shoeman, R. L., Wessels, H. J. C. T., van den Heuvel, L. P., Russ, L., Schlichting, I., Jetten, M. S. M., and den Camp, H. J. M. O. (2011) Evolution of a new enzyme for carbon disulphide conversion by an acidothermophilic archaeon, *Nature* **478**, 412-414.

Lomb, L., **Barends, T. R. M.**, Kassemeyer, S., Aquila, A., Epp, S. W., Erk, B., Foucar, L., Hartmann, R., Rudek, B., Rolles, D., Rudenko, A., Shoeman, R. L., Andreasson, J., Bajt, S., Barthelmess, M., Barty, A., Bogan, M. J., Bostedt, C., Bozek, J. D., Caleman, C., Coffee, R., Coppola, N., DePonte, D. P., Doak, R. B., Ekeberg, T., Fleckenstein, H., Fromme, P., Gebhardt, M., Graafsma, H., Gumprecht, L., Hampton, C. Y., Hartmann, A., Hauser, G., Hirsemann, H., Holl, P., Holton, J. M., Hunter, M. S., Kabsch, W., Kimmel, N., Kirian, R. A., Liang, M., Maia, F. R. N. C., Meinhart, A., Marchesini, S., Martin, A. V., Nass, K., Reich, C., Schulz, J., Seibert, M. M., Sierra, R., Soltau, H., Spence, J. C. H., Steinbrener, J., Stellato, F., Stern, S., Timneanu, N., Wang, X., Weidenspointner, G., Weierstall, U., White, T. A., Wunderer, C., Chapman, H. N., Ullrich, J., Strueder, L., and Schlichting, I. (2011) Radiation damage in protein serial femtosecond crystallography using an x-ray free-electron laser, *Physical Review B* **84**.

Lai, J., Niks, D., Wang, Y., Domratcheva, T., **Barends, T. R. M.**, Schwarz, F., Olsen, R. A., Elliott, D. W., Fatmi, M. Q., Chang, C.-e. A., Schlichting, I., Dunn, M. F., and Mueller, L. J. (2011) X-ray and NMR Crystallography in an Enzyme Active Site: The Indoline Quinonoid Intermediate in Tryptophan Synthase, *Journal of the American Chemical Society* **133**, 4-7.

Chapman, H. N., Fromme, P., Barty, A., White, T. A., Kirian, R. A., Aquila, A., Hunter, M. S., Schulz, J., DePonte, D. P., Weierstall, U., Doak, R. B., Maia, F. R. N. C., Martin, A. V., Schlichting, I., Lomb, L., Coppola, N., Shoeman, R. L., Epp, S. W., Hartmann, R., Rolles, D., Rudenko, A., Foucar, L., Kimmel, N., Weidenspointner, G., Holl, P., Liang, M., Barthelmess, M., Caleman, C., Boutet, S., Bogan, M. J., Krzywinski, J., Bostedt, C., Bajt, S., Gumprecht, L., Rudek, B., Erk, B., Schmidt, C., Hoemke, A., Reich, C., Pietschner, D., Strueder, L., Hauser, G., Gorke, H., Ullrich, J., Herrmann, S., Schaller, G., Schopper, F., Soltau, H., Kuehnel, K.-U., Messerschmidt, M., Bozek, J. D., Hau-Riege, S. P., Frank, M., Hampton, C. Y., Sierra, R. G., Starodub, D., Williams, G. J., Hajdu, J., Timneanu, N., Seibert, M. M., Andreasson, J., Rocker, A., Joensson, O., Svenda, M., Stern, S., Nass, K., Andritschke, R., Schroeter, C.-D., Krasniqi, F., Bott, M., Schmidt, K. E., Wang, X., Grotjohann, I., Holton, J. M., **Barends, T. R. M.**, Neutze, R., Marchesini, S., Fromme, R., Schorb, S., Rupp, D., Adolph, M., Gorkhover, T., Andersson, I., Hirsemann, H., Potdevin, G., Graafsma, H., Nilsson, B., and Spence, J. C. H. (2011) Femtosecond X-ray protein nanocrystallography, *Nature* **470**, 73-U81.

Jaenicke, E., Buechler, K., Markl, J., Decker, H., and **Barends, T. R. M.** (2010) Cupredoxin-like domains in haemocyanins, *Biochemical Journal* **426**, 373-378.

Barends, T. R. M., Werbeck, N. D., and Reinstein, J. (2010) Disaggregases in 4 dimensions, *Current Opinion in Structural Biology* **20**, 46-53.

Werbeck, N. D., Kellner, J. N., **Barends, T. R. M.**, and Reinstein, J. (2009) Nucleotide Binding and Allosteric Modulation of the Second AAA plus Domain of C1pB Probed by Transient Kinetic Studies, *Biochemistry* **48**, 7240-7250.

Glas, A. F., Maul, M. J., Cryle, M., **Barends, T. R. M.**, Schneider, S., Kaya, E., Schlichting, I., and Carell, T. (2009) The archaeal cofactor F-0 is a light-harvesting antenna chromophore in eukaryotes, *Proceedings of the National Academy of Sciences of the United States of America* **106**, 11540-11545.

Barends, T. R. M., Hartmann, E., Griese, J. J., Beitlich, T., Kirienko, N. V., Ryjenkov, D. A., Reinstein, J., Shoeman, R. L., Gomelsky, M., and Schlichting, I. (2009) Structure and mechanism of a bacterial light-regulated cyclic nucleotide phosphodiesterase, *Nature* **459**, 1015-U1150.

Maul, M. J., **Barends, T. R. M.**, Glas, A. F., Cryle, M. J., Domratcheva, T., Schneider, S., Schlichting, I., and Carell, T. (2008) Crystal Structure and Mechanism of a DNA (6-4) Photolyase, *Angewandte Chemie-International Edition* **47**, 10076-10080.

Dunn, M. F., Niks, D., Ngo, H., **Barends, T. R. M.**, and Schlichting, I. (2008) Tryptophan synthase: the workings of a channeling nanomachine, *Trends in Biochemical Sciences* **33**, 254-264.

Brouns, S. J. J., **Barends, T. R. M.***, Worm, P., Akerboom, J., Turnbull, A. P., Salmon, L., and van der Oost, J. (2008) Structural insight into substrate binding and catalysis of a novel 2-keto-3-deoxy-D-arabinonate dehydratase illustrates common mechanistic features of the FAH superfamily, *Journal of Molecular Biology* **379**, 357-371.

Barends, T. R. M., Dunn, M. F., and Schlichting, I. (2008) Tryptophan synthase, an allosteric molecular factory, *Current Opinion in Chemical Biology* **12**, 593-600.

Barends, T. R. M., Domratcheva, T., Kulik, V., Blumenstein, L., Niks, D., Dunn, M. F., and Schlichting, I. (2008) Structure and mechanistic implications of a tryptophan synthase quinonold intermediate, *Chembiochem* **9**, 1024-1028.

van Straaten, K. E., **Barends, T. R. M.**, Dijkstra, B. W., and Thunnissen, A.-M. W. H. (2007) Structure of Escherichia coli lytic transglycosylase MltA with bound chitohexaose - Implications for peptidoglycan binding and cleavage, *Journal of Biological Chemistry* **282**, 21197-21205.

Ngo, H., Kimmich, N., Harris, R., Niks, D., Blumenstein, L., Kulik, V., **Barends, T. R.**, Schlichting, I., and Dunn, M. F. (2007) Allosteric regulation of substrate channeling in tryptophan synthase: Modulation of the L-Serine reaction in stage I of the ss-reaction by alpha-site ligands, *Biochemistry* **46**, 7740-7753.

Ngo, H., Harris, R., Kimmich, N., Casino, P., Niks, D., Blumenstein, L., **Barends, T. R.**, Kulik, V., Weyand, M., Schlichting, I., and Dunn, M. F. (2007) Synthesis and characterization of allosteric probes of substrate channeling in the tryptophan synthase bienzyme complex, *Biochemistry* **46**, 7713-7727.

Casino, P., Niks, D., Ngo, H., Pan, P., Brzovic, P., Blumenstein, L., **Barends, T. R.**, Schlichting, I., and Dunn, M. F. (2007) Allosteric regulation of tryptophan synthase channeling: The internal aldimine probed by trans-3-indole-3'-acrylate binding, *Biochemistry* **46**, 7728-7739.

Barends, T. R. M., Bultema, J. B., Kaper, T., van der Maarel, M. J. E. C., Dijkhuizen, L., and Dijkstra, B. W. (2007) Three-way stabilization of the covalent intermediate in amylomaltase, an alpha-amylase-like transglycosylase, *Journal of Biological Chemistry* **282**, 17242-17249.

Barends, T. R. M., Polderman-Tijmes, J. J., Jekel, P. A., Williams, C., Wybenga, G., Janssen, D. B., and Dijkstra, B. W. (2006) Acetobacter turbidans alpha-amino acid ester hydrolase - How a single mutation improves an antibiotic-producing enzyme, *Journal of Biological Chemistry* **281**, 5804-5810.

Barends, T. R. M., de Jong, R. M., van Straaten, K. E., Thunnissen, A., and Dijkstra, B. W. (2005) Escherichia coli MltA: MAD phasing and refinement of a tetartohedrally twinned protein crystal structure, *Acta Crystallographica Section D-Biological Crystallography* **61**, 613-621, erratum *Acta Crystallographica Section D-Biological Crystallography* **61**, 1172-1172.

Barends, T. R. M., Yoshida, H., and Dijkstra, B. W. (2004) Three-dimensional structures of enzymes useful for beta-lactam antibiotic production, *Current Opinion in Biotechnology* **15**, 356-363.

Barends, T. R. M., Polderman-Tijmes, J. J., Jekel, P. A., Hensgens, C. M. H., de Vries, E. J., Janssen, D. B., and Dijkstra, B. W. (2003) The sequence and crystal structure of the alpha-amino acid ester hydrolase from Xanthomonas citri define a new family of beta-lactam antibiotic acylases, *Journal of Biological Chemistry* **278**, 23076-23084.

Barends, T. R. M., Hensgens, C. M. H., Polderman-Tijmes, J. J., Jekel, P. A., de Vries, E., Janssen, D. B., and Dijkstra, B. W. (2003) X-ray analysis of two antibiotic-synthesizing bacterial ester hydrolases: preliminary results, *Acta Crystallographica Section D-Biological Crystallography* **59**, 158-160.

Barends, T. R. M., and Dijkstra, B. W. (2003) Oils used in microbatch crystallization do not remove a detergent from the drops they cover, *Acta Crystallographica Section D-Biological Crystallography* **59**, 2345-2347.

Barends, T. R. M., and Dijkstra, B. W. (2003) Acetobacter turbidans alpha-amino acid ester hydrolase: merohedral twinning in P2(1) obscured by pseudo-translational NCS, *Acta Crystallographica Section D-Biological Crystallography* **59**, 2237-2241.

Bokma, E., **Barends, T.**, van Scheltinga, A. C. T., Dijkstra, B. W., and Beintema, J. J. (2000) Enzyme kinetics of hevamine, a chitinase from the rubber tree Hevea brasiliensis, *Febs Letters* **478**, 119-122.

Teaching experience, Lectures, Formal Education etc.

STUDENTS SUPERVISED	
2016 - 2017	**Nicole Mertes, MSc student** Department of Biomolecular Mechanisms, Max Planck Institute for Medical Research, Heidelberg, Germany
2013 - present	**Akram Mohd., PhD student** Department of Biomolecular Mechanisms, Max Planck Institute for Medical Research, Heidelberg, Germany
2011 - 2016	**Andreas Dietl, PhD student** Department of Biomolecular Mechanisms, Max Planck Institute for Medical Research, Heidelberg, Germany
2010 – 2011	**Andreas Dietl, MSc student** Department of Biomolecular Mechanisms, Max Planck Institute for Medical Research, Heidelberg, Germany
2003 – 2004	**Jelle Bultema, MSc student** Faculty of Mathematics and Natural Sciences, University of Groningen, The Netherlands
2003 – 2004	**Hilda Korff, BSc student** Faculty of Mathematics and Natural Sciences, University of Groningen, The Netherlands

OTHER TEACHING ACTIVITIES	
2015	**Phasing of XFEL data**, lecture for Dutch and Belgian students, SyNew meeting, Utrecht
2013	**Lecture "Biological Science with X-rays"** For students at the XFEL-2013 school of Rennes University at Dinard
2008	**Protein Crystallography** Methods Course, ZMBH, Heidelberg University
2006 - present	**Practical Course "Structural Biology"** For students in the Molecular and Cellular Biology program of Heidelberg University

MAJOR COLLABORATIONS	
2006 - present	**M.S.M. Jetten, B. Kartal, H. Op den Camp, J. Keltjens,** Department of Microbiology, Radboud University Nijmegen, the Netherlands -Structural Biology of the Anammox Pathway -Mechanism of Biological Carbon Disulfide Conversion -Structure and Function of Lanthanide-dependent Enzymes
2006 - 2010	**E. Jaenicke,** Institute for Molecular Biophysics, Johannes-Gutenberg University Mainz, Germany -Structure determination of Molluscan and Arthropod Haemocyanins by hybrid methods

SELECTED INVITED LECTURES	
2017	**Observing Protein Dynamics with Sub-Picosecond Time Resolution SFX,** BioXFEL 4th International Conference, Las Vegas, USA
2016	**Ultrafast Functional Motions in Myoglobin Probed by Serial Femtosecond Crystallography**, Gordon Research Conference on Diffraction Methods in Structural Biology, Lewiston, USA
2016	**Direct Observation of Functional Motions In Myoglobin by Serial Femtosecond Crystallography**, 3rd Ringberg Workshop on Structural Biology with FELs, Tegernsee, Germany
2015	**Free-Electron Lasers…New X-ray Sources for Structural Biology**, SyNew meeting, Utrecht, The Netherlands
2015	**Phasing Free-electron Laser Data**, 2nd Ringberg Workshop on Structural Biology with FELs, Tegernsee, Germany
2015	***De novo* Phasing of SFX Data**, XFEL workshop, RIKEN, Hyogo, Japan
2014	**Structural Biology with Free-Electron Lasers**, symposium of the Groningen Biomolecular Sciences and Biotechnology Institute, The Netherlands
2014	**Unusual Cofactors in Anammox Enzymes**, IVth International Cofactors and Coenzymes Meeting, *Parma, Italy*
2014	***De novo* Phasing of XFEL Data**, IUCR 2014, Montreal, Canada
2014	**Protein crystallography with XFELs**, TRSC Protein Dynamics Workshop, Les Houches, France
2014	**Introduction to Crystallography using XFELs**, satellite workshop to IUCr2014, Montreal, Canada
2013	***De novo* Phasing of Data from an FEL**, Satellite meeting "X-ray lasers in biology - techniques", Chichely Hall, UK
2012	**FELs: Emerging Opportunities for Structural Biology**, Workshop of the Finnish Organization of Synchrotron Radiation Users, Tampere, Finland
2011	**Imaging Biological Molecules with FELs**, IUCR2011, Madrid
2011	**FELs: Emerging Opportunities for Structural Biology**, workshop free electron laser project of Groningen University, Utrecht, The Netherlands
2010	**Femtosecond Free-Electron Laser Pulses Yield Accurate Diffraction Intensities for Protein Crystal Structure Determination**, satellite workshop to sri2010, Chicago, USA
2009	**The Mechanism of DNA Damage Repair by (6-4)-Photolyases**, ECM25, Session "Novel Enzyme Mechanisms", Istanbul, Turkey

EDUCATION	
2004 / 4 / 16	**PhD** Faculty of Mathematics and Natural Sciences, University of Groningen, The Netherlands PhD Supervisor: Prof. Dr. Bauke W. Dijkstra
1998 / 8 / 27	**MSc** Faculty of Mathematics and Natural Sciences, University of Groningen, The Netherlands