Crystallography Times

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ACS – Great Lakes Regional Meeting
Lisle, Illinois, May 1 – 4, 2019

24th Sealy Center for Structural Biology Symposium
Galveston, Texas, May 4, 2019

Second Annual Industrial Biostructures America (IBA) Conference
La Jolla, California, May 19 – 21, 2019

ACS – Middle Atlantic Regional Meeting
Baltimore, Maryland, May 30 – June 1, 2019

102nd Canadian Chemistry Conference and Exhibition
Québec City, Canada, June 3 – 7, 2019

ACS – Central Regional Meeting
Midland, Michigan, June 4 – 7, 2019

First Annual CSB Symposium
Montreal, Canada, June 17, 2019

ACS – Northwest Regional Meeting
Portland, Oregon, June 16 – 19, 2019

International Conference on the Chemistry of the Organic Solid State (ICCOSS XXIV)
New York, New York, June 16 – 21, 2019

ACS – Northeast Regional Meeting
Saratoga Springs, New York, June 22 – 27, 2019

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Crystallography in the News

April 2, 2019. Researchers led by Kelly Manthei, a Postdoctoral Fellow at the University of Michigan Life Sciences Institute, found the structure of activated lecithin:cholesterol acyltransferase (LCAT) enzyme and how it helps to return excess cholesterol to the liver. Using X-ray crystallography, the scientists determined the mechanism of the enzyme and its reaction in association with a drug-like chemical.

April 3, 2019. New work from the D. E. Shaw research team covers fragment binding, and even if you don't do fragment-based drug discovery, it's worth a read. That's because the mechanisms by which fragments bind to proteins are most likely the fundamental ones by which larger molecules bind as well; this is the reductionist look at small molecule-protein interactions.

April 8, 2019. As a gifted young graduate student in physics at Cambridge in the late 1940s, June Broomhead mapped out the crystal structures of two components critical to DNA — adenine and guanine — using X-ray crystallography and painstaking calculations. In an era of rapid scientific discovery, that research for her PhD thesis was significant.

April 10, 2019. Based on true events, Anna Ziegler's one-act drama, Photograph 51, is a riveting and amazing story told in superior style in the curent production impeccably directed by Ellie Schwetye at West End Players Guild. Schwetye's direction is especially telling when Nicole Angeli as Rosalind Franklin takes center stage, while the men in the cast lurk in the background, arms crossed disapprovingly for the most part.

April 11, 2019. HIV, Ebola, and Zika are ugly, nasty viruses. David Goodsell makes them look beautiful, even alluring. And the unusual precision of his depictions is driven by science—some of it his own research. A structural biologist at Scripps Research in San Diego, California, Goodsell paints watercolors of viruses and cells with exacting scientific specifications.

April 11, 2019. Scientists have captured the first "snapshot" of two proteins involved in delivering a bacterial stress-response master regulator to the cell's recycling machinery. The Brown University-led team found that RssB—a protein that specifically recognizes the master regulator and delivers it to the recycling machinery somewhat like a recycling truck—forms a compact structure with a factor that inhibits RssB activity. The inhibition factor, called IraD, is triggered by DNA damage, one of many stresses the master regulator helps bacteria survive by turning on important genes.

April 12, 2019. The Royal Swedish Academy of Sciences has just awarded the 2019 Gregori Aminoff Prize in Crystallography to ASU Emeritus Regents' Professor Michael O'Keeffe and Professor Omar M. Yaghi, of the University of California, Berkeley, "for their fundamental contributions to the development of reticular chemistry." The honor was personally awarded by His Majesty King Carl XVI Gustaf of Sweden.

April 12, 2019. Scientists at Scripps Research have identified a group of small molecules that prevent structural changes to proteins that are at the root of AL amyloidosis, a progressive and often fatal disease. The small molecules bind to immunoglobulin proteins, which play an essential role in the body's immune system, and then stabilize subunits of the protein called immunoglobulin light chains.

April 15, 2019. Rice University scientists have developed a new method for making accurate structural models of proteins that takes far less computational power than existing brute-force approaches. Led by Peter Wolynes and alumnus Xingcheng Lin, the research applies force at strategic points during the simulation of protein models so as to speed up the computation.

April 15, 2019. In 2016, a group of Japanese researchers discovered a bacterium that grows on PET and partially feeds on it. They found out that this bacterium possesses two special enzymes, PETase and MHETase, which are able to digest PET plastic polymers. In April 2018, the structure of PETase was finally solved independently by several research groups. Research teams have now obtained the complex three-dimensional structure of MHETase at BESSY II, the synchrotron source at Helmholtz-Zentrum Berlin.

[Rigaku Oxford Diffraction LinkedIn group](#) shares information and fosters discussion about X-ray crystallography and SAXS topics. Connect with other research groups and receive updates on how they use these techniques in their own laboratories. You can also catch up on the latest newsletter or Rigaku Journal issue. We also hope that you will share information about your own research and laboratory groups.

**Rigaku Reagents:
Human Serum Albumin SAXS Standard Kit, Item 1019893**

This kit includes ~10 mg of HSA along with 5 − 10 mL of an HSA buffer (50 mM phosphate buffer pH 6.5, 50 mM Sodium chloride). This kit is designed to prepare HSA protein for measurement.

Contact ReagentOrders@Rigaku.com
For more information, visit the
[Rigaku Reagents website.](#)

Cold Spring Harbor Laboratory: X-Ray Methods in Structural Biology

The June 15th deadline for applications to the [CSHL X-ray Methods in Structural Biology Course](#) to be October 15 through October 30, 2019 is rapidly approaching.

The course is designed for researchers who are either new to, or who wish to increase their in-depth knowledge of, macromolecular crystallography.

This immersive course is an outstanding place to learn both the theoretical and practical aspects of macromolecular crystallography because of the extensive lectures from world-renowned teachers, which are combined with hands-on experiments. This 2019 course will be led by Jim Pflugrath (Rigaku, ret.), Tassos Perrakis (NKI), Paul Adams (LBL), Janet Newman (CSIRO) and an all-star cast of lecturers. Attendees can expect to participate in a course that is unparalleled in the world, with experts each devoting several days to teaching the fundamentals, theory and practical considerations of crystallographic structure solution.

We expect to have the participants crystallize several proteins and determine their structures all in about two weeks. Students may also work on their own projects, but not exclusively. They will also become well-versed in the theory of X-diffraction and crystal structure determination while having lots of fun, but not much sleep. There will be a trip to the state-of-the-art beamlines at NSLS-II to collect data.

The course is limited to 16 participants due to the very hands-on nature of the experiments and the intimate seminar room and laboratory settings. Please [check the course page](#) for more details. In particular, please note the information about fellowships, scholarships, and stipends that are available. It is often possible for applicants to receive some level of support to help offset the course fee.

This course is supported with funds provided by

April 16, 2019. Theory had predicted a [direct single bond between two yttrium centres](#) but researchers had struggled to realise it experimentally. Now, scientists in China have become the first to make the elusive bond as part of an endohedral metallofullerene. Xing Lu from Huazhong University of Science and Technology and colleagues used the stabilising effect of a fullerene cage to assist them in making the yttrium–yttrium bond.

Product Spotlights

CrysAlis^{Pro} v40

Now with full 64-bit compatibility!
Rigaku Oxford Diffraction single crystal X-ray diffractometers come complete with CrysAlis^{Pro}, our user-inspired data collection and data processing software for small molecule and protein crystallography. Designed around an easy-to-use graphical user interface, CrysAlis^{Pro} can be operated under fully automatic, semi-automatic or manual control.

The latest release, CrysAlis^{Pro} v.40, is now fully 64-bit compatible and ready for the future. As modern diffractometers increase in performance and speed, your experiments generate bigger and bigger images and datasets. Additionally, supporting large detectors with very high pixel counts, such as those commonly found at synchrotrons, requires large amounts of memory. Moving to 64-bit gives applications access to more memory, enabling the handling of these very large image sizes and data sets.

Also, in this release, is further expanded support for older Rigaku instrumentation. New third party hardware support is also increased. See below for other new software features that have recently been introduced.

How to get CrysAlis^{Pro}
CrysAlis^{Pro} is freely available for users of Rigaku Oxford Diffraction single crystal X-ray instruments and can be downloaded from our forum. Please register at https://www.rigakuxrayforum.com. Any queries related to the software may be answered on the forum.

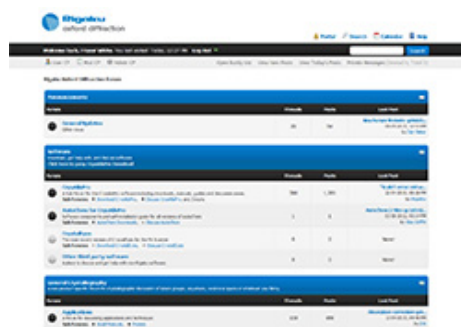### CrysAlis^{Pro}: Seamless from start to finish
CrysAlis^{Pro} combines automated crystal screening, the fastest and most accurate strategy available, concurrent data reduction and automatic small molecule structure solution. Visual feedback is provided for each step with clear, color-coded guidance so that both novices and experts can collect high-quality data in the shortest time possible.

CrysAlis^{Pro} is built on a command line interface and the GUI retains full manual control options for those that want them. It is your choice how to analyse your data.

CrysAlis^{Pro} processes data using sophisticated algorithms to provide the highest quality data. As technology or approaches change, our software team incorporates these to further advance data analysis and processing.

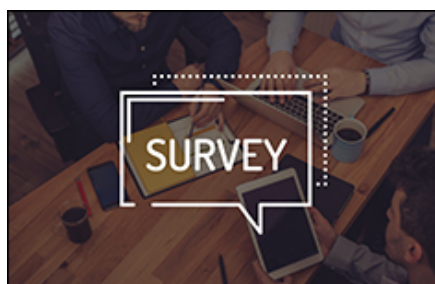## Rigaku Oxford Diffraction Forum

www.Rigakuxrayforum.com

Here you can find discussions about software, general crystallography issues and more. It's also the place to download the latest version of Rigaku Oxford Diffraction's CrysAlis^{Pro} software for single crystal data processing.

We look forward to seeing you on there soon.
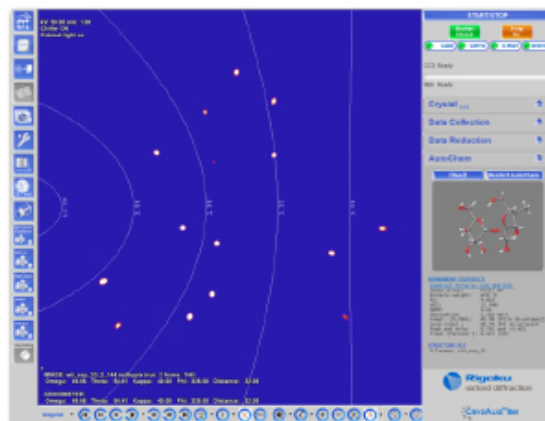

Survey of the Month
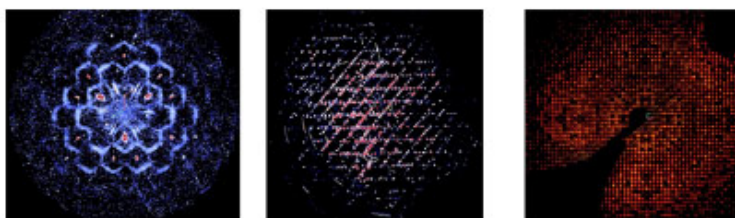

Processing of challenging and non-standard data collections

CrysAlis^Pro^ contains a comprehensive and highly effective range of tools for dealing with a full range of samples from easy to challenging, and non-standard crystal samples. EwaldExplorer and Ewald3D (NEW!) are the tools that have been developed to easily identify effects, problems or artifacts in difficult or problematic datasets.

Ewald3D allows visualization of measured reciprocal space in 3 dimensions and in an undistorted way. Identifying diffuse scatter, modulation, subtle twinning, or incorrect instrument models is quick and easy with this new feature.

From left to right: An example of diffuse scattering, multiple crystals and a protein.

Supporting a range of crystallographic setups and applications

In addition to standard data collection routines, CrysAlis^Pro^ contains tools for working with non-standard experimental setups and sample types, including:

- High pressure data collections
- Variable temperature and multi-wavelength experiments
- Powder experiments (data collection and processing)
- Automatic screening or full data collections of several *in situ* protein crystals
- Highly absorbing samples
- Up to 8-fold twinned samples
- Charge density measurements
- Absolute structure determination

Software Compatibility

Exporting frames or data from CrysAlis^Pro^ into suitable alternative formats such as mosFLM, XDS, Denzo (HKL 2000) or another Esperanto format is easily achieved. Use CrysAlis^Pro^'s data collection strategy to achieve the best data coverage in the quickest possible time and then automatically output into HKLF format for small molecule datasets or into the MTZ format for protein datasets.
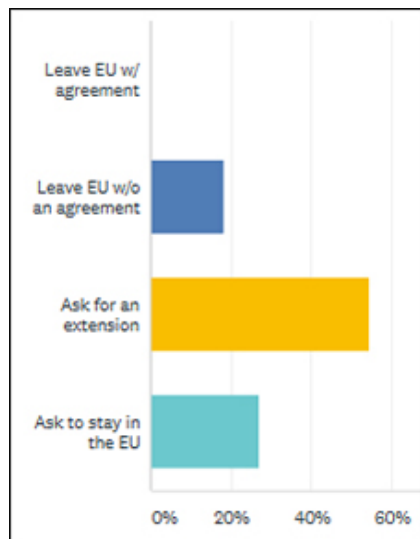
CrysAlis^Pro^ is used by numerous research groups to process their synchrotron data. Our software is capable of importing data from several different detector types; known or unknown.

AutoChem

AutoChem is the ultimate productivity tool for small molecule chemists, offering fast, fully automatic structure solution and refinement during data collection. Developed in collaboration with OlexSys Ltd (Durham University, UK), AutoChem works in conjunction with Olex2 where more advanced structure solution and refinement functionality exists. AutoChem is seamlessly integrated within CrysAlis^Pro^, and forms an integral part of our 'What is this?' feature.
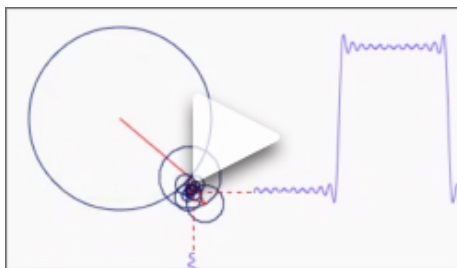
Last Month's Survey

Let us test our ability to prognosticate. This edition of *Crystallography Times* is scheduled to post a couple of days before March 29, the deadline for Brexit.

Videos of the Month

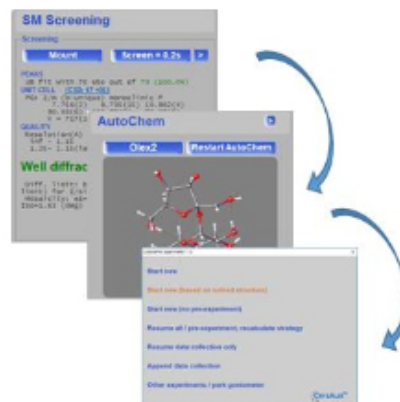Here is a nifty explanation of Fourier series using epicycles.

And here is a longer video that provides a more detailed description of this approach, where a refinement process is used to draw a fairly complex two-dimensional image: https://youtu.be/ds0cmAV-Yek. Now we just inverse the FT to make it complete.

Subscribe to Rigaku eNewsletters

Each month, Rigaku distributes two eNewsletters: *The Bridge*, which focuses on

The 'What is this?' feature gives you structures in seconds and ensures you are not wasting time collecting full datasets on known samples or starting materials. It is an alternative pre-experiment option, which is used to plan your full data collections.

Lab in the Spotlight

The Central Department of X-ray Structure Analysis at the Technische Universität Braunschweig

Left: Cu XtaLAB Synergy-S, right: Mo XtaLAB Synergy-S, both with 800 Series Cryostream systems. Not shown is an Xcalibur with an Eos detector.

The Central Department of X-ray Structure Analysis at the Technische Universität Braunschweig has three single-crystal diffractometers, a copper XtaLAB Synergy-S and a molybdenum XtaLAB Synergy-S both with HyPix-6000HE HPC, and a molybdenum Xcalibur with an Eos CCD. The Synergys are recent additions and already providing a boost in productivity. In addition to the structure elucidation of small molecules, which represents the main job of the facility, data collection on protein crystals and powder diffraction measurements can be performed. The group has considerable experience in dealing with highly reactive, air-sensitive samples. Education is very important to the university and the center provide guidance in structural analysis. The facility is managed by Dr. Christian Kleeberg.

Useful Link

Inspiring women in crystallography

Here is an article by Suzanna Ward on women in crystallography.

Selected Recent Crystallographic Papers

Organic crystallography: three decades after Kitaigorodskii. Slovokhotov, Yuri L. *Structural Chemistry*. Apr2019, Vol. 30 Issue 2, p551-558. 8p. DOI: 10.1007/s11224-018-1254-6.

Lattice versus structure, dimensionality versus periodicity: a crystallographic

Babel? Nespolo, Massimo. *Journal of Applied Crystallography*. Apr2019, Vol. 52 Issue 2, p451-456. 6p. DOI: 10.1107/S1600576719000463.

Aquarium: an automatic data-processing and experiment information management system for biological macromolecular crystallography beamlines. Yu, Feng; Wang, Qisheng; Li, Minjun; Zhou, Huan; Liu, Ke; Zhang, Kunhao; Wang, Zhijun; Xu, Qin; Xu, Chuanyan; Pan, Qiangyan; He, Jianhua. *Journal of Applied Crystallography*. Apr2019, Vol. 52 Issue 2, p472-477. 6p. DOI: 10.1107/S1600576719001183.

A simple adaptation to a protein crystallography station to facilitate difference X-ray scattering studies. Sharma, Amit; Berntsen, Peter; Harimoorthy, Rajiv; Appio, Roberto; Sjöhamn, Jennie; Järvå, Michael; Björling, Alexander; Hammarin, Greger; Westenhoff, Sebastian; Brändén, Gisela; Neutze, Richard. *Journal of Applied Crystallography*. Apr2019, Vol. 52 Issue 2, p378-386. 9p. DOI: 10.1107/S1600576719001900.

Design, biological evaluation and X-ray crystallography of nanomolar multifunctional ligands targeting simultaneously acetylcholinesterase and glycogen synthase kinase-3. Oukoloff, Killian; Coquelle, Nicolas; Bartolini, Manuela; Naldi, Marina; Le Guevel, Rémy; Bach, Stéphane; Josselin, Béatrice; Ruchaud, Sandrine; Catto, Marco; Pisani, Leonardo; Denora, Nunzio; Iacobazzi, Rosa Maria; Silman, Israel; Sussman, Joel L.; Buron, Frédéric; Colletier, Jacques-Philippe; Jean, Ludovic; Routier, Sylvain; Renard, Pierre-Yves. *European Journal of Medicinal Chemistry*. Apr2019, Vol. 168, p58-77. 20p. DOI: 10.1016/j.ejmech.2018.12.063.

High Consistency of Structure-Based Design and X-Ray Crystallography: Design, Synthesis, Kinetic Evaluation and Crystallographic Binding Mode Determination of Biphenyl-N-acyl-ß-d-Glucopyranosylamines as Glycogen Phosphorylase Inhibitors. Fischer, Thomas; Koulas, Symeon M.; Tsagkarakou, Anastasia S.; Kyriakis, Efthimios; Stravodimos, George A.; Skamnaki, Vassiliki T.; Liggri, Panagiota G.V.; Zographos, Spyros E.; Riedl, Rainer; Leonidas, Demetres D. *Molecules*. Apr2019, Vol. 24 Issue 7, p1322-1322. 1p. DOI: 10.3390/molecules24071322.

Synthesis of a new 24-membered tetramide macrocycle and X-ray crystal structure determination. Santa María, Dolores; Claramunt, Rosa M.; Torralba, M. Carmen; Torres, M. Rosario; Elguero, José. *Tetrahedron Letters: International Organ for the Rapid Publication of Preliminary Communications in Organic Chemistry*. Apr2019, Vol. 60 Issue 17, p1206-1209. 4p. DOI: 10.1016/j.tetlet.2019.03.066.

Highly efficient adsorption of benzothiophene from model fuel on a metal-organic framework modified with dodeca-tungstophosphoric acid. Ullah, Latif; Zhao, Guoying; Hedin, Niklas; Ding, Xunlei; Zhang, Suojiang; Yao, Xiaoqian; Nie, Yi; Zhang, Yanqiang. *Chemical Engineering Journal*. Apr2019, Vol. 362, p30-40. 11p. DOI: 10.1016/j.cej.2018.12.141.

Using powder XRD and pair distribution function to determine anisotropic atomic displacement parameters of orthorhombic tridymite and tetragonal cristobalite. Lee, Seungyeol; Xu, Huifang. *Acta Crystallographica: Section B, Structural Science, Crystal Engineering & Materials*. Apr2019, Vol. 75 Issue 2, p160-167. 8p. DOI: 10.1107/S2052520619000933.

Martini bead form factors for nucleic acids and their application in the refinement of protein—nucleic acid complexes against SAXS data. Paissoni, Cristina; Jussupow, Alexander; Camilloni, Carlo. *Journal of Applied Crystallography*. Apr2019, Vol. 52 Issue 2, p394-402. 9p. DOI: 10.1107/S1600576719002450.

Discovery of a new class of MTH1 inhibitor by X-ray crystallographic screening. Yokoyama, Takeshi; Kitakami, Ryota; Mizuguchi, Mineyuki. *European Journal of Medicinal Chemistry*. Apr2019, Vol. 167, p153-160. 8p. DOI: 10.1016/j.ejmech.2019.02.011.

Refinement of protein structures using a combination of quantum-mechanical calculations with neutron and X-ray crystallographic data. Caldararu, Octav; Manzoni, Francesco; Oksanen, Esko; Logan, Derek T.; Ryde, Ulf. *Acta Crystallographica: Section D, Structural Biology*. Apr2019, Vol. 75 Issue 4, p368-380. 13p. DOI: 10.1107/S205979831900175X.

Heavy-atom labeling of RNA by PLOR for *de novo* crystallographic phasing. Stagno, Jason R.; Yu, Ping; Dyba, Marzena A.; Wang, Yun-Xing; Liu, Yu. *PLoS ONE*. 4/15/2019, Vol. 14 Issue 4, p1-9. 9p. DOI: 10.1371/journal.pone.0215555.

Design, synthesis and biological evaluation of novel human monoamine oxidase B inhibitors based on a fragment in an X-ray crystal structure. Cheng, Kai; Li, Shiyu; Lv, Xiao; Tian, Yongbin; Kong, Haiyan; Huang, Xufeng; Duan, Yajun; Han, Jihong; Xie, Zhouling; Liao, Chenzhong. *Bioorganic & Medicinal Chemistry Letters*. Apr2019, Vol. 29 Issue 8, p1012-1018. 7p. DOI: 10.1016/j.bmcl.2019.02.008.

A direct approach to estimate the anisotropy of protein structures from small-angle X-ray scattering. Roig-Solvas, Biel; Brooks, Dana; Makowski, Lee. *Journal of Applied Crystallography*. Apr2019, Vol. 52 Issue 2, p274-283. 10p. DOI: 10.1107/S1600576719000918.

Crystallization of the human tetraspanin protein CD9. Umeda, Rie; Nishizawa, Tomohiro; Nureki, Osamu. *Acta Crystallographica: Section F, Structural Biology Communications*. Apr2019, Vol. 75 Issue 4, p254-259. 6p. DOI: 10.1107/S2053230X1801840X.

Low-resolution structure, oligomerization and its role on the enzymatic activity of a sucrose-6-phosphate hydrolase from *Bacillus licheniformis*. Mera, Alain; de Lima, Mariana Zuliani Theodoro; Bernardes, Amanda; Garcia, Wanius; Muniz, João Renato Carvalho. *Amino Acids*. Apr2019, Vol. 51 Issue 4, p599-610. 12p. DOI: 10.1007/s00726-018-02690-2.

ß-Lactoglobulin associative interactions: a small-angle scattering study. Anghel, Lilia; Rogachev, Andrey; Kuklin, Alexander; Erhan, Raul Victor. *European Biophysics Journal*. Apr2019, Vol. 48 Issue 3, p285-295. 11p. DOI: 10.1007/s00249-019-01360-9.

Challenging structure determination from powder diffraction data: two pharmaceutical salts and one cocrystal with Z' = 2. Schlesinger, Carina; Bolte, Michael; Schmidt, Martin U. Zeitschrift für Kristallographie. *Crystalline Materials*. Apr2019, Vol. 234 Issue 4, p257-268. 12p. DOI: 10.1515/zkri-2018-2093.

A 3D inorganic-organic hybrid constructed from Strandberg-type polyoxometalates and silver complexes: Synthesis, structure and properties. Shi, Zhenyu; Li, Feifei; Zhao, Jie; Yu, Xiao-Yang; Zheng, Yuguo; Chen, Zhe; Guo, Qingqing; Zhang, Guoyi; Luo, Yuhui. *Inorganic Chemistry Communications*. Apr2019, Vol. 102, p104-107. 4p. DOI: 10.1016/j.inoche.2019.02.018.

X-Ray powder diffraction — A non-destructive and versatile approach for the identification of new psychoactive substances. Jurásek, Bronislav; Bartunek, Vilém; Huber, Štepán; Kuchar, Martin. *Talanta*. Apr2019, Vol. 195, p414-418. 5p. DOI: 10.1016/j.talanta.2018.11.063.

Book Review

[The Big Nine: How the Tech Titans and Their Thinking Machines Could Warp Humanity](#)
By Amy Webb, ISBN: 978-1541773752

Forget Stephen King. If you want to read something nightmare-inducing, pick up Amy Webb's newest book, *The Big Nine*. Webb, a quantitative futurist and professor of strategic foresight at NYU's Stern School of Business, presents a vision of humanity's future that doesn't have much humanity in it. It is scary—real world scary, not vampires and haunted hotels scary.

The rise of artificial intelligence in recent years (newsflash: it's already here) gives many in the academic community like Webb reason to pause. For a lot of laypeople, their understanding of artificial intelligence—and perhaps fear or skepticism of it—stems from representations in popular culture, like HAL in *2001: A Space Odyssey*. The concern that AI is ultimately created by humans, who are inherently flawed, and therefore, AI might be inherently flawed, is a real one. However, as Webb herself notes in the introduction, "This is not a book about the usual AI debates." Instead, "it is both a warning and a blueprint for a better future."

The Big Nine refers to the nine big tech companies around the world at the forefront of artificial intelligence research and development. They are: Google, Microsoft, Amazon, Facebook, IBM, Apple, Baidu, Alibaba and Tencent. The first six form America's "G-MAFIA," as Webb calls it. The latter three form China's "BAT"—and Webb suggests they are the ones we should really be concerned about. In America, the AI business is driven by capitalism and the desire to be better and faster than the competition. Here, it's all about the bottom dollar. In China, it's about something else entirely.

But before Webb really digs into these companies, their corporate missions, and the future impact of their actions on humanity, she steps back a few centuries, providing her readers with a brief history of AI. The first part of her book, "Ghosts in the Machine," begins with a deep dive into the philosophical debate regarding mind, man, and machine. In other words, if man has a mind, and man makes machine, can the machine have a mind? René Descartes, in his Treatise of Man, expressed his belief that even if humans could make a believable automaton (or robot), it would never pass as a human because it

would lack a human mind and therefore a human soul.

Technology has advanced significantly since Descartes' time. The first computational machines were invented, automation made industrial work more efficient and oftentimes safer. However, computer scientists and researchers have always strived to bridge the gap Descartes described between machine and mind. And that's where the Big Nine come in.

The Big Nine are all about pushing boundaries and surpassing the limit of previously developed technologies. Webb introduces each of the companies in the G-MAFIA and BAT, and describes their role in AI research and development, as well as her concerns regarding each. One of the most interesting concerns Webb expresses regards the limited pool of people culled to work on AI projects, especially in the United States. The G-MAFIA's AI divisions consist largely of people with degrees from elite East Coast and occasionally West Coast universities. They typically have a liberal political perspective. But humans are diverse—and as a corollary, human thought is diverse. So, shouldn't the pool of people developing artificial intelligence—artificial thought, one might say—be more diverse?

In the second part, "Our Futures", Webb describes three possible (and seemingly probable) future states of humanity. Webb's writing is so descriptive and detailed it's easy to forget that these events haven't happened yet. It feels like reading a history textbook where our future is already the past. Or like something Aldous Huxley and George Orwell co-wrote with Isaac Asimov about a future where artificial intelligence overrides human intelligence. If Part One didn't spook you out of your skin, Part Two will.

In Part Three, Webb hits rewind, bringing her readers back to the present and reminding them that the future isn't set in stone. It is an admirable attempt at optimistic pragmatism, but I had a hard time feeling like anything could substantially change. Unless some kind of technological plague wipes out all our electronics, parts of what Webb describes seems inevitable. AI is already here—and the responsibility for making sure that it doesn't wipe out humanity (not humans, just humanity) lies not only on the shoulders of these tech giants, but on the shoulders of individual consumers. Holding these companies—and the AI they develop—accountable to an ethical and moral code of conduct is our responsibility.

Review by Jeanette S. Ferrara, MA

Speaking of Stephen King, our own Bev Vincent has coedited with King an anthology of flight-related short stories (and a poem) titled *Flight or Fright: 17 Turbulent Tales*. (Cemetery Dance Publications, Forest Hill, MD, © 2018, 332 pages, ISBN: 978-15877676796). Included are some classics like Sir Arthur Conan Doyle's "The Horror of the Heights" and "Nightmare at 20,000 Feet". As some of you may remember, the latter became a Twilight Zone segment starring William Shatner. Other authors include Ray Bradbury, Joe Hill, Roald Dahl and King himself. Bev included his short story from 2010, "Zombies on a Plane".

King provides an introduction to the book and a paragraph introducing each of the stories. Bev provides the epilogue and reminded me of the time Jan Troup, Paul Swepston, he and I were trying to get from Hong Kong to Houston without passing through LAX. What a story that was!

Anyway, to get the most value from the book, I recommend going all in and reading it on a plane as I did.

Review by Joseph Ferrara
Deputy Director, X-ray Research Laboratory, Rigaku

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