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Rigaku Newsletter Vol. 5, No. 4, Spring 2008

**A word from our president: Some things never change, but thankfully, some things do.**

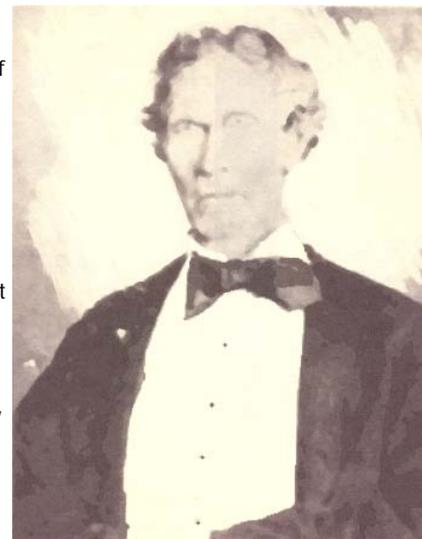
My great-great-great grandfather, Judge John Brown, was born in 1800 and is remembered in our family because he kept a detailed diary of his life during the period 1852-1865. He chronicled the day-to-day activities of raising 10 children, working as a farmer and lawyer, and most interestingly, the lead up to and culmination of the American Civil War. Fifty years ago a distant relative transcribed the diary using a typewriter. My new hobby is digitizing the typewritten version using a scanner and OCR software and using Google to annotate the historical aspects of the diary.

It is interesting to note the things that will probably never change, as it helps to put everyday life into context. Like most fathers, he worried about the quality of the man who married his first daughter. Even though the man was a trained lawyer and had a nice bank account, Judge Brown was highly concerned about the younger generation and their lack of commitment to hard work. He worried about the candidates running for political office and the fact that there never seemed to be any high quality candidates from any political party. In spite of the worthlessness of the succeeding generations and the horrible group of elected officials, civilization somehow managed to muddle along for another 150 years. Perhaps there is hope for us yet.

But some things do change and perhaps the biggest contrast he chronicles is the change in medicine. Of course he didn't realize he was doing this but his descriptions of family illnesses and the treatments that were administered make you glad to live in the modern world. One of the most common ingredients in the medicine of his day appears to be different forms of mercury. If he was sick for more than a couple of days he would take a "Blue Mass" pill which contains a large amount of mercury; Abraham Lincoln is thought to have suffered a number of mental conditions due to a large intake of Blue Mass. If someone in the family was constipated he gave them calomel (dimercury dichloride), a drug that is suspected of contributing to the premature death of George Washington. If a baby was sick they received a mercury/chalk mixture. And if all else failed, he would administer a glass of turpentine.

Based on my lineage, perhaps it is a good thing that I didn't have the grades necessary to get into medical school: the world is indeed a safer place.

Paul N. Swepston



Calendar of events

Rigaku will be attending the following conferences in the coming months:

- [APS Users Meeting](#), Argonne, IL, May 5-9
- [ICCBM12](#) (International Conference on the Crystallization of Biological Macromolecules), Cancun, Mexico, May 6-9
- [Sealy Center for Structural Biology Symposium](#), Galveston, TX, May 16-17
- [Mid-Atlantic Macromolecular Crystallography Meeting](#), Chapel Hill, NC, May 22-24

Visit the Rigaku booth at the ACA meeting in Knoxville

Rigaku will be exhibiting at this year's [ACA in Knoxville, Tennessee](#). Please drop by the Rigaku booth, #101, to see the latest in crystallographic hardware and software. On display will be automation systems (Alchemist™II, Desktop Minstrel™UV, and ACTOR™ accessories), our benchtop XRD and small molecule systems (MiniFlex™II XRD system and SCXmini™ small molecule system), the new Saturn 944+ 18-bit CCD detector, X-ray optics and accessories such as MtGUI and the Proteros® Free Mounting® System.

Rigaku employees will be available to show you the systems that spark your interest and to conduct software demonstrations on 2DP, CrystalClear™, d*TREK®, CrystalTrak™ and MIFit+.

During the poster sessions the Alchemist II will display its versatility in liquid handling by serving up its famous Alchetini cocktails!

Sunday, June 1st, Rigaku will hold a "Lunch and Learn" at noon in the convention center, featuring presentations by Tom McNulty ("Diverse Applications with the RAPID II Curved Imaging Plate Diffraction System"), Angela Criswell ("Expanding the Crystallographers Toolkit: New Tools for Your Structure Solution Pipeline"), and Craig Sterling ("The New Desktop Minstrel UV with Clean Light Technology"). Everyone is welcome! Please RSVP to [Michelle Goodwin](#) to ensure your lunch accommodations.

Everyone is invited to the 23rd Annual Rigaku Fun Run/Walk, which will take place at World Fair Park on Monday, June 2, 2008 at 7 a.m. Refreshments, prizes and t-shirts will be given away after the event. The Fun Run Waiver can be filled out prior to or at the event.

- **CSC** (Canadian Society for Chemistry), Edmonton, Alberta, Canada, May 24-28
- **ACA** (American Crystallographic Association), Knoxville, TN, May 31-June 5
- **ICDD: Fundamentals of X-ray Powder Diffraction**, Newtown Square, PA, June 2-6
- **ICDD: Advanced Methods in X-ray Powder Diffraction**, Newtown Square, PA, June 9-13
- **Bio International Convention**, San Diego, CA, June 17-20
- **10th Northwest Crystallography Workshop**, Eugene, OR, June 20-22
- **Diffraction Methods in Structural Biology Gordon Conference**, Lewiston, ME, July 13-18
- **Semicon West**, San Francisco, CA, July 15-17
- **PRChem 2008**, Puerto Rico, July 27-Aug 2

Training Sessions

Rigaku is pleased to announce the following training sessions in 2008:

- Macromolecular
 - September 17-19
- XRD (MiniFlex II):
 - September 23-24
- XRD (Jade software):
 - May 20-21 (22)
 - November 4-5 (6)
- XRF:
 - June 17-19

All classes are held at Rigaku's applications laboratory in The Woodlands, TX.



Introducing Supermini™ — the first high-power benchtop WDXRF spectrometer

Representing the next stage in the evolution of Rigaku's unique and historic line of "mini" X-ray instrumentation, the new Rigaku

Rigaku employees are involved in the following presentations during the conference:

Date	Time	Authors	Title (click for abstract)	Presentation
Sunday, June 1	8:20 a.m.	Lee Daniels	Joint SIG Sessions: Introduction to Modulated Structures	13.01
	4:30-6:30 p.m.	Jian Xu, Craig Sterling, Michael Willis	Poster: Desktop Minstrel UV: A Novel Protein Crystal Monitoring Automation System, Using UV Fluorescence Microscopy	SP174 (W0420)
Monday, June 2	5:30-7:30 p.m.	Angela Criswell, Amber Dowell, Robert Bolotovskiy, Cheng Yang, Jim Pflugrath	Poster: Automated Sample Handling, Data Collection and Structure Solution with ACTOR	MP082 (W0327)
Tuesday, June 3	5:30-7:30 p.m.	Mark Pressprich	Poster: New Algorithms for Single Crystal Photometry	TP152 (W0343)
Wednesday, June 4	8:30 a.m.	James Pflugrath	Macromolecular Crystal Diffraction Data Collection: Opinions about Best Practices	01.05.01 (W0320)
	11:00 a.m.	Kris Tesh, Angela Criswell, Lcai Jiang, Bret Simpson, Boris Verman, Cheng Yang, Joseph Ferrara	New Optics for Macromolecular Crystallography	03.01.04 (W0390)

Stay apprised of Rigaku's activities at ACA at our web site. We hope to see you in Knoxville!

Desktop Minstrel UV and CrystalMation win prize for *Most Innovative New Technology* at ELRIG

Rigaku Americas Corporation is pleased to announce the receipt of the "Most Innovative New Technology" award for the Desktop Minstrel UV ultraviolet crystal imaging and analysis system and CrystalMation automated crystallization system at the [ELRIG Protein Crystallography Conference](#), held in Cambridge, U.K. on April 1, 2008.

Rigaku Desktop Minstrel UV is the world's first fully automated ultraviolet (UV) imaging and protein crystal monitoring system that uses ultraviolet fluorescence (UVF) microscopy. Engineered and optimized for use in protein crystallization experiments, this new instrument is a major advance over previous visible light microscopy techniques because its UVF technology can easily distinguish protein crystals from non-protein crystals (such as salt). The system is bundled with advanced CrystalTrak software for automatic imaging of crystallization experiments; furthermore, it links the acquired images with crystallization conditions in a SQL relational database, providing a complete virtual crystallization laboratory.

Rigaku CrystalMation is a fully integrated platform for protein crystallization, automating every step from custom screen making to crystallization trial imaging and analysis. Modular design means that CrystalMation systems can be configured to meet a wide range of requirements and evolve as needs change. Each of the innovative workstations is available as a stand-alone instrument or in combination with one or more additional components.



50th ACTOR™ robot installed

Rigaku Americas Corporation is pleased to announce the sale of the 50th Rigaku ACTOR robotic protein crystal handling system to the Medical Research Council (MRC) Laboratory of Molecular Biology in Cambridge, UK. The system was chosen by the MRC as an upgrade for their in-house X-ray diffraction facilities and in support of crystallographic studies carried out in the laboratory, which seek to understand the structure, function and interactions of biologically important molecules at the atomic, molecular and supra-molecular level. A significant milestone for Rigaku, sale of the 50th ACTOR will be marked by a special commemorative plaque affixed to the exterior of the instrument. Dr. Andrew Leslie, Group Leader for structural studies of macromolecular complexes within the Division of Structural Studies, commented, "I'm personally delighted that we are getting the 50th system, congratulations to all concerned!"

As the world's first commercial robotic system for automated crystal sample mounting and storage, ACTOR eliminates much of the physical handling of samples by crystallographers required during routine screening and data collection either in the lab or at the beamline. It is an automated system designed to store frozen protein crystals, mount them sequentially, align them to the X-ray beam, collect complete data sets, and return the crystals to storage.

The ACTOR automated crystal mounting and data collection technology was co-developed by Rigaku with Oceanering Space Systems (OSS), a division of Oceanering International, Inc., under a license from [Abbott® Laboratories](#) for the

Supermini was designed to deliver high-precision, non-destructive analysis of elements from fluorine (F) through uranium (U) in solids, liquids, powders, and thin films. The Rigaku Supermini delivers performance and value in a compact package that has heretofore not been available in a commercial XRF elemental analyzer. Perfect for certifying compliance with WEEE/RoHS & ELV directives, the Rigaku Supermini affords superior reproducibility at the low concentration levels common to today's applications.

Recently shown at PITTCON 2008 in New Orleans, LA, the new Rigaku Supermini is offered as a compact sequential WDXRD that is both a cost-effective and high-precision, high-resolution alternative to energy dispersive X-ray fluorescence technology. This benchtop WDXRF employs three analyzing crystals, two detectors, a 12-position sample changer and a choice of analysis in an air, vacuum or helium (He) atmosphere. An air-cooled 50 kV, 200W tube provides exceptional light element performance and does not require external cooling.

Rigaku Supermini fits between the low-cost Rigaku Primini® 50W benchtop sequential WDXRF spectrometer and the high-power Rigaku ZSX Primus "mainframe" sequential WDXRF spectrometer. The Supermini is part of the broadest line of laboratory XRF instruments available today, which affords Rigaku the ability to provide an optimized high-value analytical solution for every conceivable XRF application. As with all Rigaku XRF instruments, the Rigaku Supermini is equipped with exceptionally powerful yet easy-to-use software, featuring: multiple sample handling, flowbar based application building, fundamental parameters (FP) and the EZ scan measurement user interface. Software options include: SQX software with FP, theoretical overlap correction, matching library, phase identification, glass bead correction and remote diagnostics.

Rigaku Automation open house

On April 3rd, Rigaku Automation hosted their third annual Open House at their facilities in Carlsbad, CA. Twenty-four companies, universities, and core labs from around the world turned out.

Craig Sterling started the day with an overview of the entire CrystalMation™ platform. After the presentations, attendees were divided into groups of six and were given the opportunity to attend

purpose of offering a commercial high-throughput crystallography automation system. Astex™ Therapeutics Ltd. (Cambridge, UK) purchased the first ACTOR system in 2001. In 2002, the Rigaku ACTOR was honored with an R&D 100 Award for technical innovation. In 2005, Rigaku introduced a version of robot for small molecule chemical crystallography called the ACTOR SM.

Rigaku continues to dominate home lab PDB submissions

A revised survey of the PDB¹ shows that Rigaku generators and detectors continue to provide the highest level of productivity for crystallographers collecting data and solving protein structures in a home laboratory environment. X-ray crystal structure data were compiled and analyzed for years from 2003 through 2006, the last year for which released deposits are essentially complete. All data were employed, including incidences where multiple sources and detectors were employed for a reported structure.

In 2006, users deposited 875 structures from data collected with Rigaku detectors and 953 structures from Rigaku generators. Of the 5,924 X-ray structure deposits for 2006, 4,671 (79%) were from data collected at beamlines. During the period studied, overall submissions grew at a 13.5% Compound Annual Growth Rate (CAGR). Trends for 2007 look similar but with an average time from submission to release of five months, accurate statistics for 2007 will not be available until next year.

Further analysis of the data revealed other reasons to be proud of Rigaku's continuing contribution to basic research in structural biology. For submissions where home laboratory X-ray source equipment was employed, Rigaku commanded an 88% share of citations for 2006. For non-beamline data, Rigaku lead with a 55% citation share for detectors.

Since 1996, the productivity share for Rigaku has been increasing steadily. In the most recent four-year period, for home lab source submission citations, Rigaku showed a 7.6% CAGR, contrasted with negative growth by the next closest competitor (-3.3% CAGR) over the same period. Even more impressive is the finding that, for home lab detector submissions, Rigaku showed a 14.1% CAGR over the 2003-2006 period. Again, this is juxtaposed against our next closest competitor showing a -2.0% CAGR over the same period. In all, the findings reinforce the position of Rigaku as the #1 provider of home lab X-ray instrumentation for protein and macromolecular crystallography, as well as the industry leader for consistently delivering superior home laboratory productivity.

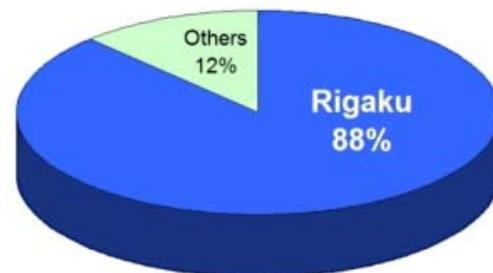
¹H.M.Berman, J.Westbrook, Z.Feng, G.Gilliland, T.N.Bhat, H.Weissig, I.N.Shindyalov, P.E.Bourne, The Protein Data Bank. Nucleic Acids Research, 28 pp. 235-242 (2000).

Introducing the RAPID™ II curved detector X-ray diffraction (XRD) system

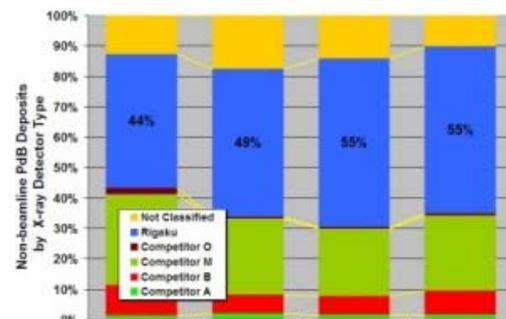
A new, compact, fully-integrated high-resolution X-ray diffractometer system, the RAPID II, has just been introduced by Rigaku. Incorporating the latest member of the RAPID family of large area curved imaging plate (IP) detectors, the Rigaku RAPID II combines every component needed for a high performance X-ray diffraction system delivering no-compromise performance for applications spanning from applied crystallography to chemical crystallography. Typical applications include: high-resolution charge density measurement, micro-diffraction, diffuse scattering, measurement of weakly diffracting disordered materials, small molecule crystallography, wide angle X-ray scattering (WAXS), stress and texture measurements, as well as general purpose powder diffraction.

Central to the performance of the Rigaku RAPID II is the new 2DP software that delivers the extraordinary power of project-based batch processing of two dimensional (2D) X-ray diffraction data. This capability allows manipulation of multiple images at the same time with various analytical protocols. In addition to general 2D intensity image processing, the software provides for: the integration of single crystal diffraction patterns, display and automatic calculation of stress and texture data, as well as line and azimuthal integration for general purpose powder diffraction.

RAPID II is so versatile that it can replace several instruments without compromising data quality. Its unique, curved large area detector subtends a 2θ range of 204°, at a single detector setting, for maximum reciprocal space coverage. Inherent to the flexibility of this system is a choice of X-ray sources, ranging from: a high-frequency 3 kW sealed tube, to a MicroMax™.002+ microfocus sealed tube, to a 1.2 kW MicroMax-007 HF microfocus rotating anode generator, and to a 18kW ultra high power ultraX 18 rotating anode generator. Available optics range from a traditional graphite monochromator or high performance SHINE optic to an VariMax™ confocal X-ray optic. Two goniometer configurations are available: a partial-χ arrangement for chemical crystallography and a fixed-χ system, with manual or automatic XY translation, for applied crystallography. The RAPID II includes a fully integrated CCD video camera system, with zoom capabilities, to image sample areas down to 1 micron. As the Rigaku RAPID II is capable of analyzing samples as small as 10 microns, the system is ideal for the non-destructive identification of small



2006 PDB home laboratory source citation distribution by vendor



2003-2006 PDB home laboratory detector citation distribution by vendor

hands-on demonstrations of the core technologies in the CrystalMation platform: CrystalTrak software, the Phoenix™ RE, the Alchemist II, the Minstrel HT, the Desktop UV. Each group was given the opportunity to work with each of the stations.

After the hands-on portion concluded, attendees were taken to The Scripps Research Institute for a complete tour of the full CrystalMation system in operation at the Joint Center for Structural Genomics. Dinner was held at the Beach House restaurant in Cardiff-by-the-Sea. With great food and drinks on hand, the event was thoroughly enjoyed by all in attendance! We look forward to next year!

S-SAD using Cr radiation: Another success story

James Liu, of the National Laboratory of Biomacromolecule, Institute of Biophysics, Chinese Academy of Sciences, and BC Wang, of the SECSG, Department of Biochemistry and Molecular Biology, University of Georgia report the crystal structure of a novel non-Pfam protein AF1514 from *Archeoglobus fulgidus* DSM 4304 solved by S-SAD using a Cr X-ray source in the online journal [Proteins, Structure, Function and Bioinformatics](#). The structure consists of 87 residues with 2 cysteines and 1 methionine, from which the structure was phased. This is the first Cr-SAD structure from James' lab since he took responsibility for it from Zihe Rao and we expect to seem many more.

SmartLab® application byte

In recent years, air purification and water decomposition using photocatalysts has become an active area of research and, in particular, oxide semiconductors are promising materials for photocatalysts because they hardly change even when used under severe atmospheric conditions. Zinc oxide, ZnO, is currently attracting attention as an environment-conscious material with photocatalytic activity. Its direct band gap energy at room temperature is 3.37 eV .

The reason for its behavior is thought to be related to its characteristic surface structure and the crystallite size. Using data obtained from X-ray diffraction measurements, the crystallite size distribution can be easily analyzed.

In this example, ZnO crystals are heated for one hour in oxygen gas at 400°C, 500°C, 600°C and 700°C. The Cu Kα lines of the heated ZnO

particles (and incorporated aggregates) from a wide range of samples. In addition, XY mapping capabilities allow the measurement at precise locations of larger samples.

At the heart of this versatile system is the RAPID II's curved IP detector, which has numerous advantages over other types of X-ray detectors - the most obvious being an extremely large active area, exceptionally low noise, and wide dynamic range. The large curved active area is advantageous because an outsized solid angle of data is collected in a single exposure. For example, chemical crystallographic data exceeds by 7° the target resolution for publication of single crystal structures determined using copper radiation for IUCr journals. While the wide dynamic range eliminates worrying about detector saturation, the curved-plate geometry of the RAPID II reduces oblique-incidence X-ray absorption effects seen with flat detectors of any kind.

deCODE biostructures, Inc. chooses Ultimate HomeLab™ system for throughput

With the recent order for a top-of-the-line Ultimate HomeLab system, deCODE biostructures became a repeat Rigaku customer for protein crystallography instrumentation. Their new system, which includes an FR-E+ SuperBright™ X-ray source, two Saturn 944+ CCD detectors, and two ACTOR robots with RFID capability, represents the pinnacle of current highly-automated home laboratory technology.

Dr. Hidong Kim, Chief Scientific Officer, in commenting on the purchase decision, said that the new system would allow for decreased reliance on synchrotron time for structure determination work. Dr. Kim elaborated that high synchrotron beamline costs and the need for increased throughput to support deCODE's protein structure determination research as part of the NIAID funded [Seattle Structural Genomics Center for Infectious Disease](#), as well as a growing number of Fragments of Life™ projects for fragment lead discovery research, were factors influencing deCODE biostructures' decision to expand the capabilities of their home crystallography laboratory.

When asked what factors were primary contributors to the selection of Rigaku over other vendors, Dr. Kim cited X-ray intensity and automation. He stated that the level of development and overall integration of the automation platform was such that it would allow unattended 24/7 data collection, a capability central to the cost/benefit analysis. In addition, the deCODE biostructures system will be equipped with RFID pins to allow beginning to end automatic tracking of every crystal with data linked to our existing Crystal Miner™ database.

About deCODE chemistry, Inc. & deCODE biostructures, Inc.

deCODE chemistry, Inc. & deCODE biostructures, Inc. are wholly-owned subsidiaries of deCODE genetics (NASDAQ: DCGN) providing contract research services to world-class pharmaceutical companies, biotechnology companies, academic institutions, and government facilities. deCODE chemistry & biostructures takes a collaborative approach to pharmaceutical research services by combining the expertise of deCODE chemistry in drug discovery and development chemistry with the expertise of deCODE biostructures in structure determination of protein-ligand complexes. deCODE biostructures is one of the largest gene-to-structure contract research organizations in the U.S.

UV fluorescence imaging of protein crystals for enhanced productivity

While much has been in the news of late about the numerous R&D and patent expiration problems besetting the pharmaceutical and biotechnology industries, there are new technologies and approaches that can address many of the historical bottlenecks. For example, the rational drug design approach—that uses information about the molecular structure of a drug receptor (protein) to identify or create candidate (small molecule) drugs—determination of high resolution 3D structures of target proteins using X-ray crystallography is key.

Rigaku has developed the Desktop Minstrel UV, the world's first fully automated UV imaging and protein crystal monitoring system, to solve the twin problems of: 1) detecting tiny protein crystals in microarray plate wells and 2) optimizing experiments to grow suitable crystals. The system employs a novel (patent pending) UV illumination source and CCD camera system that can unambiguously detect protein crystals without damaging them. Unambiguous detection, in a well defined matrix of experimental conditions, enables crystallization conditions to be further optimized for growth and identification of crystals suitable for harvesting and structure determination.

The system includes robotics to allow automated and unassisted monitoring for up to 160 microarray crystallization plates when equipped with the Rigaku Gallery 160 robotic plate hotel. With an Oracle 9i database backside, the CrystalTrak software tracks information such as chemicals, screens, protein samples, images, and image scores. An integral part of the Desktop Minstrel UV solution, this advanced software differentiates the product by simplifying the crystallization experiment process, including: providing tools that enable users to improve crystallization trial productivity with minimal user intervention, assisting in the design of well-targeted experiments, making efficient use of protein samples, and setting up reproducible optimization experiments.

The Desktop Minstrel UV revolutionizes the entire protein crystal recognition process by employing UV Fluorescence (UVF) imaging for fail-safe protein crystal identification—eliminating guesswork, saving a vast amount of time, increasing productivity, and dramatically lowering research costs. Unlike the traditional optical microscopy approach which images everything in a microplate well, UV illumination causes protein crystals to fluoresce (glow)—providing a definitive level of contrast with respect to the well solution, salt crystals, and other artifacts of the crystallization experiment.



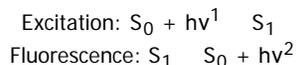
crystals are measured using the focusing beam X-ray optical system on Rigaku's SmartLab multipurpose diffractometer to obtain diffraction profiles that can be analyzed to obtain the crystallite size distribution.

The 110 diffraction line has a suitable intensity for analysis and does not overlap with any other reflections. The diffraction line width becomes narrower as the processing temperature increases, revealing that the crystallite size becomes larger qualitatively.

What's new?

- 4/21/2008 CrystalClear 1.4.0 SP1 now available
- 03/03/2008 Rigaku postdoctoral bursary program for 2008 announced
- 02/27/2008 XRF training session announced
- 02/14/2008 The March 2008 macromolecular training class is now filled
- 02/11/2008 New customer document: CCD FAQ (customer ID required)
- 01/28/2008 Job postings updated

Fluorescence occurs when a molecule relaxes to its ground state after being electrically excited:



where hv is a generic term for photon energy, h = Planck's constant and v = frequency of light. State S_0 is called the ground state of the fluorophore (fluorescent molecule) and S_1 is its first (electronically) excited state. In this case, the absorbed photon is in the ultraviolet (UV) range and the emitted light is in the visible range.

Innovation and creative engineering behind the Desktop Minstrel UV occurs at many levels: UV illumination and detection, robotic automation for relatively high throughput and unattended operation, advanced software that plans crystallizations experiments, a sophisticated SQL database architecture that links images with experiments, and provision for interfacing with other robotic automation tools. While each aspect of the Desktop Minstrel UV is innovative in its own right, the whole of the tool represents a new paradigm for basic and applied research so critical to the human race—new drug development.

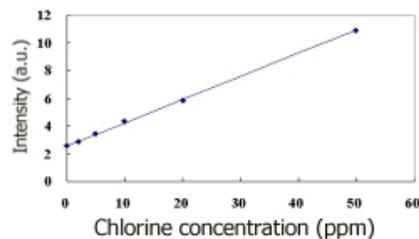
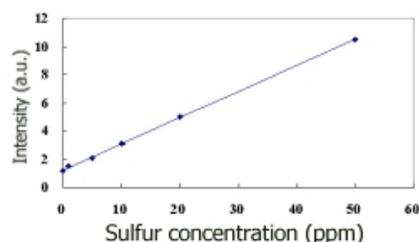
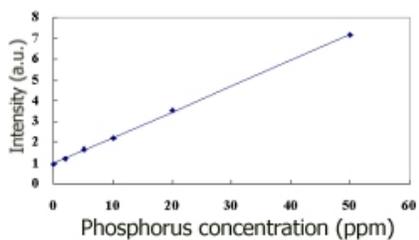
Analysis of biodiesel with a Mini-Z analyzer

Phosphorus in biodiesel, which comes from lipids in the fuel, is harmful to diesel engines, so control of phosphorus content is crucial. Sulfur content in the raw material is very low, which means that the content of sulfur in biodiesel is also very low. However, since the sulfur contents in regular gasoline is regulated for environmental reasons, the content of sulfur in biodiesel oil is regulated as well.

	Phosphorus	Sulfur	Remarks
EU	10 ppm max.	10 ppm max.	EN14214
USA	10 ppm max.	15 ppm max.	ASTM D6751

Regulations for phosphorus and sulfur limits in biodiesel fuel (B100)

Rigaku's Mini-Z P, S, Cl Analyzer is suitable for phosphorus analysis in biodiesel for EN14214, ASTM D6751. It is optimized for sub-ppm detection limits of P, S and Cl and features easy operation without chemical treatment of the samples. Easy sample preparation and operation reduces the need for a highly skilled operator. A helium atmosphere is maintained in the spectroscopic chamber and sealing film separates the sample chamber from the spectroscopic chamber, protecting the X-ray tube and the spectrometer in the event of a spilled oil sample.



Calibration curves for phosphorus, sulfur and chlorine using the P, S, Cl Analyzer
 Samples tested were prepared by mixing with hydrocarbons. Measuring time is 300 sec.



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