

# ORCID, CrossRef, and FundRef

연세대학교 생명공학과  
Mycobiology 편집위원장  
과편협 교육분과 부위원장  
반용선

## ORCID

- ❑ Open Research and Contributor ID
- ❑ 개인연구자를 다른 연구자와 구별하는 영구적인 디지털 식별자
- ❑ 논문 투고나 연구비를 신청할 때 연구자와 연구 활동을 자동으로 연결하여 연구업적을 쉽게 알 수 있게 함.

## ORCID 현황

- ❑ ORCID는 2012년 10월 16일 서비스 시작
- ❑ 서비스를 시작한 지 1년도 되지 않았으나 이미 2013년 9월 3일 자로 25만 명이 등록하였고, 2013년 말에는 50만 명이 등록할 것으로 예상
- ❑ 출판사, 정부기관, 대학, 정보관련회사, CrossRef 등이 참여하는 비영리 조직

### ORCID team

ORCID is governed by an elected Board of Directors, majority non-profit, comprised of fourteen members of the global scholarly research community. Membership in the Board of Directors is drawn from and representative of ORCID member organizations. The Board is responsible for establishing general policies for the governance of ORCID, based on a set of core principles, among them openness and transparency. In addition to the Board of Directors, ORCID has several Working Groups, open to the research community.

#### 2013 Board of Directors

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- Laurel L. Haak, Executive Director
- Rebecca Bryant, Director of Community
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- Rob Peters, Lead Developer
- Catalina Oyler, Technical Support and Writing
- Eleese Bohannon-Scott, Office Manager

## ORCID 등록

- ❑ 등록시스템은 개별 연구자에게 무료
- ❑ ORCID를 받아서 연구 활동을 관리할 수 있고 다른 연구자의 업적을 검색할 수 있음.
- ❑ 기관도 회원이 될 수 있는데 기관의 기록과 ORCID 식별자와 연결하고 ORCID 자료를 갱신하고 ORCID에서 최신 정보를 받으며 구성원이나 학생을 ORCID에 등록할 수 있음

## ORCID 정보 취급 범위

- ❑ ORCID 가 취급하는 정보는 민감하지 않은 것으로 이름, 이메일, 기관명과 연구 활동임.
- ❑ 참여 회원의 정보를 보호하기 위하여 미상무부가 정한 Safe Harbor Principles (사용자에게 목적, 제3자 공개, 연락처를 알려야 하며, 제3자 사용이나 인정하기 어려운 사용에 대해서는 opt-out 선택권을 주고, 민감한 사안은 opt-in 선택권 준다.
- ❑ 제3자 역시 같은 고지와 선택을 따름) 을 따른다

## ORCID 운영 원칙 -1

- ❑ 저자나 기여자가 공신력 있는 과정을 통하여 등록하여 학문 사회에서 영구적이고 명확하게 업적을 기록할 수 있도록 지원함.
- ❑ 학문 분야, 지리, 국가, 기관, 경계를 모두 초월함.
- ❑ 연구와 학문 사회에 관심가진 모든 기관이 참가할 수 있음.
- ❑ 서비스에 접근은 투명하고 차별이 없음.

## ORCID 운영 원칙 -2

- ❑ 연구자는 식별자와 연구 업적을 생성, 수정, 유지할 수 있으며 이런 작업은 무료로 가능하다.
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- ❑ 집행부에는 대개 비영리단체가 있으며, 모든 회의나 회계는 공중에 공개하여 투명하게 운영한다.

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<https://orcid.org/signin> 에 방문하여 ID가 있으면 사인하고 들어가고, 없으면

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Register for an ORCID iD

신규로 회원등록을 한다

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### Register for an ORCID iD

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First name



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### Yong-Sun Bahn

<http://orcid.org/0000-0001-9573-5752>

[View Public ORCID Record](#)

Keywords: Mycology, Fungal Geneticist, Fungal Pathogenesis

Websites:

Bahn Lab Homepage

Other IDs:

ResearcherID C-1211-2012

Scopus Author ID 6506207620



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개인정보업데이트

Biography

I'm professor at department of Biotechnology in Yonsei University. I'm a fungal geneticist, who studies fungal virulence and pathogenesis mechanism.

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Essential Roles of the Kar2/BiP Molecular Chaperone Downstream of the UPR Pathway in *Cryptococcus neoformans*: PLoS ONE 2013



Global transcriptome analysis of eukaryotic genes affected by gromwell extract: Journal of the Science of Food and Agriculture 2013



Sulphiredoxin plays peroxiredoxin-dependent and -independent roles via the



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### EDIT PERSONAL INFORMATION

#### Names

First Name

Yong-Sun

Last Name

Bahn

Published Name

Yong-Sun Bahn

Other Names

#### About Me

Biography

I'm professor at department of Biotechnology in Yonsei University. I'm a fungal geneticist, who studies fungal virulence and pathogenesis mechanism.

Keywords

Mycology, Fungal Geneticist, Fungal Pathogenesis

Country

South Korea

#### Websites

Website

Bahn Lab Homepage

www.bahnlab.com

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## ORCID에 연구자 업적 업데이트

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ORCID has been working with many member organizations to make it easy to connect your ORCID ID, and import information from their records. Choose one of the imports wizards to get started.

#### Australian National Data Service (ANDS) Registry

Import your research datasets into ORCID from Australian National Data Service (ANDS) and Research Data Australia (RDA). ANDS is partnering with Australian research institutions and data producing agencies to improve discovery and reusability of research data across many research domains from earth science to technology and engineering.

#### CrossRef Metadata Search

Search CrossRef's comprehensive metadata on journal articles, conference proceedings and monographs. Easily add search results to your ORCID profile.

#### Europe PubMed Central

Europe PubMed Central (Europe PMC) offers this tool to enable you to link anything in Europe PMC to your ORCID. Europe PMC contains all of PubMed, 500K records from Agricola that cannot be found in PubMed, 4 million Patents and 2.6 million full text articles that we share with PMC in the USA.

#### ResearcherID

ResearcherID is a global, multi-disciplinary scholarly research community where members can register for unique identifier, build a profile of their scholarly works, view citation metrics, and search for like-minded researchers.

#### Scopus to ORCID

Import your Identifier, profile and publications. The wizard helps you find the correct Scopus profile and to confirm your publications. You can then import the identifier and list of publications into ORCID. Any changes you make will be submitted to the Feedback team to update your Scopus

## CrossRef Metadata 검색을 통한 업데이트

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### CONNECTING

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### WITH YOUR ORCID RECORD

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has asked for the following access to your ORCID Record

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Read limited info from your ORCID Record

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This application will not be able to see your ORCID password, or other private info in your ORCID Record

Deny

Authorize



## CrossRef Metadata 검색을 통한 업데이트

FundRef Status API Help Yong-Sun Bahn

TYPE

- ☐ Journal Article (385,421)
- ☐ Conference Paper (52,253)
- ☐ Chapter (26,517)
- ☐ Report (661)
- ☐ Book (461)
- ☐ Entry (283)
- ☐ Dissertation (182)
- ☐ Monograph (113)
- ☐ Other (99)
- ☐ Journal Issue (10)

YEAR

- ☐ 2013 (58,242)
- ☐ 2012 (54,605)
- ☐ 2011 (48,898)
- ☐ 2010 (37,745)
- ☐ 2009 (32,320)
- ☐ 2008 (26,440)
- ☐ 2007 (23,890)
- ☐ 2006 (20,060)
- ☐ 2005 (16,446)
- ☐ 2004 (12,416)

OA STATUS

- ☐ Other (442,310)
- ☐ DOAJ (23,712)

PUBLICATION

- ☐ Advanced Materials Research

SORT BY: **RELEVANCE** PUBLICATION YEAR

PAGE 1 OF 466,022 RESULTS

**CO2 sensing in fungi and beyond**  
 Journal Article published Dec 2006 in Current Opinion in Microbiology volume 9 issue 6 on pages 572 to 578  
 Authors: Yong-Sun Bahn, Fritz A Mühlschlegel  
 Other IDs: S1369527406001524  
<http://dx.doi.org/10.1016/j.mib.2006.09.003> IN YOUR PROFILE

**DOAJ Effects of Alcohol Compounds on the Growth and Lipid Accumulation of Oleaginous Yeast Trichosporon fermentans**  
 Journal Article published 5 Oct 2012 in PLoS ONE volume 7 issue 10 on page e46975  
 Authors: Chao Huang, Hong Wu, Li-ping Liu, Wen-yong Lou, Min-hua Zong  
 Editors: Yong-Sun Bahn  
<http://dx.doi.org/10.1371/journal.pone.0046975> ADD TO ORCID

**DOAJ Oxygen and an Extracellular Phase Transition Independently Control Central Regulatory Genes and Conidiogenesis in Aspergillus fumigatus**  
 Journal Article published 5 Sep 2013 in PLoS ONE volume 8 issue 9 on page e74805  
 Authors: Myoung-Hwan Chi, Kelly D. Craven  
 Editors: Yong-Sun Bahn  
<http://dx.doi.org/10.1371/journal.pone.0074805> ADD TO ORCID

**DOAJ Characterization of the Chromosome 4 Genes That Affect Fluconazole-Induced Disomy Formation in Cryptococcus neoformans**  
 Journal Article published 7 Mar 2012 in PLoS ONE volume 7 issue 3 on page e33022

## ResearcherID를 통한 연구업적 업데이트

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**Australian National Data Service (ANDS) Registry**  
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**CrossRef Metadata Search**  
 Search CrossRef's comprehensive metadata on journal articles, conference proceedings and monographs. Easily add search results to your ORCID profile.

**Europe PubMed Central**  
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RESEARCHERID



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Return to My Researcher Profile

Exchange Profile Data Between ResearcherID and ORCID | Add ORCID Publications to: My Publications

My Publications: 33 record(s)

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If My Publications privacy setting is private, the privacy setting of the publications sent to ORCID will be set to limited.

Page 1 of 1 Go

Sort by: Publication Year Results per page: 50

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- ☒ 1. Title: [A Fluconazole-Responsive Mps1/Bwl4-Like Protein, Mps1, Plays Pleiotropic Roles in Antifungal Drug Resistance, Stress Response, and Virulence of \*Cryptococcus neoformans\*](#) (record added 22-Mar-12)  
 Author(s): Song, Min-Hae; Lee, Jang-Won; Kim, Min-Su; et al.  
 Source: Eukaryotic Cell Volume: 11 Issue: 1 Pages: 53-67 Published: JAN 2012  
 Times Cited: 1  
 DOI: 10.1128/EC.05236-11
- ☒ 2. Title: [Cryptococcal Titan Cell Formation Is Regulated by G-Protein Signaling in Response to Multiple Stimuli](#) (record added 22-Mar-12)  
 Author(s): Okagaki, Laura H.; Wang, Yina; Ballou, Elizabeth R.; et al.  
 Source: Eukaryotic Cell Volume: 10 Issue: 10 Pages: 1306-1316 Published: OCT 2011  
 Times Cited: 16  
 DOI: 10.1128/EC.05179-11
- ☒ 3. Title: [Hrk1 Plays Both Hsp1-Dependent and -Independent Roles in Controlling Stress Response and Antifungal Drug Resistance in \*Cryptococcus neoformans\*](#) (record added 22-Mar-12)  
 Author(s): Kim, Seo-Young; Ko, Young-Joon; Jung, Kwang-Woo; et al.  
 Source: Plos One Volume: 6 Issue: 4 Published: APR 13 2011  
 Times Cited: 2  
 DOI: 10.1371/journal.pone.0016769
- ☒ 4. Title: [Multifaceted Roles of Yop1 Phosphotransfer Protein in Viability, Stress Response, and Virulence Factor Regulation in \*Cryptococcus neoformans\*](#) (record added 22-Mar-12)  
 Author(s): Lee, Jang-Won; Ko, Young-Joon; Kim, Seo-Young; et al.  
 Source: Eukaryotic Cell Volume: 10 Issue: 7 Pages: 998-1002 Published: JUL 2011  
 Times Cited: 4  
 DOI: 10.1128/EC.05124-11
- ☒ 5. Title: [Ste50 adaptor protein governs sexual differentiation of \*Cryptococcus neoformans\* via the pheromone-response MAPK signaling pathway](#) (record added 22-Mar-12)  
 Author(s): Lee, Kwang-Ho; Kim, Seo-Young; Park, J.; et al.

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## IMPORT WORKS

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1 | Select profiles   2 | Select profile name   3 | Review publications   4 | Review profile   5 | Send Author ID   6 | Send publications

### Select your Scopus profiles

Please select all profiles that contain publications authored by you and click the next button to continue.

You searched for: Authname (Bahn, Yong-Sun) | [edit](#)   Sort by: Relevancy

All	Authors	Documents	Subject area	Affiliation	City	Country
1	<input checked="" type="checkbox"/> Bahn, Yongsun Bahn, Yong-Sun	42	Nursing, Immunology and Microbiology, Biochemistry, Genetics and Molecular Biology, Agricultural and Biological Sciences, Medicine, Dentistry	Yonsei University	Seoul	South Korea
<a href="#">Show recent documents</a>						
2	<input checked="" type="checkbox"/> Bahn, Yongsun Bahn, Yong-Sun	1	Pharmacology, Toxicology and Pharmaceutics, Biochemistry, Genetics and Molecular Biology	Yonsei University	Seoul	South Korea
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- ❑ CrossMark는 CrossRef에서 운영하며 2012년 4월 27일 첫 서비스를 시작
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- ❑ CrossMark는 CrossRef DOI를 기탁한 모든 내용물에 붙일 수 있음

## CrossMark의 적용예

Acta Crystallographica Section A  
Foundations of Crystallography  
Volume 67, Part 1 (January 2011)

research papers

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Acta Cryst. (2011). A67, 56-62 [ doi:10.1107/S0108767310044892 ]

**PVMR: assembling small helix fragments as structural solutions for molecular replacement**

**F. Jiang and W. Ding**

**Abstract:** A new real-space implementation of the molecular-replacement method is described. The method locates the search model in the target crystal by maximizing the matching between the search-model vectors and the Patterson self and cross vectors. In previous work, a new rotation function was introduced for the molecular-replacement method [Jiang (2008), *Acta Cryst.* D64, 561-566]. This rotation function is calculated by matching the search model directly with both the Patterson self and cross vectors in real space. All the matches are summed and averaged to enhance the overall signal-to-noise ratio for a given orientation of the search model. Recently, to avoid the dependence of the weights derived from the linear regression on the properties of the search model and the target crystal structure, such as secondary structures, space groups and cell parameters, a dynamic correlation coefficient has been designed and used as the total rotation function score [Jiang & Ding (2010), *Chin. Phys. B*, 19, 106101]. This work further extends this idea to the implementation of translation search. A new real- or direct-space translation function has been implemented by matching the cross vectors between the symmetry mates of the search model to the Patterson cross vectors. This method enables effective searching for small helix fragments in the target crystal. Although the solution model assembled by using multiple fragments of helix is insufficient to start *ab initio* phasing of the target crystal, it can be used to identify the known protein folds in the Protein Data Bank that are homologous to the target structure. It can also be combined with other experimental and theoretical models to screen and select for better search models for molecular replacement.

**Keywords:** Patterson vectors; scoring functions; dynamic correlation coefficient; homologous folds.

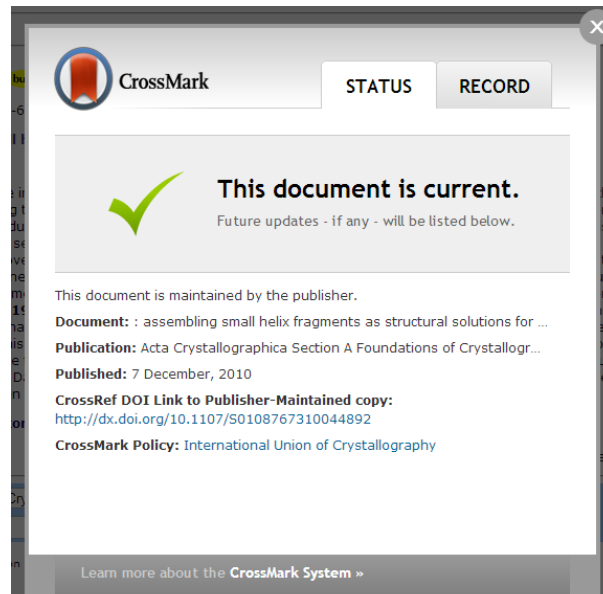
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**Publication:** Acta Crystallographica Section A Foundations of Crystallogr...

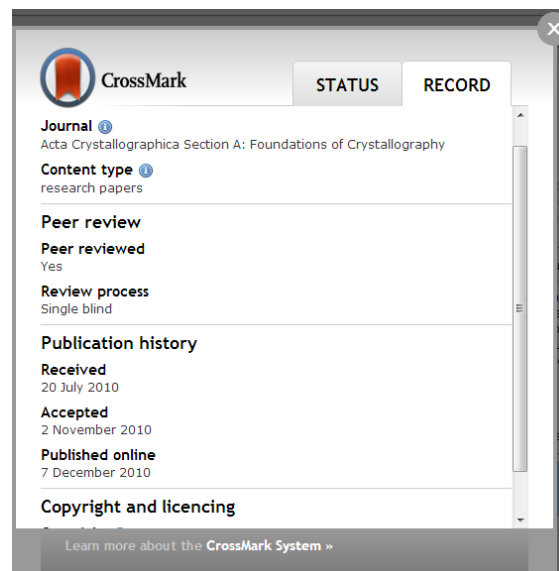
**Published:** 7 December, 2010

**CrossRef DOI Link to Publisher-Maintained copy:**  
<http://dx.doi.org/10.1107/S0108767310044892>

**CrossMark Policy:** International Union of Crystallography

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## CrossMark의 적용예



The image shows a CrossMark record window with a "STATUS" tab and a "RECORD" tab. The "RECORD" tab is active, displaying detailed information about the document, including the journal name, content type, peer review status, publication history, and copyright/licensing information.

**CrossMark** STATUS RECORD

**Journal** ⓘ  
Acta Crystallographica Section A: Foundations of Crystallography

**Content type** ⓘ  
research papers

**Peer review**  
**Peer reviewed**  
Yes

**Review process**  
Single blind

**Publication history**  
**Received**  
20 July 2010  
**Accepted**  
2 November 2010  
**Published online**  
7 December 2010

**Copyright and licencing**

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## CrossMark의 적용예

Acta Crystallographica Section D  
**Biological Crystallography**  
Volume 62, Part 10 (October 2006)

research papers

[html](#) [pdf](#) [cited in](#) [contents of issue](#) [erratum](#) [open access](#)

Acta Cryst. (2006). D62, 1196-1207 [ doi:10.1107/S0907444906030915 ]

Application of the use of high-throughput technologies to the determination of protein structures of bacterial and viral pathogens



M. J. Fogg, P. Alzari, M. Bahar, I. Bertini, J.-M. Betton, W. P. Burmeister, C. Cambillau, B. Canard, M. Carrondo, M. Coll, S. Daenke, O. Dym, M.-P. Egloff, F. J. Enguita, A. Geerlof, A. Haouz, T. A. Jones, Q. Ma, S. N. Manicka, M. Migliardi, P. Nordlund, R. J. Owens, Y. Peleg, G. Schneider, R. Schnell, D. I. Stuart, N. Tarbouriech, T. Unge, A. J. Wilkinson, M. Wilmanns, K. S. Wilson, O. Zimhony and J. M. Grimes

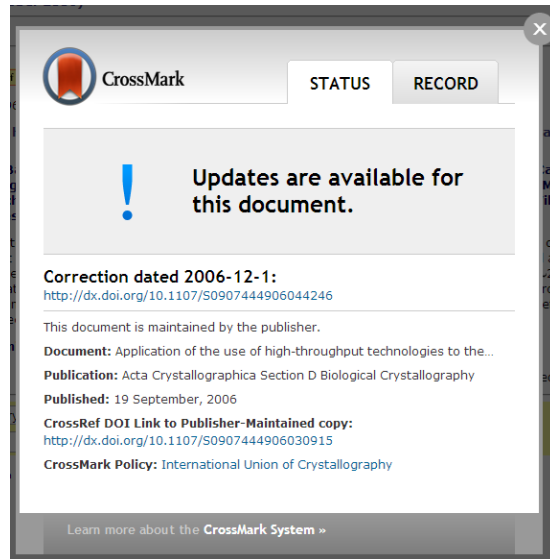
**Abstract:** The Structural Proteomics In Europe (SPINE) programme is aimed at the development and implementation of high-throughput technologies for the efficient structure determination of proteins of biomedical importance, such as those of bacterial and viral pathogens linked to human health. Despite the challenging nature of some of these targets, 175 novel pathogen protein structures (~220 including complexes) have been determined to date. Here the impact of several technologies on the structural determination of proteins from human pathogens is illustrated with selected examples, including the parallel expression of multiple constructs, the use of standardized refolding protocols and optimized crystallization screens.

**Keywords:** automation; miniaturization; cloning; expression; viruses; bacteria.

## CrossMark의 적용예

The screenshot shows a web browser window displaying a CrossMark document. At the top, there is a CrossMark logo and two buttons: "STATUS" and "RECORD". Below this, a large blue exclamation mark icon is followed by the text "Updates are available for this document." Underneath, it states "Correction dated 2006-12-1:" and provides a URL: <http://dx.doi.org/10.1107/S0907444906044246>. The text continues: "This document is maintained by the publisher." followed by "Document: Application of the use of high-throughput technologies to the...". Below that, it says "Publication: Acta Crystallographica Section D Biological Crystallography" and "Published: 19 September, 2006". Then, it provides a "CrossRef DOI Link to Publisher-Maintained copy:" with the URL <http://dx.doi.org/10.1107/S0907444906030915>. Finally, it mentions "CrossMark Policy: International Union of Crystallography". At the bottom, there is a link: "Learn more about the CrossMark System »".

## CrossMark의 적용예



The screenshot shows a CrossMark notification window. At the top left is the CrossMark logo. To its right are two tabs: 'STATUS' and 'RECORD'. Below the tabs is a large blue exclamation mark icon followed by the text 'Updates are available for this document.' Below this, it says 'Correction dated 2006-12-1:' followed by a URL: <http://dx.doi.org/10.1107/S0907444906044246>. Below the URL, it states 'This document is maintained by the publisher.' Then, it lists 'Document: Application of the use of high-throughput technologies to the...', 'Publication: Acta Crystallographica Section D Biological Crystallography', and 'Published: 19 September, 2006'. Next, it says 'CrossRef DOI Link to Publisher-Maintained copy:' followed by a URL: <http://dx.doi.org/10.1107/S0907444906030915>. Below that, it says 'CrossMark Policy: International Union of Crystallography'. At the bottom, there is a link: 'Learn more about the CrossMark System »'.

## CrossMark의 적용예

Acta Crystallographica Section D  
**Biological Crystallography**  
Volume 62, Part 12 (December 2006)

addenda and errata

[html](#) [pdf](#) [open access](#)

Acta Cryst. (2006). D62, 1571 [ doi:10.1107/S0907444906044246 ]

Application of the use of high-throughput technologies to the determination of protein structures of bacterial and viral pathogens. Corrigendum

M. J. Fogg, P. Alzari, M. Bahar, I. Bertini, J.-M. Betton, W. P. Burmeister, C. Cambillau, B. Canard, M. A. Carrondo, M. Coll, S. Daenke, O. Dym, M.-P. Egloff, F. J. Enguita, A. Geerlof, A. Haoz, T. A. Jones, Q. Ma, S. N. Manicka, M. Migliardi, P. Nordlund, R. J. Owens, Y. Peleg, G. Schneider, R. Schnell, D. I. Stuart, N. Tarbouriech, T. Unge, A. J. Wilkinson, M. Wilmanns, K. S. Wilson, O. Zimhony and J. M. Grimes

**Abstract:** A correction is made to the name of one of the authors in Fogg *et al.* (2006), *Acta Cryst.* D62, 1196-1207.

**Keywords:** automation; miniaturization; cloning; expression; viruses; bacteria.



CrossMark

## FundRef

❑ Funder identification service 서비스로 CrossRef에 기탁한 출판물에서 연구비 정보를 표준을 만들어 제공.

❑ 2013년 5월 정식으로 출범하여 서비스를 시작

## 왜 FundRef가 필요할까?

❑ 표준화된 연구비지원에 대한 이름이나 메타자료가 없어서 텍스트 마이닝이나 분석이 어렵다.

❑ 연구비 지원 기관도 지원한 결과물을 쉽게 찾기가 어렵다

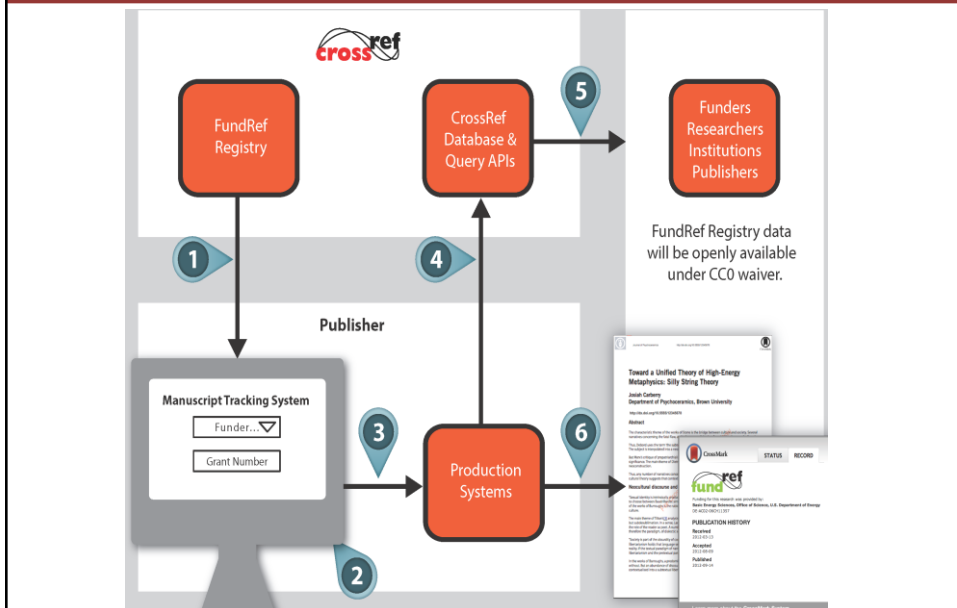
➢ 미국 NIH 에서는 Medline 에 반드시 그 연구가 미국 정부 연구비 지원 받은 것인지 여부를 기록하게 하였고 연구비 번호를 기록한다. 그럼으로써 정부 연구비 지원한 논문을 쉽게 추적할 수 있고 또한 국민에게도 쉽게 연구비가 이렇게 효율적으로 쓰였다는 것을 알릴 수 있다.



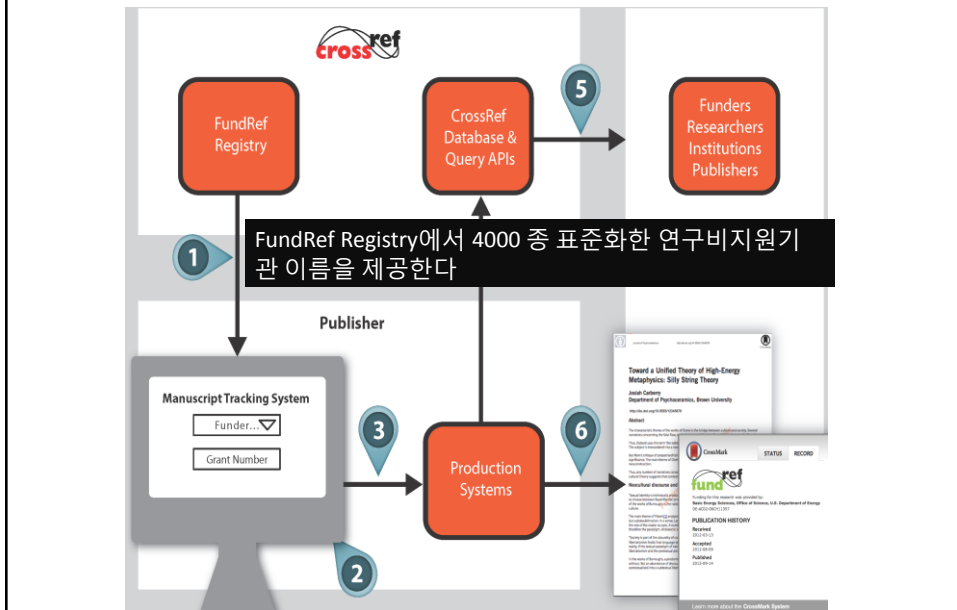
## 왜 FundRef가 필요할까?

- ❑ 발행인도 출판하는 연구를 지원한 주요 기관을 쉽게 추적하기 어렵다.
- ❑ 연구자 소속 연구 기관에서도 구성원의 학문 업적에 대한 주요 지원기관을 쉽게 확인하기 어렵다.

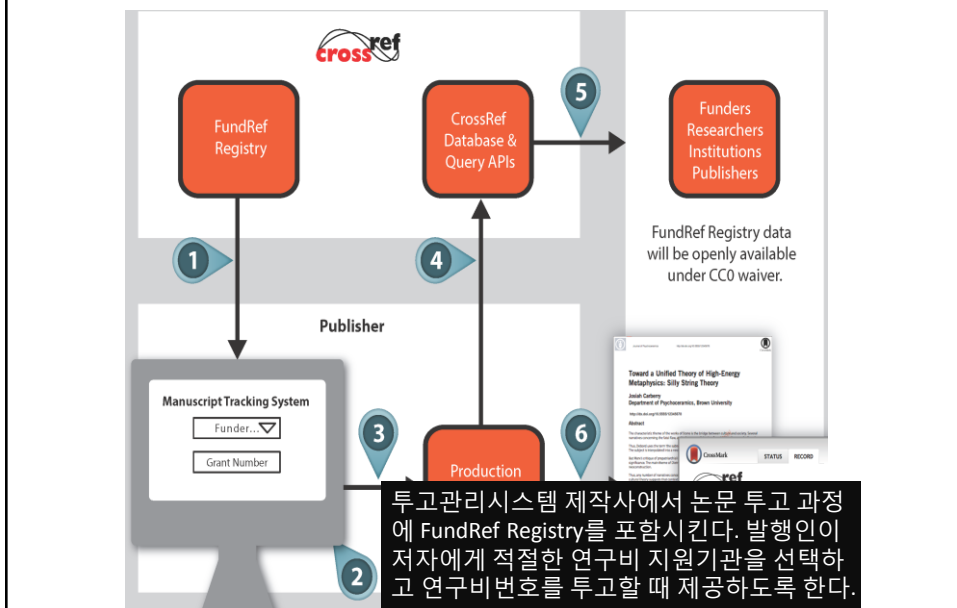
## FundRef workflow



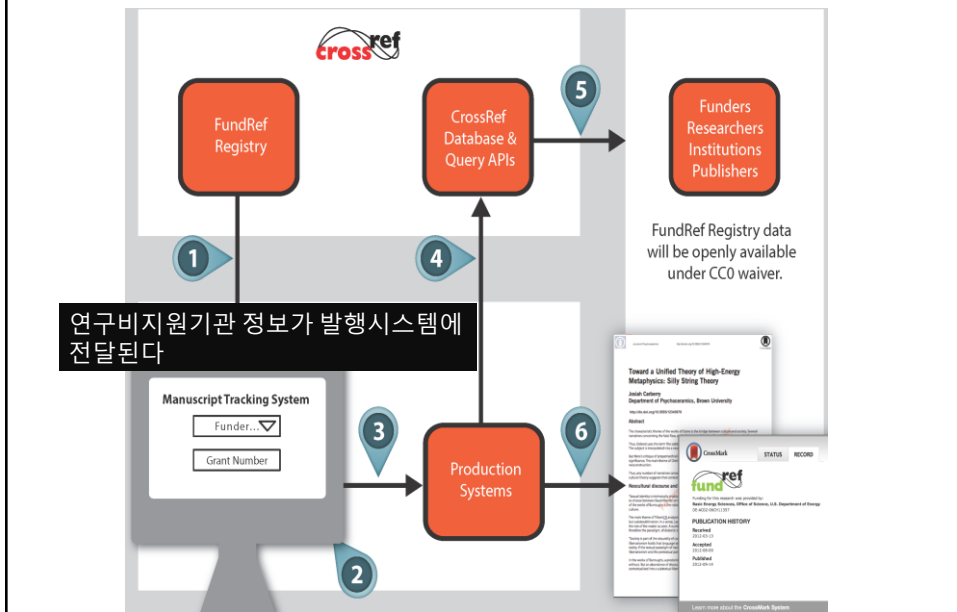
## FundRef workflow



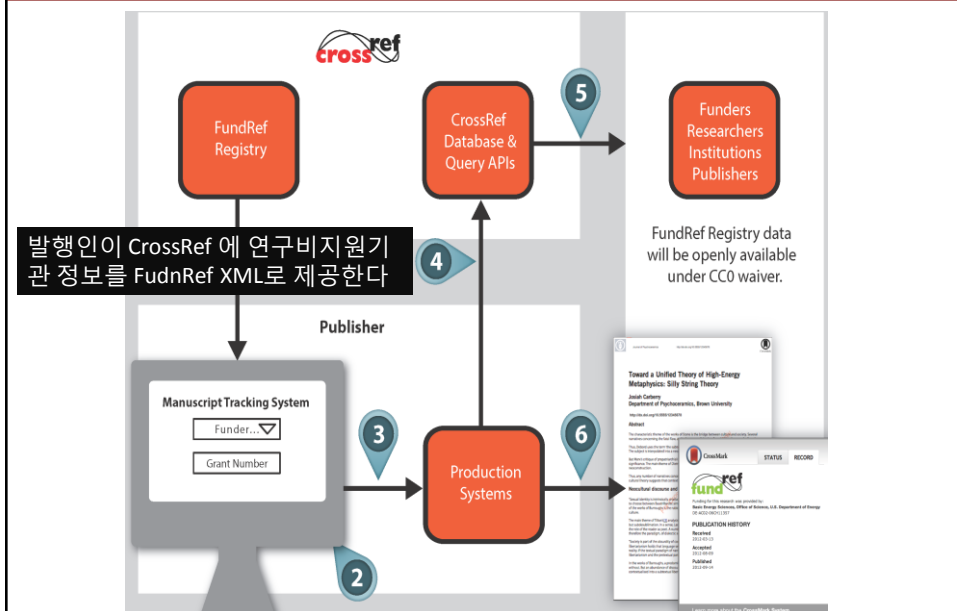
## FundRef workflow



## FundRef workflow



## FundRef workflow



# FundRef workflow

The diagram illustrates the FundRef workflow, a process for linking research outputs to their funding sources. The workflow is divided into two main sections: the Publisher side and the Funders side.

**Publisher Side:**

- Manuscript Tracking System:** The process begins here, where a manuscript is submitted. It includes a dropdown menu for "Funder..." and a field for "Grant Number".
- Production Systems:** The manuscript is then processed through the Production Systems, which are connected to the Manuscript Tracking System via a bidirectional arrow (labeled 3).
- CrossRef Database & Query APIs:** The Production Systems interact with the CrossRef Database & Query APIs (labeled 4).
- FundRef Registry:** The CrossRef Database & Query APIs interact with the FundRef Registry (labeled 5).

**Funders Side:**

- Funders Researchers Institutions Publishers:** The FundRef Registry provides data to these entities.
- Data Availability:** A note states: "FundRef Registry data will be openly available under CC0 waiver."

**Additional Information:**

- A screenshot of the CrossRef website is shown, displaying the "Toward a Unified Theory of High-Energy Metaphysics: Sisy String Theory" by Jason Calvert, Department of Physics, Brown University.
- A screenshot of the FundRef website is shown, displaying the "PUBLICATION HISTORY" for the same work, listing the journal, volume, issue, and date.

# FundRef workflow

## FundRef 서비스로 누가 어떤 혜택을 받는가?

- ① 연구비지원기관: 연구비 지원 결과를 쉽게 추적할 수 있다.
- ② 저자: 투고 시스템에서 쉽게 입력 가능하다.
- ③ 연구기관: 구성원의 연구 성과를 쉽게 추적할 수 있다.
- ④ 발행인: 연구비 제공 기관을 쉽게 분석할 수 있다.
- ⑤ 독자와 대중: 국민에게 연구비 사용 결과물을 더 투명하게 제공한다.

## FundRef에는 어떻게 참여하는가 – 연구비 지원기관

- ① FundRef 등록 담당자(fundref.registry@crossref.org) 에게 메일을 보내어 정보를 제공하면 심사 후 등록된다.
- ② 제공할 정보는 연구비지원기관 이름(영문명)이고 URL 주소이며 기관 설명이다. 왜냐하면 제대로 된 연구비 지원기관인지 확인하는 과정이 필요하기 때문이다.
- ③ 주요 정부산하 연구비 지원 기관은 물론, 모든 대학이 교내 연구비를 지원하므로 등록이 필요하다. 또한 상업회사에서도 연구비를 지원하므로 등록이 필요하다. 우리나라는 연구비 규모가 정부 지원액보다 상업회사가 2 배가 넘는다. 정부 산하 기관은 국가 차원에서 일괄 정리하여 제공하는 것도 좋은 방법이다. 또한 대교협 같은 기관은 대학 정보를 모두 가지고 있으므로 모든 대학과 협력하여 제공하는 것도 좋을 것이다.

## FundRef에는 어떻게 참여하는가 – 연구비 지원기관

Metadata Search  Sign in with ORCID

beta  
**fundref**  
search

Q National Research Foundation X

National Foundation for Cancer Research United States  
National Research Foundation South Africa  
National Organization for Hearing Research Foundation United States  
Danish National Research Foundation Denmark  
Arthritis National Research Foundation United States  
National Research Foundation-Prime Minister's office, Republic of Singapore Singapore

## FundRef에는 어떻게 참여하는가 – 연구비 지원기관

crossref.org

Contact

Members Area

ABOUT CROSSREF FOR PUBLISHERS FOR LIBRARIES FOR AFFILIATES FOR RESEARCHERS



### FundRef Registry

The FundRef Registry provides a common taxonomy of over 4000 funding body names that FundRef participants should use to normalize Funder Names and IDs for deposit.

The list should be used to present authors with a pre-populated "Funder Name" option at the time of submission, and can also be used to match the funding names in backfile content if this data has been previously extracted.

The list is available to download as an RDF file, and is freely available under a CC0 license waiver.

**DOWNLOAD 4.2 MB (RDF)**

#### Version History

- **November 19th 2013**  
Bug fixes to correct some labeling errors in the RDF. Funder count: 4,817.
- **November 6th 2013**  
New Registry file incorporating corrected hierarchy information for the US Department of Energy, separating out second and third tier organisations. Funder count: 4,817.
- **May 28th 2013**  
First Registry File. Funder count: 4,785



To the extent possible under law, CrossRef has waived all copyright and related or neighboring rights to the FundRef Registry.

#### Additional Options

Download a CSV file of the funder names and identifiers in the FundRef Registry.

To suggest modifications to the registry, contact [fundref.registry@crossref.org](mailto:fundref.registry@crossref.org). For more information about FundRef, visit <http://www.crossref.org/fundref>.

Sign up for CrossRef updates.

Email  Go



## FundRef에는 어떻게 참여하는가 – 연구비 지원기관

### FUNDING AGENCIES

Funding Agencies do not need to do anything to join FundRef. Publishers will deposit funding information from content that they publish, and anyone can search this data using [FundRef Search](#). Feedback from funding agencies, or questions about FundRef can be sent to [fundref@crossref.org](mailto:fundref@crossref.org)

### PUBLISHERS

1. Sign up for FundRef by agreeing to the simple Terms and Conditions. There are no fees for participating in FundRef.
2. Incorporate the [FundRef Registry](#) into your submission system.
3. Ask authors to input funding information on submission using the controlled vocabulary from the Registry.
4. Make sure your production system can support the [additional FundRef metadata elements](#)
5. Submit standardized FundRef data to CrossRef with your regular metadata deposits. Funder IDs from the FundRef Registry must be included for any funder that is listed in the Registry.
6. Query CrossRef for funding data.

For an overview of FundRef watch our 20 minute [pre-recorded FundRef Webinar](#) (.mov)

Technical information on how to deposit FundRef data within the CrossRef schema can be found in [FundRef Help](#)

### THE FUNDREF REGISTRY

The [FundRef Registry](#) is a taxonomy of international funder names, IDs, abbreviations, and alternate names donated by Elsevier. This controlled vocabulary is freely available and should be incorporated into manuscript submission systems or used to reconcile funder names in backfile content ahead of deposit.

### PARTICIPATING PUBLISHERS

American Chemical Society (ACS)  
American Diabetes Association  
American Institute of Physics (AIP)  
American Physical Society (APS)  
American Psychiatric Publishing  
American Psychological Association (APA)  
American Society of Neuroradiology (ASNR)  
Association for Computing Machinery (ACM)  
BioMed Central  
BioScientifica  
Copernicus Publications (Copernicus GmbH)  
eLife Sciences Organisation  
FapUNIFESP (SciELO)  
Hindawi Publishing Corporation  
IEEE, Inc.

## FundRef에는 어떻게 참여하는가 – 발행인(학회)

- ① FundRef 에 사인한다.
- ② 투고관리시스템 제작사에 FundRef 등록을 포함시켜 달라고 요청한다.
- ③ XML 제작 회사에 FundRef 메타자료를 CrossRef Schema 에 맞추어 기탁하도록 요청한다.
- ④ 투고자에게 연구비 정보를 선택하라고 요청하고 투고 규정에 삽입한다.
- ⑤ FundRef 자료를 CrossRef에 제공한다.
- ⑥ FundRef 자료를 CrossMark 자료에 넣는다(선택사항)
- ⑦ CrossRef를 검색하여 연구비 정보를 찾는다.
- ⑧ 참여하는 데 아무런 별도 경비 없고 단지 CrossMark에 참여하면 경비가 든다(2011년 이후는 건당 0.2 미국달러, 2010년도까지 과거 분은 0.02 미국달러).

## FundRef에는 어떻게 참여하는가 – 연구자

- ① 투고할 때 FundRef 정보를 완성한다.
- ② CrossMark Record tab에서 FundRef 정보를 본다
- ③ FundRef Search에서 연구비 정보를 확인한다.

감사합니다