

Data citation and persistent identifiers: the DataCite approach

Elizabeth Newbold, The British Library

April 30, 2013

Presented at PREPARDE workshop on linking
datasets and articles for publication



What is DataCite?

The image shows the DataCite logo and tagline on a blue background with a network diagram of nodes and lines. The logo 'DataCite' is in a white box, and the tagline 'Creating a global citation framework for data' is in white text below it.

DataCite

Creating
a global
citation
framework
for data

- Established in 2009 (December)
- A member of the International DOI Foundation
- A Registration Agency for DOI names
- Not for profit organisation
- 18 full members from Europe, North America, Asia and Australia
- Members work with data centres in their own countries
- Provide a shared infrastructure for minting DOIs

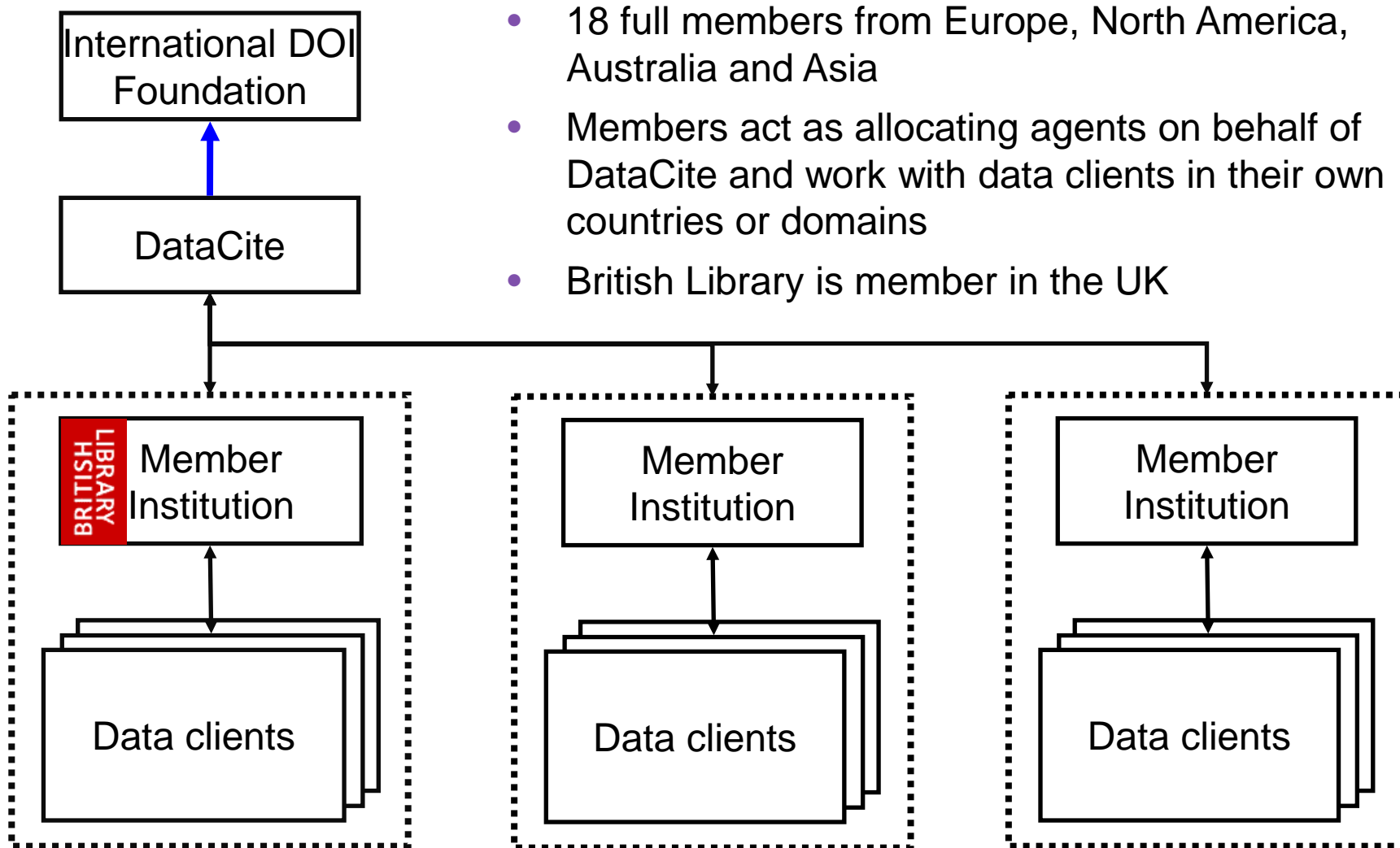
A global registration agency with local representation



SND Swedish National Data Service



DataCite structure



Stepping back - why the need?

Finding data it not easy!

- No widely used methods to **identify** and **locate** data
 - How can data be found and reused?
- No widely used method to **cite** data
 - How can researchers get credit for data sharing
 - How can data creators obtain credit of dataset creation efforts
- No effective way to **link** between articles and datasets

Why use DOIs?

- Global
- Widely adopted - most **widely used** identifier for research articles
 - Permits the scientists and publishers to use the same syntax and technical infrastructure for datasets and articles
- Governance and infrastructure
 - Standardised - ISO 26324:2012

The **Digital Object Identifier** is a persistent identifier that directs users to an object, even if it changes location.

If an object moves, the new location is given to the existing DOI, so that it directs users to the **same object in the new location.**

Back to basics: Anatomy of a DOI

- A DOI is formed of a prefix, in the form of “10.#####” and a suffix, separated by /
- Assign a prefix to data centres – unique to an organisation
- The format of the suffix is determined by the data centre –unique for each object

10.5072/chosen_by.DataCentre-1



Prefix Suffix

- These are used to form URLs by adding the resolving domain, e.g.:

http://dx.doi.org/10.5072/chosen_by.DataCentre-1

What is expected of data centres?

We supply DOIs for datasets as long as a data centre:

- Provides **mandatory metadata** for its datasets
- Provides a **landing page** for each dataset
- Can maintain **working URLs** for its registered datasets
- Has trusted **curation and preservation policies** in place

Open Resolution Target

- DOIs must resolve to a publicly accessible landing page
- The landing page must be open
- Describe the data objects and include at least the mandatory metadata and DOI

Economic and Social Data Service



Economic and Social Data Service

About

Data

Access and support

Resources

Offer and deposit

News

Events

Which service?

Select service

National Child Development Study: Sweep 4 Feasibility Study and Tobacco Research Council Study, 1978

A new Digital Object Identifier (DOI) is assigned to the data collection each time there is a major change to data, documentation or metadata. The new DOI will resolve to an updated version of this page containing a log of changes to this data collection since the allocation of its first DOI. The DOI system supports resource discovery and simplifies citation for users of data collections. Data producers benefit directly through increased visibility of their work.

10.5255/UKDA-SN-2025-1

Citation:

National Children's Bureau, *National Child Development Study: Sweep 4 Feasibility Study and Tobacco Research Council Study, 1978* [computer file]. Colchester, Essex: UK Data Archive [distributor], 1984. SN: 2025, <http://dx.doi.org/10.5255/UKDA-SN-2025-1>

Change log:

7 October 2011: DOI created

Minor changes

5 April 2012: Minor changes to catalogue record

11 April 2012: Minor changes to catalogue record

[Full catalogue record >](#)

This is the latest release

Maintaining persistence

- The ‘persistence’ of identifiers can only be determined by the holders of the data
- So data must be stored some where that is **accessible**, and **well managed** for **the long term**
- This means that we need to make sure data centres we work with are appropriately managed for data curation and preservation

Data Discovery

- Mandatory metadata must be provided according to the DataCite metadata scheme
- Metadata must be made freely available for discovery purposes
- Develop and implement suitable quality control measures to ensure compliance with the metadata scheme



Aims of the metadata schema

“...a core list of metadata properties chosen for accurate identification of data for citation and retrieval purposes...”

- Support citation and discovery of datasets
- Must be suitable for all types of data
- Must work with all disciplines and subjects – domain agnostic
- Do this in the simplest manner

The Metadata Schema – mandatory properties

DataCite Metadata Schema: <http://schema.datacite.org/>

- Identifier (with type attribute)
 - A unique string that identifies a resource – the allowed value is the DOI
- Creator (with type and name identifier attributes)
 - The main researchers involved in producing the dataset
- Title (with optional type attribute)
 - A name by which the resource is known
- Publisher
- PublicationYear
 - Year in which the data was or will be made publicly available

Citation

The mandatory metadata elements are required for registration and minting DOIs but also provide the elements for the citation.

Recommend citation style:

Creator (Publication Year): Title. Publisher. Identifier

Rees, A.P.; (2012): Impact of phosphate and iron fertilisation on rates of nitrogen fixation in surface waters by stable-isotope mass spectrometry during the FEEP programme cruise PO311. British Oceanographic Data Centre (BODC), Natural Environment Research Council (NERC).

<http://dx.doi.org/10.5285/6B0962C8-574B-473B-A18A-1F9AC95AA7BF>

Metadata

- Optional metadata elements
 - Subject
 - Contributor
 - Date
 - Language
 - Resource Type
 - Alternate Identifier
 - **Related Identifier**
 - Size
 - Format
 - Version

IsReferencedBy

http://search.datacite.org/ui?q=relatedIdentifier:*		Page	Safety	Tools
contributor	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.5284/1007840			
creator	Land at Hudson's Field, Salisbury, Wiltshire	#2		
publicationYear	doi:10.5284/1000135 Wessex Archaeology			
publisher	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.5284/1007804			
language	East Tytherley Manor House, East Tytherley, Hampshire	#3		
refQuality	doi:10.5284/1000142 Wessex Archaeology			
has_metadata	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.5284/1007363			
	Timsbury Lake, Romsey, Hampshire	#4		
	doi:10.5284/1000176 Wessex Archaeology			
	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.5284/1008310			
	Land Warfare Centre, Warminster	#5		
	doi:10.5284/1000149 Wessex Archaeology			
	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.5284/1008280			
	Genomic data from Escherichia coli O104:H4 isolate TY-2482	#6		
	doi:10.5524/100001 Dataset : GigaDB Dataset Li, D • Xi, F • Zhao, M • Chen, W • Cao, S • (et. al.)			
	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.1056/NEJMoa1107643			
	Genomic data from the Chinese Rhesus macaque (Macaca mulatta lasiota)	#7		
	doi:10.5524/100002 Dataset : GigaDB Dataset Yan, G • Zhang, G • Fang, X • Zhang, Y • Li, C • (et. al.)			
	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.1038/nbt.1992			
	Genomic data from the crab-eating macaque/cynomolgus monkey (Macaca fascicularis)	#8		
	doi:10.5524/100003 Dataset : GigaDB Dataset Yan, G • Zhang, G • Fang, X • Zhang, Y • Li, C • (et. al.)			
	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.1038/nbt.1992			
	Genomic data from the giant panda (Ailuropoda melanoleuca)	#9		
	doi:10.5524/100004 Dataset : GigaDB Dataset Li, R • Fan, W • Tian, G • Zhu, H • He, L • (et. al.)			
	<i>relatedIdentifier:</i> IsReferencedBy:DOI:10.1038/nature08696			
	The genomic sequence of the Chinese hamster ovary (CHO) K1 cell line (Cricetulus griseus)	#10		
	doi:10.5524/100005 Dataset : GigaDB Dataset			

IsCitedBy

publicationYear	Kohler, Martin • Kalthoff, Norbert <i>relatedIdentifier:</i> IsCitedBy:DOI:10.1002/qj.686	
publisher	Climate change projections for the Greater Alpine Region "CC_GAR" doi:10.5675/BFG_CC_GAR_2011 Dataset : Dataset	#3
language	Dr. Enno Nilson • Peter Krahe <i>relatedIdentifier:</i> IsCitedBy:DOI:10.	
refQuality	Ratings of sweets [version 1] doi:10.5881/RATINGS-OF-SWEETS Lukasz Kidzinski <i>relatedIdentifier:</i> IsCitedBy:DOI:10.5881/RATINGS-OF-SWEETS	#4
has_metadata	Internet Ad2 [version 1] doi:10.5881/INTERNET-AD2 i Bayer <i>relatedIdentifier:</i> IsCitedBy:DOI:10.5881/INTERNET-AD2	#5
	Szenarienstudie für das Abflussregime des Rheins doi:10.5675/BFG_KLIWAS_ABFLUSSRHEIN_IKSR_WORKSHOP Text : NonGeographicDataset Moser, Hans • Nilson, Enno <i>relatedIdentifier:</i> IsCitedBy:DOI:10.	#6
	Chars74K Kannada hnd [version 3] doi:10.5881/CHARS74K-KANNADA-HND Teofilo de Campos <i>relatedIdentifier:</i> IsCitedBy:DOI:10.5881/CHARS74K-KANNADA-HND	#7
	Chars74K English hnd [version 12] doi:10.5881/CHARS74K-ENGLISH-HND Teofilo de Campos <i>relatedIdentifier:</i> IsCitedBy:DOI:10.5881/CHARS74K-ENGLISH-HND	#8
	Chars74K Kannada img [version 5] doi:10.5881/CHARS74K-KANNADA-IMG Teofilo de Campos <i>relatedIdentifier:</i> IsCitedBy:DOI:10.5881/CHARS74K-KANNADA-IMG	#9
	(Table 1) Benthic foraminiferal distribution at ODP Site 127-794 doi:10.1594/PANGAEA.770908 Dataset : Dataset Nomura, Ritsuo <i>relatedIdentifier:</i> IsCitedBy:DOI:10.2973/odp.proc.sr.127128-1.187.1992	#10

Examples

DataCite Content Service Beta

doi:10.5523/BRIS.12MJTNRTSDJFS17SL4PQ2UCQRK

This page represents DataCite's metadata for *doi:10.5523/BRIS.12MJTNRTSDJFS17SL4PQ2UCQRK*.

For a landing page of this dataset please follow <http://dx.doi.org/10.5523/BRIS.12MJTNRTSDJFS17SL4PQ2UCQRK>

Citation David Matthews; (2012): Integrated Omics - Human; University of Bristol.

<http://dx.doi.org/10.5523/BRIS.12MJTNRTSDJFS17SL4PQ2UCQRK> [RIS](#) [BIBTEX](#)

Descriptions

Abstract

This is an integrated data set of transcriptomic and proteomic data for a set of cells infected with a human virus over time. This raw data will be available to any academic who requests it once the paper has been accepted. Vanessa C Evans, Gary Barker, Kate J Heesom, Jun Fan, Conrad Bessant & David A Matthews, 2012. 'De novo derivation of proteomes from transcriptomes for transcript and protein identification', Nature Methods, 2012/11/11/ online, accessed 29 November 2012, ISSN: 1548-7105.

Subjects

proteomics
transcriptomics

Language

eng

Other formats

[text/html](#)
[application/x-datacite+xml](#)
[application/vnd.datacite.datacite+xml](#)

Join Date: Sep 2011
Location: Oslo, Norway
Posts: 21

proteins can be identified by searching genome database.

I suppose difference is mostly due to sample prep used. The articles with the deep coverage are FASP-based if I remember correctly, +4 hour gradients etc. The first article mentioned here is 1d gel fractionated instead, slightly above 2 hour gradient. I have data here in my lab with same sample ran in similar comparison (i.e., MED-FASP 6 fractions 4h grad, or 1d-gel 15 fractions 2h grad) and I get double the amount of IDs in the FASP preparation using a QExc.

Reply With Quote

01-09-2013 06:42 AM

#8

Davidbristol

Proton Member



Join Date: Jan 2013
Posts: 1

Hi everyone,

Thanks for your interest and discussion of our paper, (I'm the senior author). Thought I'd join in the discussion if thats OK! A couple of things to say is that firstly it is true to say that the number of proteins identified is indeed a limitation of the dataset and not the PIT method so I would expect that larger datasets would get larger numbers of hits (the original experiments were done almost 2 years ago!!). Secondly, the big benefit to me as a virologist is that the method copes with more than one genome in the sample under analysis. Thirdly, on the question of dataset size and FDR, we were concerned about that which is why we included data on the size of the search space in each case (Table 2 I think in the paper). Fourthly, the problem of isoform assignment is one we are wrestling with right now!! I would say that the problem is easier in some respects as, if you look at the information attached to the GFF3 data files generated by PIT, we can assign a peptide to the exon number on the transcript and we are hopeful that will help but it is a problem to be sure. Fifthly (and finally?) you can access all the data in its raw format directly from one site now at the University of Bristol (RNAseq files and ms/ms spectra) using the following link:

<http://dx.doi.org/10.5523/bris.12mjt...s17sl4pq2ucqrk>

As you can see it has a DOI attached to it which means (I think) this should be permanently accessible to anyone who wants to dig into it for themselves. This is very important to us as we think access to this kind of matched dataset is going to be useful for others developing this kind of bespoke analysis. Anyway if anyone has more questions I'm more than happy to help (I should say, though, that my co-author Conrad Bessant is the real ms/ms expert...!).

Reply With Quote

01-15-2013 10:58 AM

#9



Metadata shows a related identifier



doi:10.5524/100002

This page represents DataCite's metadata for doi:10.5524/100002

For a landing page of this dataset please follow <http://dx.doi.org/10.5524/100002>

Citation Yan, G; Zhang, G; Fang, X; Zhang, Y; Li, C; Ling, F; Cooper, DN; Li, O; Li, Y; van Gool, AJ; Du, H; Chen, J; Chen, R; Zhang, P; Huang, Z; Thompson, JR; Meng, Y; Bai, Y; Wang, J; Zhuo, M; Wang, T; Huang, Y; Wei, L; Li, J; Wang, Z; Hu, H; Le, L; Stenson, PD; Li, B; Liu, X; Ball, EV; An, N; Huang, Q; Zhang, Y; Fan, W; Zhang, X; Li, Y; Wang, W; Katze, MG; Su, B; Nielsen, R; Yang, H; Wang, J; Wang, X; Wang, J. (2011): Genomic data from the Chinese Rhesus macaque (*Macaca mulatta lasiota*). *IGLSolence*. <http://dx.doi.org/10.5524/100002>  

Descriptions

Abstract The Chinese rhesus macaque (*Macaca mulatta lasiota*) is a subspecies of rhesus macaques that mainly resides in western and central China. Due to their anatomical and physiological similarity with human beings, macaques are a common laboratory model. Also, as several macaques species have been sequenced, such as the Indian rhesus macaque and the crab-eating macaque, examination of the Chinese rhesus macaque (CR) genome offers interesting insights into the entire *Macaca* genus. The DNA sample for data sequencing and analyses was obtained from a five-year old female CR from southwestern China. The genome was sequenced on the IlluminaGAIIx platform, from which 142-Gb of high-quality sequence, representing 47-fold genome coverage for CR. The total size of the assembled CR genome was about 2.84 Gb, providing 47-fold on average. Scaffolds were assigned to the chromosomes according to the synteny displayed with the Indian rhesus macaque and human genome sequences. About 97% of the CR scaffolds could be placed onto chromosomes.

Resource type

Dataset GigaDB Dataset

Subjects Genomic

License <http://creativecommons.org/publicdomain/zero/1.0/>

Size 1 GB

Language eng

Dates

Available 2011-07-06

Updated 2012-04-27

Related Identifiers

IsReferencedBy doi:[10.1038/nbt.1992](https://doi.org/10.1038/nbt.1992)

Other formats

[text/html](#)

[application/vnd.datacite+xml](#)

[application/vnd.datacite.datacite+xml](#)

[application/vnd.datacite+text](#)

[application/vnd.datacite.datacite+text](#)

[application/rdf+xml](#)

[text/turtle](#)

[application/x-bibtex](#)

[application/x-research-info-systems](#)

[application/citeproc+json](#)

[application/vnd.citationstyles.csl+json](#)

Linking from the related identifier to the journal article

nature
biotechnology

Search Advanced search

Login Cart

[nature.com](#) ▶ [journal home](#) ▶ [archive](#) ▶ [issue](#) ▶ [research](#) ▶ [letter](#) ▶ [full text](#)

NATURE BIOTECHNOLOGY | RESEARCH | LETTER **OPEN**



Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques

Guangmei Yan, Guojie Zhang, Xiaodong Fang, Yanfeng Zhang, Cai Li, [Fei Ling](#), David N Cooper, Qiye Li, Yan Li, Alain J van Gool, Hongli Du, Jiesi Chen, Ronghua Chen, Pei Zhang, Zhiyong Huang, John R Thompson, Yuhuan Meng, Yinqi Bai, Jufang Wang, Min Zhuo, Tao Wang, Ying Huang, Liqiong Wei, Jianwen Li, Zhiwen Wang *et al.*

[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

Nature Biotechnology, 29, 1019–1023, (2011) | doi:10.1038/nbt.1992

Journal home

Current issue

For authors

Subscribe

E-alert sign up

RSS feed

[Click here](#) to see statistics

SCIENTIFIC REPORTS

News and Views

by Zhang *et al.*

Comprehensive studies of the kinome set the stage for discovering the next generation of kinase-

DOI in journal article

To characterize the polymorphisms of several important variants between the CE and CR macaques, we carried out a population survey in 33 unrelated CE macaque individuals of Vietnamese origin and 28 CR macaque individuals using PCR amplification and sequencing.

Accession codes.

The CR macaque (*M. mulatta*) and the CE macaque (*M. fascicularis*) whole genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers [AEHK000000000](#) and [AEHL000000000](#). The versions described in this Letter are [AEHK01000000](#) and [AEHL01000000](#). All short read data have been deposited into the Short Read Archive under accession numbers [SRA023855](#) and [SRA023856](#). Raw sequencing data of transcriptome have been deposited in Gene Expression Omnibus as [GSE29629](#). Genome assemblies are also available using the following data DOIs at our CLiMB repository: [doi:10.5524/100002](#) and [doi:10.5524/100003](#) <<http://dx.doi.org/10.5524/100002> and < <http://dx.doi.org/10.5524/100003>>.

- Accession codes

[Main](#) • [Methods](#) • [Accession codes](#) • [References](#) • [Acknowledgments](#) • [Author information](#) • [Supplementary information](#)

Referenced accessions

DDBJ/GenBank/EMBL	Gene Expression Omnibus	Sequence Read Archive
AEHK000000000	GSE29629	SRA023855
AEHL000000000		SRA023856
AEHK01000000		
AEHL01000000		

- References

[Main](#) • [Methods](#) • [Accession codes](#) • [References](#) • [Acknowledgments](#) • [Author information](#) • [Supplementary](#)

Data DOI and related manuscript both on the landing page

Revolutionizing data dissemination, organization, and use

search

Chinese Rhesus macaque

The Chinese rhesus macaque (*Macaca mulatta lasiota*) is a subspecies of rhesus macaques that mainly resides in western and central China. Due to their anatomical and physiological similarity with human beings, macaques are a common laboratory model. Also, as several macaques species have been sequenced, such as the Indian rhesus macaque and the crab-eating macaque, examination of the Chinese rhesus macaque (CR) genome offers interesting insights into the entire *Macaca* genus.

The DNA sample for data sequencing and analyses was obtained from a five-year old female CR from southwestern China. The genome was sequenced on the IlluminaGAIIx platform, from which 142-Gb of high-quality sequence, representing 47-fold genome coverage for CR. The total size of the assembled CR genome was about 2.84 Gb, providing 47-fold on average. Scaffolds were assigned to the chromosomes according to the synteny displayed with the Indian rhesus macaque and human genome sequences. About 97% of the CR scaffolds could be placed onto chromosomes.

Additional information can be found at: <http://macaque.genomics.org.cn/>

download

readme
[readme.txt](#)

Genome sequence
[CR.cns.all.fa.gz](#)

Coding sequence
[CR.ods.fa.gz](#)

Protein sequence
[CR.pep.fa.gz](#)

Annotation data
[CR.gff.gz](#)
[CR.ipr.gz](#)
[CR.kegg.gz](#)
[CR.wego.gz](#)
[CR.name.gz](#)

Genome depth
[CR.genome.depth.gz](#)



Citation

In accordance with our [terms of use](#), please cite this dataset as:

Yan, G; Zhang, G; Fang, X; Zhang, Y; Li, C; Ling, F; Cooper, DN; Li, O; Li, Y; van Gool, AJ; Du, H; Chen, J; Chen, R; Zhang, P; Huang, Z; Thompson, JR; Meng, Y; Bai, Y; Wang, J; Zhuo, M; Wang, T; Huang, Y; Wei, L; Li, J; Wang, Z; Hu, H; Le, L; Stenson, PD; Li, B; Liu, X; Ball, EV; An, N; Huang, Q; Zhang, Y; Fan, W; Zhang, X; Li, Y; Wang, W; Katze, MG; Su, B; Nielsen, R; Yang, H; Wang, J; Wang, X; Wang, J (2011): Genomic data from the Chinese Rhesus macaque (*Macaca mulatta lasiota*). GigaScience. <http://dx.doi.org/10.5524/100002>

Related manuscript available at:
[doi:10.1038/nbt.1992](https://doi.org/10.1038/nbt.1992)

Accession codes associated with this data:
NCBI Study [SRP003590](#)
NCBI BioProject [PRJNA51409](#)
NCBI GenBank [AEHK00000000](#)
NCBI WGS Project [AEHK00000000](#)

Thickness-dependent magnetic properties of oxygen-deficient EuO

M. Barbagallo¹*, T. Stollenwerk², J. Kroha², N.-J. Steinke¹, N.D.M. Hine^{1,3},
J.F.K. Cooper¹, C.H.W. Barnes¹†, A. Ionescu¹, P.M.D.S. Monteiro¹, J.-Y. Kim¹,
K.R.A. Ziebeck¹, C.J. Kinane⁴, R.M. Dalgliesh⁴, T.R. Charlton⁴, and S. Langridge⁴

¹ *Cavendish Laboratory, Physics Department, University of Cambridge, Cambridge CB3 0HE, United Kingdom*

² *Physikalisches Institut and Bethe Center for Theoretical Physics, Universität Bonn, D-53115 Bonn, Germany*

³ *Thomas Young Centre, Department of Materials and Department of Physics,
Imperial College London, Exhibition Road SW7 2AZ, United Kingdom*

⁴ *ISIS, Harwell Science and Innovation Campus, STFC, Oxon OX11 0QX, United Kingdom*

(Dated: April 25, 2011)

We have studied how the magnetic properties of oxygen-deficient EuO sputtered thin films vary as a function of thickness. The magnetic moment, measured by polarized neutron reflectometry, and the Curie temperature are found to decrease with reducing thickness. Our results indicate that the reduced number of nearest neighbors, band bending and the partial depopulation of the electronic states that carry the spins associated with the $4f$ orbitals of Eu are all contributing factors in the surface-induced change of the magnetic properties of EuO_{1-x} .

PACS numbers: 75.70.-i, 75.50.Pp, 75.47.Lx, 71.15.Mb

Electron-doped EuO is a semiconductor which undergoes a simultaneous ferromagnetic and insulating-conducting phase transition, across which the resistivity drops by 8 to 13 orders of magnitude [1, 2] and the conduction electrons become nearly 100 % spin polarized [3, 4], making EuO a strong candidate for efficient spin filtering

length and the spatial extension of the RKKY interaction in EuO_{1-x} .

Thin films of EuO_{1-x} with $x=4\%$ were deposited by co-sputtering of Eu_2O_3 and Eu on Si substrates with a Pt buffer and capping layer of 10 nm each, as described in Ref. [6]. The samples were characterized by superconducting

DOI in references – would be better to have the citation – but does link through to the data

face [29].

To conclude, we have performed systematic measurements of the Curie temperature and layer-average magnetic moment in thin, oxygen-deficient EuO films in dependence of the film thickness. These measurements enabled us to study the influence of the film interface on these quantities and to analyze the physical effects contributing to their reduction. In stoichiometric EuO the Curie temperature is reduced for film thicknesses smaller than 10 nm, and we found that this reduction can be well explained semiquantitatively by the reduced number of neighboring magnetic atoms at the surface of the Eu sublattice. In electron doped, i.e., semiconducting EuO_{0.96} there is an overall, numerical enhancement of the Curie temperature with respect to stoichiometric EuO, but the surface-induced reduction extends up to higher film thicknesses of about 40 nm. The overall absolute-value enhancement and the thickness-dependent reduction can both be understood qualitatively in terms of the conduction-electron mediated, long-range RKKY spin-exchange interaction operative in these conducting films. Analyzing the reduction of the layer-average magnetic moment per Eu atom, we found interface-induced band bending and concomitant partial depopulation of the Eu 4*f* band to be the dominant mechanism, besides possible pinning effects. This conclusion was reached by estimating the energy gain for transferring Eu 4*f* electrons at the interface with the Pt capping layers. Our results are also relevant for applications of EuO in spintronics, where interface effects naturally play an important role. Especially, our conjec-

- Rev. B **81**, 235216 (2010).
- [7] H. Miyazaki, H. J. Im, and K. T. *et al.*, Appl. Phys. Lett. **96**, 232503 (2010).
- [8] A. Mauger and C. Godart, Phys. Rep. **141**, 51 (1986).
- [9] M. Arnold and J. Kroha, Phys. Rev. Lett. **100**, 046404 (2008).
- [10] C. A. F. Vaz, J. Bland, and G. Lauhoff, Rep. Prog. Phys. **71**, 056501 (2008).
- [11] M. Sperl, F. Maccherozzi, and F. B. *et al.*, Phys. Rev. B **81**, 035211 (2010).
- [12] F. Maccherozzi, M. Sperl, and G. P. *et al.*, Phys. Rev. Lett. **101**, 267201 (2008).
- [13] V. N. Men'shov, V. V. Tugushev, S. Caprara, and E. V. Chulkov, Phys. Rev. B **81**, 235212 (2010).
- [14] S. Okamoto, Phys. Rev. B **82**, 024427 (2010).
- [15] J. W. Freeland, K. E. Gray, and L. O. *et al.*, Nat. Mat. **4**, 62 (2005).
- [16] J. Lee, N. Sai, and A. A. Demkov, Phys. Rev. B **82**, 235305 (2010).
- [17] Y. Wang, M. K. Niranjana, J. D. Burton, J. M. An, K. D. Belashchenko, and E. Y. Tsybal, Phys. Rev. B **79**, 212408 (2009).
- [18] doi: 10.5286/ISIS.E.24066298 (2009).
- [19] T. S. Santos, J. S. Moodera, and K. V. R. *et al.*, Phys. Rev. Lett. **101**, 147201 (2008).
- [20] M. Müller, G.-X. Miao, and J. S. Moodera, J. Appl. Phys. **105**, 07C917 (2009).
- [21] P. Gustafsson, H. Ohlsen, and L. Nordborg, Phys. Rev. B **33**, 3749 (1986).
- [22] G. van der Laan, E. Arenholz, A. Schmehl, and D. G. Schlom, Phys. Rev. Lett. **100**, 067403 (2008).
- [23] E. Arenholz, A. Schmehl, D. G. Schlom, and G. van der

But the DOI does resolve to the landing page and the data



Data collected on the CRISP instrument at the ISIS facility

RB820232.

Investigation title: Magnetic moment of EuO in spin filtering magnetic tunnel structures.

Creator: *Easton, S*

Creator: *Griffin, T*

Creator: *Barnes, C H W*

Creator: *Ionescu, A*

DOI: 10.5286/ISIS.E.24066298

Date of Experiment: Thu Feb 19 13:34:31 GMT 2009

Publisher: STFC ISIS Facility

Data format: RAW/Nexus

Select the data format above to find out more about it.

Data Citation

The recommended format for citing this dataset in a research publication is as:
[author], [date], [title], [publisher], [doi]

For Example:

Easton, S. et al; (2009): 820232, STFC ISIS Facility, doi:10.5286/ISIS.E.24066298

Abstract

EuO is the ferromagnetic oxide semiconductor with the highest demonstrated value of conduction band exchange splitting (0.6 eV), which makes it at present one of the most promising material for achieving high spin filtering in magnetic tunnelling junctions. We intend to study the tunnelling of single electrons in quantum dots through a spin filtering EuO barrier, as a collaboration merging the expertise in our group on ferromagnetic thin film structures with the Semiconductor Physics group expertise on quantum dots at the Cavendish Laboratory in Cambridge. In this light we strongly believe that it is now necessary to study how EuO interacts with different metallic electrodes such as NiFe, Co and Y, and with substrates commonly used in spintronic devices, Si and GaAs, and how the magnetic moment of EuO is influenced by and influences the adjacent layers.



DOWNLOAD

download
the dataset

doi:10.5286/ISIS.E.24066298

This page represents DataCite's metadata for *doi:10.5286/ISIS.E.24066298*.

For a landing page of this dataset please follow <http://dx.doi.org/10.5286/ISIS.E.24066298>

Citation Easton,S; Barnes,C H W; Ionescu,A; (2011): RB820232: Magnetic moment of EuO in spin filtering magnetic tunnel structures.; STFC ISIS Facility. <http://dx.doi.org/10.5286/ISIS.E.24066298> **RIS** **BIBTEX**

Other formats

[text/html](#)

[application/x-datacite+xml](#)

[application/vnd.datacite.datacite+xml](#)

[application/x-datacite+text](#)

[application/vnd.datacite.datacite+text](#)

[application/rdf+xml](#)


[text/turtle](#)

[application/x-bibtex](#)

[application/x-research-info-systems](#)

[application/citeproc+json](#)

[application/vnd.citationstyles.csl+json](#)



In summary DataCite aims to provide a framework of support

- Support **researchers** by enabling them to locate, identify and cite research datasets with confidence
- Support **data centres** by providing workflows and infrastructure to identify and cite datasets
- Support **publishing** by enabling research articles to be linked to underlying data

Useful Links

DataCite Metadata

- The DataCite metadata schema is available at <http://schema.datacite.org>
- [isCitedBy: A Metadata Scheme for DataCite](#). Joan Starr from CDL explains the background to DataCite's metadata schema

DataCite Metadata Store (MDS)

- Documentation on the API and using the metadata store is available from <http://mds.datacite.org>
- You can also search DOIs already added to the MDS at <http://search.datacite.org>

Best practice for data citation

- <http://www.dcc.ac.uk/resources/how-guides/cite-datasets> from the DCC
- <http://ands.org.au/cite-data/> from the Australian National Data Service

Data curation and preservation

- <http://www.dcc.ac.uk/resources/curation-lifecycle-model> - the DCC can also run on-site courses on applying the data management lifecycle.

Thank you

Email: datasets@bl.uk

Web: www.bl.uk/datasets
www.datacite.org