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June 29, 2010

Two-thirds of Wiley-Blackwell's Journal Portfolio now has an Impact Factor

Hoboken, N.J.

Wiley-Blackwell, the scientific, technical, medical, and scholarly business of John Wiley & Sons, Inc., today announced that **two thirds of its journals (67% and 1,013 titles) have an Impact Factor** according to the Thomson ISI® 2009 Journal Citation Reports (JCR). This is a higher proportion of the list than any other major journals publisher. Of these ranked titles, **nearly a quarter are in the top ten of their subject category (332 titles) whilst two thirds are in the top half of their category.**

Wiley-Blackwell has **36 number 1 rankings** (**from 33 titles**, with *Econometrica* top of three, and *Worldviews on Evidence-Based Nursing* top of two categories respectively), the joint highest number of top ranked titles as a proportion of the list. **The Wiley-Blackwell journal** *CA-A Cancer Journal for Clinicians* remains in first place **overall with an Impact Factor of 87.925.**

51 new titles were added to Wiley-Blackwell's listing in the JCR for 2009 with 4 titles re-listed.

Wiley-Blackwell's average Impact Factor saw a 5.3% rise last year. **This year, the company's average was 2.1, compared to 2.0 last year.** This is in the context of an overall 1.7% reduction in average Impact Factor between JCR 2008 and 2009.

Overall, Wiley-Blackwell published 11.2% of the journals, 11.3 % of the articles, and received 11.1% of the citations.

"We are delighted with the Impact Factor results this year", said Steve Miron, Senior Vice President, Wiley-Blackwell. "They reflect the hard work of our external Editors, society partners and Wiley colleagues to continually drive the quality of the journals that we publish and to ensure they meet the needs of authors and researchers alike".

Impact factors are a metric that reflect the frequency that peer-reviewed journals are cited by researchers, making them an important tool for evaluating a journal's quality.

Within the 2009 Journal Citation Report were a number of key changes in the rankings for individual titles.



Highlights in Chemistry and Physical Sciences:

Angewandte Chemie, a journal of the German Chemical Society published under the Wiley-VCH brand, has further increased its Impact Factor to 11.829, strengthening its position as the leading chemistry journal publishing primary research and review articles.

ChemSusChem, also from Wiley-VCH and co-owned and supported by ChemPubSoc Europe (an association of 16 European Chemical Societies), received an impressive first Impact Factor of 4.767.

Biofuels, Bioproducts, Biorefining - Biofpr, published on behalf of the Society for Chemical Industry, increased its Impact Factor by over 68% to 4.885 and now ranks 2nd after just two years.

There are four number one ranked journals in physical sciences, including *Mass Spectrometry Reviews* for the 11th consecutive year and *Advanced Synthesis and Catalysis* for its 7th year.



Highlights in Life Sciences:

Within Life Sciences we have achieved 9 number one rankings. 4 journals retain their number one rankings - *Aging Cell* in the Geriatrics and Gerontology category, *Global Ecology and Biogeography* in Physical Geography, *Human Brain Mapping* in the Neuroimaging category and *Journal of Avian Biology* in Ornithology.

5 journals rise to number one ranking – *Fish and Fisheries* in the Fisheries category, *Global Change Biology* in the Biodiversity Conservation category, *Journal of Comparative Neurology* has risen to number one in Zoology and *Molecular Nutrition and Food Research* is now number one in the Food Science and Technology category. *Evolutionary Anthropology* is ranked first in the Anthropology category.

Recently launched journals that achieved an Impact Factor for the first time include *Evolutionary Applications* – 4.744 and is ranked 9th in the Evolutionary Biology category, and *Insect Conservation and Diversity* which also receives its first Impact Factor of 2.828 and is ranked 4th in the Entomology category. *Autism Research* gets its first Impact Factor of 1.375 and *Ecohydrology*, which launched in 2008, gains its first Impact Factor at 1.719.

FEMS Microbiology Reviews Impact Factor rose from 7.963 to 9.783 and is ranked 6/94 in the Microbiology category and for the sixth consecutive year *Ecology Letters* increased its Impact Factor to 10.318 and remains the highest ranking primary research journal in Ecology



Highlights in Social Sciences & Humanities:

Wiley-Blackwell's consistent leadership in social science is demonstrated through our publishing more titles listed in the Social Science JCR than any other publisher.

11 of our journals were ranked number one within their subject category – these included *Child Development* (ranked number one for the fifth consecutive year), *Econometrica*, *Industrial Relations* and *Journal of Computer-Mediated Communication*.

75 of our journals are ranked in the top ten of their respective SSCI categories.

24 journals have received their first Impact Factor with *Developing World Bioethics* entering the Ethics category at number seven.

In 18 categories we publish the most journals in the category confirming our exceptional market presence in anthropology, business - finance, demography, economics, family studies, geography, gerontology, health policy & services, history of social sciences, law, management, nursing, planning and development, psychology (developmental and social), public, environmental & occupational health, public administration and social sciences – mathematical methods.



Highlights in Health Sciences: (I)

291 Wiley-Blackwell health science journals received an Impact Factor in 2009 with an average of 2.62, 26 journals increased their score by 0.5 or more and 24 titles received their first Impact Factor. In addition 30 titles achieved an Impact Factor of 5 or more, with 9 titles ranked number 1 in their category and a further 50 in the top 10.

The journal *CA* – *A Cancer Journal for Clinicians*, published on behalf of The American Cancer Society, was awarded an Impact Factor of 87.925 - the highest Impact Factor among all medical titles. In the Oncology category, Wiley is now the third leading Publisher with 17 titles.

The Wiley EBM portfolio continues to gain strength, with *Worldviews on Evidence-Based Nursing*, an official journal of the Honor Society of Nursing, Sigma Theta Tau International, claiming the number 1 spot of 72 journals in the Nursing (science) category with an impact factor of 1.944, an increase from 1.294 in 2008. The *Cochrane Database of Systematic Reviews* climbed to 5.653, moving up the rankings for the 2nd year, since its inclusion in the Journal Citation Reports in 2007, to 11th place in Medicine, General & Internal.



Highlights in Health Sciences: (II)

From our Nursing portfolio, in addition to *Worldviews on Evidence-Based Nursing* now being ranked number 1, *Birth* is now ranked as the number 2 journal with an impact factor of 1.919.

BJOG's Impact Factor has increased to 3.437, while *Ultrasound in Obstetrics & Gynecology* now has an Impact Factor of 3.154. *American Journal of Transplantation*, published on behalf of the American Society of Transplantation (AST) and the American Society of Transplant Surgeons (ASTS) received a 2009 Impact Factor of 6.433, maintaining its status as the number 1 ranked journal in Transplantation. *Hepatology*, published on behalf of The American Association of the Study of the Liver, is the highest ranking hepatology journal and second in the gastroenterology and hepatology category, with an Impact Factor of 10.840.

The journal *Allergy*, published on behalf of The European Academy of Allergy and Clinical Immunology, was awarded an Impact Factor of 6.380, ranking it number 2 in the category for the fifth year. In dentistry, Wiley-Blackwell has 11 titles ranked in the top 20. *Journal of Clinical Periodontology* and *Periodontology 2000* are ranked as number 1 and 4 respectively.

In veterinary sciences 14 of our titles saw a rise in impact factor, notably *Journal of Veterinary Internal Medicine* increasing from 1.885 to 2.168 and now ranking in the top 10 at number 8. *Zoonoses and Public Health*'s impact factor leapt from 1.333 to 1.912.



Highlights in Health Sciences: (III)

Addiction and Addiction Biology keep their number 1 ranking in the categories of Substance Abuse (Social Science) and Substance Abuse respectively and Alcoholism's Impact Factor has increased to 3.392. Bipolar Disorders, published by Wiley-Blackwell on behalf of the International Society for Bipolar Disorders, jumped up 13 places in the Psychiatry category with an increased Impact Factor of 5.502.

The journals of the BPS (British Pharmacological Society) received increased Impact Factors, with BJP (British Journal of Pharmacology) increasing to 5.204, confirming it as the highest ranked general pharmacology research journal. The Journal of Pathology's 2009 Impact Factor of 6.466 places it number 2 in the Pathology category. Brain Pathology has also seen its Impact Factor rise for the 2nd year running, rising to 5.903.





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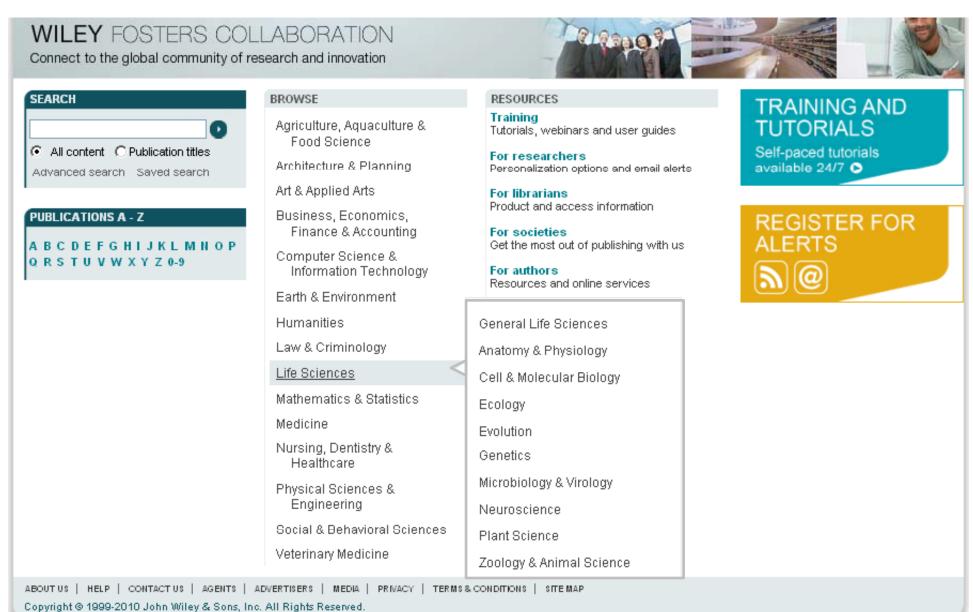


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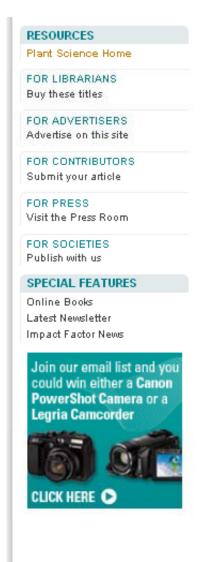


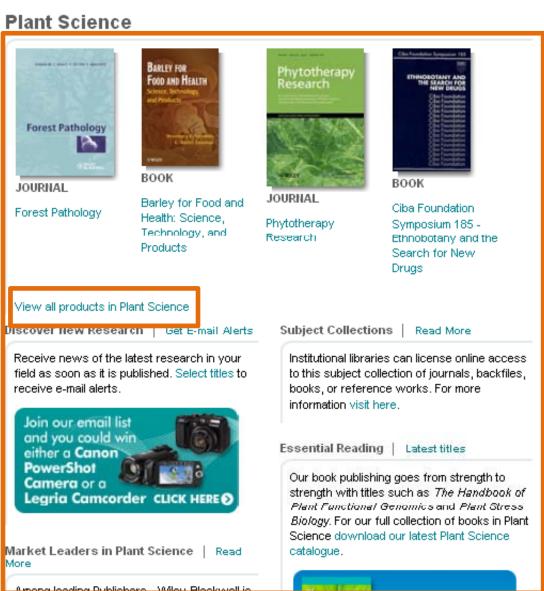
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NOTE: Users can also search with wildcard characters to find a broader range of term variants. See "Search Conventions" chart below for more information on using wildcards (or truncation).

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 Word root
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 word root + ed (past tense)
 CLEARED

 word root + ing (gerund)
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 word root + er (comparative adjective)
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 word root + est (superlative adjective)
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. This search will find all of the following variants.

. Searching any of these variants (e.g., TUMOUR) will also find all term variants.

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 TUMOR
 CENTER

 American English (plural)
 TUMORS
 CENTERS

 British (singular)
 TUMOUR
 CENTRE

 British (plural)
 TUMOURS
 CENTRES

3. NON-STANDARD PLURAL VARIANTS

Search MOUSE

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Singular MOUSE Plural MICE

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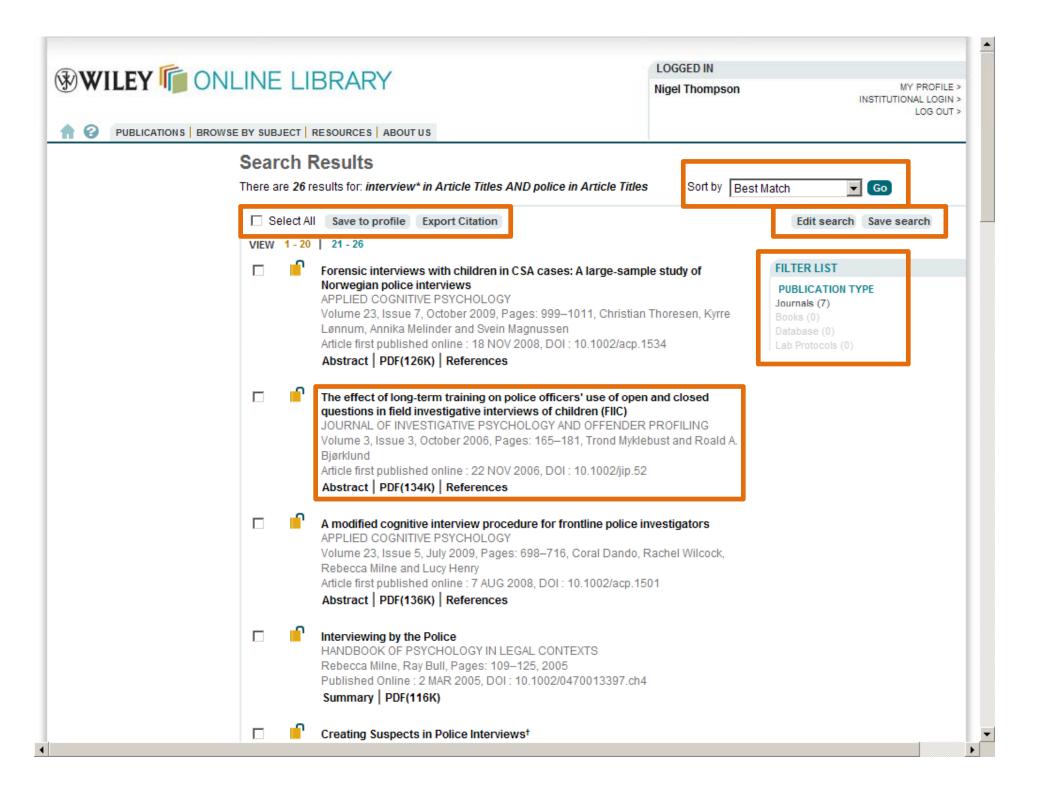
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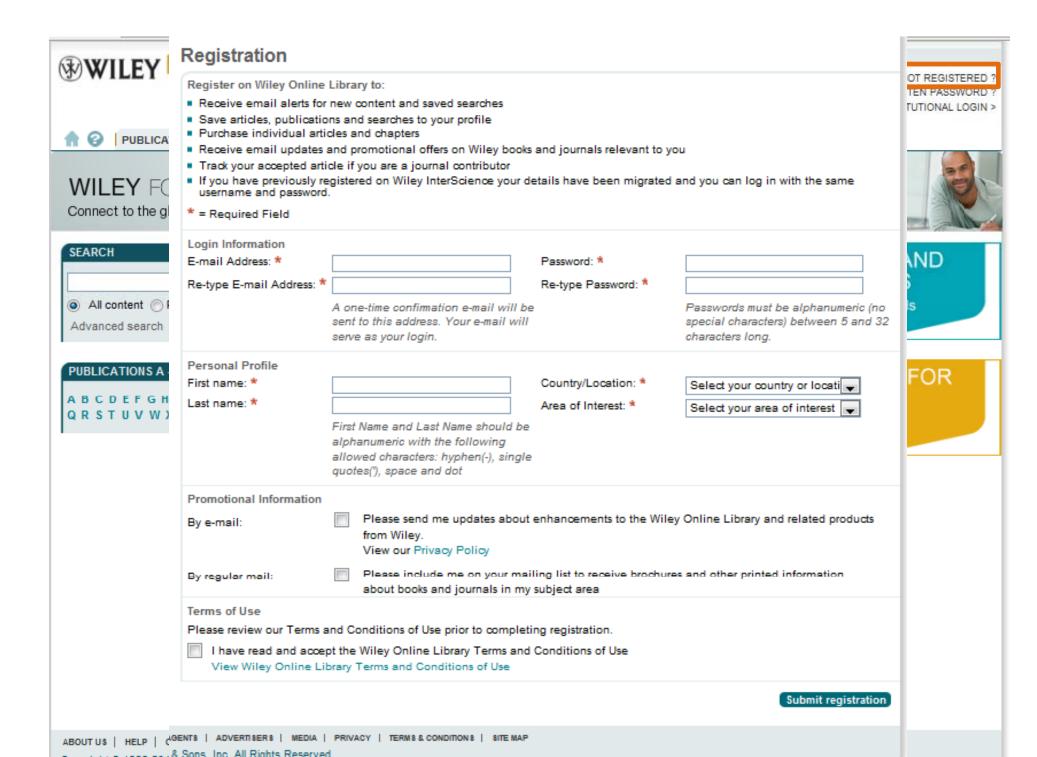
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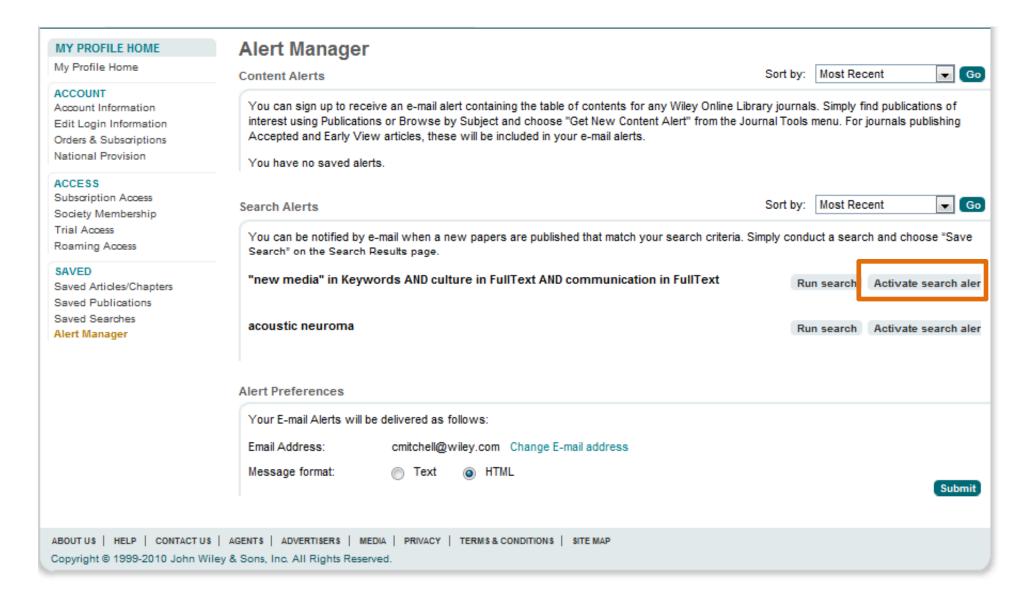
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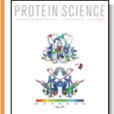
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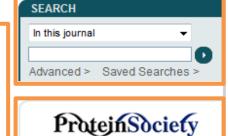
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A novel method for the production of in vivo-assembled, recombinant Escherichia coli RNA polymerase lacking the α C-terminal domain

Kelly-Anne Twist, Seyyed I. Husnain, Josef D. Franke, Deepti Jain, Elizabeth A. Campbell, Bryce E. Nickels, Mark S. Thomas, Seth A. Darst and Lars F. Westblade Accepted manuscript online: 17 MAR 2011 03:39PM EST | DOI: 10.1002/pro.622

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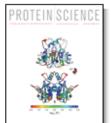
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Jean-François Trempe, Solomon Shenker, Guennadi Kozlov and Kalle Gehring Article first published online: 11 MAR 2011 | DOI: 10.1002/pro.608

Abstract | Full Article (HTML) | PDF(645K) | References

Binding of small molecules to cavity forming mutants of a de novo designed protein

Aditi Das, Yinan Wei, Istvan Pelczer and Michael H. Hecht

Article first published online: 7 MAR 2011 | DOI: 10.1002/pro.601

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Reviews

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Mei Hong and Yongchao Su

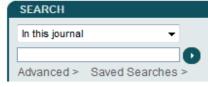
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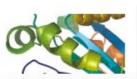
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The following Virtual Issues are available:

- Protein Folding: Short Question Long Answer (July, 2010)
- Learning about proteins that live in membranes (November, 2009)
- Celebrating the Structure of Myoglobin and its Impact on the Science of Proteins (May, 2009)

ISSUE 3, JULY 2010: PROTEIN FOLDING: SHORT QUESTION - LONG ANSWER

Arguably, more articles in *Protein Science* deal with the folding of proteins than any other subject. Solving the protein folding problem also remains as one of the major challenges in biology. This Virtual Issue combines two groups of articles from Protein Science that deal with this subject. The first selections have already established themselves as "citation classics". The second group of selections includes articles published within the past three years that can be characterized as "up-and-coming citation classics". Together, these contributions revisit established highlights and provide pointers to future developments.

Introduction to the Virtual issue

Brian W. Matthews

Principles of protein folding-A perspective from simple exact models

Ken A. Dill, Sarina Bromberg, Kaizhi Yue, Hue Sun Chan, Klaus M. Ftebig, David P. Yee

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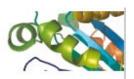
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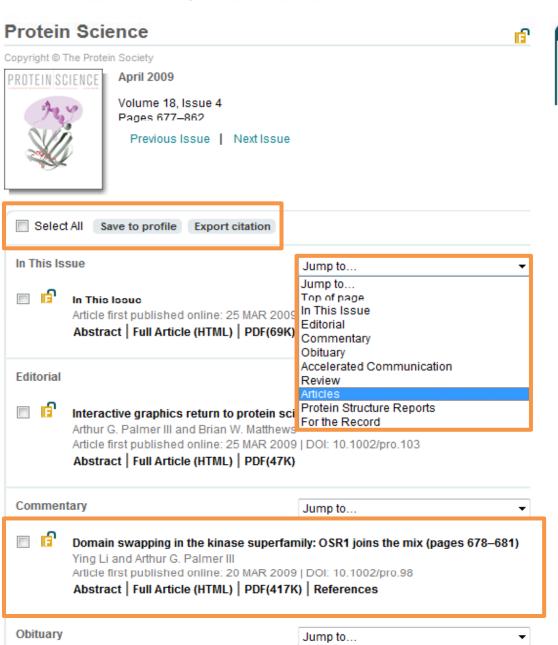
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Commentary

Domain swapping in the kinase superfamily: OSR1 joins the mix[†]

Ying Li, Arthur G. Palmer III

Article first published online: 20 MAR 2009

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Volume 18, Issue 4, pages 678-681, April 2009

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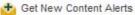
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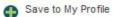
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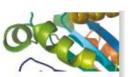
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Domain swapping in the kinase superfamily: OSR1 joins the mix†

Ying Li, Arthur G. Palmer III

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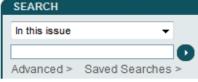
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Protein kinases constitute a large family of proteins that participate in the majority of cell signaling pathways. $\underline{1}$ Kinases act as mediators of a variety of biological processes in both normal physiology and pathogenesis, through specific interactions with upstream and downstream signaling molecules. Most kinases are multidomain proteins consisting of a catalytic kinase domain and several regulatory domains. The structures of kinase domains are conserved and have a two-lobed architecture consisting of a predominantly β -sheet N-terminal lobe and a predominantly α -helical C-terminal lobe. $\underline{2}$ In contrast, the regulatory domains of different kinases often have distinct overall folds and local structural motifs required for maintaining pathway specificity. Structure determinations of protein kinases have provided more detailed descriptions of the regulation of kinase activity at the molecular level; however, the mechanisms of critical events, such as autophosphorylation, are still not fully understood.

Some recently determined structures of kinase domains, including Ste20-like kinase (SLK; PDB 2JFL, 2J51) and lymphocyte-originated kinase (LOK; PDB 2J7T) of the Ste20 family and death-associated kinase 3 (DAPK3, PDB 2J90) and checkpoint kinase 2 (CHK2, PDB 2CN5) of the CaMK family, suggest that domain swapping serves as a possible mechanism for trans autophosphorylation between two identical protein kinases. 3, 4 In a domain-swapped dimer, one structural element of a molecule is replaced by the identical element from the partner molecule. Domain swapping is a general mechanism for forming protein oligomers and an efficient one from the evolutionary



Domain swapping in the kinase superfamily: OSR1 joins the mix

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Department of Biochemistry and Molecular Biophysics, Columbia University, New York, New York 10032

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Protein kinases constitute a large family of proteins that participate in the majority of cell signaling pathways. Kinases act as mediators of a variety of biological processes in both normal physiology and pathogenesis, through specific interactions with upstream and downstream signaling molecules. Most kinases are multidomain proteins consisting of a catalytic kinase domain and several regulatory domains. The structures of kinase domains are conserved and have a two-lobed architecture consisting of a predominantly β-sheet N-

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Protein kinases constitute a large family of proteins that participate in the majority of cell signaling pathways. 1 Kinases act as mediators of a variety of biological processes in both normal physiology and pathogenesis, through specific interactions with upstream and downstream signaling molecules. Most kinases are multidomain proteins consisting of a catalytic kinase domain and several regulatory domains. The structures of kinase domains are conserved and have a two-lobed architecture consisting of a predominantly β-sheet N-terminal lobe and a predominantly α-helical C-terminal lobe. 2 In contrast, the regulatory domains of different kinases often have distinct overall folds and local structural motifs required for maintaining pathway specificity. Structure determinations of protein kinases have provided more detailed descriptions of the regulation of kinase activity at the molecular level; however, the mechanisms of critical events, such as autophosphorylation, are still not fully understood.

Some recently determined structures of kinase domains, including Ste20-like kinase (SLK; PDB 2JFL, 2J51) and lymphocyte-originated kinase (LOK: PDB 2J7T) of the Ste20 family and death-associated kinase 3 (DAPK3, PDB 2J90) and checkpoint kinase 2 (CHK2, PDB 2CN5) of the CaMK family, suggest that domain swapping serves as a possible mechanism for trans autophosphorylation between two identical protein kinases.3, 4 In a domain-swapped dimer, one structural element of a molecule is replaced by the identical element from the partner molecule. Domain swapping is a general mechanism for forming protein oligomers and an efficient one from the evolutionary point of view, because the interactions between monomers in the domain-swapped interface are native-like and new recognition sites need not be evolved. In the February, 2009 issue of Protein Science, Lee et al.5 reported the X-ray crystal structure of the kinase domain of oxidative stress responsive 1 (OSR1), which represents another example of a domain-swapped protein kinase. A similar report by Villa et al.6 appeared in the December 2008 issue of Proteins: Structure, Function and Bioinformatics, The structural coordinates have been deposited in the Protein Data Bank (PDB) as 3DAK and 2VWI, respectively. OSR1 is a Ser/Thr protein kinase belonging to the Ste20 family. It is one of the two human homologues of the putative Drosophila mitogen-activated protein kinase kinase kinase (MAP4K) Fray,7 and a component of the recently identified WNK-OSR1/SPAK pathway, which is responsible for cell volume control and ion homeostasis in mammals and is activated by osmotic stress.8 In the pathway, with-no-lysine kinases (WNKs) activate OSR1, which in turn activates the Na+/K+/2CI cotransporters through direct phosphorylation.9, 10 Mutations in WNKs lead to Gordon's syndrome, an autosomal dominant form of hypertension. 11 Full-length OSR1 contains an C-terminal extension, residues 291–527; within this sequence, the unique PF1 region, residues 291–344, is required for kinase activity, although the basis for this requirement is unknown. The structures of the OSR1 kinase domains reported by Lee et al.5 and Villa et al.6 used constructs that encompassed residues 1-295 and 1-303, respectively, and neither contains a complete PF1 region.

Both structural studies show that the OSR1 kinase domain forms a domain-swapped dimer (Fig. 1). The dimer interface is formed by exchange of the P+1 loop, located in the C-terminus of the activation segment, and the following helix αΕF (Fig. 2). The interface is stabilized by a salt bridge between Glu196 in helix αΕF of one monomer and Arg279, located between helices αl and αJ, in the other monomer, as well as van der Waals contacts between several hydrophobic residues from helix αΕF of one monomer and the hydrophobic pocket located between helices αG and αF of the partner monomer. The activation segment, which commonly is 20–30 residues in length and contains one or several phosphorylation sites, is a critical structural element for regulation of kinase activity. 12 Electron density is not clearly defined in either study for the phosphorylation site, Thr185, or the C-terminal part of the activation loop. The partially disordered activation segment suggests that the OSR1 kinase domain structures represent an inactive conformation, because a correctly positioned activation segment is required for ATP binding.



Figure 1. The kinase domain of oxidative stress responsive 1 (OSR1) forms a domain-swapped dimer. Each monomer binds one molecule of Mg-AMP-

mammals and is activated by osmotic stress. In the pathway, with-no-lysine kinases (WNKs) activate OSR1, which in turn activates the Na+/K+/2Cl⁻ cotransporters through direct phosphorylation. 9, 10 Mutations in WNKs lead to Gordon's syndrome, an autosomal dominant form of hypertension. 11 Full-length OSR1 contains an C-terminal extension, residues 291–527; within this sequence, the unique PF1

Α N lobe C lobe

Figure 2. Structure of the OSR1 kinase domain monomer. (A) The first monomer from the coordinate file PDB 3DAK is shown. OSR1 has the typical bilobal kinase architecture consisting of a largely β -sheet N-terminal lobe (blue) and a helical C-terminal domain (aquamarine). (B) The domain-swapped interface between monomers contains a salt bridge between Arg279 of one monomer and Glu196 of the partner molecule, a cation- π interaction between Lys148 of one monomer and Trp192 of the partner molecule, and hydrophobic interactions between residues in α F and α G of one monomer with residues in α F of the partner. (C) The structure shows characteristics of an inactive kinase, including absence of an ion pair between Lys46 and Glu63. An interactive view is available in the electronic version of the article, which also depicts superpositions with other kinase structures. Interactive View

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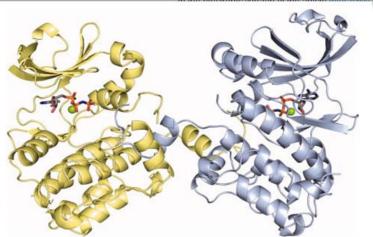
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This outward movement has been observed in the structure of catalytically active cyclin-dependent kinase 2 (Cdk2) in complex with a phosphatase. 13 Solution NMR and kinetic data on dimeric p21-activated kinase 2 (PAK2) combined with the crystal structure of the highly homologous p21-activated kinase 1 (PAK1, PDB 1YHV) in its active state suggest that dimerization, which allows positioning of the activation loop of one manager in the active site of the partner melocule, is assential for the transquired partner manager.

Figure 1. The kinase domain of oxidative stress responsive 1 (OSR1) forms a domain-swapped dimer. Each monomer binds one molecule of Mg-AMP-PNP. The two monomers from the coordinate file PDB <u>3DAK</u> are depicted in blue and yellow, respectively; the AMP-PNP molecules are shown as CPK-colored bonds; and the Mg ²⁺ ions are shown as green spheres. An interactive view is available



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Figure 1. The kinase domain of oxidative stress responsive 1 (OSR1) forms a domain-swapped dimer. Each monomer binds one molecule of Mg-AMP-PNP. The two monomers from the coordinate file PDB 3DAK are depicted in blue and yellow, respectively; the AMP-PNP molecules are shown as CPK-colored bonds; and the Mg²⁺ ions are shown as green spheres. An interactive view is available in the electronic version of the article.Interactive View

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Lee et al. did not identify any key differences in the amino acid sequences between homologous domain-swapped and non-swapped kinases. Swapped domains often do not share similarity in sizes and sequences, based on the currently available high-resolution structures. 19 Owing to the relatively small differences in free energy of monomers and oligomers, many domain-swapped oligomers show low-affinity and are only observed in crystals. 20 Indeed, OSR1 kinase domain is monomeric in solution. 5, 6 In contrast, the previously identified domain-swapped kinase domains of SLK, LOK, and DAPK3 form stable dimers in solution. 4 Biochemical data for these kinases strongly support the involvement of dimers in the autophosphrylation reaction. However, the functional relevance of dimerization cannot be judged solely from the affinity in aqueous solution and coimmunoprecipitation experiments indicate that both the kinase domain alone and the full-length OSR1 are capable of forming oligomers in cells. 10

Intrinsic conformational plasticity is critical for structural transitions between active and inactive states of protein kinases, and biophysical evidence suggests that conformational dynamics may be coupled to catalysis.21–24 Results from NMR spectroscopy and molecular dynamics simulations have linked conformational flexibility to domain swapping in other protein molecules.25, 26 Therefore, domain swapping may be a consequence of the intrinsic conformational flexibility of kinase domains. The impact of domain swapping on the autophosphorylation reaction, if indeed they are coupled, remains to be fully elucidated, and additional structural and biochemical data are required to clarify the functional role



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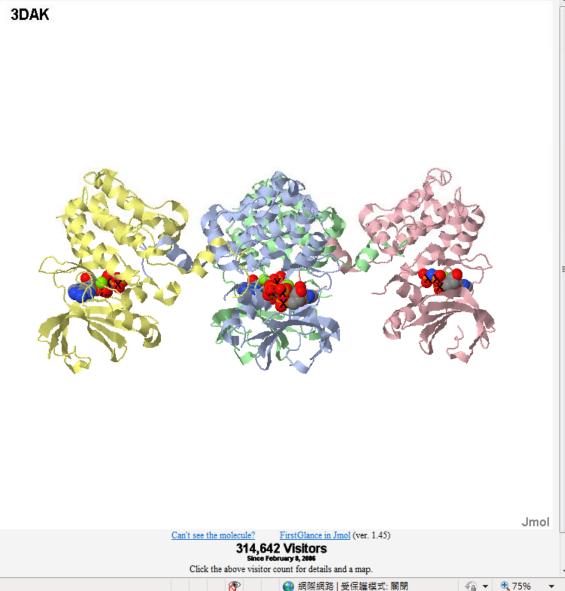
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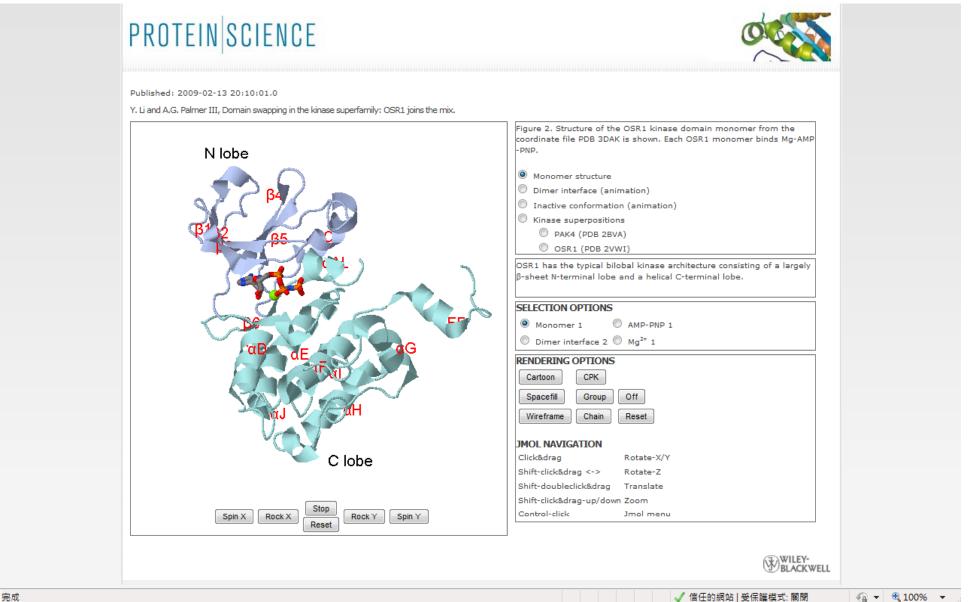
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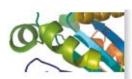
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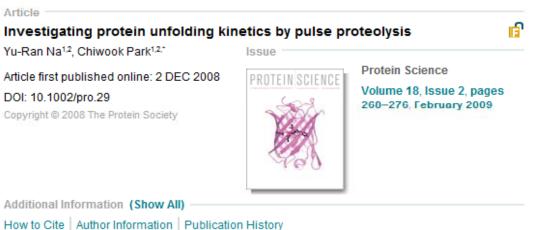
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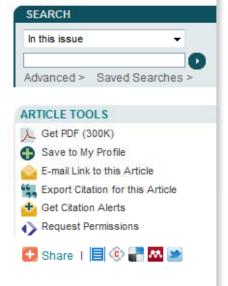
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Yu-Ran Na1,2, Chiwook Park1,2,1

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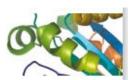
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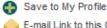
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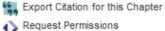
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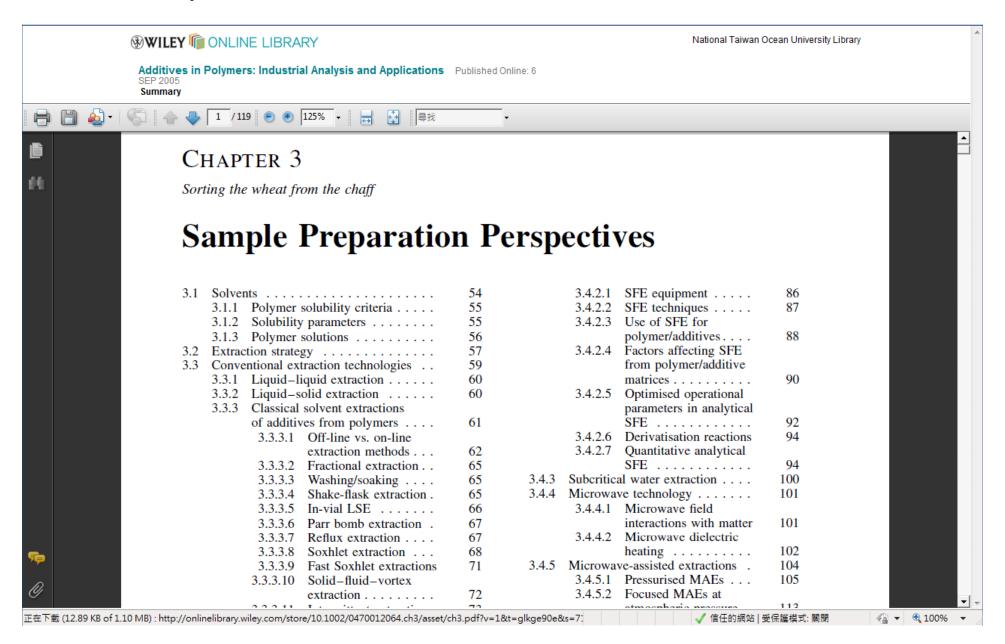
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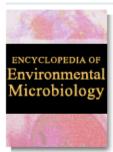
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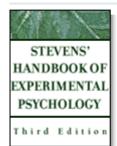
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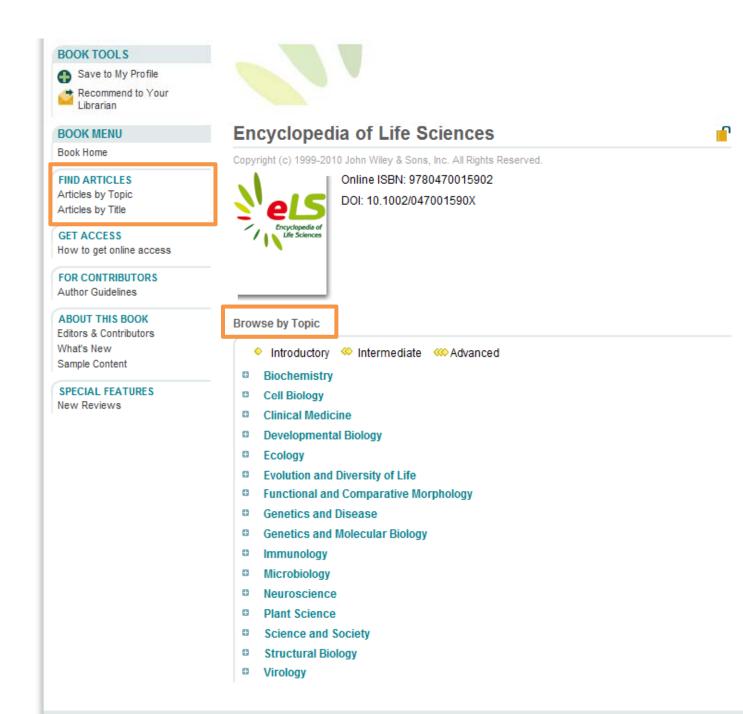
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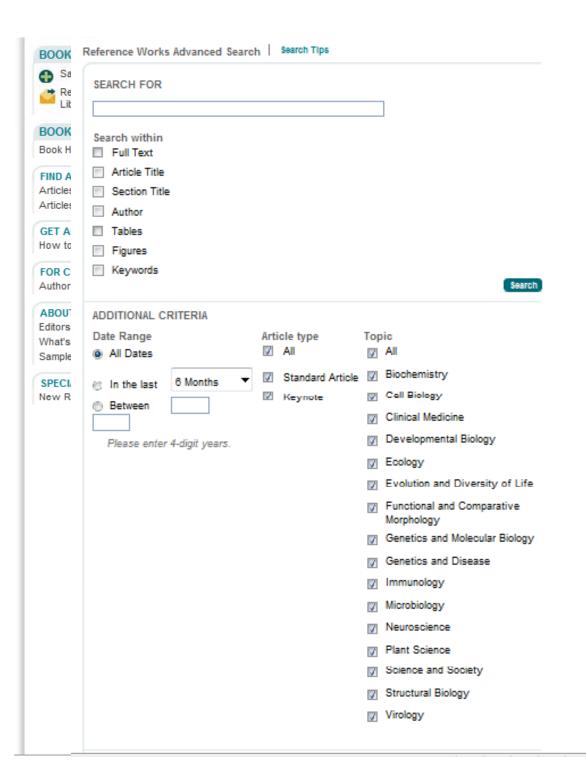
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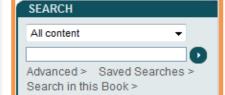
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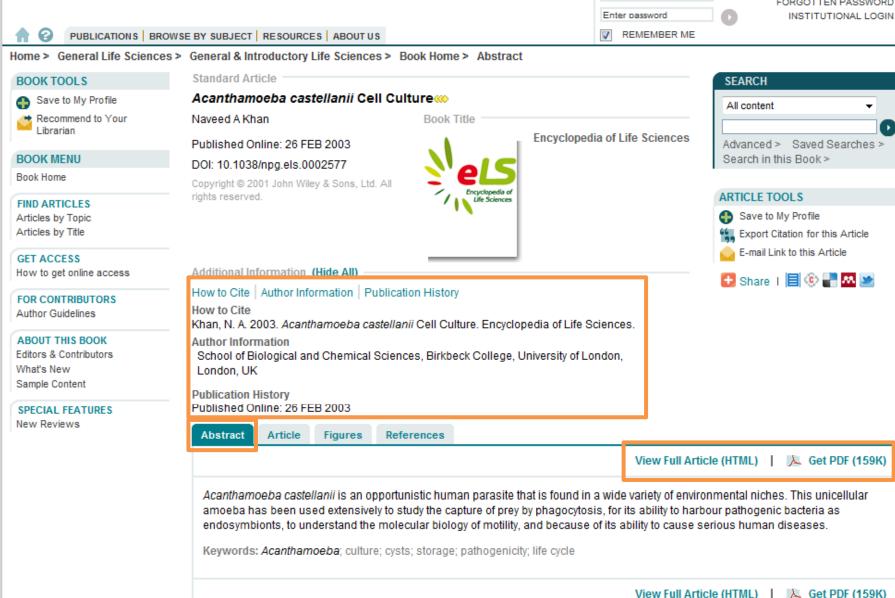


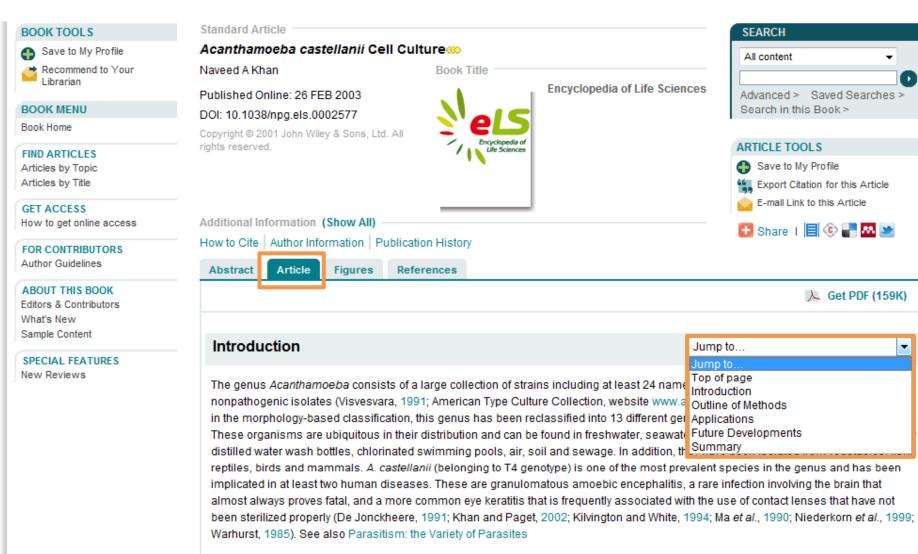




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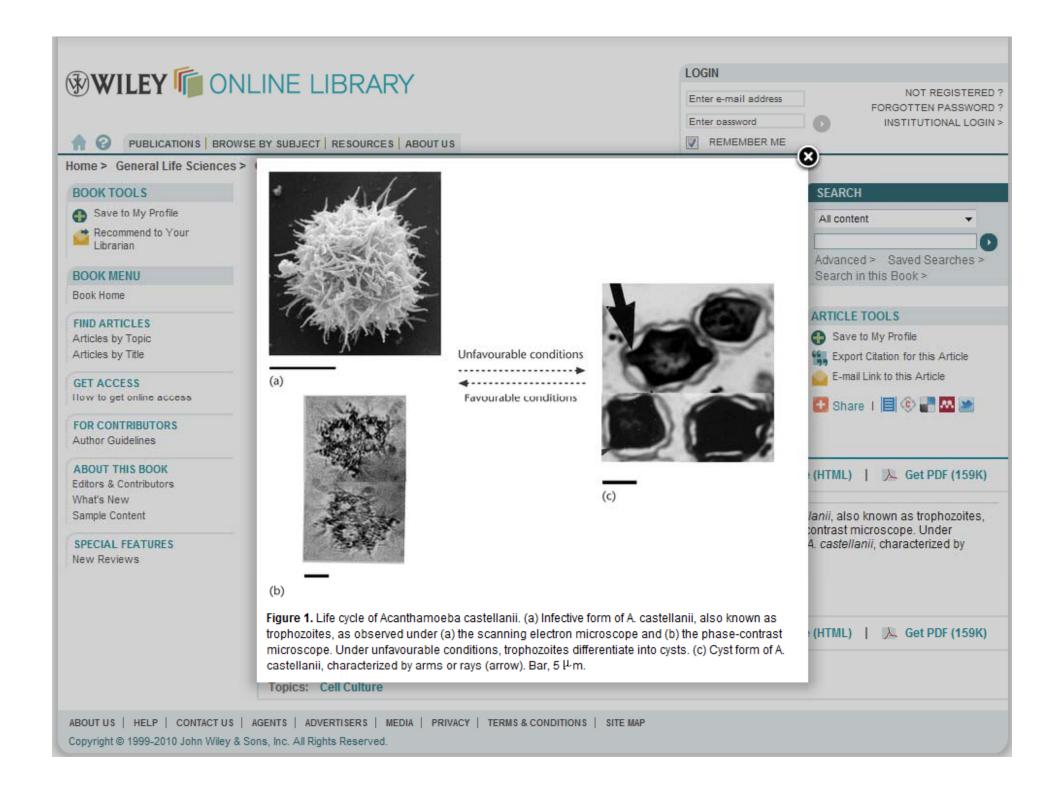


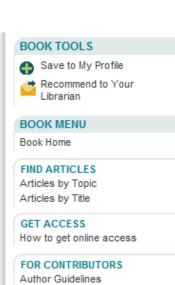




The life cycle of A. castellanii consists of vegetative infective trophozoites that reproduce by binary fission, and a dormant cyst form (Figure 1) (Byers, 1979; Byers et al., 1991; Ma et al., 1990). Trophozoites possess characteristic spines on their surface known as acanthopodia that are used for motility and adherence to host cells (Figure 1a, b). The latter is a primary step in pathogenesis (Cao et al., 1998; Khan, 2001). Trophozoites differentiate into cysts, a process known as encystment, under unfavourable conditions such as starvation (lack of nutrients), cold, heat and increased osmolarity. Cysts are double walled, consisting of an outer ectocyst and an inner endocyst. Both walls meet at points known as arms or rays. A. castellanii has a maximum number of six rays (Figure 1c). Cysts are resistant to various antimicrobial agents, thus presenting a problem in chemotherapy because this may lead to recurrence of the disease. In addition, cysts can survive harsh environmental conditions such as high temperatures and desiccation, and they can be airborne (Byers, 1979; Cordingley et al., 1996; Turner et al., 2000; Weisman, 1976). Furthermore, Acanthamoeba cysts can survive for several years while maintaining their pathogenicity. These characteristics suggest that the primary functions of cysts may be to withstand adverse conditions and to spread amoebae throughout the environment (Mazur et al., 1995). Under favourable conditions, cysts transform into trophozoites, a

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