
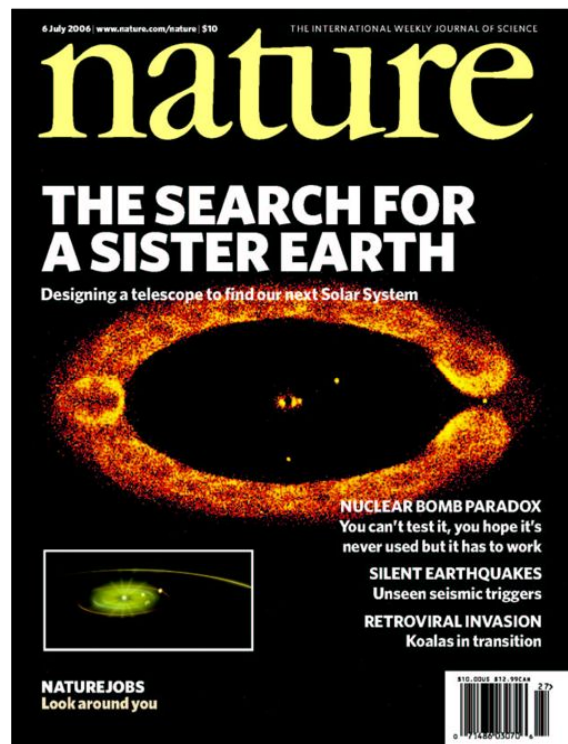


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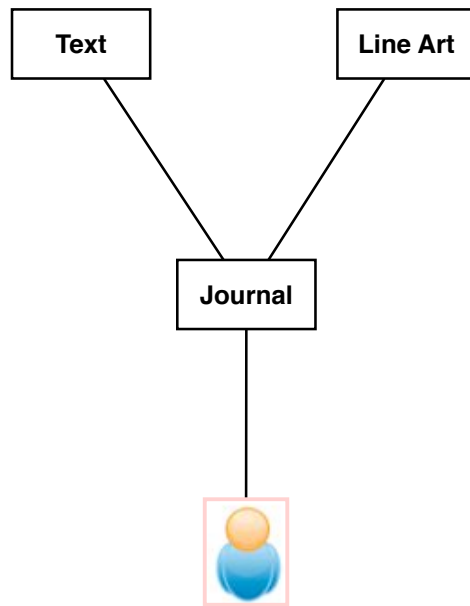
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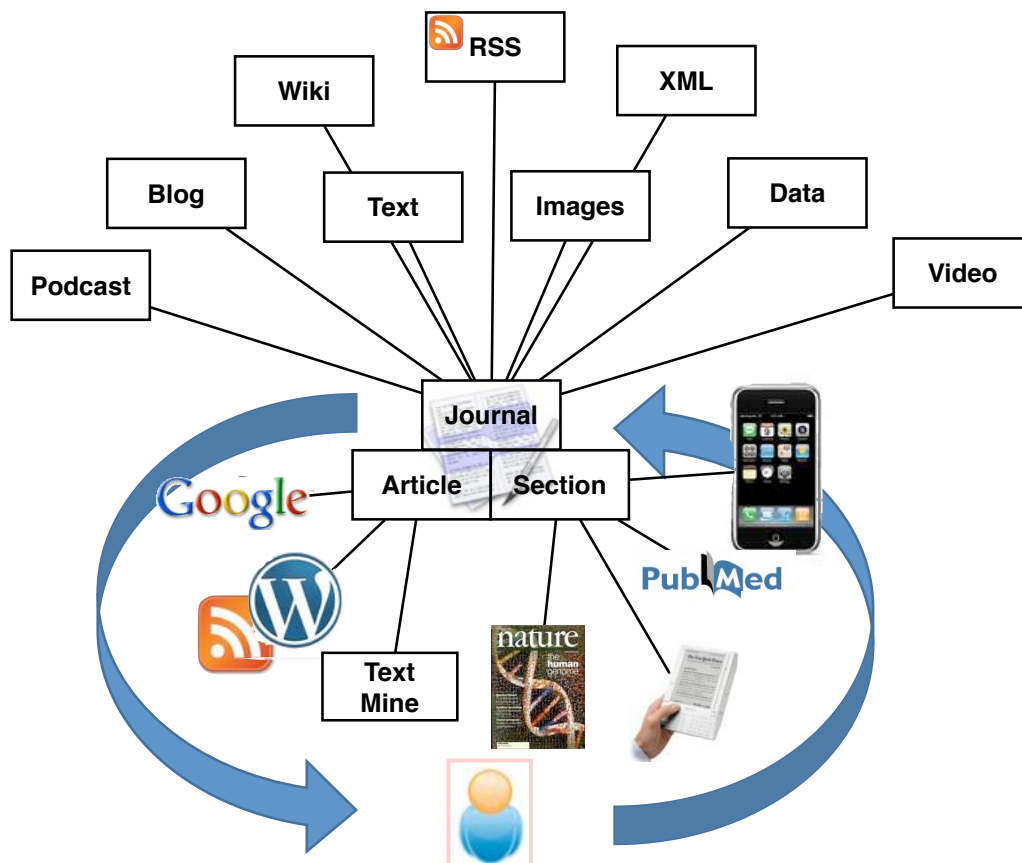
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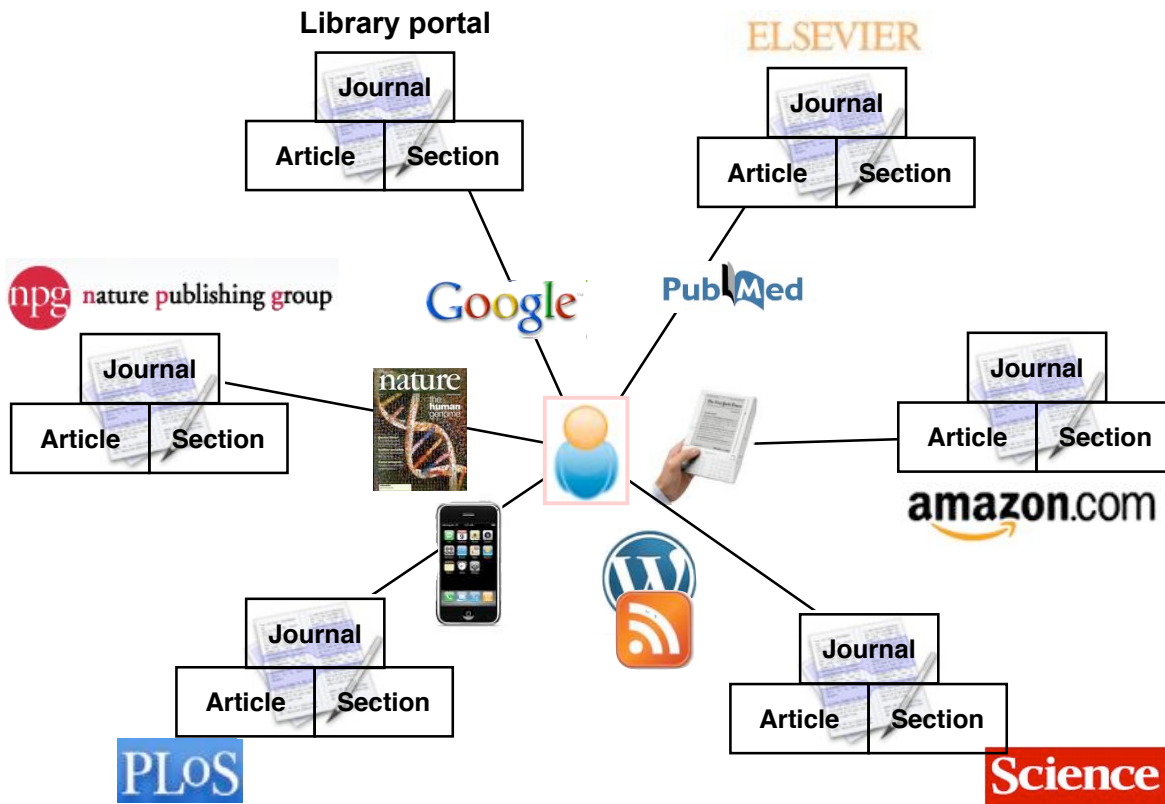


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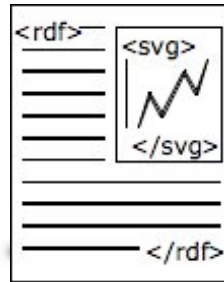
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Michael Lammers, Heinz Neumann, Jason W Chin & Leo C James

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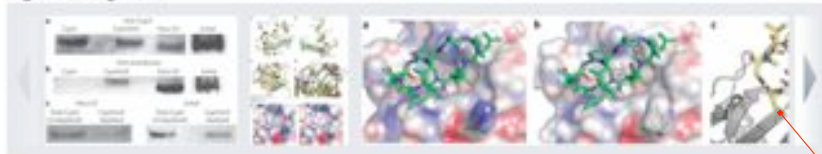
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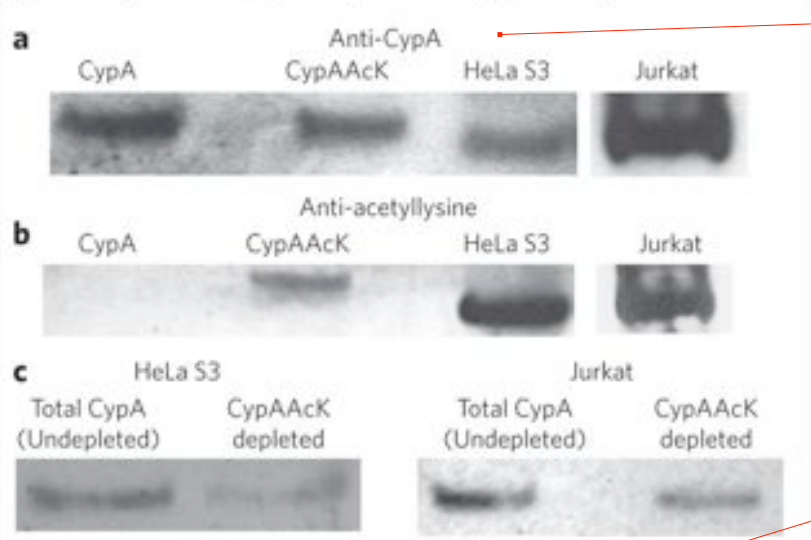
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Figure 1: Homogenous and site-specific incorporation of acetyllysine into CypA.



(a,b) CypA can be immunoprecipitated from HeLa and Jurkat T cells (a) and the acetylated fraction detected by anti-acetyllysine in both cell types (b). Recombinant CypA and CypAAcK represent controls. (c) Quantification of acetylated CypA in HeLa and Jurkat cells using an immunodepletion approach. Endogenous CypA from cell lysate was depleted with anti-acetyllysine and compared to undepleted material by western blot with anti-CypA. A substantial proportion of CypA is acetylated in both HeLa and Jurkat cells. See Supplementary Figure 1 for full-length gels and blots.

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To determine the proportion of endogenous CypA that was acetylated in each cell type, we performed an immunodepletion experiment. Acetylated CypA was depleted from lysate using anti-acetyllysine bound to

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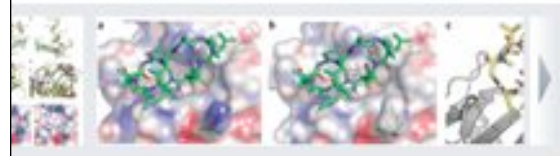
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### Contributions

M.L., H.N., J.W.C. and L.C.J. designed experiments and analyzed data.

### Competing financial interests

The authors declare no competing financial interests.

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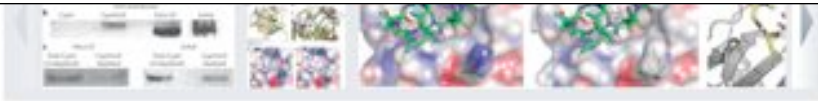
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Acetylation of the  $\epsilon$ -amine of specific lysine residues in proteins is a reversible post-translational modification with diverse roles and a functional importance that rivals that of phosphorylation<sup>13</sup>. Acetylation is mediated by acetyl-CoA-dependent histone acetyltransferases<sup>14</sup> and reversed by zinc-dependent histone deacetylases or NAD dependent sirtuins<sup>15</sup>. Acetylated targets can be specifically recognized by bromodomain-containing proteins<sup>16</sup>. Recent mass spectrometry and immunofluorescence studies demonstrate that hundreds of nonhistone proteins are acetylated in mammalian cells<sup>17</sup>; however, the molecular mechanisms by which acetylation may control protein function and effect cellular regulation are largely unknown.

A recent proteomics screen isolated a peptide whose sequence matched CypA but which contained an N<sup>6</sup>-acetyl-L-lysine (acetylysine, 2) in place of Lys125 (ref. 17). However, because there are many CypA gene fusions in the genome, the origin of this peptide was ambiguous. Here we show that the free enzyme form of CypA is acetylated in human cells. We produced homogeneously and site-specifically acetylated recombinant CypA using an acetylysyl-tRNA synthetase/tRNA<sup>Cys</sup> pair that co-translationally directs the incorporation of acetylysine in response to an amber codon<sup>18</sup> placed in a CypA gene. This approach allowed us to perform

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When activated, it will highlight key entities...

## Abstract

Abstract | Introduction | Results | Discussion | Methods | Additional information | Accession codes | References | Acknowledgments | Author information | Supplementary information

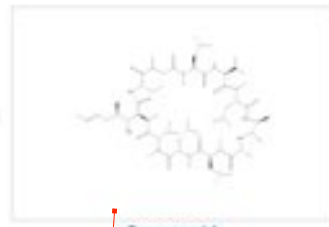
Cyclophilin A (CypA) is a ubiquitous *cis-trans* prolyl isomerase with key roles in immunity and viral infection. CypA suppresses T-cell activation through cyclosporine complexation and is required for effective HIV-1 replication in host cells. We show that CypA is acetylated in diverse human cell lines and use a synthetically evolved acetyllysyl-tRNA synthetase/tRNA<sub>CysA</sub> pair to produce recombinant acetylated CypA in *Escherichia coli*. We determined atomic-resolution structures of acetylated CypA and its complexes with cyclosporine and HIV-1 capsid. Acetylation markedly inhibited CypA catalysis of *cis* to *trans* isomerization and stabilized *cis* rather than *trans* forms of the HIV-1 capsid. Furthermore, CypA acetylation antagonized the immunosuppressive effects of cyclosporine by inhibiting the sequential steps of cyclosporine binding and

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## Inside this article

### Compounds



Compound 1

1/2

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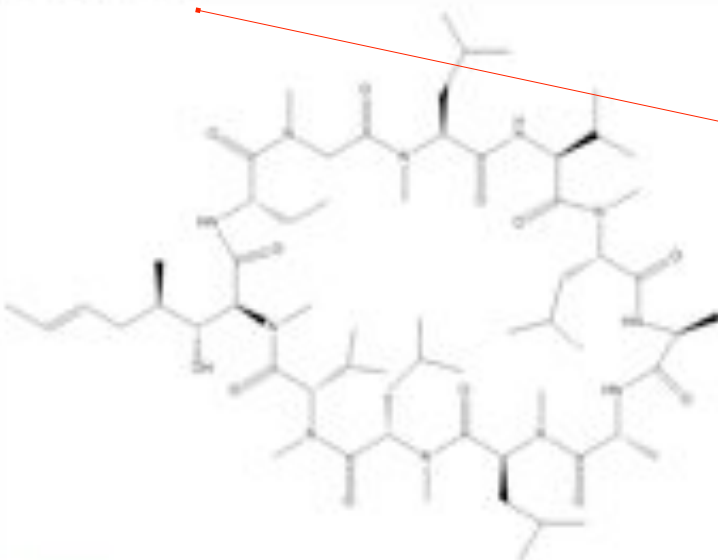
## Compound 1

From  
Acetylation regulates Cyclophilin A catalysis, immunosuppression and HIV isomerization  
Michael Lemmers, Heinz Neumann, Jason W Chin & Leo C James  
Nature Chemical Biology 6, 331-337 (2010) | doi:10.1038/nchembio.342

Compound pages recognise article context...

Back to article

### Compound 1: Cyclosporine



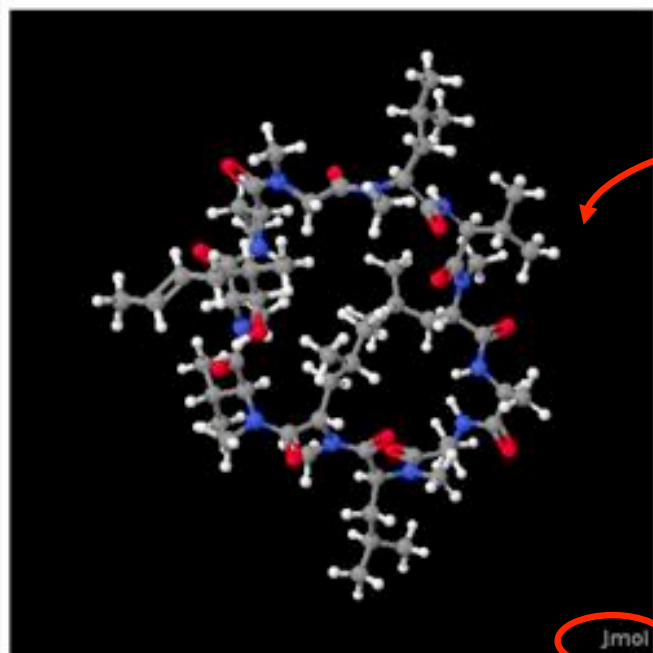
...but link to common information...







Compound 1: Cyclosporine



3D ball-and-stick model of Cyclosporine

Jmol

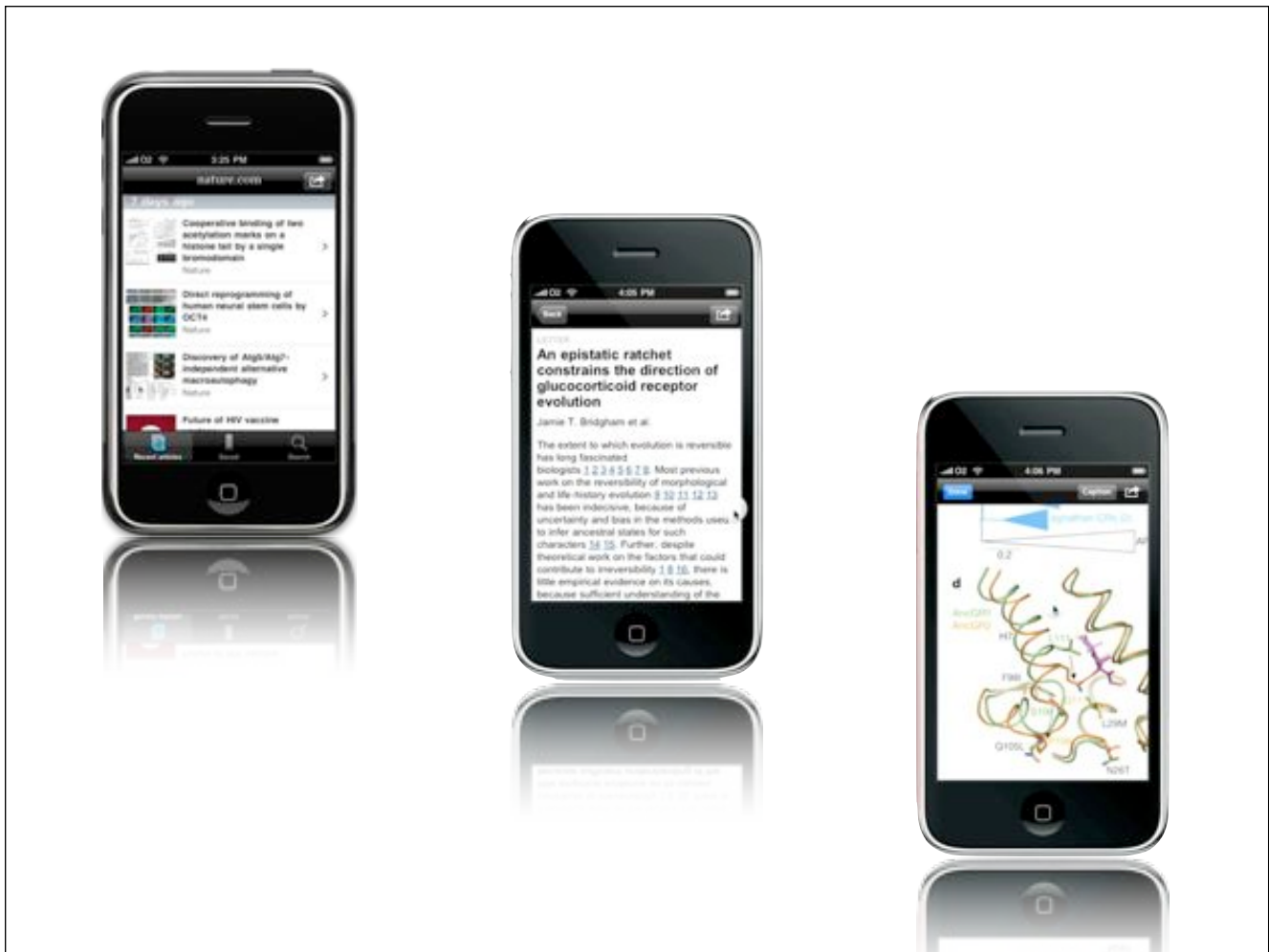
Chemical structure of Cyclosporine (C<sub>34</sub>H<sub>61</sub>N<sub>7</sub>O<sub>12</sub>)  
Molecular weight: 757.68 g/mol  
CAS number: 598-36-2  
SMILES: CC1(C)CC2(C)CC3(C)CC4(C)CC5(C)CC6(C)CC7(C)CC8(C)CC9(C)CC10(C)CC20(C)CC21(C)CC22(C)CC23(C)CC24(C)CC25(C)CC26(C)CC27(C)CC28(C)CC29(C)CC30(C)CC31(C)CC32(C)CC33(C)CC34(C)CC1

## Article Improvement Project

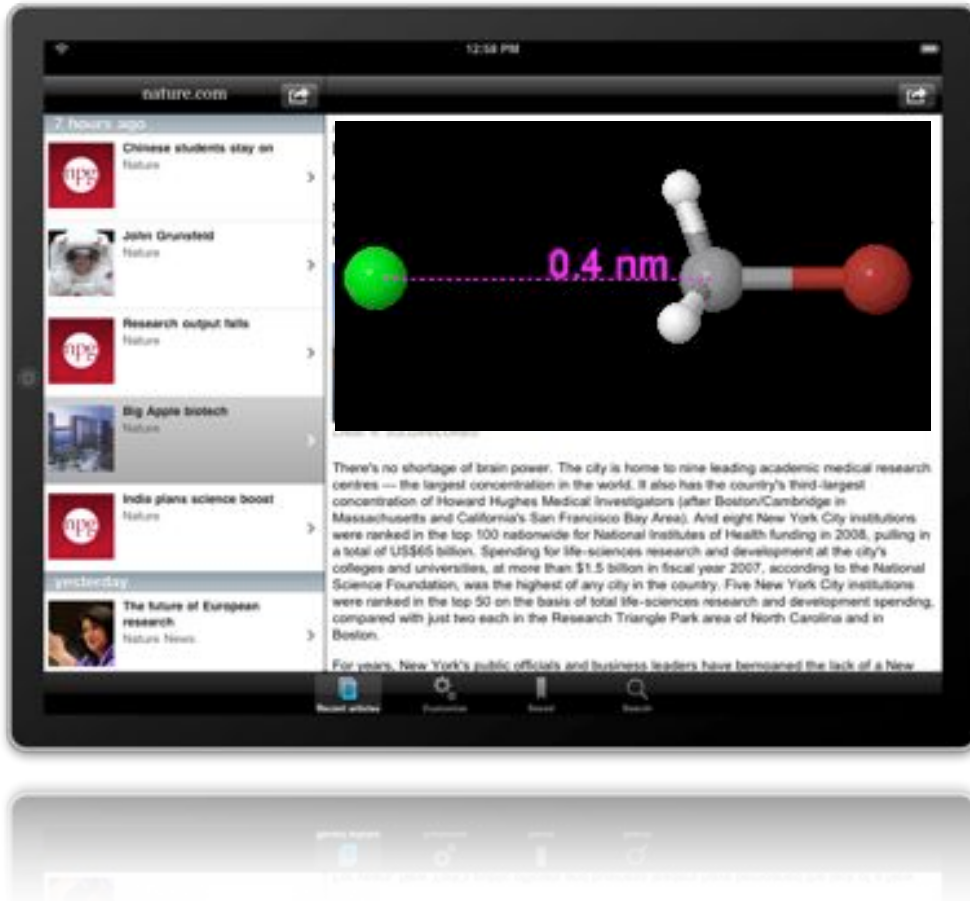
- ▶The article as a hub
- ▶Modular framework
- ▶From electronic print to digitally-optimised
- ▶On-going
- ▶Roll-out through 2010 and early 2011

# Just a beginning









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