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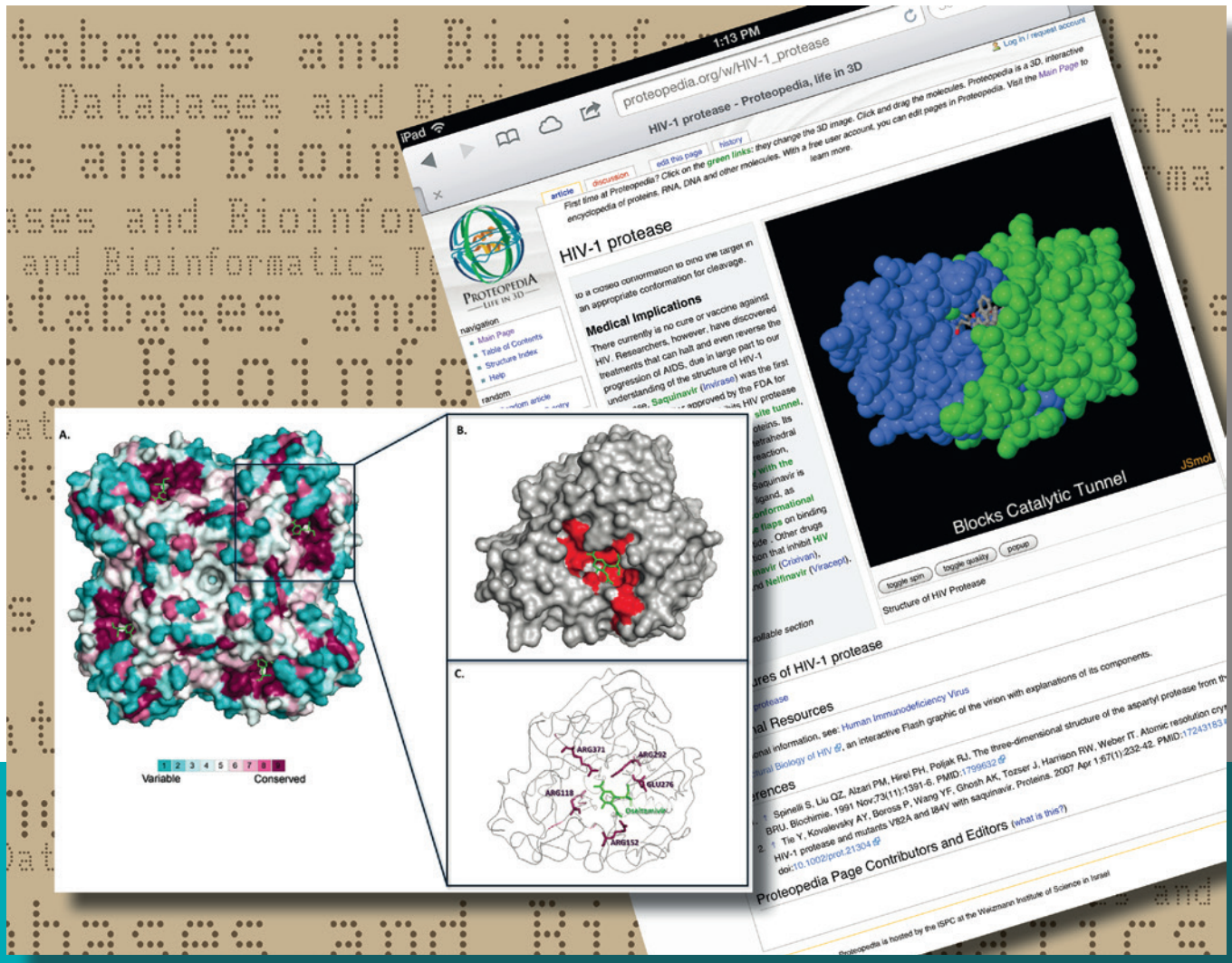

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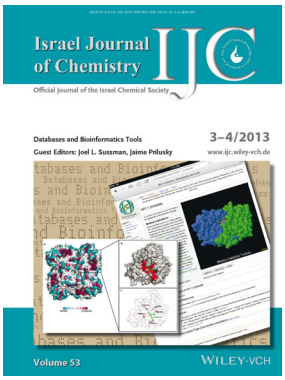
Cover Picture



Gershon Celniker, Guy Nimrod, Haim Ashkenazy, Fabian Glaser, Eric Martz, Itay Mayrose, Tal Pupko, and Nir Ben-Tal*

Robert M. Hanson, Jaime Prilusky, Zhou Renjian, Takanori Nakane, and Joel L. Sussman*

The cover shows on the left a ConSurf analysis of the influenza neuraminidase protein. The 3D tetramer colored by conservation grades is shown in (A) with maroon indicating the most conserved amino acids, and close-up views (B,C) are shown of one of the conserved regions with the anti-flu drug, oseltamivir (tamiflu) bound; see Celniker et al. for details, page 199. On the right is a page from Proteopedia as viewed on an iPad, via the JSmol viewer, showing a complex of HIV-Protease and Saquinavir (Invirase), the first protease inhibitor approved by the FDA for the treatment of HIV; see Hanson et al. for details, page 207.

Review

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JSmol and the Next-Generation Web-Based Representation of 3D Molecular Structure as Applied to *Proteopedia*

Robert M. Hanson,[a] Jaime Prilusky,[b] Zhou Renjian,[c] Takanori Nakane,[d] and Joel L. Sussman*[e]

Abstract: Although Java does not run on some handheld devices, e.g., iPads and iPhones, JavaScript does. The development of JSmol, a JavaScript-only version of Jmol, is described, and its use in *Proteopedia* is demonstrated. A key aspect of JSmol is that it includes the full implementation of the entire set of Jmol functionalities, including file reading and writing, scripting, and rendering. The relative performances of Java-based Jmol and JavaScript-only JSmol are discussed. We can now confirm that the guiding principles of Java programming can be completely and relatively straightforwardly transformed directly into JavaScript, requiring no Java applet, and producing identical graphical results. JSmol is thus the first full-featured molecular viewer, and the first ever viewer for proteins, which can be utilized with an internet browser on handheld devices lacking Java. Since the MediaWiki features of *Proteopedia* have been modified to optionally use JSmol, the wealth of crowd-sourced content in *Proteopedia* is now directly available on such devices, without the need to download any additional applet.

Keywords: bioinformatics · databases · Java · JavaScript · *Proteopedia*

Communicating Science Widely

There is a great need to improve the communication of scientific concepts at all levels, so as to generate a passion for science in the next generation, as well as to increase the public understanding of science. *Proteopedia*[1–3] was developed to tackle this issue via a novel approach. The novelty of *Proteopedia* lies in the implementation of a wiki web resource that presents information on the 3D structure and function of biological macromolecules (Figure 1) as a way of showing the principles of structural biology to a broad audience. This includes a wide range of web users, from high school students to medical school students, from educators looking for a way to engage their students in molecular structure to scientists doing basic and applied research, as well as the general public.

Structural biology is concerned with accumulating structural information at the atomic level for proteins, nucleic acids, and other biological macromolecules. Such detailed information can then be utilized to understand how these macromolecules function, and how they recognize other molecules with which they interact. However, biological macromolecules contain many thousands of atoms and, even when displayed on a computer screen as high-quality 3D representations, are often very difficult to fathom, even for a trained biochemist, let alone for a clinician, a layman, or a high school student.

Proteopedia was constructed with the specific objective of providing a user-friendly tool that would enable under-

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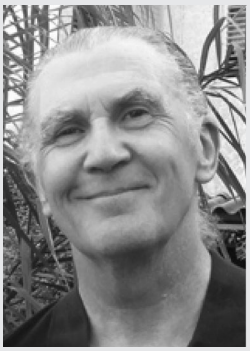
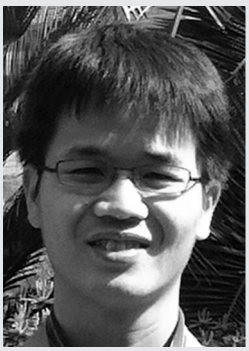
Robert Hanson is the Edolph A. Larson and Truman E. Anderson Sr. Chair of Chemistry and currently serves as chair of the St. Olaf College Chemistry Dept. He joined the St. Olaf faculty in 1986 after earning a B. S. from Caltech, a PhD from Columbia University, and completing postdoctoral work at MIT. Over the course of his career, Hanson has been the recipient of many awards and grants from organizations that include the NSF, NIH, the ACS, DuPont, Eli Lilly, and the W. M. Keck Foundation. Hanson has published numerous articles in the areas of chemistry, material science, informatics, and mathematics, as well as two books: *Molecular Origami: Precision Scale Models from Paper* and *Introduction to Molecular Thermodynamics*. He is the co-inventor on one patent titled *Catalytic Asymmetric Epoxidation* (with K. Barry Sharpless, who received the Nobel Prize in Chemistry in 2001). Since 2006 Hanson has been the project leader and principal developer for the Jmol Molecular Visualization Project, a global open-source interdisciplinary effort to develop novel web-based capabilities for the visualization of molecular structure and energetics. Applicable in a wide range of fields, the Jmol applet can be found on thousands of websites, including the PDB and Proteopedia. In 2010 Jmol became part of an exhibit on nanotechnology in the Innoventions pavilion at the Walt Disney Epcot theme park, where more than 300,000 visitors have interacted with it. He also developed the Interim course Medicinal Chemistry in Jamaica: An International Perspective, which brings students to the University of the West Indies in Kingston, Jamaica, every other year for an in-depth look into how drugs work and how they are designed and developed, with a particular focus on the interactions of culture, traditional healing, and pharmaceutical medicine. Prof. Hanson may be reached at hansonr@stolaf.edu.



Jaime Prilusky is the Head of the Bioinformatics Unit at the Weizmann Institute of Science in Rehovot, Israel. He received his PhD in neuroendocrinology from the National University of Cordoba, Argentina in 1974, and was a full professor at the National Technological University in Argentina before joining the Weizmann Institute in 1989. An early online pioneer in bioinformatics, Jaime developed the first web interface to search and retrieve PDB data, called 3DB, and founded BioMOO (a virtual meeting place for biologists). In addition to Proteopedia his projects include OCA (oca.weizmann.ac.il), a browser-database for protein structure/function and GeneCards (www.genecards.org), an electronic encyclopedia integrating information about the functions of human genes and their products, and of biomedical applications based on this knowledge. For more, see http://miw.weizmann.ac.il. Most recently he, together with Joel Sussman & Eran Hodis, has developed Proteopedia, the free, collaborative 3D encyclopedia of proteins & other molecules (http://proteopedia.org). Prof. Prilusky may be reached at Jaime.Prilusky@weizmann.ac.il.

graduates, graduate students, scientists, and clinical investigators, amongst others, to understand such complex macromolecular structures and how they function as microscopic bio-nano machines. It has not escaped our notice that the development of such a tool for structural biology might serve as a paradigm for developing similar tools for other disciplines, such as astronomy, neuroanatomy, architecture, and paleontology.

Structural biology has played a cutting edge role in the immense progress of life science research over the past 60 years. There have been more than a dozen Nobel Prizes in structural biology since the early 1950s, when Watson and Crick[4] determined the 3D structure of the DNA double helix (Figure 2a). Understanding the basic mechanisms of how protein and nucleic acid molecules function is crucial for biology. For example, without structural insight (Figure 2b), it is impossible to comprehend how the ribosome (the nano-machine that synthesizes all proteins



Zhou Renjian earned his B. S. in Mathematics at Shanghai Jiao Tong University. He worked as a software engineer for IDSignet, Primeton, and Koretide, doing research and development in digital signatures, enterprise software platforms, and computer operating systems. He created the open source project Java2Script, providing an Eclipse plugin for converting existing Java code into JavaScript. He also developed and operated WeBuzz.IM service, providing web messengers for users to connect with their friends on popular instant messaging networks, such as Gtalk, MSN, YMSG, and AIM. Recently, he co-founded Coco Voice with Guo Lei, an app for iOS and Android devices, helping people to send text, voice, and pictures to their friends. Mr. Renjian may be reached at zhourenjian@gmail.com.

Takanori Nakane graduated from Kyoto University's School of Medicine in 2010. After passing Japan's national board exam and qualifying as a medical doctor, Nakane decided to enter a four-year PhD course in X-ray crystallography at Kyoto University instead of clinical practice. While working on "wet" experiments, he realized that he is more attracted to "dry" (computational) aspects of science. Over the last two years, Nakane has been developing molecular viewers for web browsers and mobile devices, including the NDKMol molecular viewer that has been incorporated with the RCSB PDB Mobile app. Nakane also contributes to several open-source projects, including PyMOL and Jmol. Visit http://webglmol.sourceforge.jp to download Nakane's GLmol (Molecular viewer on WebGL/Javascript) and ESmol & NDKmol (Molecular viewer for Android). Dr. Nakane may be reached at nakane.t@gmail.com.

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in all living systems) works. Structural information is also crucial for understanding how regulatory proteins turn genes on and off, by recognizing specific regions of DNA (Figure 2c).

Proteopedia has been used particularly successfully in conjugation with SMART Teams ("Students Modeling A Research Topic" [http://proteopedia.org/w/Group:SMART:Teams], a project developed by Dr. Timothy Herman, Milwaukee School of Engineering). Within the SMART framework, the students, together with their mentors, e.g., professors and/or graduate or undergraduate students at nearby universities, design and build physical models of proteins. They then make an oral presentation explaining their work to a lay audience, and prepare a poster that is presented to a scientific audience. Following this, a number of such teams have also produced *Proteopedia* pages, some of which are spectacular. A striking example of one such *Proteopedia* page is "A Physical Model of the β2-Adrenergic Receptor." This was one of the first examples of a SMART Team *Proteopedia* page, and it is a model of just how well high school students can communicate the essence of the relationship of the 3D structure of a protein to its function (Figure 3).

Joel L. Sussman is the Morton and Gladys Pickman Professor of Structural Biology at the Weizmann Institute of Science, and the Director of the Israel Structural Proteomics Center (ISPC, http://www.weizmann.ac.il/ISPC). He is a member of EMBO, a Fellow of the AAAS, on the Executive Board of the Int'l Structural Genomics Org (ISGO) and on the editorial board of *Proteins*, *PEDS* & *PLoS ONE*. He is an Honorary Professor of the Chinese Academy of Sciences, received the Bergmann Prize for Outstanding Research in Chemistry in Israel (1979), the U.S. Army Science Conference Award for Outstanding Research (1991), the Elkeles Prize for Outstanding Scientist in Medicine in Israel (2005) and the Teva Founders Prize for Breakthroughs in Molecular Medicine (2006). From 1994 to 1999 he was the director of the Brookhaven PDB. He obtained his B. A. at Cornell University in 1965, and his PhD in biophysics at MIT in 1972. His research group, at the Weizmann, is studying the 3D structure/function of nervous system proteins, including β-secretase, acetylcholinesterase, cholinesterase-like adhesion molecules (CLAMs), β-glucosidase (the enzyme that is defective in Gaucher disease) and paraoxonase (a key enzyme that helps rid the arteries of plaque-forming clumps of LDL, "bad" cholesterol, that can lead to arteriosclerosis). The goal of his research is to use the 3D structures of proteins as a basis for new leads for treating neurological disorders, such as Alzheimer's Disease, autism, and in developing new therapies for Gaucher and arteriosclerosis. He is also studying intrinsically disordered proteins. Most recently he, together with Jaime Prilusky & Eran Hodis, has developed Proteopedia, the free, collaborative 3D encyclopedia of proteins and other molecules (http://proteopedia.org).

Proteopedia also enables users to supplement their scientific publications with Interactive 3D Complements (I3DCs) (http://proteopedia.org/w/Interactive_3D_Complements_in_Proteopedia). A new "Workbench" feature (http://proteopedia.org/w/Workbenches), intended expressly for the creation of articles complementing upcoming scientific publications, allows authors to hide their protected article during its development. These hidden pages may be made accessible for viewing and editing by co-authors, referees and editors, and can quickly be made public upon publication of the accompanying paper. Such I3DCs for publications have already been used effectively (Figure 4). Already 65 such I3DCs, associated with articles published in 12 different journals, have been generated (http://proteopedia.org/w/Special:SpecialI3DC).

Interactive Molecular Visualization

Proteopedia's unique character hinges on the fact that it allows a relative novice to create a story around an interactive molecular visualization that the reader can then explore on his or her own, or with a variable amount of guidance. This capability has been made possible by a rich history of technological developments. Over the course of the last 50 years, the interactive 3D representation of molecular structures has changed dramatically. From Levinthal's Kluge[5,6] (Figure 5) to current capabilities, we have seen an enormous transition from graphics intended for private viewing on specialized main-frame computers, to graphics that run on literally billions of personal hand-held devices. With the advent of the web, and the development of the Chime plug-in in the 1990s, chemists,[7] biochemists, and molecular biologists finally obtained a means of communicating their research results and teaching lessons that related to molecular structure in an interactive form. Chime's nature as a Netscape browser plug-in was both its strength and its downfall. While it made interactive structure manipulation widely available, it was not compatible with newer technologies, and had to be abandoned.

One of these newer technologies was Java, introduced into browsers as its own Netscape plug-in in 1995.[8] For roughly two decades, Java has served the web community as a ubiquitous mechanism for delivering interactive web-based content. Capitalizing on the widespread availability of Java, the developers of Jmol found ways to deliver essentially all of the capabilities of RasMol and Chime, along with many additional capabilities that crossed into additional scientific fields, such as inorganic chemistry, crystallography, and materials science. To date, hundreds, if not thousands, of web sites–far too many to list here–utilize the Jmol Java applet (Figure 6) to enhance their content and provide an interactive visitor experience.

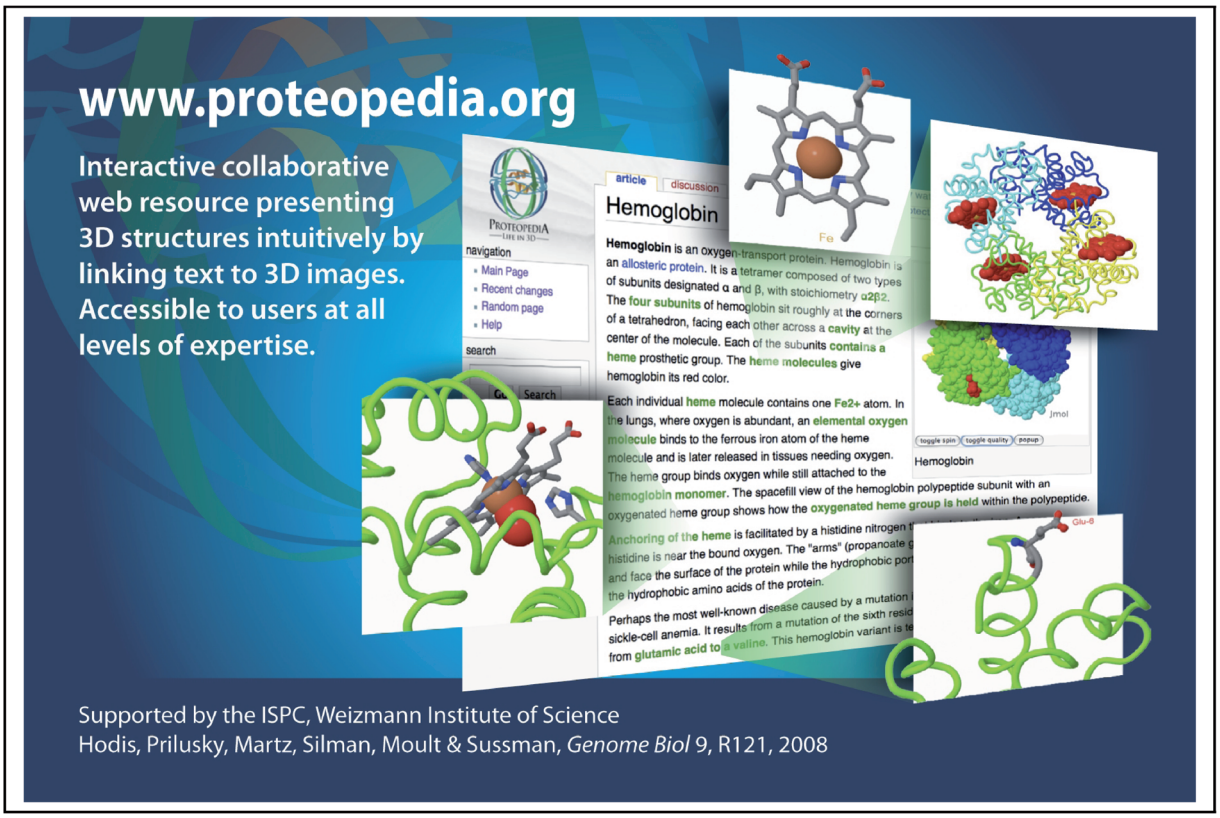

Figure 1. The hemoglobin page in *Proteopedia* (http://proteopedia.org/w/Hemoglobin), a typical *Proteopedia* page. It displays the red blood cell protein, hemoglobin, in the center, surrounded by representations of individual 3D images of functional parts of the protein, which are displayed as the viewer clicks on a particular highlighted hyperlink in the explanatory text.

Creating Value

The key to Jmol's success and wide acceptance by the web development community has been the way it, like its predecessor Chime, has enabled a completely new type of "developer" to create value. Whereas traditional 3D software development (still) involves a software developer (usually a professional engineering team or a motivated computer-savvy amateur) and a user (often a well-trained, experienced scientist), these web-based tools are different. The Jmol[3] software designers are programmers in the traditional sense. The ultimate users of these tools, however, are true *novices,* who have, most probably, absolutely no experience in running 3D software tools. Instead, they are simply visitors to web sites–students, non-scientists, and professional scientists alike. What lies in between these two constituents is what makes Jmol so interesting: a large group of web page designers, mostly amateurs in the programming world, including scientists and educators who have learned a bit of JavaScript and HTML and are able to express their creativity in the form of web sites. In effect, the Jmol applet provides a blank slate upon which molecularly minded scientists in a wide variety of fields can create customized visual portals into their worlds. The "value-added" nature of Jmol includes a rich high-level scripting language with nearly 1,000 semantic tokens embedded in a fully functional, mathematically based programming language that permits the sophisticated manipulation of molecular "objects." On top of that, Jmol's user-developers have designed a JavaScript library that makes customization exceptionally easy.

Due to the flexibility and wide-ranging capabilities of Jmol, the crowd-sourcing of web page content creation to this group of dedicated "Jmol users" (in effect, web page developers) has been enormously productive over the past 5–10 years. Pages range from very simple to highly complex, and from displays of just one molecule to full web-based applications, e.g., *Proteopedia*, First Glance,[9] the CheMagic Virtual Molecular Model Kit,[10] and many others.

The Java Dilemma

Recently, however, between Apple's decision not to allow Java on their iOS platform and the Java browser plug-in coming under fire as a possible security risk,[11] we find ourselves once more at a technology cusp. No longer is the Java plug-in ubiquitous. As a consequence, as technol-

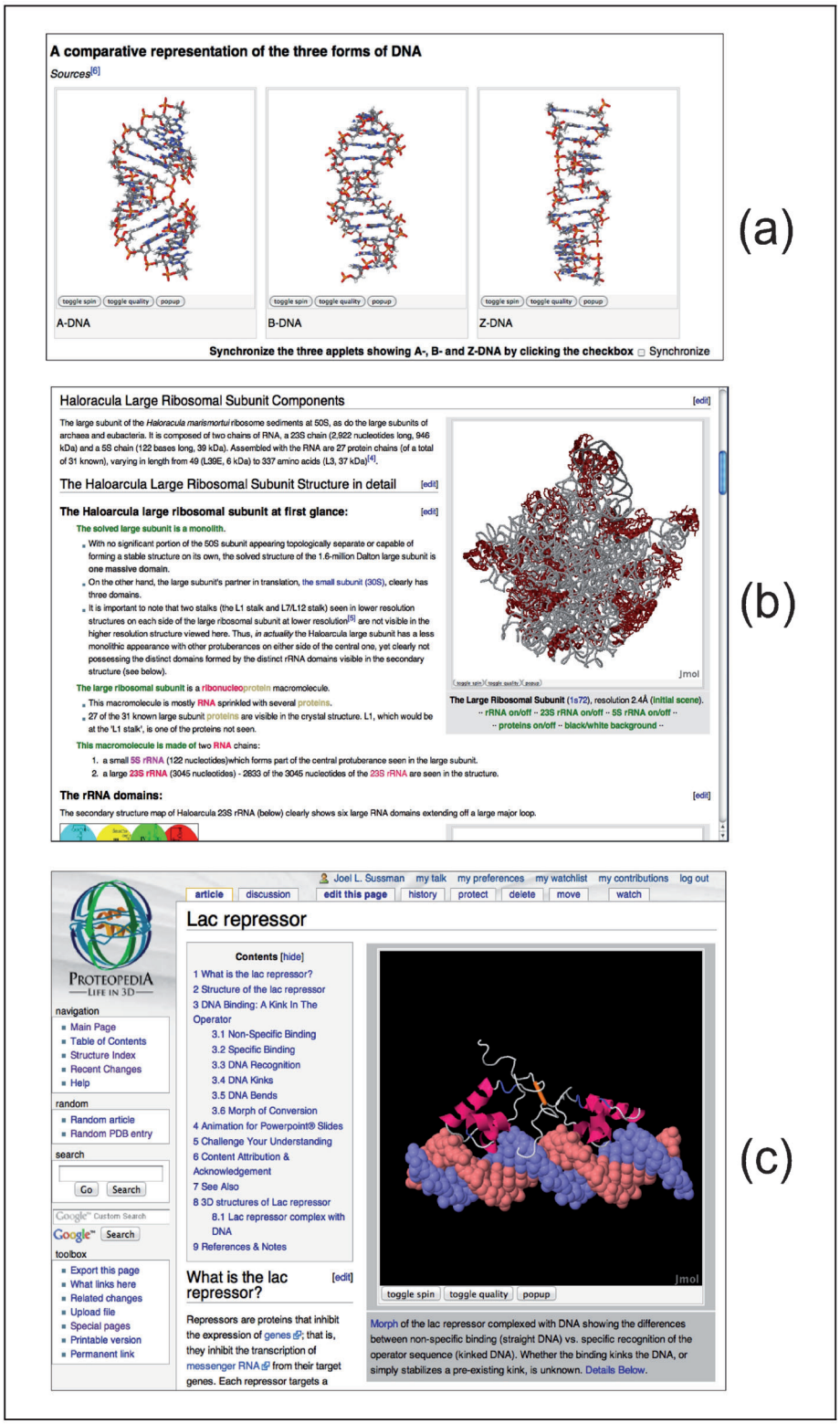

Figure 2. Important biomacromolecules as represented in *Proteopedia*. (a) Forms of DNA; showing 3D models of A-, B-, and Z-DNA that can be synchronized to illustrate differences between them (by Adithya Sagar, a visiting student at the Weizmann Institute of Science from the India Institute of Technology;[22] http://proteopedia.org/w/Forms_of_DNA). (b) Large ribosomal subunit (by Dr. Wayne Decatur, postdoctoral fellow at University of New Hampshire;[23] http://proteopedia.org/w/Large_Ribosomal_Subunit_of_Haloarcula). (c) Structure of a complex of a regulatory protein with its gene (by Prof. Eric Martz at University of Massachusetts; http://proteopedia.org/w/Lac_repressor).

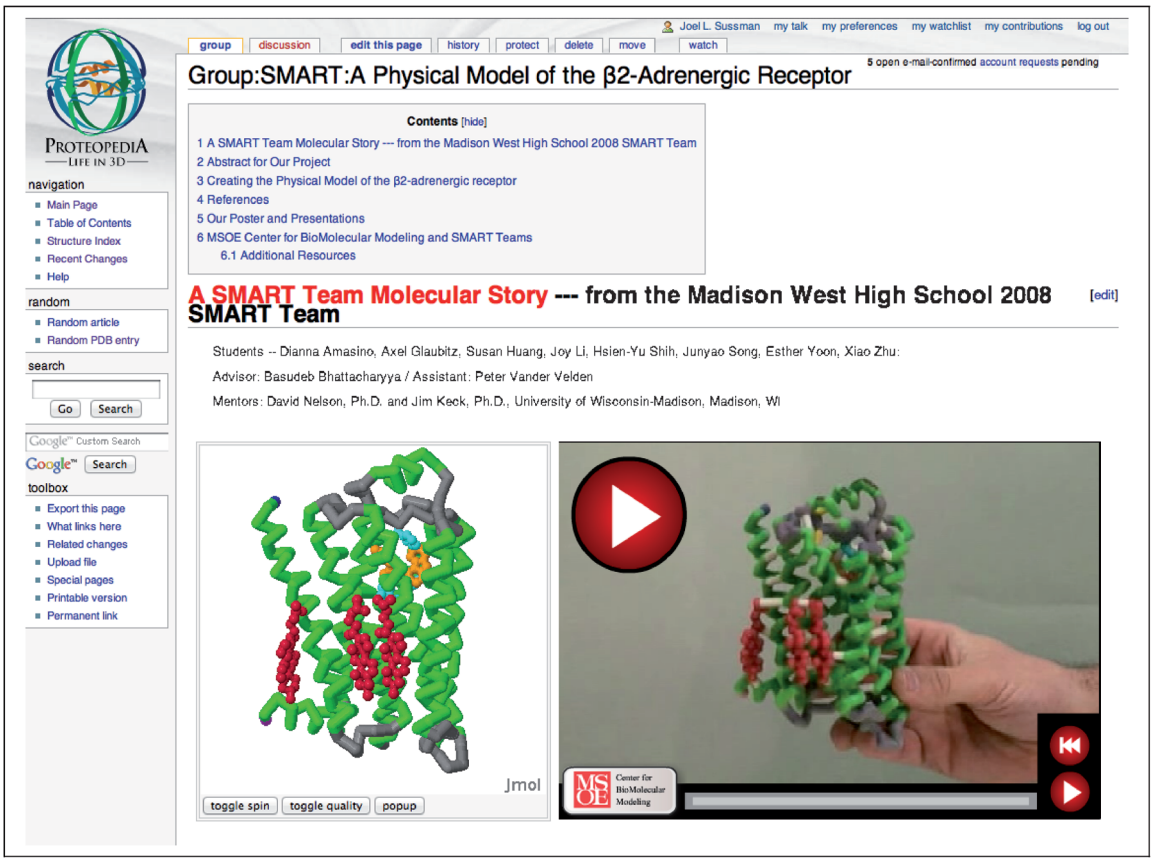

Figure 3. *Proteopedia* use in pedagogy. *Proteopedia* page: "A Physical Model of the β2-Adrenergic Receptor" (http://proteopedia.org/w/Group:SMART:A_Physical_Model_of_the_β2-Adrenergic_Receptor) authored by the Madison West High School SMART team. To the right of the interactive 3D structure is a movie that the SMART team created and uploaded, which uses a physical model of the receptor to explain its structure and function.

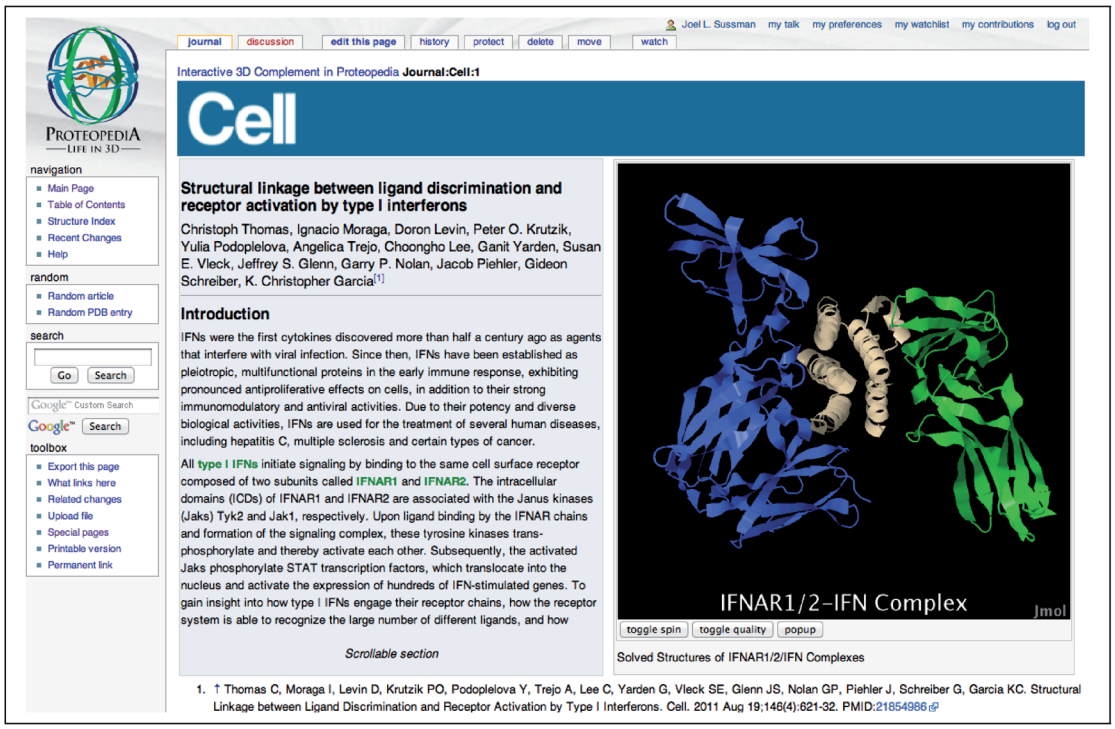

Figure 4. Example of an I3DC (http://proteopedia.org/w/Journal:Cell:1) for a recent paper on interferon, published in Cell.[24]

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Figure 5. Image of the Kluge, one of the earliest (if not the earliest) molecular graphics systems, which was developed by Cyrus Levinthal at MIT in the early 1960s. The computer was a Digital Equipment Corp. (DEC) PDB-7, and the glass hemisphere was a powerful interactive device that permitted rotation in three dimensions.

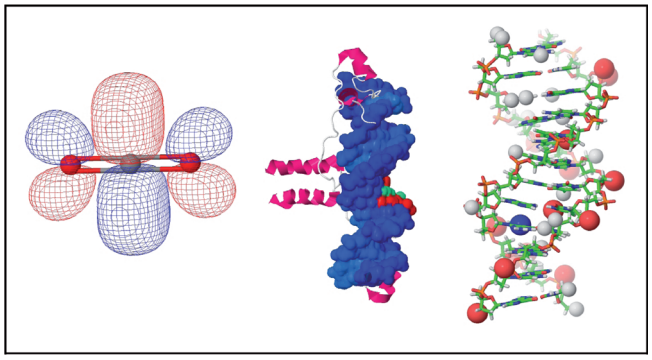


Figure 6. Examples of the broad range of visualizations possible with Jmol/JSmol, including a small molecule with molecular orbitals, a biomolecule with surfaces, and a PyMOL session.

ogy advances, web applications, such as *Proteopedia*, are at risk of losing their audience. This time it is Java that is losing its hold, and the new technology is HTML5.[12] Combined with WebGL[13] (a browser-based version of OpenGL[14]), HTML5 allows reasonable speed in rendering complex 3D graphical scenes. Now available in all significant browsers, HTML5 holds the promise of delivering 3D molecular content without Java. However, WebGL is not generally available on mobile operating systems (most notably not on iOS or Android).

Will HTML5 indeed serve as a suitable replacement for Java, in terms of the interactive graphical representation of molecular structure on the web? This was the question that we, as Jmol and *Proteopedia* developers, posed in the fall of 2012. The fear was that we would have to start all over again, as some bold developers have attempted to do, e.g., iChemLabs.[15] However, such an option seemed extremely daunting for such a feature-filled program as Jmol and such a complex application as *Proteopedia*. Nonetheless, the decision was made to explore the possibility of using HTML5, with or without WebGL, and the results of that exploration are presented here.

Java-less Jmol?

The fact that Jmol is written in Java suggests that perhaps its run is over, that it needs to give way to a new generation of technology. However, there are two important aspects of Jmol that suggest that this might not be necessary. First, Jmol is written in a highly modularized style of Java programming. From the start, it was recognized that success on the web involves targeted downloads, allowing only the parts necessary for a given application to be downloaded, and the program to be delivered incrementally. This modularization might easily be transferable into JavaScript,[16] allowing, again, targeted download of Jmol features on a need-to-use basis. Second, Jmol has been developed in a truly unusual way, utilizing absolutely *no* external 3D graphics packages. Every pixel that a user sees as a model is manipulated in a Jmol rendering, and is created on the fly, using exceptionally efficient rastering techniques. This allows Jmol (in whatever programming language) to be completely independent of the computer/tablet operating system employed, and allows it to be the first full-featured molecular viewer for web browsers to become available on Apple's iPad.

We can now confirm that these guiding principles of Java programming can be completely and relatively straightforwardly transformed directly into JavaScript, requiring no Java applet, and producing identical graphical results. Thus, over the course of the past six months, we have been able to completely recreate Jmol in pure JavaScript, in the form we now refer to as JSmol.[17] Key to this development has been the use and co-development of the Java2Script Eclipse Plug-In,[18] a remarkable piece of software that allows "compiling" of Java code directly into JavaScript. A huge benefit of using Java2Script has been that Jmol development can still be done in Java, producing all the Java compiled versions (Jmol desktop application, JmolData server application, and the signed and unsigned Jmol applets), just as before. A few simple steps within the Eclipse programming environment compile that code into JavaScript.

Substantial optimization of the Jmol Java code, of the portions of the Java language utilized by Jmol, and of the compiler itself, was necessary to achieve this success. Many routine Java techniques (such as the overriding of methods by sub-classing or the overloading of methods by using multiple "signatures") must be completely avoid-

Table 1. Relative performance comparison of Jmol and JSmol.[a]

	Jmol	JSmol
core download (MB)[b]	1.0	2.2
core + bio package download (MB)[c]	1.1	2.4
Small-molecule loading time (ms)[d]	90	60
Small-protein loading time (ms)[e]	120	140
Large-protein loading time (ms)[f]	730	2600
Large-protein rendering time (ms)[g]	11/12	95/85
Small-protein surface creation time (ms)[h]	150	1250
PyMOL session file loading (ms)[i]	96	750

[a] Performance will vary with platform, browser, and machine; the reported testing was carried out using Firefox 18.0.2/Windows 8 on a Toshiba Satellite P845t laptop with i5–3317U 1.70 GHz CPU and 6 GB memory; [b] includes JmolApplet0.jar vs. core.z.js + corescript.z.js; [c] adds JmolApplet0ShapeBio.jar or core.bio.js; [d] loading caffeine model; [e] loading 1CRN (49 KB, 327 atoms); [f] loading 2bxaH (2BXA, with hydrogen atoms, 1.4 MB, 16,731 atoms); [g] rendering of 2bxaH as balls and sticks/as cartoons; [h] 1CRN, 1.2 Å solvent-accessible surface; [i] loading dna.pse (DNA 12-mer scene, 796 atoms).

ed in critical code sections. Needless to say, a substantial amount of experimentation was necessary. In the end, however, the results achieved are impressive: A fully functional JavaScript-only version of Jmol now runs on all modern browsers, including Internet Explorer, Firefox, Safari, Chrome, and Opera, and on all platforms tested, including Windows, Linux, Apple OS X, and Apple iOS.

A comparison of Jmol and JSmol is provided in Table 1. Not surprisingly, Jmol is more compact than JSmol, by a factor of ~2–3. Much of this difference is due to the fact that the Java language library is already present on the client machine, in the form of a Java plug-in, and that the Java code is in a binary format. In contrast, when a page utilizing JSmol is accessed, the required components of the Java language, translated into non-binary JavaScript, must be downloaded in full. In both cases, however, files are cached, and subsequent page views are far faster than the first viewing.

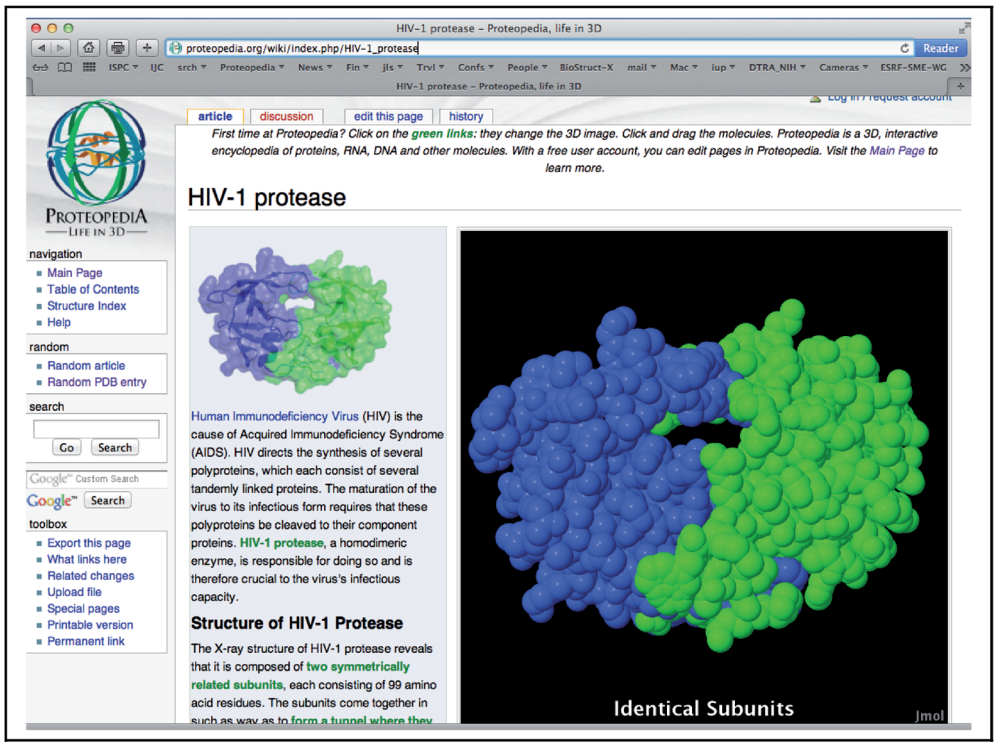
Performance with small molecules is very similar in the two versions, but clearly JavaScript does not scale at the same rate as Java. Today's JavaScript lacks many of the basic features of Java, including integer and bit set data types, both of which are widely used in Jmol/JSmol. These types have to be "faked" in JavaScript using double-precision numbers, leading to performance issues. Developers of different browsers have optimized their JavaScript implementations in different ways and to different extents, resulting in significant performance differences between browsers. The end result is that model production can take significantly more time in JavaScript, and, for large systems, model rotation may seem somewhat sluggish in comparison to Jmol.

JSmol with WebGL

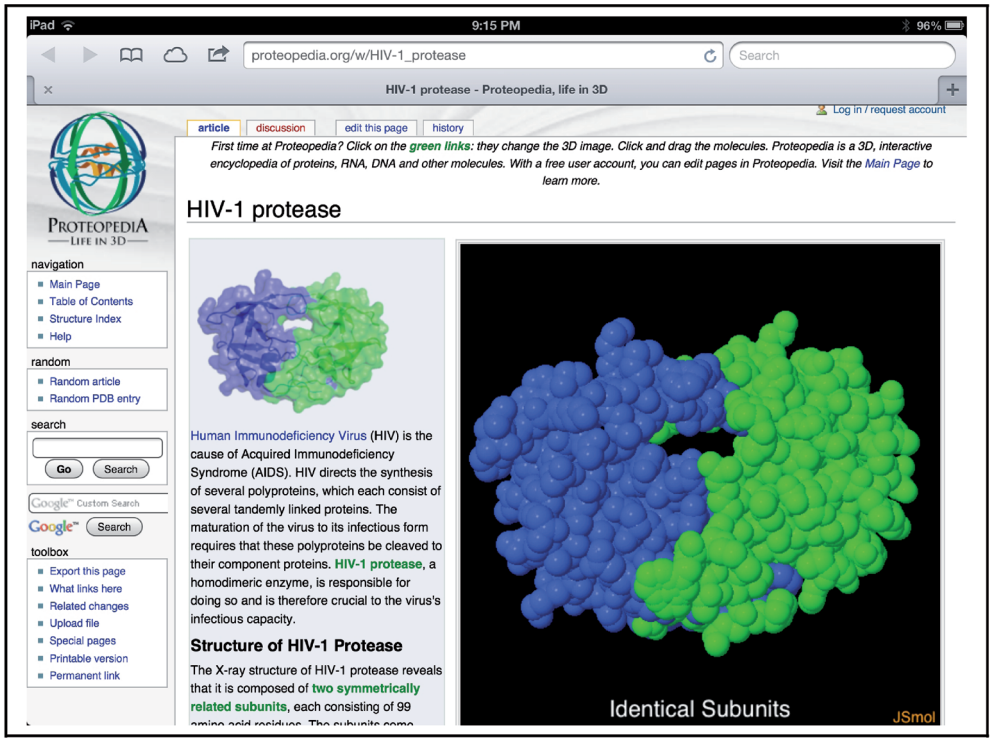
The above discussion relates to the pure HTML5 version of JSmol, which uses a 2D-only canvas to render scenes. We have also been experimenting with WebGL, which allows for hardware acceleration of 3D rendering similar to OpenGL. Our efforts have not been as advanced in this area, partially because writing WebGL export drivers for Jmol is somewhat more complicated than a direct translation of Java into JavaScript. Our starting point in this effort has been GLmol,[19] a web-based viewer that was developed by one of us (TN). The fact that Apple has also disabled WebGL in its browser for the iPad has slowed this development somewhat. Nonetheless, WebGL-based versions of JSmol could potentially provide an alternative to our current HTML5-only solution.

JSmol in Proteopedia

The sophisticated and feature-demanding nature of *Proteopedia* poses an excellent challenge for JavaScript-based interactive molecular graphics. We are happy to report that, despite the performance limitations of JavaScript, utilization of JSmol has been successfully implemented in Proteopedia. As described elsewhere,[1,2] Proteopedia runs on top of MediaWiki,[20] an open source collaborative environment that provides Proteopedia the basic infrastructure for community editing. To maintain the smooth wiki-3D structure integration characteristic of Proteopedia, we have developed JSmolExtension,[21] a dedicated software that enables MediaWiki to display 3D structures using JSmol, utilizing the best available rendering engine–whether it be WebGL, HTML5, Java–or resorting to a static image, in the unlikely case that either none of these is available or that the available engine is limited too much by performance issues. JSmolExtension provides full backward compatibility, enabling Proteopedia to display the >90,000 pages created utilizing Jmol on Java-less devices, such as the Apple iPad (Figure 7) and Google Android tablets. The Proteopedia server is able to sense the client's device, whether it is a computer or a Java-less device, and then automatically delivers the *Proteopedia* page requested with the appropriate viewer.



(a)



(b)

Figure 7. Comparison of *Proteopedia* pages showing the HIV-1 Protease in (a) Jmol on a MacBookPro (using the Safari browser), and (b) JSmol on an iPad (using the Safari browser).

Conclusions

Clearly, a new age of web-based molecular visualization is at hand. Technology is changing rapidly, and great opportunities are opening up for meaningful, interactive, 3D molecular visualization over the web that will be able to reach millions of people in ways that could not have been imagined only a decade ago. If the international collaboration that has propelled *Proteopedia* and JSmol to the frontier of this new age is any indication of what will be, we can anticipate many more full-featured web-based tools built by students, educators, and practicing scientists in the near future.

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