

Subject: YASARA now available for free download
From: Elmar Krieger <elmar.krieger@cmbi.kun.nl>
Date: Mon, 03 Nov 2003 12:01:59 +0100
To: rasmol@lists.umass.edu

Dear all,

after 10 years of development, we are happy to announce the release of YASARA - a molecular graphics, -modeling and -simulation program for Linux and Windows.

Free download from <http://www.yasara.org>

Why yet another one?

- A new approach to OpenGL graphics, up to 35 times faster than usually: atoms are truly round, and you can even walk through the ribosome (100000 atoms) fluently, also in stereo.

- Lots of multimedia elements: display text in 3D letters, load and animate images including alpha channel/transparency, create your own molecular movies and presentations. People use it instead of PowerPoint when giving a talk. See <http://www.yasara.org/movies> for examples.

- New molecular dynamics force fields, optimized for maximum accuracy required in protein structure prediction: <http://www.yasara.org/yamber>

- Interactive real-time simulations: just pull atoms and molecules around during a simulation, and work with dynamic models instead of static pictures.

- Publication-quality ray-traced images including labels and arrows. No Photoshop post-processing required, label the atoms directly in YASARA. <http://www.yasara.org/raytrace>

- Intuitive user interface with context menus and a sequence selector that zooms in on your favorite residues.

- Lots of analysis and molecular modeling functions. Building, contacts, RMSDs..

- Program your own plugins in Python to extend YASARA with new functions.

- Powerful macro language (Yanaconda) and selection syntax.

That's it for the most important features,
many thanks to Eric Martz for the invitation to post here!

Best greetings and hope to see you soon (in the download log 😊),
Elmar

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=WHAT IF YASARA knows the answer?!=

=---- <http://www.yasara.org> ----=

=- <http://www.cmbi.kun.nl/whatif> -=

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