

Hasan Baig, Pedro Fontanarossa, Vishwesh Kulkarni, James McLaughlin, Prashant Vaidyanathan, Bryan Bartley, Shyam Bhakta, Swapnil Bhatia, Mike Bissell, Kevin Clancy, Robert Sidney Cox, Angel Goñi Moreno, Thomas Gorochoowski, Raik Grunberg, Jihwan Lee, Augustin Luna, Curtis Madsen, Goksel Misirli, Tramy Nguyen, Nicolas Le Novere, Zachary Palchick, Matthew Pocock, Nicholas Roehner, Herbert Sauro, James Scott-Brown, John T. Sexton, Guy-Bart Stan, Jeffrey J. Tabor, Logan Terry, Marta Vazquez Vilar, Christopher A. Voigt, Anil Wipat, David Zong, Zach Zundel, Jacob Beal* and Chris Myers

Synthetic biology open language visual (SBOL Visual) version 2.3

<https://doi.org/10.1515/jib-2020-0045>

Received December 10, 2020; accepted January 11, 2021; published online June 7, 2021

Abstract: People who are engineering biological organisms often find it useful to communicate in diagrams, both about the structure of the nucleic acid sequences that they are engineering and about the functional relationships between sequence features and other molecular species. Some typical practices and conventions have begun to emerge for such diagrams. The Synthetic Biology Open Language Visual (SBOL Visual) has been

This document does not contain technology or technical data controlled under either the U.S. International Traffic in Arms Regulations or the U.S. Export Administration Regulations.

***Corresponding author: Jacob Beal**, Raytheon BBN Technologies, Cambridge, USA, E-mail: editors@sbolstandard.org. <https://orcid.org/0000-0002-1663-5102>

Hasan Baig, University of Connecticut, Storrs, USA

Pedro Fontanarossa, Logan Terry and Zach Zundel, University of Utah, Salt Lake City, USA. <https://orcid.org/0000-0002-0535-2684> (P. Fontanarossa)

Vishwesh Kulkarni, University of Warwick, Coventry, USA

James McLaughlin, Angel Goñi Moreno and Anil Wipat, Newcastle University, Newcastle upon Tyne, UK

Prashant Vaidyanathan, Microsoft Research, Cambridge, UK

Bryan Bartley, Tramy Nguyen and Nicholas Roehner, Raytheon BBN Technologies, Cambridge, USA

Shyam Bhakta, Jihwan Lee, John T. Sexton, Jeffrey J. Tabor and David Zong, Rice University, Houston, USA. <https://orcid.org/0000-0002-5426-2765> (J. Lee), <https://orcid.org/0000-0002-8157-4780> (D. Zong)

Swapnil Bhatia and Curtis Madsen, Boston University, Boston, USA

Mike Bissell, Shipyard Toolchains LLC, Emeryville, USA

Kevin Clancy, Thermo Fisher Scientific, San Diego, USA

Robert Sidney Cox, Kobe University, Kobe, Japan

Thomas Gorochoowski, University of Bristol, Bristol, UK

Raik Grunberg, KAUST, Thuwal, Saudi Arabia

Augustin Luna, Harvard Medical School, Boston, USA

Goksel Misirli, Keele University, Keele, UK

Nicolas Le Novere, Babraham Institute, Cambridge, UK

Zachary Palchick, Zymergen, Emeryville, USA

Matthew Pocock, Turing Ate My Hamster, Ltd., Newcastle, UK

Herbert Sauro, University of Washington, Seattle, USA

James Scott-Brown, University of Oxford, Oxford, UK

Guy-Bart Stan, Imperial College, London, UK

Marta Vazquez Vilar, Universitat Politècnica de Valencia, Valencia, Spain

Christopher A. Voigt, MIT, Cambridge, USA

Chris Myers, University of Colorado Boulder, Boulder, USA

developed as a standard for organizing and systematizing such conventions in order to produce a coherent language for expressing the structure and function of genetic designs. This document details version 2.3 of SBOL Visual, which builds on the prior SBOL Visual 2.2 in several ways. First, the specification now includes higher-level “interactions with interactions,” such as an inducer molecule stimulating a repression interaction. Second, binding with a nucleic acid backbone can be shown by overlapping glyphs, as with other molecular complexes. Finally, a new “unspecified interaction” glyph is added for visualizing interactions whose nature is unknown, the “insulator” glyph is deprecated in favor of a new “inert DNA spacer” glyph, and the polypeptide region glyph is recommended for showing 2A sequences.

Keywords: diagrams; SBOL Visual; standards.