

Synthetic Biology Open Language Visual (SBOL Visual), version 1.0.0

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1. Purpose

In this BioBricks Foundation Request for Comments (BBF RFC), we specify the Synthetic Biology Open Language Visual standard (SBOL Visual) to enable consistent, human-readable depiction of genetic designs.

2. Relation to other BBF RFCs

BBF RFC 93 REPLACES BBF RFC 16

3. Copyright Notice

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4. Description of SBOL Visual

The Synthetic Biology Open Language Visual (SBOL Visual) project is an effort to create an open-source graphical notation to support the description and specification of genetic designs. SBOL Visual is intended for use by biological engineers in forward engineering projects. It aims to encourage and support model-driven engineering by establishing a common set of symbols.

SBOL Visual Version 1.0.0 consists of a set of symbols that can be used to graphically depict functional information encoded by nucleic acid sequences. Each symbol in the set has three components: a shape, a display name, and a definition.

SBOL Visual symbol shapes are defined by spatial pattern, in a manner similar to alphanumeric characters. Stylistic features such as line width and color are left unspecified. When using symbols to represent parts or features in sequence, horizontal alignment and/or use of one or more lines to connect the symbols is RECOMMENDED. In such cases, the default configuration of the symbol shapes presented in Section 7 of this document implies that the genetic part is oriented in a 5' to 3' direction on the positive strand of the DNA molecule. Symbols that are both horizontally and vertically symmetric and represent parts on the positive strand SHOULD be positioned with their centers above the line. Negative strand conventions are a 180-

degree rotation of the positive strand. See www.sbolstandard.org/visual/bestpractices for examples.

SBOL Visual symbol display names reflect the common name for the entity represented by the relevant symbol, and are used when describing the symbol textually.

SBOL Visual symbol definitions, in version 1.0.0, are established by association with terms in the Sequence Ontology (SO). Use of the SO allows SBOL Visual to leverage the rich relational information encoded in the ontology. Use of the SO also enables greater coordination with the SBOL Core Data Model, as SBOL Core uses SO terms as a controlled vocabulary for the type field of DNA Component. Where possible, SBOL Visual symbol definitions take the form of the SO accession number for the appropriate SO term. Inclusion of symbols in SBOL Visual that represent entities not yet defined within the SO SHOULD be accompanied by a request to the SO (www.sequenceontology.org) to add a term for the undefined entity. The concise definition submitted to the SO serves as the definition for the SBOL Visual symbol while the term is awaiting approval.

The full SBOL Visual Symbol Set is presented below in Section 7 and is available in computer-readable format on the SBOL Visual Website. Details about the serialization can be found at www.sbolstandard.org/visual/serialization.

5. Adoption of SBOL Visual

SBOL Visual adoption is the use of SBOL Visual symbols when pictorially representing designs that contain sequence features covered by the standard. Use of images consistent with the SBOL Visual symbols presented in Section 7 constitutes SBOL adoption. A set of image files for the SBOL Visual symbols are available at www.sbolstandard.org/visual/download. These image files are normative and use of them is NOT REQUIRED for adoption of SBOL Visual.

SBOL Visual can be adopted in a variety of contexts, including informal human-to-human communication, such as “whiteboard” discussions, semi-formal and formal human-to-human communication, such as slide presentations and scientific publications, and human-computer communication for design specification using computer-aided design (CAD) tools. Examples of diagrams expressed using SBOL Visual can be found on the SBOL Visual Best Practices page, at www.sbolstandard.org/visual/bestpractices. SBOL Visual is currently adopted by several software tools and has been used in scientific publication.

6. Changes to SBOL Visual

SBOL Visual is community-driven and open source. An initial set of biological concepts to represent in SBOL Visual was chosen heuristically based on type presence and predominance in conventional description of genetic designs. The symbol shapes chosen to represent these initial features were inspired by conventional depictions of these features.

We expect addition and refinement of SBOL Visual symbols, as well as growth in the scope of concepts covered by the standard, i.e., entities that are not sequence feature types. For instance, development of representations for regulatory relationships between DNA Components is expected. Community input is crucial to the success of the SBOL Visual project. Feedback to the standard is gathered via comments made on the specification document, accessible as a google document from www.sbolstandard.org/visual/specification, or via email to visual@sbolstandard.org. Additions to the symbol set will be facilitated through open submission and discussion at www.sbolstandard.org/visual/sandbox. Instructions for submitting symbols can be found at this location. Questions regarding SBOL Visual can be directed to visual@sbolstandard.org.

Updates to the SBOL Visual Specification will be made by the SBOL Visual Working Group Leads in concordance with the recommendations of the SBOL Visual Working Group members. Updates will be approved by rough consensus by the SBOL Developers Group. Interested parties may join the SBOL Developers' Group and SBOL Visual Working Group by contacting sbol-editors@googlegroups.com. All members of the SBOL Visual Working Group MUST also be members of the wider SBOL Developers' Group.

All versions of the SBOL Visual Specification will be available on the SBOL Visual web page at www.sbolstandard.org/visual/specification. The working document of the latest version will also be available and open to comments. Declaration of version number when claiming adoption of SBOL Visual is RECOMMENDED.

SBOL Visual follows a versioning strategy based on that of Synthetic Biology Open Language (SBOL), specified in BBF RFC 87. SBOL Visual version numbers MUST take the form X.Y.Z where X, Y, and Z are integers. X is the major version, Y is the minor version, and Z is a patch version. Each element MUST increase numerically. For instance: 1.9.0 < 1.10.0 < 1.11.0.

Major versions (X) correspond to releases of SBOL Visual. Such releases may involve, but are not limited to, representation of new domains such as regulatory interaction, or changes to the way in which symbols shapes and definitions are specified. The submission of the specification document to the BioBrick Foundation as a Request For Comment (BBF RFC) and release of an up-to-date symbol set serialization is REQUIRED.





Minor versions (Y) correspond to revisions to the specification as approved by the SBOL Visual Working Group. Such revisions may include, but are not limited to, addition of types to the symbol set, changes to SO mappings of existing symbols, and changes to the reference shape of existing symbols. The submission of the specification document to the BioBrick Foundation as a Request For Comment (BBF RFC) is OPTIONAL and release of an up-to-date symbol set serialization is REQUIRED.







Patch versions (Z) correspond to draft revisions made by the SBOL Working Group during the specification process. Patch changes may include, but are not limited to, approval of pending SO accession numbers and copy-edits to documentation wording. The submission of the







specification document to the BioBrick Foundation as a Request For Comment (BBF RFC) is NOT RECOMMENDED.






As the standard grows, community feedback will generate bottom-up growth and maturation of the symbol set. In tandem, top-down curation by the SBOL Visual Working Group will ensure consistency of the standard. By mixing bottom-up and top-down approaches to advancing this effort, we aim to converge on a standard that is both intuitive and rigorous enough to support effective and safe biological engineering.

7. The SBOL Visual Symbol Set

Shape	Display Name	Definition
	Promoter	SO:0000167
	Operator	SO:0000057
	CDS	SO:0000316
	Ribosome Entry Site	SO:0000139

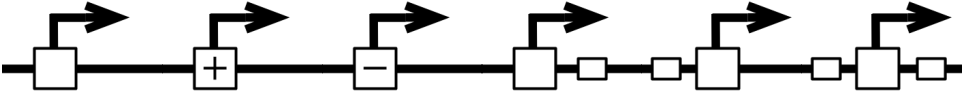









	Terminator	SO:0000141
	Insulator	SO:0000627
	Ribonuclease Site	SO Pending A region of DNA sequence that codes for a ribonuclease cleavage site on the RNA transcript.
	RNA Stability Element	SO:0001957
	Protease Site	SO:0001956
	Protein Stability Element	SO:0001955

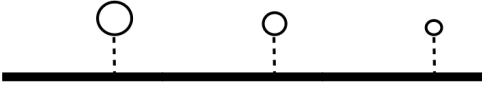

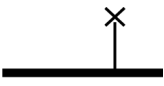

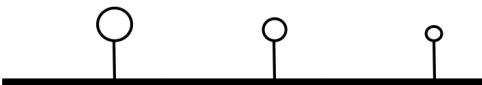

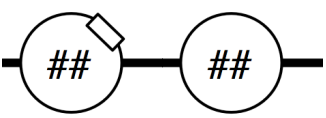



	Origin of Replication	SO:0000296
	Primer Binding Site	SO:0005850
	Restriction Enzyme Recognition Site	SO:0001687
	Blunt Restriction Site	SO:0001691
	5' Sticky Restriction Site	SO Pending A restriction enzyme recognition site that, when cleaved, results in 5' overhangs.
	3' Sticky Restriction Site	SO Pending A restriction enzyme recognition site that, when cleaved, results in 3' overhangs.









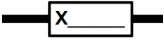

	5' Overhang	SO:0001933
	3' Overhang	SO:0001932
	Assembly Scar	SO:0001953
	Signature	SO Pending A region of DNA sequence where developer information is encoded.
	User Defined	A region of a DNA sequence not covered by other SBOL Visual symbols.


8. Transition from SBOL Visual 0.0.0 to SBOL Visual 1.0.0

SBOL Visual as specified in BBF RFC 16 has been retroactively assigned version number 0.0.0 (previously 0.9) under the current versioning scheme. Prior to BBF RFC 93, SBOL Visual's symbol set underwent some significant changes, available on the SBOL website under the title SBOL Visual 1.0 alpha, but not officially published or voted on by the SBOL Developers Group. SBOL Visual 1.0 alpha has been assigned version number 0.1.0 under the current versioning scheme. The specification of SBOL Visual versions 0.0.0 and 0.1.0 can be found at www.sbolstandard.org/visual/specification. Below is a mapping from the symbols SBOL Visual 0.0.0 to the symbol set of SBOL Visual 1.0.0.

0.0.0	1.0.0
 <p>Constitutive Promoter, Inducible Promoter, Repressible Promoter, Promoter with Downstream Operator, Promoter with Upstream Operator, Promoter with Upstream and Downstream Operators</p>	 <p>Promoter</p>
 <p>Translation Start Site</p>	 <p>Ribosome Entry Site</p>
 <p>Open Reading Frame</p>	 <p>CDS</p>
 <p>Terminator, Bidirectional Terminator</p>	 <p>Terminator</p>
 <p>Ribonuclease Site</p>	 <p>Ribonuclease Site</p>

 <p>RNA Stability Element, "Stable", RNA Stability Element, "Intermediate", RNA Stability Element, "Unstable"</p>	 <p>RNA Stability Element</p>
 <p>Protease Site</p>	 <p>Protease Site</p>
 <p>Protein Degradation Element, "Stable", Protein Degradation Element, "Intermediate", Protein Degradation Element, "Unstable"</p>	 <p>Protein Stability Element</p>
 <p>Origin of Replication, Shorthand Origin of Replication</p>	 <p>Origin of Replication</p>
 <p>Primer Site</p>	 <p>Primer Binding Site</p>

 <p>5' Overhang Restriction Site</p>	 <p>5' Sticky Restriction Site</p>
 <p>3' Overhang Restriction Site</p>	 <p>3' Sticky Restriction Site</p>
 <p>Blunt Restriction Site</p>	 <p>Blunt Restriction Site</p>
 <p>Scar</p>	 <p>Assembly Scar</p>
 <p>Barcode</p>	 <p>Signature</p>

 <p>Prefix, Shorthand Prefix, Suffix, Shorthand Suffix</p>	N/A												
<p>New Symbols</p> <table border="0" style="width: 100%; text-align: center;"> <tr> <td data-bbox="305 548 358 600"></td> <td data-bbox="719 541 786 606"></td> <td data-bbox="1130 541 1219 600"></td> </tr> <tr> <td data-bbox="269 678 391 709">Operator</td> <td data-bbox="695 678 816 709">Insulator</td> <td data-bbox="1101 678 1276 709">User Defined</td> </tr> <tr> <td data-bbox="326 814 337 869"></td> <td data-bbox="712 827 779 854"></td> <td data-bbox="1130 827 1196 854"></td> </tr> <tr> <td data-bbox="228 947 480 1014">Restriction Enzyme Recognition Site</td> <td data-bbox="667 947 824 978">5' Overhang</td> <td data-bbox="1101 947 1258 978">3' Overhang</td> </tr> </table>					Operator	Insulator	User Defined				Restriction Enzyme Recognition Site	5' Overhang	3' Overhang
Operator	Insulator	User Defined											
Restriction Enzyme Recognition Site	5' Overhang	3' Overhang											

9. Acknowledgements

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