

DSSR release notes since R24

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DSSR is an integrated software tool to identify, annotate, and quantify structural features of nucleic acids, including modified nucleotides, non-canonical base pairs, helices, stems, coaxial stacks, hairpin/internal/junction loops, kink turns, G-quadruplexes, i-motifs, and pseudoknots etc. It has a module (SNAP) for the comprehensive characterization of DNA-protein and RNA-protein interactions. DSSR can generate cartoon-block innovative schematics in PyMOL, and perform SQL-like feature queries in Jmol. The software allows for *in silico* base mutations, regular models creation, customized rebuilding, and template-based modeling.

DSSR has completely superseded 3DNA: features previously served via two dozens of core and utility programs in 3DNA v2.x have been consolidated into one DSSR program, all under an easy-to-use and consistent interface. DSSR may be [licensed from Columbia Technology Ventures \(CTV\)](#) and it is free for academic users.

v2.5.0-2025feb12

- DSSR Academic (formerly referred to as DSSR Basic for Academic users) has been significantly enhanced with features previously in the Pro version, including functionality from the classic 3DNA v2.x suite.

- The [DSSR Academic user manual](#) has also been dramatically improved and expanded, from 66 to 112 pages. DSSR Academic is a feature-rich software product with a professional manual.
- DSSR Pro shares the code base and manual contents with DSSR Academic. The Pro version is mostly for commercial users, with advanced capabilities for model building, additional features in structural analyses, annotations, and visualizations. DSSR Pro comes with direct support from the developer, *in whatever way to address their issues as effectively as possible*.

v2.4.6-2024nov15

- Fixed a buffer overflow bug which showed up when the `--nmr` (`--md`) option is used for analyzing a large number of models/frames from molecular dynamics (MD) trajectories with cross-paired pseudo-knot segments in separate chains.
- Increased default block depth from 0.5 to 0.8 Å when rendering with `--blocview` or `--cartoon-block`. For consistency with `--block-file` and `--block-color` options, now `--block-cartoon` behaves the same as `--cartoon-block`.
- Other minor bug fixes and refinements.

v2.4.5-2024sep24

- This is the first release after X3DNA-DSSR was officially funded by the NIH R24GM153869 grant as an NIGMS National Resource for structural bioinformatics of nucleic acids.
- It contains numerous bug fixes (e.g., chain id with >4 chars) and minor improvements since the v1.9.10-2020apr23 release before DSSR was licensed by the CTV.
- From now on, X3DNA-DSSR is on track to be actively maintained with more frequent releases (new features and bug fixes).