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Contract for license of software

between

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and

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1. Definition of the Software

UNIO is a software package for automated NMR data analysis. It provides the functionalities of the four existing algorithms: MATCH, for automated backbone assignment, ASCAN, for automated side-chain assignment, ATNOS, for automated peak picking and NOE identification in 2D homonuclear and 3D heteronuclear-resolved NOESY spectra, and CANDID, for automated NOE assignment of NOESY cross peaks in conjunction with protein three-dimensional structure calculation.
Details are to learn from the following publications:

Herrmann, T., Güntert, P. & Wüthrich, K.
"Protein NMR structure determination with automated NOE-identification in the NOESY spectra using the new software ATNOS."
J. Biomol. NMR 2002 Nov; 24(3): 171-189.

Herrmann, T., Güntert, P. & Wüthrich, K.
"Protein NMR structure determination with automated NOE assignment using the new software CANDID and the torsion angle dynamics algorithm DYANA."
J. Mol. Biol. 2002 May; 319(1): 209-227.

Volk, J.; Herrmann, T.; Wüthrich, K.
“Automated sequence-specific protein NMR assignment using the memetic algorithm MATCH.”
J. Biomol.NMR. 2008, 41, 127-138.

Fiorito, F.; Damberger, F.F.; Herrmann, T.; Wüthrich, K.
“Automated amino acid side-chain assignment of proteins using 13C- and 15N resolved 3D [1H, 1H]-NOESY.”
J. Biomol. NMR 2008, 42, 23-33.

This Software is composed of 3 types of files: executable (binary) files, configuration files and documentation files. Not included is the source code.
(together “Software”)

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Herrmann, T., Güntert, P. & Wüthrich, K.
"Protein NMR structure determination with automated NOE-identification in the NOESY spectra using the new software ATNOS."
J. Biomol. NMR 2002 Nov; 24(3): 171-189.

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By using this software you indicate your acceptance.

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In case of any problems, comments, questions, please contact the UNIO authors using the E-mail address torsten.herrmann@ens-lyon.fr