“HiP-FA Software” is an open source project for analyzing the data acquired by using the High performance Fluorescence Anisotropy method described in Nature Communication…. [REF].

**Main features include**:

* Loading of the raw data acquired with the microscope.
* Determination of the DNA concentrations using the reference wells.
* Display of the titration curves for the wellplate, their analysis and the extraction of the concentration of active protein and the dissociation constants obtained from an automated fitting procedure.
* Export of the data for the whole wellplate.

**Software environment**

The program is written in Labview9.0 using built-in libraries.

**Documentation**

A documentation file describing how to use the software is available (“HiP-FA Software\_Documentation.docx”) as well as a full exemplary dataset for testing (“Example of dataset\_\_pdm2\_Robot\_Matrix\_dupl1.zip”).