We are pleased to announce the release of PyRx 0.9.5. Major changes in this release include:

- Fixed a bug when toggling hydrogen bonds using toolbar icon.
- PyRx can now run docking for molecules that have quotes in their names, like in 3-hydroxy-5\_7\_3'\_4'\_5'-pentamethoxyflavone.
- Added balloon widget to draw labels when the mouse stays above a molecule. This can be helpful when there are multiple molecules in 3D scene. The mouse cursors changes to busy when you move the mouse over a molecule. You can disable this by deleting a single line [https://sourceforge.net/p/pyrx/code/278/tree/PyRxDev/PyRx/mayaviEngine.py#l110](https://sourceforge.net/p/pyrx/code/278/tree/PyRxDev/PyRx/mayaviEngine.py#l110).
Let me know if you don't like this feature; I can add an option to disable this in the next release of PyRx, if needed.
- Added RMSD from reference structure column to AutoDock Analyze Results table.

- When making flexible residues, PyRx is now using options defined in receptor preparation preferences to decide what type of changes to do.

PyRx 0.9.2, 0.9.3 and 0.9.4 users can update to this release using PyRx > Help > Check for Updates... menu. The list of changes for 0.9.4 version is available at PyRx 0.9.4 Release Announcement.