

First Steps in KNIME

and how to use BioSolveIT software inside

First, you have to install KNIME from here : https://www.knime.com/downloads/download-knime

KNIME itself provides quite good video tutorials for the general use of their software here:

https://www.knime.org/knime-online-self-training-lesson-1



KNIME has a slightly unusual way to add new nodes. Go to:





1) Paste https://www.biosolveit.de/KNIME/download/biosolveit_knime_nodes (and press enter)

2) Mark checkbox

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Available Software Check the items that you wish to install.			
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1) Install also the community nodes from:

2) Mark checkbox

https://update.knime.com/community-contributions/4.1 (and press enter) https://update.knime.com/community-contributions/trusted/4.1

(in case you have another version replace the 4.1 with your version number)

▲ Install			_	
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After restart of KNIME you will have the BioSolveIT nodes here

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1) Go to the Preferences:



2) Then this pops up. Go to >KNIME >BioSolveIT Settings and select the path to your license

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type filter text	BioSolvelT		⇒ • •
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Afterwards you can properly work with BioSolveIT nodes.





import an existing workflow

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create a new workflow

🛕 KNIME Analytics Platform						
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For now, let's create a new!



1) We need a node to read our molecule file (an sdf). So we type sdf in the search dialog and drag and drop the *SDF reader* node to the workflow









SDF Reader	3D Coordinates Generator	F	🛕 Dialog - 0:1999 - 3D Coordinates Generator ïlle	_		×
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2) We drop the *3D Coordinates Generator* node to our work-flow and configure it:

successful) turns

green.





After running a node you can see the results by right-clicking on the node. In the last section you can check the outcome.



Next we need a to prepare the receptor, which is done with the *SeeSAR Interactive GUI* node.

- 1) Execute this node to open the interface
- 2) (Down-)load a crystal structure (PDB)
- 3) Define the binding site
- 4) Add your ligand to the "Analyzer" mode
- 5) Optionally set pharmacophore constraints in the docking mode
- 6) Save your project upon closing SeeSAR.

Video tutorials how to use SeeSAR can be found here: <u>https://www.biosolveit.de/SeeSAR</u>



Now the compounds and the receptor come together in the *Docking (FlexX)* node. In the configuration dialog you can chose the number of poses (10 is default). Check 'Append all data columns' box to keep all data from your sdf. Make sure you chose the right molecule column!





After the docking, we want to score the generated poses. Therefore, we include an *Affinity Calculatotr (HYDE)* node. Connect the docking results and the *SeeSAR Interactive GUI* as indicated below.





Add the *SeeSAR Interactive GUI* node to see the results after docking and scoring. When you execute this node, a SeeSAR window will open.



Find some ready to use workflows:







Enjoy working with BioSolveIT software in KNIME and

expect actives!



More useful KNIME help:

KNIME pages (https://www.knime.com)

- **SOLUTIONS** for example workflows
- RESOURCES/LEARNING HUB <u>https://www.knime.com/learning-hub</u>
- RESOURCES/NODE GUIDE <u>https://www.knime.com/nodeguide</u>
- Book WILL THEY BLEND <u>https://www.knime.com/knimepress/will-they-blend</u>

KNIME Tech pages

- FORUM for questions and answers <u>https://forum.knime.com</u>
- **DOCUMENTATION** for docs, FAQ, changelogs, ...
- **COMMUNITY CONTRIBUTIONS** for dev instructions and third party nodes

KNIME TV on YouTube https://www.youtube.com/user/KNIMETV

