PROPEDEUTICS Seminar

Scientific Software and Databases

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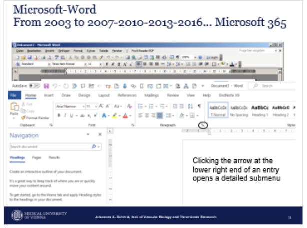
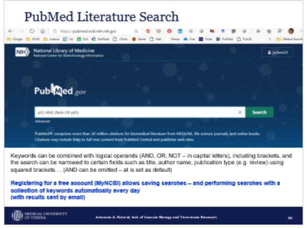
Bookmark slide



Microsoft-Word
From 2003 to 2007-2010-2013-2016… Microsoft 365

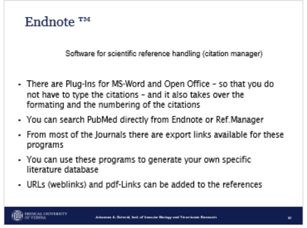
Clicking the arrow at the lower right end of an entry opens a detailed submenu



PubMed Literature Search

Keywords can be combined with logical operands (AND, OR, NOT – in capital letters), including brackets, and the search can be narrowed to certain fields such as title, author name, publication type (e.g. review) using squared brackets … (AND can be omitted – at is set as default)

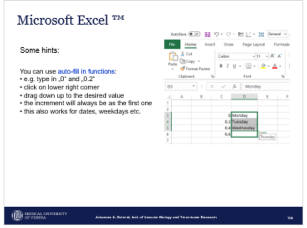
Registering for a free account (MyNCBI) allows saving searches – and performing searches with a collection of keywords automatically every day (with results sent by email)



Endnote ™

Software for scientific reference handling (citation manager)

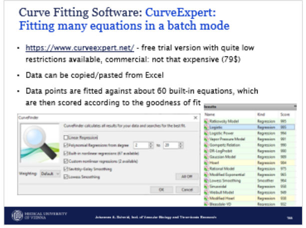
- There are Plug-Ins for MS-Word and Open Office – so that you do not have to type the citations – and it also takes over the formating and the numbering of the citations
- You can search PubMed directly from Endnote or Ref.Manager
- From most of the Journals there are export links available for these programs
- You can use these programs to generate your own specific literature database
- URLs (weblinks) and pdf-Links can be added to the references



Microsoft Excel ™

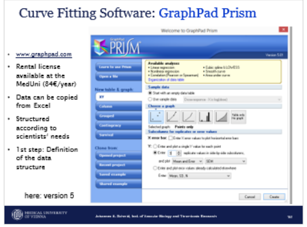
Some hints:

You can use auto-fill in functions:
- e.g. type in „0" and „0.2"
- click on lower right corner
- drag down up to the desired value
- the increment will always be as the first one
- this also works for dates, weekdays etc.



Curve Fitting Software: CurveExpert: Fitting many equations in a batch mode

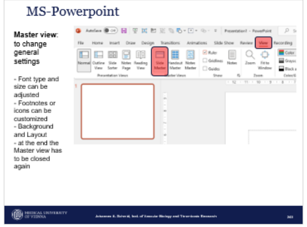
- https://www.curveexpert.net/ - free trial version with quite low restrictions available, commercial: not that expensive (79$)
- Data can be copied/pasted from Excel
- Data points are fitted against about 60 built-in equations, which are then scored according to the goodness of fit



Curve Fitting Software: GraphPad Prism

- www.graphpad.com
- Rental license available at the MedUni (84€/year)
- Data can be copied from Excel
- Structured according to scientists' needs
- 1st step: Definition of the data structure

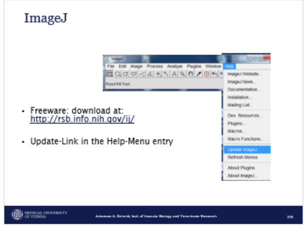
here: version 5



MS-Powerpoint

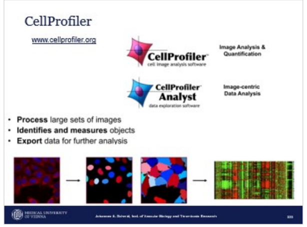
Master view: to change general settings

- Font type and size can be adjusted
- Footnotes or icons can be customized
- Background and Layout
- at the end the Master view has to be closed again



ImageJ

- Freeware: download at: http://rsb.info.nih.gov/ij/
- Update-Link in the Help-Menu entry



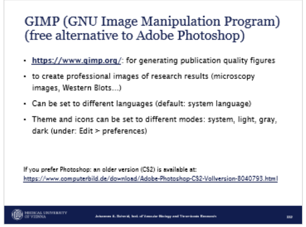
CellProfiler

www.cellprofiler.org

Image Analysis & Quantification

Image-centric Data Analysis

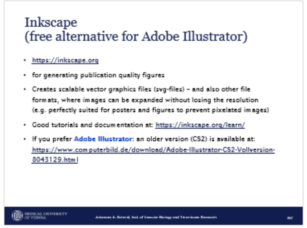
- **Process** large sets of images
- **Identifies and measures** objects
- **Export** data for further analysis



GIMP (GNU Image Manipulation Program) (free alternative to Adobe Photoshop)

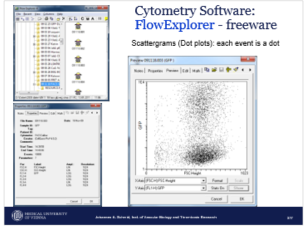
- https://www.gimp.org/: for generating publication quality figures
- to create professional images of research results (microscopy images, Western Blots…)
- Can be set to different languages (default: system language)
- Theme and icons can be set to different modes: system, light, gray, dark (under: Edit > preferences)

If you prefer Photoshop: an older version (CS2) is available at: https://www.computerbild.de/download/Adobe-Photoshop-CS2-Vollversion-8040793.html



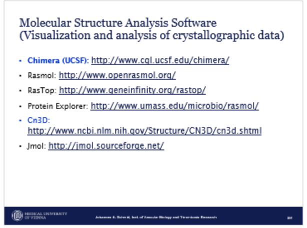
Inkscape (free alternative for Adobe Illustrator)

- https://inkscape.org
- for generating publication quality figures
- Creates scalable vector graphics files (svg-files) – and also other file formats, where images can be expanded without losing the resolution (e.g. perfectly suited for posters and figures to prevent pixelated images)
- Good tutorials and documentation at: https://inkscape.org/learn/
- If you prefer **Adobe Illustrator**: an older version (CS2) is available at: https://www.computerbild.de/download/Adobe-Illustrator-CS2-Vollversion-8043129.html



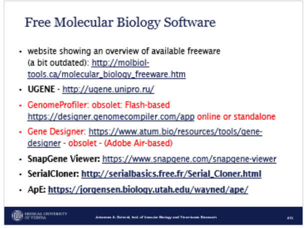
Cytometry Software: FlowExplorer - freeware

Scattergrams (Dot plots): each event is a dot



Molecular Structure Analysis Software (Visualization and analysis of crystallographic data)

- **Chimera (UCSF):** http://www.cgl.ucsf.edu/chimera/
- Rasmol: http://www.openrasmol.org/
- RasTop: http://www.geneinfinity.org/rastop/
- Protein Explorer: http://www.umass.edu/microbio/rasmol/
- Cn3D: http://www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml
- Jmol: http://jmol.sourceforge.net/



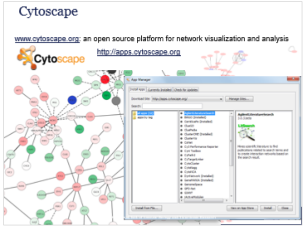
Free Molecular Biology Software

- website showing an overview of available freeware (a bit outdated): http://molbiol-tools.ca/molecular_biology_freeware.htm
- **UGENE** - http://ugene.unipro.ru/
- GenomeProfiler: obsolet: Flash-based https://designer.genomecompiler.com/app online or standalone
- Gene Designer: https://www.atum.bio/resources/tools/gene-designer - obsolet - (Adobe Air-based)
- **SnapGene Viewer:** https://www.snapgene.com/snapgene-viewer
- **SerialCloner: http://serialbasics.free.fr/Serial_Cloner.html**
- **ApE: https://jorgensen.biology.utah.edu/wayned/ape/**

Databases

Image databases

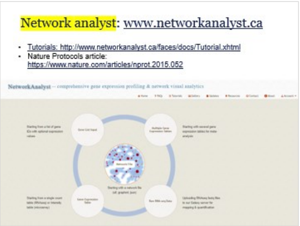
- https://imagescience.org/images/
- https://histologyguide.com
- mouse histology: https://www.emouseatlas.org/emap/home.html



Cytoscape

www.cytoscape.org: an open source platform for network visualization and analysis

http://apps.cytoscape.org



Network analyst: www.networkanalyst.ca

- Tutorials: http://www.networkanalyst.ca/faces/docs/Tutorial.xhtml
- Nature Protocols article: https://www.nature.com/articles/nprot.2015.052

Software for	Commercial Software	Freeware
Writing Calculating Presenting	MS-Word MS-Excel MS-Powerpoint	OpenOffice LibreOffice Office-Online (Word, Excel,…) Google Docs
Literature Citation managing	Endnote (Reference Manager)	Myendnoteweb **Sciwheel** (https://sciwheel.com) Zotero Bibus Mendeley
Pdf-editing	Adobe Acrobat Prof.	Pdf-XChange Editor
Image Processing	Adobe-Photoshop Adobe Illustrator both: (Vers. CS2:free)	**Gimp**, Irfanview, Paint.net **InkScape**
Image Analysis		ImageJ, Fiji, CellProfiler
Curve fitting Data analysis	GraphPad-Prism Sigmaplot, MS-Excel	CurveExpert
Cytometry	CellQuest, DIVA, …	CytExpert Cytoflow
X-ray structure analysis		Chimera, Rasmol, RasTop CN3D (iCN3D)
Sequence analysis	Snapgene, VectorNTI CloneManager	CLC Sequence Viewer UGENE, SnapGene Viewer, SerialCloner, ApE
Network visualization		Cytoscape

Download-links for software

- **Online Office packages**:
  - **OnlineWord, Excel, Powerpoint..**: https://www.office.com (You need a free MS-account: hotmail or outlook) - **GoogleDocs, Google sheets** etc: https://docs.google.com …
  - **OnlyOffice**: similar to Word.. https://www.onlyoffice.com
- *LibreOffice*: https://de.libreoffice.org
- OpenOffice: https://www.openoffice.org/de/

Offline alternatives to MS-Office

- *Mendeley*: https://www.mendeley.com/ .. If you don‘t have Endnote
- MyEndnoteWeb: https://www.myendnoteweb.com/ - free alternative to Endnote
- **Sciwheel**: https://sciwheel.com
- *pdf-xchange* editor: https://www.tracker-software.com/products
- free (older) versions of *Adobe Photoshop and Adobe Illustrator*:
  https://www.computerbild.de/download/Adobe-Photoshop-CS2-Vollversion-8040793.html
  https://www.computerbild.de/download/Adobe-Illustrator-CS2-Vollversion-8043129.html
- *Gimp*: https://www.gimp.org , Inkscape: https://inkscape.org/
- *Fiji-version of ImageJ*: https://fiji.sc
- *CellProfiler*: http://cellprofiler.org
- *Graphpad Prism* (trial version): http://www.graphpad.com/scientific-software/prism/

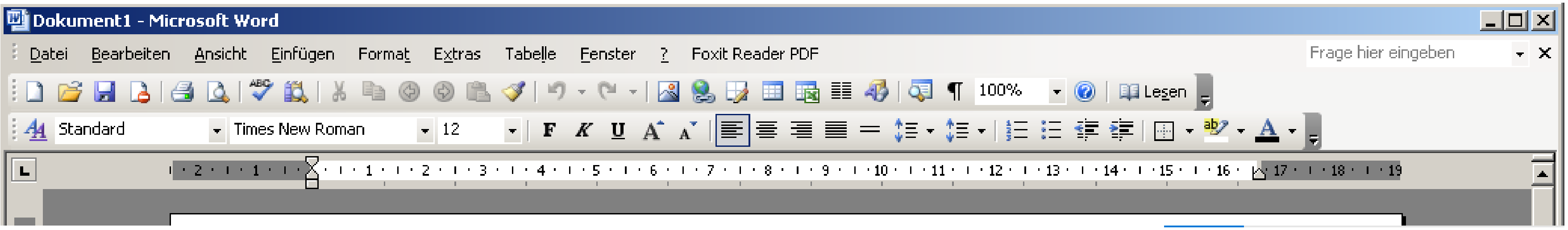
Download-links for software II

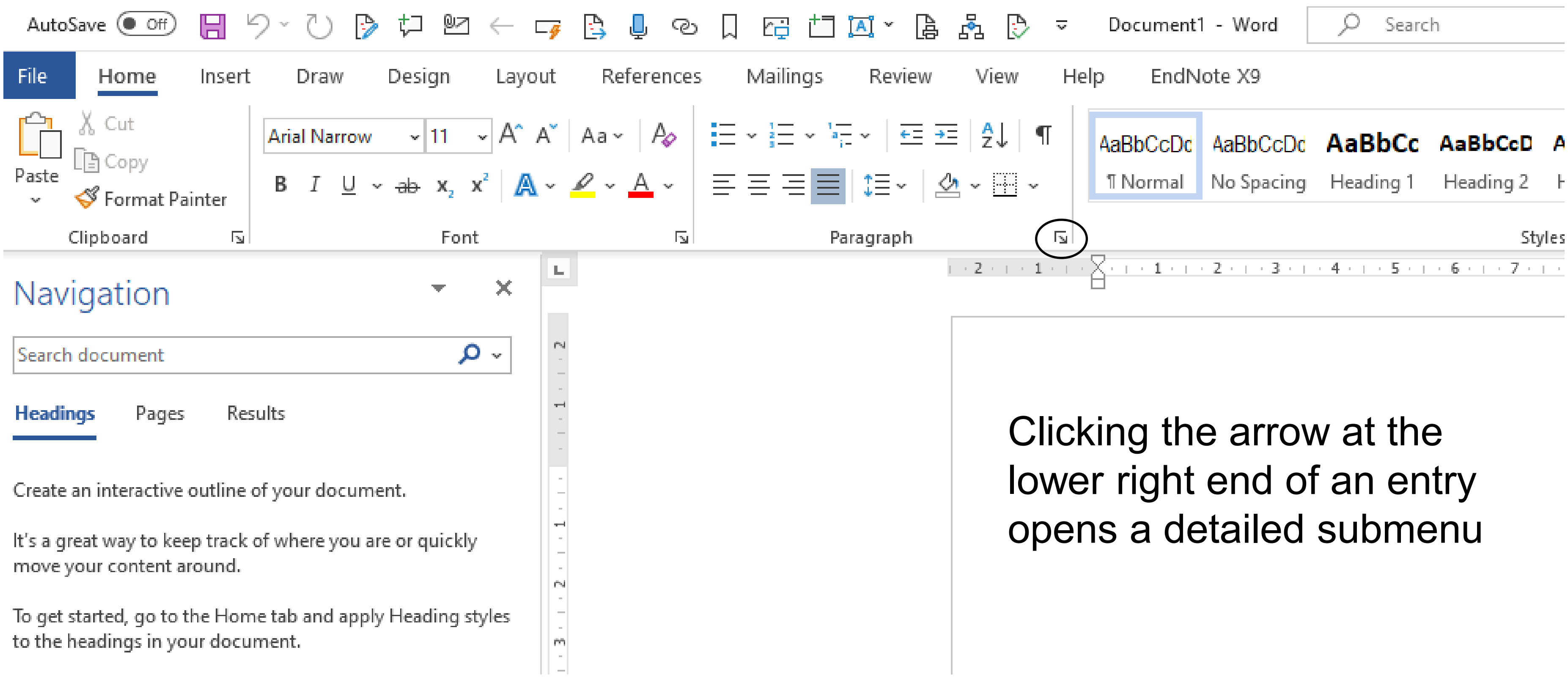
- Cytometry: *Flowing Software*: http://www.uskonaskel.fi/flowingsoftware/
  Cytexpert: https://www.beckman.com/coulter-flow-cytometers/cytoflex/cytexpert
  Cytoflow: https://cytoflow.github.io
- 3D-molecular structure viewer *ChimeraX*: https://www.cgl.ucsf.edu/chimerax/
  CN3D (from NCBI): https://www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml
- Sequence analysis (DNA, RNA, protein, plasmids):
  SnapGene Viewer: http://www.snapgene.com/products/snapgene_viewer/
  UGENE: http://ugene.net
  Serial Cloner: http://serialbasics.free.fr/Serial_Cloner.html
- Network visualization: *Cytoscape*: http://www.cytoscape.org
- *LinRegPCR* for realtime PCR (qPCR) analysis:
  http://www.hartfaalcentrum.nl/index.php?main=files&sub=LinRegPCR
- Plagiarism check: *VIPER*: http://scanmyessay.com/

Content of the 1st session

- MS-Word
- Endnote (citation manager software)
- Mendeley (free citation manager software)
- SciWheel Workspace
- PubMed database: professional search and link to citation manager

Microsoft-Word
From 2003 to 2007-2010-2013-2016… Microsoft 365





Create an interactive outline of your document.

It's a great way to keep track of where you are or quickly move your content around.

To get started, go to the Home tab and apply Heading styles to the headings in your document.

Clicking the arrow at the lower right end of an entry opens a detailed submenu

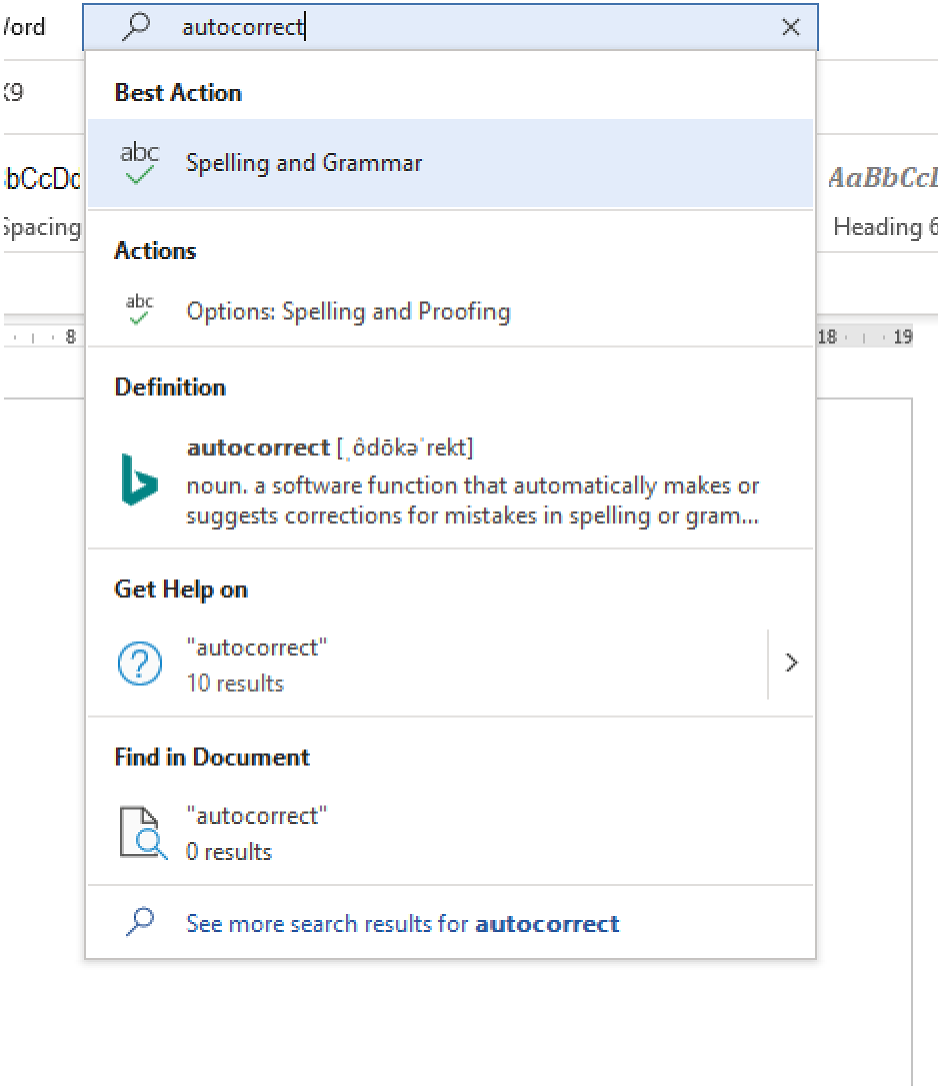
Some Hints for MS-Word

- There are three different ENTER commands:

  - ENTER alone: new paragraph
  - SHIFT / ENTER: new line (e.g. in bulleted lists)
  - CTRL (Strg) / ENTER: new page
- Use rather tables instead of tabulators (e.g. when you write a CV; you can make the lines invisible)
- You can copy all different kinds of files into a Word-file and maintain the original file in the background (e.g. Excel graphs…) by OLE (Object Linked Embedding)
- You can generate hyperlinks to other files or websites
- Use „Insert symbol“ for Greek letters instead switching to Symbol font (this maintains the symbols if you are switching the font later)
- You can apply the auto-correction feature for frequently used text (including formats such as symbols: e.g. „NF“ is replaced by „NF-κB“ or TNF is replaced by TNFα)

Finding a command

- using the search window in the toolbar, you can find most commands quickly:



autocorrect

Best Action

Spelling and Grammar

Actions

Options: Spelling and Proofing

Definition

autocorrect [ˌôdōkəˈrekt]

noun. a software function that automatically makes or suggests corrections for mistakes in spelling or gram...

Get Help on

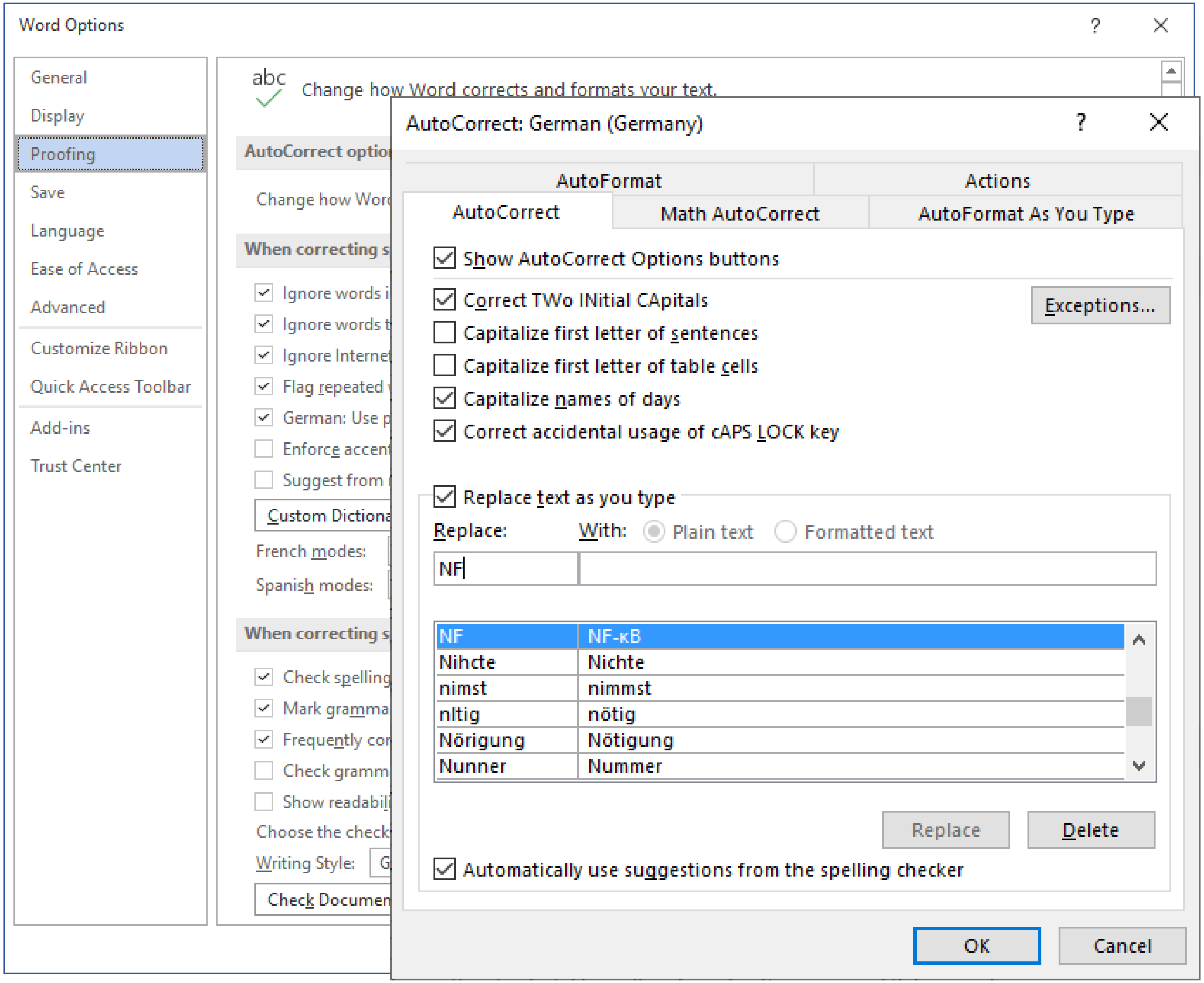
"autocorrect"
10 results

Find in Document

"autocorrect"
0 results

See more search results for **autocorrect**

Using the auto-correction feature



Change how Word corrects and formats your text.

AutoCorrect optio

Change how Word

When correcting s

☑ Ignore words i
☑ Ignore words t
☑ Ignore Internet
☑ Flag repeated
☑ German: Use p
☐ Enforce accent
☐ Suggest from

French modes:
Spanish modes:

When correcting s

☑ Check spelling
☑ Mark gramma
☑ Frequently co
☐ Check gramm
☐ Show readabili

Choose the check
Writing Style: G

☑ Show AutoCorrect Options buttons

☑ Correct TWo INitial CApitals
☐ Capitalize first letter of sentences
☐ Capitalize first letter of table cells
☑ Capitalize names of days
☑ Correct accidental usage of cAPS LOCK key

☑ Replace text as you type

Replace: With: ● Plain text ○ Formatted text

Replace: NF

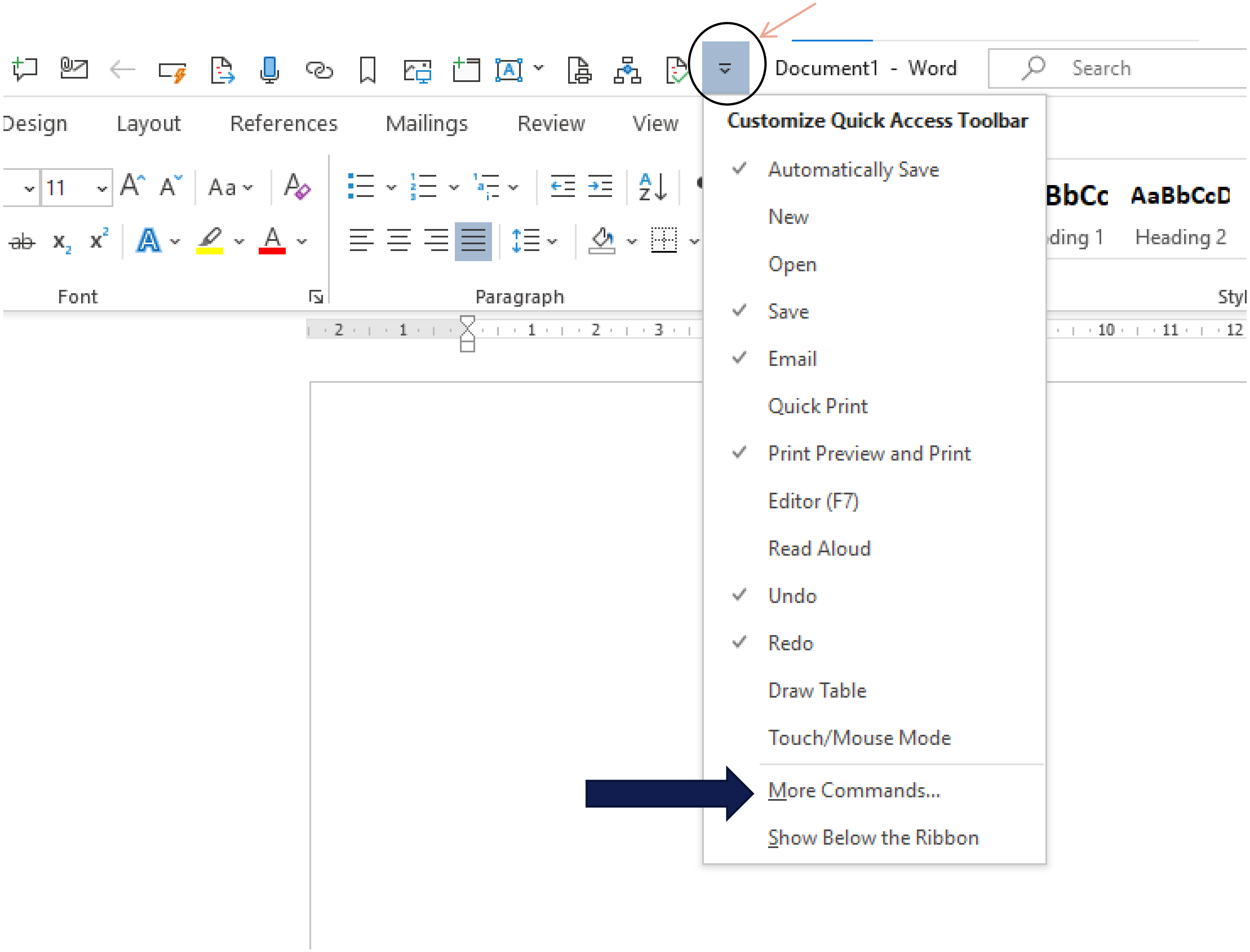
Replace	With
NF	NF-κB
Nihcte	Nichte
nimst	nimmst
nltig	nötig
Nörigung	Nötigung
Nunner	Nummer

☑ Automatically use suggestions from the spelling checker

File Menu > Options > Proofing > Autocorrection
- you can delete unwanted entries (e.g. DNA> DANN)
- you can specify that it shouldn‘t capitalize letters after a period (e.g. abbreviation p53)
- you can define your own abbreviation-autotext entries (even in a formated manner including Greek symbols e.g. NF > NF-κB)
- you can define auto-text entries, e.g. that „phos“ is always extended to „phosphorylation“

Customizing Word

There is a fast access toolbar that can be customized



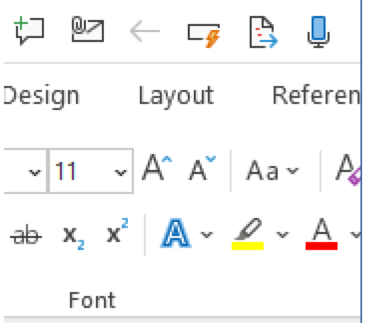
Document1 - Word

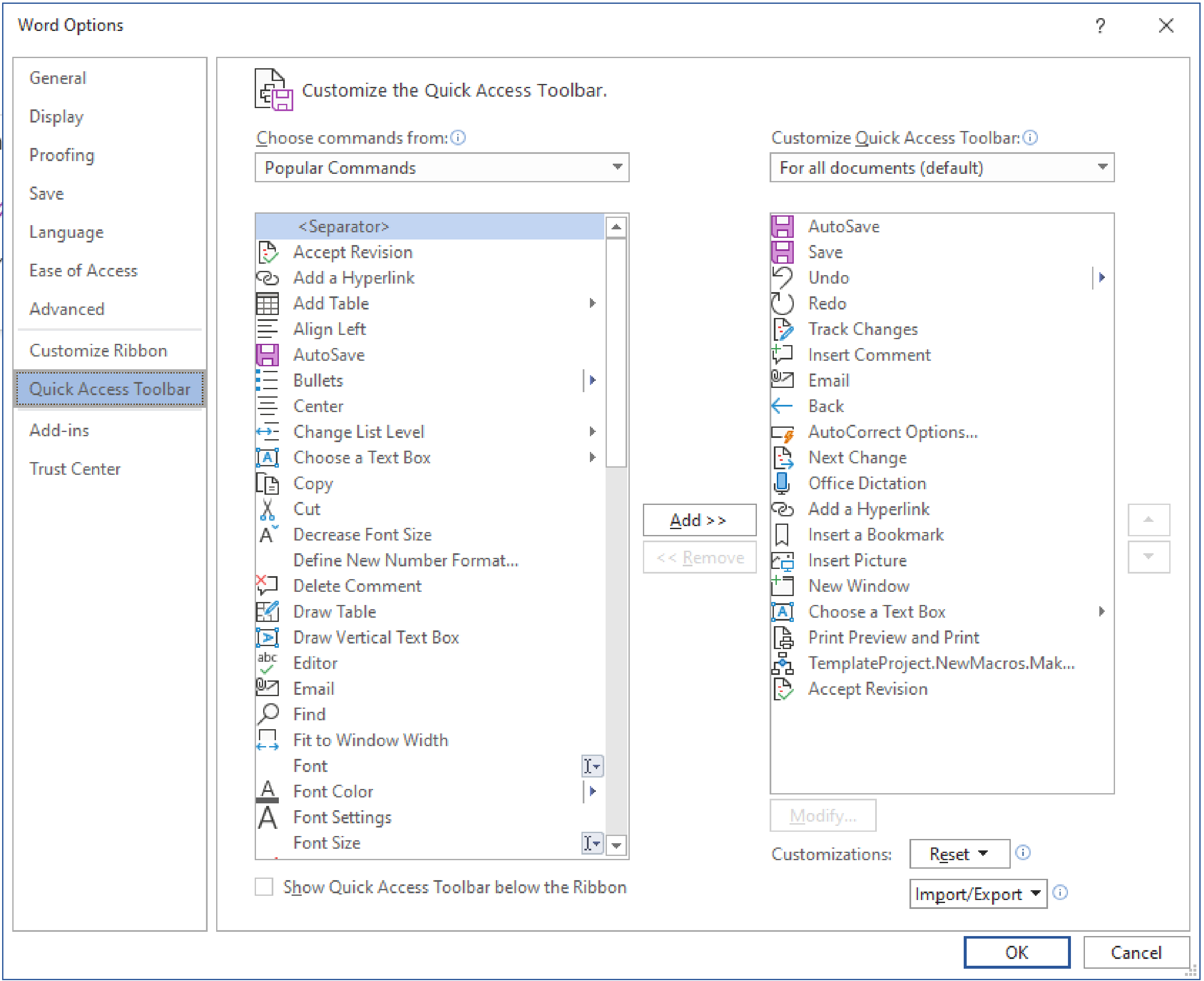
Customize Quick Access Toolbar

- ✓ Automatically Save
- New
- Open
- ✓ Save
- ✓ Email
- Quick Print
- ✓ Print Preview and Print
- Editor (F7)
- Read Aloud
- ✓ Undo
- ✓ Redo
- Draw Table
- Touch/Mouse Mode
- More Commands...
- Show Below the Ribbon

Customizing Word

There is a fast access toolbar that can be customized





Word Options

- General
- Display
- Proofing
- Save
- Language
- Ease of Access
- Advanced
- Customize Ribbon
- Quick Access Toolbar
- Add-ins
- Trust Center

Customize the Quick Access Toolbar.

Choose commands from: Popular Commands

- <Separator>
- Accept Revision
- Add a Hyperlink
- Add Table
- Align Left
- AutoSave
- Bullets
- Center
- Change List Level
- Choose a Text Box
- Copy
- Cut
- Decrease Font Size
- Define New Number Format...
- Delete Comment
- Draw Table
- Draw Vertical Text Box
- Editor
- Email
- Find
- Fit to Window Width
- Font
- Font Color
- Font Settings
- Font Size

Add >>

<< Remove

Customize Quick Access Toolbar: For all documents (default)

- AutoSave
- Save
- Undo
- Redo
- Track Changes
- Insert Comment
- Email
- Back
- AutoCorrect Options...
- Next Change
- Office Dictation
- Add a Hyperlink
- Insert a Bookmark
- Insert Picture
- New Window
- Choose a Text Box
- Print Preview and Print
- TemplateProject.NewMacros.Mak...
- Accept Revision

Modify...

☐ Show Quick Access Toolbar below the Ribbon

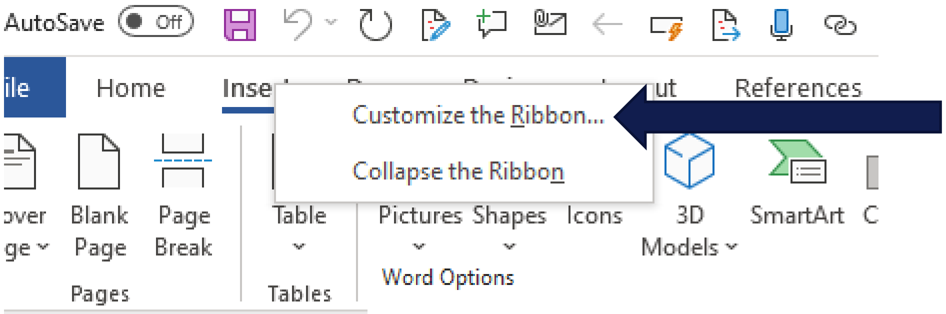
Customizations: Reset

Import/Export

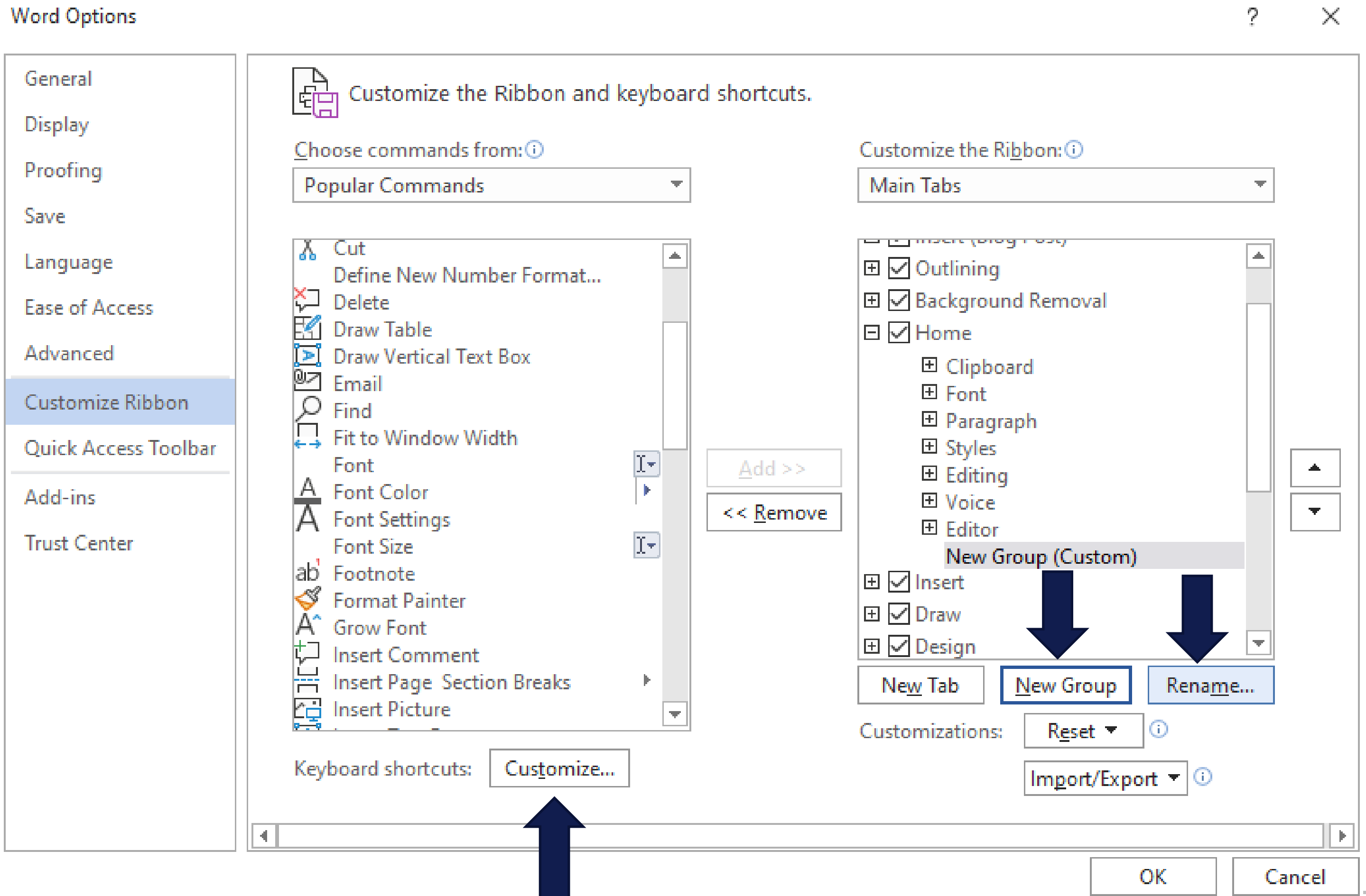
OK

Cancel

Customizing Word



Right-clicking on the menu, allows customizing each tab.

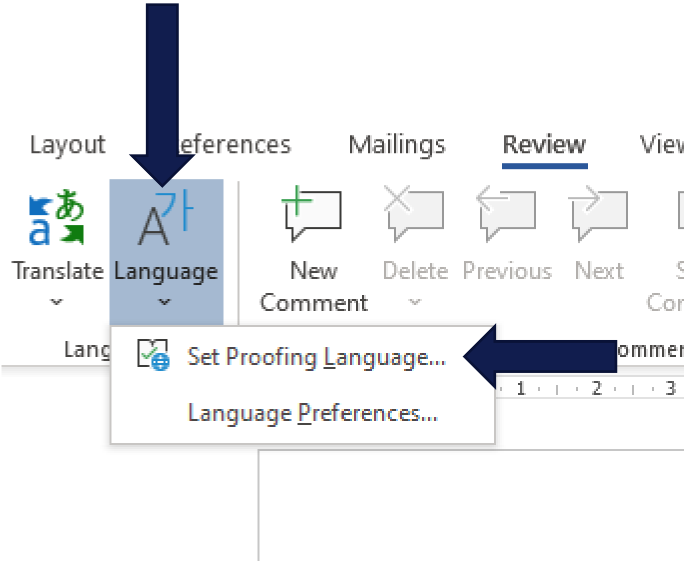

Word Options

Customize the Ribbon and keyboard shortcuts.

Choose commands from: Popular Commands

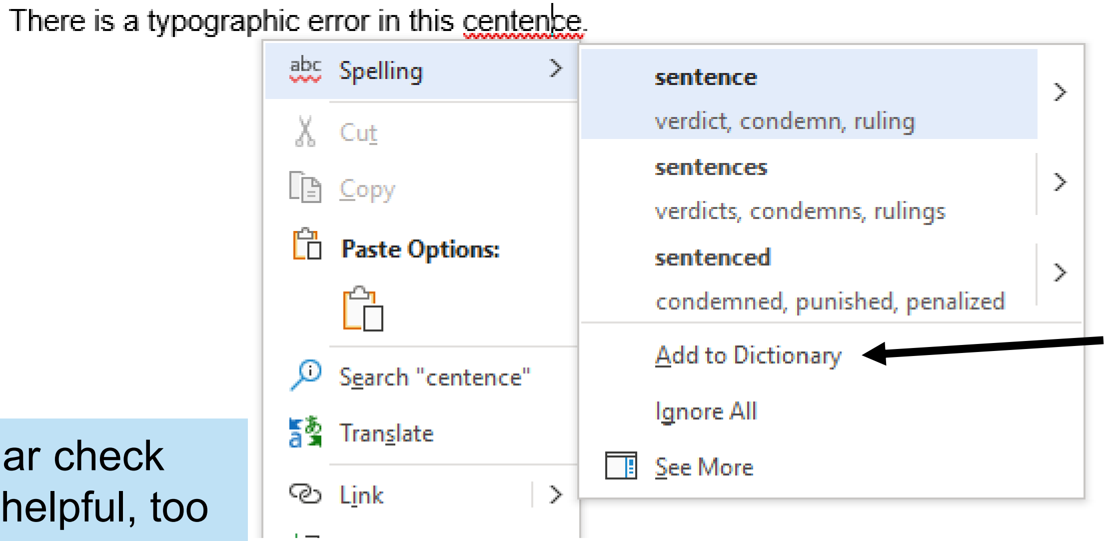
Customize the Ribbon: Main Tabs

Language and spell checking settings



Language is usually automatically set.
You might consider to set it specifically to US-English (e.g. if you are submitting a manuscript to a US-journal)

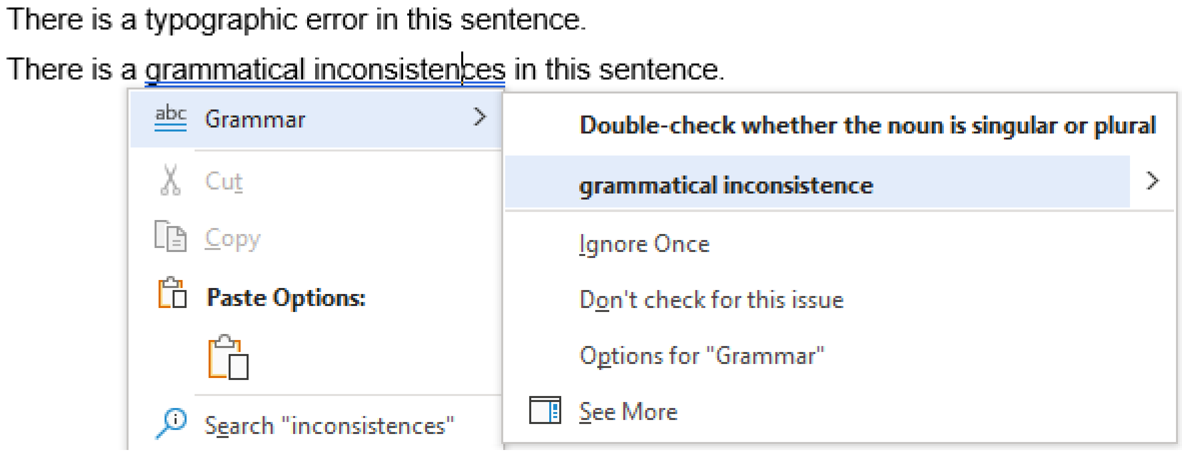
Spell-Checking in MS-Word



There is a typographic error in this centence.

mistakes are underlined in red; right-clicking on the wrong word opens a context menu: suggestions for the right word – or: option to add the unknown word to the dictionary (the latter makes sense to add scientific terms to the dictionary). It's recommendable to use this feature for correct scientific writing.

Grammar check can be helpful, too

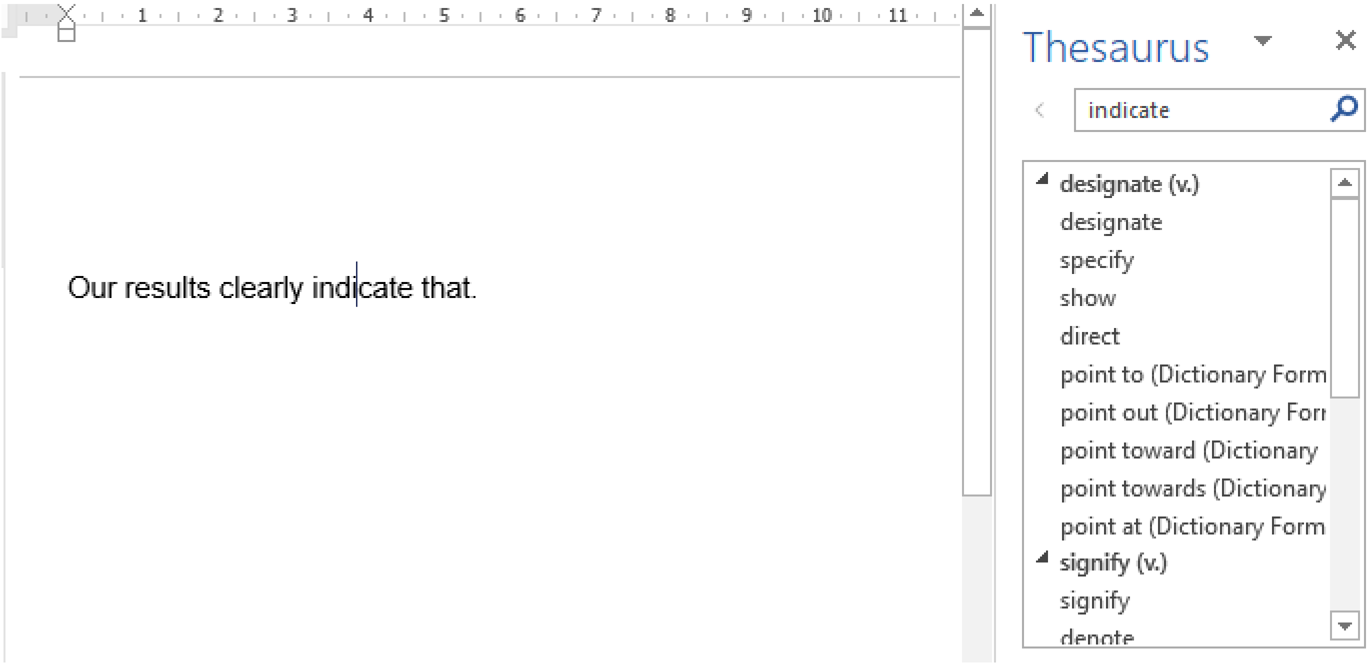


There is a typographic error in this sentence.

There is a grammatical inconsistences in this sentence.

You find your custom dictionary at:
C:\Users*username*\AppData\Roaming\Microsoft\UProof: CUSTOM.DIC
(can be transferred to other PC)

The Thesaurus: Shift-F7 (or right-click in a word)

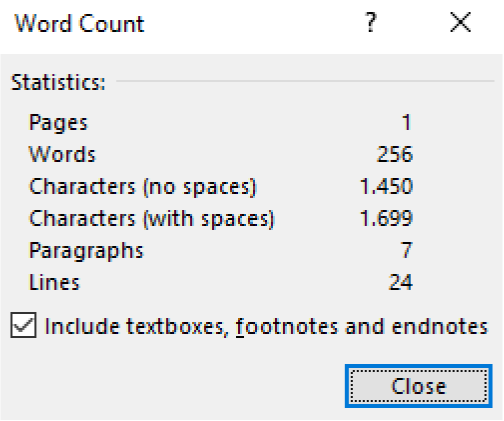


Our results clearly indicate that.

indicate

- gives you suggestions for synonyms
(quite convenient, when you write a longer text, where you don‘t want to use the same words again and again)

Other useful features: Count words, characters

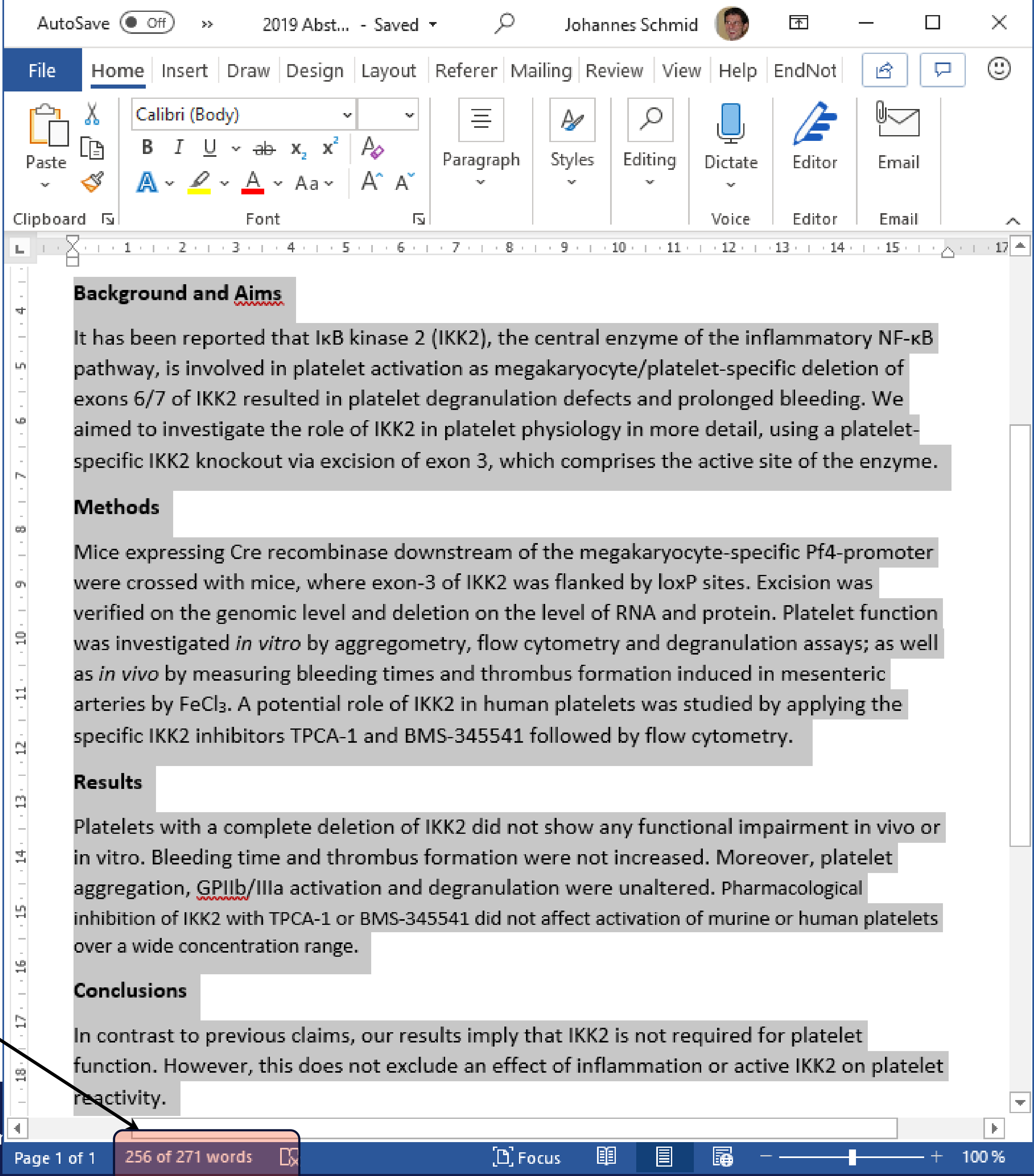


Word Count

Statistics:

Pages	1
Words	256
Characters (no spaces)	1.450
Characters (with spaces)	1.699
Paragraphs	7
Lines	24

☑ Include textboxes, footnotes and endnotes



Background and Aims

It has been reported that IκB kinase 2 (IKK2), the central enzyme of the inflammatory NF-κB pathway, is involved in platelet activation as megakaryocyte/platelet-specific deletion of exons 6/7 of IKK2 resulted in platelet degranulation defects and prolonged bleeding. We aimed to investigate the role of IKK2 in platelet physiology in more detail, using a platelet-specific IKK2 knockout via excision of exon 3, which comprises the active site of the enzyme.

Methods

Mice expressing Cre recombinase downstream of the megakaryocyte-specific Pf4-promoter were crossed with mice, where exon-3 of IKK2 was flanked by loxP sites. Excision was verified on the genomic level and deletion on the level of RNA and protein. Platelet function was investigated *in vitro* by aggregometry, flow cytometry and degranulation assays; as well as *in vivo* by measuring bleeding times and thrombus formation induced in mesenteric arteries by $FeCl_3$. A potential role of IKK2 in human platelets was studied by applying the specific IKK2 inhibitors TPCA-1 and BMS-345541 followed by flow cytometry.

Results

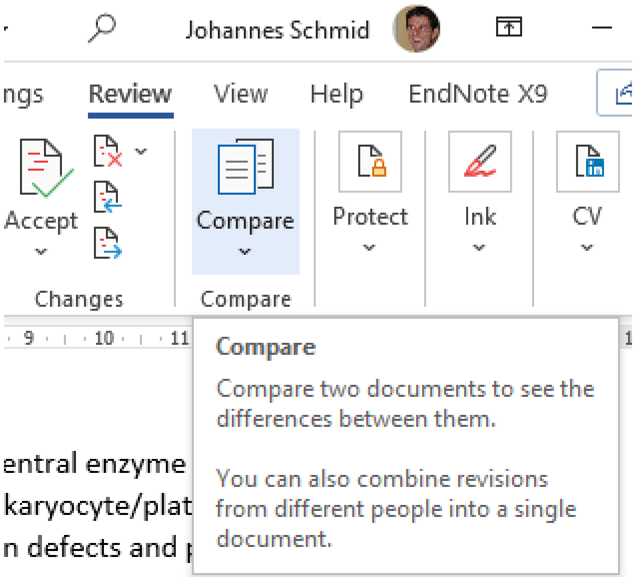
Platelets with a complete deletion of IKK2 did not show any functional impairment in vivo or in vitro. Bleeding time and thrombus formation were not increased. Moreover, platelet aggregation, GPIIb/IIIa activation and degranulation were unaltered. Pharmacological inhibition of IKK2 with TPCA-1 or BMS-345541 did not affect activation of murine or human platelets over a wide concentration range.

Conclusions

In contrast to previous claims, our results imply that IKK2 is not required for platelet function. However, this does not exclude an effect of inflammation or active IKK2 on platelet reactivity.

Page 1 of 1 256 of 271 words

Compare and merge documents
(if several people work on the same document)

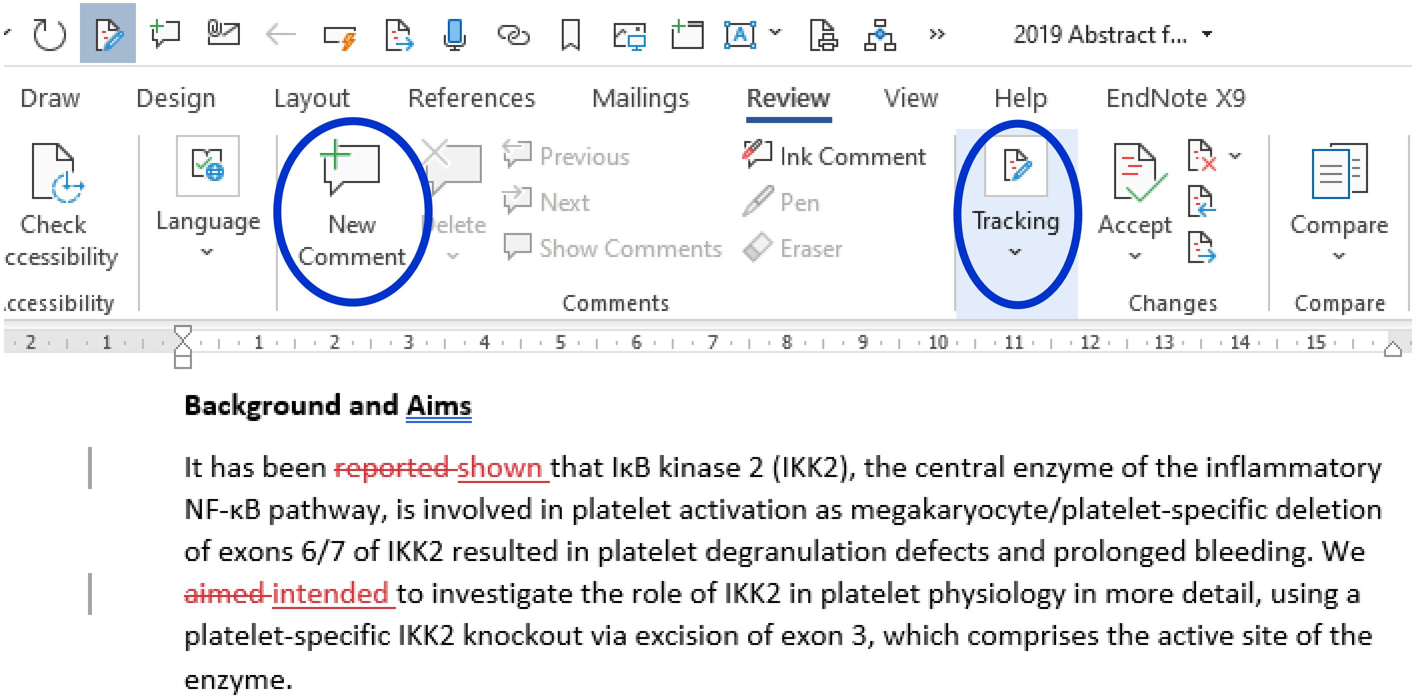


Compare

Compare two documents to see the differences between them.

You can also combine revisions from different people into a single document.

The Reviewing Mode of MS-Word: As Reviewer

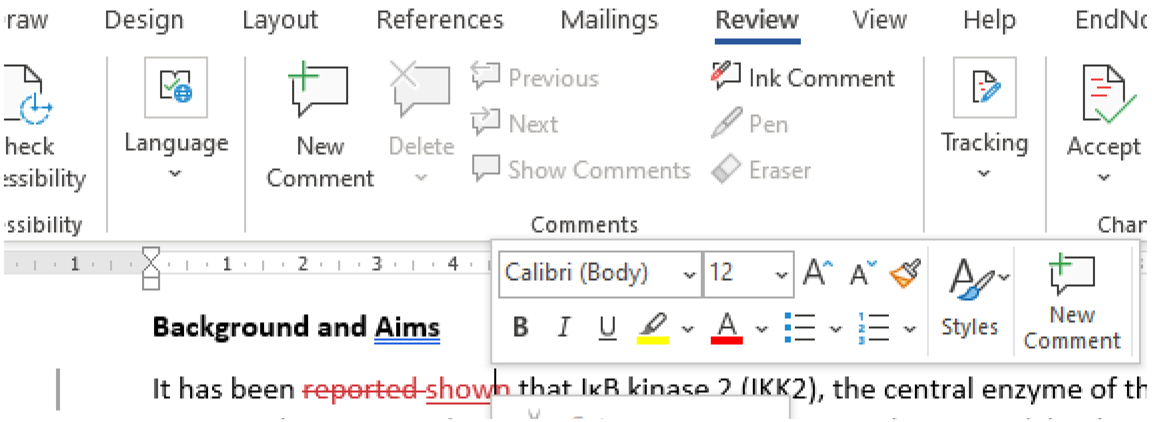


Background and Aims

It has been ~~reported~~ shown that IκB kinase 2 (IKK2), the central enzyme of the inflammatory NF-κB pathway, is involved in platelet activation as megakaryocyte/platelet-specific deletion of exons 6/7 of IKK2 resulted in platelet degranulation defects and prolonged bleeding. We ~~aimed~~ intended to investigate the role of IKK2 in platelet physiology in more detail, using a platelet-specific IKK2 knockout via excision of exon 3, which comprises the active site of the enzyme.

1. **Click on the reviewing tab**
2. **Activate the „track changes mode“ (Änderungen nachverfolgen)**
3. **Type your changes into the document (deleted text will appear struck-through) , changes are marked in a different colour (according to the reviewer-computer settings)**
4. **If necessary: add comments**
5. **You should de-activate the track-changes mode again at the end**

The Reviewing Mode of MS-Word II: accept or reject changes done by the reviewer

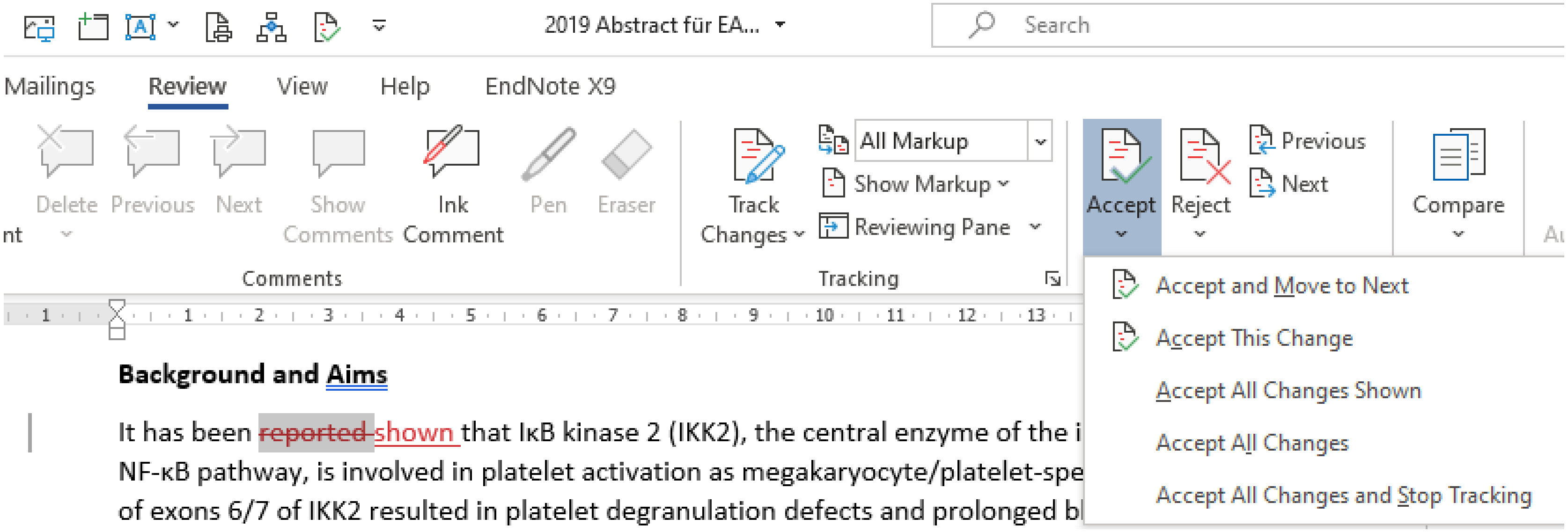


Background and Aims

It has been ~~reported~~ shown that IκB kinase 2 (IKK2), the central enzyme of th

right-click onto a change and either accept or reject a modification

- or use the Accept button

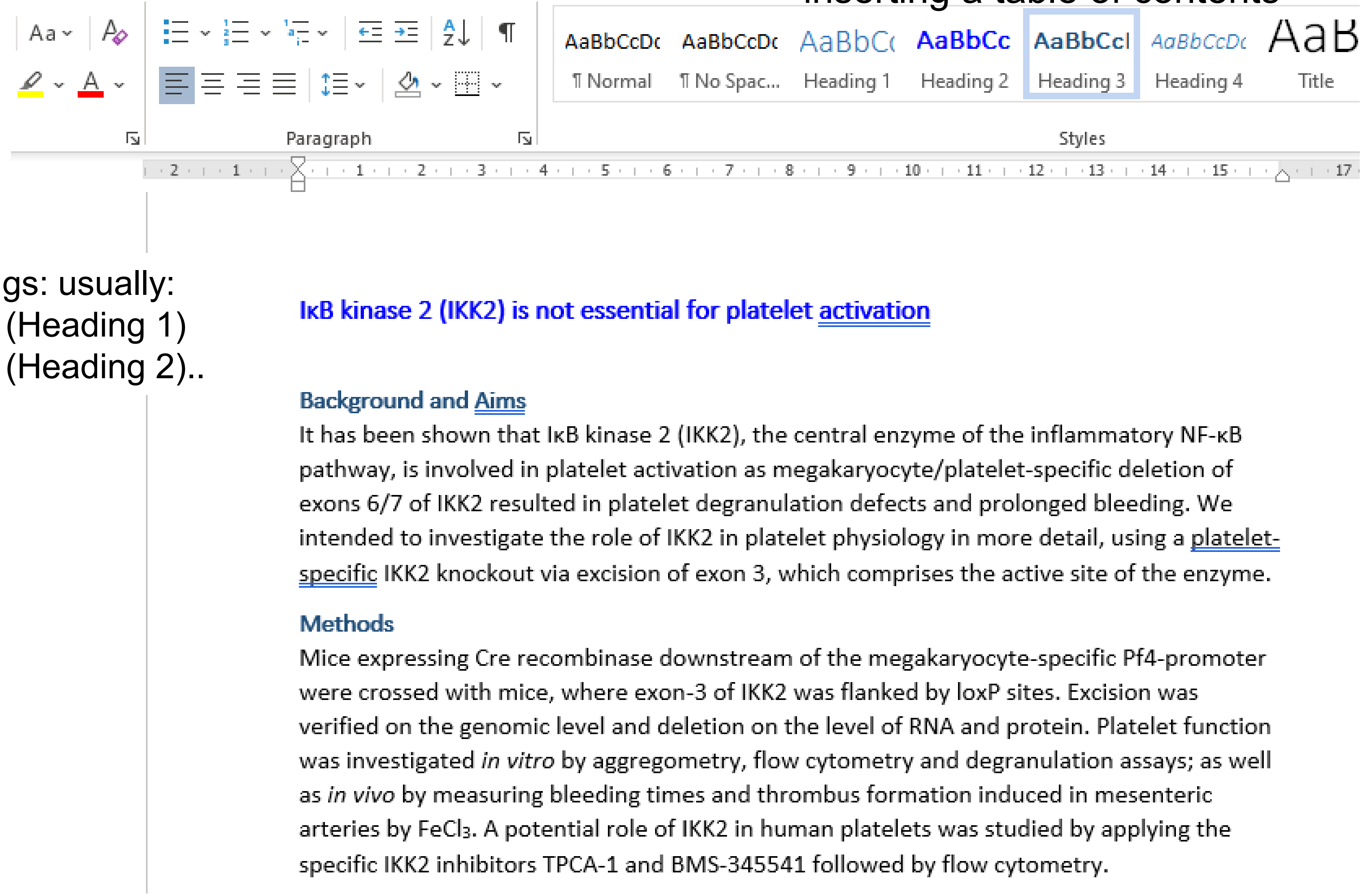


Background and Aims

It has been ~~reported~~ shown that IκB kinase 2 (IKK2), the central enzyme of the i
NF-κB pathway, is involved in platelet activation as megakaryocyte/platelet-spe
of exons 6/7 of IKK2 resulted in platelet degranulation defects and prolonged bl

Insert a Table of Contents

When you **define headings in your document**, these can be used for inserting a table of contents



IκB kinase 2 (IKK2) is not essential for platelet activation

Background and Aims

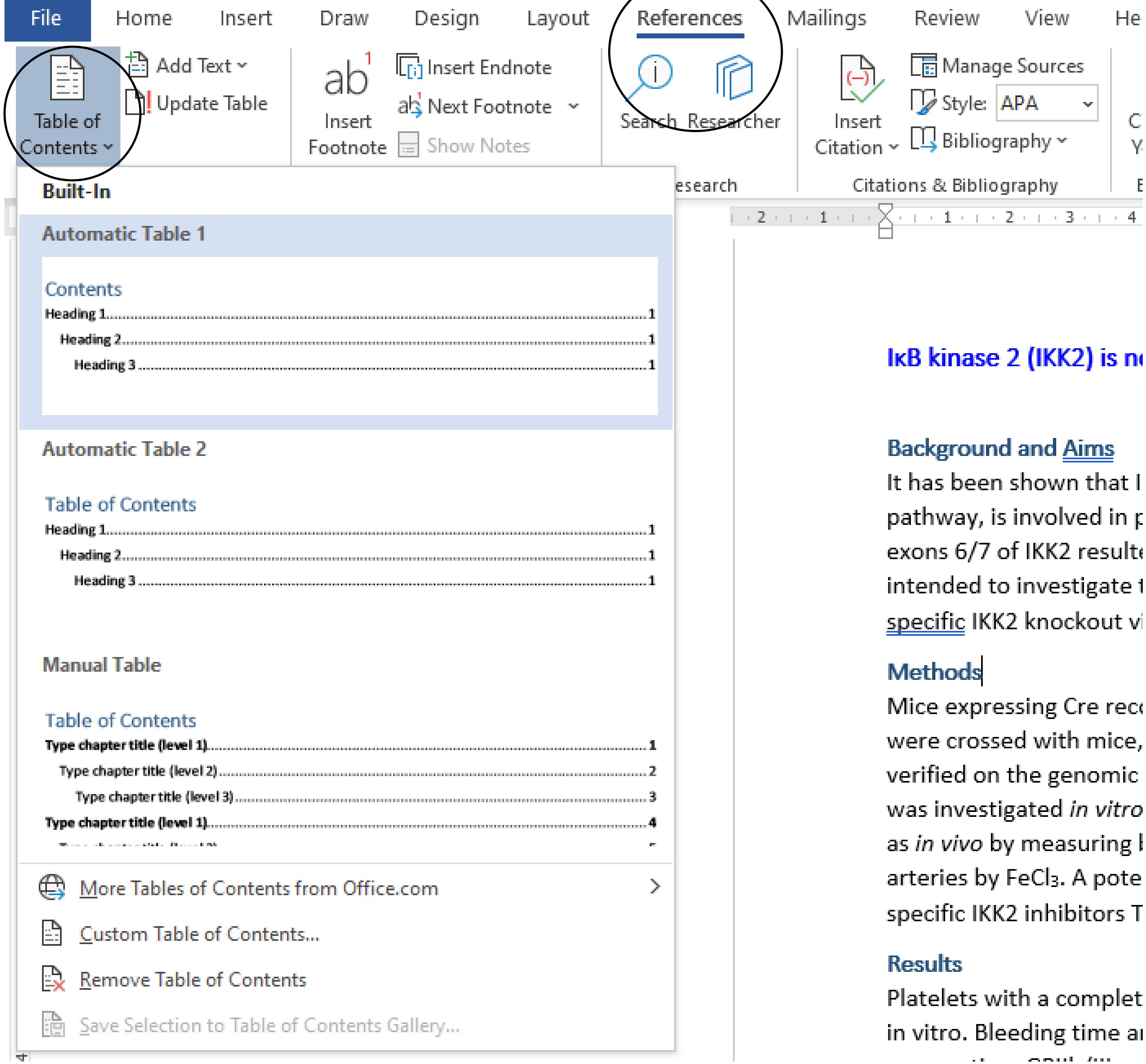
It has been shown that IκB kinase 2 (IKK2), the central enzyme of the inflammatory NF-κB pathway, is involved in platelet activation as megakaryocyte/platelet-specific deletion of exons 6/7 of IKK2 resulted in platelet degranulation defects and prolonged bleeding. We intended to investigate the role of IKK2 in platelet physiology in more detail, using a platelet-specific IKK2 knockout via excision of exon 3, which comprises the active site of the enzyme.

Methods

Mice expressing Cre recombinase downstream of the megakaryocyte-specific Pf4-promoter were crossed with mice, where exon-3 of IKK2 was flanked by loxP sites. Excision was verified on the genomic level and deletion on the level of RNA and protein. Platelet function was investigated *in vitro* by aggregometry, flow cytometry and degranulation assays; as well as *in vivo* by measuring bleeding times and thrombus formation induced in mesenteric arteries by $FeCl_3$. A potential role of IKK2 in human platelets was studied by applying the specific IKK2 inhibitors TPCA-1 and BMS-345541 followed by flow cytometry.

Headings: usually:
Ctrl +1 (Heading 1)
Ctrl +2 (Heading 2)..

Insert a Table of Contents



IκB kinase 2 (IKK2) is n

Background and Aims

It has been shown that I
pathway, is involved in p
exons 6/7 of IKK2 result
intended to investigate t
specific IKK2 knockout v

Methods

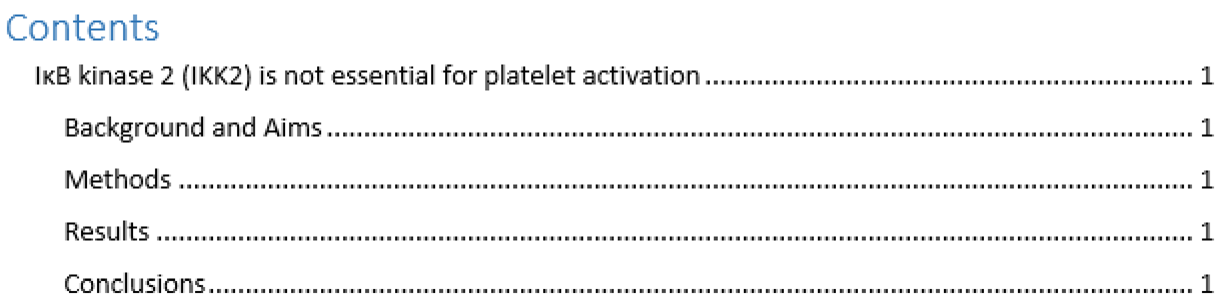
Mice expressing Cre rec
were crossed with mice,
verified on the genomic
was investigated *in vitro*
as *in vivo* by measuring
arteries by FeCl₃. A pote
specific IKK2 inhibitors T

Results

Platelets with a complet
in vitro. Bleeding time a

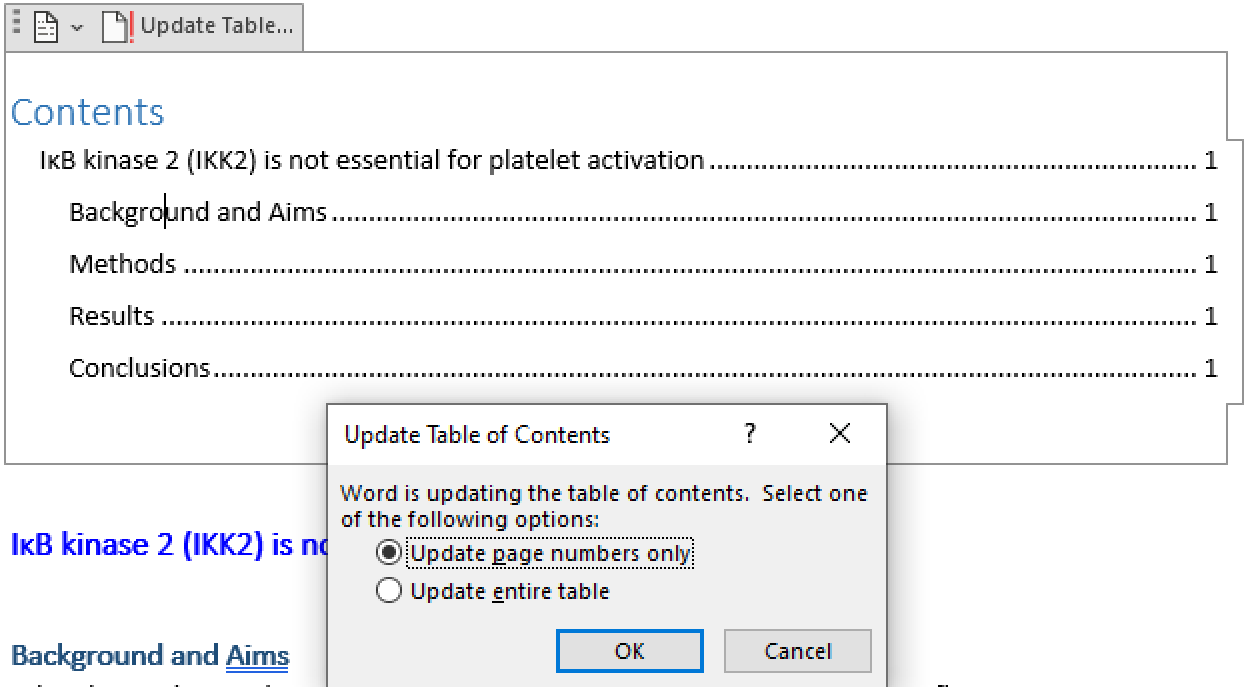
Insert a Table of Contents

„Ctrl + click“ on an entry lets you jump to the respective page of the document



Contents

Table of content can be updated by clicking on the top (or right-clicking into it)



Contents

Update Table of Contents

Word is updating the table of contents. Select one of the following options:

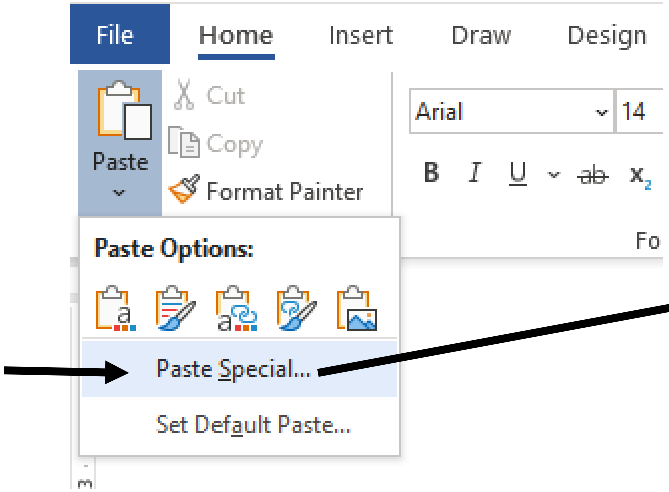
● Update page numbers only
○ Update entire table

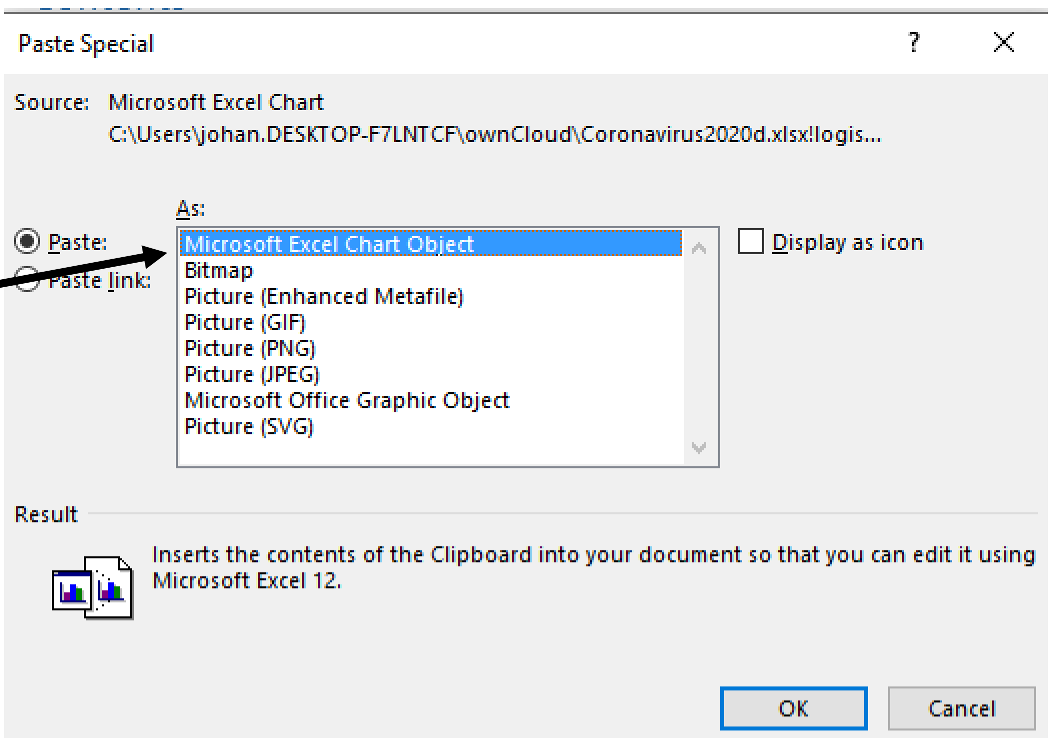
IκB kinase 2 (IKK2) is n

Background and Aims

Copying Excel Graphs into Word (as Excel file)

In Excel: click on the graph and copy it (Ctrl-C)
> in Word (Home tab): click: Paste special: and paste as Excel object




Paste Special

Source: Microsoft Excel Chart
C:\Users\johan.DESKTOP-F7LNTCF\ownCloud\Coronavirus2020d.xlsx!logis...

As:

● Paste:
○ Paste link:

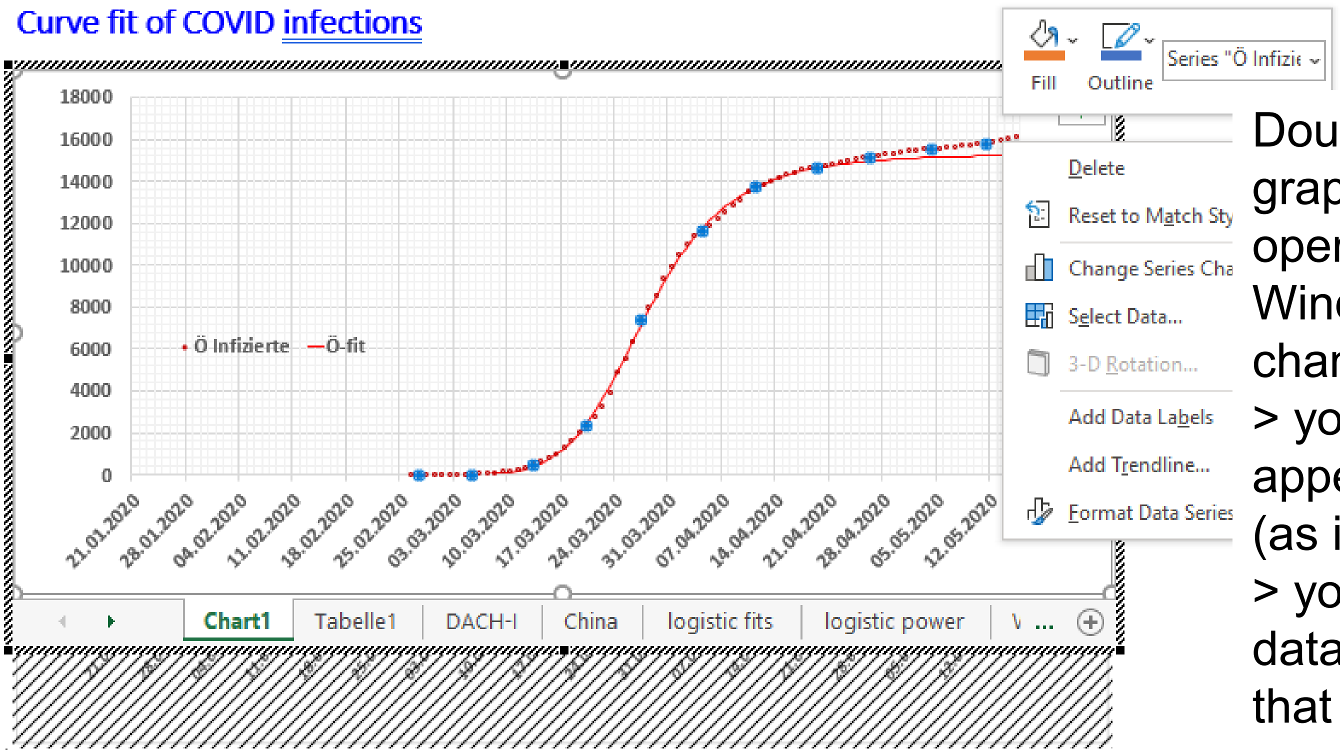
- Microsoft Excel Chart Object
- Bitmap
- Picture (Enhanced Metafile)
- Picture (GIF)
- Picture (PNG)
- Picture (JPEG)
- Microsoft Office Graphic Object
- Picture (SVG)

☐ Display as icon

Result

Inserts the contents of the Clipboard into your document so that you can edit it using Microsoft Excel 12.

Opening Excel Graphs in Word (as Excel file)



Curve fit of COVID infections

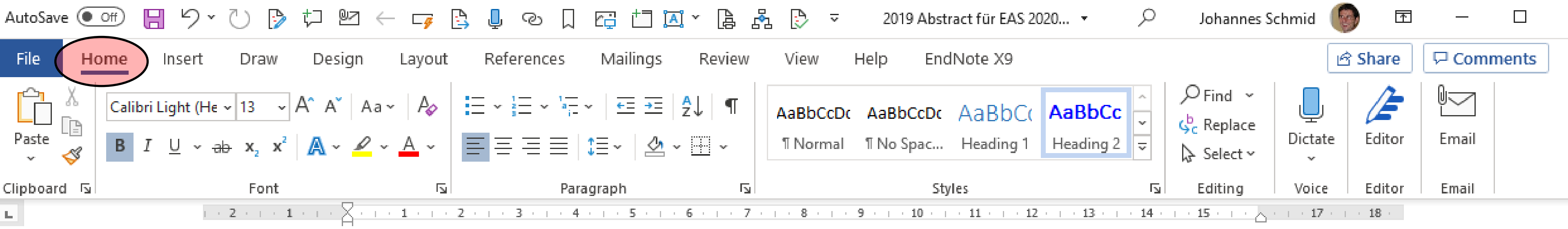
Double clicking on the graph in the Word file opens a small Excel Window (the frame changes):

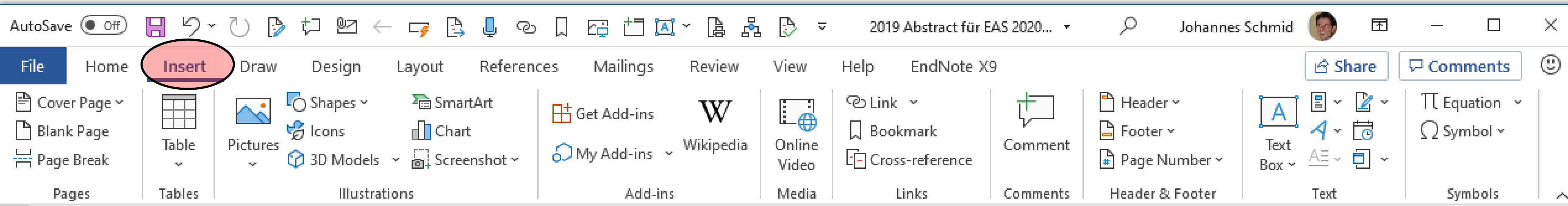
> you can change the appearance of the graph (as in Excel)

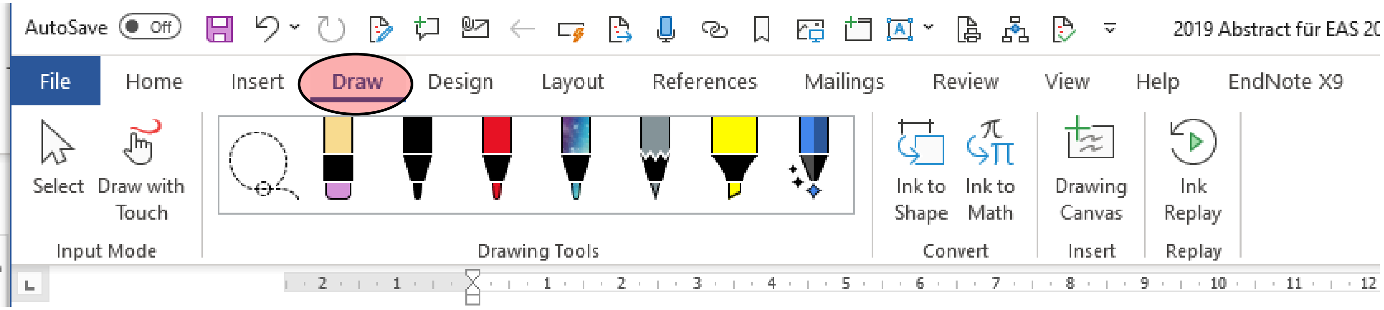
> you can also go into the data and change the data that is shown etc.

This procedure can be done with every file that allows OLE (Object Linked embedding)

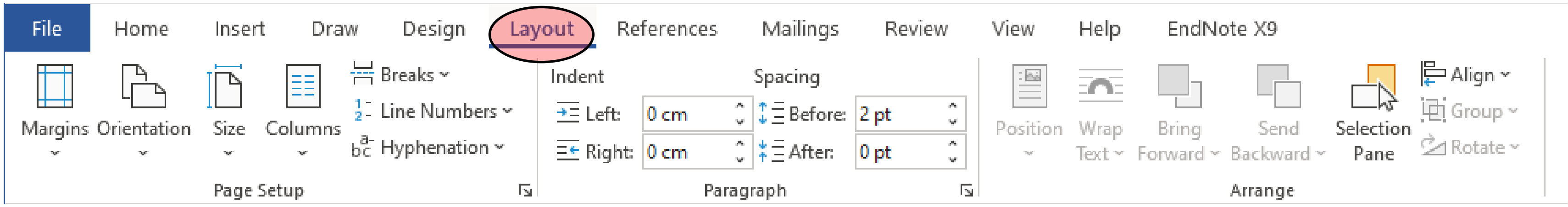
The different tabs and toolbars

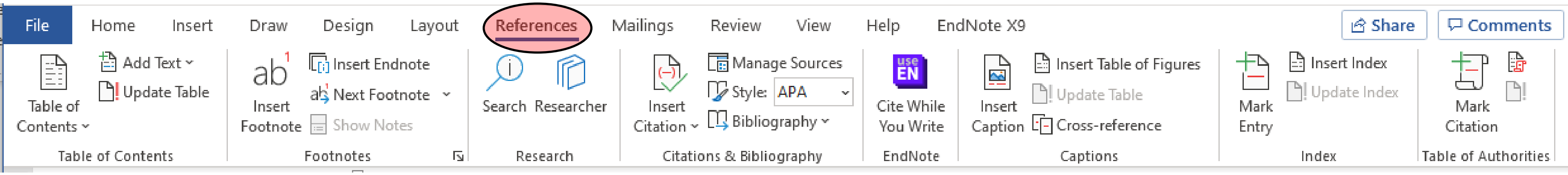


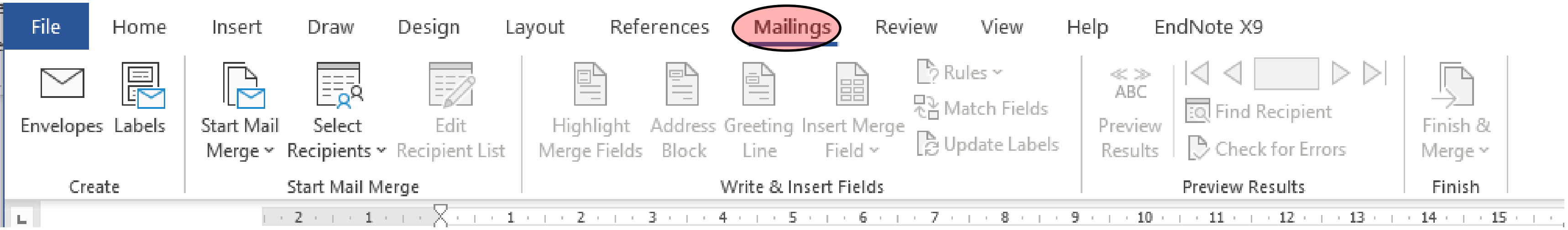


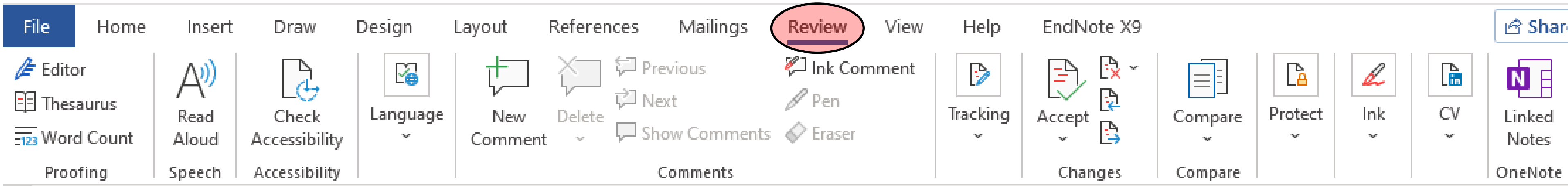


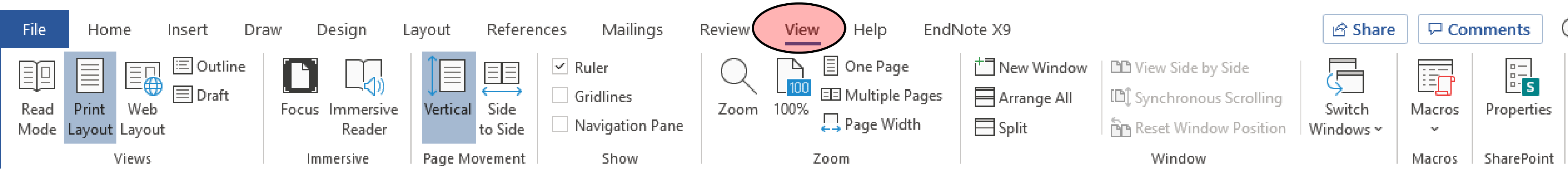
The different tabs and toolbars







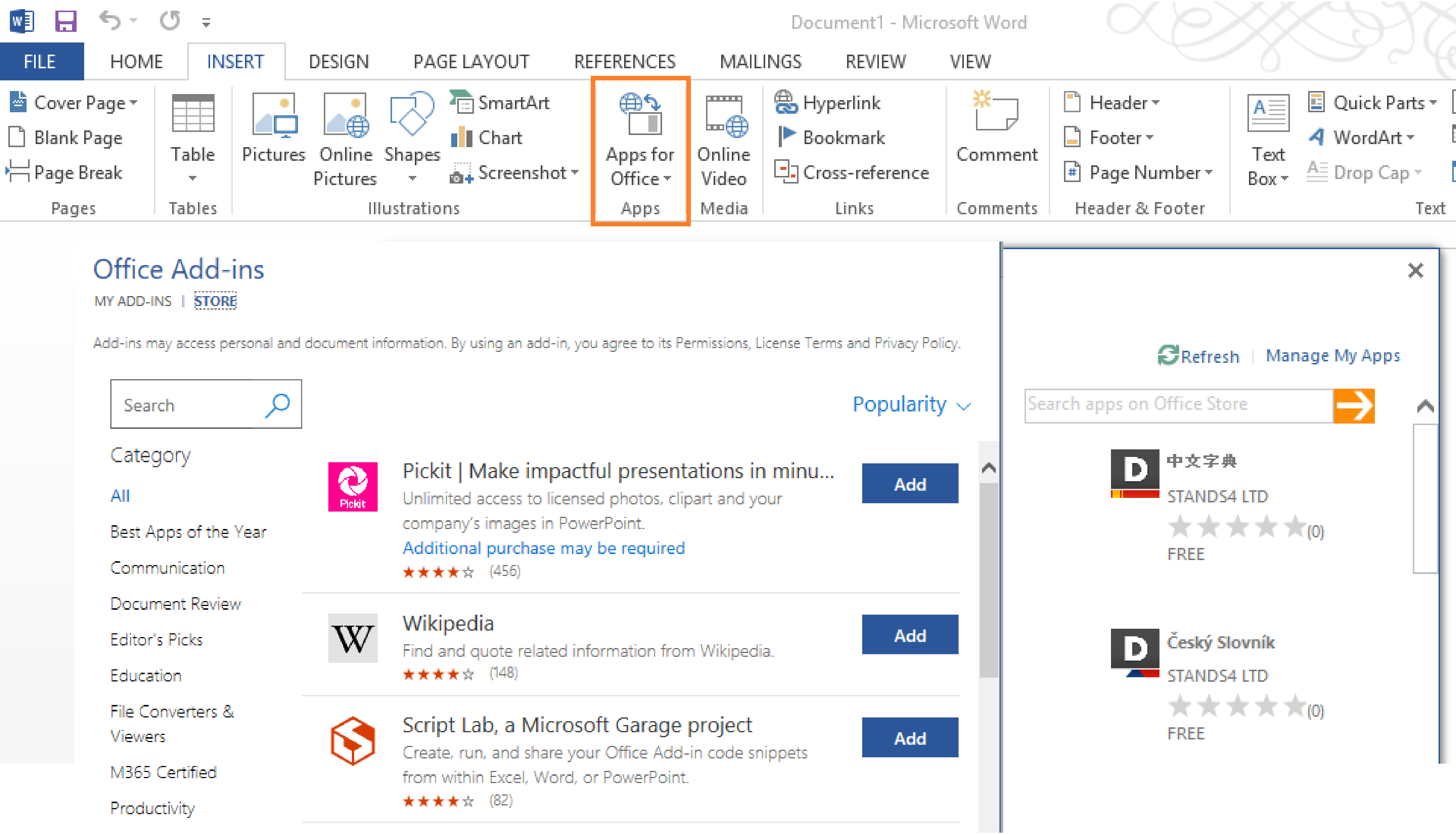




Developments since MS-Office 2013

- Usability on tablets and convertibles
- Strong connection to Onedrive the cloud-solution of Microsoft (with hotmail or outlook account)
- New licensing strategy: Microsoft365: always newest Office : (Word, Excel, Powerpoint, Outlook, OneNote, Access, Publisher): rental for students and academics possible – but not supported by our University for employees (due to data safety issues).
- Microsoft365 is free for most students with some restrictions at the Med.Univ Vienna (does not include the 1TB Onedrive space)
- pdf‘s can be converted in Word documents (format maintained, editable)
- Integration of online videos or pictures, recording of the screen…

Add-ins within Word 2013 and later



Office Add-ins

MY ADD-INS | STORE

Add-ins may access personal and document information. By using an add-in, you agree to its Permissions, License Terms and Privacy Policy.

Category

- All
- Best Apps of the Year
- Communication
- Document Review
- Editor's Picks
- Education
- File Converters & Viewers
- M365 Certified
- Productivity

Pickit | Make impactful presentations in minu...
Unlimited access to licensed photos, clipart and your company's images in PowerPoint.
Additional purchase may be required
★★★★☆ (456)

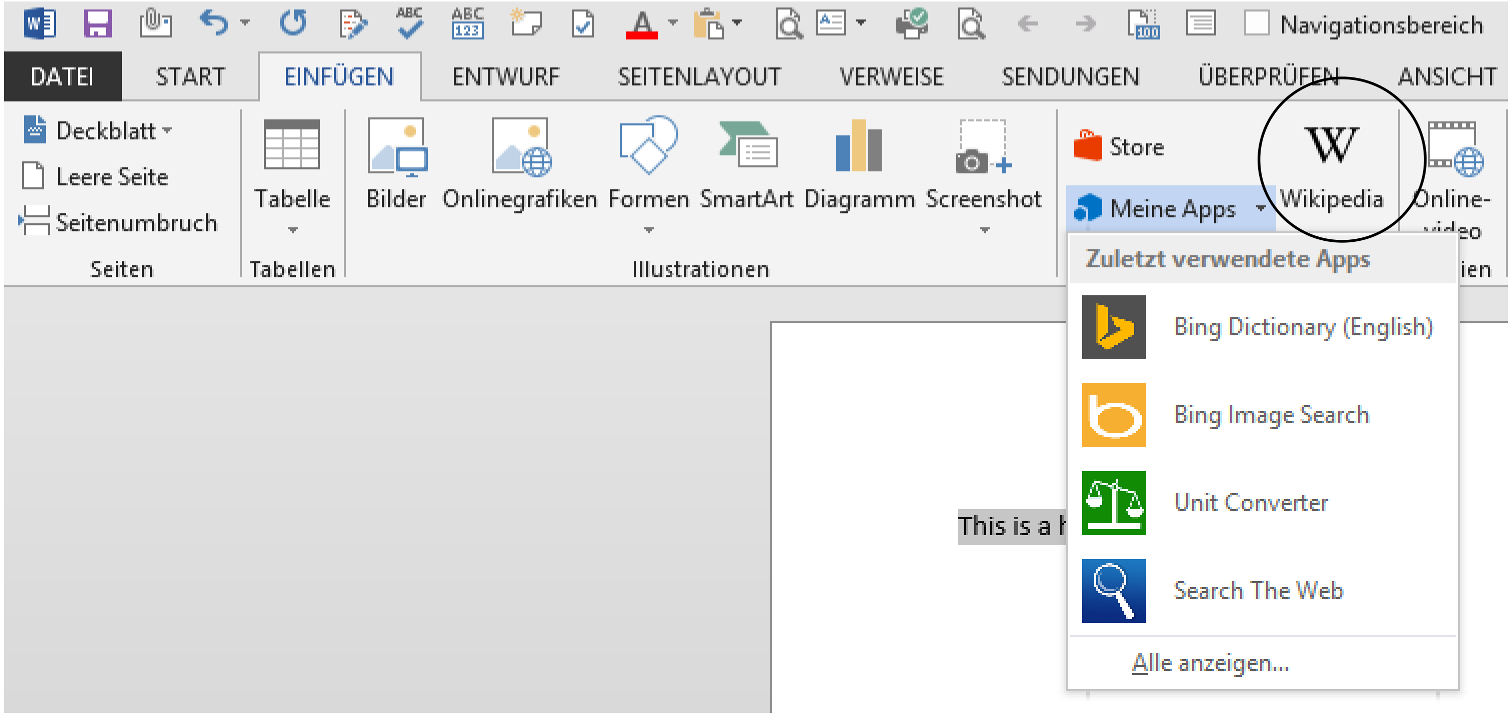
Wikipedia
Find and quote related information from Wikipedia.
★★★★☆ (148)

Script Lab, a Microsoft Garage project
Create, run, and share your Office Add-in code snippets from within Excel, Word, or PowerPoint.
★★★★☆ (82)

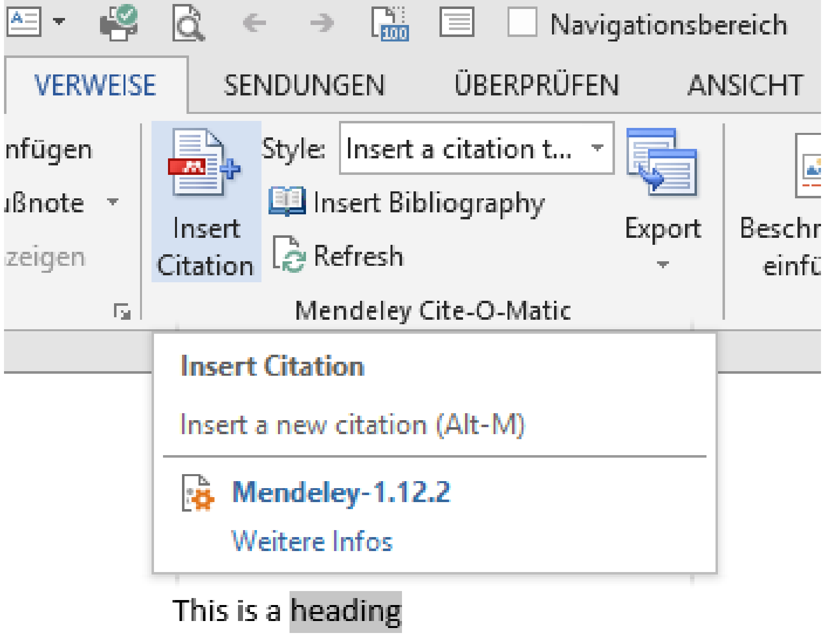
中文字典
STANDS4 LTD
☆☆☆☆☆ (0)
FREE

Český Slovník
STANDS4 LTD
☆☆☆☆☆ (0)
FREE

Apps in Word 2013



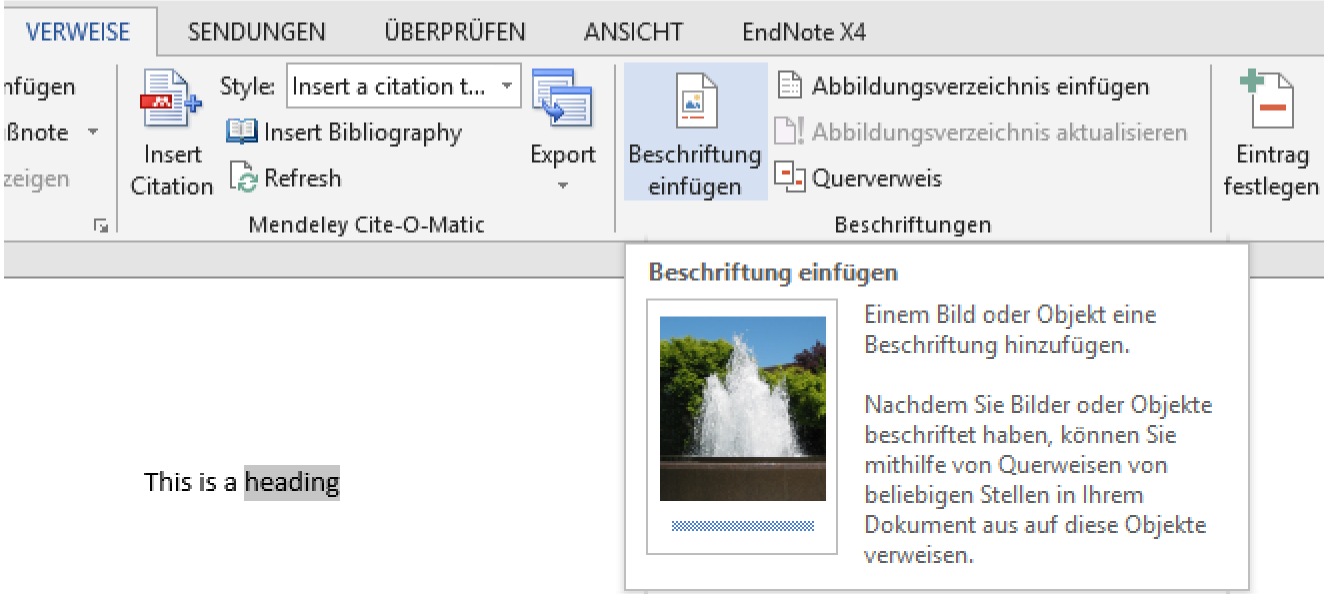
Mendeley Add-In for citations



Insert a new citation (Alt-M)

This is a heading

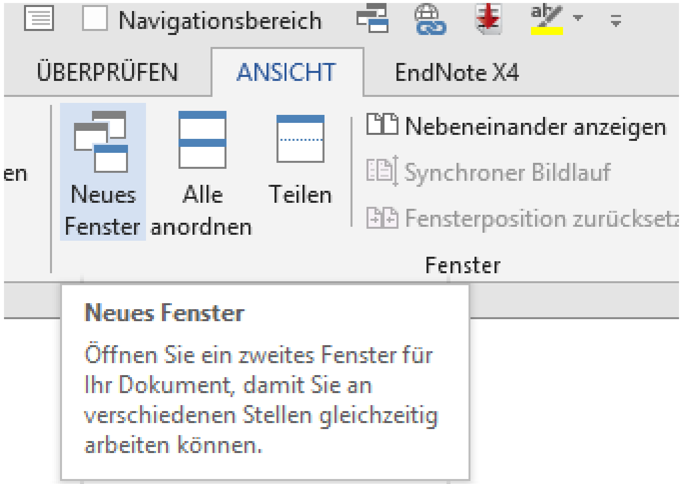
Adding of figure legends



Einem Bild oder Objekt eine Beschriftung hinzufügen.

Nachdem Sie Bilder oder Objekte beschriftet haben, können Sie mithilfe von Querweisen von beliebigen Stellen in Ihrem Dokument aus auf diese Objekte verweisen.

This is a heading

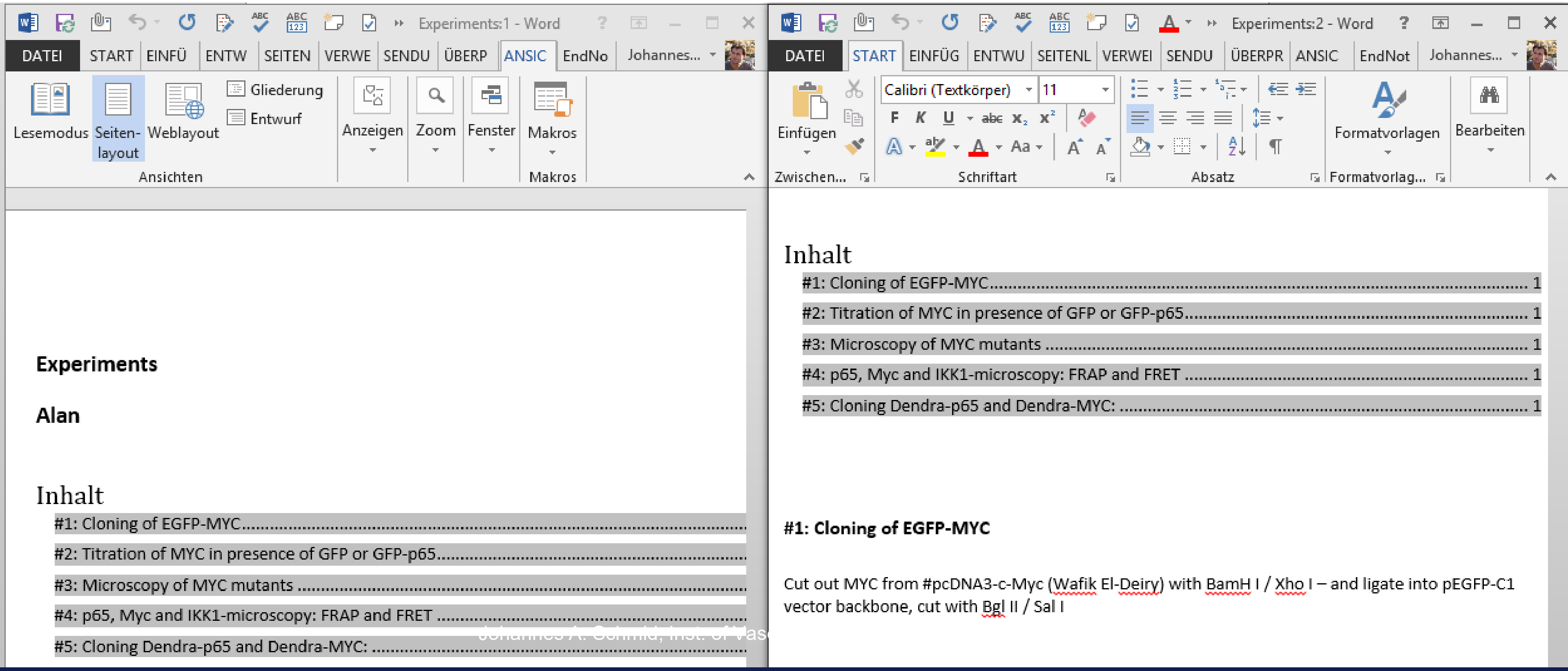


Neues Fenster

Öffnen Sie ein zweites Fenster für Ihr Dokument, damit Sie an verschiedenen Stellen gleichzeitig arbeiten können.

You can open the same document twice (e.g. to work on 2 different positions simultaneously)

(Dragging the window to the left margin of the monitor will scale it exactly to the left half of the monitor >> and vice versa on the right side)



Experiments

Alan

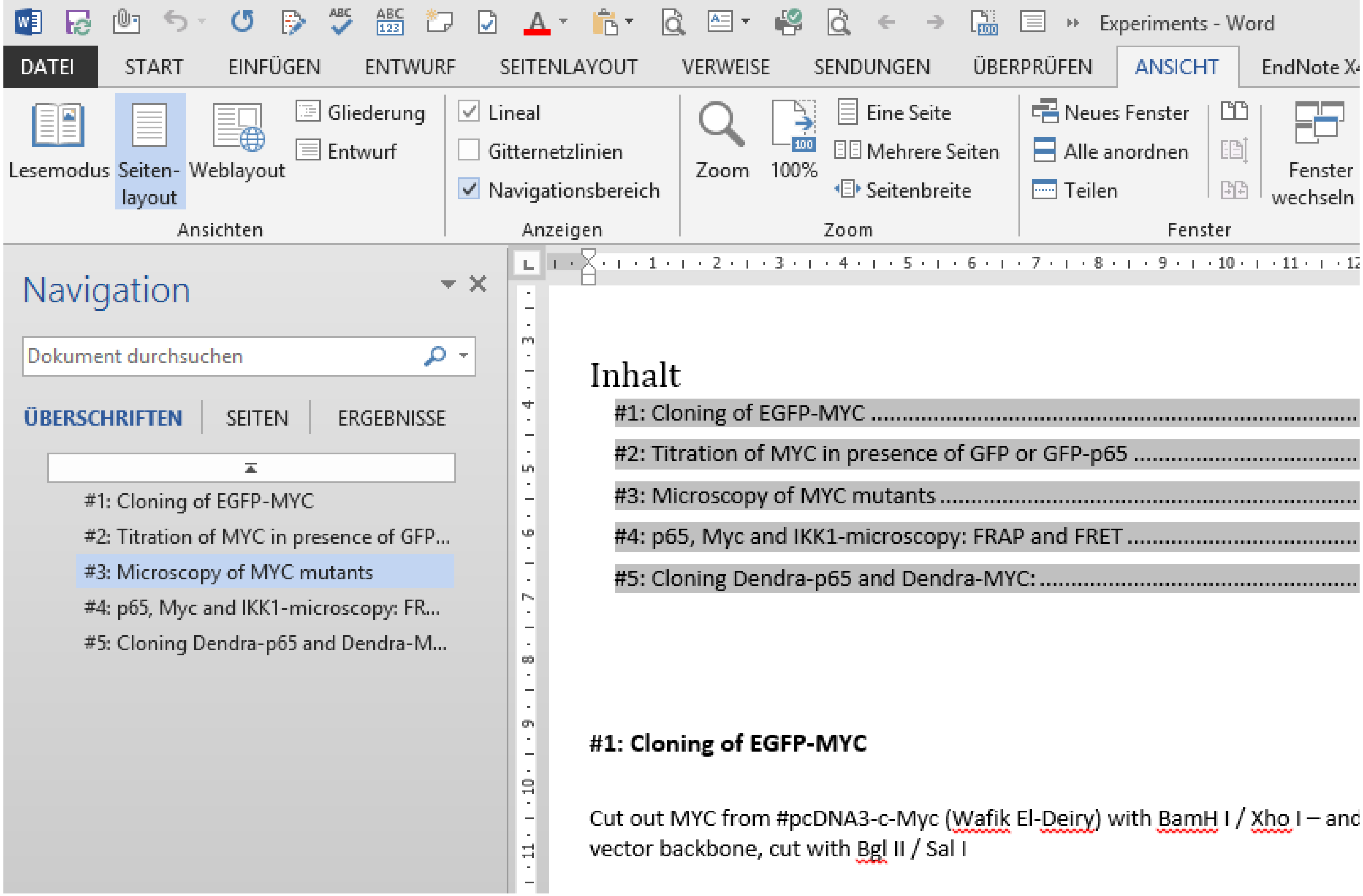
Inhalt

Inhalt

#1: Cloning of EGFP-MYC

Cut out MYC from #pcDNA3-c-Myc (Wafik El-Deiry) with BamH I / Xho I – and ligate into pEGFP-C1 vector backbone, cut with Bgl II / Sal I

The Navigation Window



☑ Lineal
☐ Gitternetzlinien
☑ Navigationsbereich

#1: Cloning of EGFP-MYC
#2: Titration of MYC in presence of GFP...
#3: Microscopy of MYC mutants
#4: p65, Myc and IKK1-microscopy: FR...
#5: Cloning Dendra-p65 and Dendra-M...

Inhalt

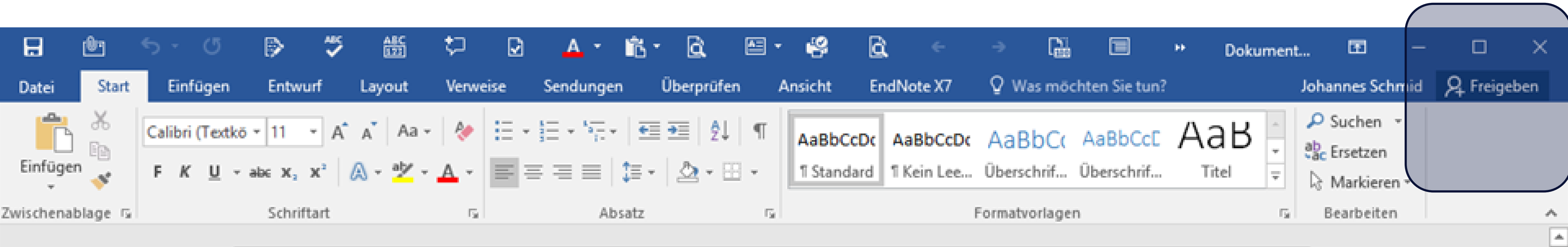
#1: Cloning of EGFP-MYC ....
#2: Titration of MYC in presence of GFP or GFP-p65 ....
#3: Microscopy of MYC mutants ....
#4: p65, Myc and IKK1-microscopy: FRAP and FRET ....
#5: Cloning Dendra-p65 and Dendra-MYC: ....

#1: Cloning of EGFP-MYC

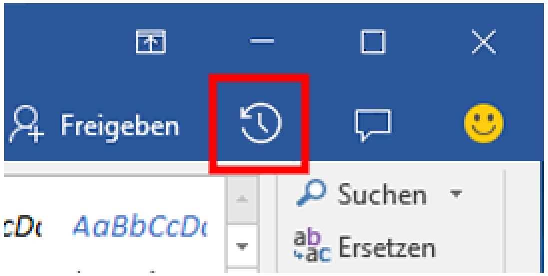
Cut out MYC from #pcDNA3-c-Myc (Wafik El-Deiry) with BamH I / Xho I – and
vector backbone, cut with Bgl II / Sal I

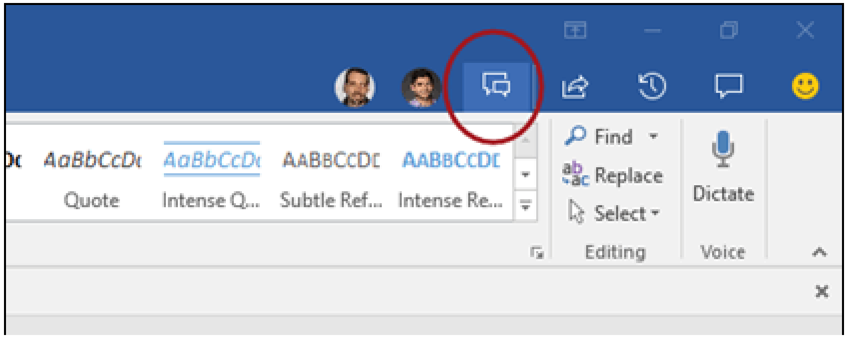
Some features since Word 2016

- Better sharing options
- Authors can work simultaneously on the same document on the cloud (Onedrive)
  → You can work with others on a manuscript or grant proposal simultaneously and see changes in real time: BUT: frequent error messages with large or complex documents



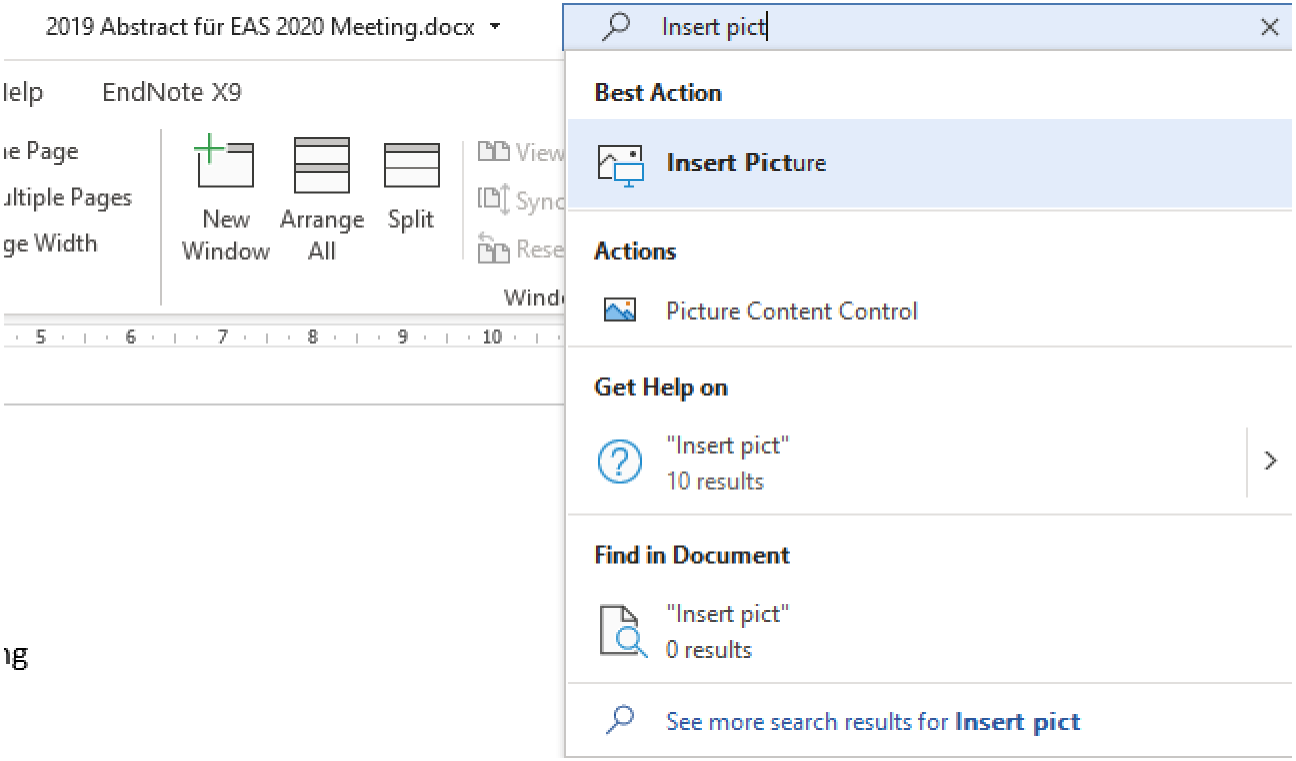
Changes done by co-authors can be checked and previous versions can be restored





Chat function for co-authors

„Search“ Button
> Help function that initiates the command immediately



2019 Abstract für EAS 2020 Meeting.docx

Insert pict

Best Action

Insert Picture

Actions

Picture Content Control

Get Help on

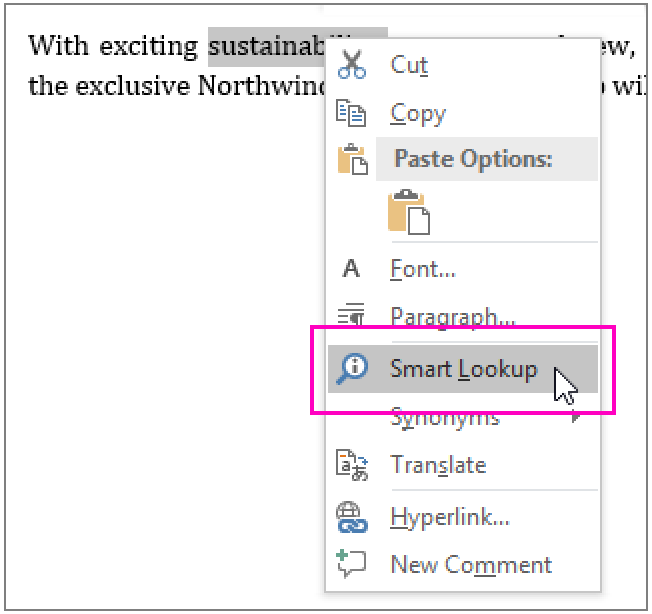
"Insert pict"
10 results

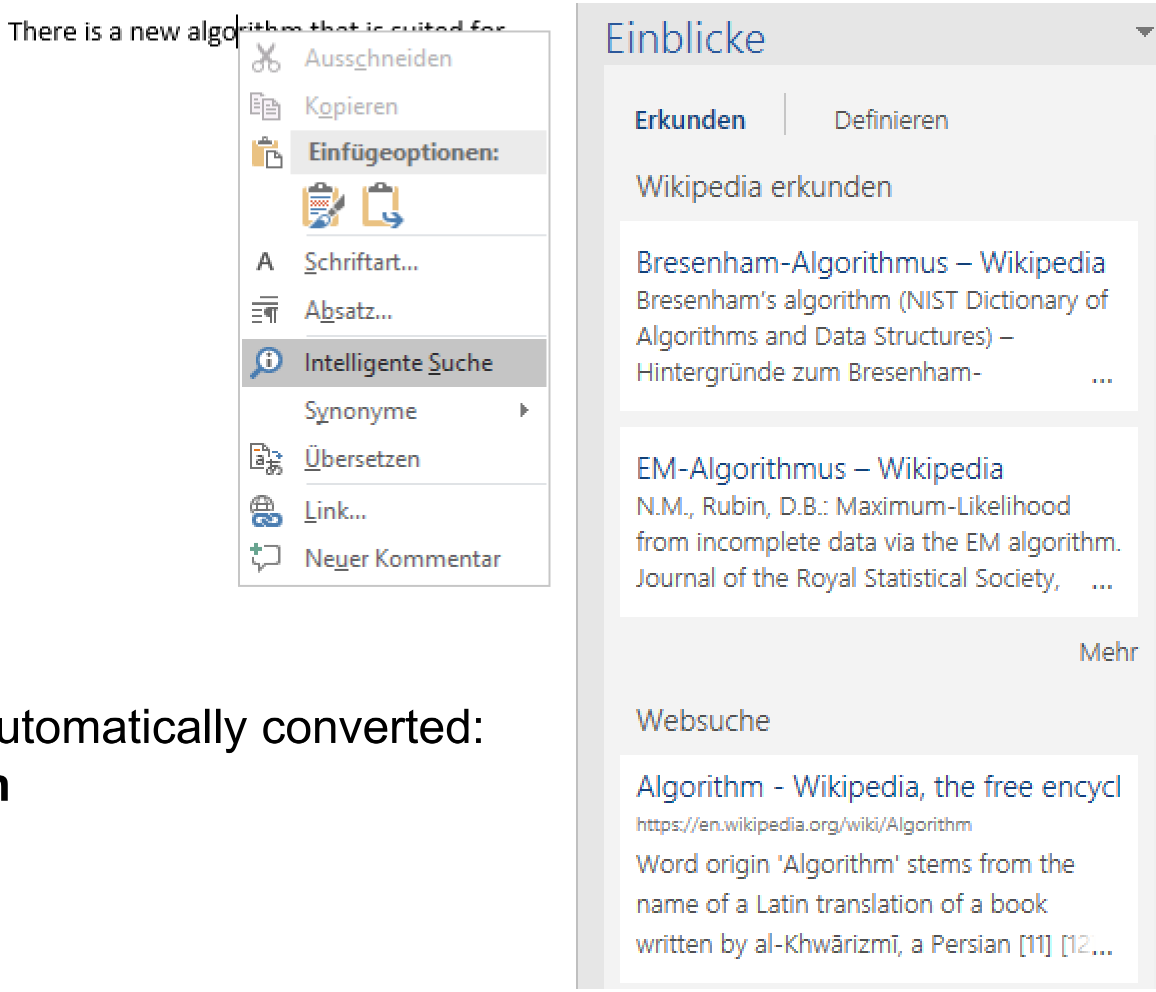
Find in Document

"Insert pict"
0 results

See more search results for **Insert pict**

Smart Look up function within a document (by right-clicking a word)


With exciting sustainab ew,
the exclusive Northwin wi


There is a new algo

Wikipedia erkunden

Bresenham-Algorithmus – Wikipedia
Bresenham's algorithm (NIST Dictionary of Algorithms and Data Structures) – Hintergründe zum Bresenham- ...

EM-Algorithmus – Wikipedia
N.M., Rubin, D.B.: Maximum-Likelihood from incomplete data via the EM algorithm. Journal of the Royal Statistical Society, ...

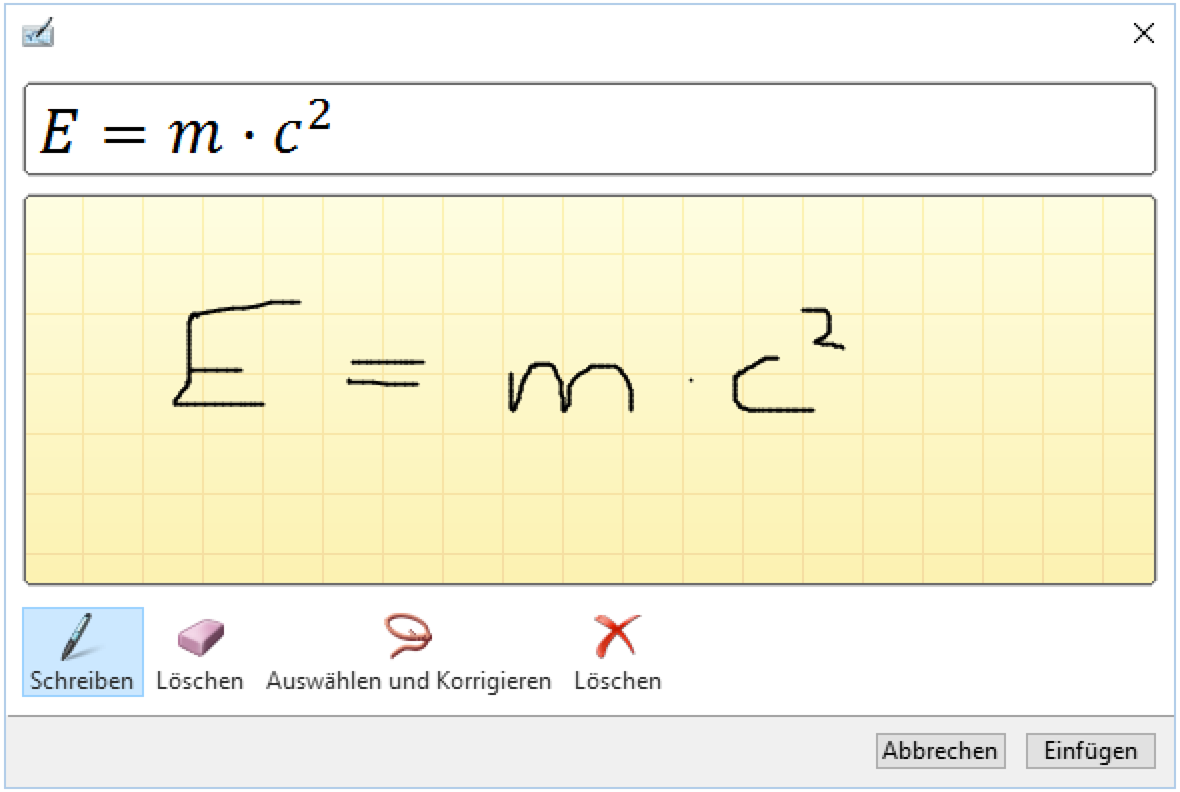
Mehr

Websuche

Algorithm - Wikipedia, the free encycl
https://en.wikipedia.org/wiki/Algorithm
Word origin 'Algorithm' stems from the name of a Latin translation of a book written by al-Khwārizmī, a Persian [11] [12...

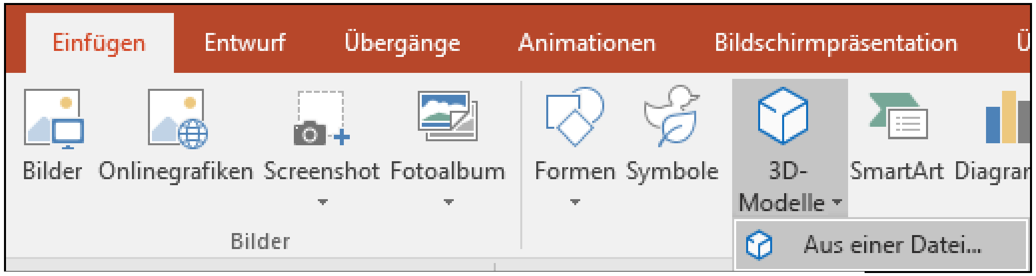
Hand-written equations can be automatically converted:
Insert > Equation > **Ink Equation**

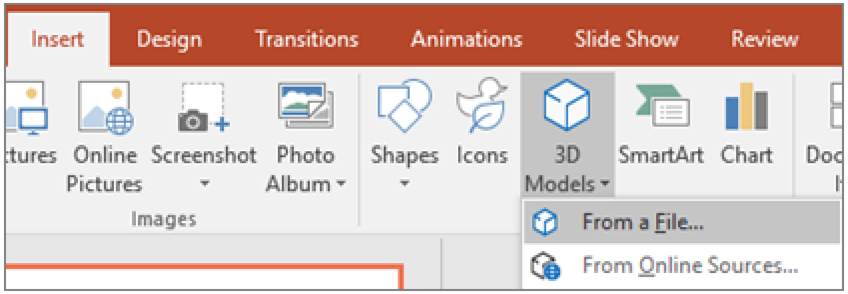
Hand-written equations can be automatically converted:
Insert > Equation > **Ink Equation**

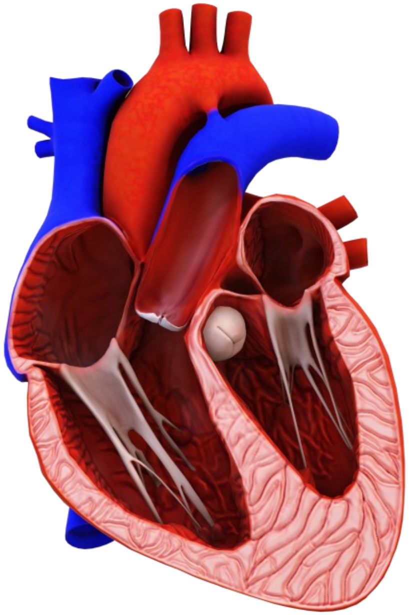


$$E = m \cdot c^2$$

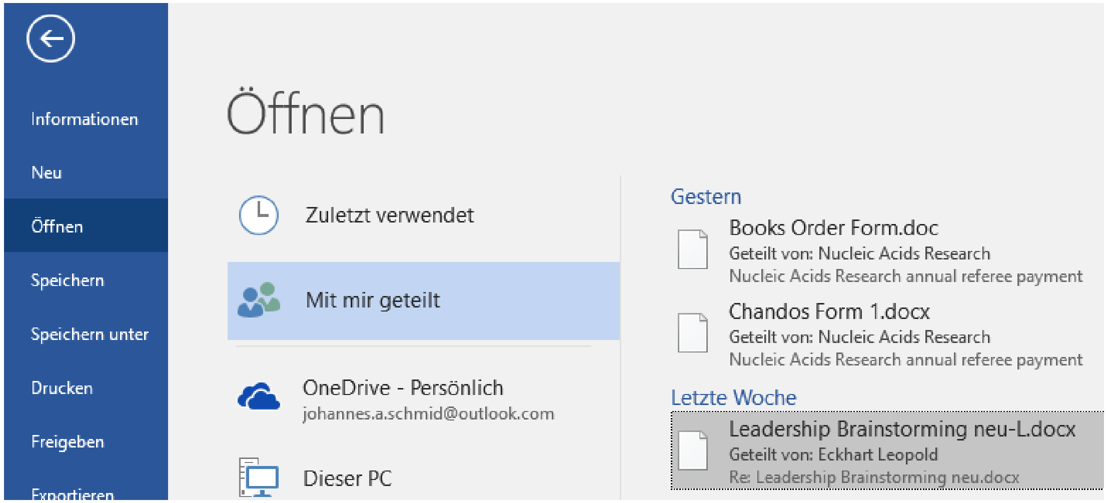
Inserting of 3D models







Some features of Office 365 users: Opening of Word-files, which had been received as email attachment:

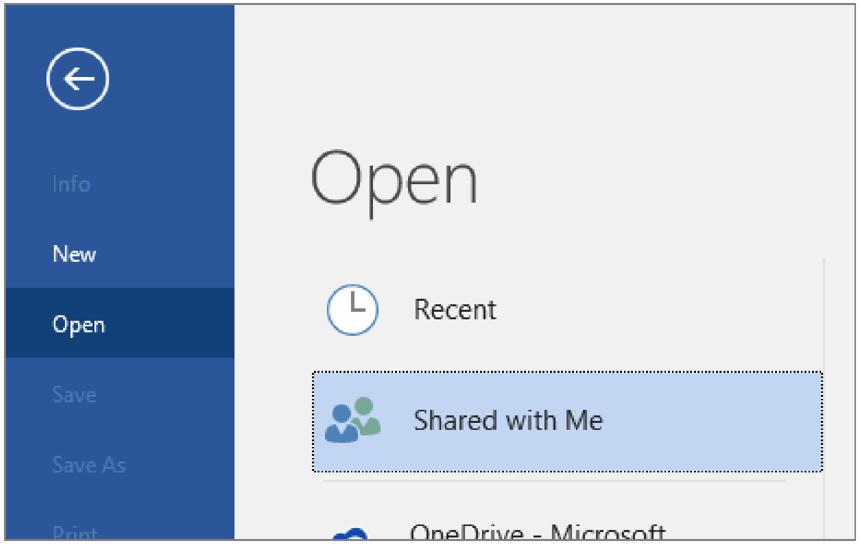


johannes.a.schmid@outlook.com

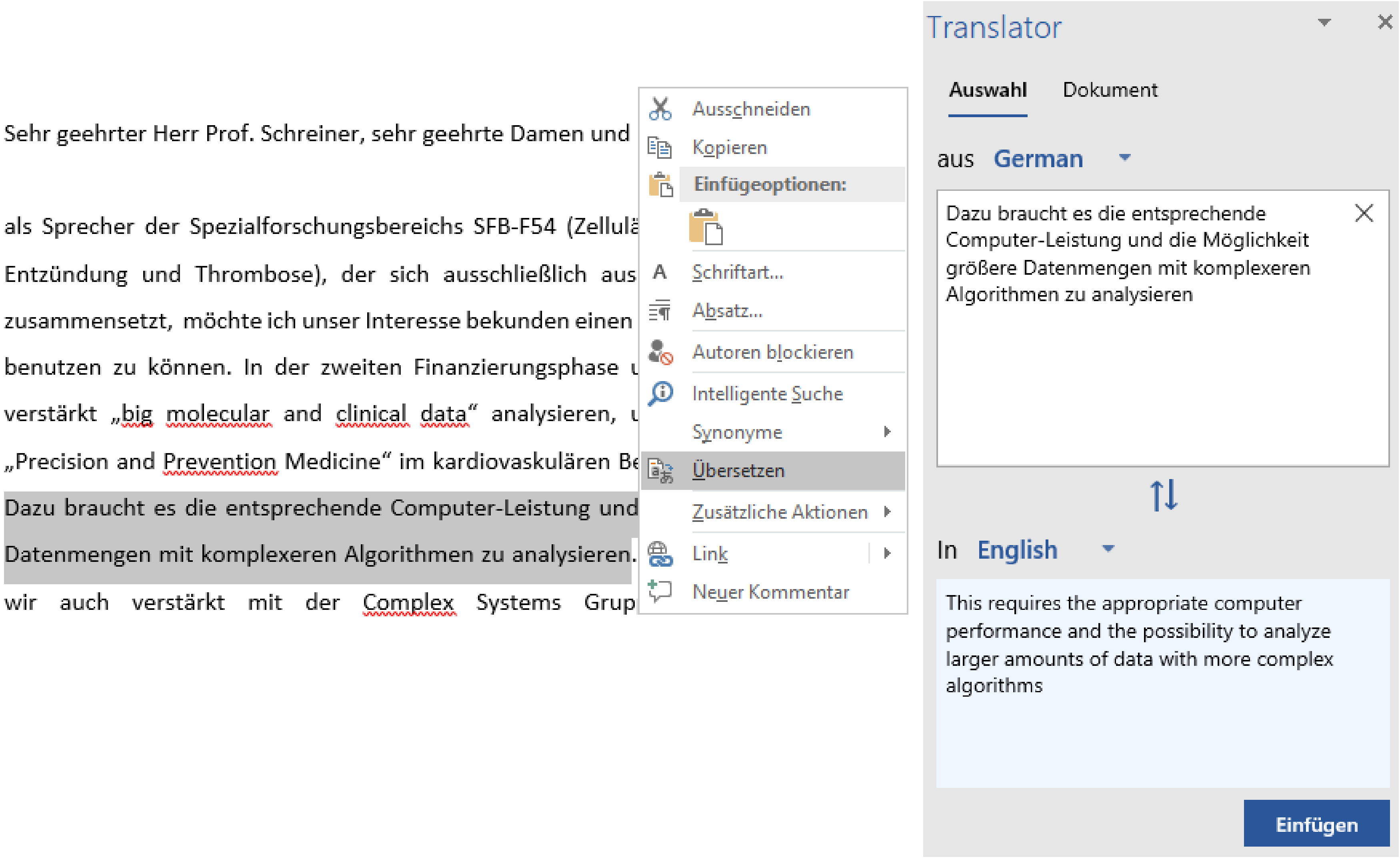
Books Order Form.doc
Geteilt von: Nucleic Acids Research
Nucleic Acids Research annual referee payment

Chandos Form 1.docx
Geteilt von: Nucleic Acids Research
Nucleic Acids Research annual referee payment

Leadership Brainstorming neu-L.docx
Geteilt von: Eckhart Leopold
Re: Leadership Brainstorming neu.docx



Translations within a document



Sehr geehrter Herr Prof. Schreiner, sehr geehrte Damen und

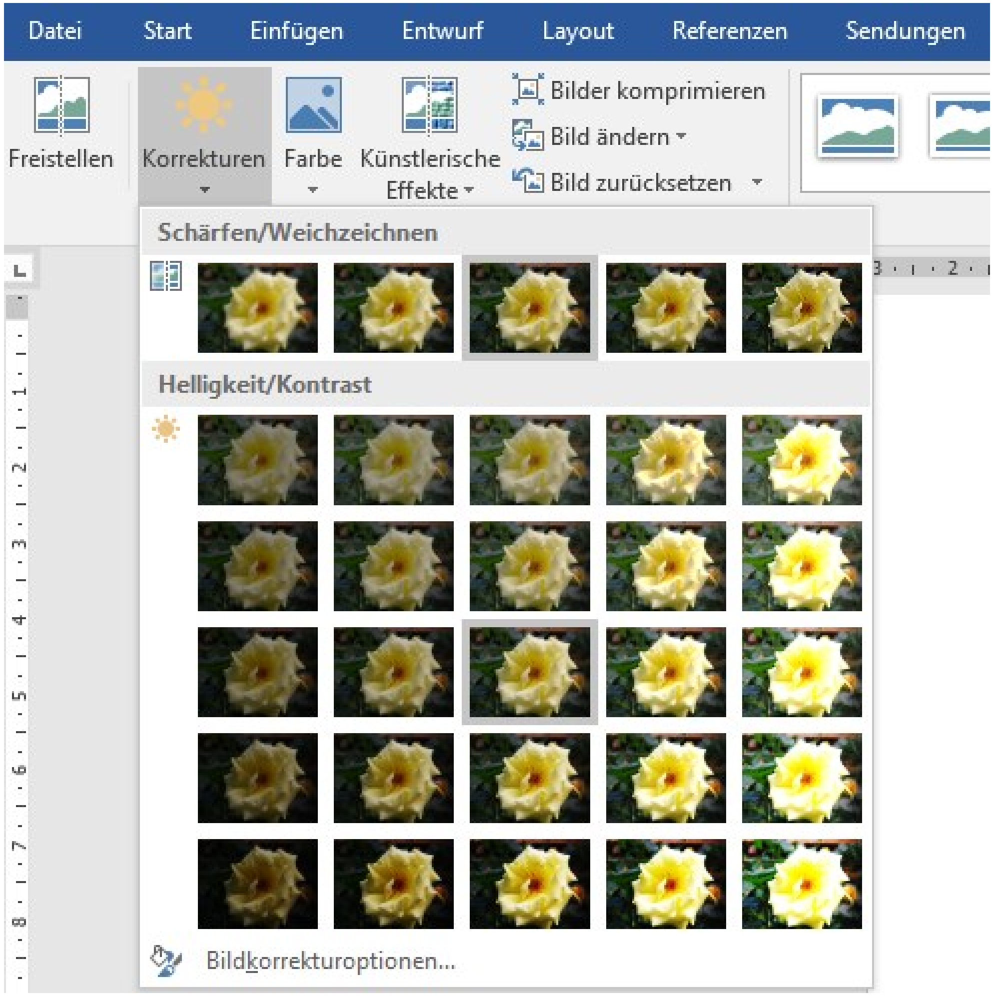
als Sprecher der Spezialforschungsbereichs SFB-F54 (Zellulä
Entzündung und Thrombose), der sich ausschließlich aus
zusammensetzt, möchte ich unser Interesse bekunden einen
benutzen zu können. In der zweiten Finanzierungsphase u
verstärkt „big molecular and clinical data“ analysieren, u
„Precision and Prevention Medicine“ im kardiovaskulären Be
Dazu braucht es die entsprechende Computer-Leistung und
Datenmengen mit komplexeren Algorithmen zu analysieren.
wir auch verstärkt mit der Complex Systems Grup

Dazu braucht es die entsprechende Computer-Leistung und die Möglichkeit größere Datenmengen mit komplexeren Algorithmen zu analysieren

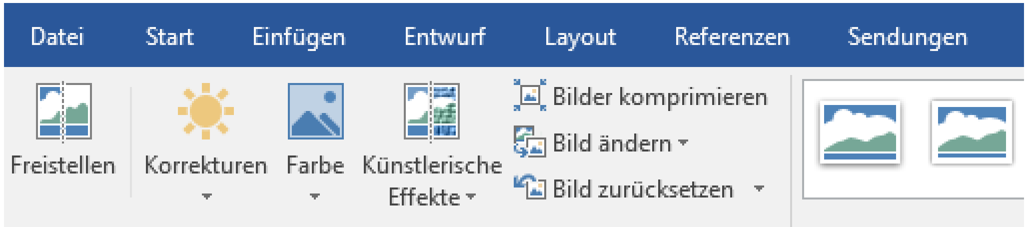
This requires the appropriate computer performance and the possibility to analyze larger amounts of data with more complex algorithms

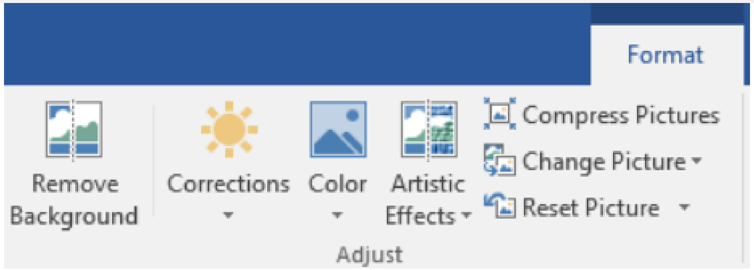
Working with images in Office files

Double click on an image and perform brightness/contrast adjustments, changes of colors or removal of background…



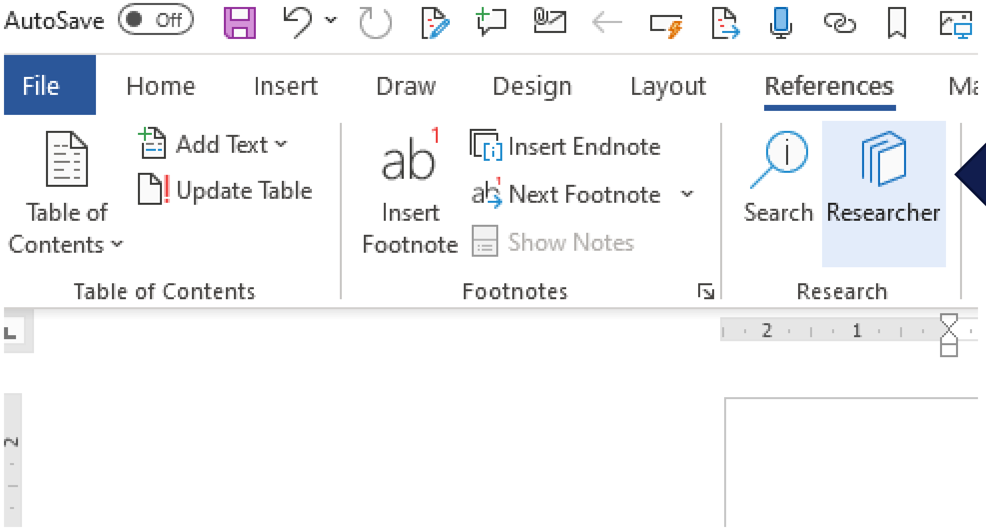
Working with images in Office files

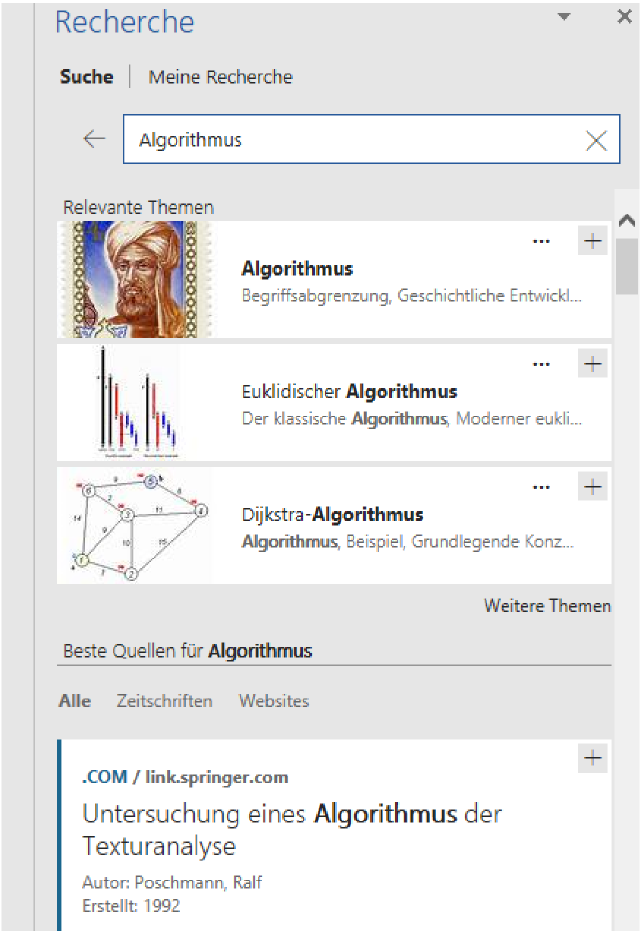




Easier background removal

The “Researcher” function





Algorithmus

Relevante Themen

Algorithmus
Begriffsabgrenzung, Geschichtliche Entwickl...

Euklidischer **Algorithmus**
Der klassische **Algorithmus**, Moderner eukli...

Dijkstra-**Algorithmus**
Algorithmus, Beispiel, Grundlegende Konz...

Weitere Themen

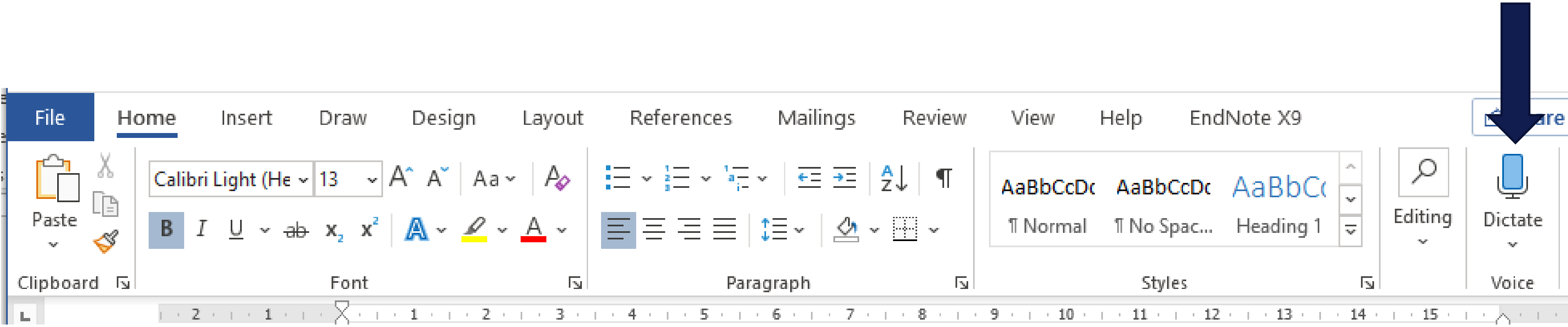
Beste Quellen für **Algorithmus**

Alle Zeitschriften Websites

.COM / link.springer.com
Untersuchung eines **Algorithmus** der Texturanalyse
Autor: Poschmann, Ralf
Erstellt: 1992

Speech recognition (Dictating text)

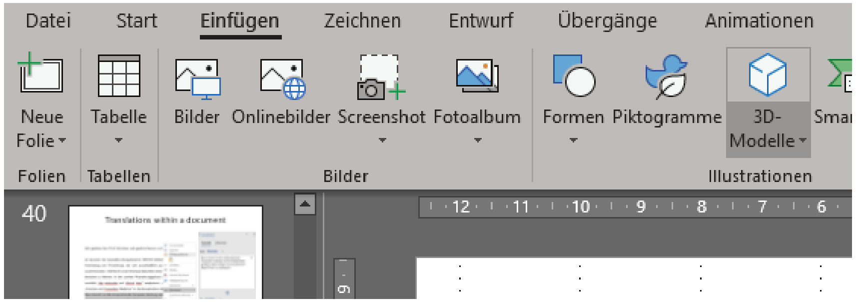
Included into the Start-tab of the latest version without the need of an Add-in



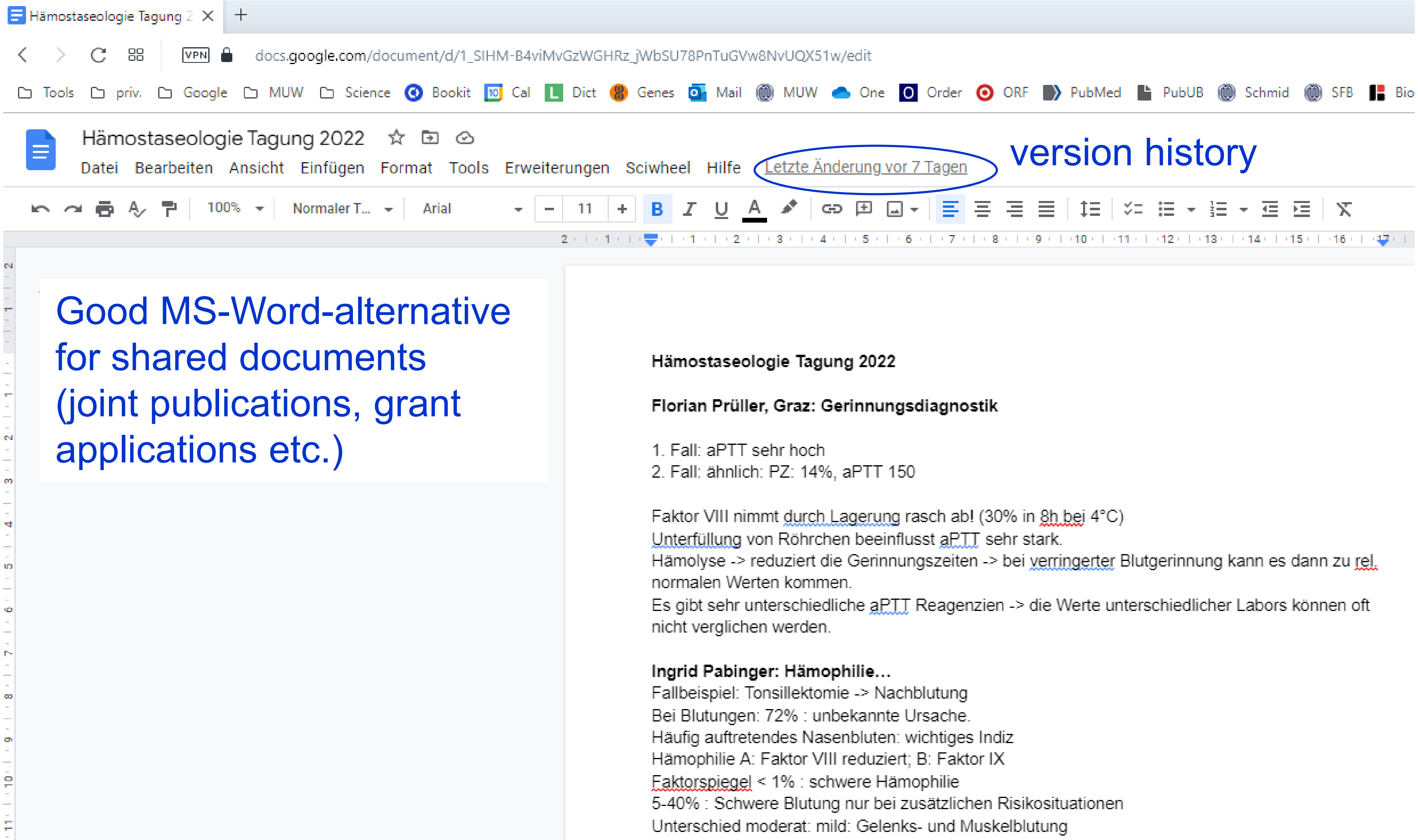
Newest functions in Office 365

- Transparency of images

- Integration of animated 3D models



Google Docs for text documents



version history

Good MS-Word-alternative for shared documents (joint publications, grant applications etc.)

Hämostaseologie Tagung 2022

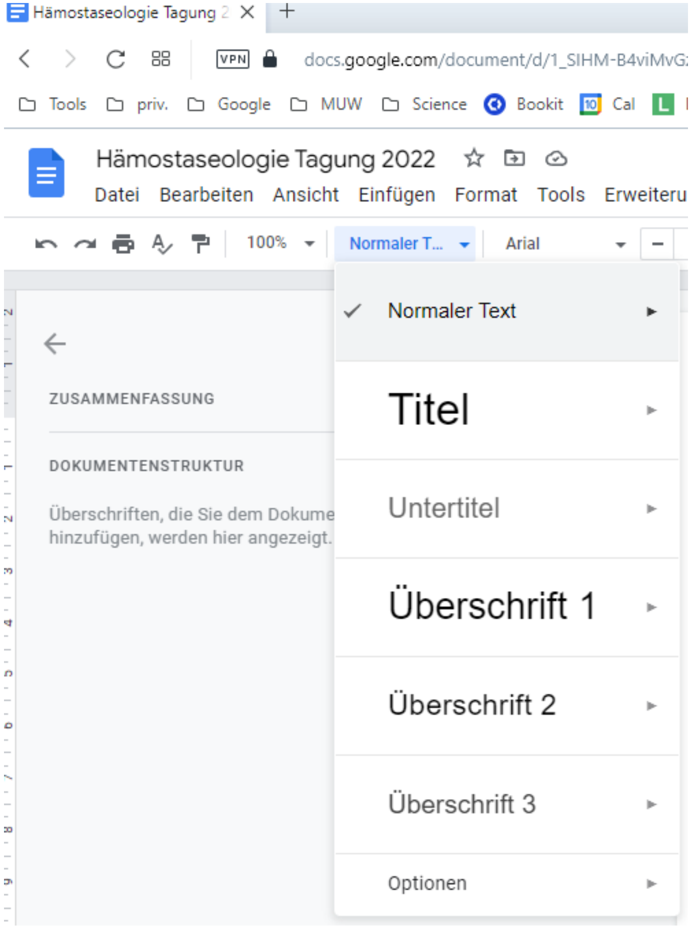
Florian Prüller, Graz: Gerinnungsdiagnostik

1. Fall: aPTT sehr hoch
2. Fall: ähnlich: PZ: 14%, aPTT 150

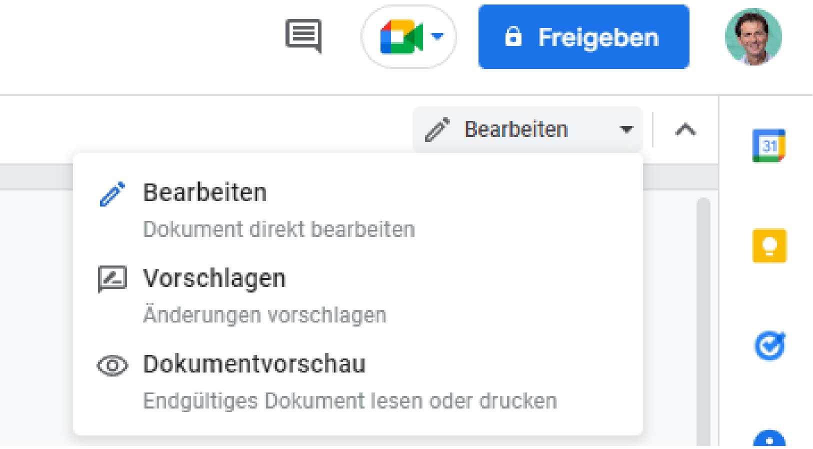
Faktor VIII nimmt durch Lagerung rasch ab! (30% in 8h bei 4°C)
Unterfüllung von Röhrchen beeinflusst aPTT sehr stark.
Hämolyse -> reduziert die Gerinnungszeiten -> bei verringerter Blutgerinnung kann es dann zu rel. normalen Werten kommen.
Es gibt sehr unterschiedliche aPTT Reagenzien -> die Werte unterschiedlicher Labors können oft nicht verglichen werden.

Ingrid Pabinger: Hämophilie…
Fallbeispiel: Tonsillektomie -> Nachblutung
Bei Blutungen: 72% : unbekannte Ursache.
Häufig auftretendes Nasenbluten: wichtiges Indiz
Hämophilie A: Faktor VIII reduziert; B: Faktor IX
Faktorspiegel < 1% : schwere Hämophilie
5-40% : Schwere Blutung nur bei zusätzlichen Risikosituationen
Unterschied moderat: mild: Gelenks- und Muskelblutung

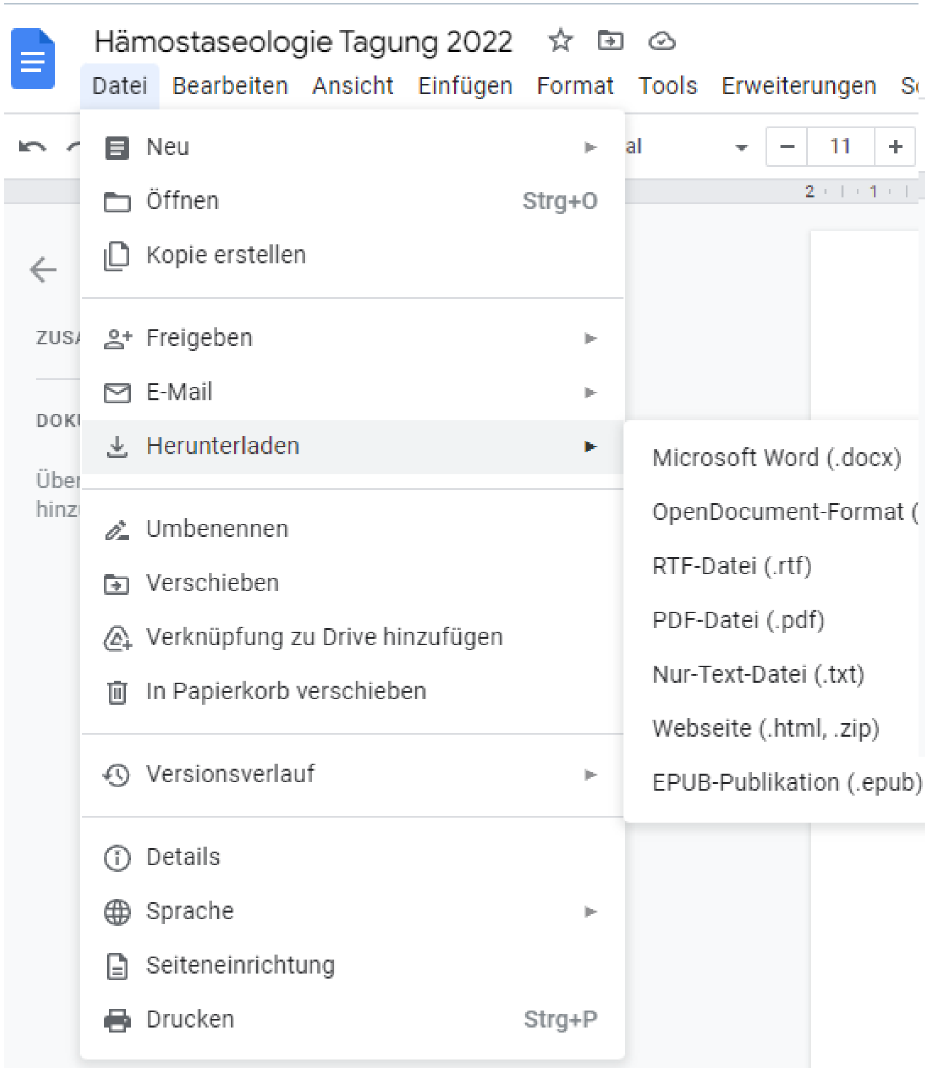
Google Docs features

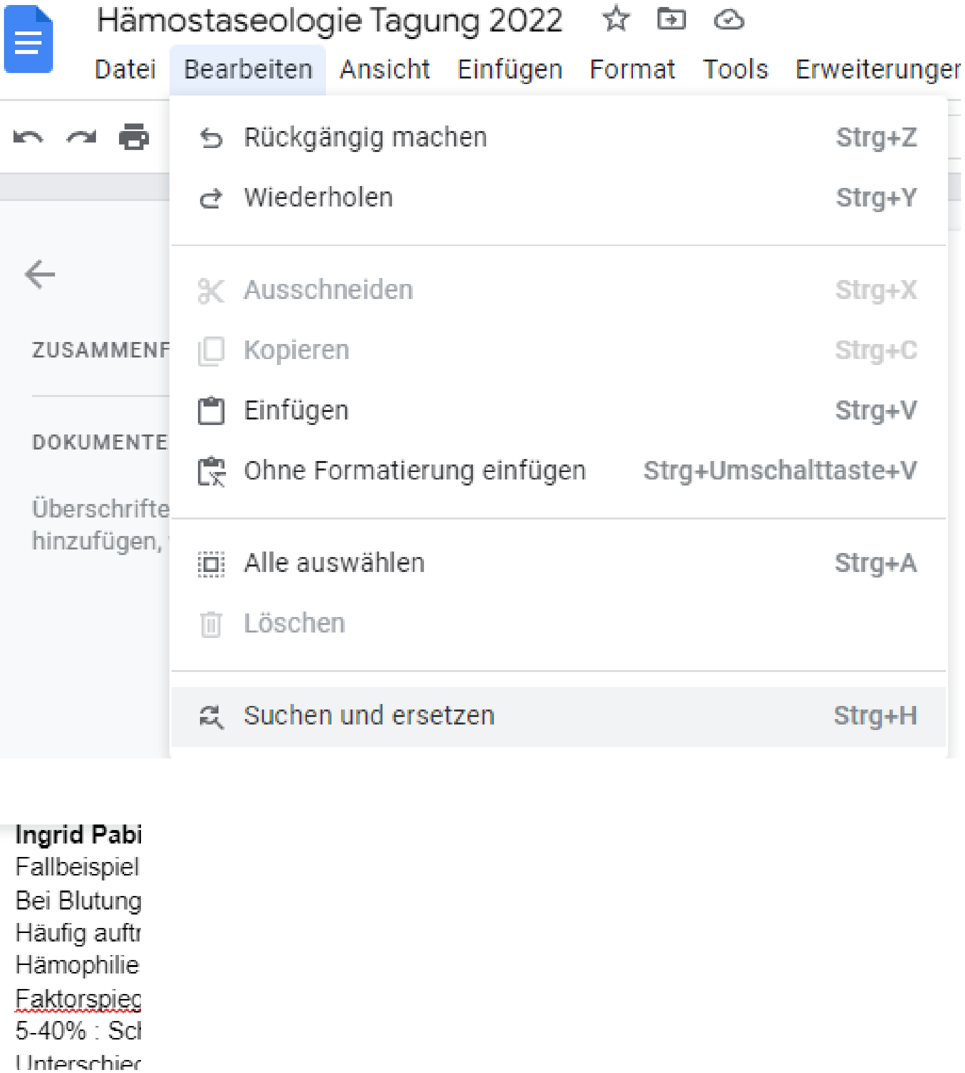


upper right corner:

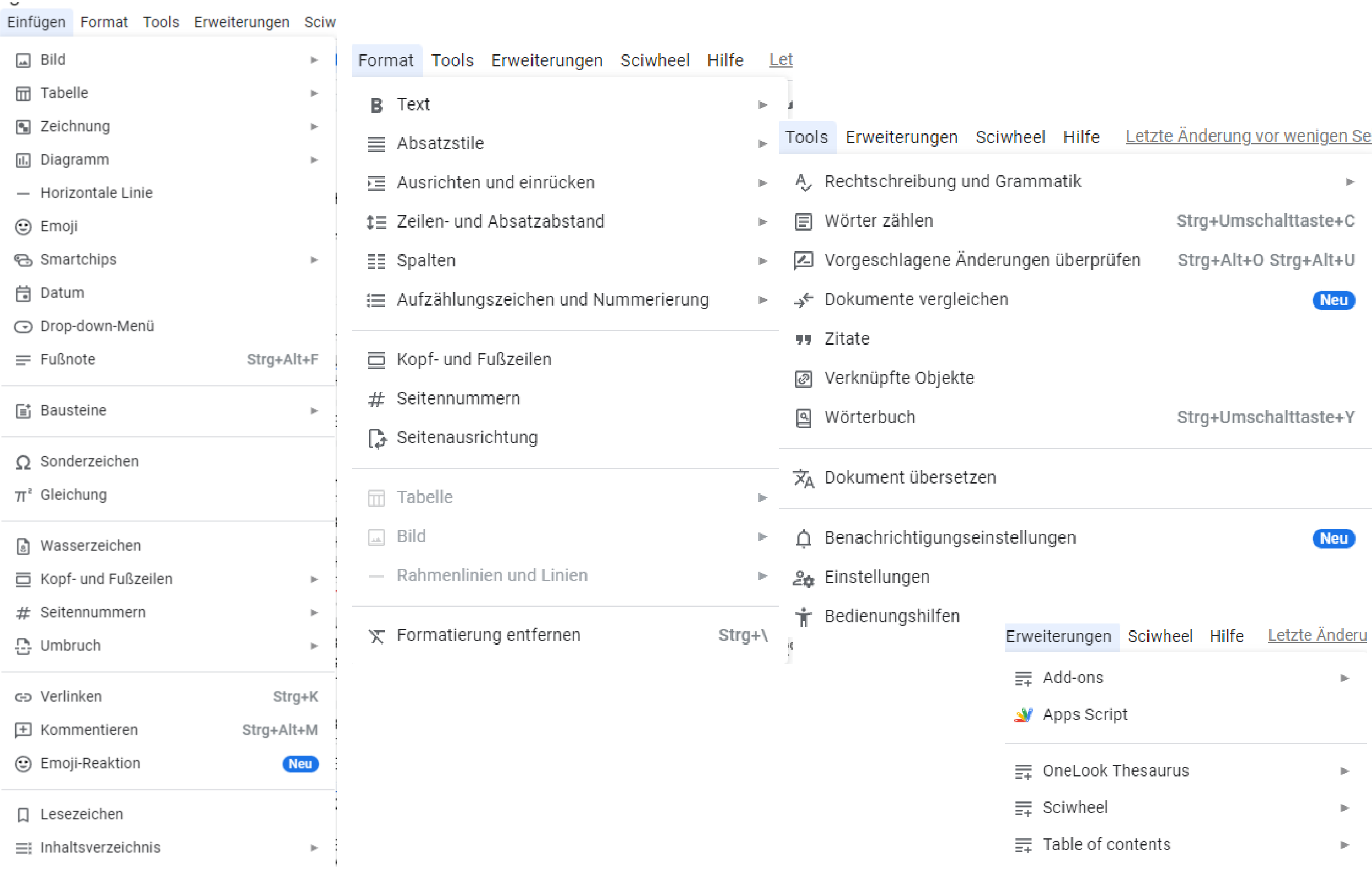


Google Docs features



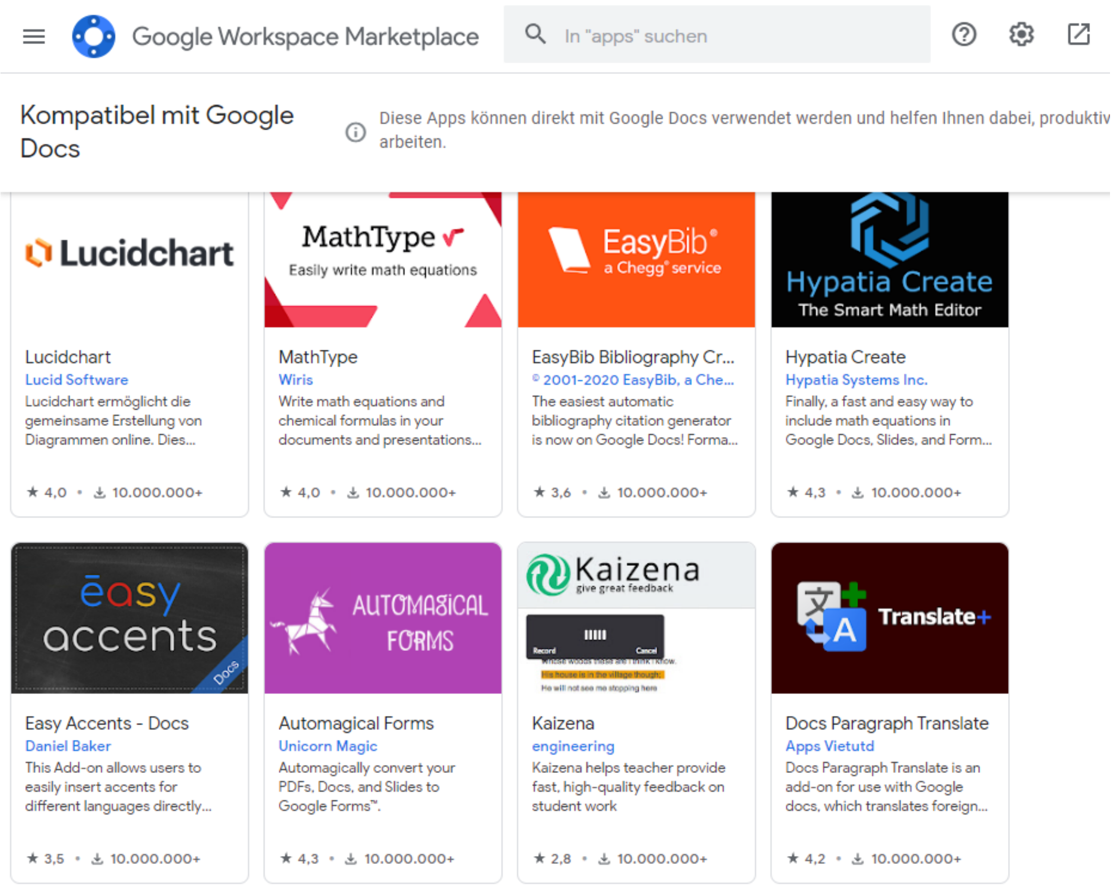


Google Docs features



Google Docs Add-ons

Many useful extensions:
- Sciwheel
- Paperpile
- Thesaurus



Kompatibel mit Google Docs

Diese Apps können direkt mit Google Docs verwendet werden und helfen Ihnen dabei, produktiv arbeiten.

Lucidchart
Lucid Software
Lucidchart ermöglicht die gemeinsame Erstellung von Diagrammen online. Dies...
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engineering
Kaizena helps teacher provide fast, high-quality feedback on student work
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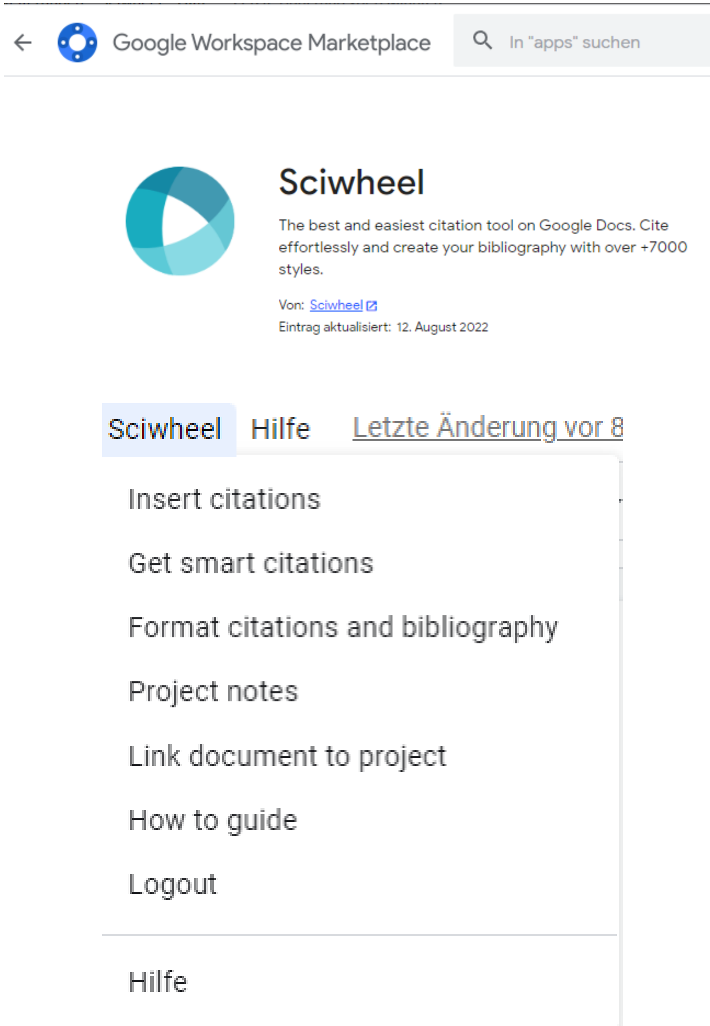
Docs Paragraph Translate
Apps Vietutd
Docs Paragraph Translate is an add-on for use with Google docs, which translates foreign...
★ 4,2 • 10.000.000+



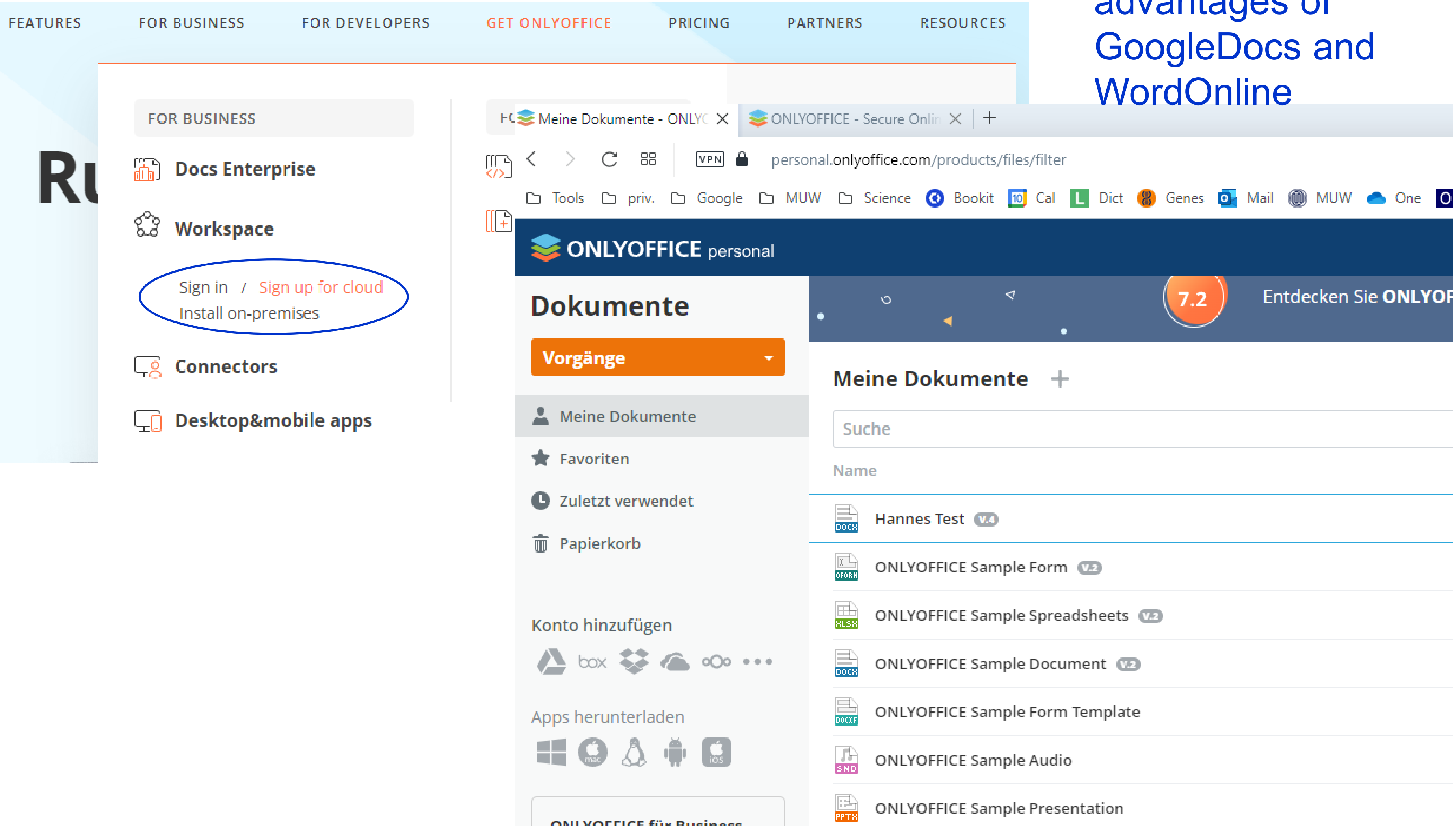
Sciwheel

The best and easiest citation tool on Google Docs. Cite effortlessly and create your bibliography with over +7000 styles.

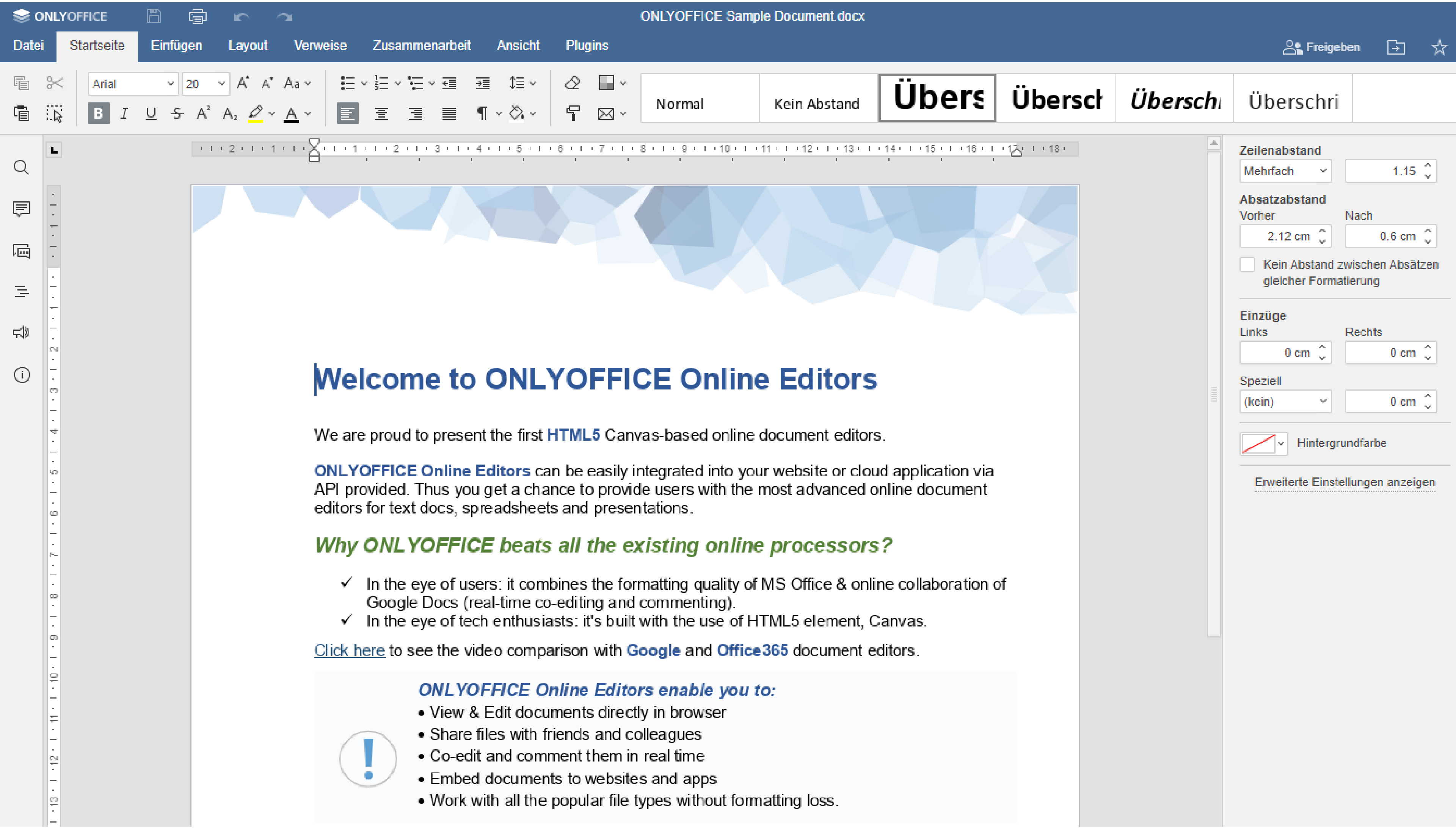
Von: Sciwheel
Eintrag aktualisiert: 12. August 2022

OnlyOffice: www.onlyoffice.com

Online Office Package, which seems to combine advantages of GoogleDocs and WordOnline



OnlyOffice: www.onlyoffice.com



Zeilenabstand: Mehrfach 1.15

Absatzabstand: Vorher 2.12 cm, Nach 0.6 cm

☐ Kein Abstand zwischen Absätzen gleicher Formatierung

Einzüge: Links 0 cm, Rechts 0 cm

Speziell: (kein) 0 cm

Hintergrundfarbe

Erweiterte Einstellungen anzeigen

Welcome to ONLYOFFICE Online Editors

We are proud to present the first **HTML5** Canvas-based online document editors.

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Click here to see the video comparison with **Google** and **Office365** document editors.

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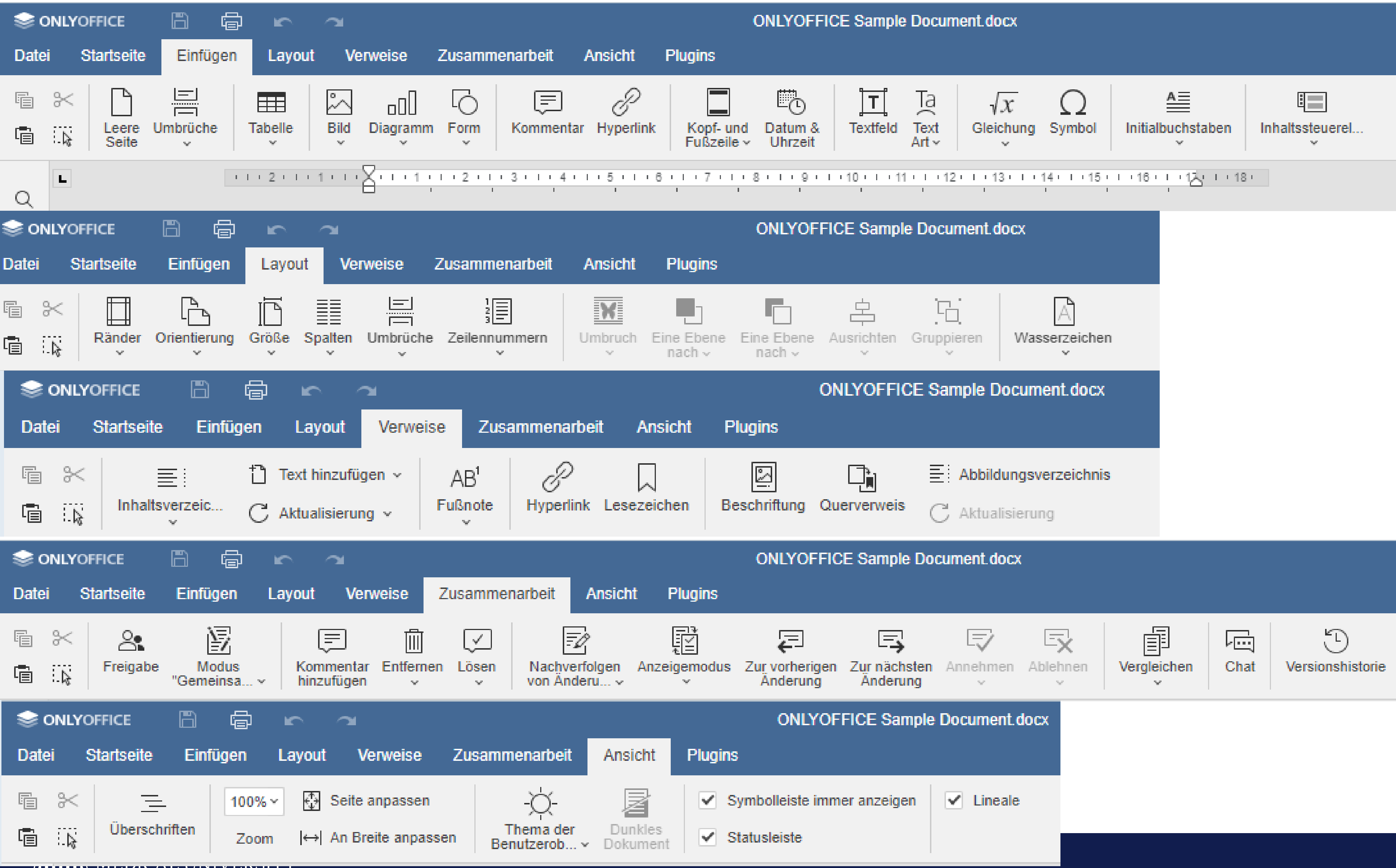
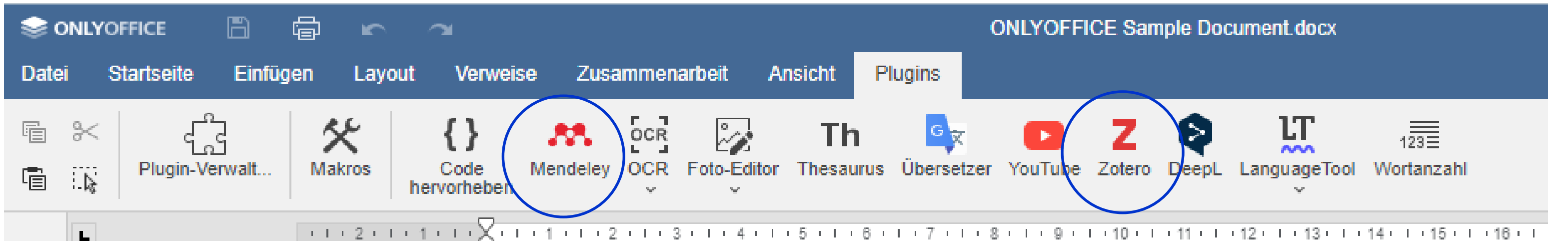
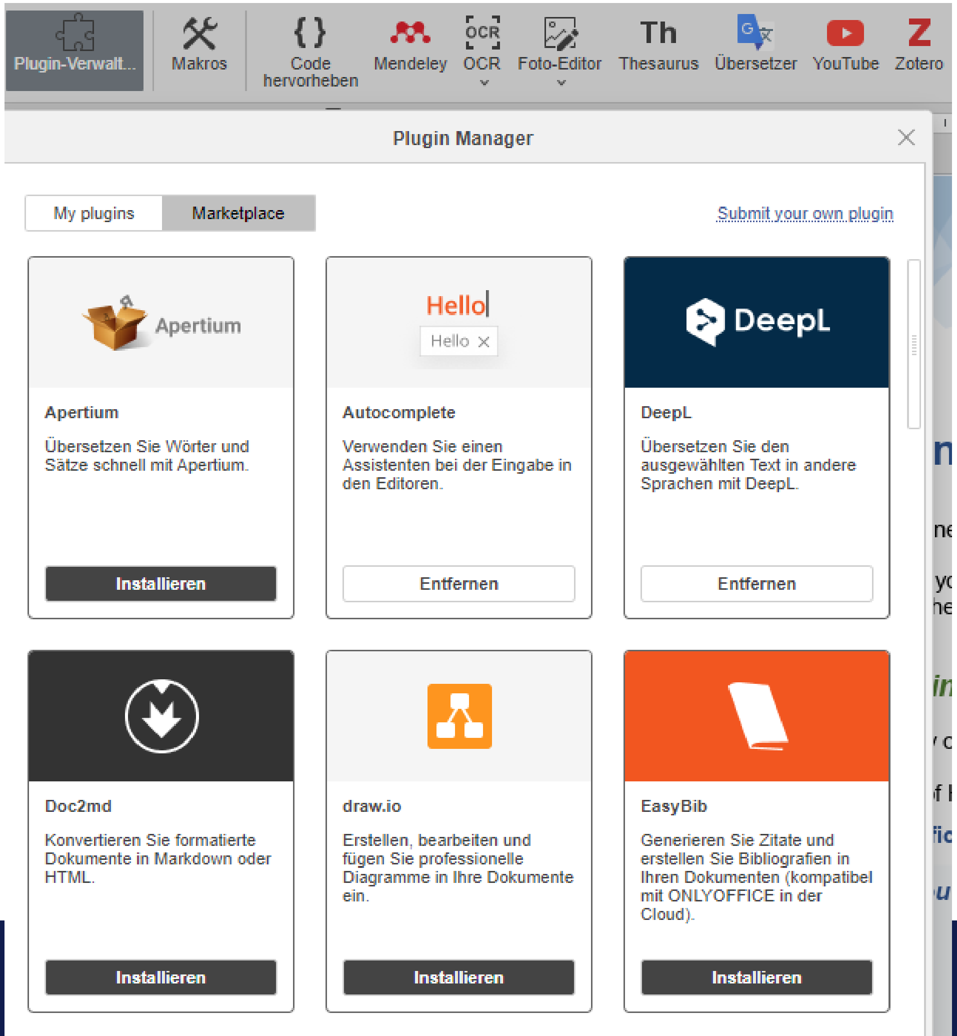
- Share files with friends and colleagues
- Co-edit and comment them in real time
- Embed documents to websites and apps
- Work with all the popular file types without formatting loss.

OnlyOffice: www.onlyoffice.com



OnlyOffice: www.onlyoffice.com





Apertium

Übersetzen Sie Wörter und Sätze schnell mit Apertium.

Installieren

Autocomplete

Verwenden Sie einen Assistenten bei der Eingabe in den Editoren.

Entfernen

DeepL

Übersetzen Sie den ausgewählten Text in andere Sprachen mit DeepL.

Entfernen

Doc2md

Konvertieren Sie formatierte Dokumente in Markdown oder HTML.

Installieren

draw.io

Erstellen, bearbeiten und fügen Sie professionelle Diagramme in Ihre Dokumente ein.

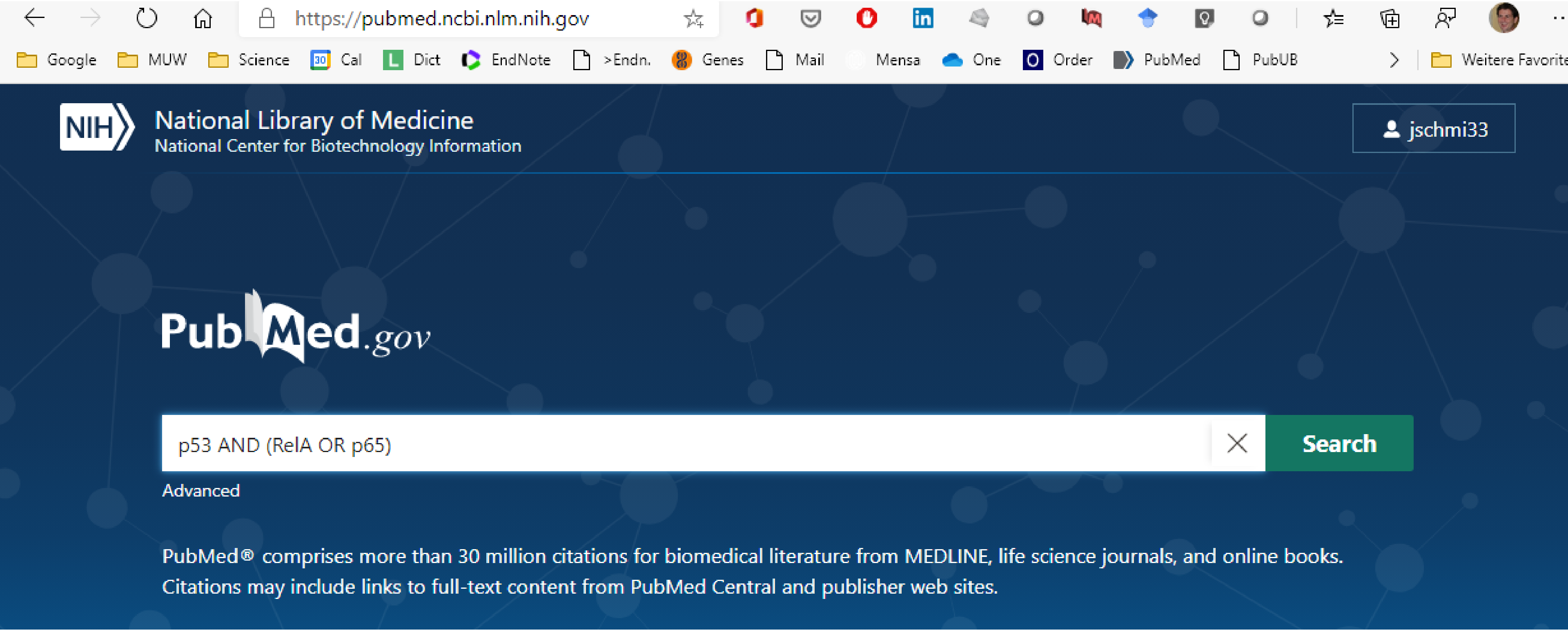
Installieren

EasyBib

Generieren Sie Zitate und erstellen Sie Bibliografien in Ihren Dokumenten (kompatibel mit ONLYOFFICE in der Cloud).

Installieren

PubMed Literature Search



p53 AND (RelA OR p65)

PubMed® comprises more than 30 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites.

Keywords can be combined with logical operands (AND, OR, NOT – in capital letters), including brackets, and the search can be narrowed to certain fields such as title, author name, publication type (e.g. review) using squared brackets ... (AND can be omitted – at is set as default)

Registering for a free account (MyNCBI) allows saving searches – and performing searches with a collection of keywords automatically every day (with results sent by email)

PubMed search tags

Affiliation [AD]
All Fields [ALL]
Author [AU]
Comment Corrections
Corporate Author [CN]
EC/RN Number [RN]
Entrez Date [EDAT]
Filter [FILTER]
First Author Name [1AU]
Full Author Name [FAU]
Grant Number [GR]
Investigator [IR]
Issue [IP]
Journal Title [TA]
Language [LA]
Last Author [LASTAU]
MeSH Date [MHDA]
MeSH Major Topic [MAJR]
MeSH Subheadings [SH]
MeSH Terms [MH]
NLM Unique ID [JID]
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Pharmacol. Action MSH Terms [PA]
Place of Publication [PL]
Publication Date [DP]
Publication Type [PT]
Publisher Identifier [AID]
Secondary Source ID [SI]
Subset [SB]
Substance Name [NM]
Text Words [TW]
Title [TI]
Title/Abstract [TIAB]
Transliterated Title [TT]
UID [PMID]
Volume [VI]

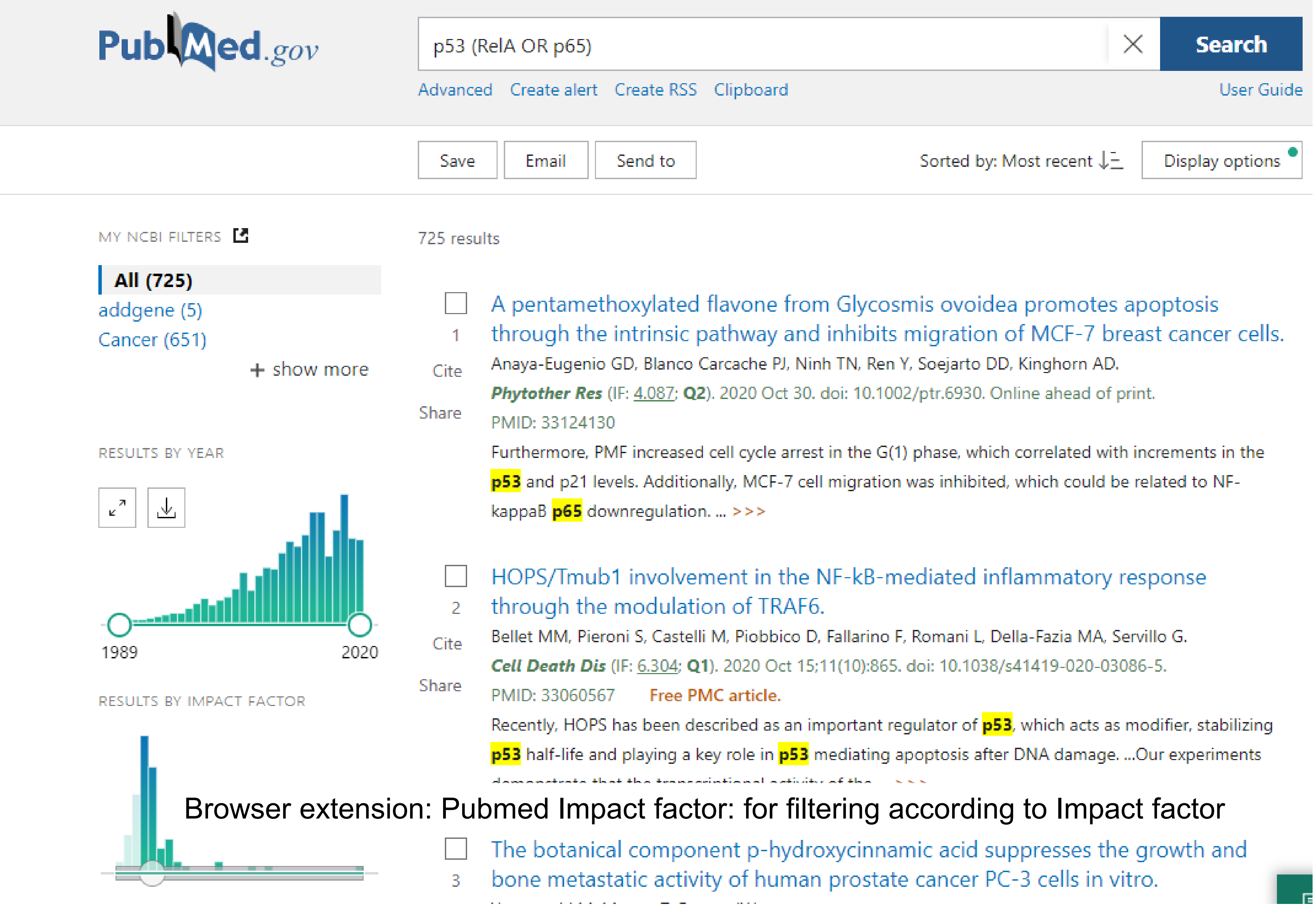
p53[ti] AND (RelA OR p65)

208 results

☐ 1 NF-kappaB is involved in the regulation of autophagy in mutant **p53** cells in response to ionizing radiation.
Zhu Y, Zuo W, Shen X, Liu Y, Zhao Y, Xiong Y, Cao H, Wang Y, Liang Z.
Cell Death Discov (IF: 4.11; **Q2**). 2021 Jun 25;7(1):159. doi: 10.1038/s41420-021-00533-w.
PMID: 34226514 Free PMC article.
The nuclear translocation of **p65** was mediated by p300; this factor also regulates the nuclear behavior of NF-kappaB. The knockdown of p300 in p53-R273H cells led to an inhibition of **p65** expression and an increase in autophagy. In addition, the inhibition of p300 or ... >>>

☐ 3 Inhibitor of apoptosis-stimulating **p53** protein protects against inflammatory bowel disease in mice models by inhibiting the nuclear factor kappa B signaling.
Qian K, Yuan L, Wang S, Kuang Y, Jin Q, Long D, Jiang Y, Zhao H, Liu K, Yao H.
Clin Exp Immunol (IF: 4.33; **Q2**). 2021 Aug;205(2):246-256. doi: 10.1111/cei.13613. Epub 2021 Jun 7.
PMID: 33942299
Meanwhile, in both types of colitis mice models, iASPP over-expression inhibited **p65** phosphorylation

- when you are signed in, search results are highlighted.
- Phrases or exact word combinations can be searched with quotation marks (e.g. „prostate cancer“)
- Filters can be applied (left side)



725 results

1 A pentamethoxylated flavone from Glycosmis ovoidea promotes apoptosis through the intrinsic pathway and inhibits migration of MCF-7 breast cancer cells.

Anaya-Eugenio GD, Blanco Carcache PJ, Ninh TN, Ren Y, Soejarto DD, Kinghorn AD.

Phytother Res (IF: 4.087; **Q2**). 2020 Oct 30. doi: 10.1002/ptr.6930. Online ahead of print.

PMID: 33124130

Furthermore, PMF increased cell cycle arrest in the G(1) phase, which correlated with increments in the **p53** and p21 levels. Additionally, MCF-7 cell migration was inhibited, which could be related to NF-kappaB **p65** downregulation. ... >>>

2 HOPS/Tmub1 involvement in the NF-kB-mediated inflammatory response through the modulation of TRAF6.

Bellet MM, Pieroni S, Castelli M, Piobbico D, Fallarino F, Romani L, Della-Fazia MA, Servillo G.

Cell Death Dis (IF: 6.304; **Q1**). 2020 Oct 15;11(10):865. doi: 10.1038/s41419-020-03086-5.

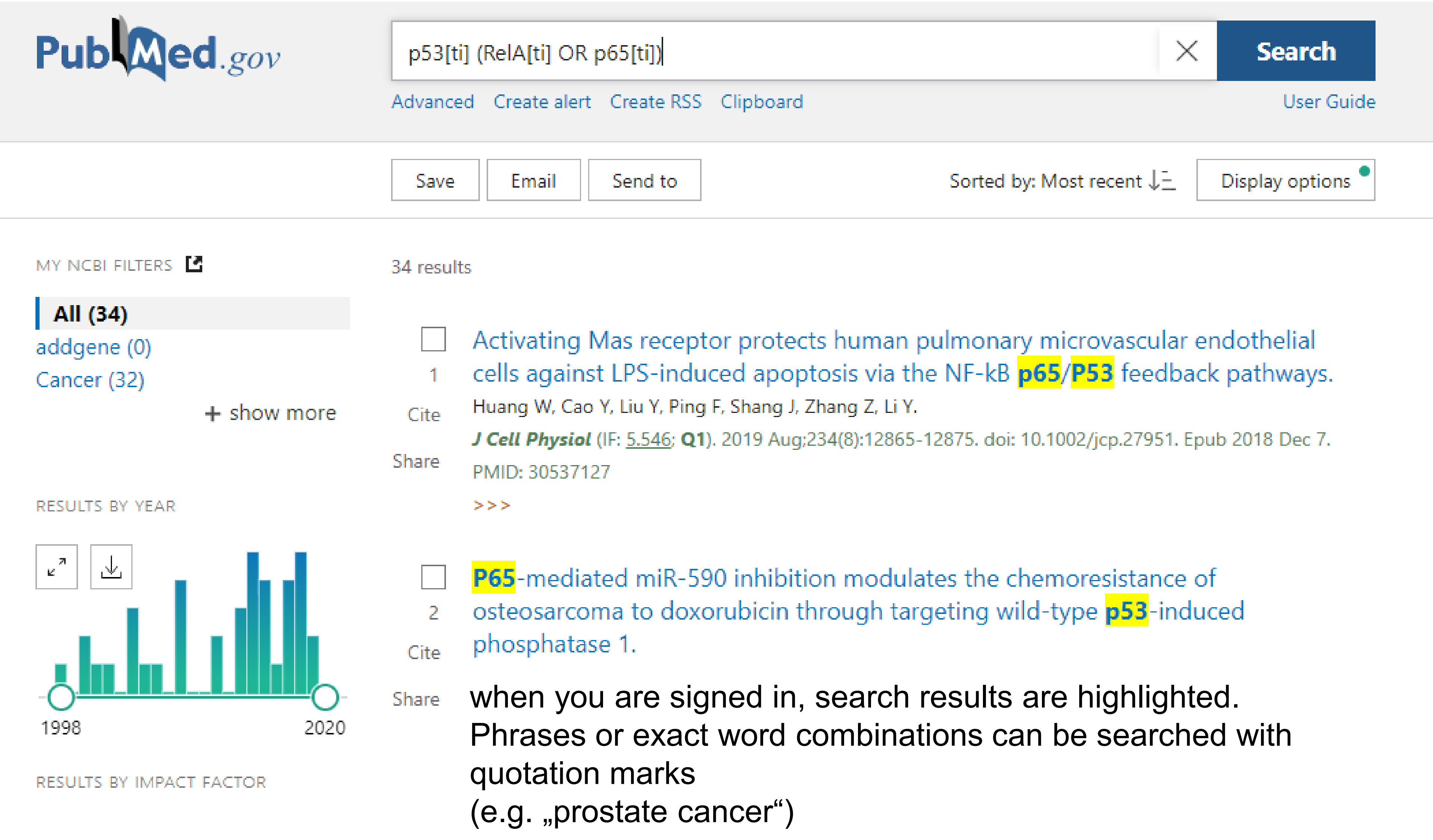
PMID: 33060567 Free PMC article.

Recently, HOPS has been described as an important regulator of **p53**, which acts as modifier, stabilizing **p53** half-life and playing a key role in **p53** mediating apoptosis after DNA damage. ...Our experiments

Browser extension: Pubmed Impact factor: for filtering according to Impact factor

3 The botanical component p-hydroxycinnamic acid suppresses the growth and bone metastatic activity of human prostate cancer PC-3 cells in vitro.

Using [ti] to search for title words



p53[ti] (RelA[ti] OR p65[ti])

34 results

☐ 1 Activating Mas receptor protects human pulmonary microvascular endothelial cells against LPS-induced apoptosis via the NF-kB **p65**/**P53** feedback pathways.

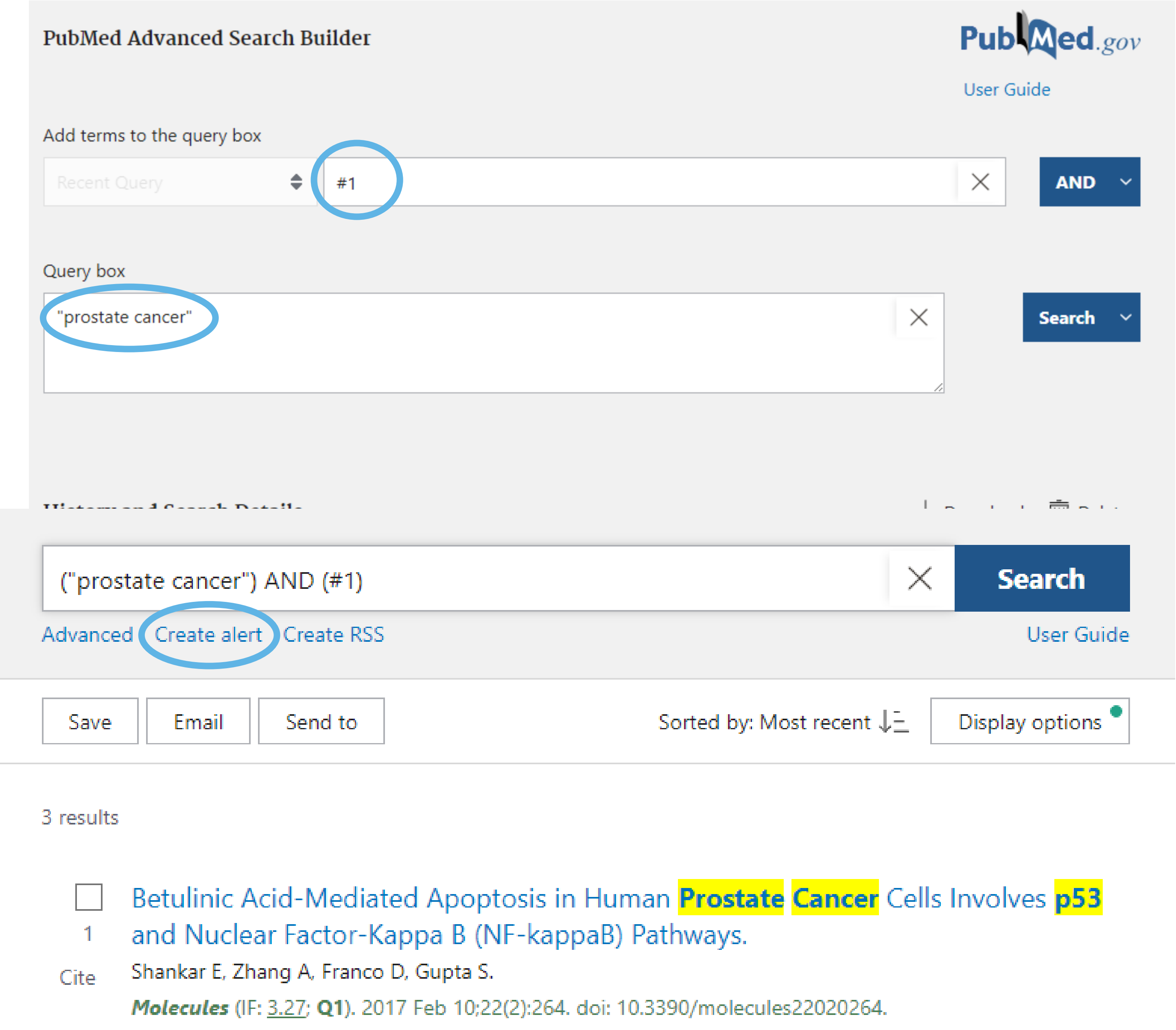
Huang W, Cao Y, Liu Y, Ping F, Shang J, Zhang Z, Li Y.

J Cell Physiol (IF: 5.546; **Q1**). 2019 Aug;234(8):12865-12875. doi: 10.1002/jcp.27951. Epub 2018 Dec 7.

PMID: 30537127

☐ 2 **P65**-mediated miR-590 inhibition modulates the chemoresistance of osteosarcoma to doxorubicin through targeting wild-type **p53**-induced phosphatase 1.

when you are signed in, search results are highlighted. Phrases or exact word combinations can be searched with quotation marks
(e.g. „prostate cancer“)



#1

"prostate cancer"

("prostate cancer") AND (#1)

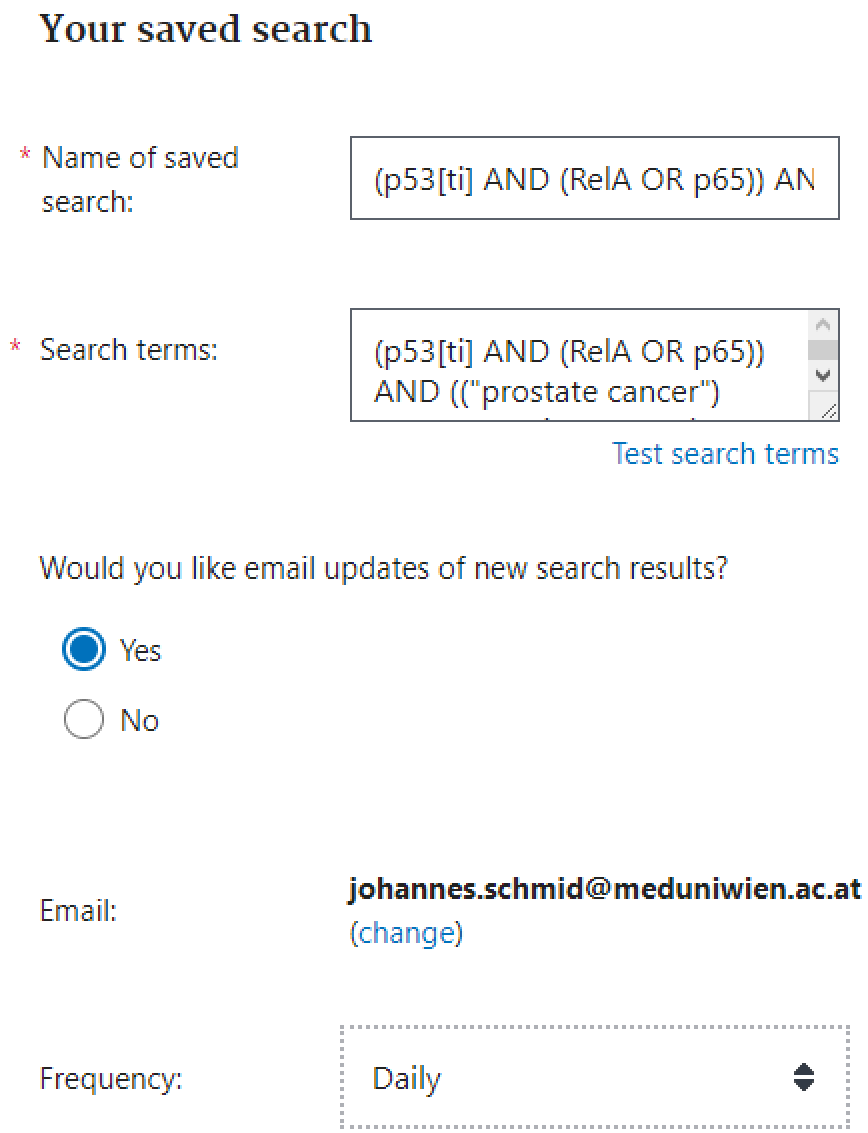
3 results

☐ 1 Betulinic Acid-Mediated Apoptosis in Human Prostate Cancer Cells Involves p53 and Nuclear Factor-Kappa B (NF-kappaB) Pathways.

Shankar E, Zhang A, Franco D, Gupta S.

Molecules (IF: 3.27; **Q1**). 2017 Feb 10;22(2):264. doi: 10.3390/molecules22020264.

Advanced search: additional options, search history (search #1, #2 ...), the single searches can be combined (e.g. #1 AND #2) – and the resulting search (#3) can be set as automatic search („create alert“). In this way, a collection of keywords can be searched automatically every day – and the results sent by email



Your saved search

* Name of saved search: (p53[ti] AND (RelA OR p65)) AN

* Search terms: (p53[ti] AND (RelA OR p65)) AND (("prostate cancer")

Would you like email updates of new search results?

● Yes

○ No

Email: **johannes.schmid@meduniwien.ac.at**

Frequency: Daily

Advanced search: additional options, search history (search #1, #2 ...), the single searches can be combined (e.g. #1 AND #2) – and the resulting search (#3) can be set as automatic search („create alert“). In this way, a collection of keywords can be searched automatically every day – and the results sent by email

Email of the search results

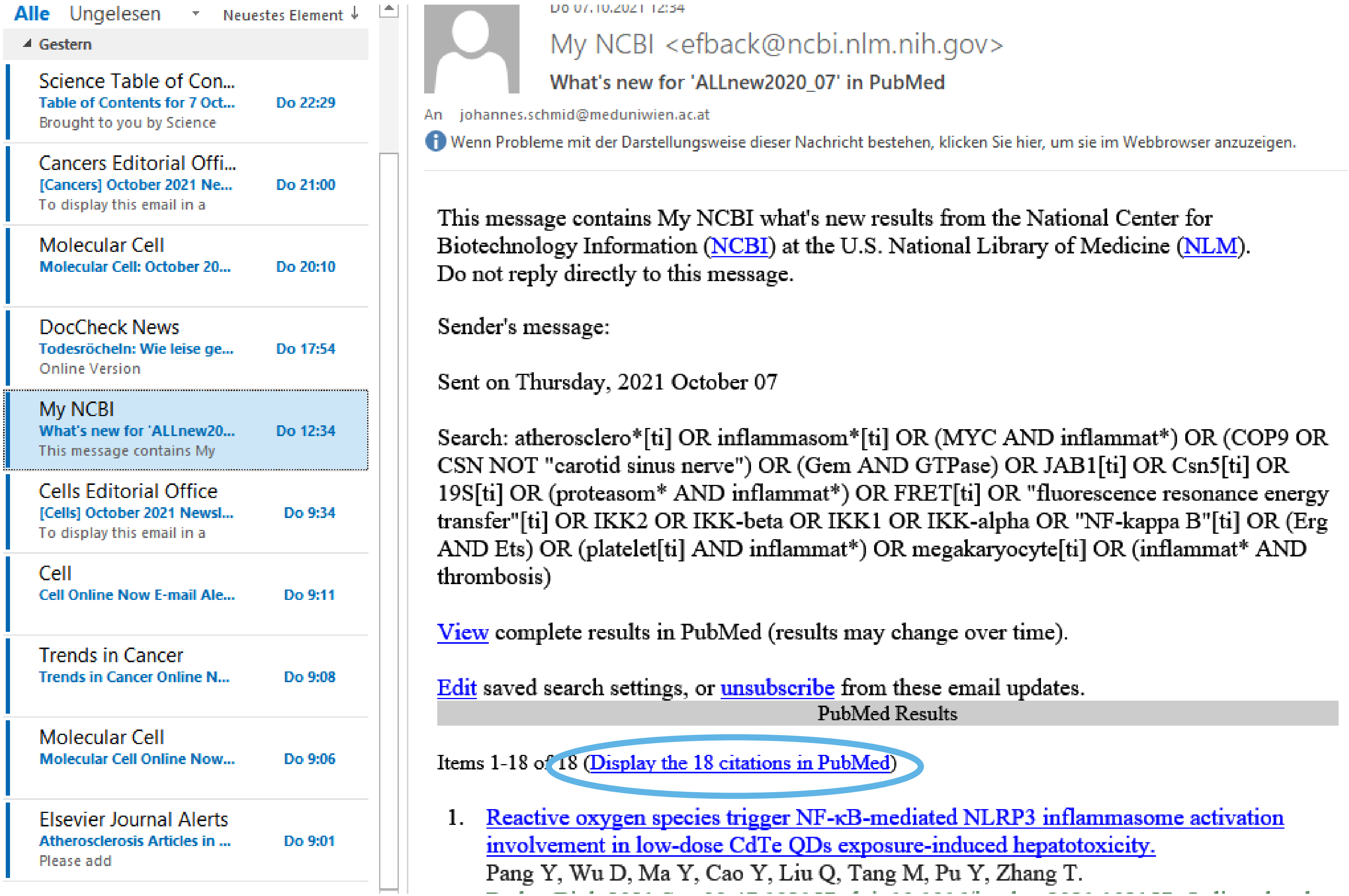


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Table of Contents for 7 Oct... Do 22:29
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To display this email in a

Molecular Cell
Molecular Cell: October 20... Do 20:10

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Online Version

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[Cells] October 2021 Newsl... Do 9:34
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Trends in Cancer
Trends in Cancer Online N... Do 9:08

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An johannes.schmid@meduniwien.ac.at
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This message contains My NCBI what's new results from the National Center for Biotechnology Information (NCBI) at the U.S. National Library of Medicine (NLM).
Do not reply directly to this message.

Sender's message:

Sent on Thursday, 2021 October 07

Search: atheroscler o*[ti] OR inflammasom*[ti] OR (MYC AND inflammat*) OR (COP9 OR CSN NOT "carotid sinus nerve") OR (Gem AND GTPase) OR JAB1[ti] OR Csn5[ti] OR 19S[ti] OR (proteasom* AND inflammat*) OR FRET[ti] OR "fluorescence resonance energy transfer"[ti] OR IKK2 OR IKK-beta OR IKK1 OR IKK-alpha OR "NF-kappa B"[ti] OR (Erg AND Ets) OR (platelet[ti] AND inflammat*) OR megakaryocyte[ti] OR (inflammat* AND thrombosis)

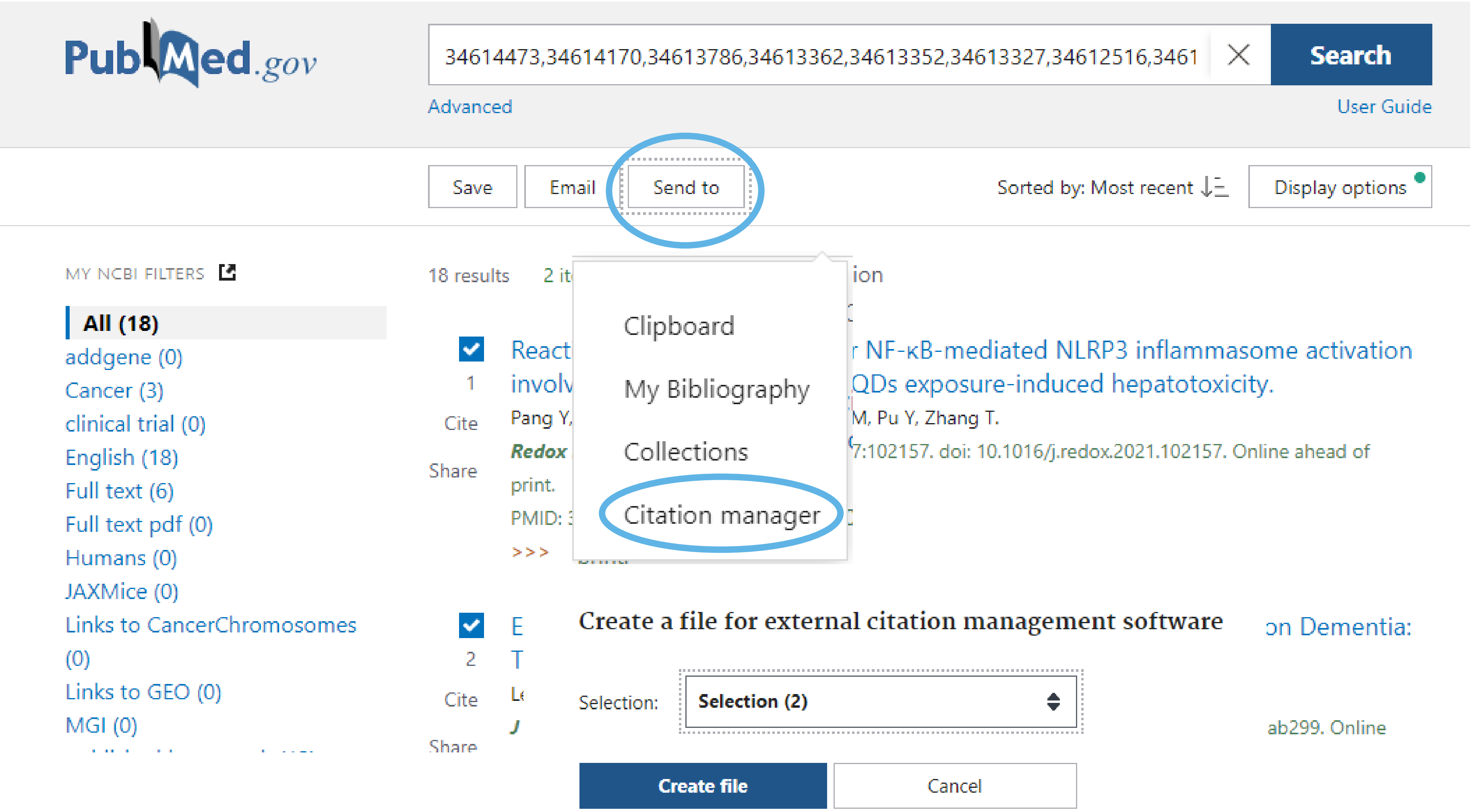
View complete results in PubMed (results may change over time).

Edit saved search settings, or unsubscribe from these email updates.

PubMed Results

Items 1-18 of 18 (Display the 18 citations in PubMed)

1. Reactive oxygen species trigger NF-κB-mediated NLRP3 inflammasome activation involvement in low-dose CdTe QDs exposure-induced hepatotoxicity.
Pang Y, Wu D, Ma Y, Cao Y, Liu Q, Tang M, Pu Y, Zhang T.



React… NF-κB-mediated NLRP3 inflammasome activation involv… QDs exposure-induced hepatotoxicity.

Pang Y, … M, Pu Y, Zhang T.

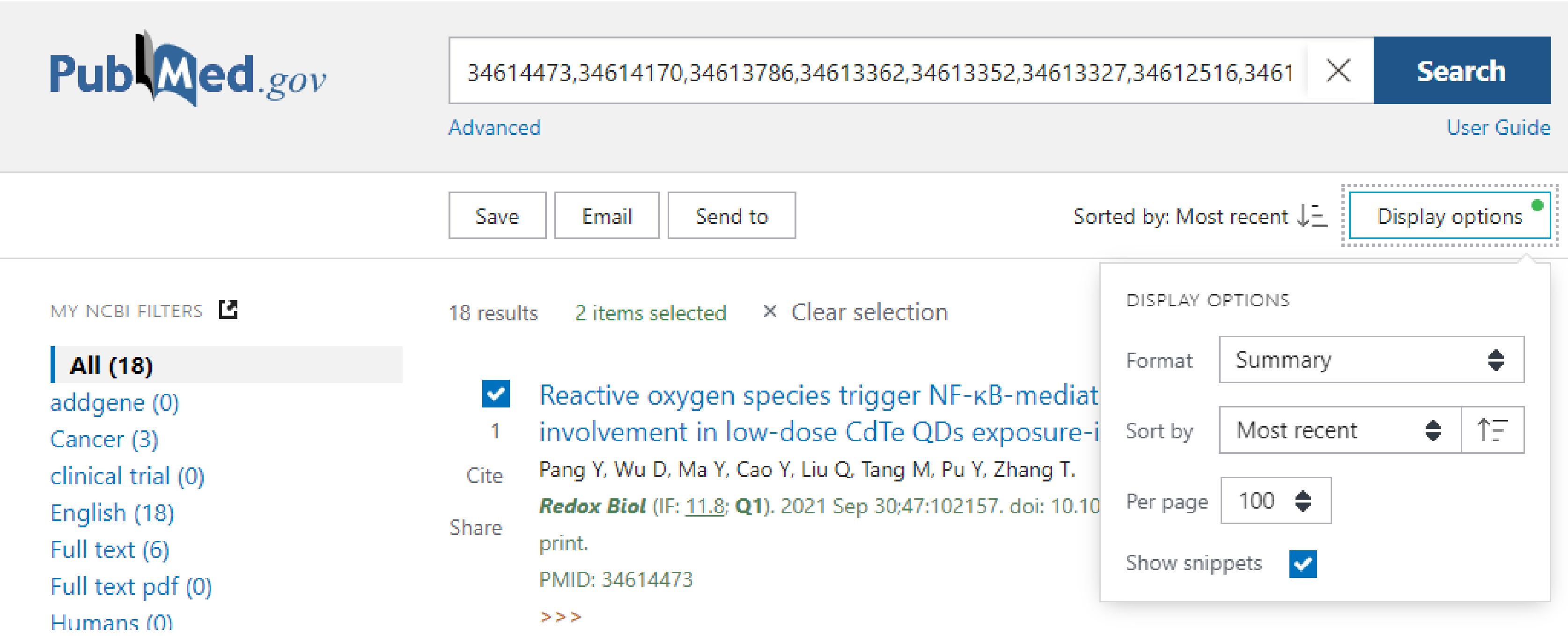
Redox … 7:102157. doi: 10.1016/j.redox.2021.102157. Online ahead of print.

Create a file for external citation management software

Selection: **Selection (2)**

The downloaded file can be directly opened with Endnote (or other citation software)

In this way many search results can be imported at once into the reference software.



34614473,34614170,34613786,34613362,34613352,34613327,34612516,3461

Sorted by: Most recent

18 results 2 items selected × Clear selection

All (18)
addgene (0)
Cancer (3)
clinical trial (0)
English (18)
Full text (6)
Full text pdf (0)
Humans (0)

☑ 1

Reactive oxygen species trigger NF-κB-mediat
involvement in low-dose CdTe QDs exposure-i
Pang Y, Wu D, Ma Y, Cao Y, Liu Q, Tang M, Pu Y, Zhang T.
Redox Biol (IF: 11.8; **Q1**). 2021 Sep 30;47:102157. doi: 10.10
print.
PMID: 34614473
\>>>

DISPLAY OPTIONS

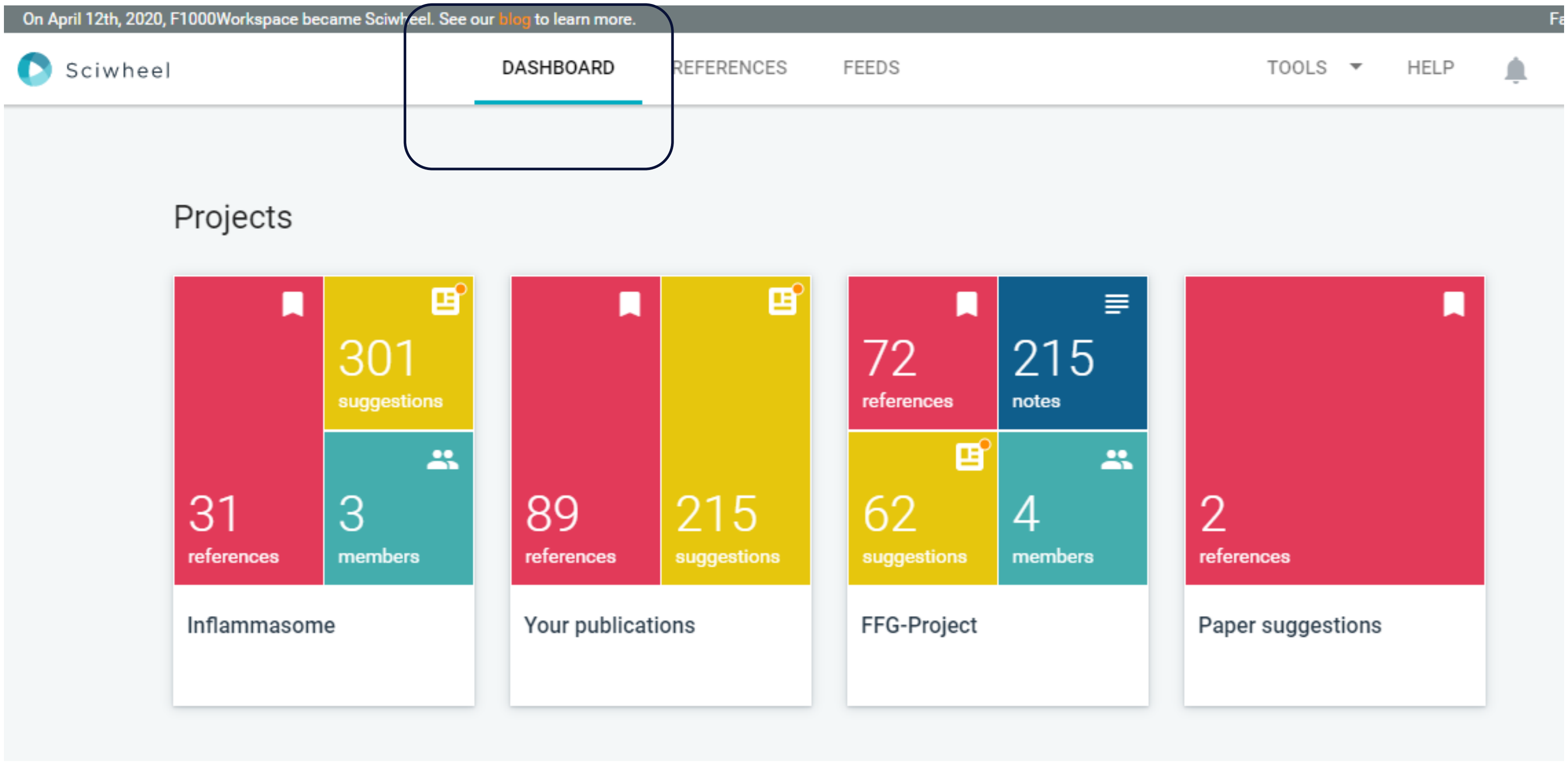
Format: Summary
Sort by: Most recent
Per page: 100
Show snippets ☑

Display settings can be changed:

Abstract display: contains „Link-Outs“ to the article on the journal website https://sciwheel.com/

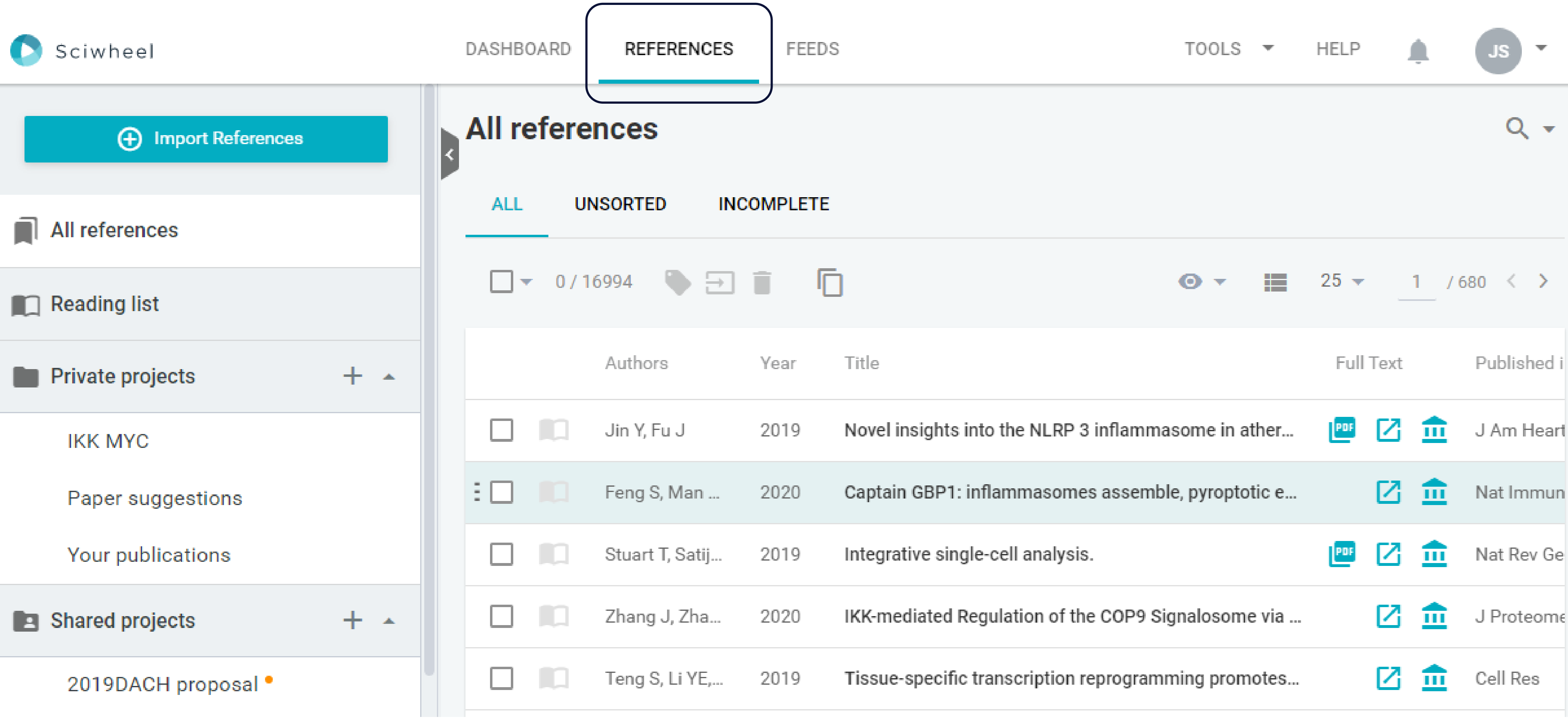
Sciwheel – web-based citation manager

- Browser and Word add-on available (as well as Google-Docs add-on)
- Projects: can be shared
- Makes suggestions of new literature based on the existing projects
- License available for our university



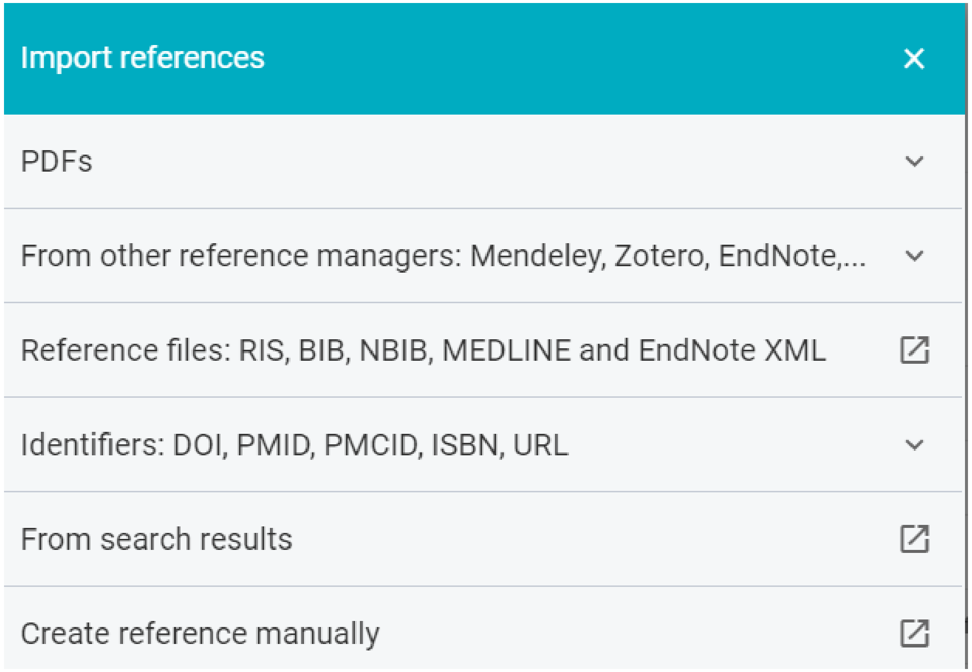
On April 12th, 2020, F1000Workspace became Sciwheel. See our blog to learn more.

Sciwheel – web-based citation manager



Authors	Year	Title	Full Text	Published i
Jin Y, Fu J	2019	Novel insights into the NLRP 3 inflammasome in ather...	PDF	J Am Heart
Feng S, Man ...	2020	Captain GBP1: inflammasomes assemble, pyroptotic e...		Nat Immun
Stuart T, Satij...	2019	Integrative single-cell analysis.	PDF	Nat Rev Ge
Zhang J, Zha...	2020	IKK-mediated Regulation of the COP9 Signalosome via ...		J Proteome
Teng S, Li YE,...	2019	Tissue-specific transcription reprogramming promotes...		Cell Res

Import references to Sciwheel



Import references

PDFs

From other reference managers: Mendeley, Zotero, EndNote,...

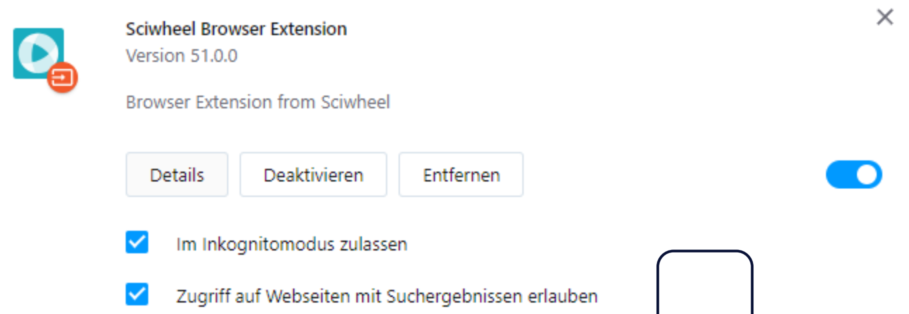
Reference files: RIS, BIB, NBIB, MEDLINE and EndNote XML

Identifiers: DOI, PMID, PMCID, ISBN, URL

From search results

Create reference manually

Import references to Sciwheel from Pubmed with Browser extension

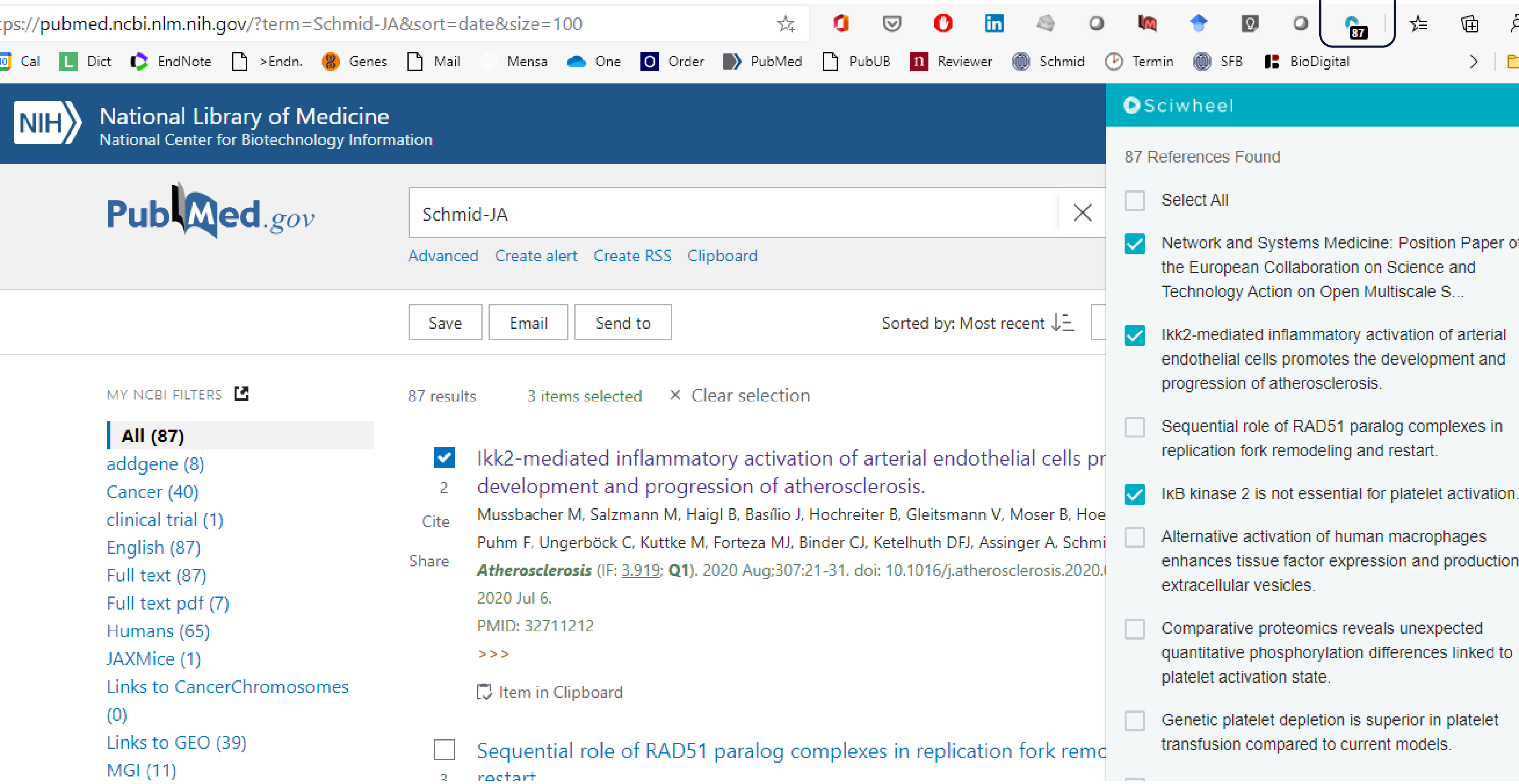


Sciwheel Browser Extension
Version 51.0.0

Browser Extension from Sciwheel

☑ Im Inkognitomodus zulassen

☑ Zugriff auf Webseiten mit Suchergebnissen erlauben



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Schmid-JA

Sorted by: Most recent

MY NCBI FILTERS

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addgene (8)
Cancer (40)
clinical trial (1)
English (87)
Full text (87)
Full text pdf (7)
Humans (65)
JAXMice (1)
Links to CancerChromosomes (0)
Links to GEO (39)
MGI (11)

87 results 3 items selected × Clear selection

☑ 2 Ikk2-mediated inflammatory activation of arterial endothelial cells pr development and progression of atherosclerosis.
Mussbacher M, Salzmann M, Haigl B, Basílio J, Hochreiter B, Gleitsmann V, Moser B, Hoe Puhm F, Ungerböck C, Kuttke M, Forteza MJ, Binder CJ, Ketelhuth DFJ, Assinger A, Schmi
Atherosclerosis (IF: 3.919; Q1). 2020 Aug;307:21-31. doi: 10.1016/j.atherosclerosis.2020.(2020 Jul 6.
PMID: 32711212
>>>
Item in Clipboard

☐ 3 Sequential role of RAD51 paralog complexes in replication fork remo restart

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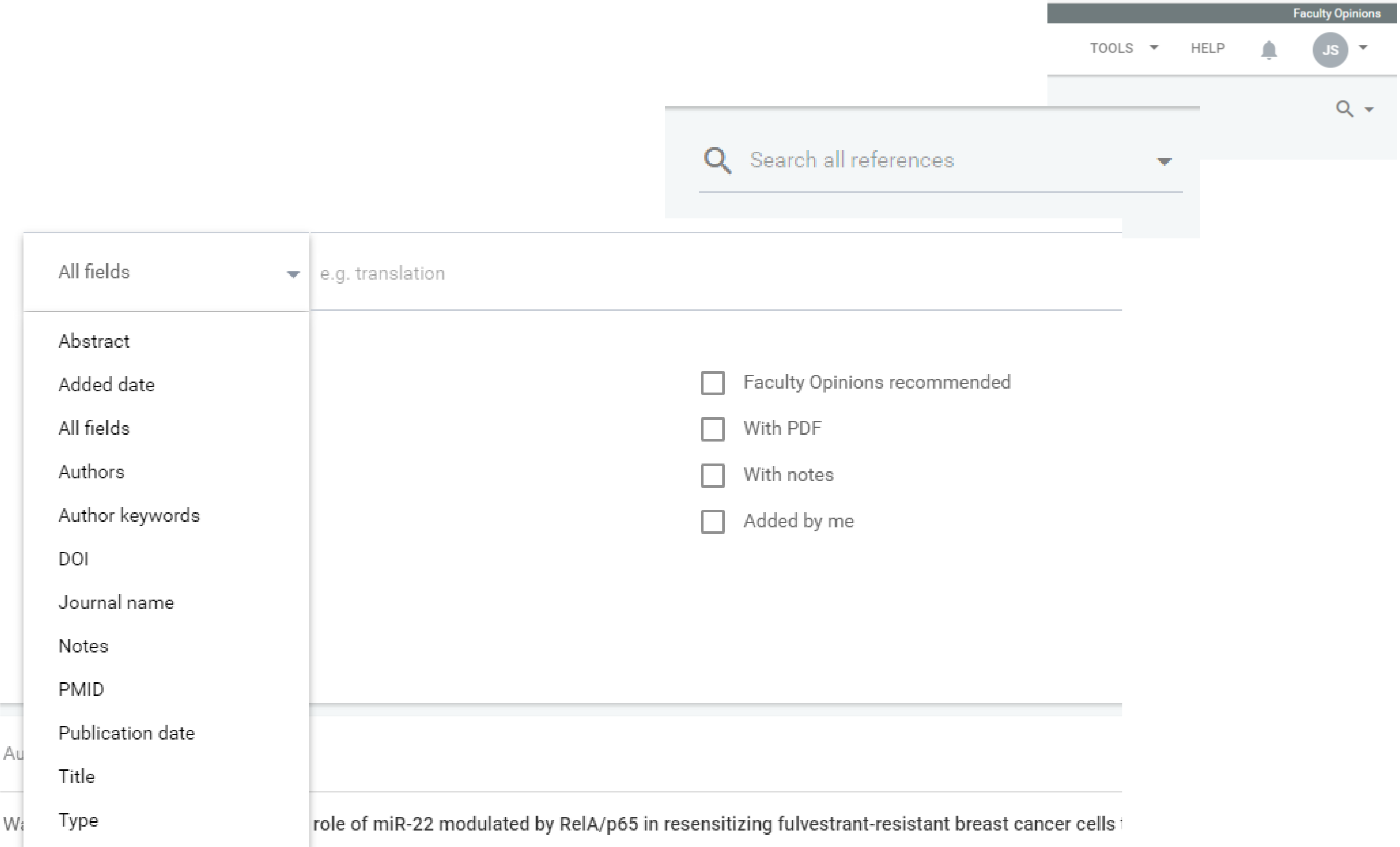
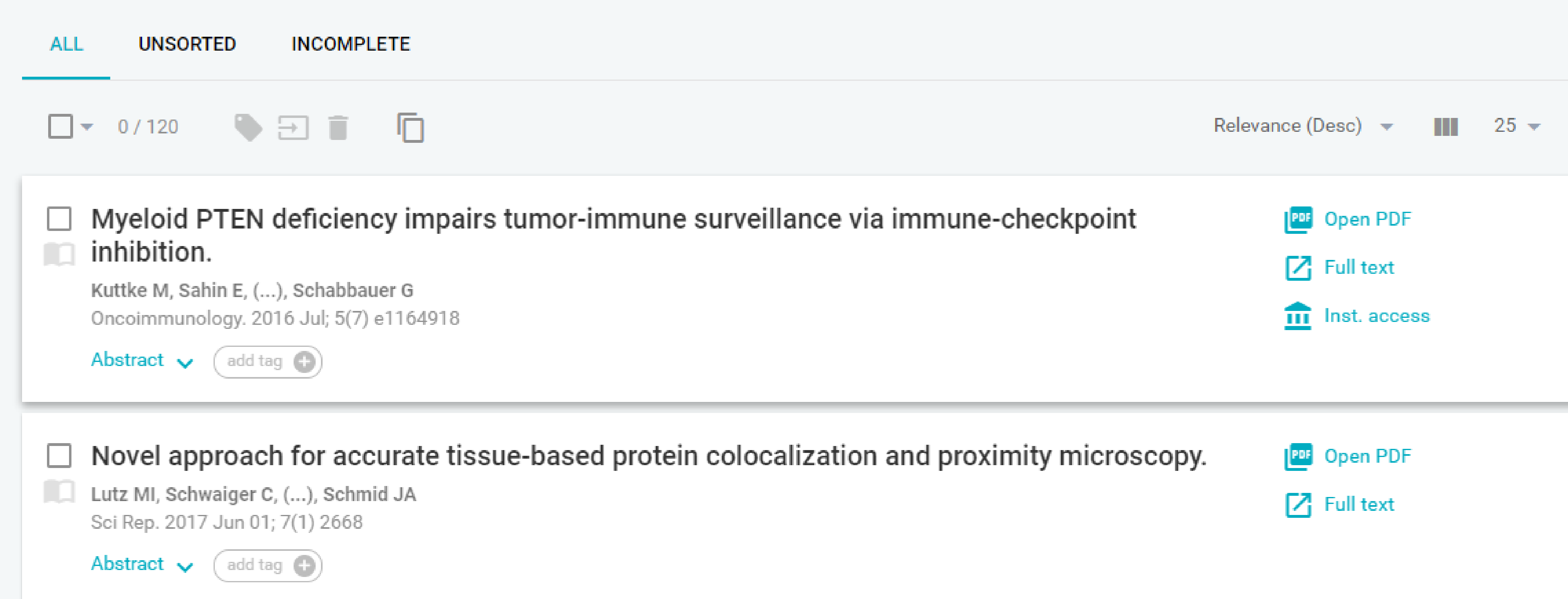
☑ Network and Systems Medicine: Position Paper of the European Collaboration on Science and Technology Action on Open Multiscale S...
☑ Ikk2-mediated inflammatory activation of arterial endothelial cells promotes the development and progression of atherosclerosis.
☐ Sequential role of RAD51 paralog complexes in replication fork remodeling and restart.
☑ IκB kinase 2 is not essential for platelet activation.
☐ Alternative activation of human macrophages enhances tissue factor expression and production extracellular vesicles.
☐ Comparative proteomics reveals unexpected quantitative phosphorylation differences linked to platelet activation state.
☐ Genetic platelet depletion is superior in platelet transfusion compared to current models.

Search data base with Sciwheel



role of miR-22 modulated by RelA/p65 in resensitizing fulvestrant-resistant breast cancer cells

Working with references in Sciwheel



☐ Myeloid PTEN deficiency impairs tumor-immune surveillance via immune-checkpoint inhibition.

Kuttke M, Sahin E, (...), Schabbauer G

Oncoimmunology. 2016 Jul; 5(7) e1164918

☐ Novel approach for accurate tissue-based protein colocalization and proximity microscopy.

Lutz MI, Schwaiger C, (...), Schmid JA

Sci Rep. 2017 Jun 01; 7(1) 2668

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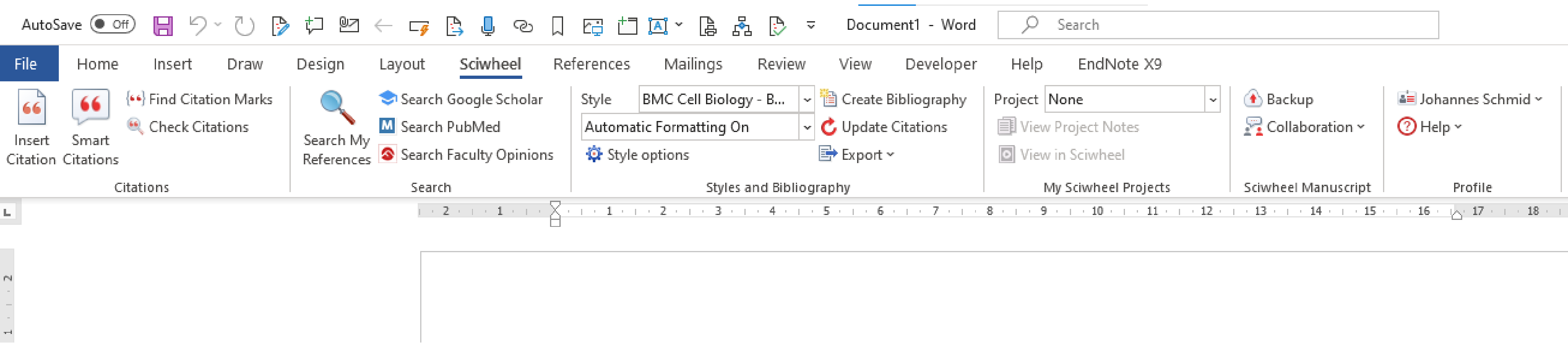

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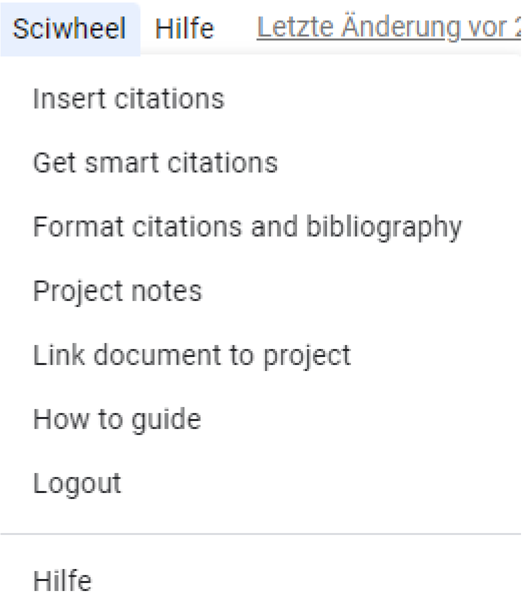
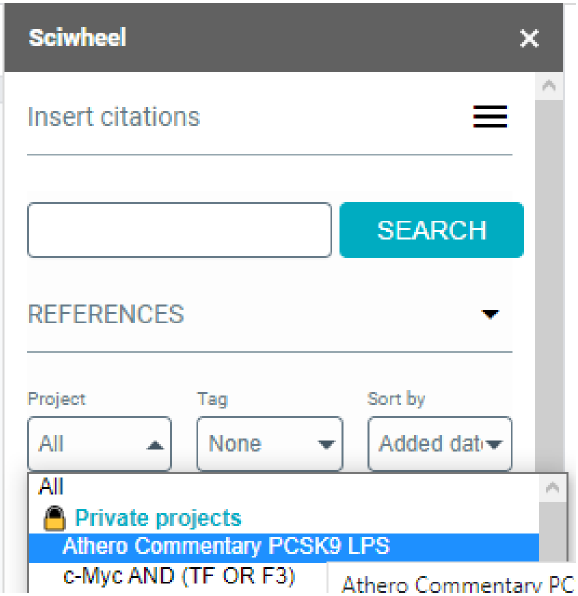
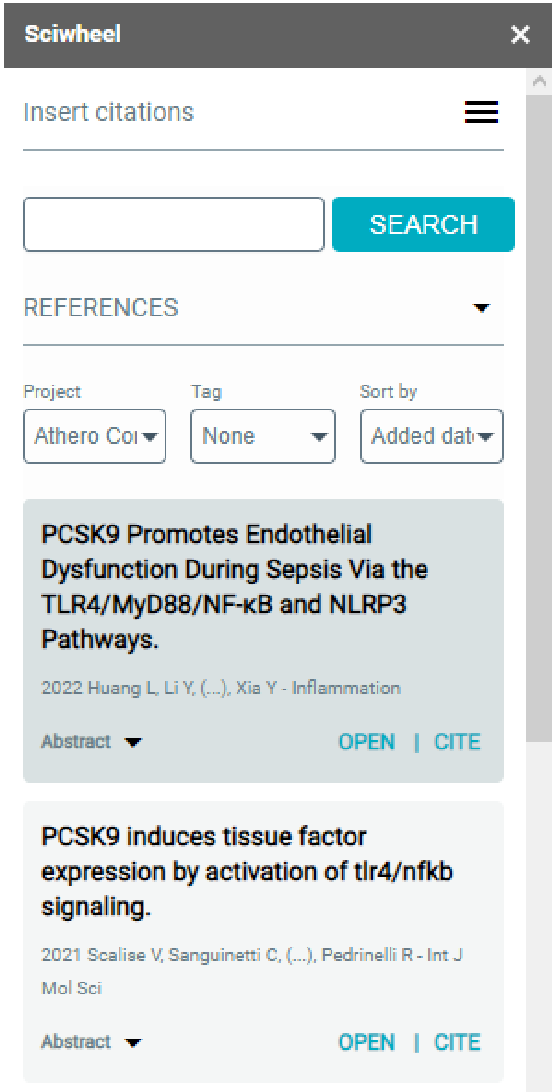






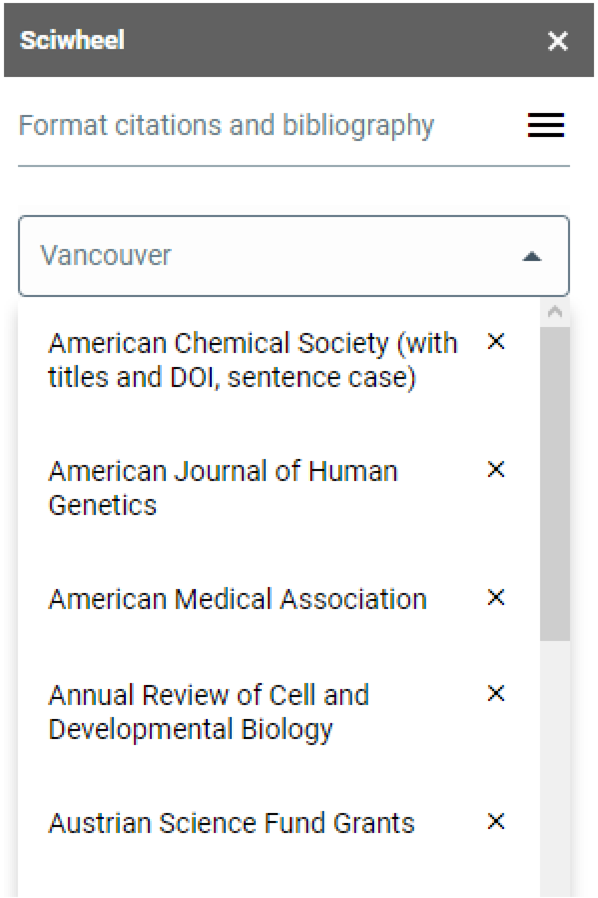
PCSK9 Promotes Endothelial Dysfunction During Sepsis Via the TLR4/MyD88/NF-κB and NLRP3 Pathways.

2022 Huang L, Li Y, (...), Xia Y - Inflammation

PCSK9 induces tissue factor expression by activation of tlr4/nfkb signaling.

2021 Scalise V, Sanguinetti C, (...), Pedrinelli R - Int J Mol Sci

Google Docs Plug-in for Sciwheel



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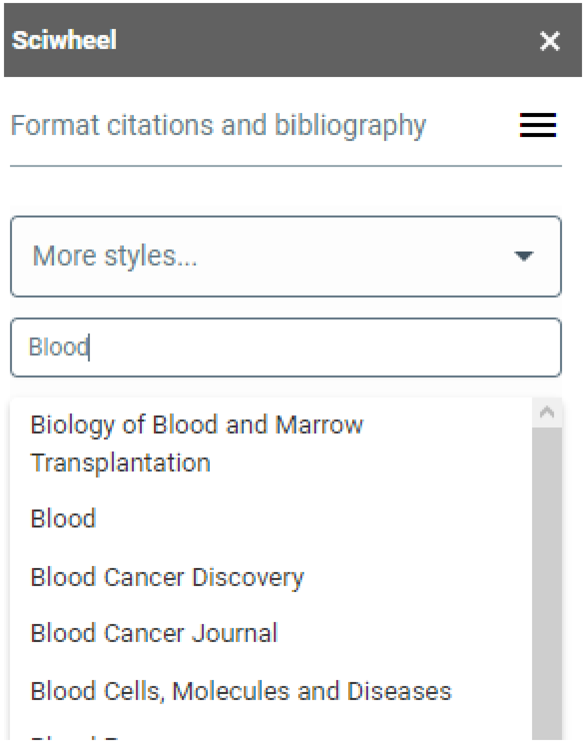

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Blood

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- Blood
- Blood Cancer Discovery
- Blood Cancer Journal
- Blood Cells, Molecules and Diseases

Sciwheel ✕

Format citations and bibliography ☰

Blood ▼

Blood

Inline citation

1

Bibliography

1. Accadia T, Acernese F, Alshourbagy M, et al. Virgo: a laser interferometer to detect gravitational waves. *J. Instrum.* 2012;7(03):P03012–P03012.

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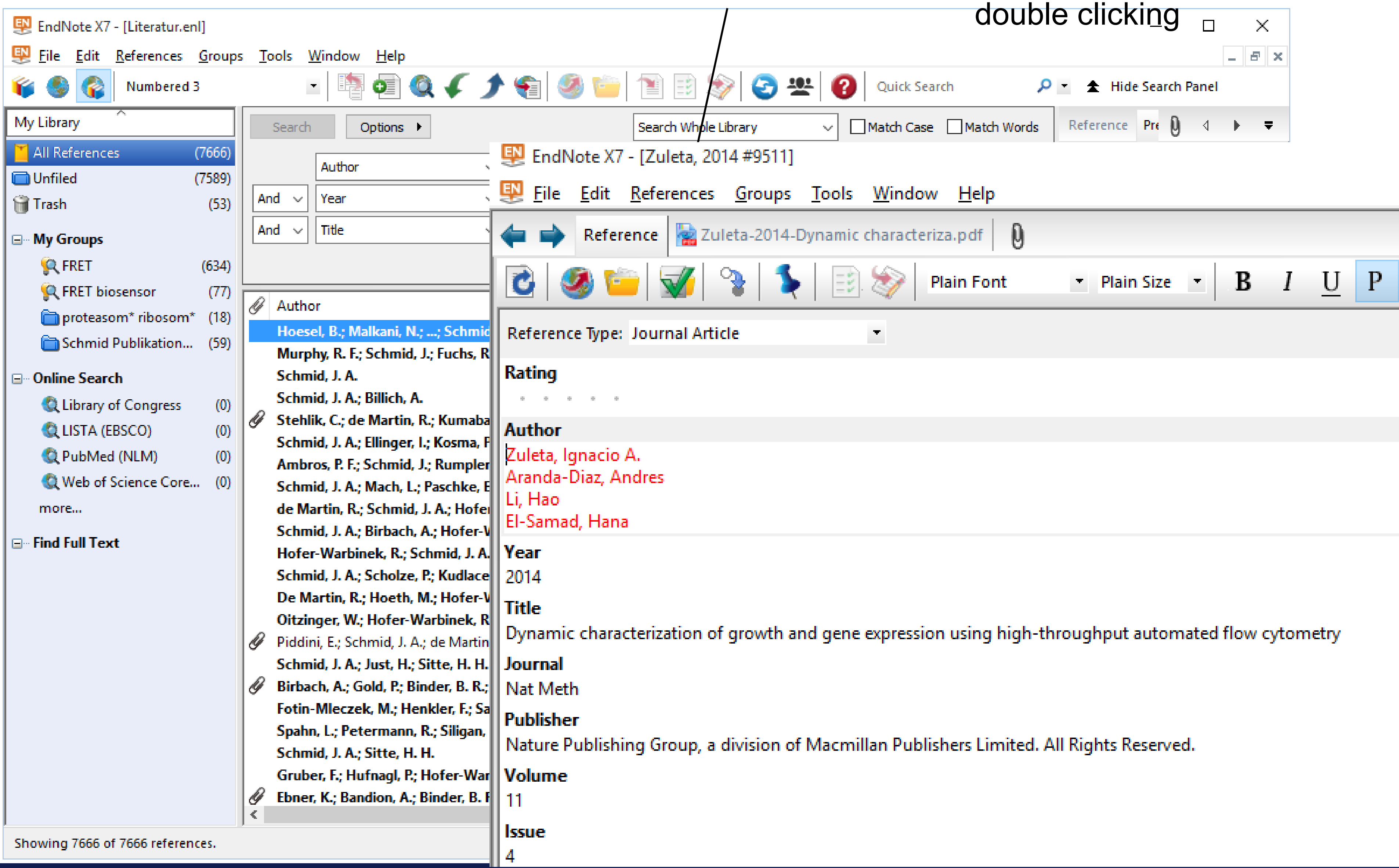

Author

Hoesel, B.; Malkani, N.; ...; Schmid
Murphy, R. F.; Schmid, J.; Fuchs, R
Schmid, J. A.
Schmid, J. A.; Billich, A.
Stehlik, C.; de Martin, R.; Kumaba
Schmid, J. A.; Ellinger, I.; Kosma, F
Ambros, P. F.; Schmid, J.; Rumpler
Schmid, J. A.; Mach, L.; Paschke, E
de Martin, R.; Schmid, J. A.; Hofer
Schmid, J. A.; Birbach, A.; Hofer-V
Hofer-Warbinek, R.; Schmid, J. A.
Schmid, J. A.; Scholze, P.; Kudlace
De Martin, R.; Hoeth, M.; Hofer-V
Oitzinger, W.; Hofer-Warbinek, R
Piddini, E.; Schmid, J. A.; de Martin
Schmid, J. A.; Just, H.; Sitte, H. H.
Birbach, A.; Gold, P.; Binder, B. R.;
Fotin-Mleczek, M.; Henkler, F.; Sa
Spahn, L.; Petermann, R.; Siligan,
Schmid, J. A.; Sitte, H. H.
Gruber, F.; Hufnagl, P.; Hofer-War
Ebner, K.; Bandion, A.; Binder, B. F

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Reference Type: Journal Article

Rating

Author
Zuleta, Ignacio A.
Aranda-Diaz, Andres
Li, Hao
El-Samad, Hana

Year
2014

Title
Dynamic characterization of growth and gene expression using high-throughput automated flow cytometry

Journal
Nat Meth

Publisher
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Volume
11

Issue
4

Connections to Databases (Pubmed)

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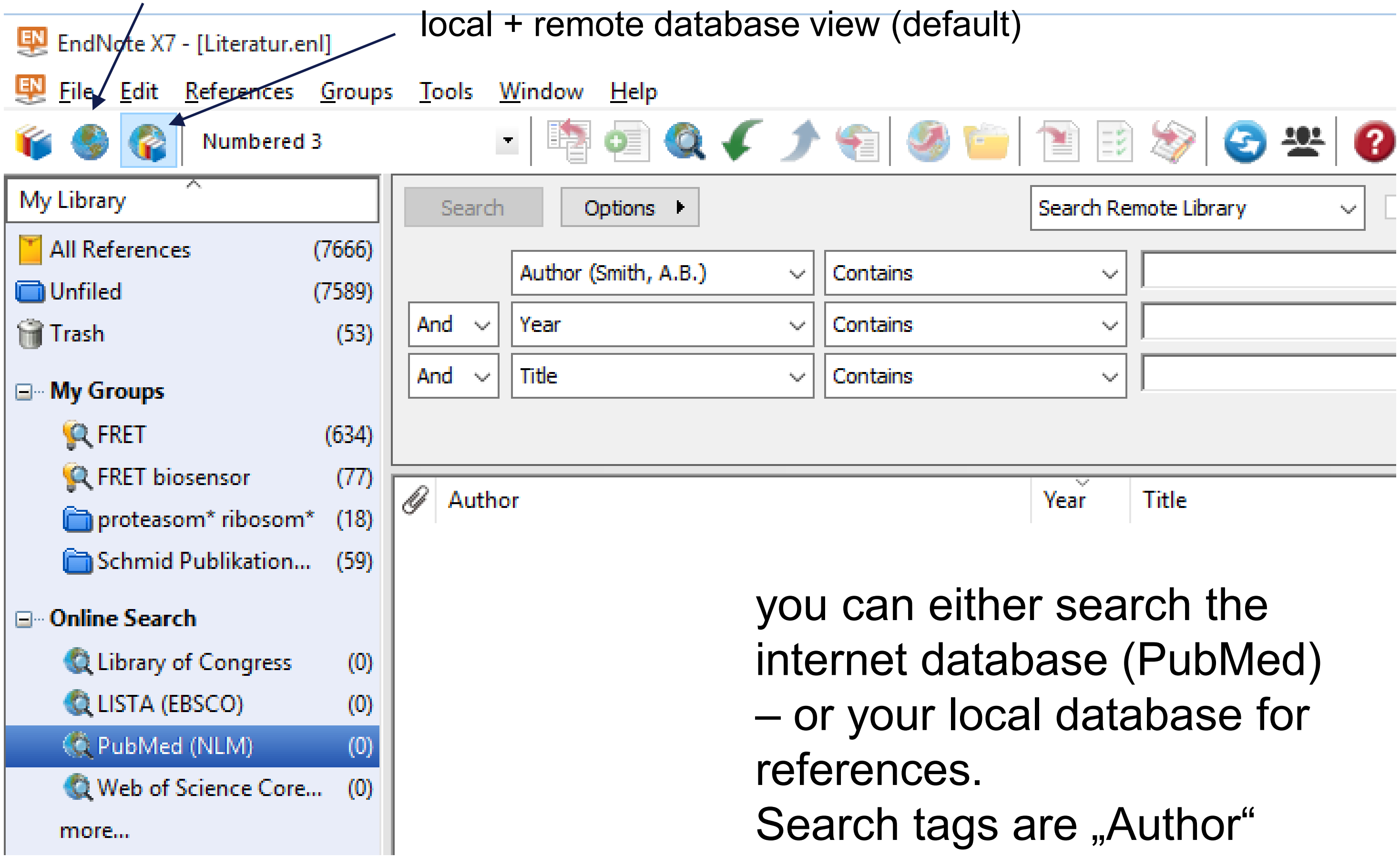

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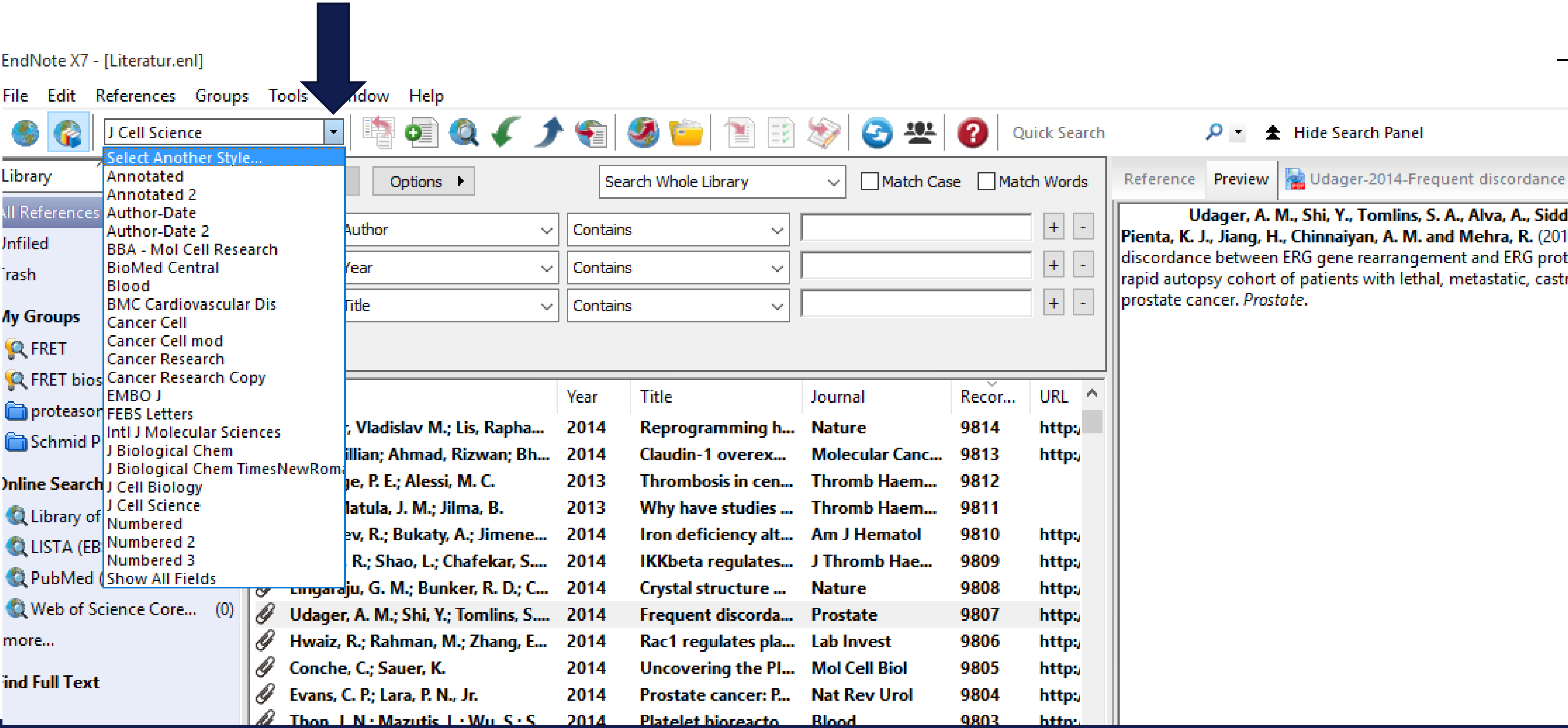
„Output styles“ – in the Edit Tab



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Year | Contains
Title | Contains

	Year	Title	Journal	Recor...	URL
, Vladislav M.; Lis, Rapha...	2014	Reprogramming h...	Nature	9814	http:/
illian; Ahmad, Rizwan; Bh...	2014	Claudin-1 overex...	Molecular Canc...	9813	http:/
ge, P. E.; Alessi, M. C.	2013	Thrombosis in cen...	Thromb Haem...	9812	
latula, J. M.; Jilma, B.	2013	Why have studies ...	Thromb Haem...	9811	
ev, R.; Bukaty, A.; Jimene...	2014	Iron deficiency alt...	Am J Hematol	9810	http:/
R.; Shao, L.; Chafekar, S....	2014	IKKbeta regulates...	J Thromb Hae...	9809	http:/
ingaraju, G. M.; Bunker, R. D.; C...	2014	Crystal structure ...	Nature	9808	http:/
Udager, A. M.; Shi, Y.; Tomlins, S....	2014	Frequent discorda...	Prostate	9807	http:/
Hwaiz, R.; Rahman, M.; Zhang, E....	2014	Rac1 regulates pla...	Lab Invest	9806	http:/
Conche, C.; Sauer, K.	2014	Uncovering the PI...	Mol Cell Biol	9805	http:/
Evans, C. P.; Lara, P. N., Jr.	2014	Prostate cancer: P...	Nat Rev Urol	9804	http:/
Thon, J. N.; Mazutis, L.; Wu, S.; S	2014	Platelet bioreacto	Blood	9803	http:/

Udager, A. M., Shi, Y., Tomlins, S. A., Alva, A., Sidd
Pienta, K. J., Jiang, H., Chinnaiyan, A. M. and Mehra, R. (201
discordance between ERG gene rearrangement and ERG prot
rapid autopsy cohort of patients with lethal, metastatic, castr
prostate cancer. *Prostate*.

Endnote- Journal Styles

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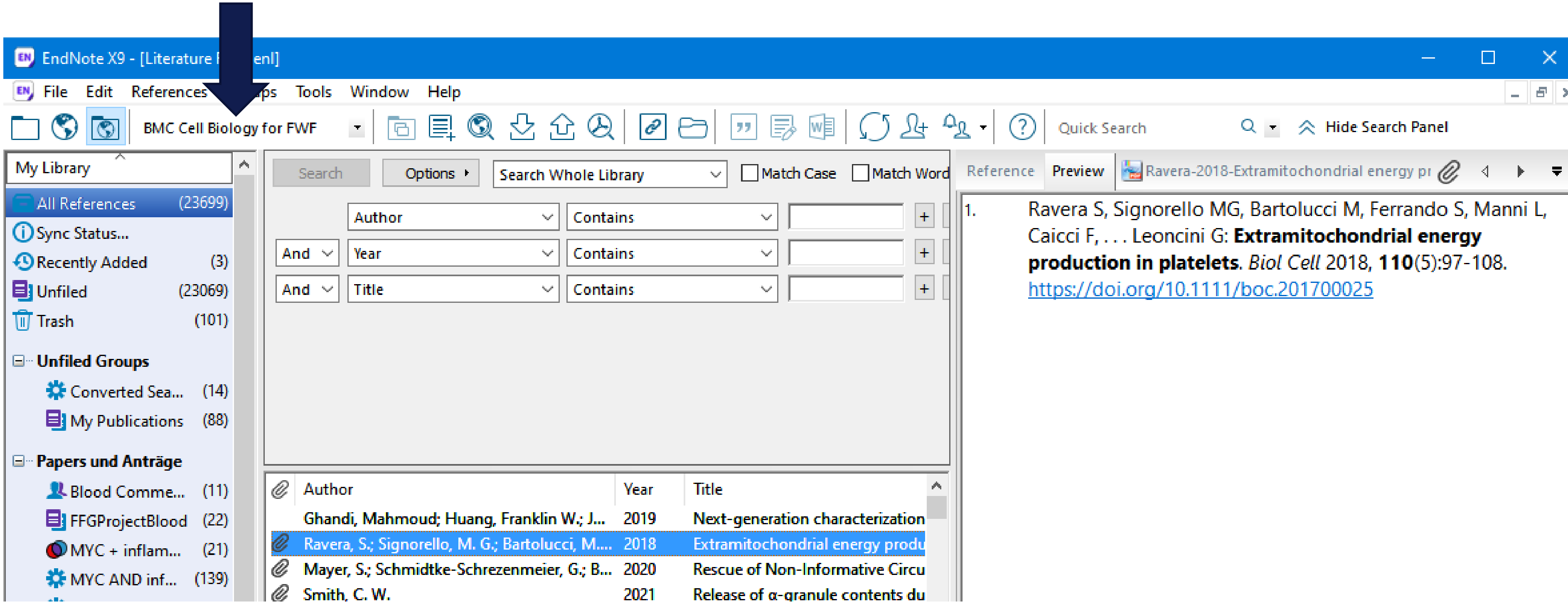

BMC Cell Biology for FWF

1. Ravera S, Signorello MG, Bartolucci M, Ferrando S, Manni L, Caicci F, . . . Leoncini G: **Extramitochondrial energy production in platelets**. *Biol Cell* 2018, **110**(5):97-108. https://doi.org/10.1111/boc.201700025

Author	Year	Title
Ghandi, Mahmoud; Huang, Franklin W.; J...	2019	Next-generation characterization
Ravera, S.; Signorello, M. G.; Bartolucci, M....	2018	Extramitochondrial energy produ
Mayer, S.; Schmidtke-Schrezenmeier, G.; B...	2020	Rescue of Non-Informative Circu
Smith, C. W.	2021	Release of α-granule contents du

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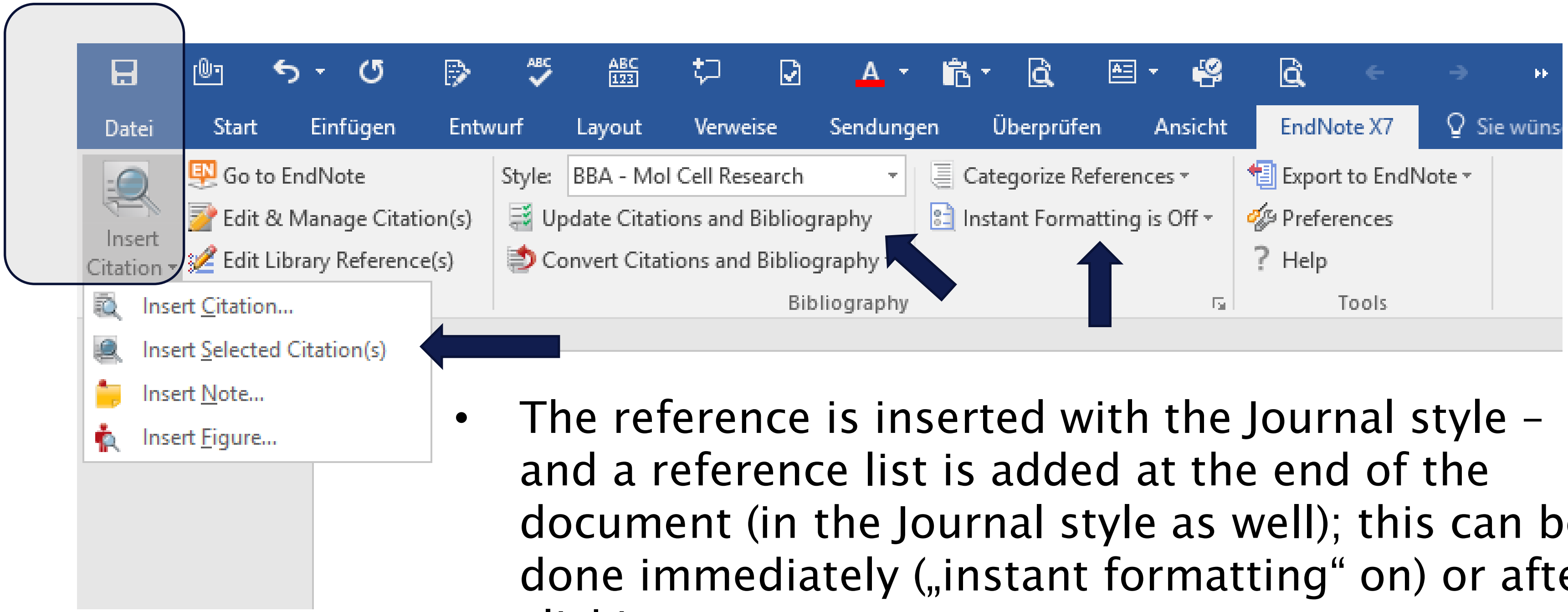

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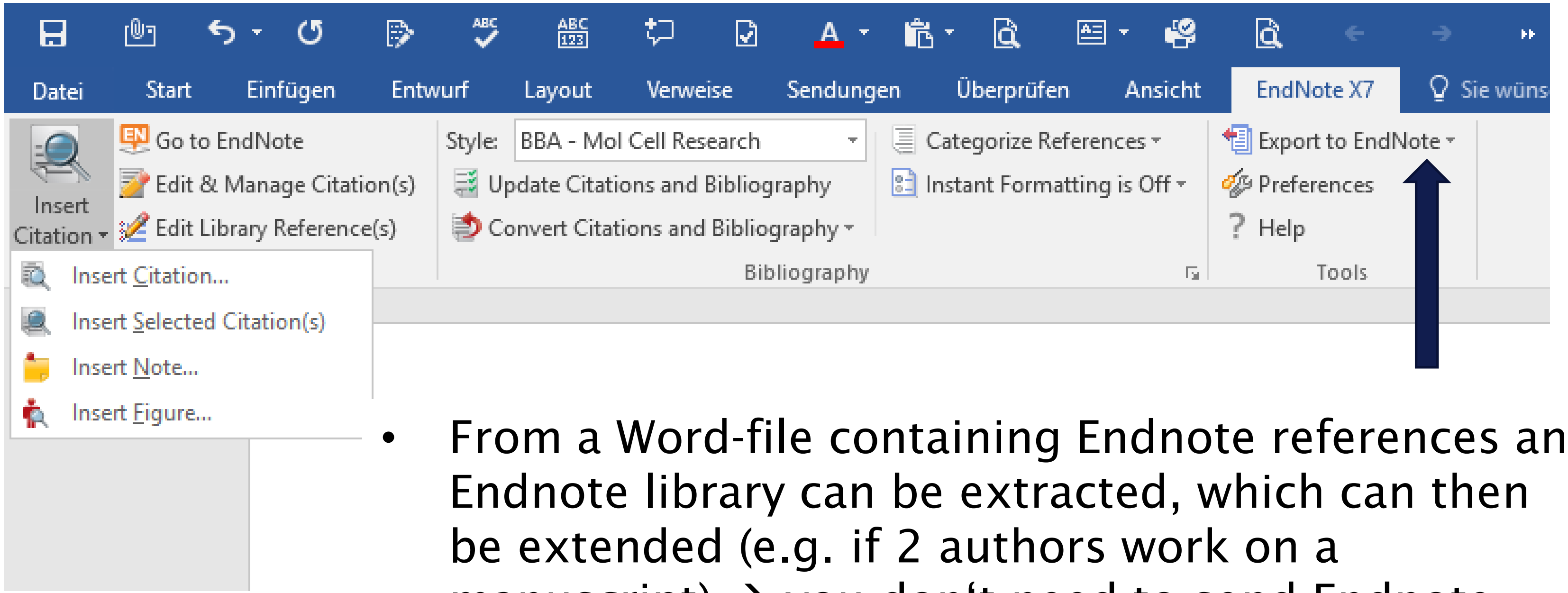

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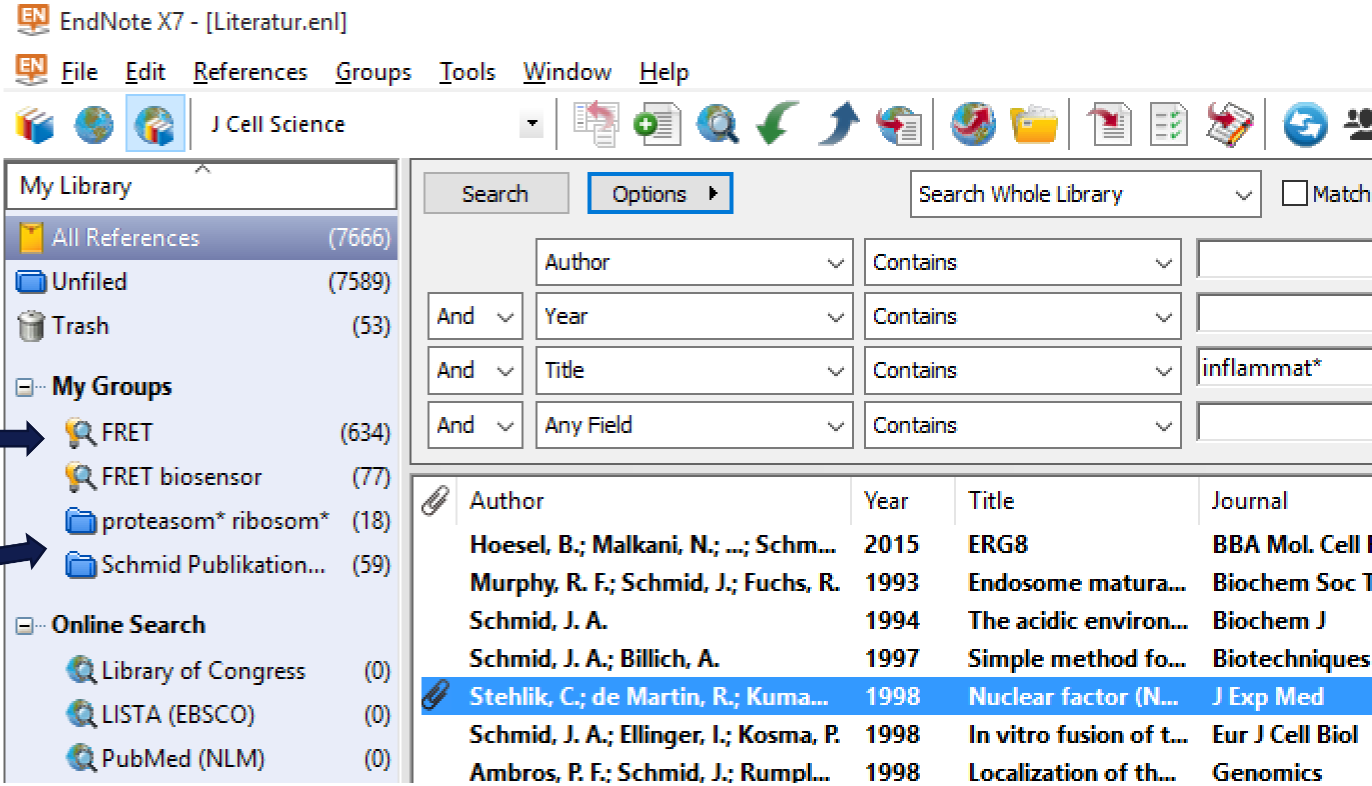

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J Cell Science

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All References	(7666)
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Schmid Publikation...	(59)
Online Search	
Library of Congress	(0)
LISTA (EBSCO)	(0)
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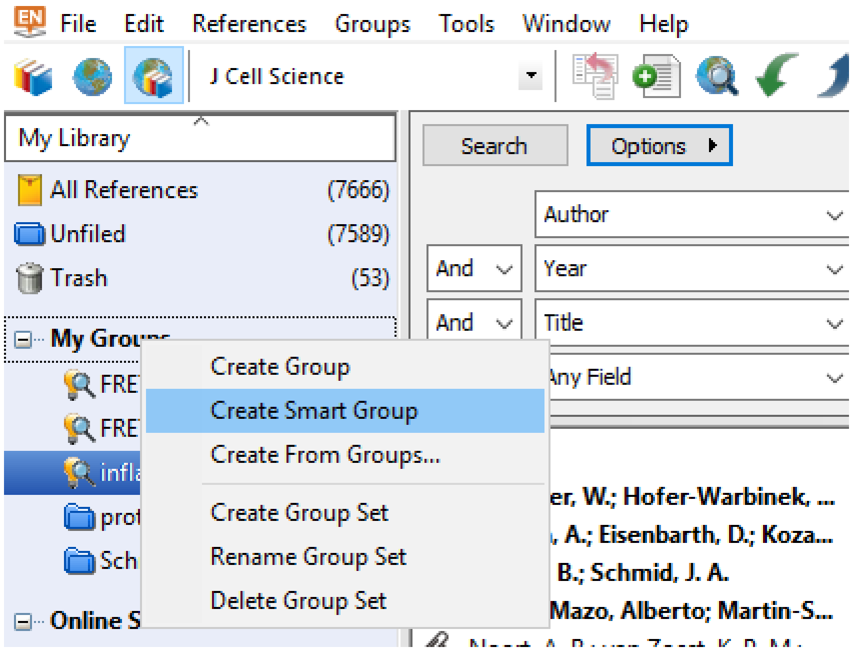
	Author	Contains	
And	Year	Contains	
And	Title	Contains	inflammat*
And	Any Field	Contains	

Author	Year	Title	Journal
Hoesel, B.; Malkani, N.; ...; Schm...	2015	ERG8	BBA Mol. Cell
Murphy, R. F.; Schmid, J.; Fuchs, R.	1993	Endosome matura...	Biochem Soc T
Schmid, J. A.	1994	The acidic environ...	Biochem J
Schmid, J. A.; Billich, A.	1997	Simple method fo...	Biotechniques
Stehlik, C.; de Martin, R.; Kuma...	1998	Nuclear factor (N...	J Exp Med
Schmid, J. A.; Ellinger, I.; Kosma, P.	1998	In vitro fusion of t...	Eur J Cell Biol
Ambros, P. F.; Schmid, J.; Rumpl...	1998	Localization of th...	Genomics

Right-click on „My Groups“ can be used to create groups or smart groups



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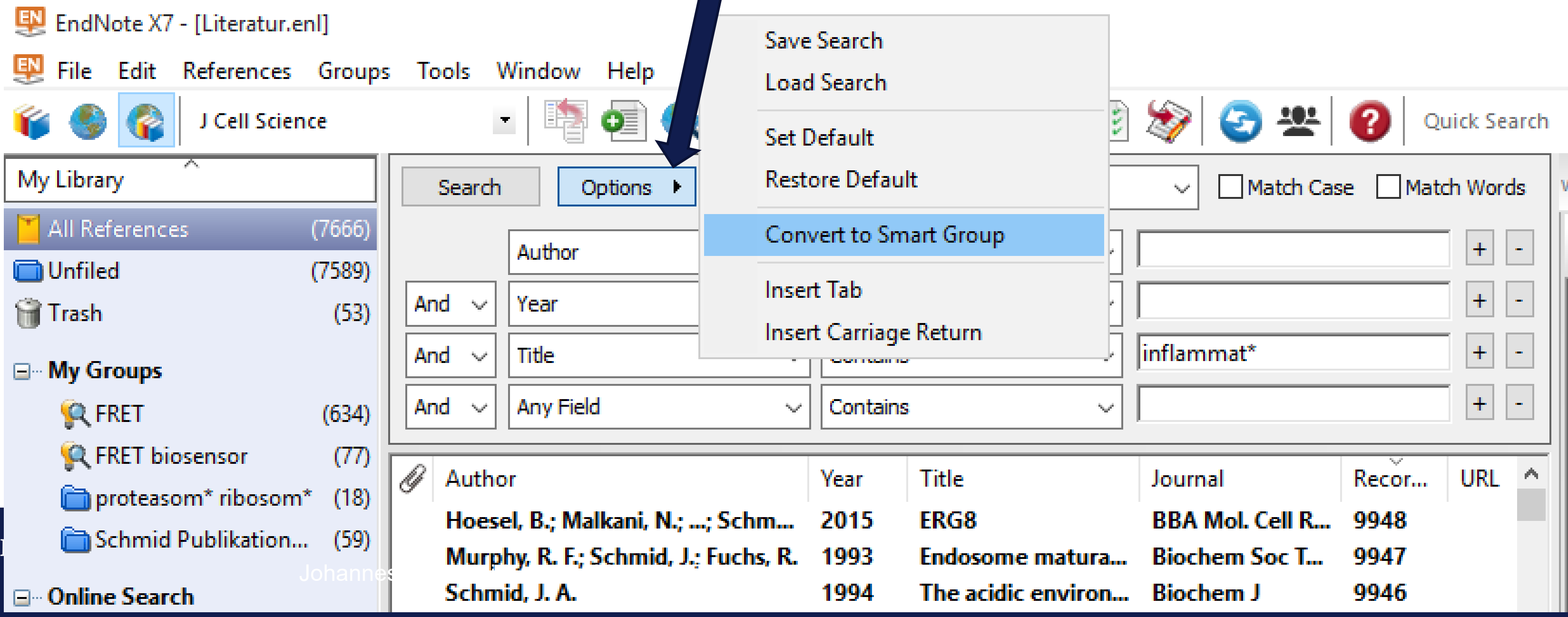

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Author	Year	Title	Journal	Recor...	URL
Hoesel, B.; Malkani, N.; ...; Schm...	2015	ERG8	BBA Mol. Cell R...	9948	
Murphy, R. F.; Schmid, J.; Fuchs, R.	1993	Endosome matura...	Biochem Soc T...	9947	
Schmid, J. A.	1994	The acidic environ...	Biochem J	9946	

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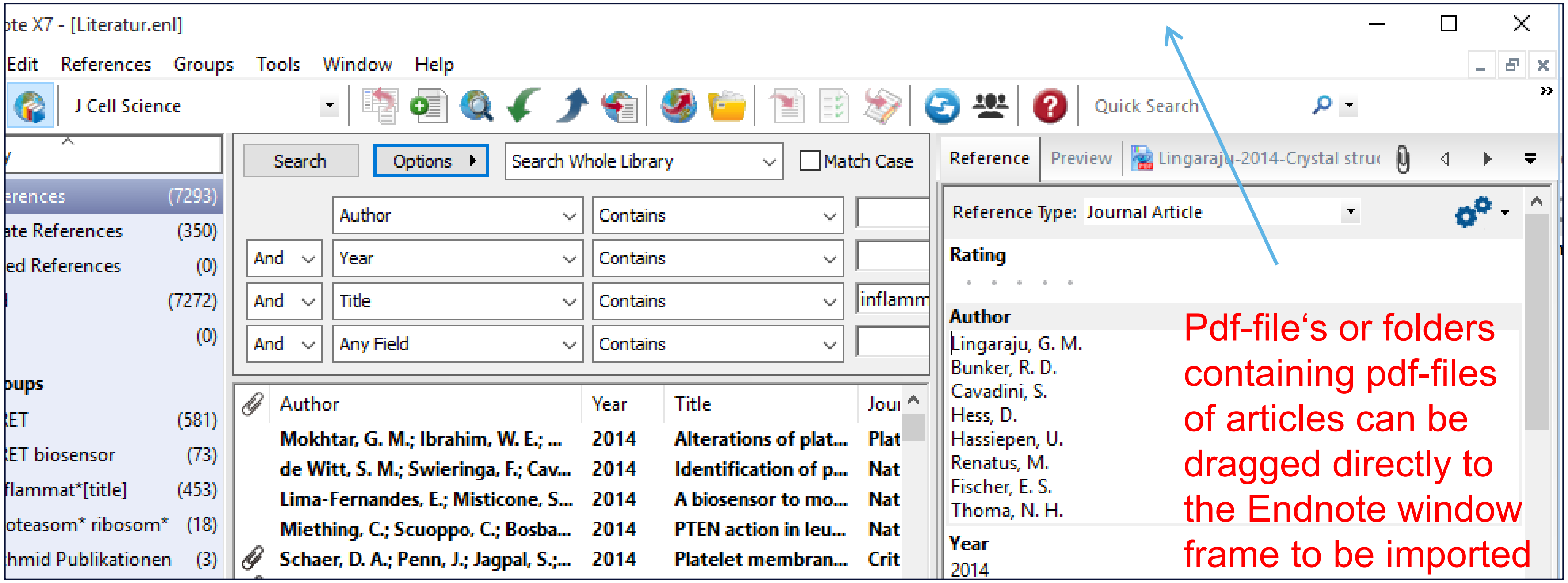

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Author	Year	Title	Jour
Mokhtar, G. M.; Ibrahim, W. E.; ...	2014	Alterations of plat...	Plat
de Witt, S. M.; Swieringa, F.; Cav...	2014	Identification of p...	Nat
Lima-Fernandes, E.; Misticone, S...	2014	A biosensor to mo...	Nat
Miething, C.; Scuoppo, C.; Bosba...	2014	PTEN action in leu...	Nat
Schaer, D. A.; Penn, J.; Jagpal, S.;...	2014	Platelet membran...	Crit

Reference Type: Journal Article

Rating

Author
Lingaraju, G. M.
Bunker, R. D.
Cavadini, S.
Hess, D.
Hassiepen, U.
Renatus, M.
Fischer, E. S.
Thoma, N. H.

Year
2014

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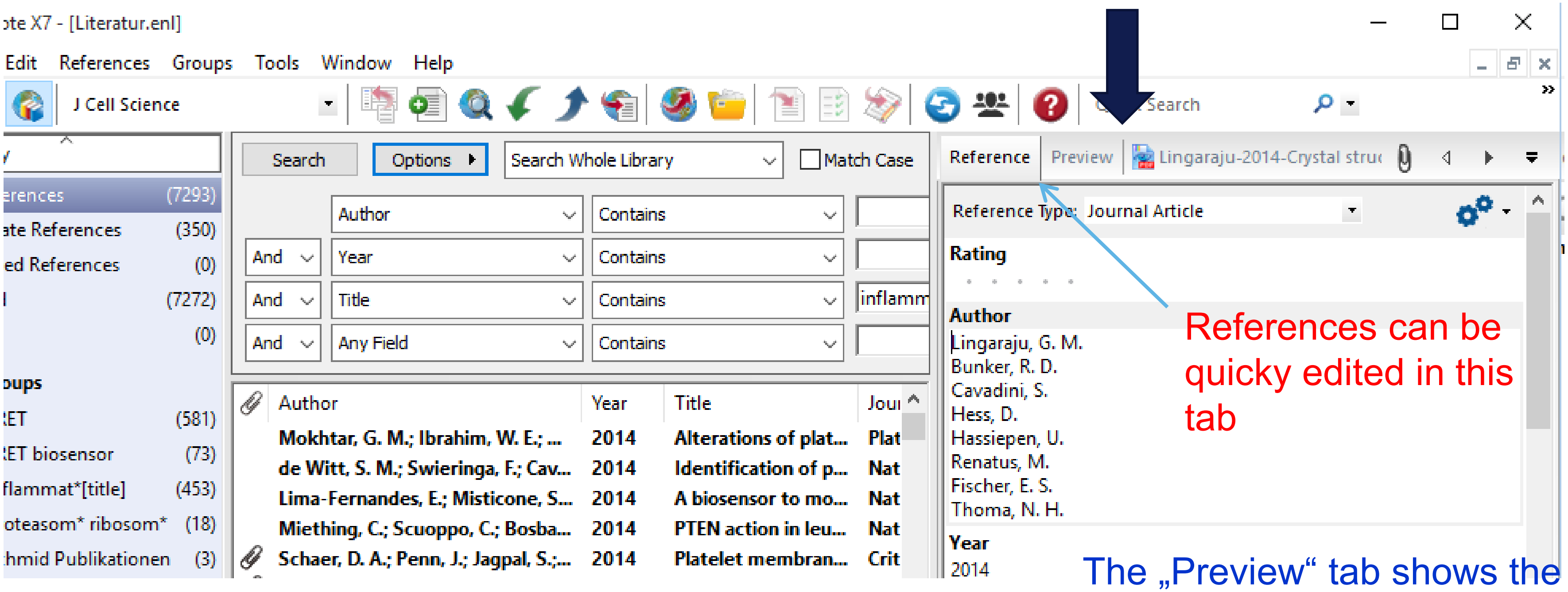

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Author	Year	Title	Jour
Mokhtar, G. M.; Ibrahim, W. E.; ...	**2014**	**Alterations of plat...**	**Plat**
de Witt, S. M.; Swieringa, F.; Cav...	**2014**	**Identification of p...**	**Nat**
Lima-Fernandes, E.; Misticone, S...	**2014**	**A biosensor to mo...**	**Nat**
Miething, C.; Scuoppo, C.; Bosba...	**2014**	**PTEN action in leu...**	**Nat**
Schaer, D. A.; Penn, J.; Jagpal, S.;...	**2014**	**Platelet membran...**	**Crit**

Reference Type: Journal Article

Rating

Author
Lingaraju, G. M.
Bunker, R. D.
Cavadini, S.
Hess, D.
Hassiepen, U.
Renatus, M.
Fischer, E. S.
Thoma, N. H.

Year
2014

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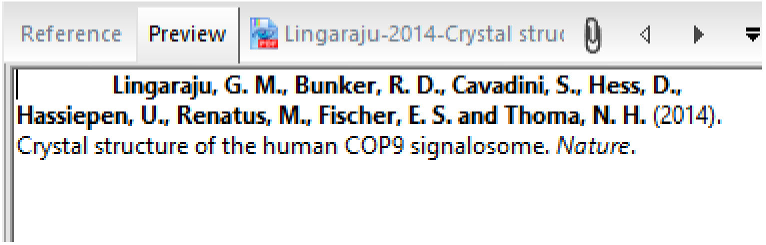

Lingaraju, G. M., Bunker, R. D., Cavadini, S., Hess, D., Hassiepen, U., Renatus, M., Fischer, E. S. and Thoma, N. H. (2014). Crystal structure of the human COP9 signalosome. *Nature*.

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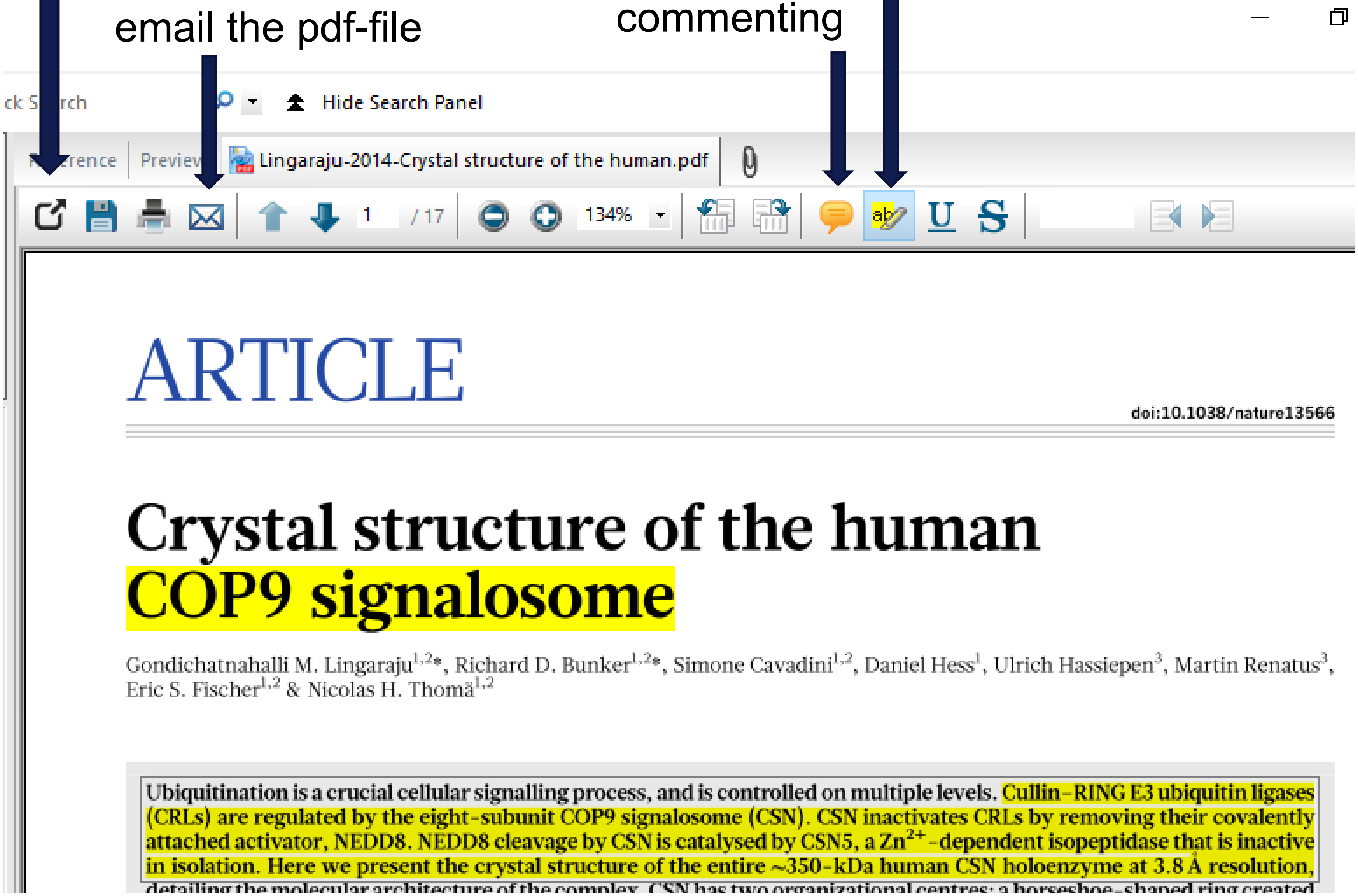

ARTICLE

doi:10.1038/nature13566

Crystal structure of the human COP9 signalosome

Gondichatnahalli M. Lingaraju[1,2]*, Richard D. Bunker[1,2]*, Simone Cavadini[1,2], Daniel Hess[1], Ulrich Hassiepen[3], Martin Renatus[3], Eric S. Fischer[1,2] & Nicolas H. Thomä[1,2]

Ubiquitination is a crucial cellular signalling process, and is controlled on multiple levels. Cullin–RING E3 ubiquitin ligases (CRLs) are regulated by the eight-subunit COP9 signalosome (CSN). CSN inactivates CRLs by removing their covalently attached activator, NEDD8. NEDD8 cleavage by CSN is catalysed by CSN5, a Zn^{2+}-dependent isopeptidase that is inactive in isolation. Here we present the crystal structure of the entire ~350-kDa human CSN holoenzyme at 3.8 Å resolution, detailing the molecular architecture of the complex. CSN has two organizational centres: a horseshoe-shaped ring created

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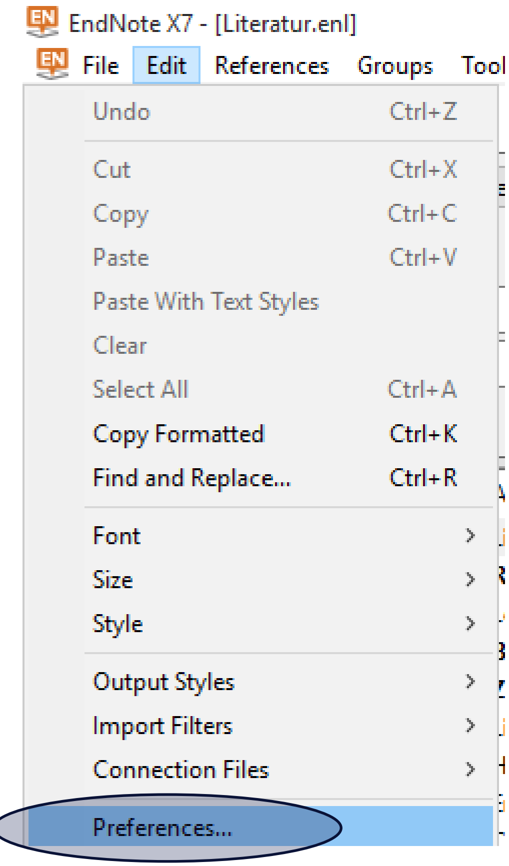
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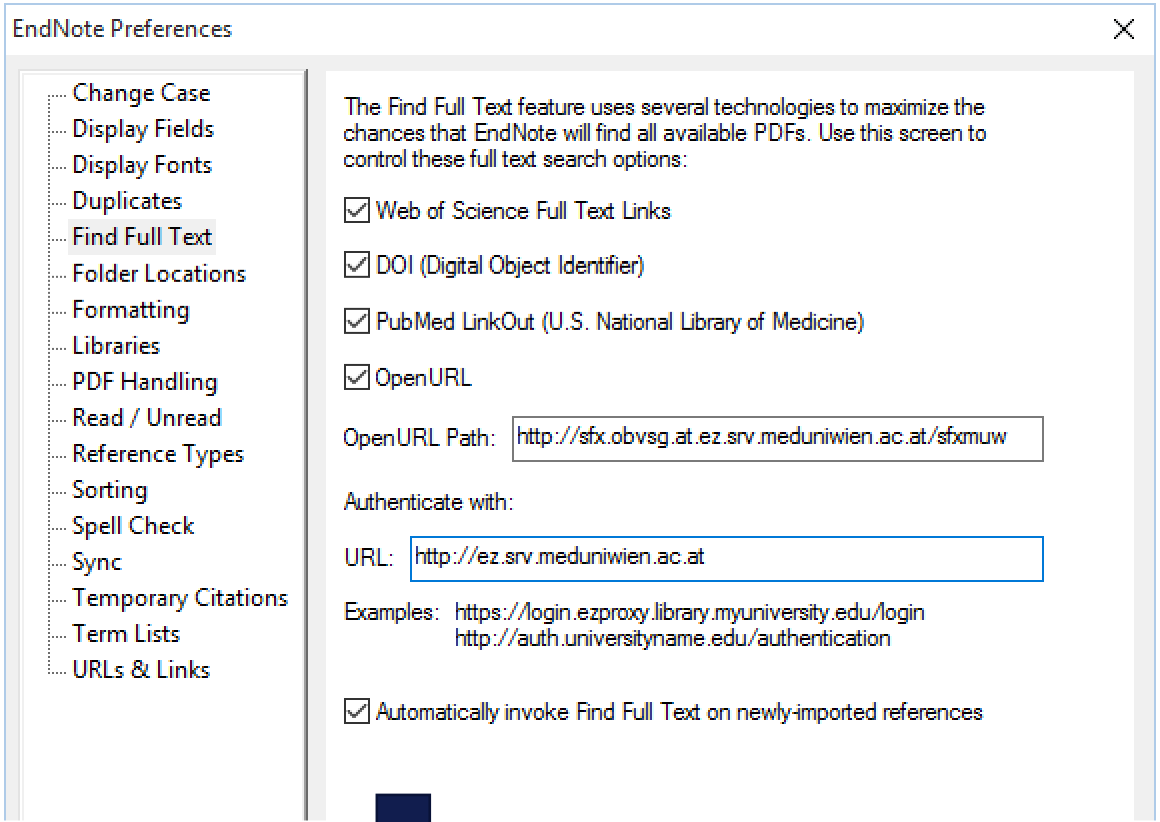
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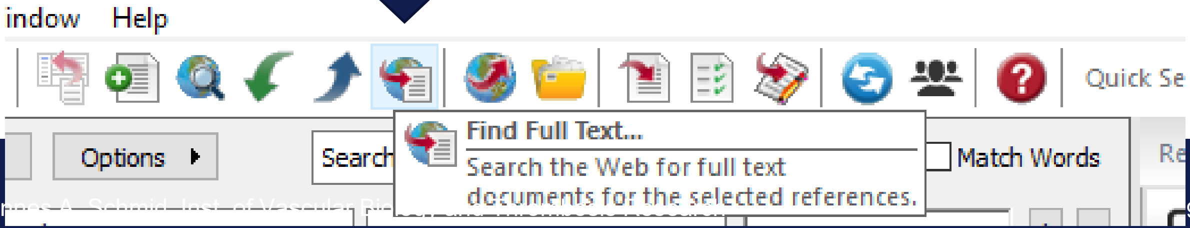

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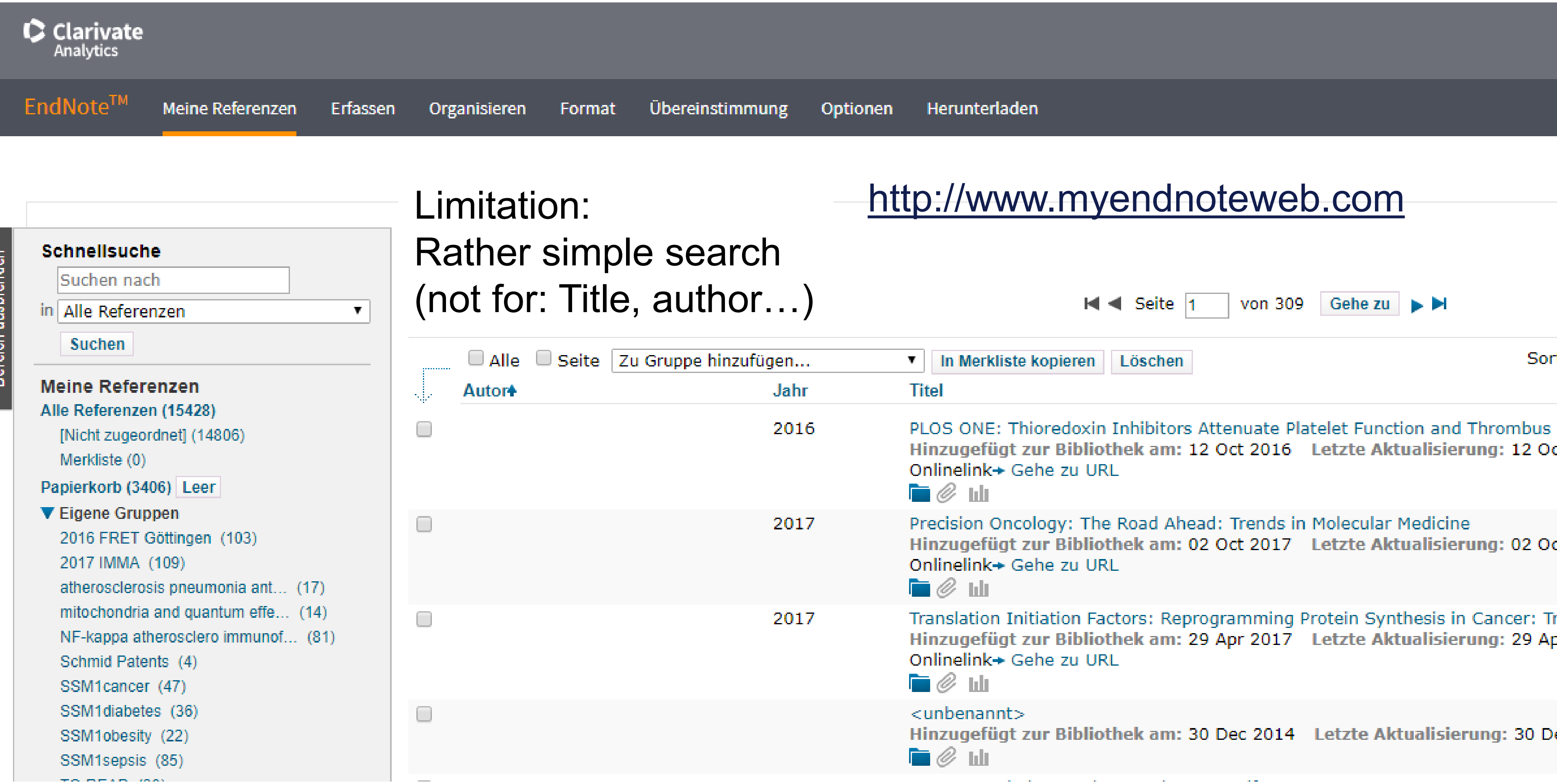

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Schmid Patents (4)
SSM1cancer (47)
SSM1diabetes (36)
SSM1obesity (22)
SSM1sepsis (85)

☐ 2016 PLOS ONE: Thioredoxin Inhibitors Attenuate Platelet Function and Thrombus
Hinzugefügt zur Bibliothek am: 12 Oct 2016 **Letzte Aktualisierung:** 12 Oc
Onlinelink→ Gehe zu URL

☐ 2017 Precision Oncology: The Road Ahead: Trends in Molecular Medicine
Hinzugefügt zur Bibliothek am: 02 Oct 2017 **Letzte Aktualisierung:** 02 Oc
Onlinelink→ Gehe zu URL

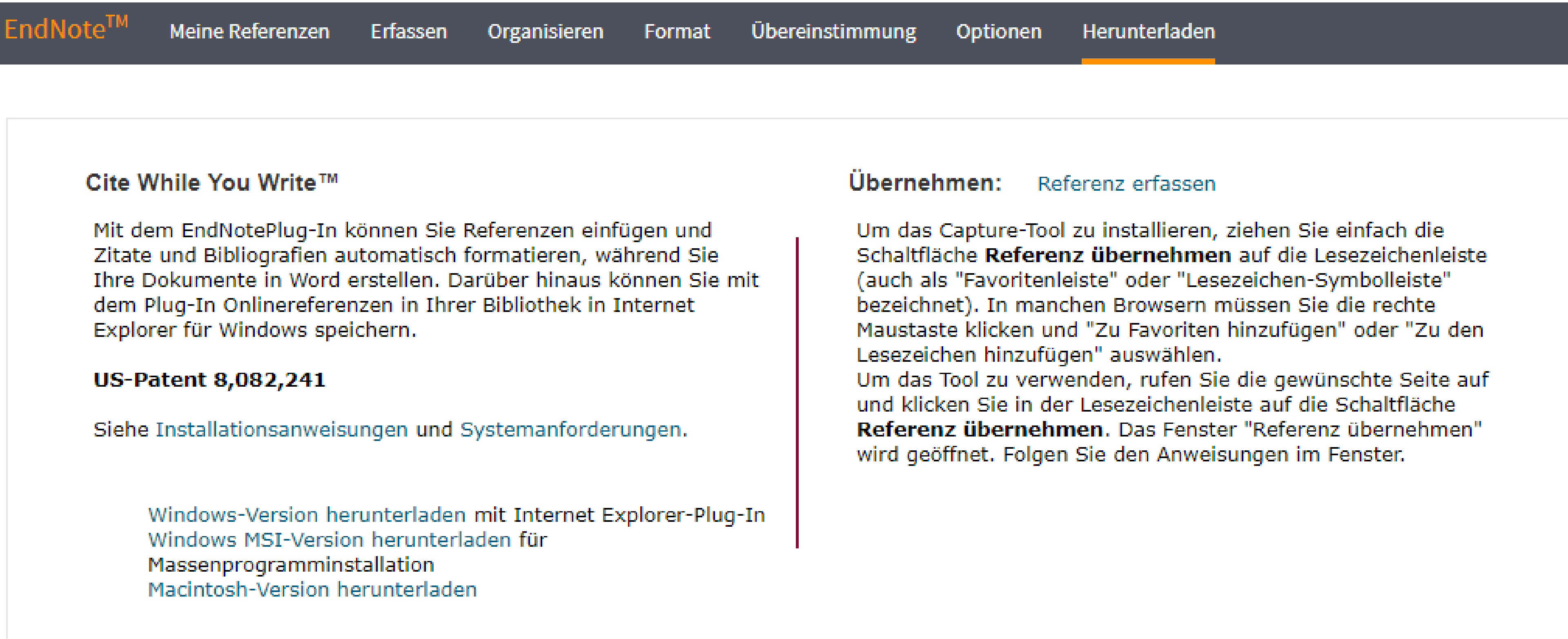
☐ 2017 Translation Initiation Factors: Reprogramming Protein Synthesis in Cancer: Tr
Hinzugefügt zur Bibliothek am: 29 Apr 2017 **Letzte Aktualisierung:** 29 Ap
Onlinelink→ Gehe zu URL

☐ <unbenannt>
Hinzugefügt zur Bibliothek am: 30 Dec 2014 **Letzte Aktualisierung:** 30 De

Free online Endnote: MyEndnoteWeb

http://www.myendnoteweb.com

Plug-in available for inserting references into Word



Cite While You Write™

Mit dem EndNotePlug-In können Sie Referenzen einfügen und Zitate und Bibliografien automatisch formatieren, während Sie Ihre Dokumente in Word erstellen. Darüber hinaus können Sie mit dem Plug-In Onlinereferenzen in Ihrer Bibliothek in Internet Explorer für Windows speichern.

US-Patent 8,082,241

Siehe Installationsanweisungen und Systemanforderungen.

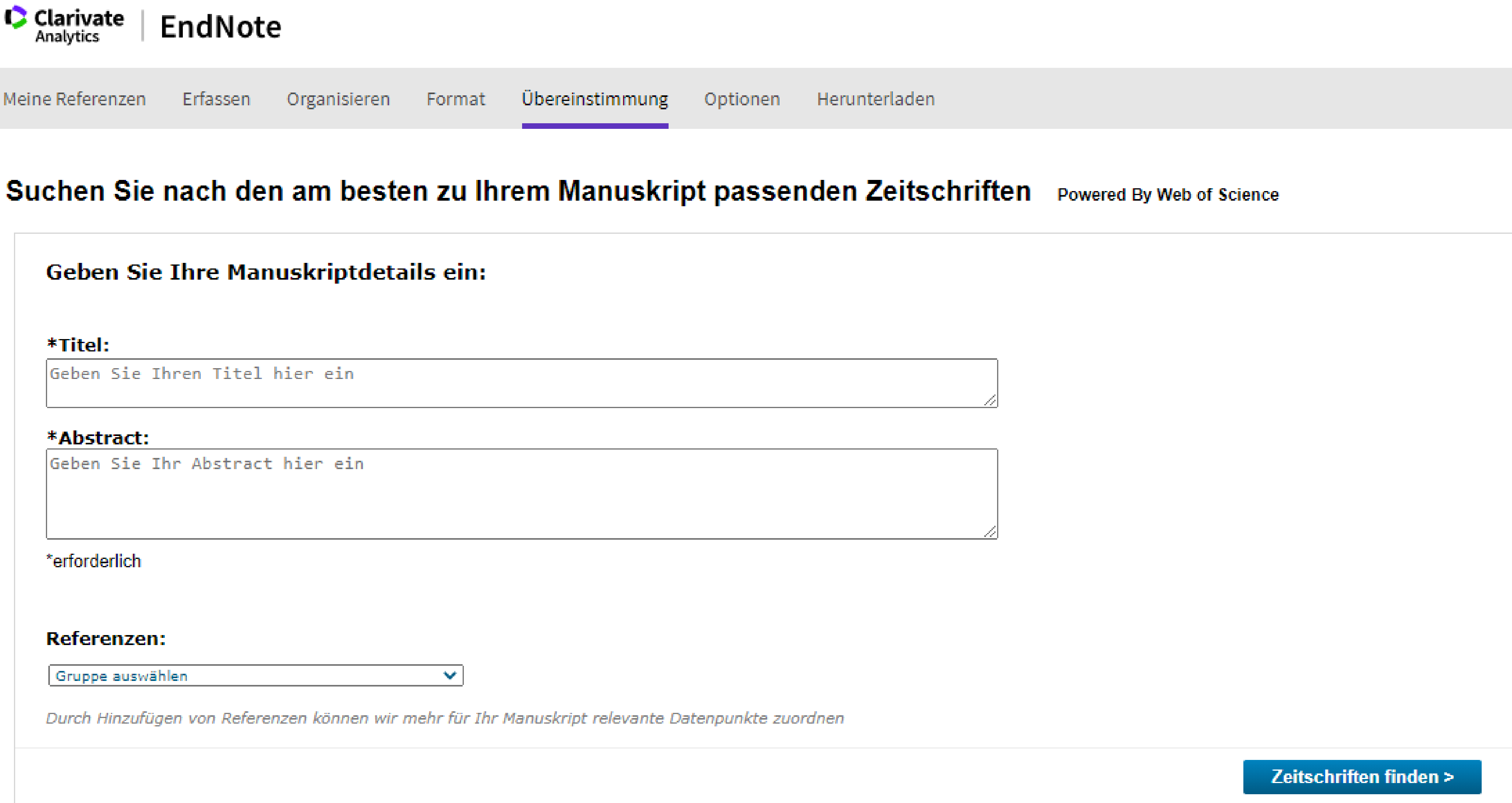
Windows-Version herunterladen mit Internet Explorer-Plug-In
Windows MSI-Version herunterladen für Massenprogramminstallation
Macintosh-Version herunterladen

Übernehmen: Referenz erfassen

Um das Capture-Tool zu installieren, ziehen Sie einfach die Schaltfläche **Referenz übernehmen** auf die Lesezeichenleiste (auch als "Favoritenleiste" oder "Lesezeichen-Symbolleiste" bezeichnet). In manchen Browsern müssen Sie die rechte Maustaste klicken und "Zu Favoriten hinzufügen" oder "Zu den Lesezeichen hinzufügen" auswählen.
Um das Tool zu verwenden, rufen Sie die gewünschte Seite auf und klicken Sie in der Lesezeichenleiste auf die Schaltfläche **Referenz übernehmen**. Das Fenster "Referenz übernehmen" wird geöffnet. Folgen Sie den Anweisungen im Fenster.

Find appropriate journals for your manuscript

http://www.myendnoteweb.com



Suchen Sie nach den am besten zu Ihrem Manuskript passenden Zeitschriften Powered By Web of Science

Geben Sie Ihre Manuskriptdetails ein:

***Titel:**
Geben Sie Ihren Titel hier ein

***Abstract:**
Geben Sie Ihr Abstract hier ein

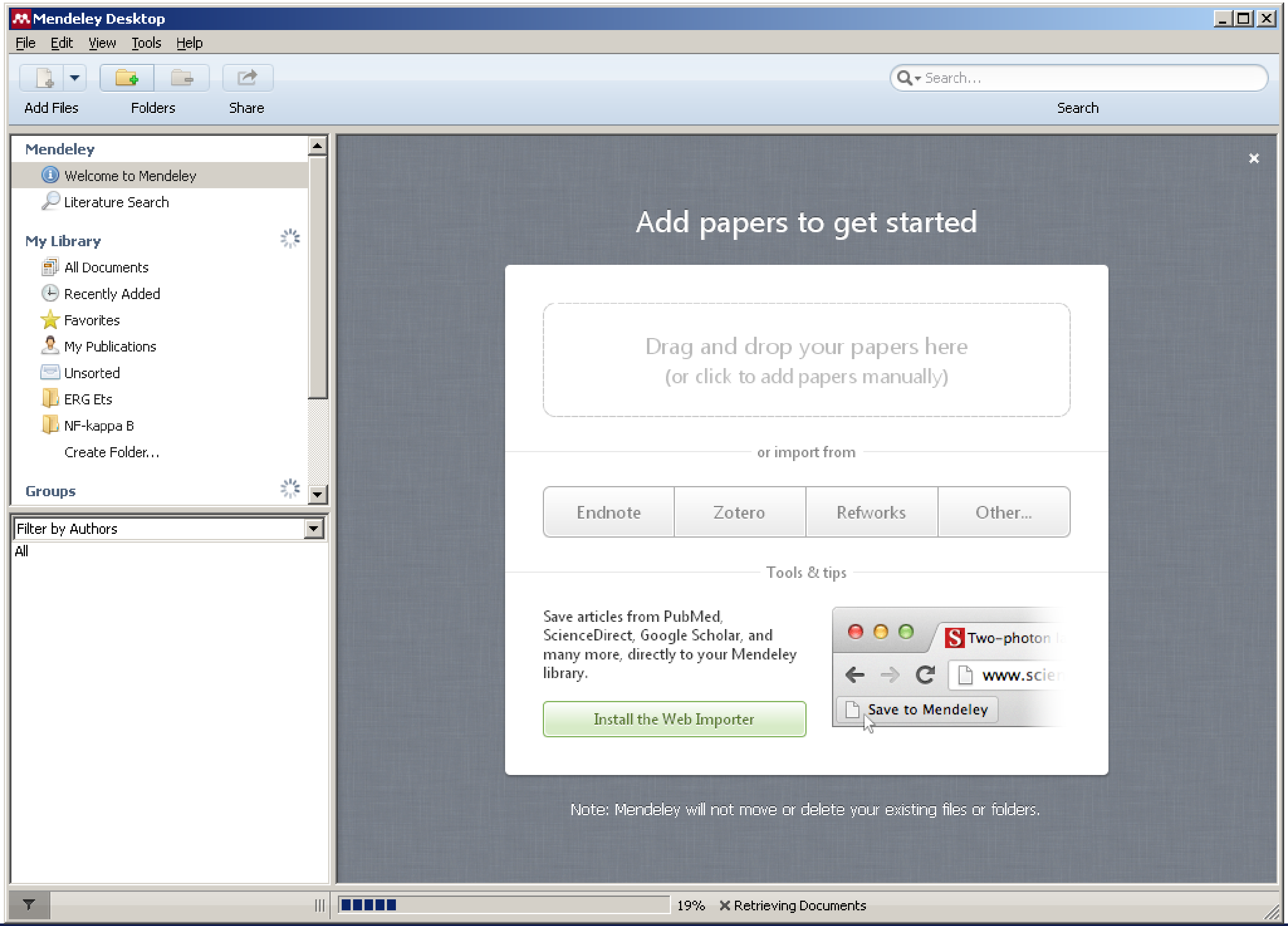
*erforderlich

Referenzen:

Durch Hinzufügen von Referenzen können wir mehr für Ihr Manuskript relevante Datenpunkte zuordnen

Mendeley-Freeware alternative to Endnote

http://www.mendeley.com/



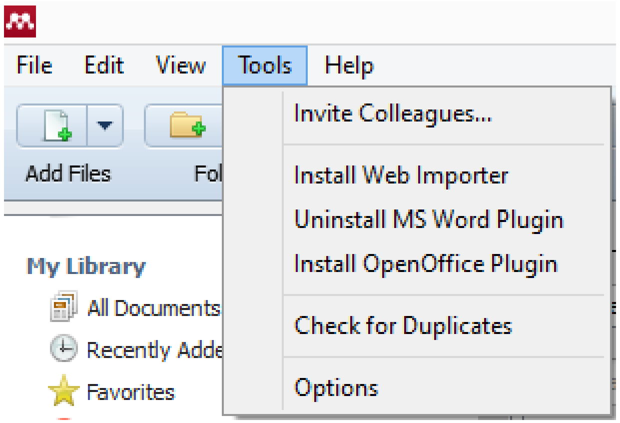
Add papers to get started

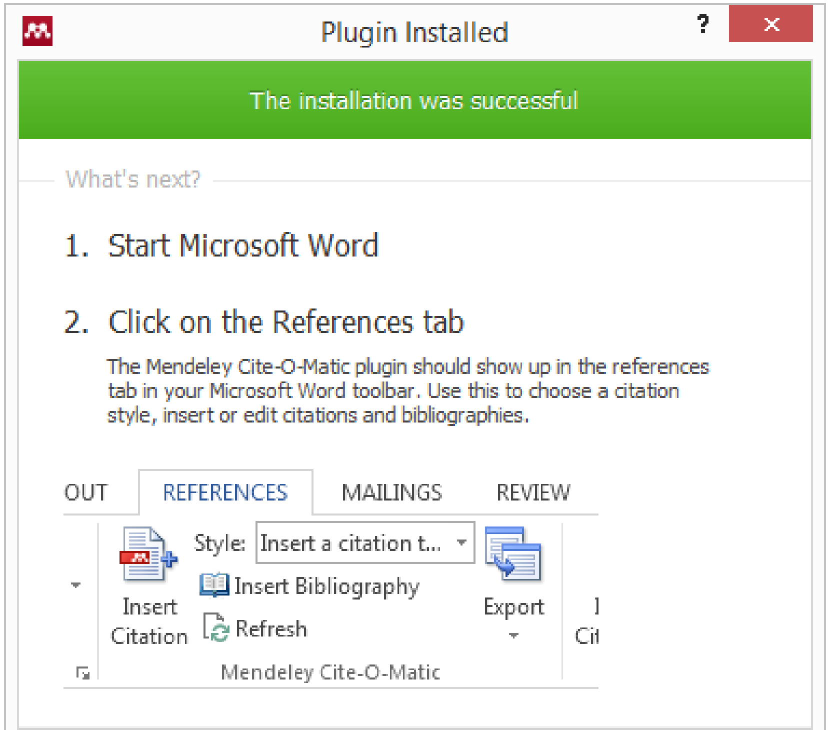
Drag and drop your papers here
(or click to add papers manually)

Save articles from PubMed, ScienceDirect, Google Scholar, and many more, directly to your Mendeley library.

Note: Mendeley will not move or delete your existing files or folders.

Mendeley Web Importer and Plugins for Word and OpenOffice




Plugin Installed

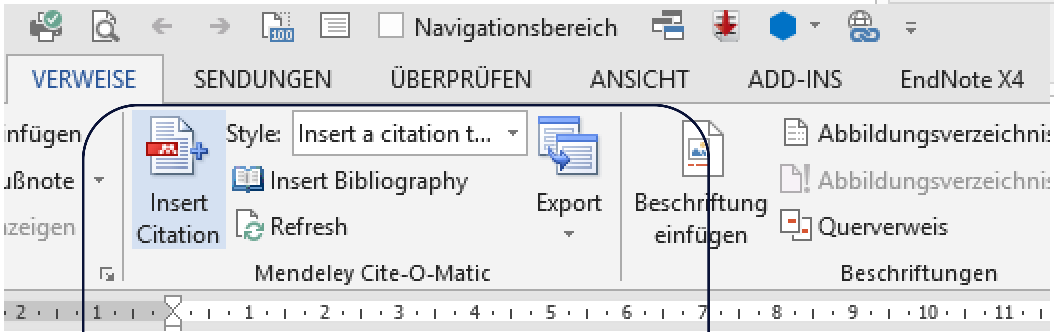
The installation was successful

What's next?

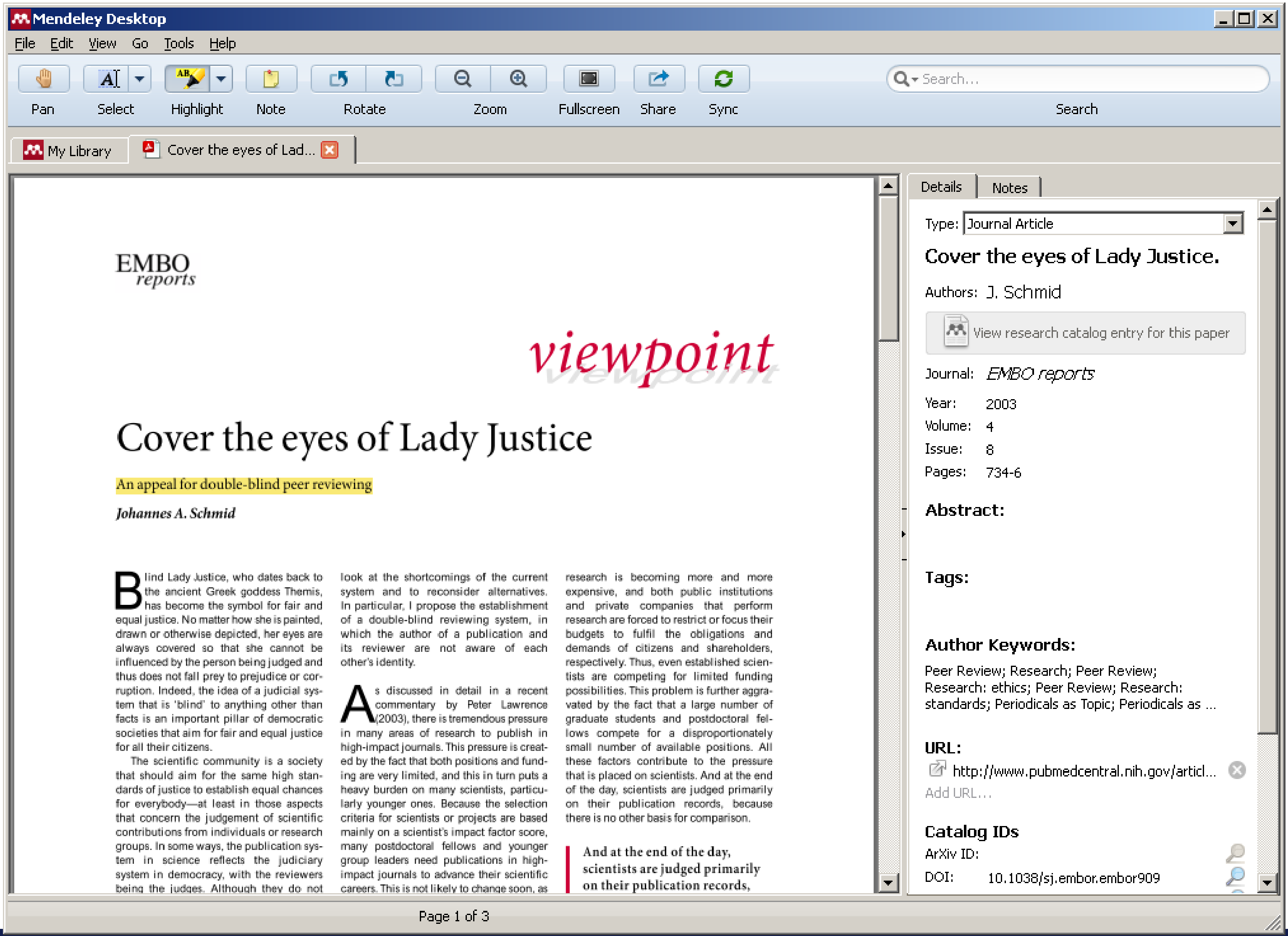
1. Start Microsoft Word

2. Click on the References tab

The Mendeley Cite-O-Matic plugin should show up in the references tab in your Microsoft Word toolbar. Use this to choose a citation style, insert or edit citations and bibliographies.



pdf‘s can be dragged to the program window and are recognized; they can also be edited in the software (highlighting, adding notes…)



EMBO *reports*

viewpoint

Cover the eyes of Lady Justice

An appeal for double-blind peer reviewing

Johannes A. Schmid

Blind Lady Justice, who dates back to the ancient Greek goddess Themis, has become the symbol for fair and equal justice. No matter how she is painted, drawn or otherwise depicted, her eyes are always covered so that she cannot be influenced by the person being judged and thus does not fall prey to prejudice or corruption. Indeed, the idea of a judicial system that is ‘blind’ to anything other than facts is an important pillar of democratic societies that aim for fair and equal justice for all their citizens.

The scientific community is a society that should aim for the same high standards of justice to establish equal chances for everybody—at least in those aspects that concern the judgement of scientific contributions from individuals or research groups. In some ways, the publication system in science reflects the judiciary system in democracy, with the reviewers being the judges. Although they do not look at the shortcomings of the current system and to reconsider alternatives. In particular, I propose the establishment of a double-blind reviewing system, in which the author of a publication and its reviewer are not aware of each other's identity.

As discussed in detail in a recent commentary by Peter Lawrence (2003), there is tremendous pressure in many areas of research to publish in high-impact journals. This pressure is created by the fact that both positions and funding are very limited, and this in turn puts a heavy burden on many scientists, particularly younger ones. Because the selection criteria for scientists or projects are based mainly on a scientist's impact factor score, many postdoctoral fellows and younger group leaders need publications in high-impact journals to advance their scientific careers. This is not likely to change soon, as research is becoming more and more expensive, and both public institutions and private companies that perform research are forced to restrict or focus their budgets to fulfil the obligations and demands of citizens and shareholders, respectively. Thus, even established scientists are competing for limited funding possibilities. This problem is further aggravated by the fact that a large number of graduate students and postdoctoral fellows compete for a disproportionately small number of available positions. All these factors contribute to the pressure that is placed on scientists. And at the end of the day, scientists are judged primarily on their publication records, because there is no other basis for comparison.

And at the end of the day, scientists are judged primarily on their publication records,

Type: Journal Article

Cover the eyes of Lady Justice.

Authors: J. Schmid

Journal: *EMBO reports*

Year: 2003
Volume: 4
Issue: 8
Pages: 734-6

Abstract:

Tags:

Author Keywords:

Peer Review; Research; Peer Review; Research: ethics; Peer Review; Research: standards; Periodicals as Topic; Periodicals as …

URL:

http://www.pubmedcentral.nih.gov/articl…

Catalog IDs

ArXiv ID:
DOI: 10.1038/sj.embor.embor909

Other Citation Managers

- Zotero: https://www.zotero.org/

Zotero for Firefox

Zotero for Firefox lets you capture and organize all your research without ever leaving the browser.

Add a plugin for Word or LibreOffice

Trouble installing Zotero?

Zotero Standalone

Zotero Standalone runs as a separate application and plugs into your choice of browser.

Add one of the following browser extensions:

Plugins for Word and LibreOffice are included

- Papers (Mac and Windows): http://www.papersapp.com/

  Recommendation: When co-authoring a manuscript find an agreement on the citation software before starting to write.

Task1: Citing literature in text documents

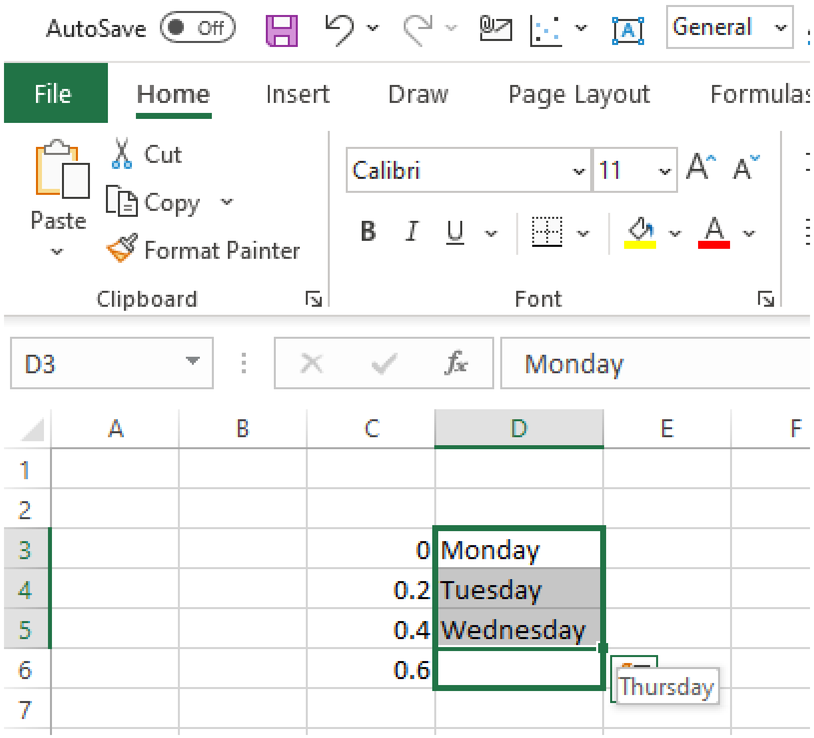
(Pubmed / GoogleDoc / Sciwheel)

- Register for a gmail account (to use Google Docs)
- Register for an account on the Sciwheel literature database platform: https://sciwheel.com – and get the Browser extension of Sciwheel and the Google Add-on (under Tools)
- Register for a Pubmed account and search for papers that contain the word roots “inflammat*” and “thrombo*” as well as the word “cancer” in the title and save it to your Sciwheel account.
- Start a new Google document – and write any text.
- Insert the citation of Franco et al. 2015
- Format citations and bibliography with the style of “The Lancet”
- How many words does the bibliography have including the preceding number of the citation? (Highlight the text and use the tool: Word count)
  Put this number into the results field and upload a screenshot of your Google Doc.

Microsoft Excel ™

Some hints:

You can use auto-fill in functions:
- e.g. type in „0“ and „0.2“
- click on lower right corner
- drag down up to the desired value
- the increment will always be as the first one
- this also works for dates, weekdays etc.



D3: Monday

	A	B	C	D	E	F
1						
2						
3			0	Monday		
4			0.2	Tuesday		
5			0.4	Wednesday		
6			0.6			
7						

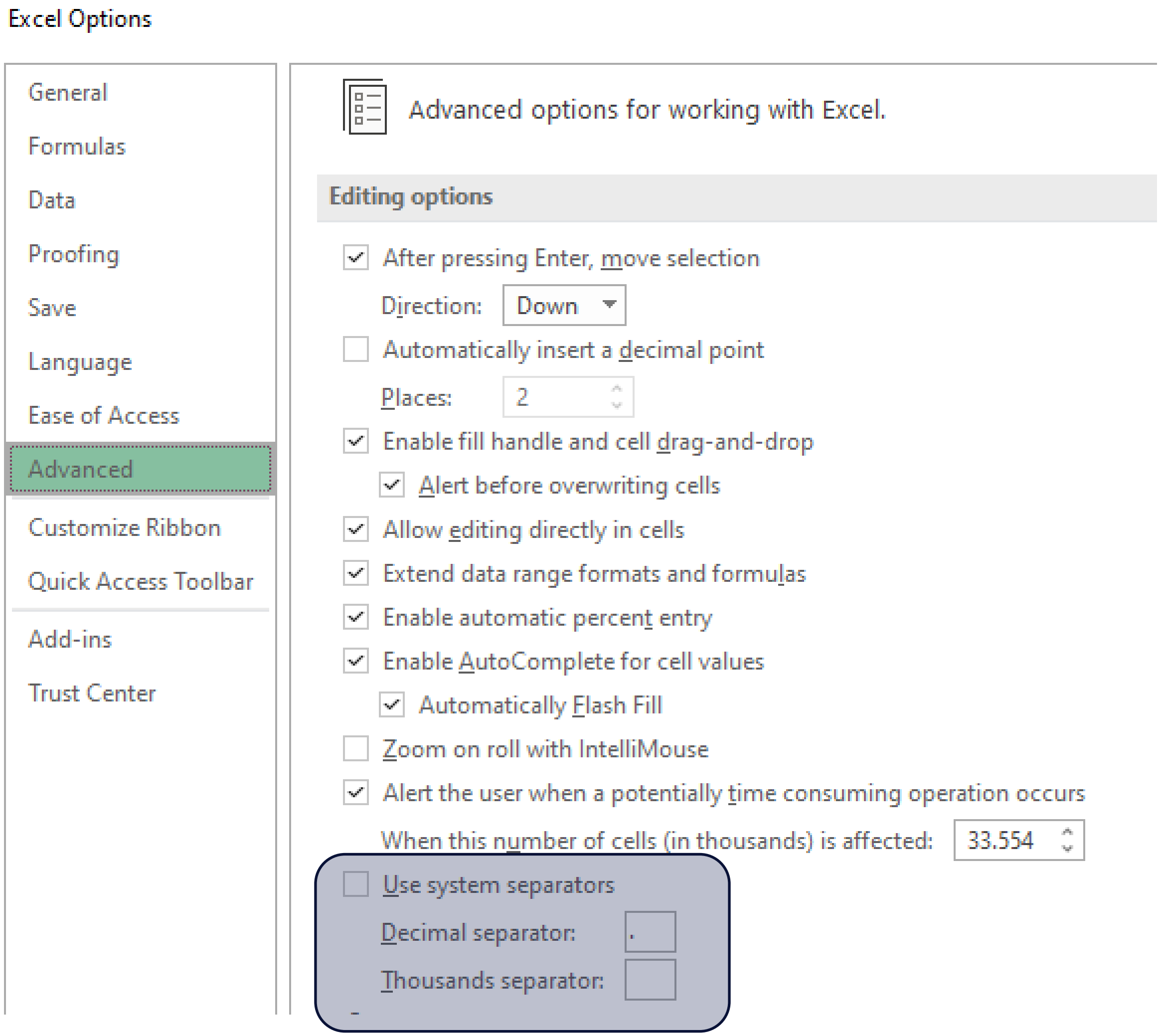
Microsoft Excel ™

Some hints:

By default text is left-aligned and
numbers are right-aligned

If you have troubles that numbers (with commas) are recognized as text:
You can change that in the Excel options:

- specify whether „.“ or „,“ is used as decimal point



Advanced options for working with Excel.

Editing options

☑ After pressing Enter, move selection

Direction: Down

☐ Automatically insert a decimal point

Places: 2

☑ Enable fill handle and cell drag-and-drop

☑ Alert before overwriting cells

☑ Allow editing directly in cells

☑ Extend data range formats and formulas

☑ Enable automatic percent entry

☑ Enable AutoComplete for cell values

☑ Automatically Flash Fill

☐ Zoom on roll with IntelliMouse

☑ Alert the user when a potentially time consuming operation occurs

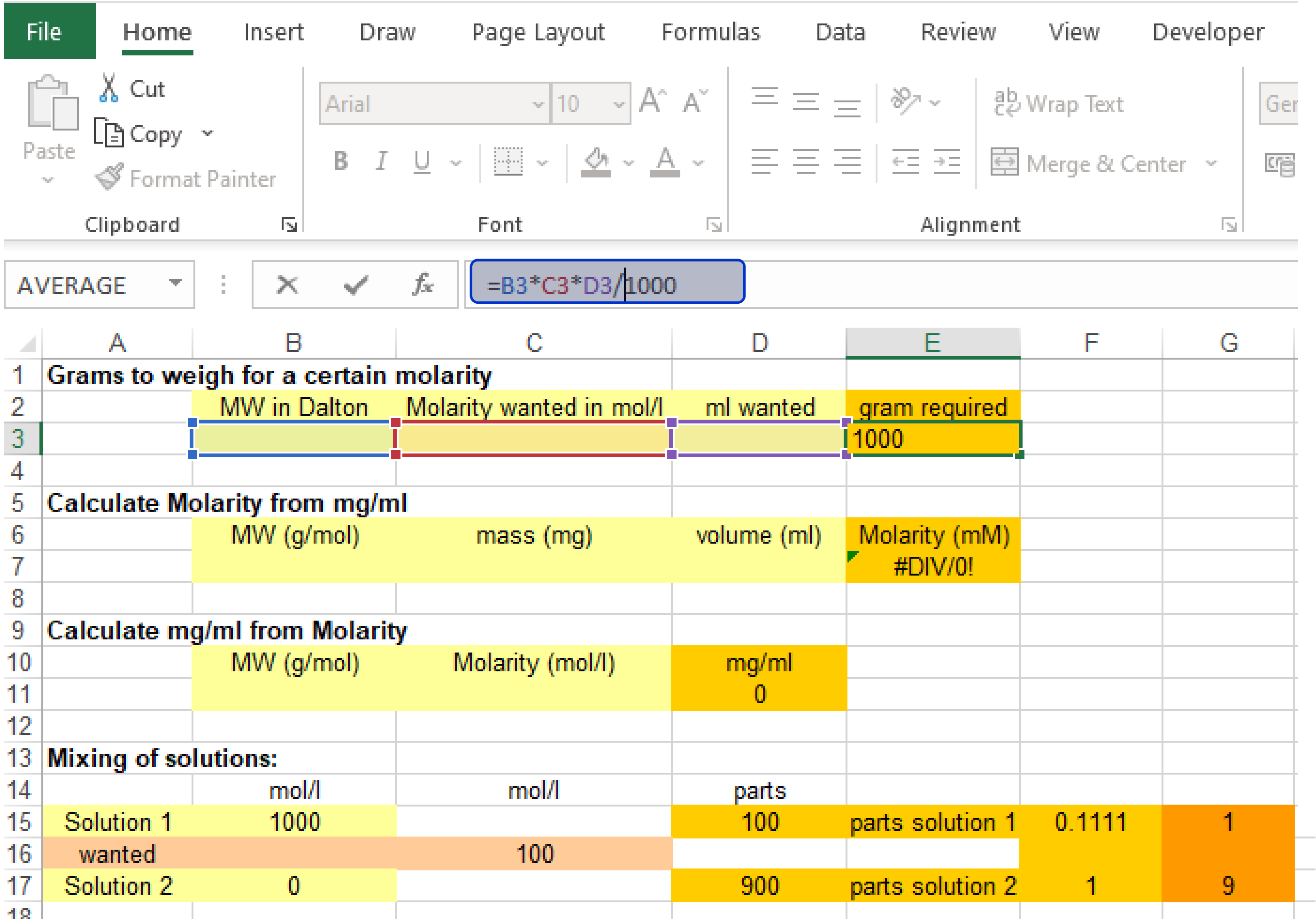
When this number of cells (in thousands) is affected: 33.554

☐ Use system separators

Decimal separator: .

Thousands separator:

Working with Excel: Calculations



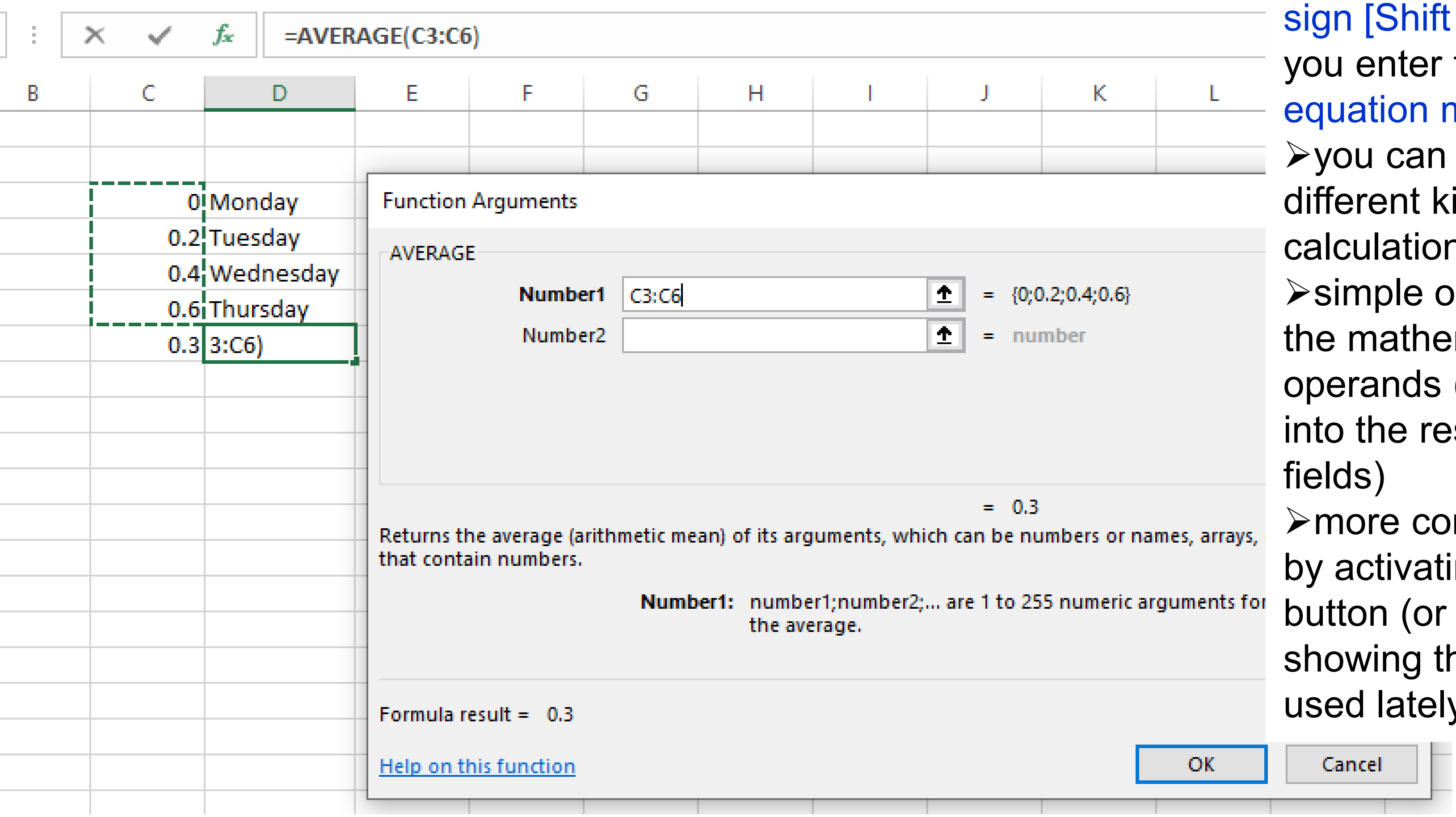
AVERAGE =B3*C3*D3/1000

	A	B	C	D	E	F	G
1	**Grams to weigh for a certain molarity**						
2		MW in Dalton	Molarity wanted in mol/l	ml wanted	gram required		
3					1000		
4							
5	**Calculate Molarity from mg/ml**						
6		MW (g/mol)	mass (mg)	volume (ml)	Molarity (mM)		
7					#DIV/0!		
8							
9	**Calculate mg/ml from Molarity**						
10		MW (g/mol)	Molarity (mol/l)	mg/ml			
11				0			
12							
13	**Mixing of solutions:**						
14		mol/l	mol/l	parts			
15	Solution 1	1000		100	parts solution 1	0.1111	1
16	wanted		100				
17	Solution 2	0		900	parts solution 2	1	9

By typing the equation sign [Shift =] in a cell, you enter the equation mode

- ➢you can perform all different kinds of calculations:
- ➢simple ones: with the mathematical operands (by clicking into the respective fields)
- ➢more complex ones by activating the *fx* button (or the field showing the functions used lately)

Working with Excel: Calculations



=AVERAGE(C3:C6)

C	D
0	Monday
0.2	Tuesday
0.4	Wednesday
0.6	Thursday
0.3	3:C6)

Function Arguments

AVERAGE

Number1 C3:C6 = {0;0.2;0.4;0.6}

Number2 = number

= 0.3

Returns the average (arithmetic mean) of its arguments, which can be numbers or names, arrays, that contain numbers.

Number1: number1;number2;... are 1 to 255 numeric arguments for the average.

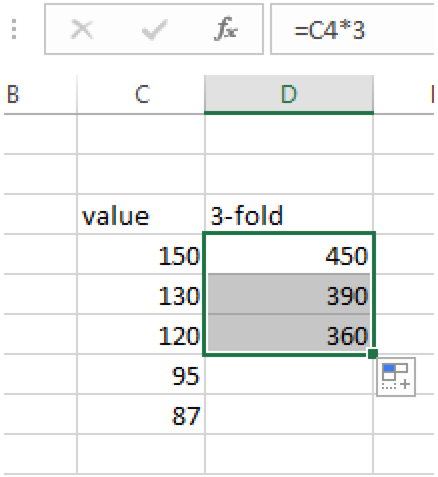
Formula result = 0.3

Help on this function

By typing the equation sign [Shift =] in a cell, you enter the equation mode

- ➢you can perform all different kinds of calculations:
- ➢simple ones: with the mathematical operands (by clicking into the respective fields)
- ➢more complex ones by activating the *fx* button (or the field showing the functions used lately)

Executing a calculation on a whole column

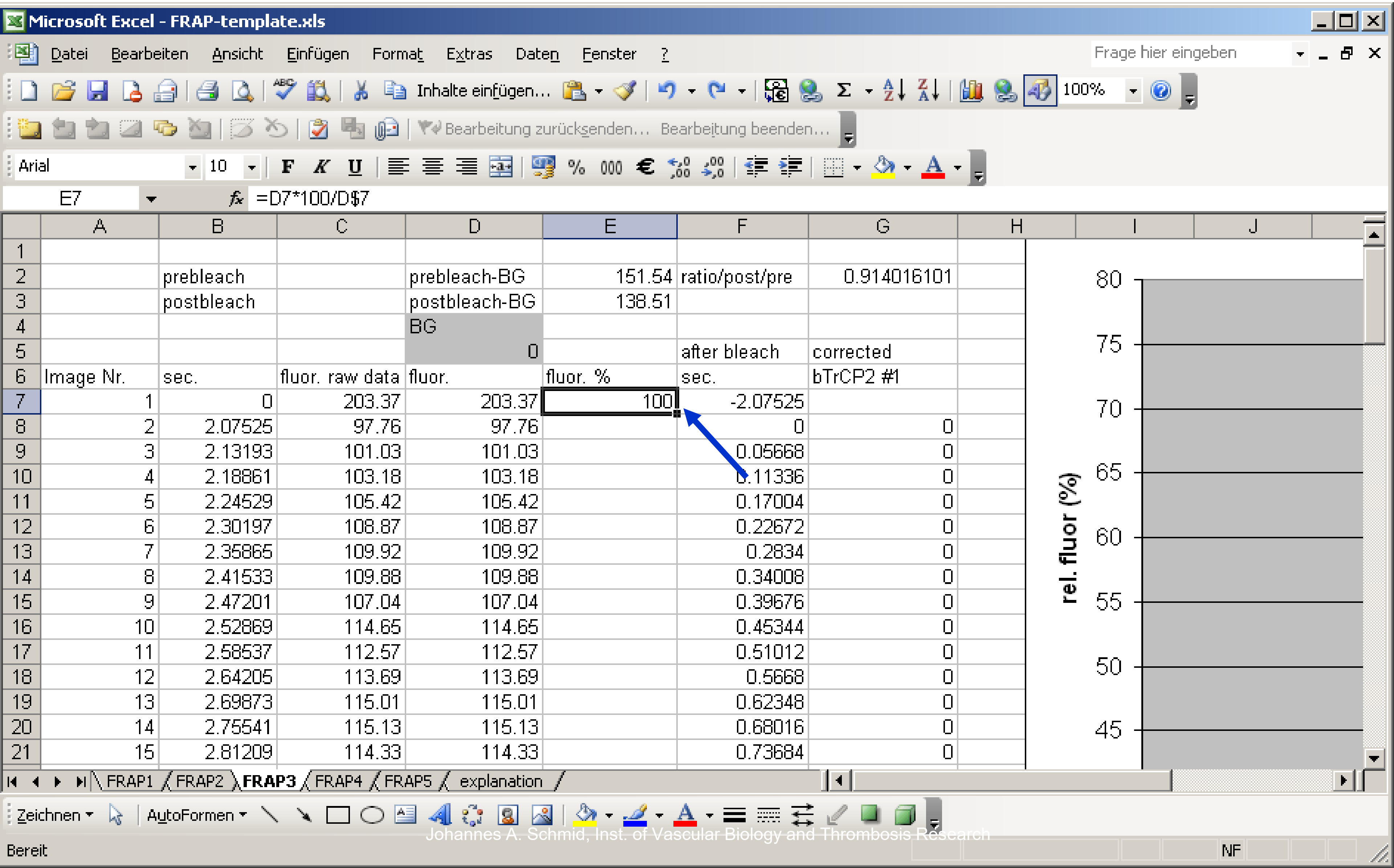


=C4*3

B	C	D
	value	3-fold
	150	450
	130	390
	120	360
	95	
	87	

- Grabbing a calculation cell at the bottom right corner and dragging it down, executes the calculation based on the cells next to that column
- double clicking onto the bottom right corner of the cell with the equation, performs the calculation for the whole column (even if it‘s very long!)
  (the cursor changes its shape to a thin cross, when it is at that corner)

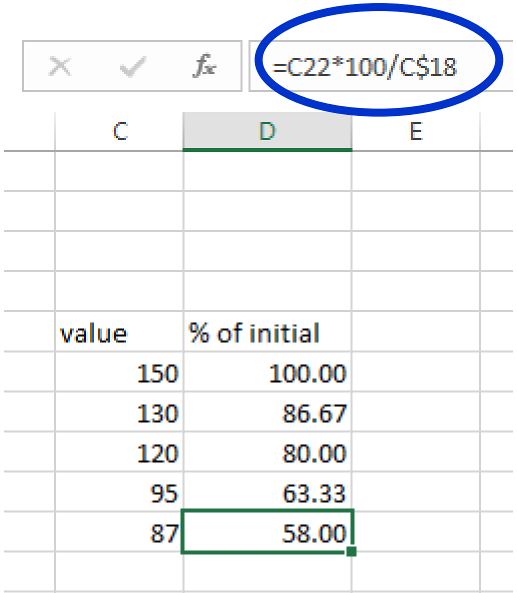
If you want to calculate a long column double click onto the lower right corner of the cell with the equation



E7 =D7*100/D$7

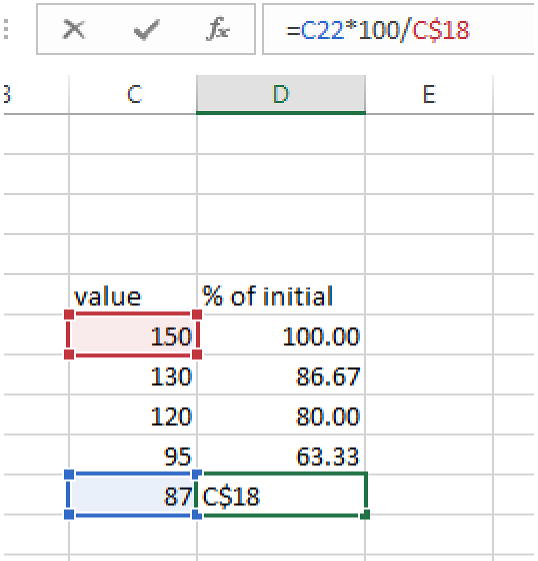
	A	B	C	D	E	F	G
1							
2		prebleach		prebleach-BG	151.54	ratio/post/pre	0.914016101
3		postbleach		postbleach-BG	138.51		
4				BG			
5				0		after bleach	corrected
6	Image Nr.	sec.	fluor. raw data	fluor.	fluor. %	sec.	bTrCP2 #1
7	1	0	203.37	203.37	100	-2.07525	
8	2	2.07525	97.76	97.76		0	0
9	3	2.13193	101.03	101.03		0.05668	0
10	4	2.18861	103.18	103.18		0.11336	0
11	5	2.24529	105.42	105.42		0.17004	0
12	6	2.30197	108.87	108.87		0.22672	0
13	7	2.35865	109.92	109.92		0.2834	0
14	8	2.41533	109.88	109.88		0.34008	0
15	9	2.47201	107.04	107.04		0.39676	0
16	10	2.52869	114.65	114.65		0.45344	0
17	11	2.58537	112.57	112.57		0.51012	0
18	12	2.64205	113.69	113.69		0.5668	0
19	13	2.69873	115.01	115.01		0.62348	0
20	14	2.75541	115.13	115.13		0.68016	0
21	15	2.81209	114.33	114.33		0.73684	0

Tricks: If you want to keep a field constant in an equation: type a „$“ in between column-letter and row-number



=C22*100/C$18

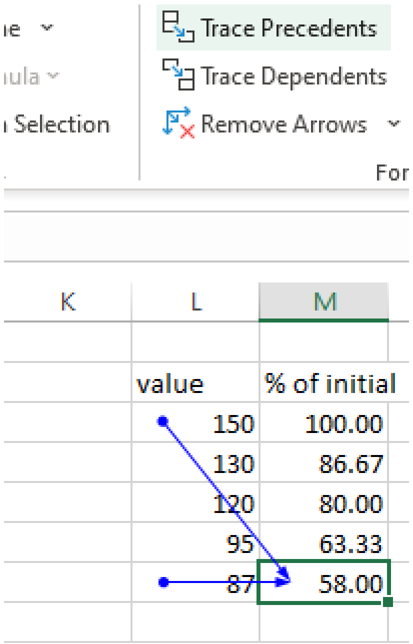
value	% of initial
150	100.00
130	86.67
120	80.00
95	63.33
87	58.00



=C22*100/C$18

value	% of initial
150	100.00
130	86.67
120	80.00
95	63.33
87	C$18

- clicking into an equation shows the cells that are used for it



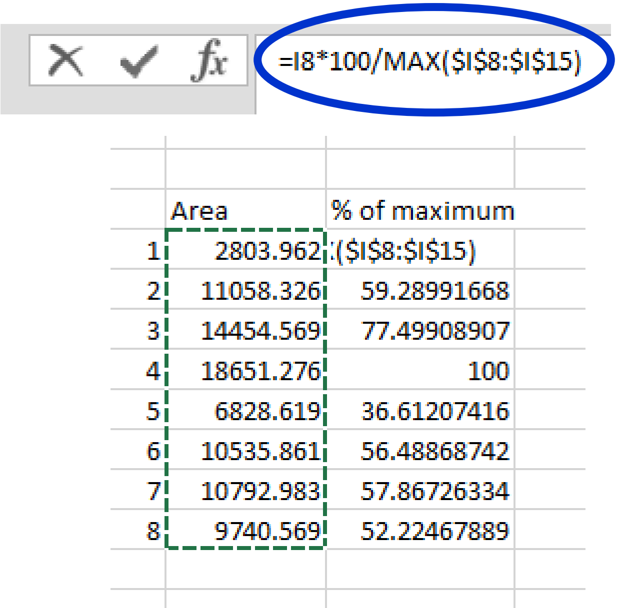
value	% of initial
150	100.00
130	86.67
120	80.00
95	63.33
87	58.00

- Formulas > Trace precedents: shows equation traces

Tricks: If you want to keep a field constant in an equation:

You can also mark the cell (or the range) and press F4

It will automatically add the $-signs correctly



=I8*100/MAX($I$8:$I$15)

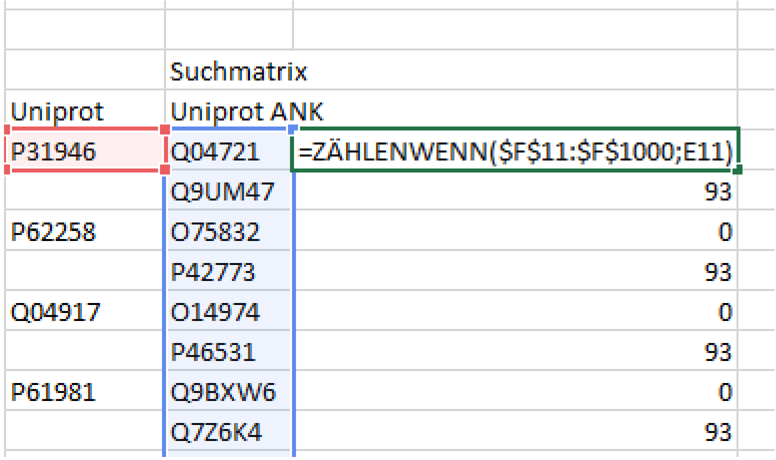
	Area	% of maximum
1	2803.962	($I$8:$I$15)
2	11058.326	59.28991668
3	14454.569	77.49908907
4	18651.276	100
5	6828.619	36.61207416
6	10535.861	56.48868742
7	10792.983	57.86726334
8	9740.569	52.22467889

Checking whether a cell is contained in another column (somewhere)

=ZÄHLENWENN($F$11:$F$1000;E11)

ENGLISH: „COUNTIF ($F$11:$F$1000;E11)

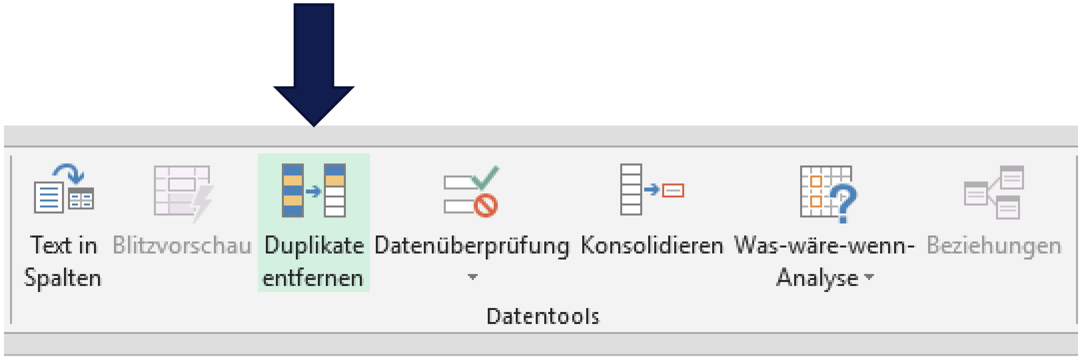
range to compare; specific cell



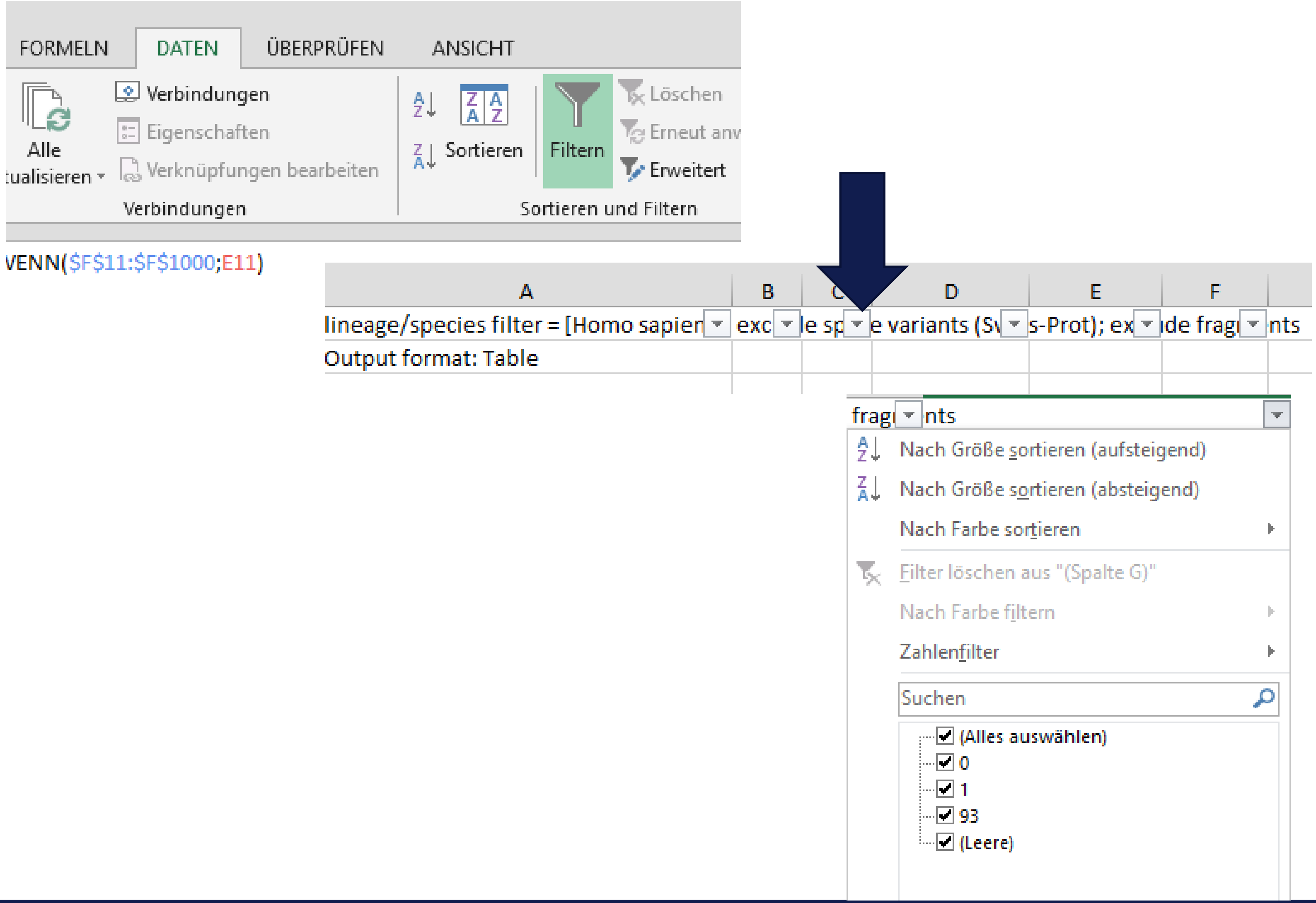
	Suchmatrix	
Uniprot	Uniprot ANK	
P31946	Q04721	=ZÄHLENWENN($F$11:$F$1000;E11)
	Q9UM47	93
P62258	O75832	0
	P42773	93
Q04917	O14974	0
	P46531	93
P61981	Q9BXW6	0
	Q7Z6K4	93

Removing of duplicate rows

- Select the range (or the whole sheet)
- In the data tools tab: click on „Remove duplicates“



Filtering of sheets



VENN($F$11:$F$1000;E11)

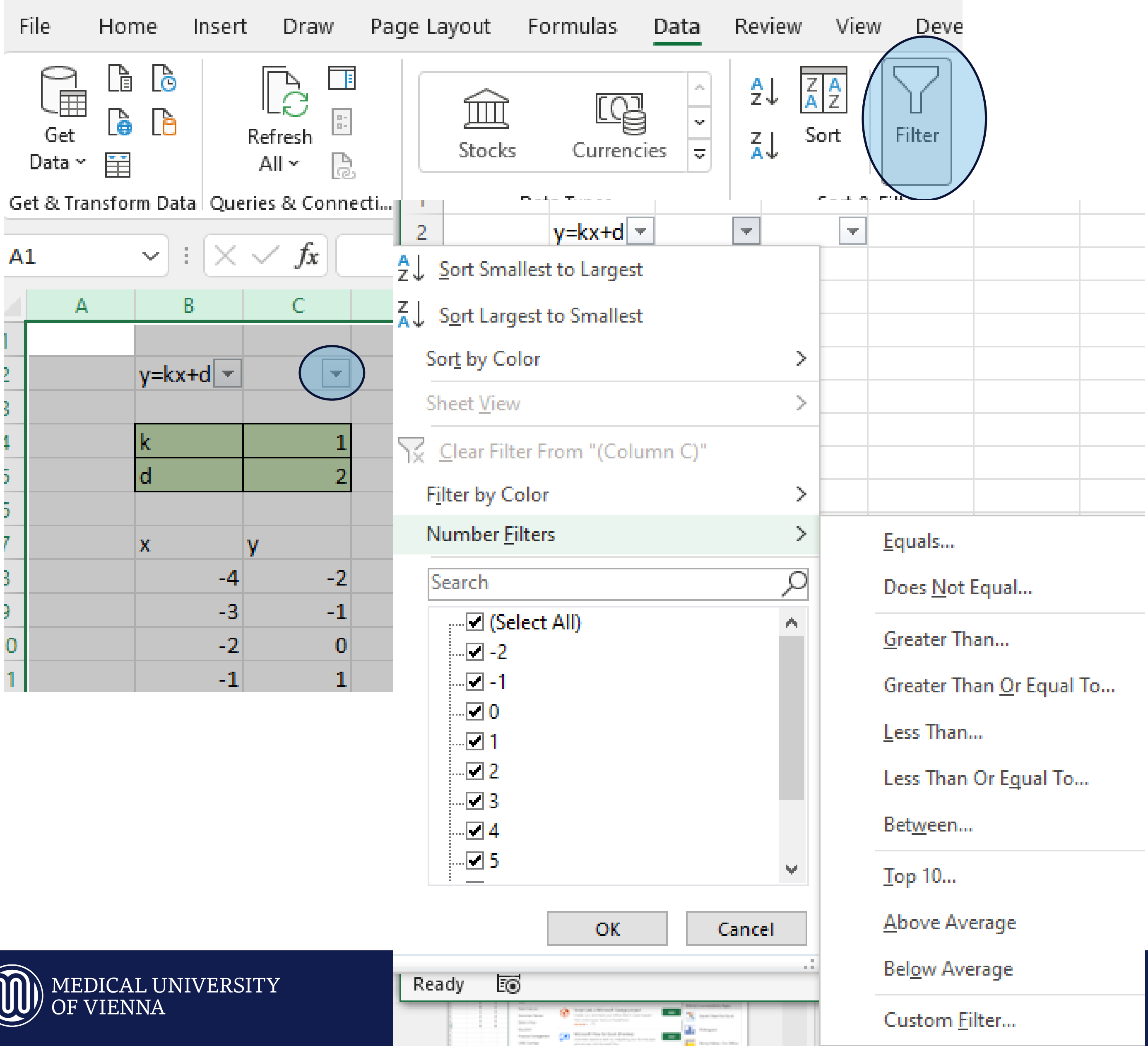
lineage/species filter = [Homo sapien exc le sp e variants (Sw s-Prot); ex ide frag nts

Output format: Table

frag nts

☑ (Alles auswählen)
☑ 0
☑ 1
☑ 93
☑ (Leere)

Filtering functions

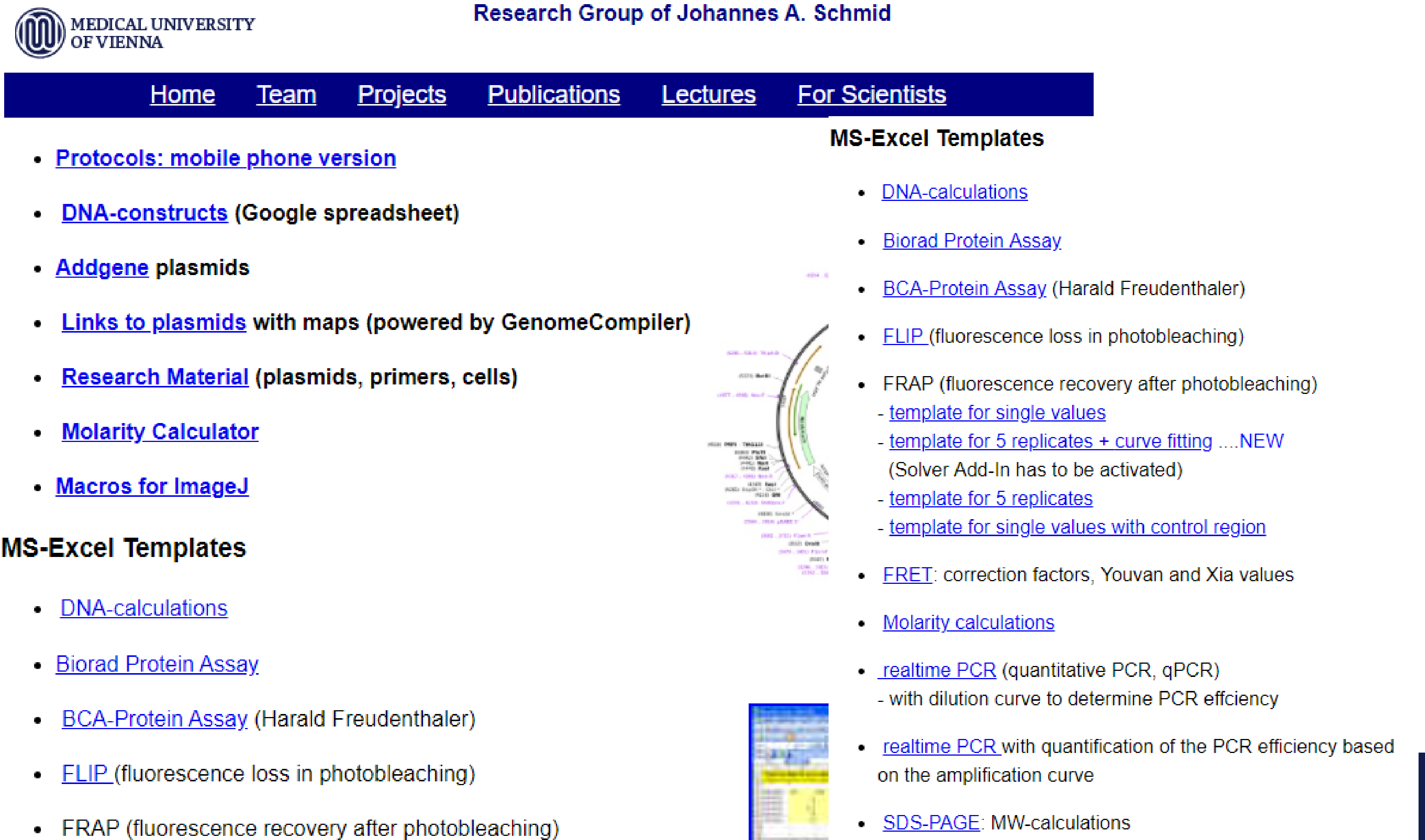


	A	B	C
1			
2		y=kx+d	
3			
4		k	1
5		d	2
6			
7		x	y
8		-4	-2
9		-3	-1
10		-2	0
11		-1	1

☑ (Select All)
☑ -2
☑ -1
☑ 0
☑ 1
☑ 2
☑ 3
☑ 4
☑ 5

You can perform frequently used calculations by using predefined Excel sheets (as templates)

Excel-templates on my website (under „For Scientists"):
http://www.meduniwien.ac.at/user/johannes.schmid/tools.html



MEDICAL UNIVERSITY OF VIENNA

Research Group of Johannes A. Schmid

- **Protocols: mobile phone version**
- **DNA-constructs (Google spreadsheet)**
- **Addgene plasmids**
- **Links to plasmids with maps (powered by GenomeCompiler)**
- **Research Material (plasmids, primers, cells)**
- **Molarity Calculator**
- **Macros for ImageJ**

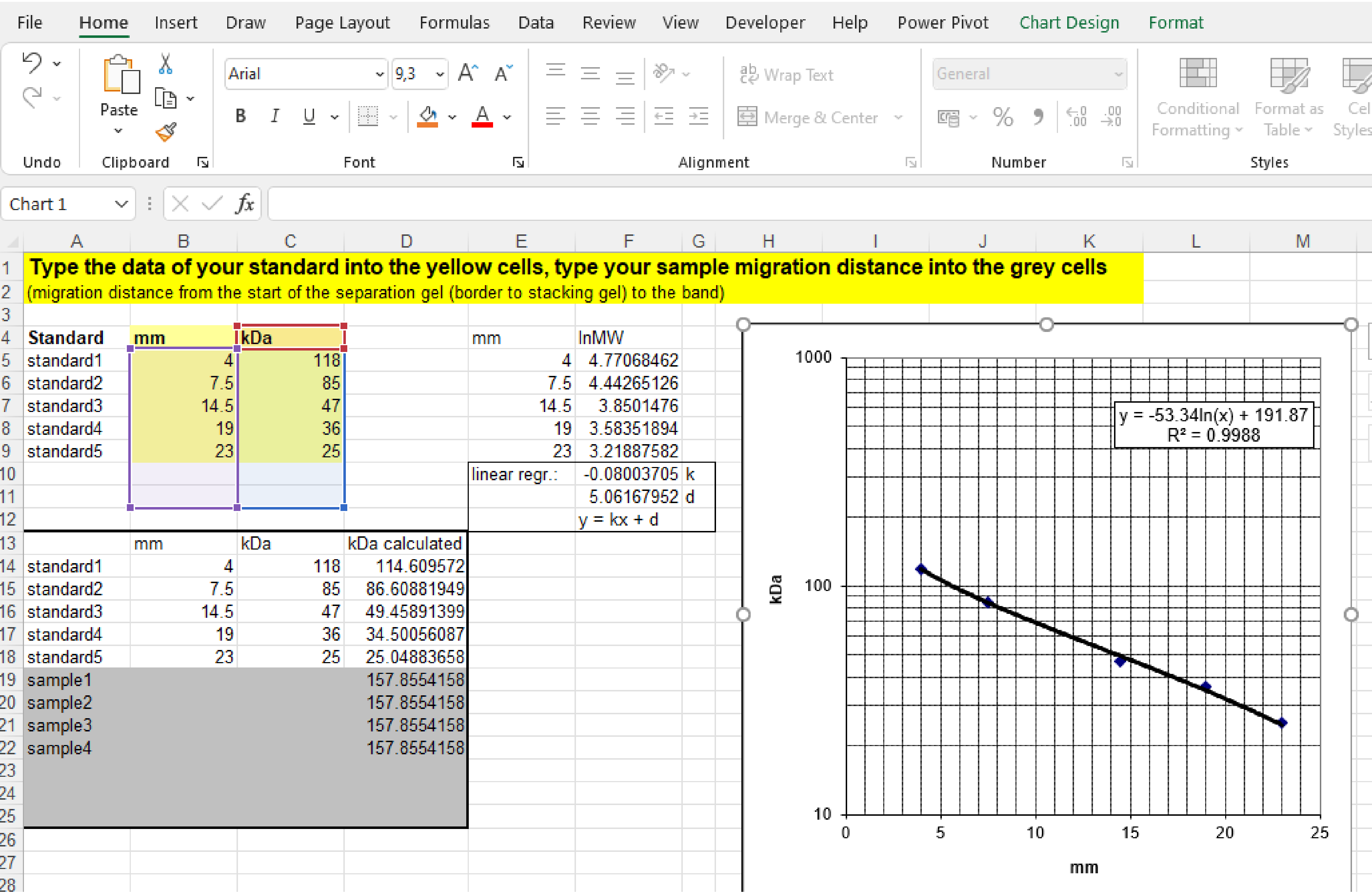
MS-Excel Templates

- DNA-calculations
- Biorad Protein Assay
- BCA-Protein Assay (Harald Freudenthaler)
- FLIP (fluorescence loss in photobleaching)
- FRAP (fluorescence recovery after photobleaching)

MS-Excel Templates

- DNA-calculations
- Biorad Protein Assay
- BCA-Protein Assay (Harald Freudenthaler)
- FLIP (fluorescence loss in photobleaching)
- FRAP (fluorescence recovery after photobleaching)

  - template for single values
  - template for 5 replicates + curve fitting ....NEW
    (Solver Add-In has to be activated)
  - template for 5 replicates
  - template for single values with control region
- FRET: correction factors, Youvan and Xia values
- Molarity calculations
- realtime PCR (quantitative PCR, qPCR)
  - with dilution curve to determine PCR effciency
- realtime PCR with quantification of the PCR efficiency based on the amplification curve
- SDS-PAGE: MW-calculations



Type the data of your standard into the yellow cells, type your sample migration distance into the grey cells

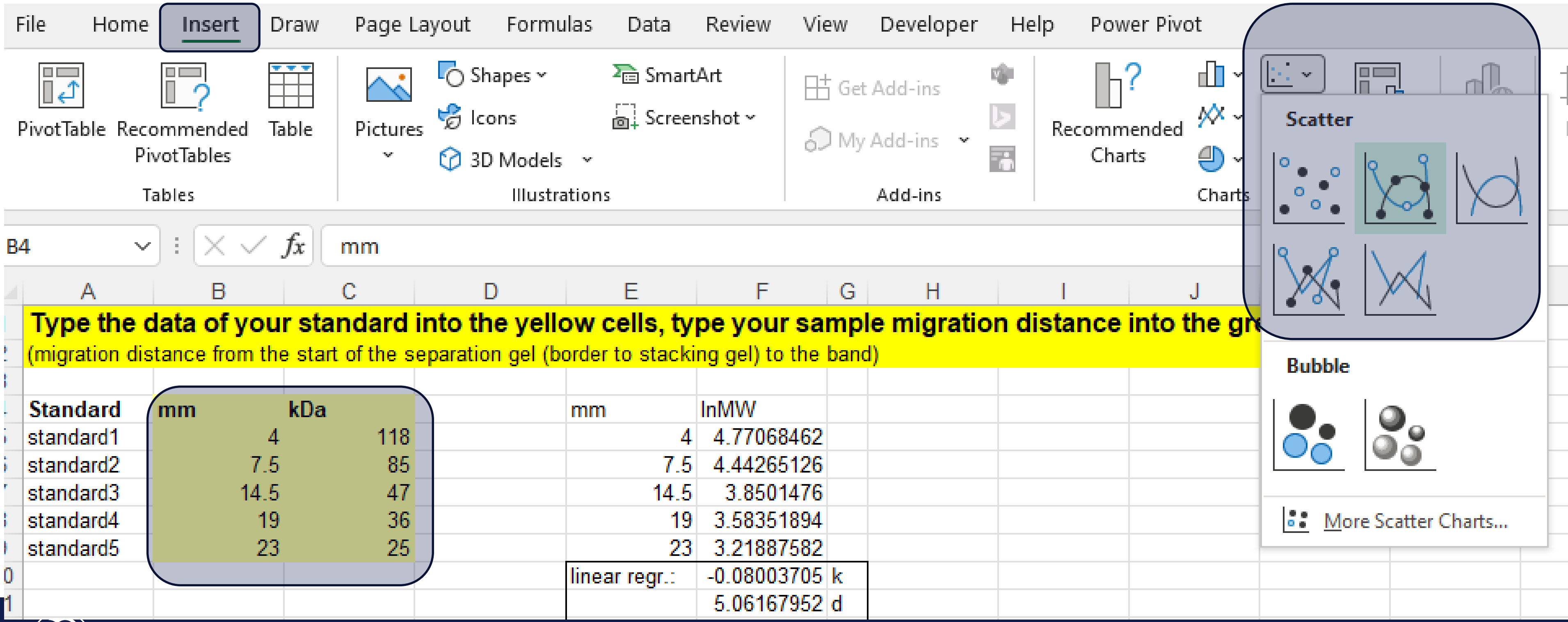
(migration distance from the start of the separation gel (border to stacking gel) to the band)

	A	B	C	D	E	F	G
4	**Standard**	**mm**	**kDa**		mm	lnMW	
5	standard1	4	118		4	4.77068462	
6	standard2	7.5	85		7.5	4.44265126	
7	standard3	14.5	47		14.5	3.8501476	
8	standard4	19	36		19	3.58351894	
9	standard5	23	25		23	3.21887582	
10					linear regr.:	-0.08003705	k
11						5.06167952	d
12						y = kx + d	
13		mm	kDa	kDa calculated			
14	standard1	4	118	114.609572			
15	standard2	7.5	85	86.60881949			
16	standard3	14.5	47	49.45891399			
17	standard4	19	36	34.50056087			
18	standard5	23	25	25.04883658			
19	sample1			157.8554158			
20	sample2			157.8554158			
21	sample3			157.8554158			
22	sample4			157.8554158			

y = -53.34ln(x) + 191.87
R² = 0.9988

Working with Excel-Graphs

- Highlight a certain cell area
  - press „Strg“ or „Ctrl“ if you want to activate separate areas
  - include the title row (if you want an appropriate legend)
- click the Insert tab and the desired graph type
  - note: don‘t use the „Line“ type if you want to generate a normal x/y-graph, but the „scatter“ type with connecting line („Line“ type generates equal x-axis distances regardless of the data)



Type the data of your standard into the yellow cells, type your sample migration distance into the gr

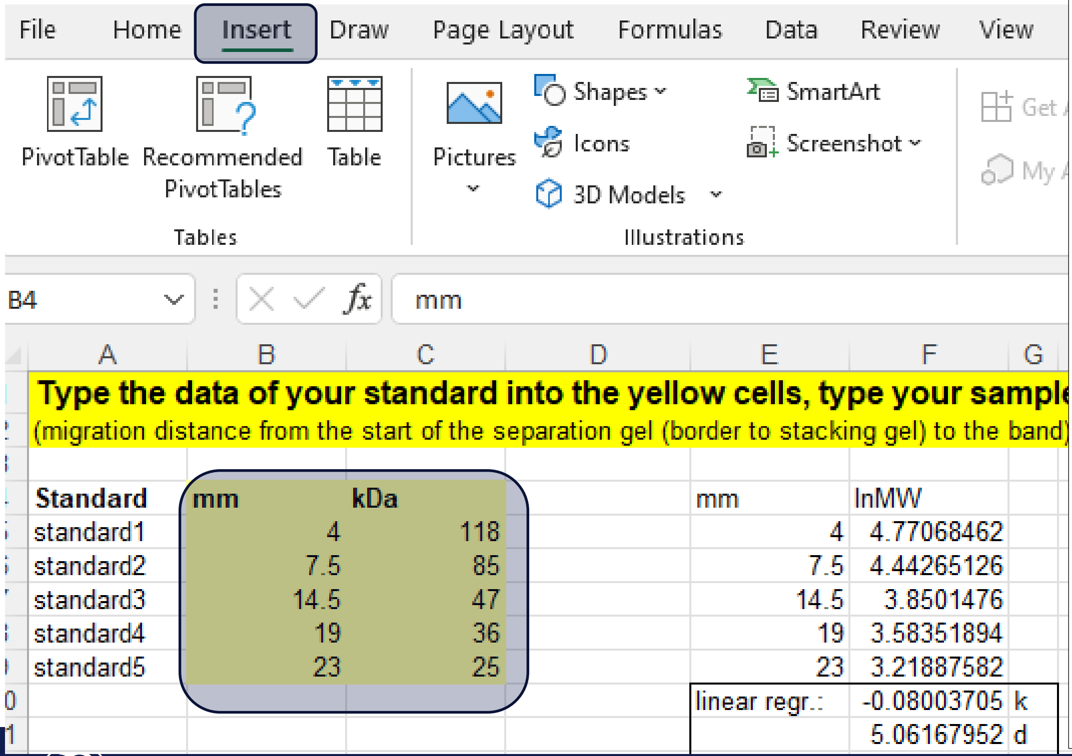
(migration distance from the start of the separation gel (border to stacking gel) to the band)

Standard	mm	kDa		mm	lnMW	
standard1	4	118		4	4.77068462	
standard2	7.5	85		7.5	4.44265126	
standard3	14.5	47		14.5	3.8501476	
standard4	19	36		19	3.58351894	
standard5	23	25		23	3.21887582	
				linear regr.:	-0.08003705	k
					5.06167952	d

Working with Excel-Graphs

- Highlight a certain cell area
  - press „Strg“ or „Ctrl“ if you want to activate separate areas
  - include the title row (if you want an appropriate legend)

- click the Insert tab and the desired graph type
  - note: don‘t use the „Line“ type if you want to generate a normal x/y-graph, but the „scatter“ type with connecting line („Line“ type generates equal x-axis distances regardless of the data)

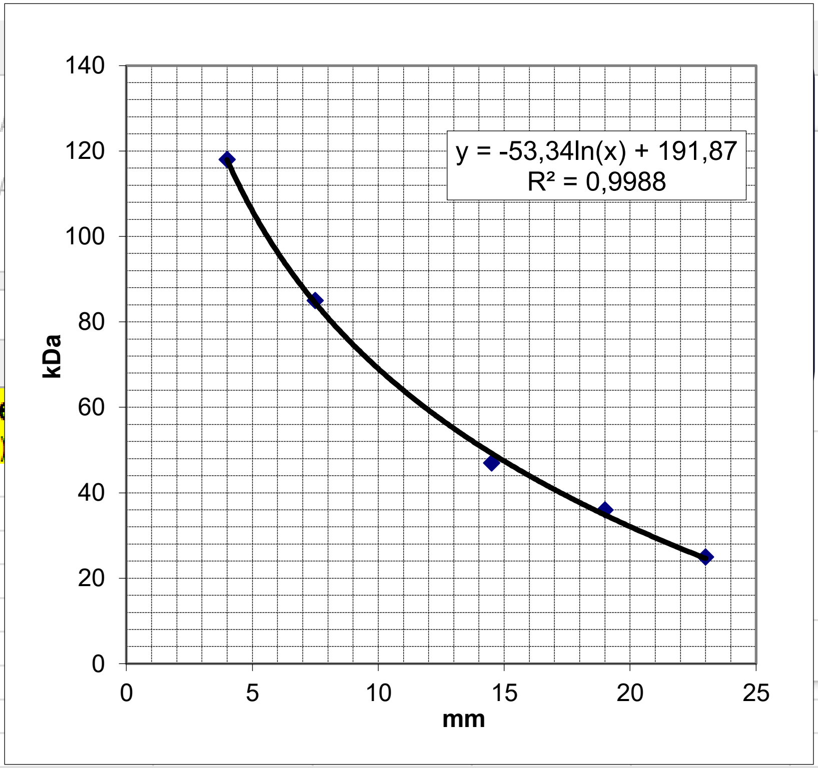


B4 mm

Type the data of your standard into the yellow cells, type your sample

(migration distance from the start of the separation gel (border to stacking gel) to the band)

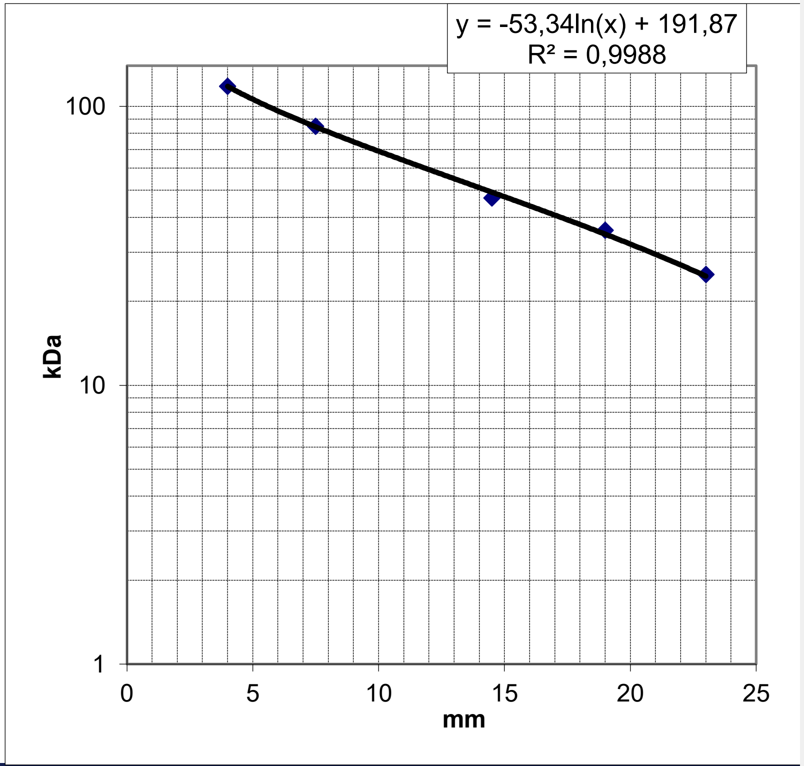
Standard	mm	kDa		mm	lnMW	
standard1	4	118		4	4.77068462	
standard2	7.5	85		7.5	4.44265126	
standard3	14.5	47		14.5	3.8501476	
standard4	19	36		19	3.58351894	
standard5	23	25		23	3.21887582	
				linear regr.:	-0.08003705	k
					5.06167952	d

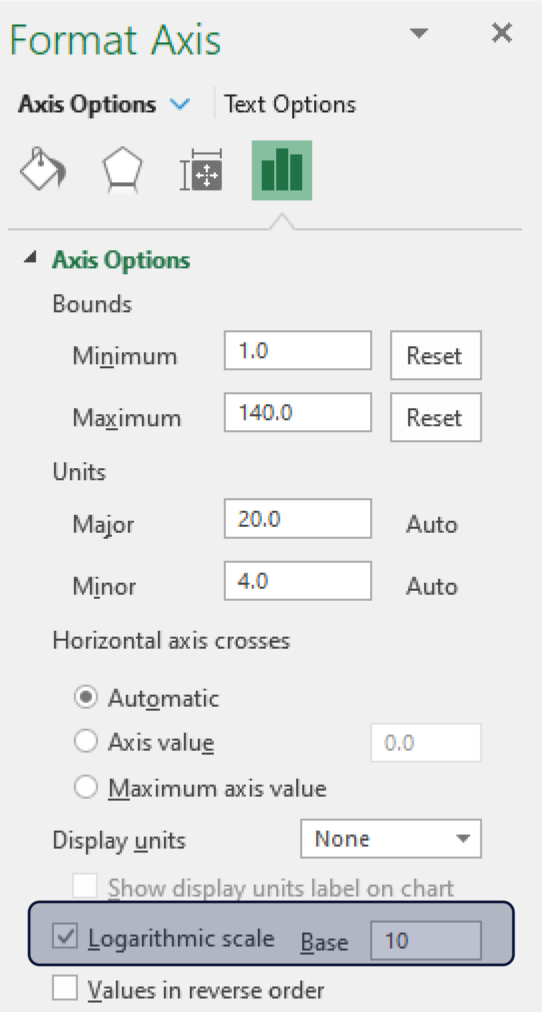


Working with Excel-Graphs

- Highlight a certain cell area
  - press „Strg“ or „Ctrl“ if you want to activate separate areas
  - include the title row (if you want an appropriate legend)
- click the Insert tab and the desired graph type
  - note: don‘t use the „Line“ type if you want to generate a normal x/y-g type with connecting line („Line“ type generates equal x-axis distances

Changes can be made by right-clicking or double clicking graph elements




Format Axis

Axis Options | Text Options

Axis Options

Bounds

Minimum 1.0 Reset

Maximum 140.0 Reset

Units

Major 20.0 Auto

Minor 4.0 Auto

Horizontal axis crosses

● Automatic

○ Axis value 0.0

○ Maximum axis value

Display units None

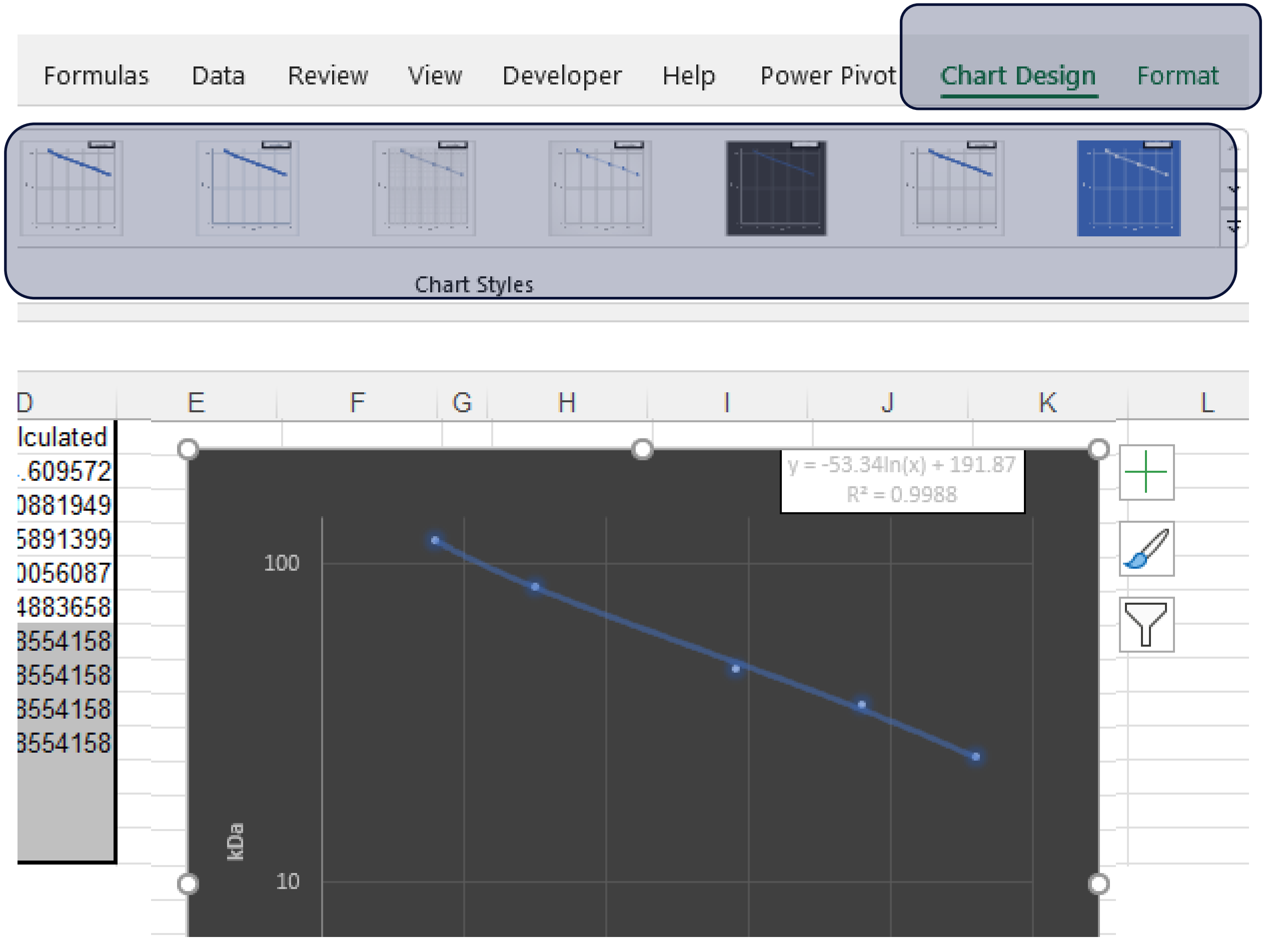
☐ Show display units label on chart

☑ Logarithmic scale Base 10

☐ Values in reverse order

Working with Excel-Graphs

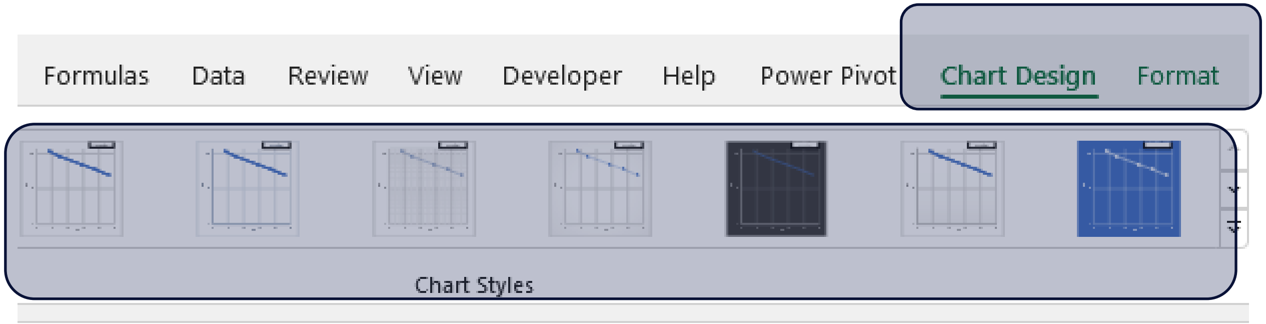
- Clicking on the graphs activates additional tabs
  (Chart Design, Format)
- Predesigned styles

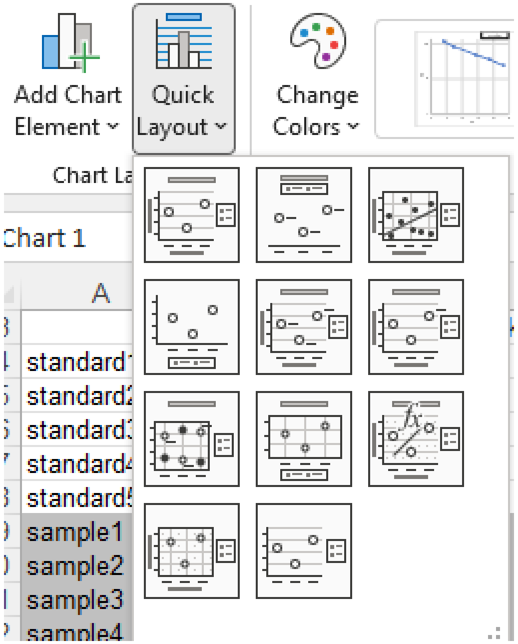


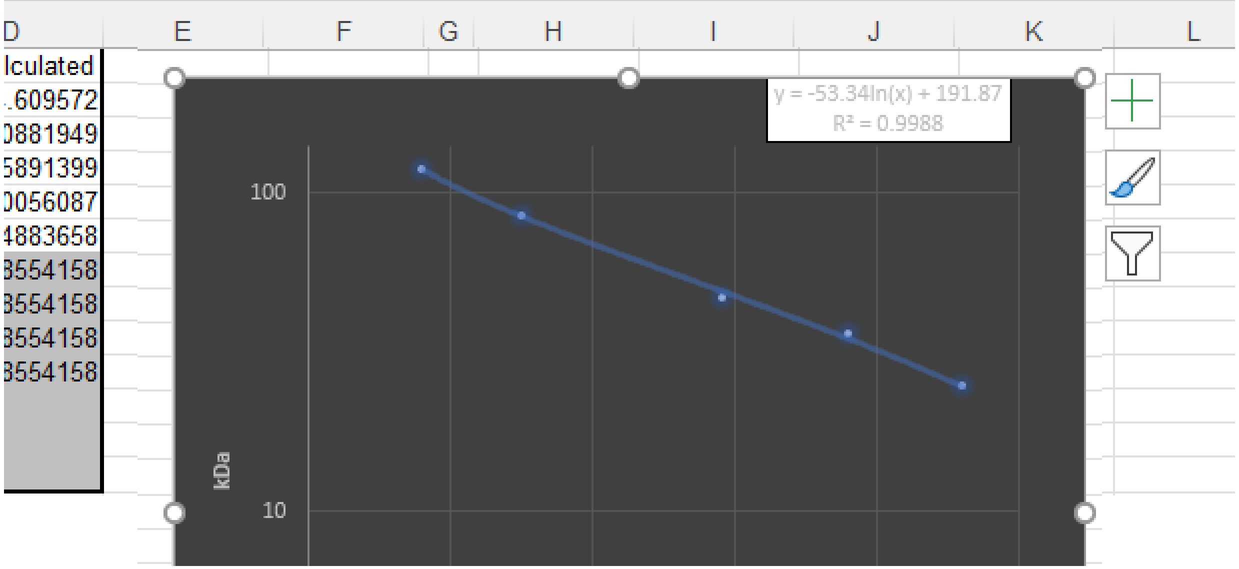
$y = -53.34\ln(x) + 191.87$
$R^2 = 0.9988$

Working with Excel-Graphs

- Quick Layout options.
  legends, titles… etc.

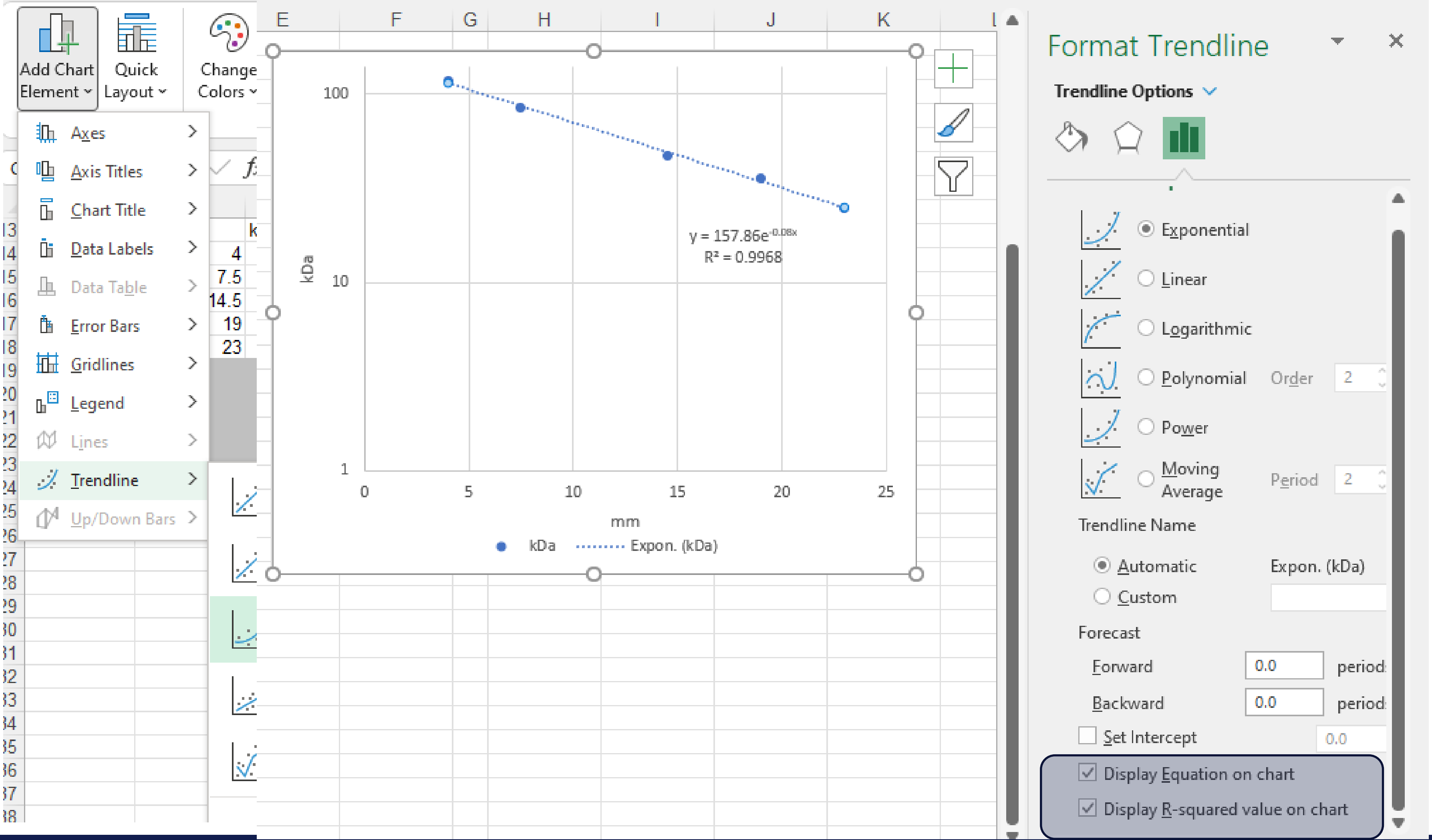






Working with Excel-Graphs

- Adding chart elements such as trendlines



$y = 157.86e^{-0.08x}$

$R^2 = 0.9968$

Format Trendline

● Exponential

○ Linear

○ Logarithmic

○ Polynomial Order 2

○ Power

○ Moving Average Period 2

Trendline Name

● Automatic Expon. (kDa)

○ Custom

Forecast

Forward 0.0 period

Backward 0.0 period

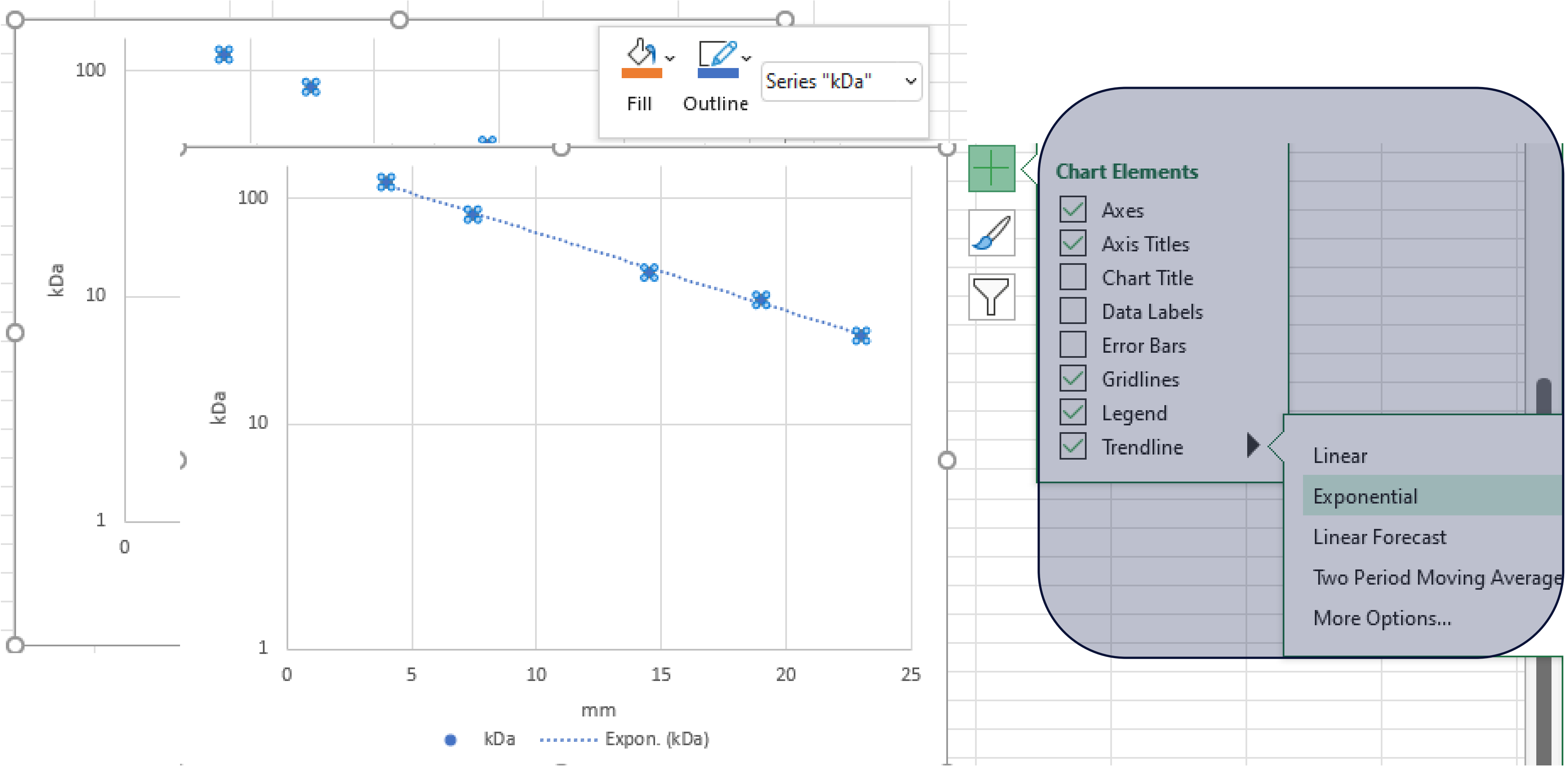
☐ Set Intercept 0.0

☑ Display Equation on chart

☑ Display R-squared value on chart

Working with Excel-Graphs

- Right-clicking on data points or clicking on the „+“ sign next to graphs allows adding a trendline, as well



Adding error bars

- Chart elements: Error bars
- Choose the last option (more options)

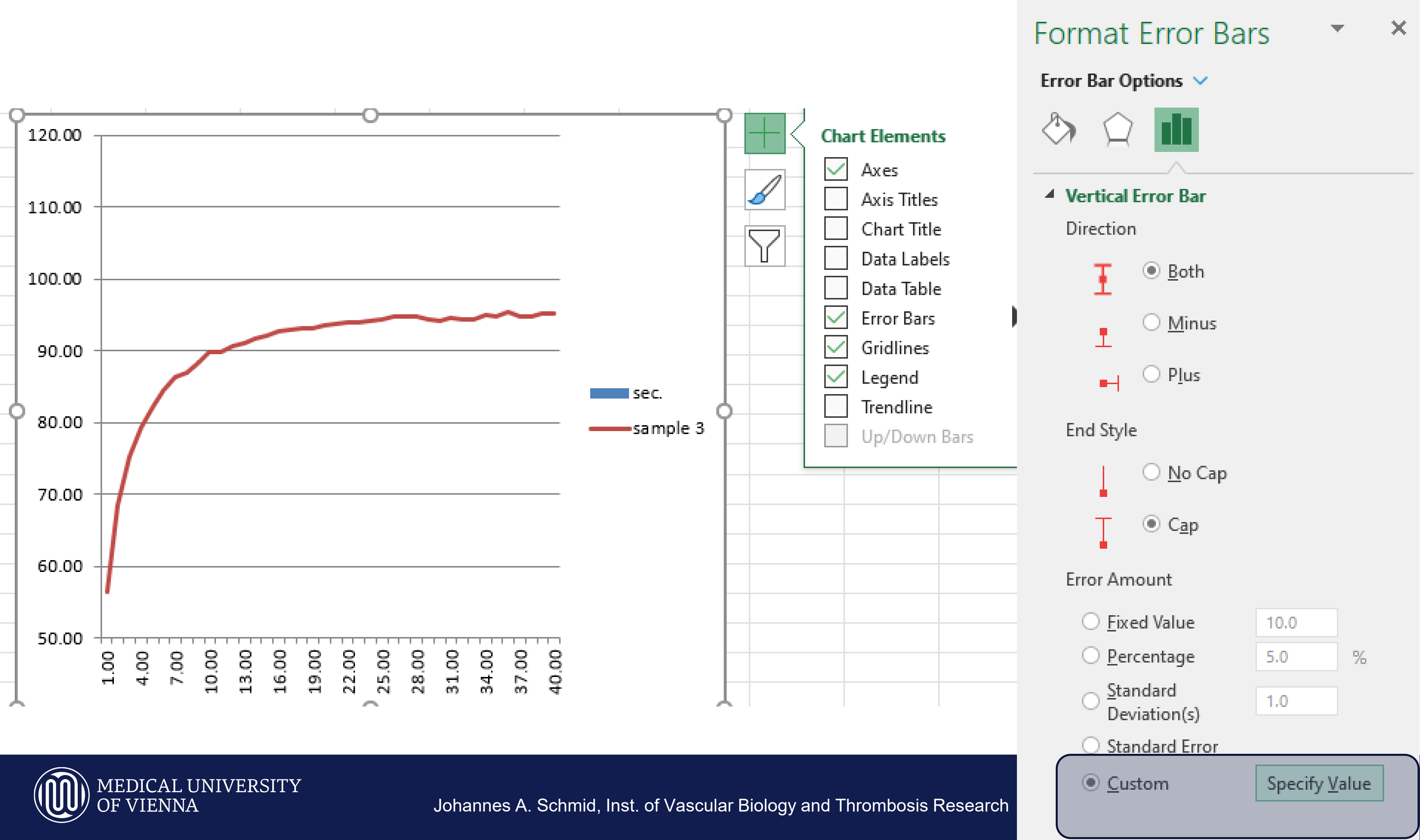


Chart Elements

- ☑ Axes
- ☐ Axis Titles
- ☐ Chart Title
- ☐ Data Labels
- ☐ Data Table
- ☑ Error Bars
- ☑ Gridlines
- ☑ Legend
- ☐ Trendline
- ☐ Up/Down Bars

Format Error Bars

Error Bar Options

Vertical Error Bar

Direction

- ● Both
- ○ Minus
- ○ Plus

End Style

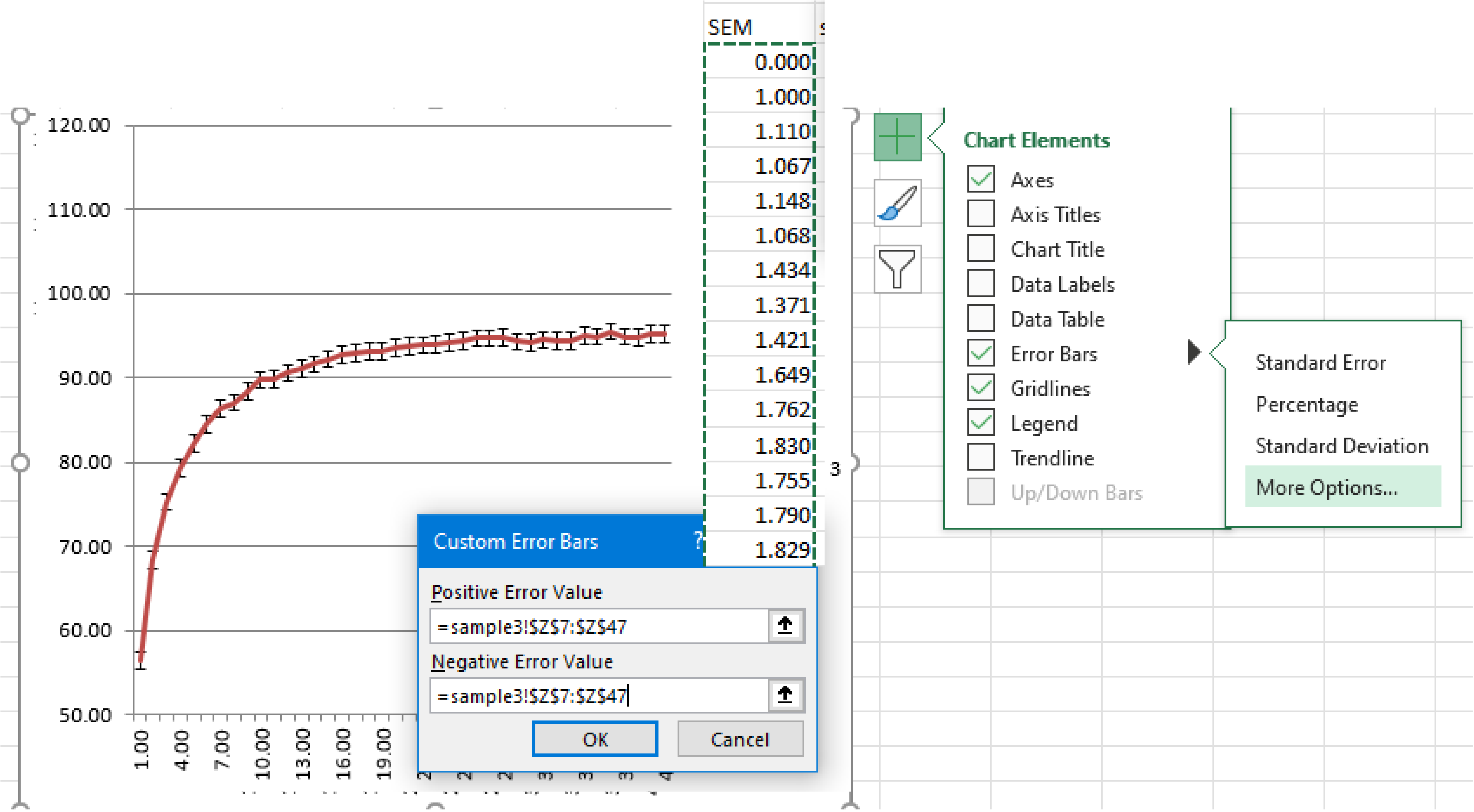
- ○ No Cap
- ● Cap

Error Amount

- ○ Fixed Value 10.0
- ○ Percentage 5.0 %
- ○ Standard Deviation(s) 1.0
- ○ Standard Error
- ● Custom Specify Value

Adding error bars

- Chart elements: Error bars
- Choose the last option (more options)
- Specify the column containing the error bars



SEM
0.000
1.000
1.110
1.067
1.148
1.068
1.434
1.371
1.421
1.649
1.762
1.830
1.755
1.790
1.829

Chart Elements

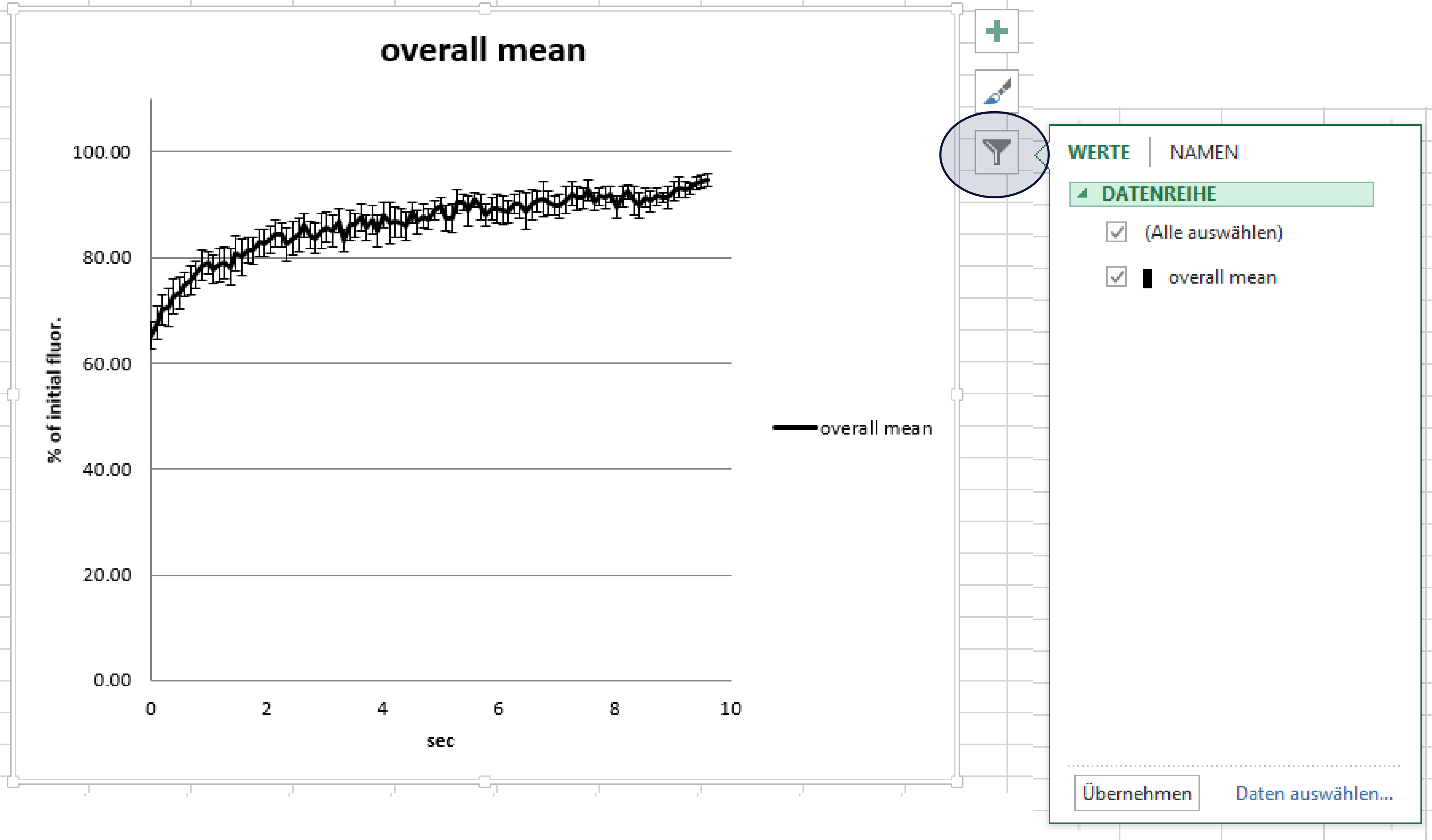
☑ Axes
☐ Axis Titles
☐ Chart Title
☐ Data Labels
☐ Data Table
☑ Error Bars
☑ Gridlines
☑ Legend
☐ Trendline
☐ Up/Down Bars

Custom Error Bars

Positive Error Value: =sample3!$Z$7:$Z$47

Negative Error Value: =sample3!$Z$7:$Z$47

Graph elements can be filtered

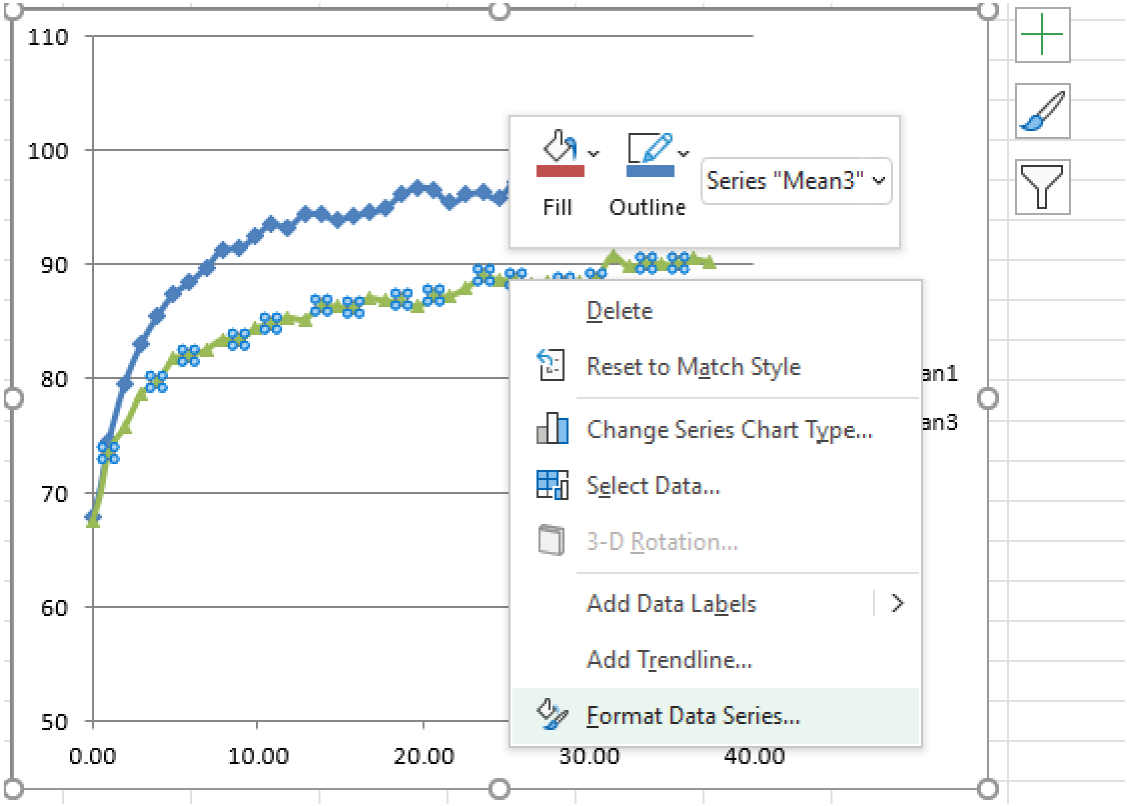


☑ (Alle auswählen)

☑ ▮ overall mean

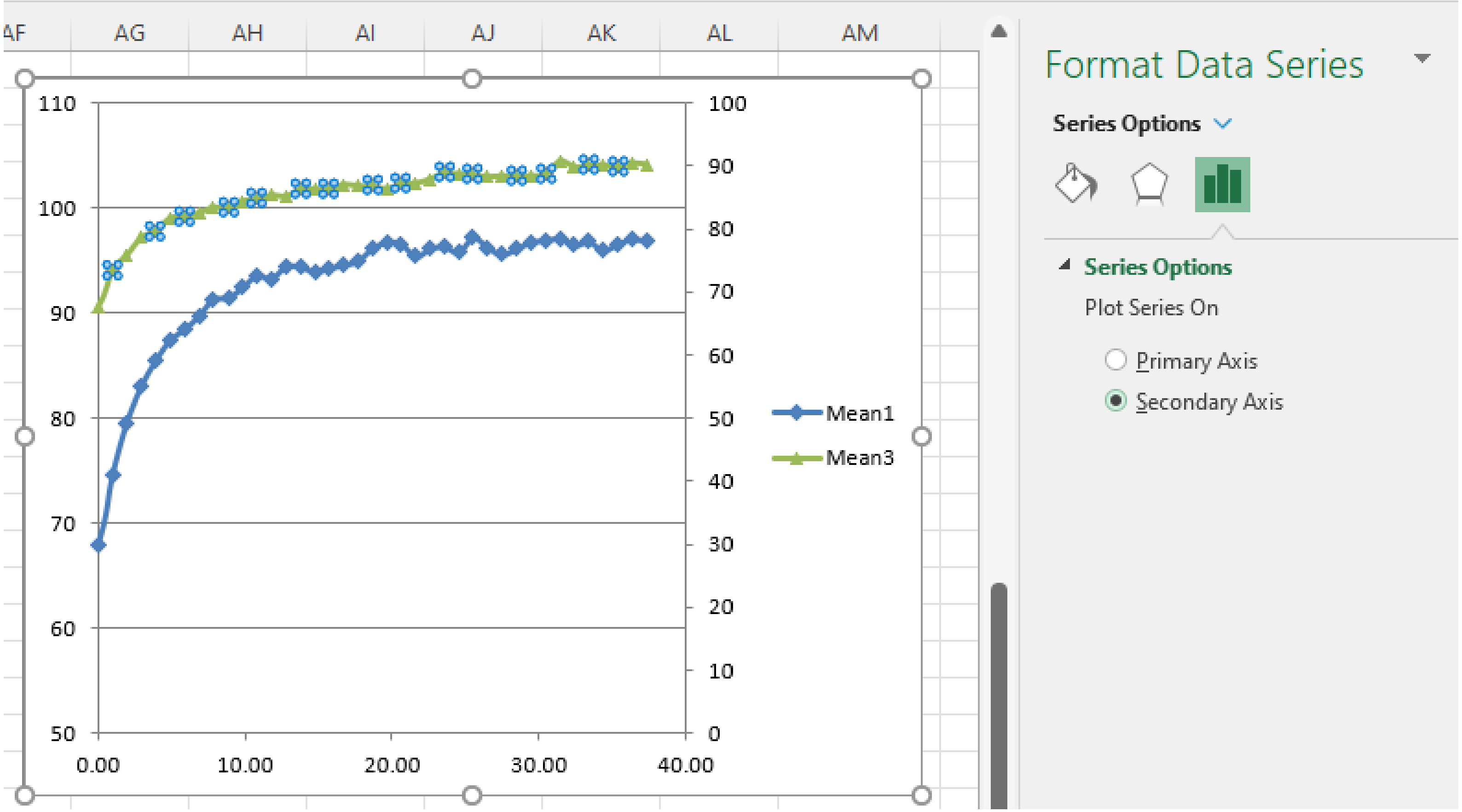
Generating graphs with two y-axes

- Right-click on a dataset > format data series



Generating graphs with two y-axes

- Right-click on a dataset > format data series
- Secondary Axis



Format Data Series

Series Options

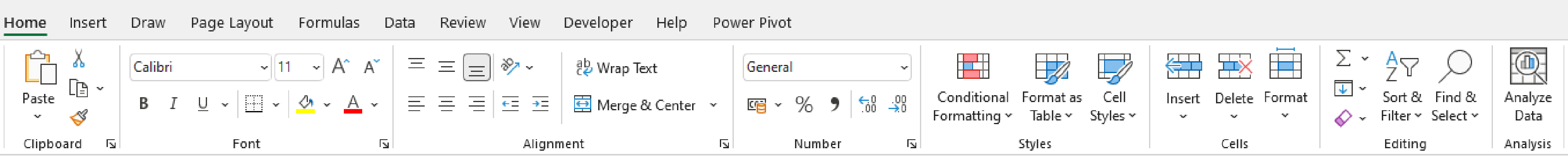
Series Options

Plot Series On

○ Primary Axis

● Secondary Axis

Tabs


Home
Insert
Draw
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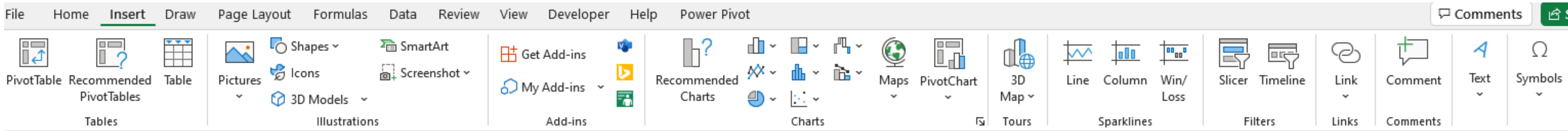
Data
Review
View
Developer
Help
Power Pivot
Paste
Calibri
11
B
I
U
Wrap Text
Merge & Center
General
%
Conditional Formatting
Format as Table
Cell Styles
Insert
Delete
Format
Sort & Filter
Find & Select
Analyze Data
Clipboard
Font
Alignment
Number
Styles
Cells
Editing
Analysis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Power Pivot
Comments
PivotTable
Recommended PivotTables
Table
Pictures
Shapes
Icons
3D Models
SmartArt
Screenshot
Get Add-ins
My Add-ins
Recommended Charts
Maps
PivotChart
3D Map
Line
Column
Win/ Loss
Slicer
Timeline
Link
Comment
Text
Symbols
Tables
Illustrations
Add-ins
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Tours
Sparklines
Filters
Links
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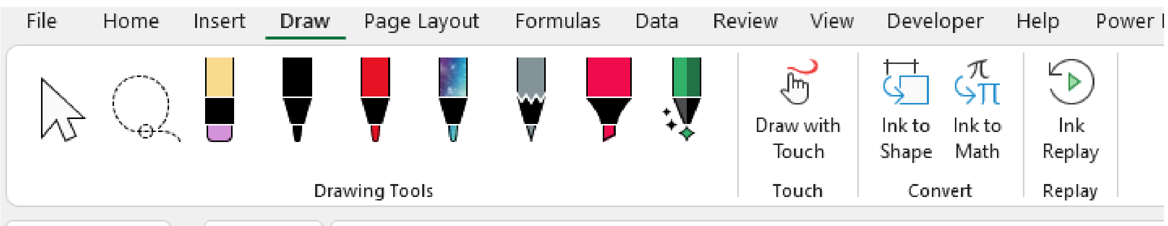
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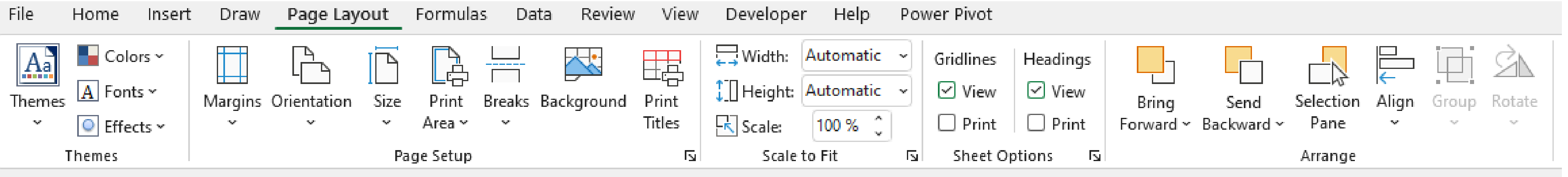
Ink to Shape
Ink to Math
Ink Replay
Drawing Tools
Touch
Convert
Replay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Orientation
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Breaks
Background
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Gridlines
☑ View
☐ Print
Headings
☑ View
☐ Print
Bring Forward
Send Backward
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Align
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Rotate
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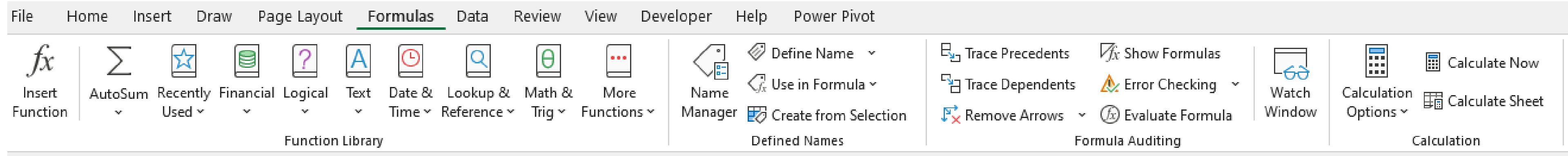
Page Setup
Scale to Fit
Sheet Options
Arrange


File
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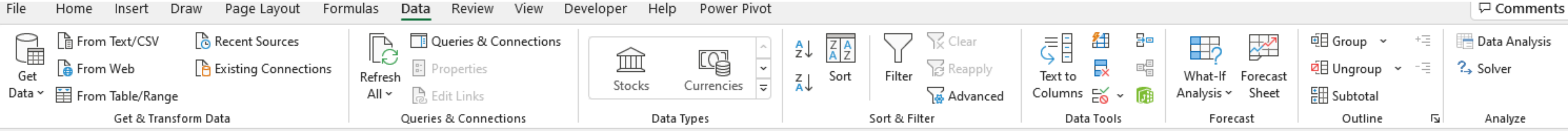
Date & Time
Lookup & Reference
Math & Trig
More Functions
Name Manager
Define Name
Use in Formula
Create from Selection
Trace Precedents
Trace Dependents
Remove Arrows
Show Formulas
Error Checking
Evaluate Formula
Watch Window
Calculation Options
Calculate Now
Calculate Sheet
Function Library
Defined Names
Formula Auditing
Calculation

Tabs


File
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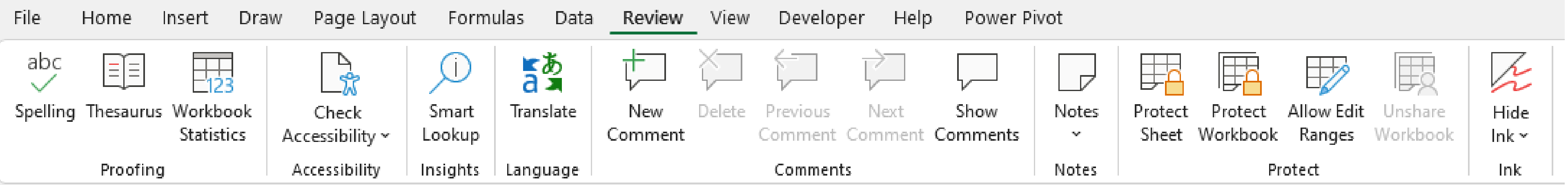
Power Pivot
Comments
Get Data
From Text/CSV
From Web
From Table/Range
Recent Sources
Existing Connections
Get & Transform Data
Refresh All
Queries & Connections
Properties
Edit Links
Queries & Connections
Stocks
Currencies
Data Types
Sort
Filter
Clear
Reapply
Advanced
Sort & Filter
Text to Columns
Data Tools
What-If Analysis
Forecast Sheet
Forecast
Group
Ungroup
Subtotal
Outline
Data Analysis
Solver
Analyze


File
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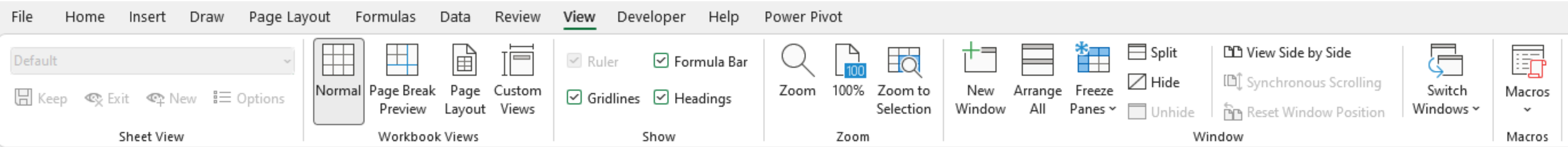
Help
Power Pivot
abc
Spelling
Thesaurus
Workbook Statistics
Proofing
Check Accessibility
Accessibility
Smart Lookup
Insights
Translate
Language
New Comment
Delete
Previous Comment
Next Comment
Show Comments
Comments
Notes
Notes
Protect Sheet
Protect Workbook
Allow Edit Ranges
Unshare Workbook
Protect
Hide Ink
Ink


File
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Power Pivot
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Keep
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Sheet View
Normal
Page Break Preview
Page Layout
Custom Views
Workbook Views
Ruler
Formula Bar
Gridlines
Headings
Show
Zoom
100%
Zoom to Selection
Zoom
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Freeze Panes
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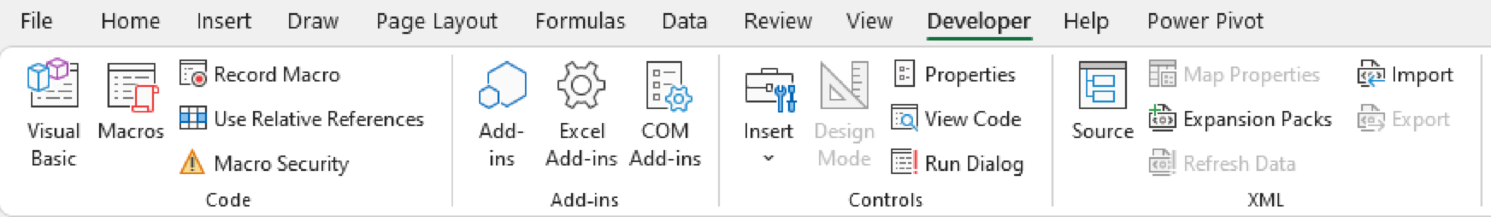
Reset Window Position
Switch Windows
Window
Macros
Macros


File
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Data
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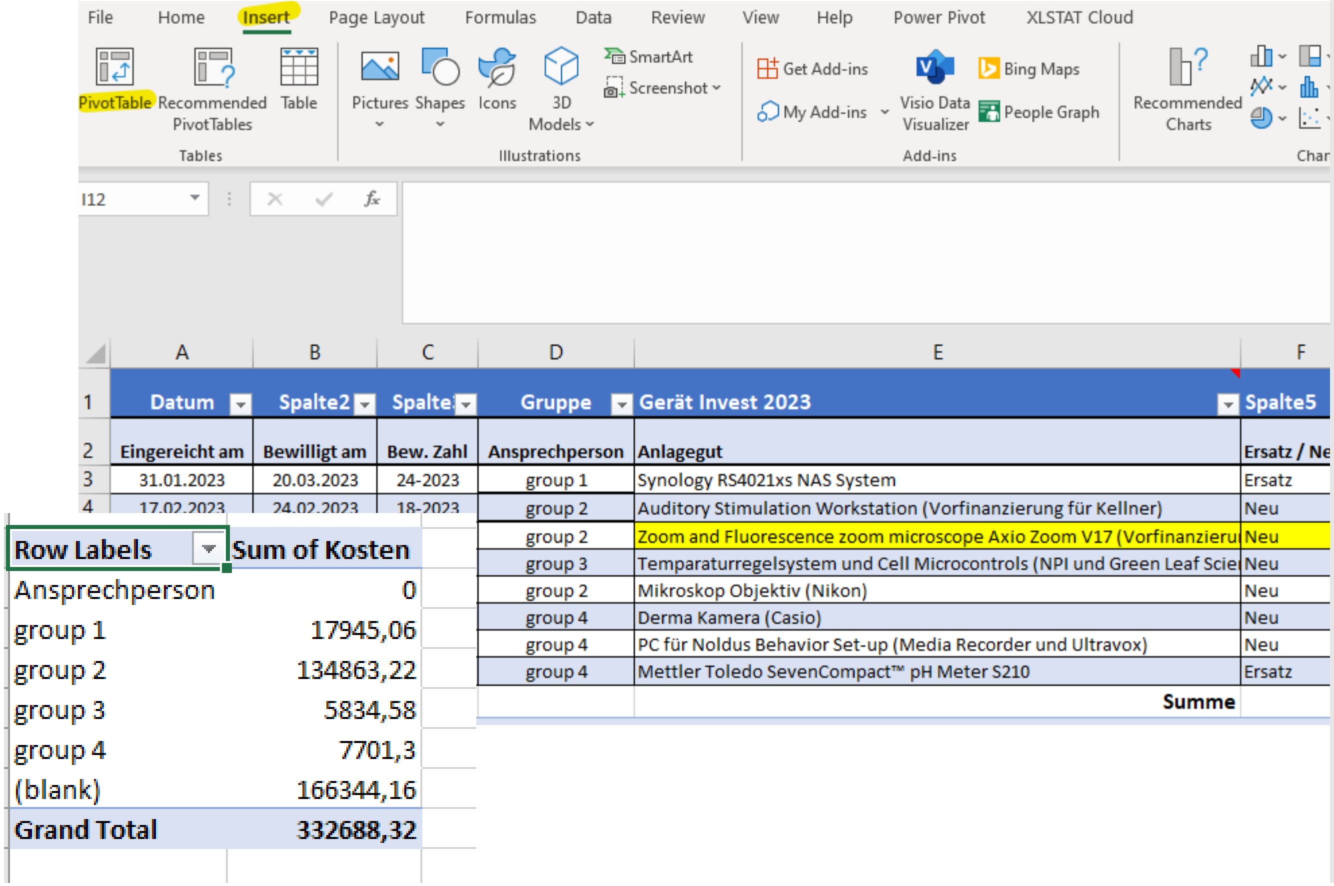
Developer
Help
Power Pivot
Visual Basic
Macros
Record Macro
Use Relative References
Macro Security
Code
Add-ins
Excel Add-ins
COM Add-ins
Add-ins
Insert
Design Mode
Properties
View Code
Run Dialog
Controls
Source
Map Properties
Expansion Packs
Refresh Data
Import
Export
XML

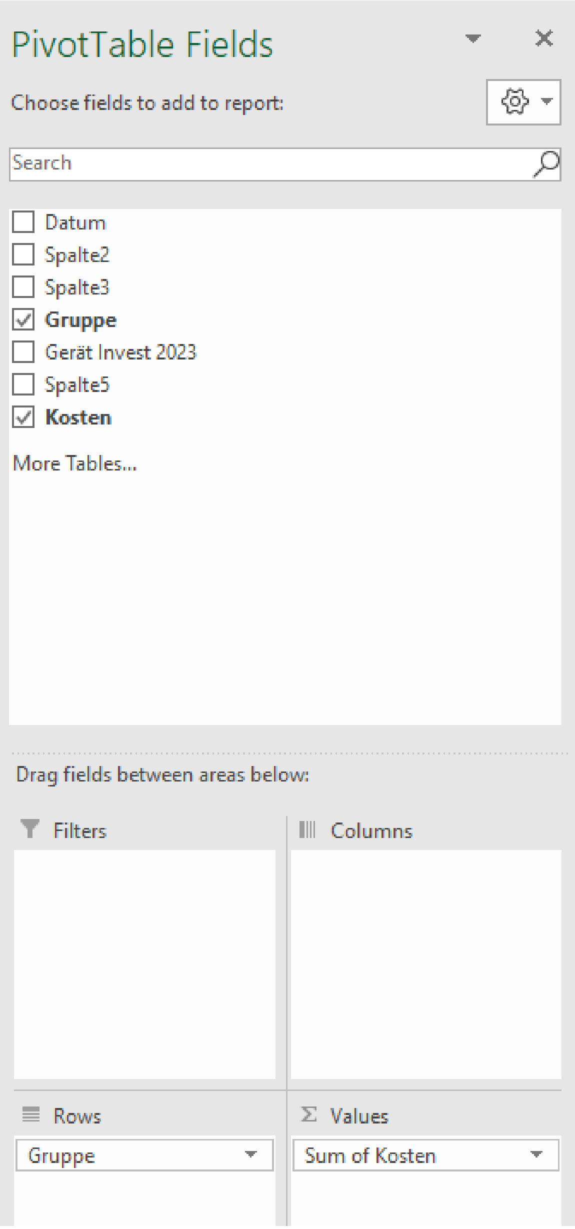
Excel Pivot Tables

- To summarize results…
- Mark table > insert PivotTable > define values to be includ



	A	B	C	D	E	F
1	Datum	Spalte2	Spalte	Gruppe	Gerät Invest 2023	Spalte5
2	Eingereicht am	Bewilligt am	Bew. Zahl	Ansprechperson	Anlagegut	Ersatz / Ne
3	31.01.2023	20.03.2023	24-2023	group 1	Synology RS4021xs NAS System	Ersatz
4	17.02.2023	24.02.2023	18-2023	group 2	Auditory Stimulation Workstation (Vorfinanzierung für Kellner)	Neu
				group 2	Zoom and Fluorescence zoom microscope Axio Zoom V17 (Vorfinanzieru	Neu
				group 3	Temparaturregelsystem und Cell Microcontrols (NPI und Green Leaf Scie	Neu
				group 2	Mikroskop Objektiv (Nikon)	Neu
				group 4	Derma Kamera (Casio)	Neu
				group 4	PC für Noldus Behavior Set-up (Media Recorder und Ultravox)	Neu
				group 4	Mettler Toledo SevenCompact™ pH Meter S210	Ersatz
					Summe	

Row Labels	Sum of Kosten
Ansprechperson	0
group 1	17945,06
group 2	134863,22
group 3	5834,58
group 4	7701,3
(blank)	166344,16
Grand Total	**332688,32**

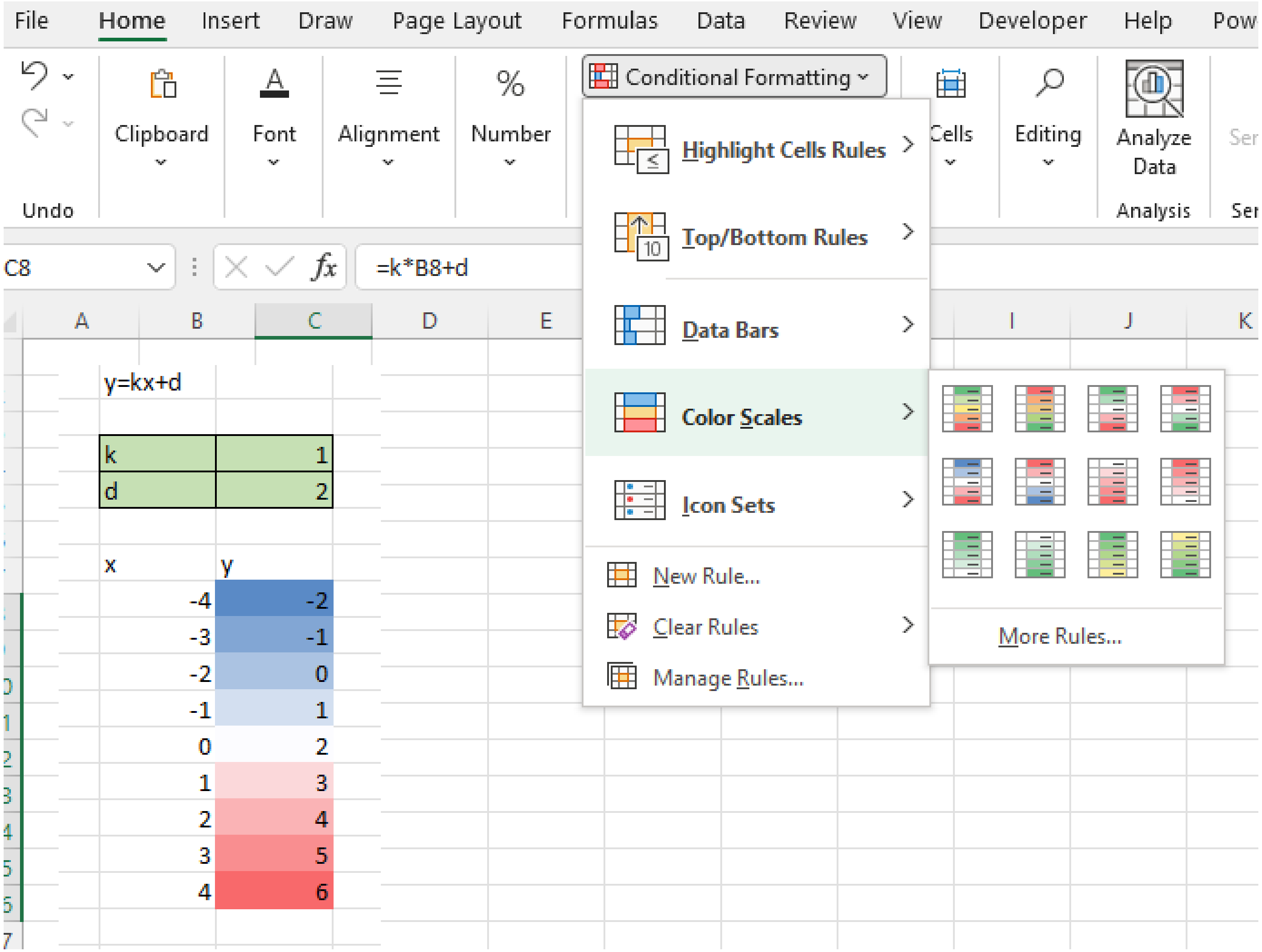


☐ Datum
☐ Spalte2
☐ Spalte3
☑ **Gruppe**
☐ Gerät Invest 2023
☐ Spalte5
☑ **Kosten**
More Tables...

Rows: Gruppe
Values: Sum of Kosten

Conditional formating of cells

Start-Tab >



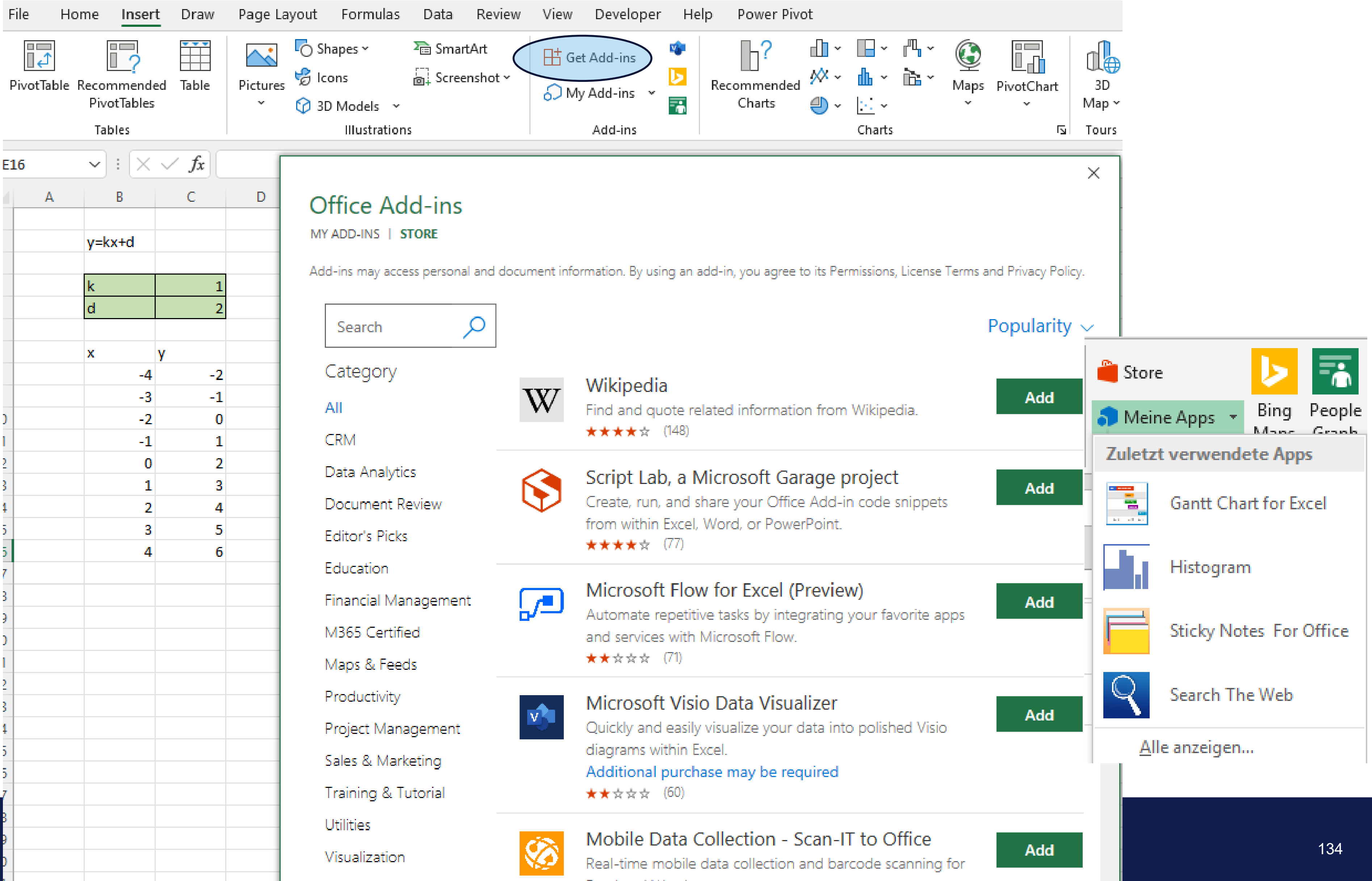
C8 =k*B8+d

y=kx+d

k	1
d	2

x	y
-4	-2
-3	-1
-2	0
-1	1
0	2
1	3
2	4
3	5
4	6

Add-ins



y=kx+d

k	1
d	2

x	y
-4	-2
-3	-1
-2	0
-1	1
0	2
1	3
2	4
3	5
4	6

Office Add-ins

MY ADD-INS | **STORE**

Add-ins may access personal and document information. By using an add-in, you agree to its Permissions, License Terms and Privacy Policy.

Category

- All
- CRM
- Data Analytics
- Document Review
- Editor's Picks
- Education
- Financial Management
- M365 Certified
- Maps & Feeds
- Productivity
- Project Management
- Sales & Marketing
- Training & Tutorial
- Utilities
- Visualization

Wikipedia
Find and quote related information from Wikipedia.
★★★★☆ (148)

Script Lab, a Microsoft Garage project
Create, run, and share your Office Add-in code snippets from within Excel, Word, or PowerPoint.
★★★★☆ (77)

Microsoft Flow for Excel (Preview)
Automate repetitive tasks by integrating your favorite apps and services with Microsoft Flow.
★★☆☆☆ (71)

Microsoft Visio Data Visualizer
Quickly and easily visualize your data into polished Visio diagrams within Excel.
Additional purchase may be required
★★☆☆☆ (60)

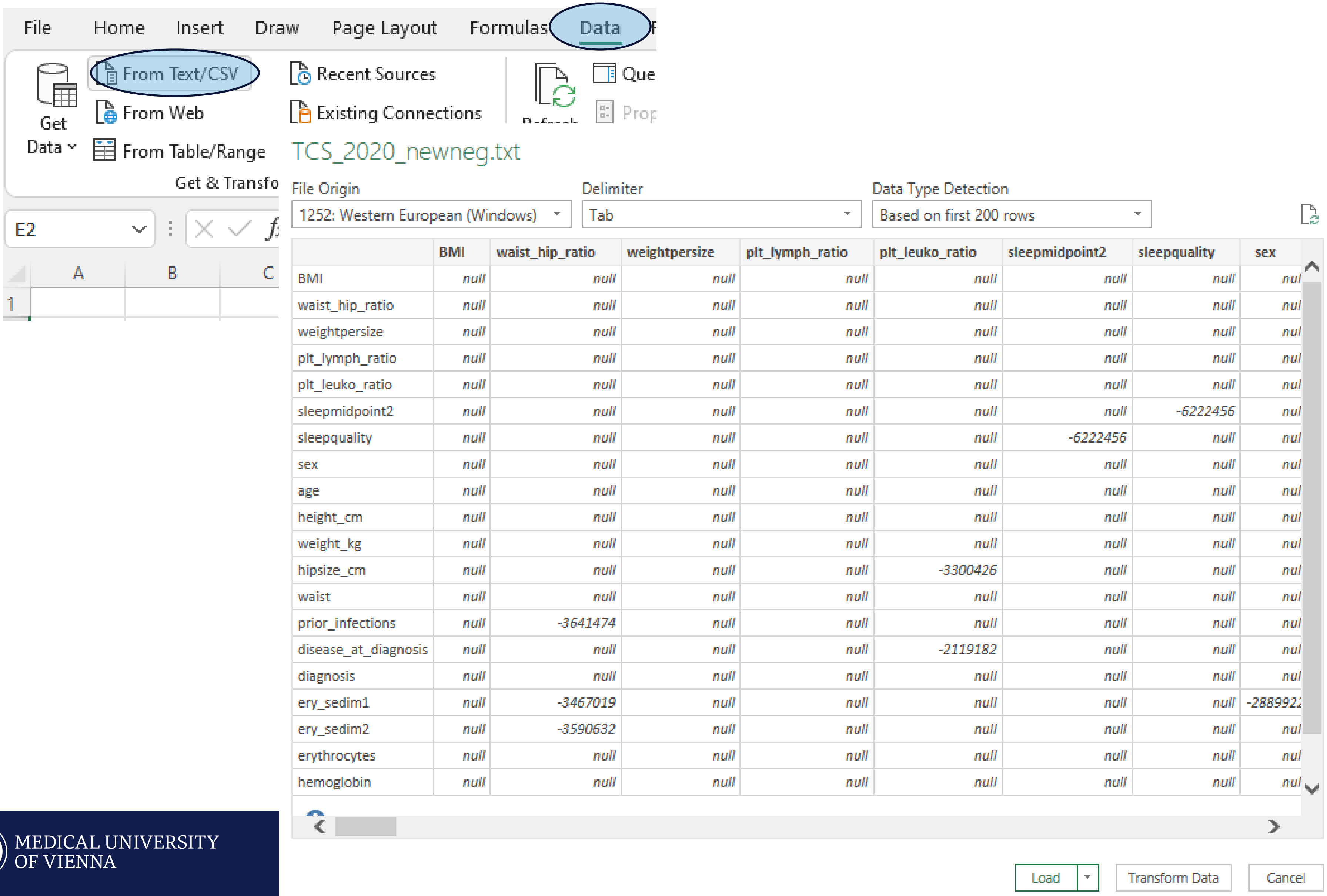
Mobile Data Collection - Scan-IT to Office
Real-time mobile data collection and barcode scanning for

Zuletzt verwendete Apps

- Gantt Chart for Excel
- Histogram
- Sticky Notes For Office
- Search The Web

Alle anzeigen...

Importing of data from text or csv sources…



TCS_2020_newneg.txt

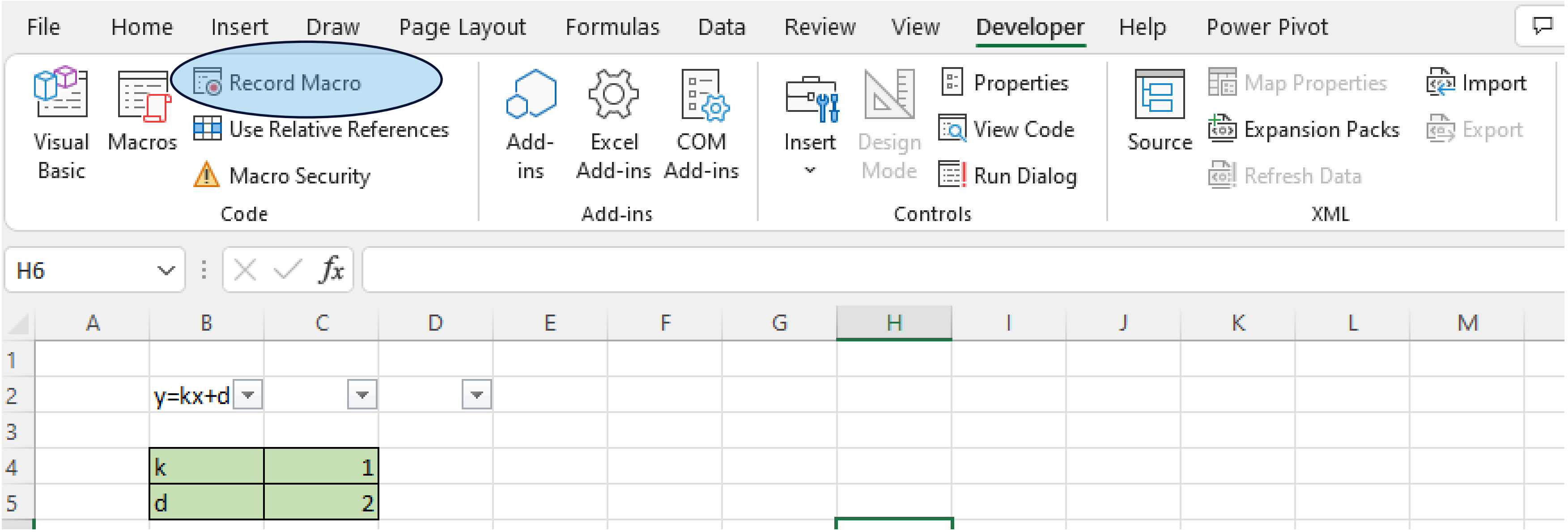
File Origin: 1252: Western European (Windows)

Delimiter: Tab

Data Type Detection: Based on first 200 rows

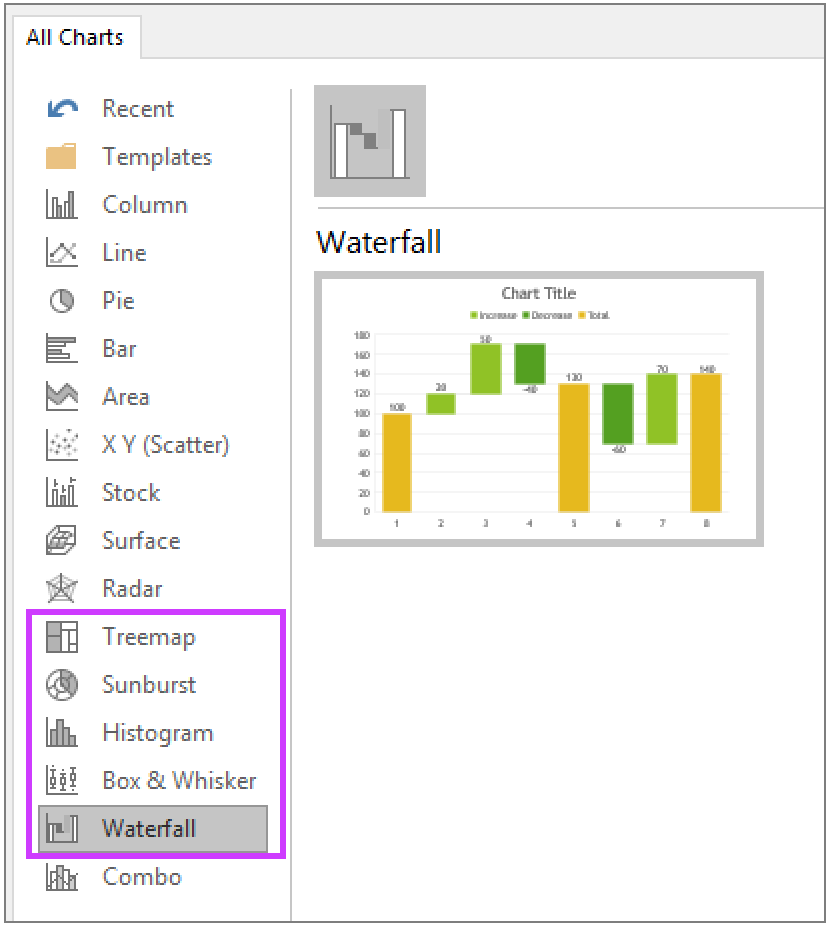
	BMI	waist_hip_ratio	weightpersize	plt_lymph_ratio	plt_leuko_ratio	sleepmidpoint2	sleepquality	sex
BMI	null	null	null	null	null	null	null	nul
waist_hip_ratio	null	null	null	null	null	null	null	nul
weightpersize	null	null	null	null	null	null	null	nul
plt_lymph_ratio	null	null	null	null	null	null	null	nul
plt_leuko_ratio	null	null	null	null	null	null	null	nul
sleepmidpoint2	null	null	null	null	null	null	-6222456	nul
sleepquality	null	null	null	null	null	-6222456	null	nul
sex	null	null	null	null	null	null	null	nul
age	null	null	null	null	null	null	null	nul
height_cm	null	null	null	null	null	null	null	nul
weight_kg	null	null	null	null	null	null	null	nul
hipsize_cm	null	null	null	null	-3300426	null	null	nul
waist	null	null	null	null	null	null	null	nul
prior_infections	null	-3641474	null	null	null	null	null	nul
disease_at_diagnosis	null	null	null	null	-2119182	null	null	nul
diagnosis	null	null	null	null	null	null	null	nul
ery_sedim1	null	-3467019	null	null	null	null	null	-288992
ery_sedim2	null	-3590632	null	null	null	null	null	nul
erythrocytes	null	null	null	null	null	null	null	nul
hemoglobin	null	null	null	null	null	null	null	nul

Development tools: Macros, Add-Ins…



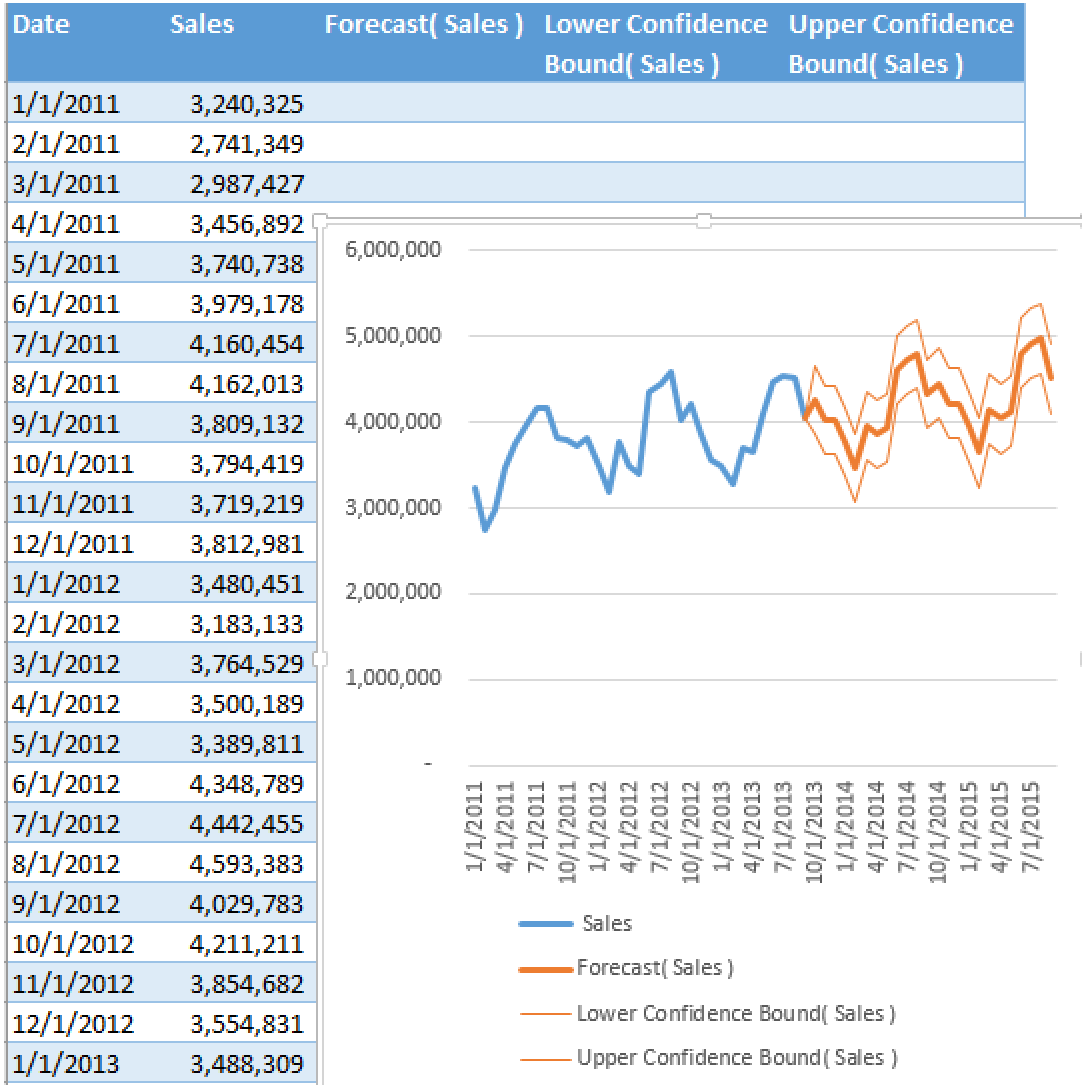
	A	B	C	D
1				
2		y=kx+d		
3				
4		k	1	
5		d	2	

Since Excel 2016



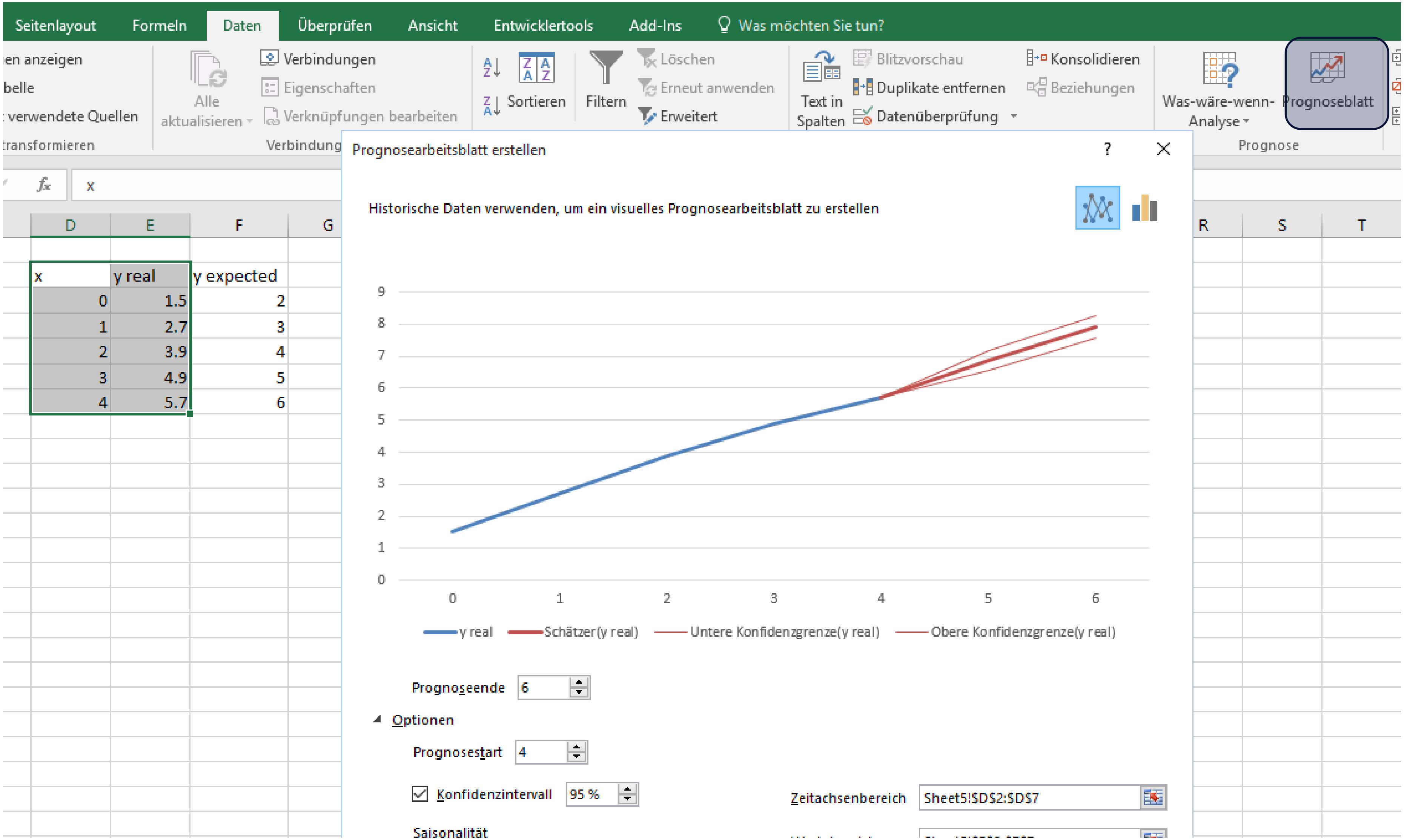
6 new graph types

Forecasting functions



Date	Sales	Forecast(Sales)	Lower Confidence Bound(Sales)	Upper Confidence Bound(Sales)
1/1/2011	3,240,325			
2/1/2011	2,741,349			
3/1/2011	2,987,427			
4/1/2011	3,456,892			
5/1/2011	3,740,738			
6/1/2011	3,979,178			
7/1/2011	4,160,454			
8/1/2011	4,162,013			
9/1/2011	3,809,132			
10/1/2011	3,794,419			
11/1/2011	3,719,219			
12/1/2011	3,812,981			
1/1/2012	3,480,451			
2/1/2012	3,183,133			
3/1/2012	3,764,529			
4/1/2012	3,500,189			
5/1/2012	3,389,811			
6/1/2012	4,348,789			
7/1/2012	4,442,455			
8/1/2012	4,593,383			
9/1/2012	4,029,783			
10/1/2012	4,211,211			
11/1/2012	3,854,682			
12/1/2012	3,554,831			
1/1/2013	3,488,309			

Forecasting functions



fx x

x	y real	y expected
0	1.5	2
1	2.7	3
2	3.9	4
3	4.9	5
4	5.7	6

Prognosearbeitsblatt erstellen

Historische Daten verwenden, um ein visuelles Prognosearbeitsblatt zu erstellen

Prognoseende 6

Optionen

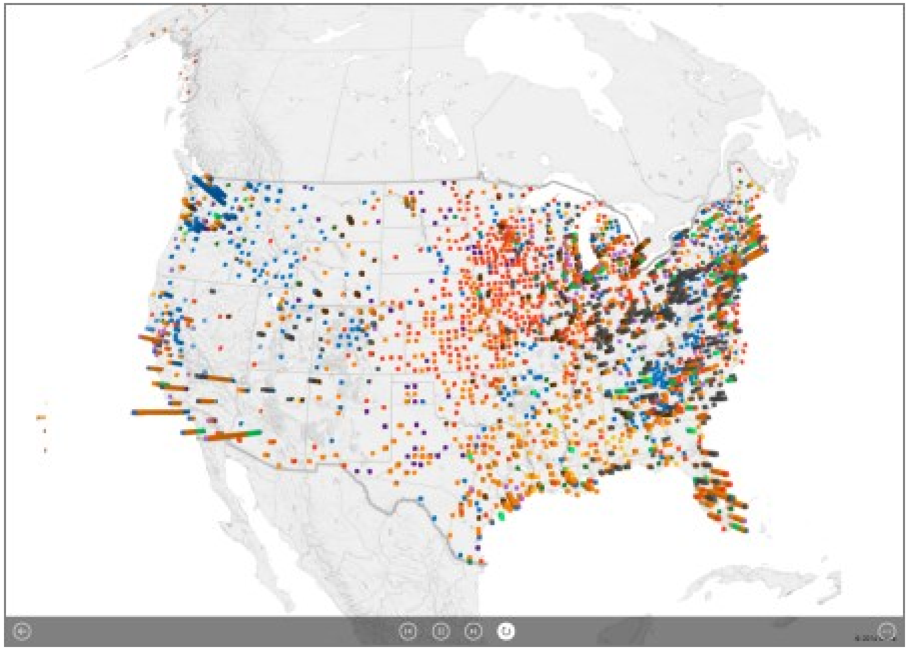
Prognosestart 4

☑ Konfidenzintervall 95 %

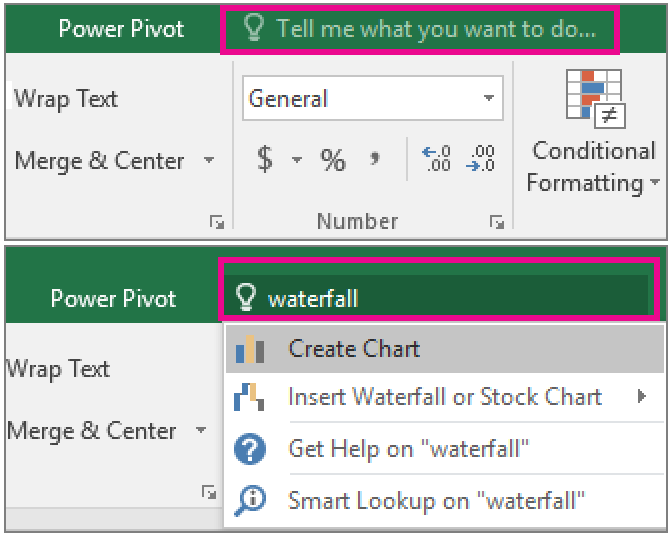
Zeitachsenbereich Sheet5!$D$2:$D$7

Saisonalität

3D maps

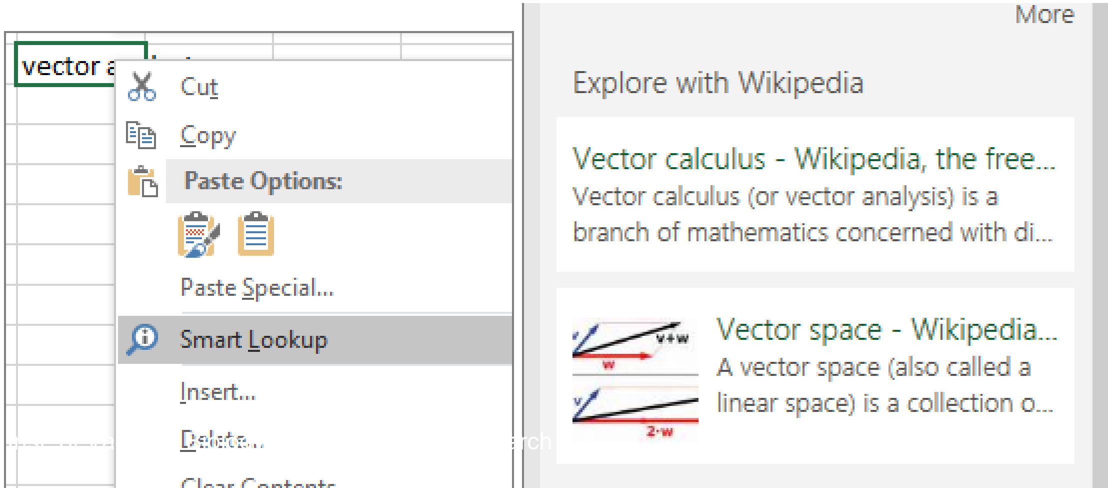


Tell me... function



… suggest available functions, which can be executed quickly

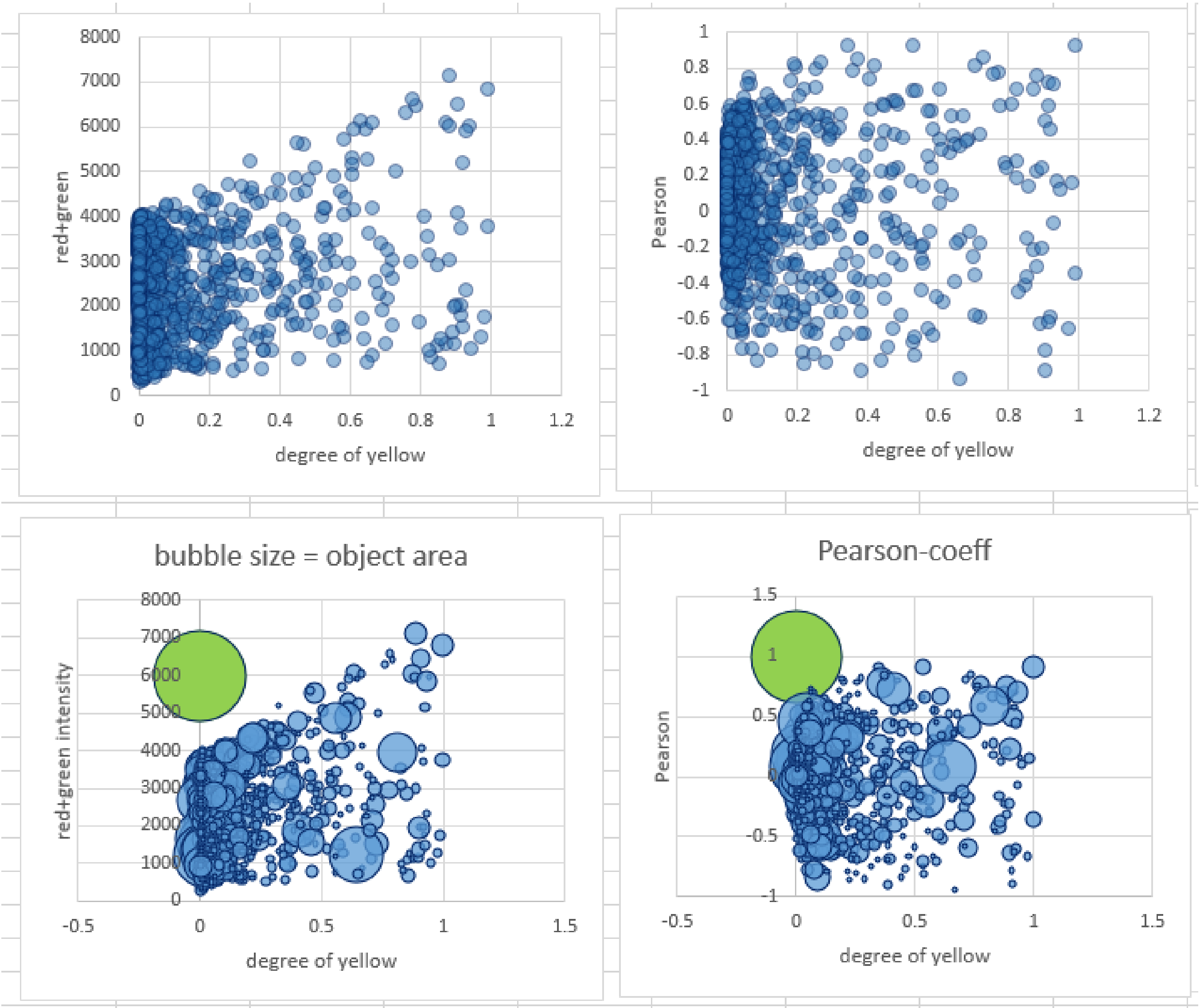
Smart Look-up



Vector calculus - Wikipedia, the free...
Vector calculus (or vector analysis) is a branch of mathematics concerned with di...

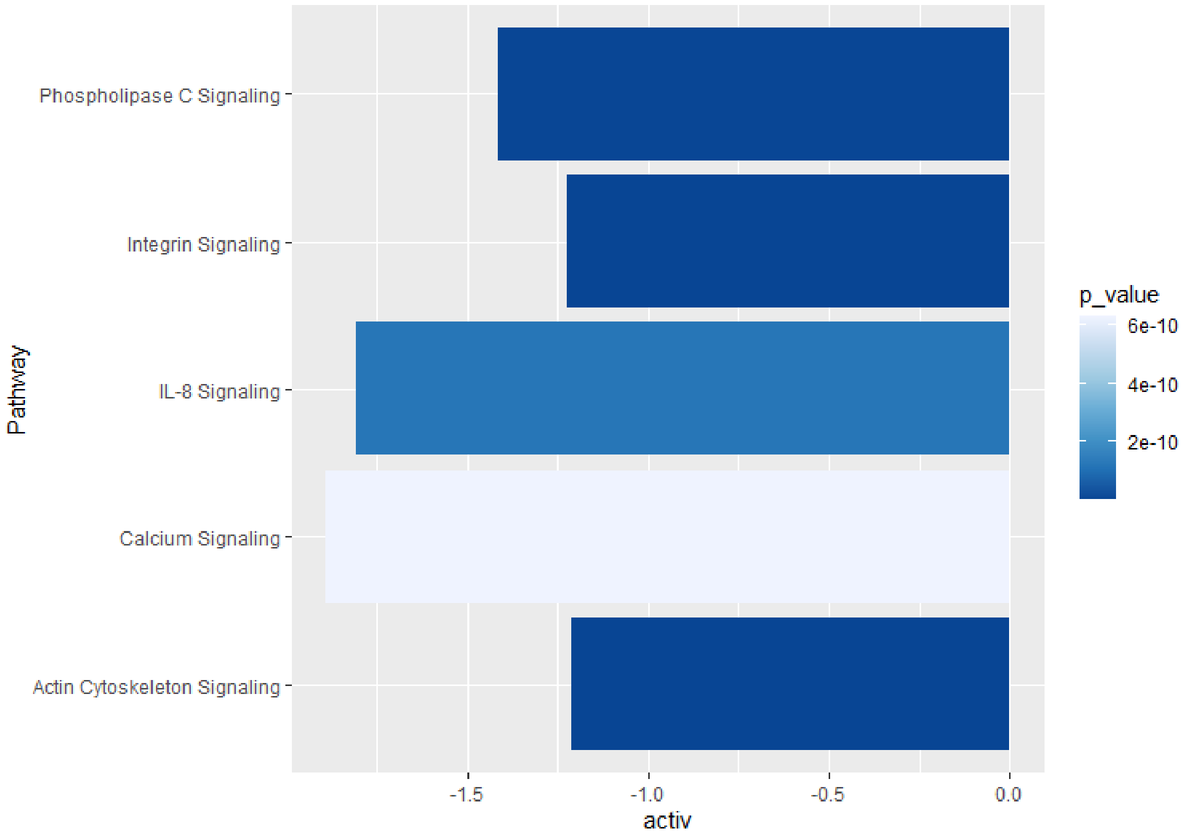
Vector space - Wikipedia...
A vector space (also called a linear space) is a collection o...

3-dimensional scattergramm (bubble charts)



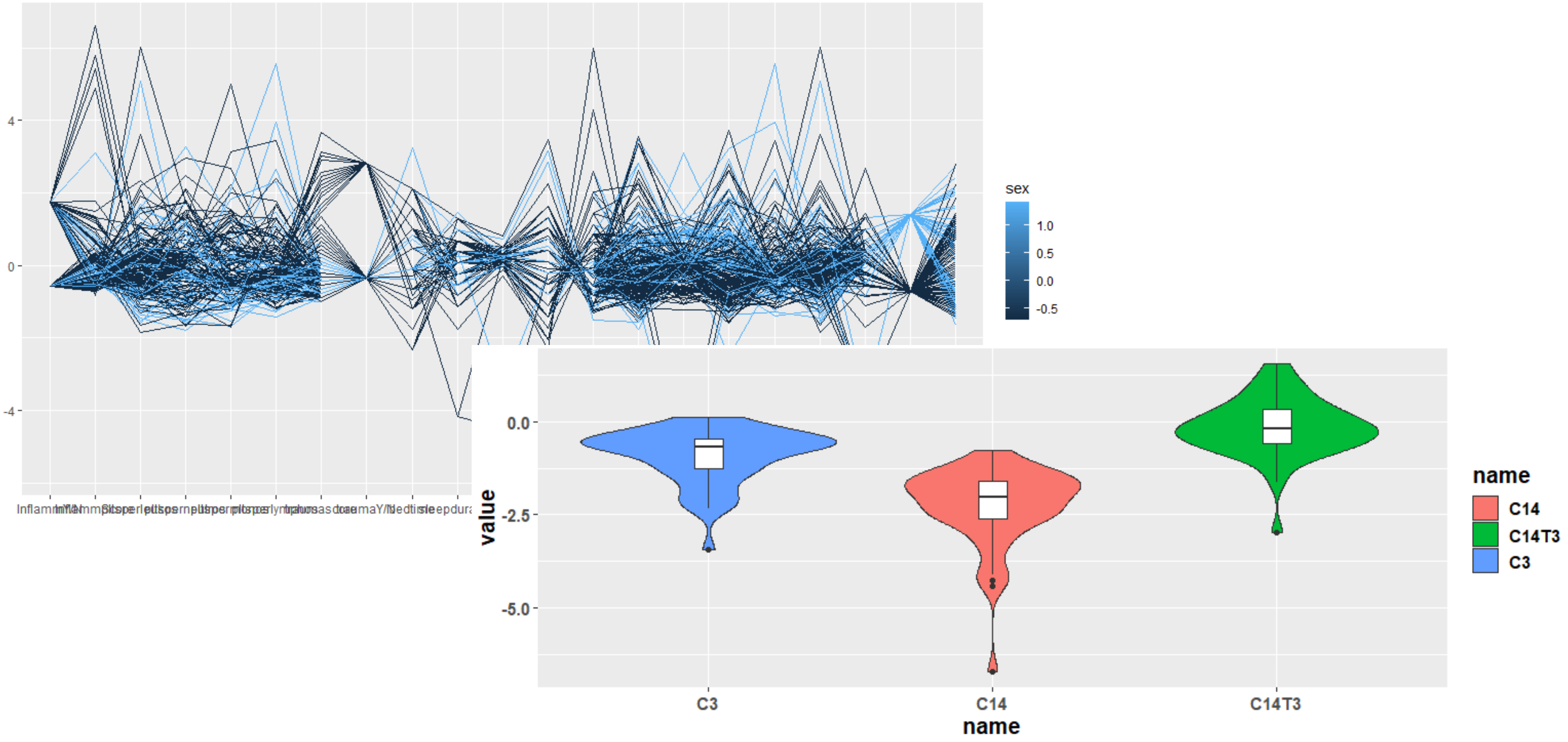
Limitations of Excel graphs (>R ggplot2)

- Colors of graph elements cannot be controlled by a numerical value (> R ggplot2 graphs)



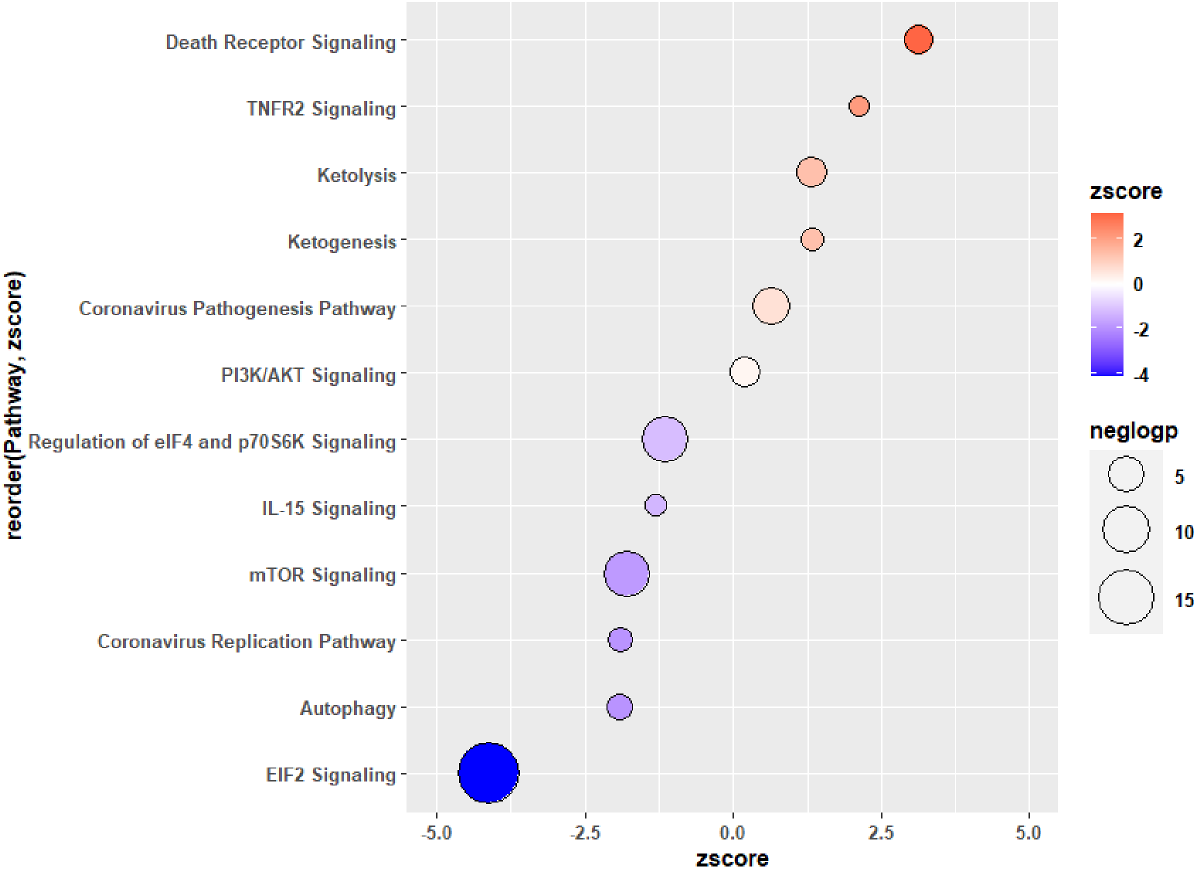
Limitations of Excel graphs (>R ggplot2)

- Excel does not have sophisticated graphs like violin plots or parallel coordinate plots



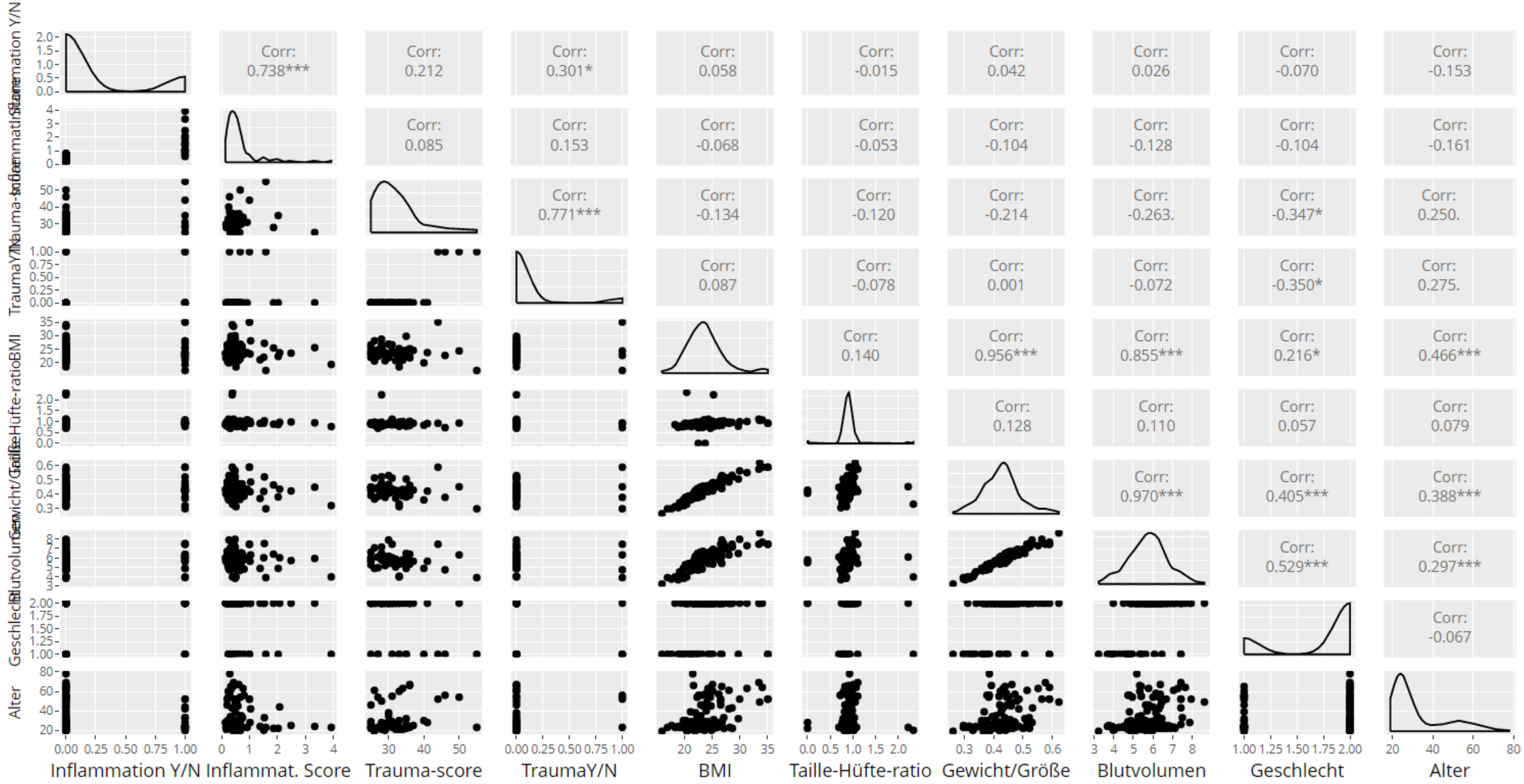
Limitations of Excel graphs (>R ggplot2)

- Excel has limitations for multi-dimensional graphs



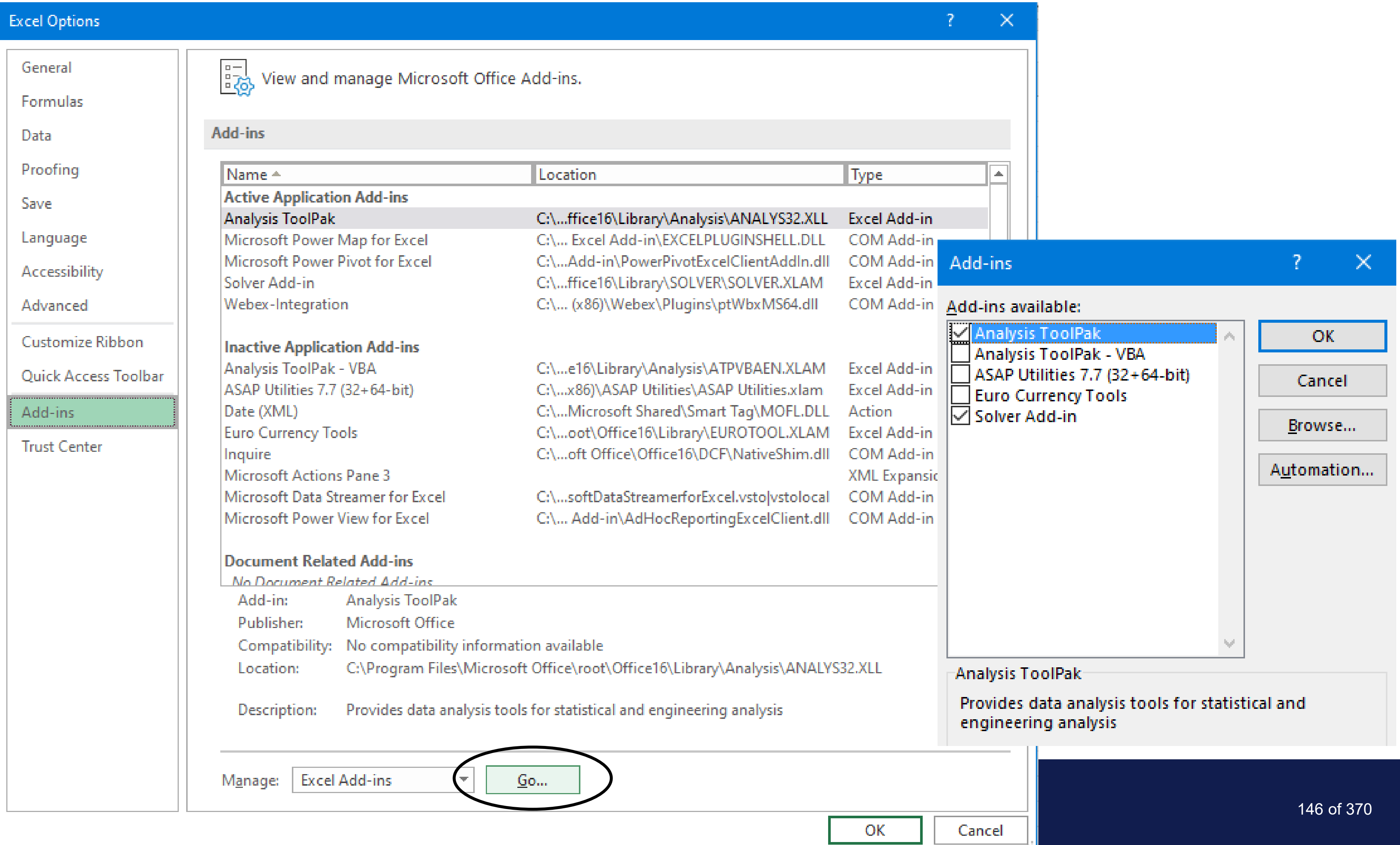
Limitations of Excel graphs (>R ggplot2)

- Excel has limitations for automated multiple graphs (like scatterplot matrices)



Data analysis and Solver functions

Have to be activated: File > options > Add-ins



View and manage Microsoft Office Add-ins.

Add-ins

Name	Location	Type
Active Application Add-ins		
Analysis ToolPak	C:\...ffice16\Library\Analysis\ANALYS32.XLL	Excel Add-in
Microsoft Power Map for Excel	C:\... Excel Add-in\EXCELPLUGINSHELL.DLL	COM Add-in
Microsoft Power Pivot for Excel	C:\...Add-in\PowerPivotExcelClientAddIn.dll	COM Add-in
Solver Add-in	C:\...ffice16\Library\SOLVER\SOLVER.XLAM	Excel Add-in
Webex-Integration	C:\... (x86)\Webex\Plugins\ptWbxMS64.dll	COM Add-in
Inactive Application Add-ins		
Analysis ToolPak - VBA	C:\...e16\Library\Analysis\ATPVBAEN.XLAM	Excel Add-in
ASAP Utilities 7.7 (32+64-bit)	C:\...x86)\ASAP Utilities\ASAP Utilities.xlam	Excel Add-in
Date (XML)	C:\...Microsoft Shared\Smart Tag\MOFL.DLL	Action
Euro Currency Tools	C:\...oot\Office16\Library\EUROTOOL.XLAM	Excel Add-in
Inquire	C:\...oft Office\Office16\DCF\NativeShim.dll	COM Add-in
Microsoft Actions Pane 3		XML Expansic
Microsoft Data Streamer for Excel	C:\...softDataStreamerforExcel.vsto|vstolocal	COM Add-in
Microsoft Power View for Excel	C:\... Add-in\AdHocReportingExcelClient.dll	COM Add-in
Document Related Add-ins		
No Document Related Add-ins		

Add-in: Analysis ToolPak
Publisher: Microsoft Office
Compatibility: No compatibility information available
Location: C:\Program Files\Microsoft Office\root\Office16\Library\Analysis\ANALYS32.XLL

Description: Provides data analysis tools for statistical and engineering analysis

Manage: Excel Add-ins Go...

Add-ins

Add-ins available:

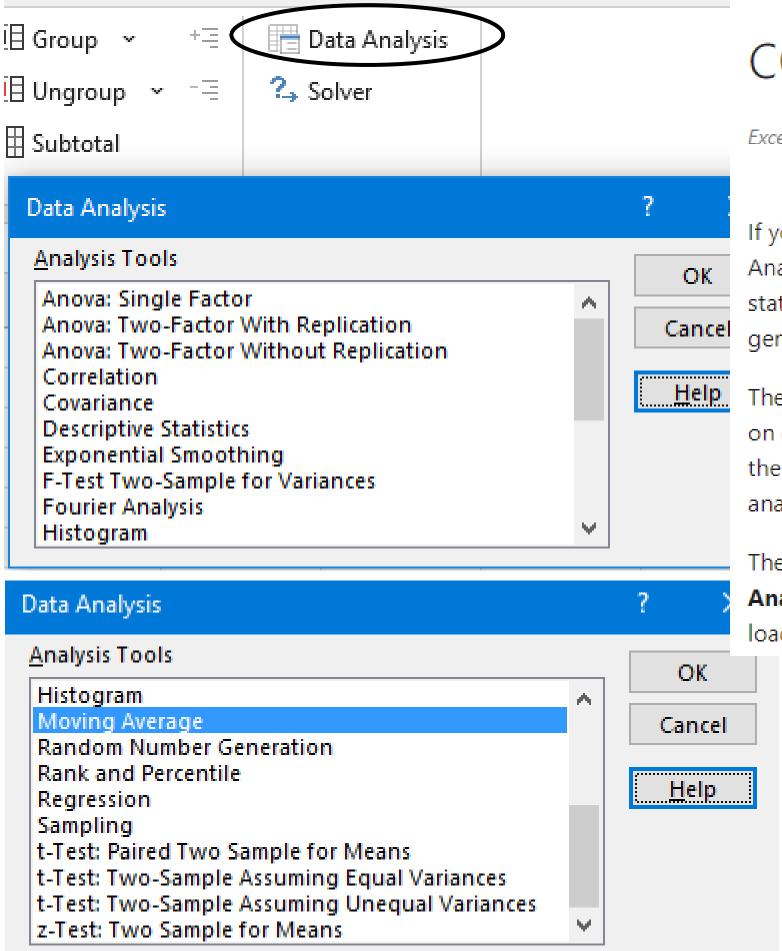
☑ Analysis ToolPak
☐ Analysis ToolPak - VBA
☐ ASAP Utilities 7.7 (32+64-bit)
☐ Euro Currency Tools
☑ Solver Add-in

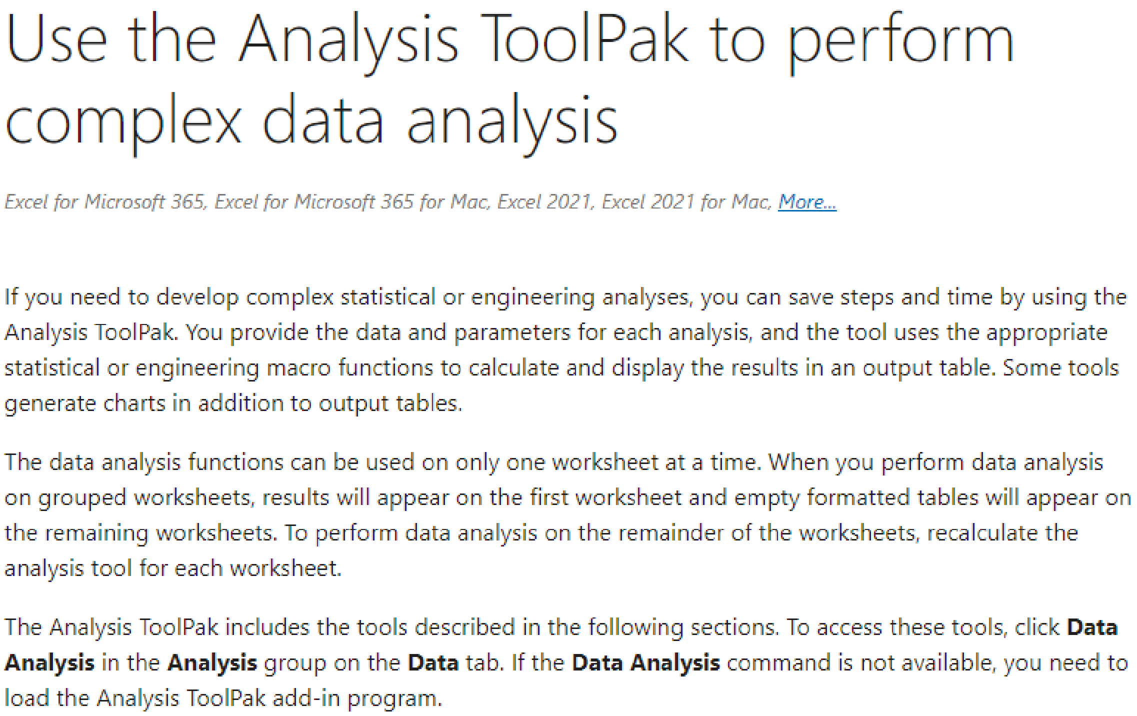
Analysis ToolPak

Provides data analysis tools for statistical and engineering analysis

Data Analysis Functions

Tab: Data >





Use the Analysis ToolPak to perform complex data analysis

Excel for Microsoft 365, Excel for Microsoft 365 for Mac, Excel 2021, Excel 2021 for Mac, More...

If you need to develop complex statistical or engineering analyses, you can save steps and time by using the Analysis ToolPak. You provide the data and parameters for each analysis, and the tool uses the appropriate statistical or engineering macro functions to calculate and display the results in an output table. Some tools generate charts in addition to output tables.

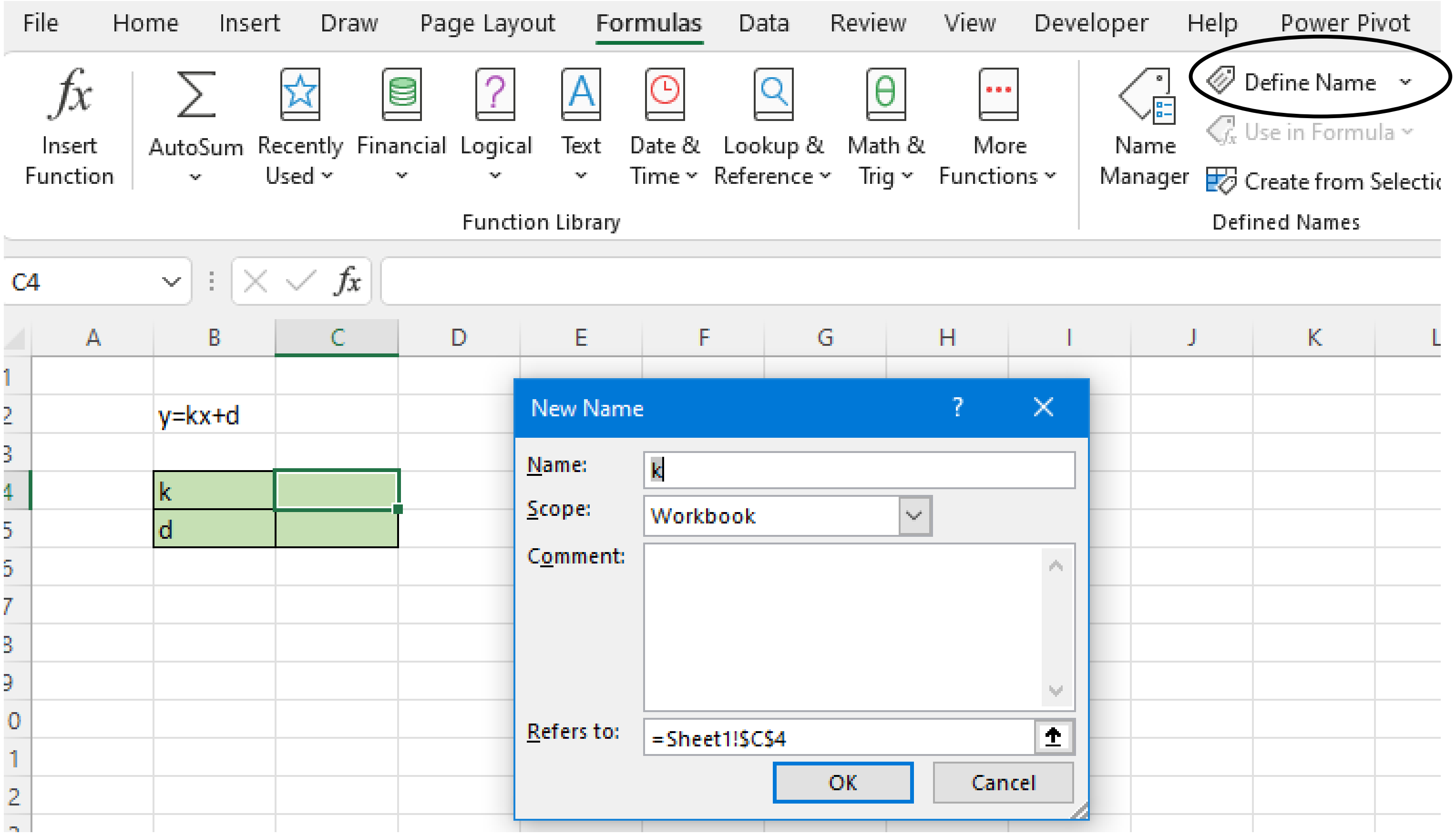
The data analysis functions can be used on only one worksheet at a time. When you perform data analysis on grouped worksheets, results will appear on the first worksheet and empty formatted tables will appear on the remaining worksheets. To perform data analysis on the remainder of the worksheets, recalculate the analysis tool for each worksheet.

The Analysis ToolPak includes the tools described in the following sections. To access these tools, click **Data Analysis** in the **Analysis** group on the **Data** tab. If the **Data Analysis** command is not available, you need to load the Analysis ToolPak add-in program.

Link to website

Defining variables for equations

1. Parameters for equations can be defined in the Formula tab („Define name“)
   e.g. *k* and *d* of a linear equation
2. These parameters can then be used in the function mode in combination with cells
3. Changing the parameters (k and d) also changes the results in y-column



y=kx+d

k	
d	

Name: k

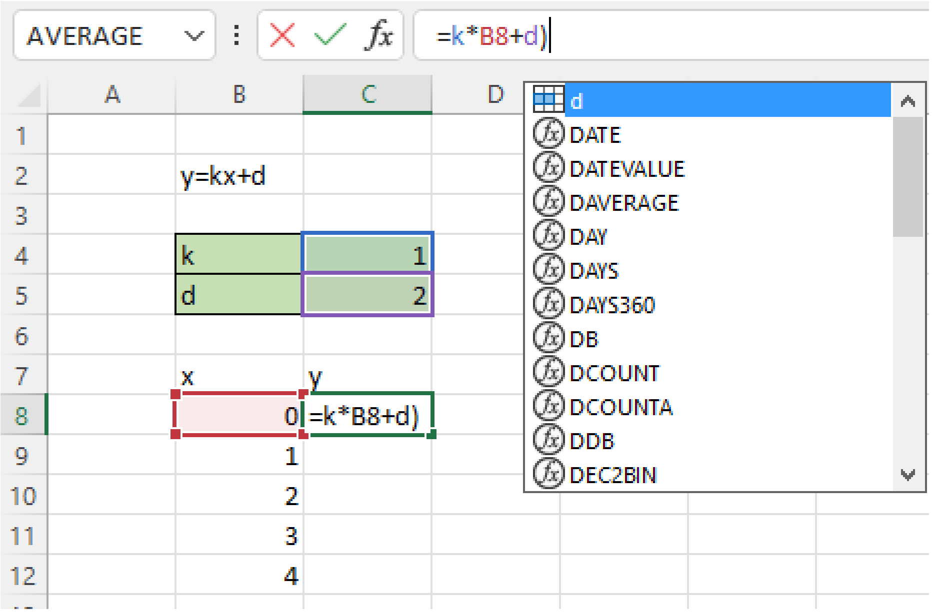
Scope: Workbook

Comment:

Refers to: =Sheet1!$C$4

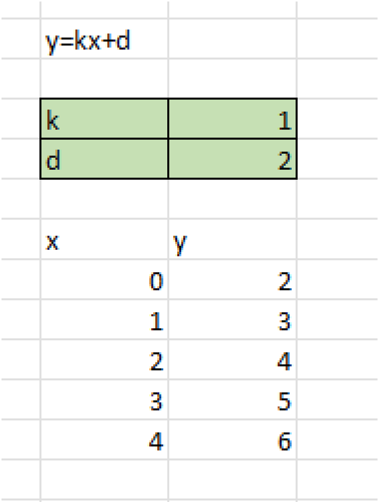
Defining variables for equations

1. Parameters for equations can be defined in the Formula tab („Define name“)
   e.g. *k* and *d* of a linear equation
2. These parameters can then be used in the function mode in combination with cells
3. Changing the parameters (k and d) also changes the results in y-column
4. An equation can be used to calculate expected y-values (dependent values) for given x-values using any starting values defined for the variables.
   (in this case k and d as defined in the green cells; the x-value is taken from column B)



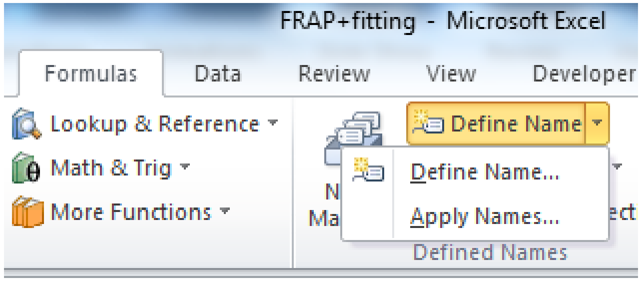
=k*B8+d)

	A	B	C	D
1				
2		y=kx+d		
3				
4		k	1	
5		d	2	
6				
7		x	y	
8		0	=k*B8+d)	
9		1		
10		2		
11		3		
12		4		

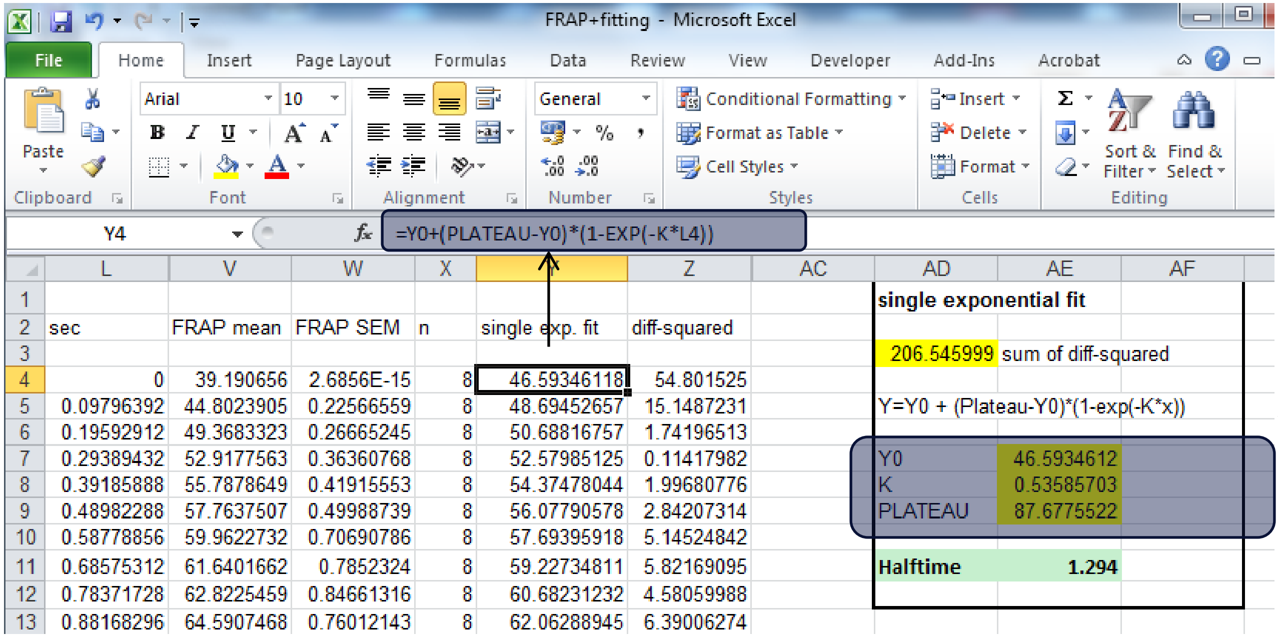


y=kx+d	
k	1
d	2
x	y
0	2
1	3
2	4
3	5
4	6

Defining more complex equations



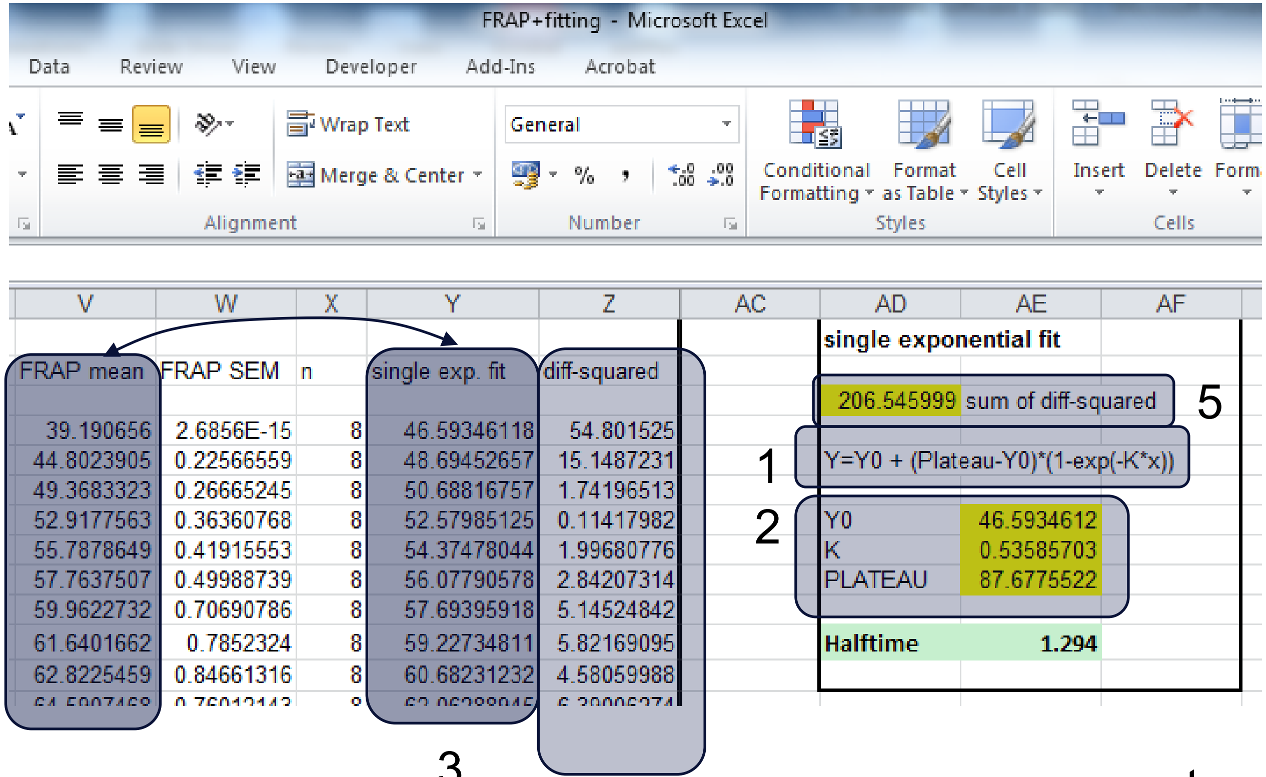
Variables



Y4 =Y0+(PLATEAU-Y0)*(1-EXP(-K*L4))

	L	V	W	X	Y	Z	AC	AD	AE	AF
1								**single exponential fit**		
2	sec	FRAP mean	FRAP SEM	n	single exp. fit	diff-squared				
3								206.545999	sum of diff-squared	
4	0	39.190656	2.6856E-15	8	46.59346118	54.801525				
5	0.09796392	44.8023905	0.22566559	8	48.69452657	15.1487231		Y=Y0 + (Plateau-Y0)*(1-exp(-K*x))		
6	0.19592912	49.3683323	0.26665245	8	50.68816757	1.74196513				
7	0.29389432	52.9177563	0.36360768	8	52.57985125	0.11417982		Y0	46.5934612	
8	0.39185888	55.7878649	0.41915553	8	54.37478044	1.99680776		K	0.53585703	
9	0.48982288	57.7637507	0.49988739	8	56.07790578	2.84207314		PLATEAU	87.6775522	
10	0.58778856	59.9622732	0.70690786	8	57.69395918	5.14524842				
11	0.68575312	61.6401662	0.7852324	8	59.22734811	5.82169095		**Halftime**	**1.294**	
12	0.78371728	62.8225459	0.84661316	8	60.68231232	4.58059988				
13	0.88168296	64.5907468	0.76012143	8	62.06288945	6.39006274				

Curve fitting with the Solver function



V	W	X	Y	Z
FRAP mean	FRAP SEM	n	single exp. fit	diff-squared
39.190656	2.6856E-15	8	46.59346118	54.801525
44.8023905	0.22566559	8	48.69452657	15.1487231
49.3683323	0.26665245	8	50.68816757	1.74196513
52.9177563	0.36360768	8	52.57985125	0.11417982
55.7878649	0.41915553	8	54.37478044	1.99680776
57.7637507	0.49988739	8	56.07790578	2.84207314
59.9622732	0.70690786	8	57.69395918	5.14524842
61.6401662	0.7852324	8	59.22734811	5.82169095
62.8225459	0.84661316	8	60.68231232	4.58059988

single exponential fit

206.545999 sum of diff-squared

Y=Y0 + (Plateau-Y0)*(1-exp(-K*x))

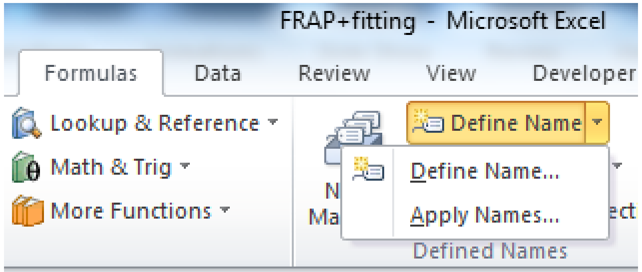
Y0	46.5934612
K	0.53585703
PLATEAU	87.6775522

Halftime **1.294**

measured

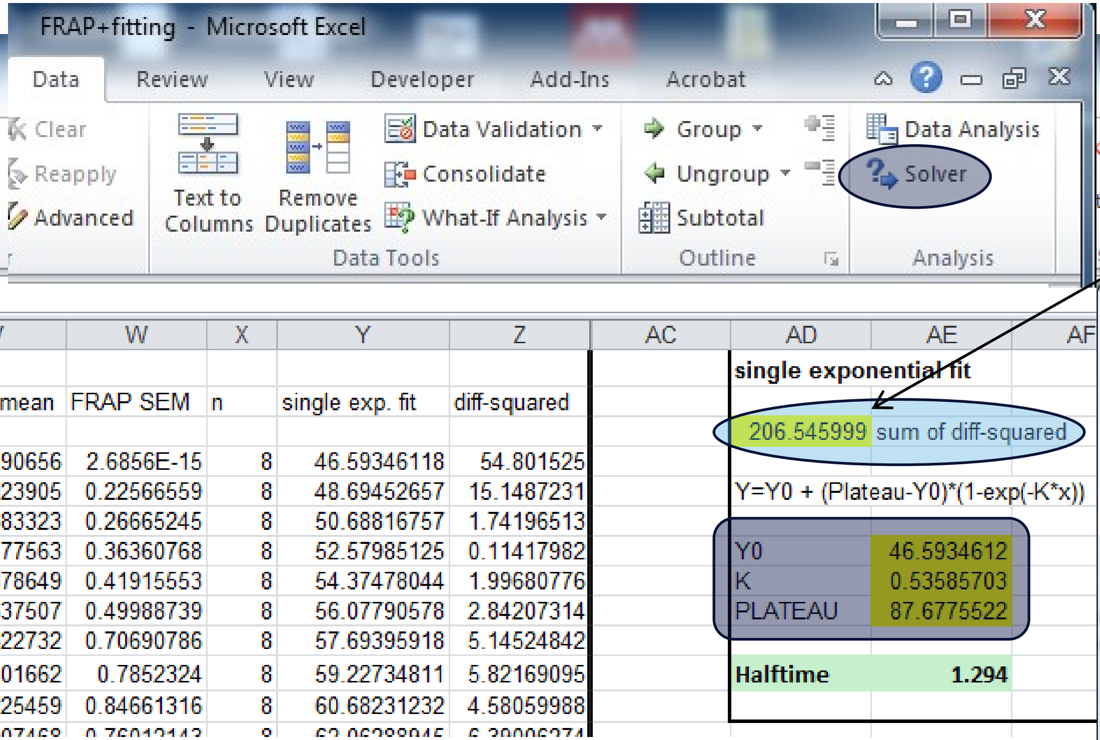
parameters

4



1. An equation is defined, which should be used for curve fitting
2. The parameters for this equation are defined as names and some initial values are given
3. This equation is used to calculate expected y-values (dependent values) for given x-values using any starting values defined for the parameters.
4. The difference between calculated values and measured vales is calculated and squared
5. The best curve fit for a given equation is obtained, when the sum of the squared differences is minimal – this can be optimized using the solver function.

Curve fitting with the Solver function II



mean	FRAP SEM	n	single exp. fit	diff-squared
90656	2.6856E-15	8	46.59346118	54.801525
23905	0.22566559	8	48.69452657	15.1487231
83323	0.26665245	8	50.68816757	1.74196513
77563	0.36360768	8	52.57985125	0.11417982
78649	0.41915553	8	54.37478044	1.99680776
37507	0.49988739	8	56.07790578	2.84207314
22732	0.70690786	8	57.69395918	5.14524842
01662	0.7852324	8	59.22734811	5.82169095
25459	0.84661316	8	60.68231232	4.58059988

single exponential fit

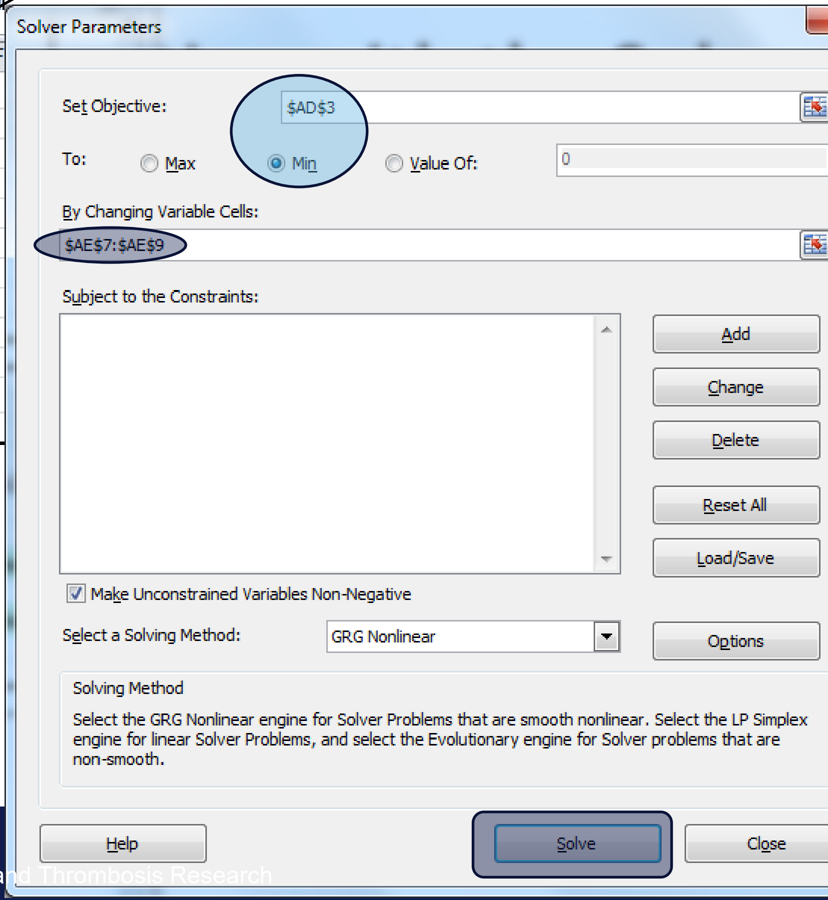
206.545999 sum of diff-squared

Y=Y0 + (Plateau-Y0)*(1-exp(-K*x))

Y0	46.5934612
K	0.53585703
PLATEAU	87.6775522

Halftime **1.294**

Σ of diff-squared (column Z)



Set Objective: $AD$3

To: ○ Max ● Min ○ Value Of: 0

By Changing Variable Cells: $AE$7:$AE$9

Subject to the Constraints:

☑ Make Unconstrained Variables Non-Negative

Select a Solving Method: GRG Nonlinear

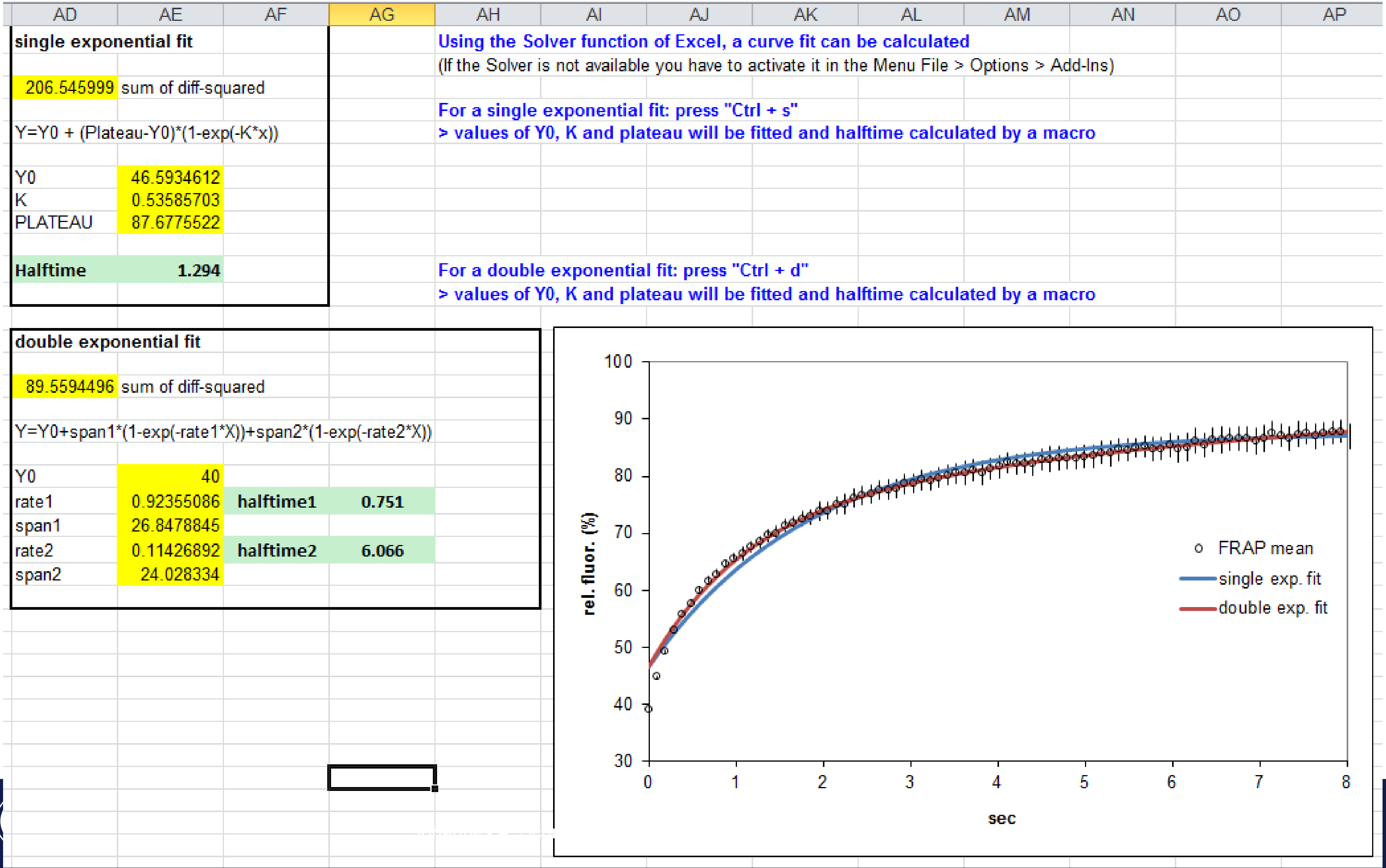
Solving Method

Select the GRG Nonlinear engine for Solver Problems that are smooth nonlinear. Select the LP Simplex engine for linear Solver Problems, and select the Evolutionary engine for Solver problems that are non-smooth.

6. Clicking the „Solver“ button in the Data tab opens a window, where you can define that the objective (sum of differences squared, red mark) is processed to a minimum (Min) by changing the variable cells (blue). Clicking the „Solve“ button then iteratively changes the variables until the minimal difference between fitting curve and the data is achieved

Example of a single and double curve fit with Excel

(from my website at: http://www.meduniwien.ac.at/user/johannes.schmid/protocols.htm - Excel templates:
FRAP template for single values + curve fitting)



single exponential fit

206.545999 sum of diff-squared

Y=Y0 + (Plateau-Y0)*(1-exp(-K*x))

Y0	46.5934612
K	0.53585703
PLATEAU	87.6775522
Halftime	**1.294**

Using the Solver function of Excel, a curve fit can be calculated

(If the Solver is not available you have to activate it in the Menu File > Options > Add-Ins)

For a single exponential fit: press "Ctrl + s"
> values of Y0, K and plateau will be fitted and halftime calculated by a macro

For a double exponential fit: press "Ctrl + d"
> values of Y0, K and plateau will be fitted and halftime calculated by a macro

double exponential fit

89.5594496 sum of diff-squared

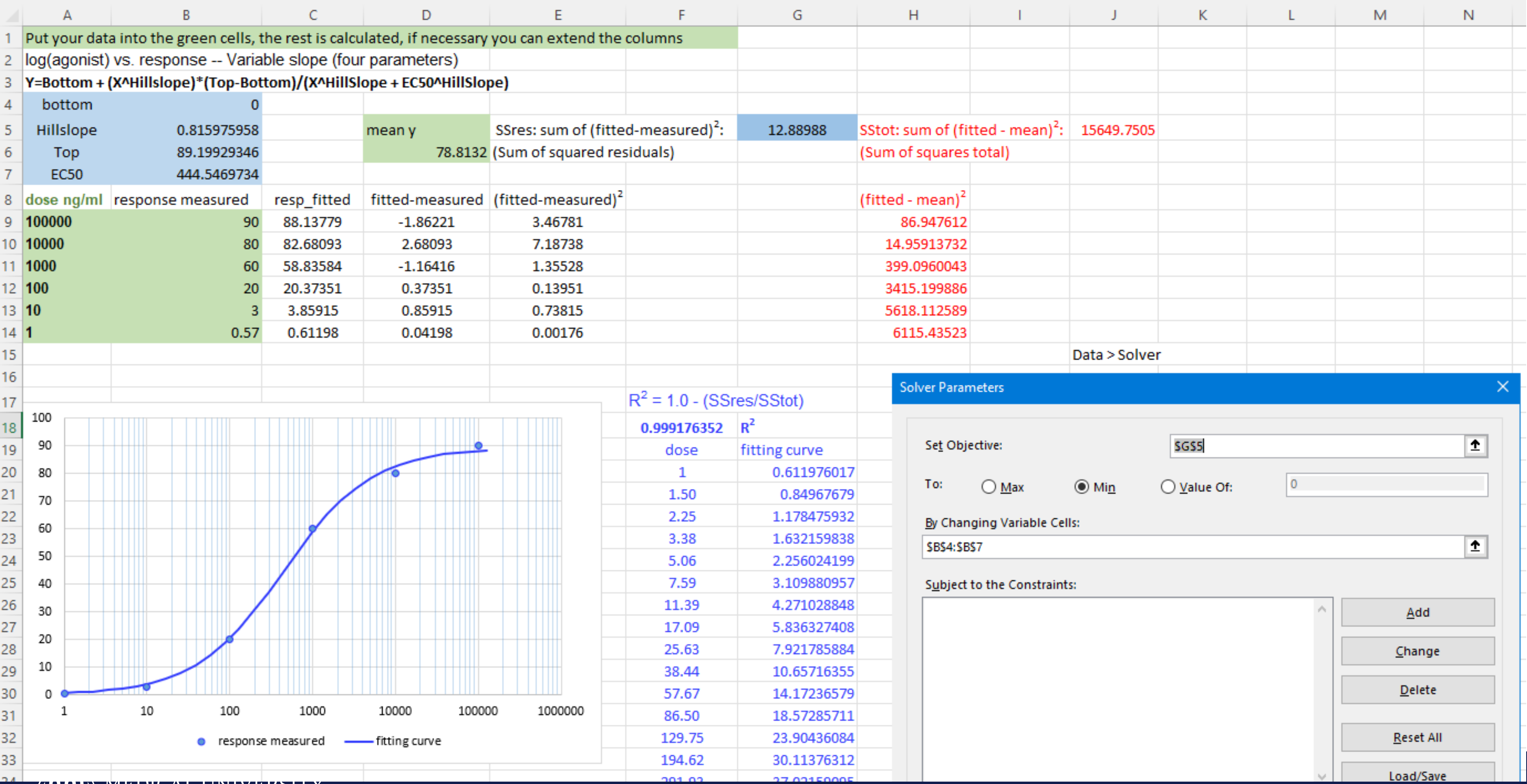
Y=Y0+span1*(1-exp(-rate1*X))+span2*(1-exp(-rate2*X))

Y0	40		
rate1	0.92355086	**halftime1**	**0.751**
span1	26.8478845		
rate2	0.11426892	**halftime2**	**6.066**
span2	24.028334		

Curve fitting incl. R² calculation

Example: dose-response curve fit (Link on my website)

R^2 = 1.0 - (SSres/SStot)
SSres: Sum of squared residuals (sum of squared differences (measured – fitted))
SStot: Sum of squares total: sum of squared differences (measured – mean of measured)



	A	B	C	D	E	F	G	H	I	J
1	Put your data into the green cells, the rest is calculated, if necessary you can extend the columns									
2	log(agonist) vs. response -- Variable slope (four parameters)									
3	Y=Bottom + (X^Hillslope)*(Top-Bottom)/(X^HillSlope + EC50^HillSlope)									
4	bottom	0								
5	Hillslope	0.815975958		mean y	SSres: sum of (fitted-measured)^2:		12.88988	SStot: sum of (fitted - mean)^2:		15649.7505
6	Top	89.19929346		78.8132	(Sum of squared residuals)			(Sum of squares total)		
7	EC50	444.5469734								
8	dose ng/ml	response measured	resp_fitted	fitted-measured	(fitted-measured)^2			(fitted - mean)^2		
9	100000	90	88.13779	-1.86221	3.46781			86.947612		
10	10000	80	82.68093	2.68093	7.18738			14.95913732		
11	1000	60	58.83584	-1.16416	1.35528			399.0960043		
12	100	20	20.37351	0.37351	0.13951			3415.199886		
13	10	3	3.85915	0.85915	0.73815			5618.112589		
14	1	0.57	0.61198	0.04198	0.00176			6115.43523		
15										Data > Solver

	F	G
17	R^2 = 1.0 - (SSres/SStot)	
18	0.999176352	R^2
19	dose	fitting curve
20	1	0.611976017
21	1.50	0.84967679
22	2.25	1.178475932
23	3.38	1.632159838
24	5.06	2.256024199
25	7.59	3.109880957
26	11.39	4.271028848
27	17.09	5.836327408
28	25.63	7.921785884
29	38.44	10.65716355
30	57.67	14.17236579
31	86.50	18.57285711
32	129.75	23.90436084
33	194.62	30.11376312

Solver Parameters

Set Objective: $G$5

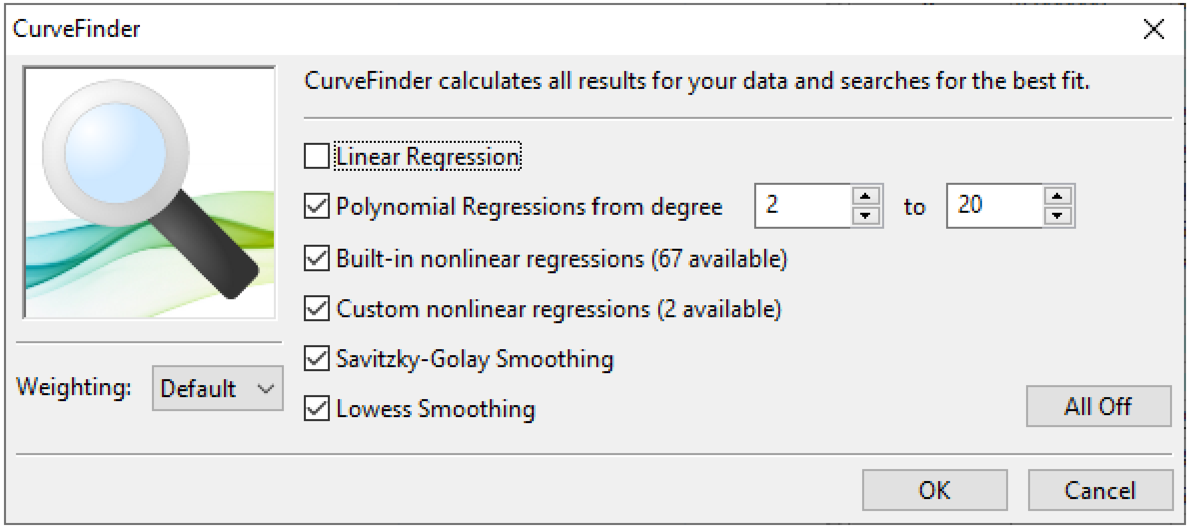
To: ○ Max ● Min ○ Value Of: 0

By Changing Variable Cells: $B$4:$B$7

Subject to the Constraints:

Curve Fitting Software: CurveExpert: Fitting many equations in a batch mode

- https://www.curveexpert.net/ - free trial version with quite low restrictions available, commercial: not that expensive (79$)
- Data can be copied/pasted from Excel
- Data points are fitted against about 60 built-in equations, which are then scored according to the goodness of fit



CurveFinder

CurveFinder calculates all results for your data and searches for the best fit.

☐ Linear Regression

☑ Polynomial Regressions from degree 2 to 20

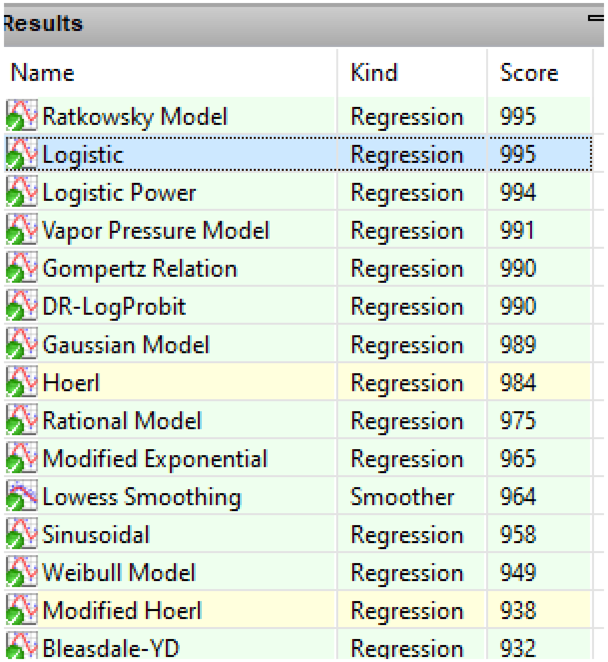
☑ Built-in nonlinear regressions (67 available)

☑ Custom nonlinear regressions (2 available)

☑ Savitzky-Golay Smoothing

☑ Lowess Smoothing

Weighting: Default



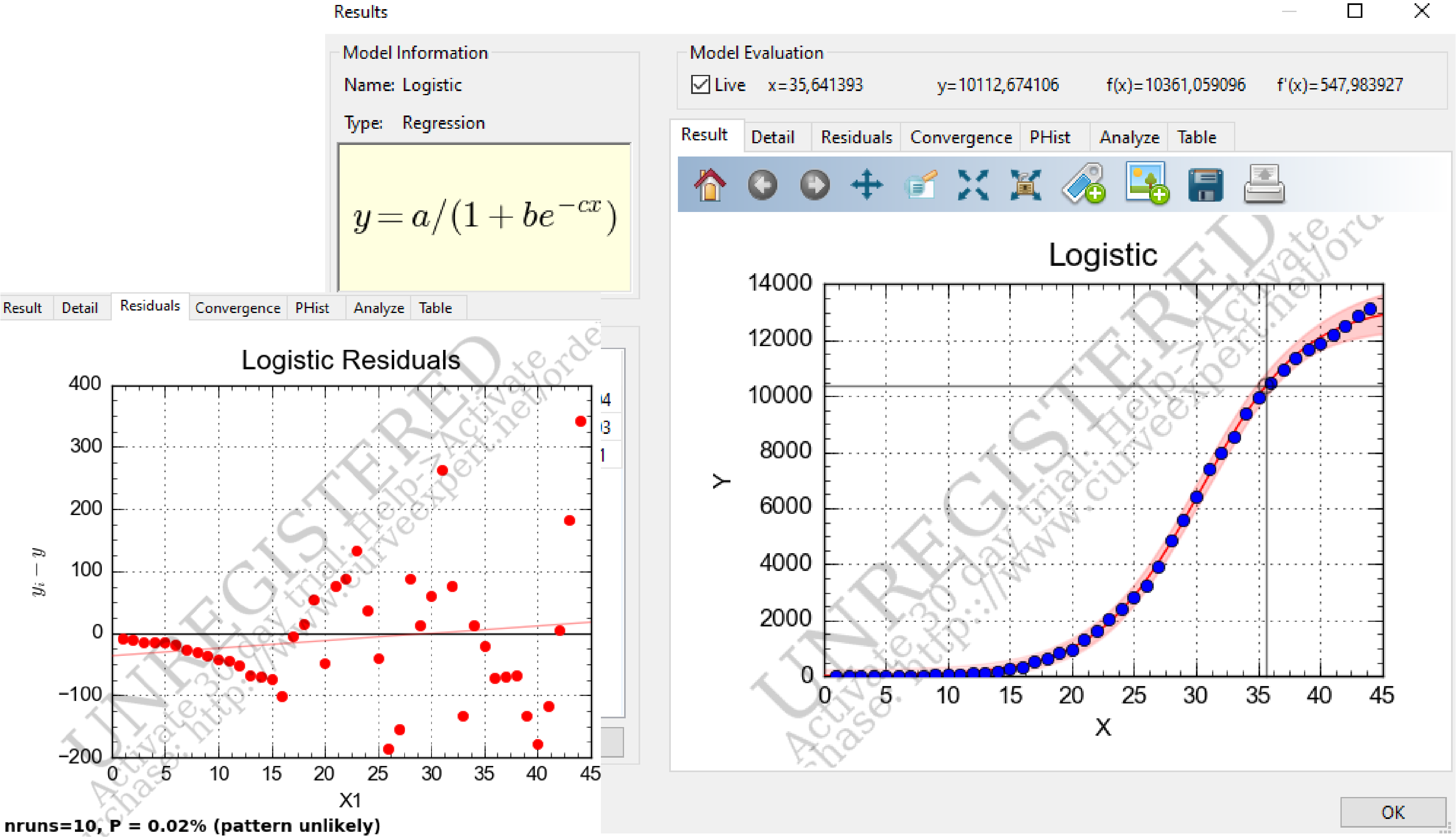
Results

Name	Kind	Score
Ratkowsky Model	Regression	995
Logistic	Regression	995
Logistic Power	Regression	994
Vapor Pressure Model	Regression	991
Gompertz Relation	Regression	990
DR-LogProbit	Regression	990
Gaussian Model	Regression	989
Hoerl	Regression	984
Rational Model	Regression	975
Modified Exponential	Regression	965
Lowess Smoothing	Smoother	964
Sinusoidal	Regression	958
Weibull Model	Regression	949
Modified Hoerl	Regression	938
Bleasdale-YD	Regression	932

Curve Fitting Software: CurveExpert

- Double clicking on a model opens a detailed graph-result

Data: COVID infections, Austria, 1st wave



Results

Model Information

Name: Logistic

Type: Regression

$$y = a/(1 + be^{-cx})$$

Model Evaluation

☑ Live x=35,641393 y=10112,674106 f(x)=10361,059096 f'(x)=547,983927

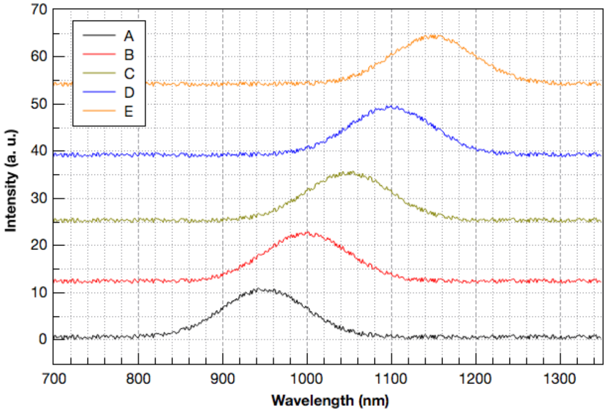
nruns=10, P = 0.02% (pattern unlikely)

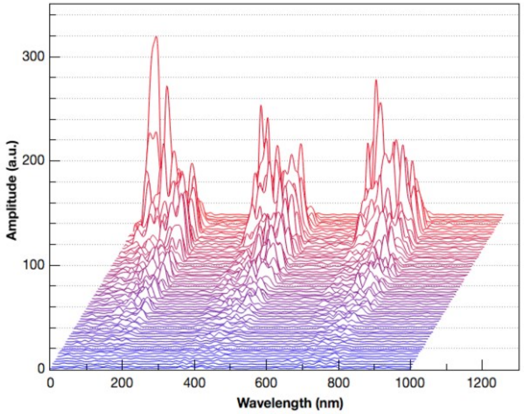
QTiPlot – a powerful Excel alternative

- Small (20MB) and powerful spreadsheet program available in many languages: https://www.qtiplot.com
- Rich graph features beyond Excel graphs
- Sophistical curve fitting is possible
- Statistical analyses beyond Excel
- Available as professional software for 10€ from our IT-dept.

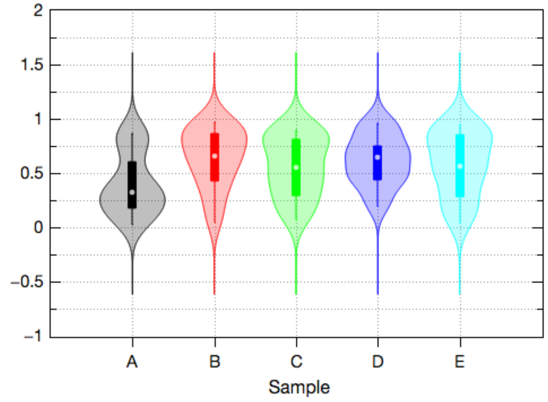
QTiPlot – graphs

stacked curves

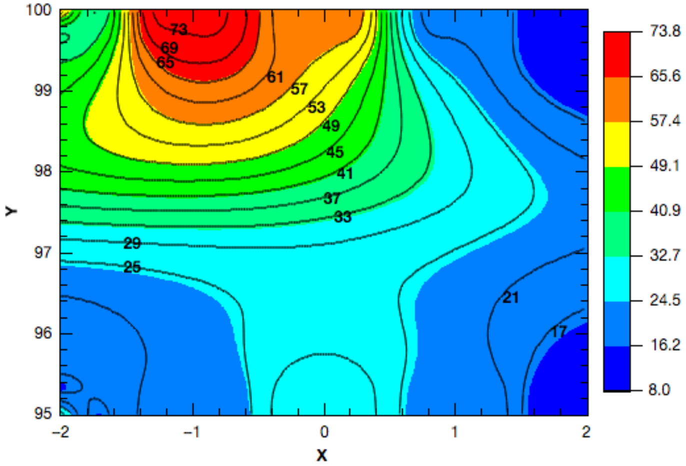




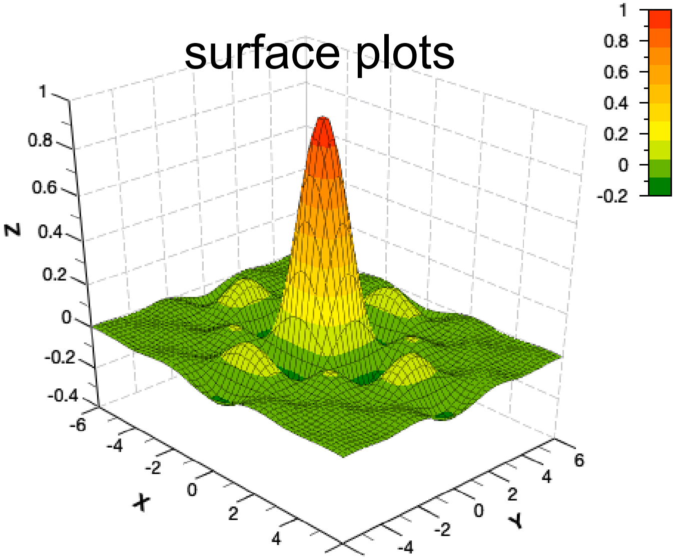
violin plots



contour plots and heatmaps

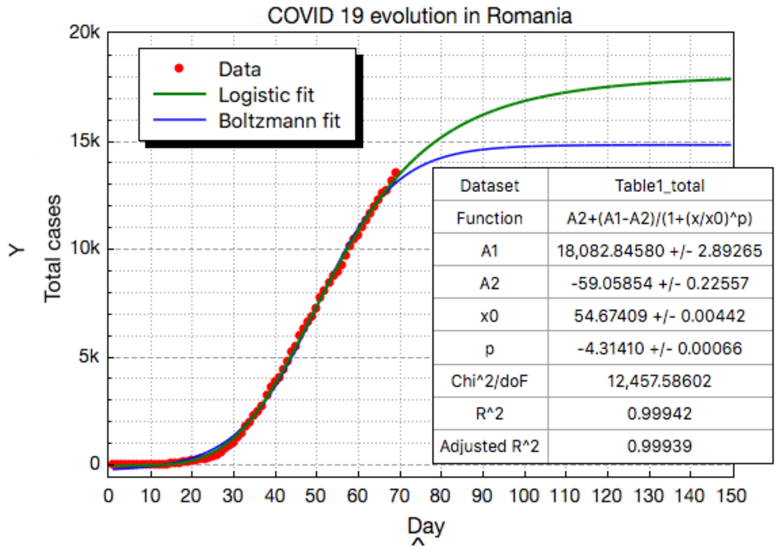


surface plots

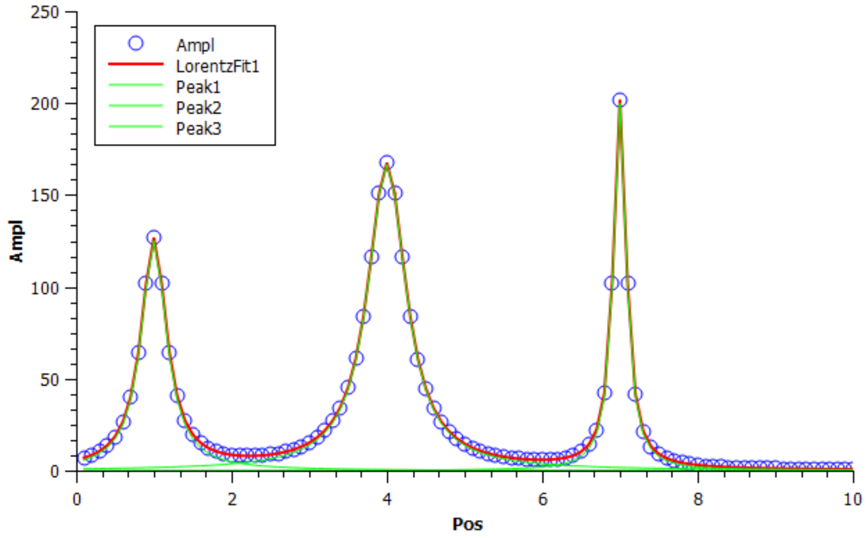


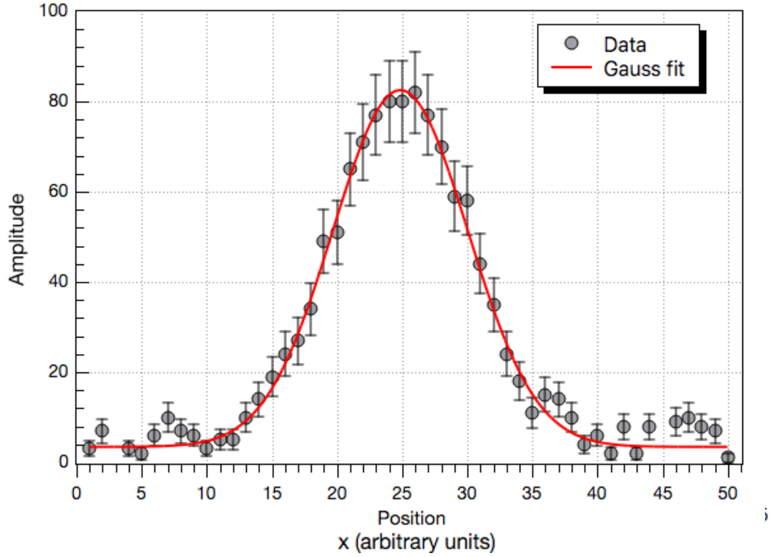
QTiPlot – data analysis

- Correlation, interpolation smoothing
- Curve fitting: Logistic, Boltzmann, Gauss, Lorentz, Multi-peak fit; custom equations



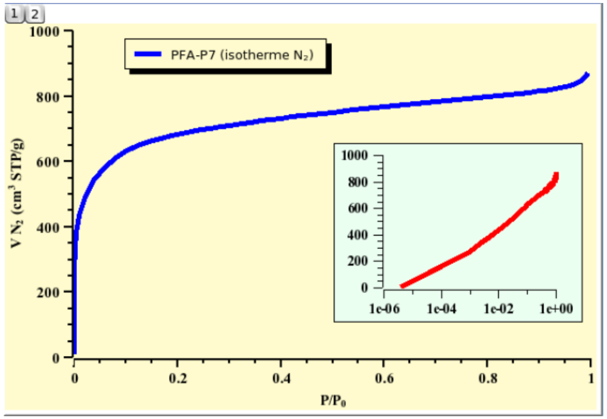
Dataset	Table1_total
Function	A2+(A1-A2)/(1+(x/x0)^p)
A1	18,082.84580 +/- 2.89265
A2	-59.05854 +/- 0.22557
x0	54.67409 +/- 0.00442
p	-4.31410 +/- 0.00066
Chi^2/doF	12,457.58602
R^2	0.99942
Adjusted R^2	0.99939





QTiPlot – statistics and data handling

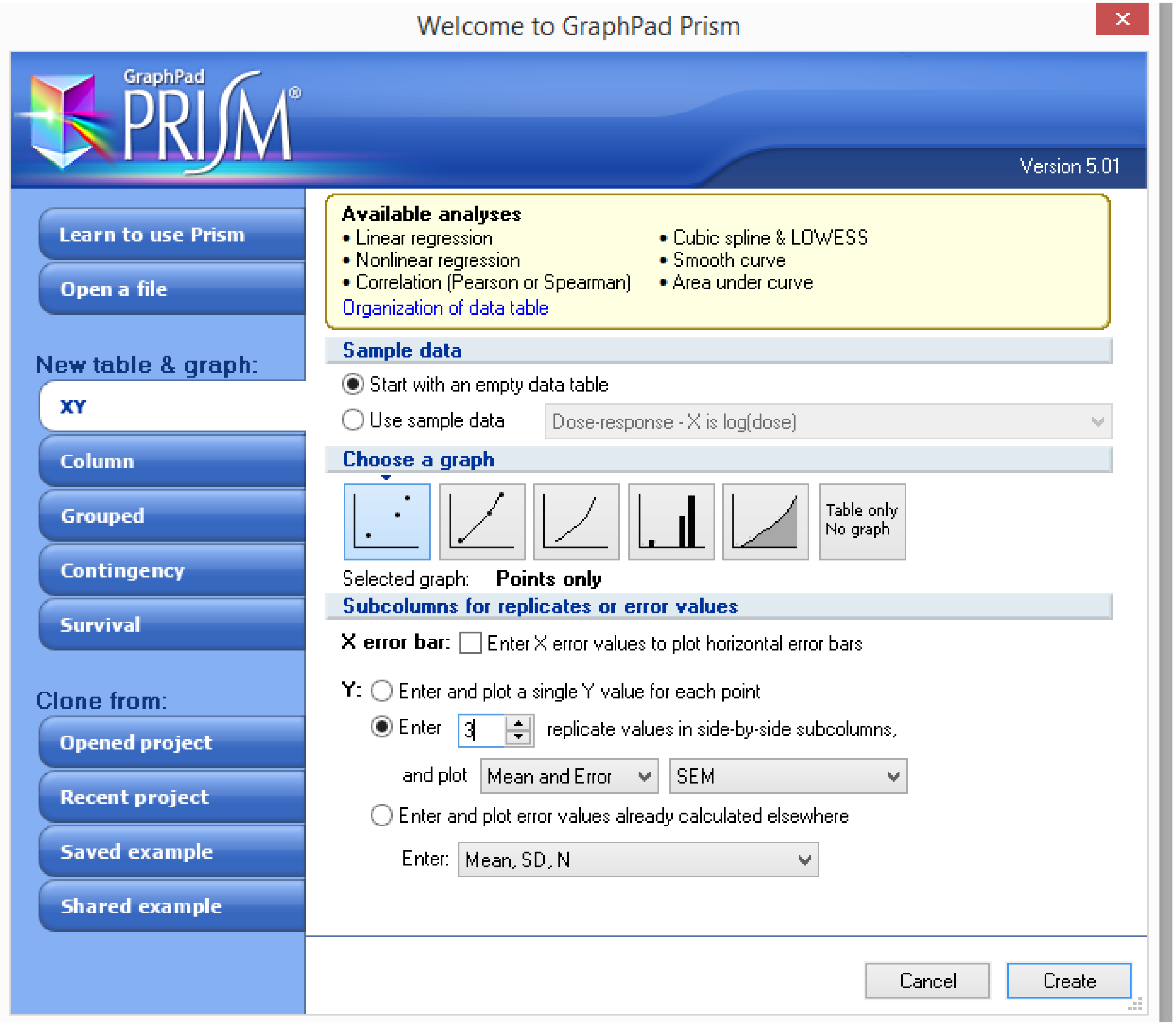
- Non-parametric tests like Mann-Whitney,
- Different types of ANOVA + posthoc tests (Bonferroni, Tukey, Sidak..)
- data exchange with Excel (including graphs with OLE), Origin, LabView
- Import from SQL-databases, MS-Access and Matlab
- direct data import via serial port
- Python scripts and automated data analysis
- Plots can have 2 or more layers



Curve Fitting Software: GraphPad Prism

- www.graphpad.com
- Rental license available at the MedUni (84€/year)
- Data can be copied from Excel
- Structured according to scientists‘ needs
- 1st step: Definition of the data structure

here: version 5



Available analyses
- Linear regression
- Nonlinear regression
- Correlation (Pearson or Spearman)
- Cubic spline & LOWESS
- Smooth curve
- Area under curve

Organization of data table

Sample data

● Start with an empty data table

○ Use sample data: Dose-response - X is log(dose)

Choose a graph

Selected graph: **Points only**

Subcolumns for replicates or error values

X error bar: ☐ Enter X error values to plot horizontal error bars

Y: ○ Enter and plot a single Y value for each point

● Enter 3 replicate values in side-by-side subcolumns,

and plot Mean and Error SEM

○ Enter and plot error values already calculated elsewhere

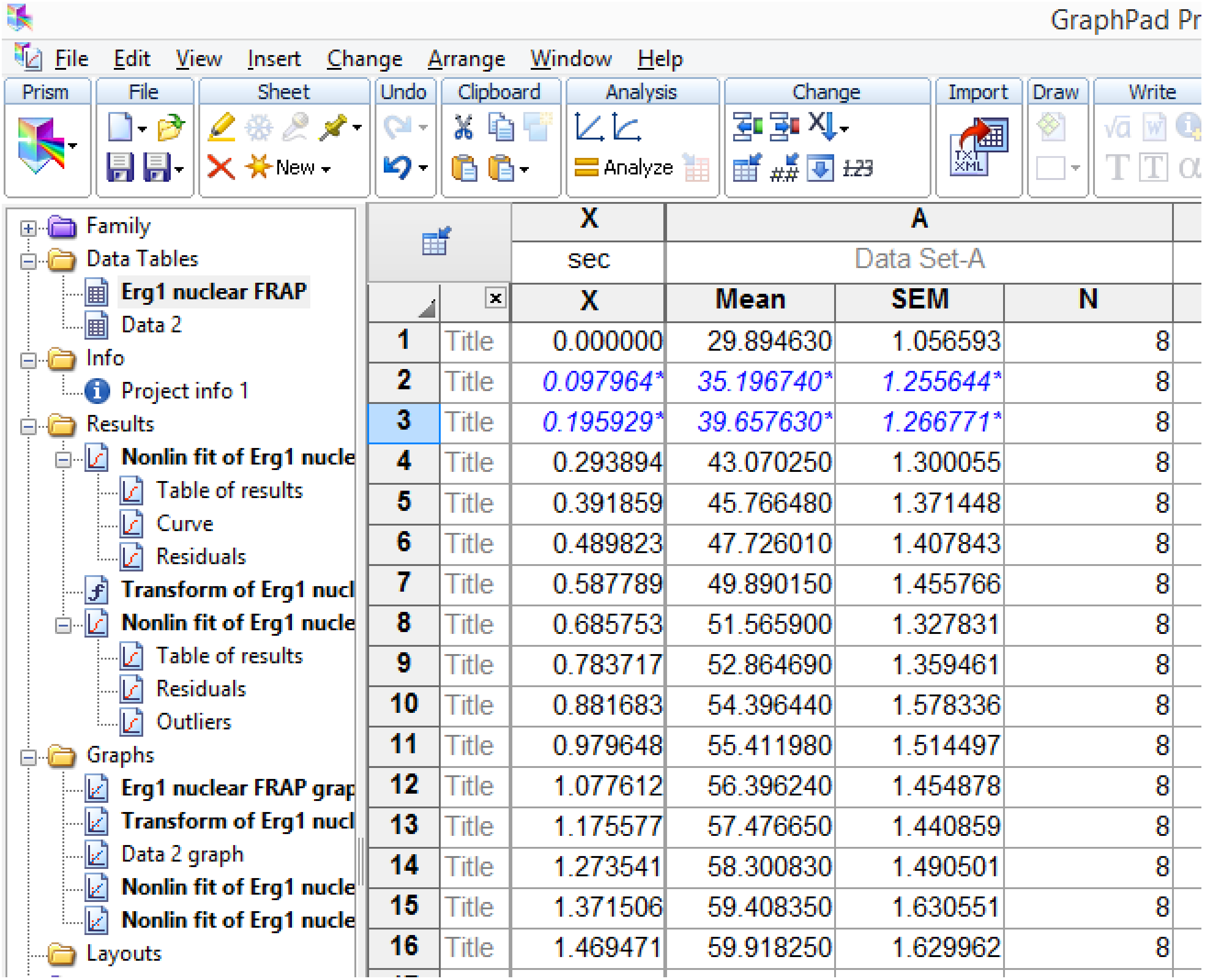
Enter: Mean, SD, N

GraphPad user interface

Data tables → (data can be excluded with „Ctrl-E“)

Results tables →

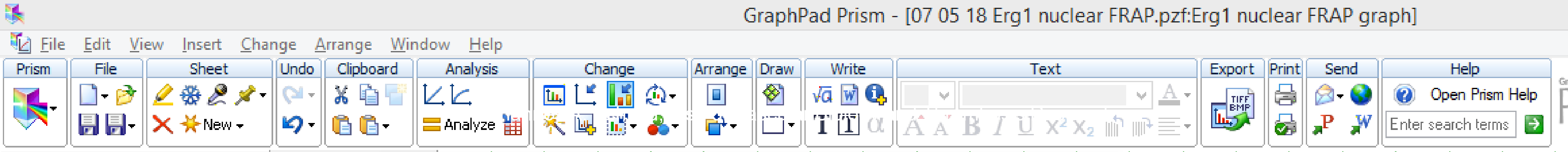
Graphs: → automatically generated (including error bars, if replicates or SD are specified)



- Family
- Data Tables
  - Erg1 nuclear FRAP
  - Data 2
- Info
  - Project info 1
- Results
  - Nonlin fit of Erg1 nucle
    - Table of results
    - Curve
    - Residuals
  - Transform of Erg1 nucl
  - Nonlin fit of Erg1 nucle
    - Table of results
    - Residuals
    - Outliers
- Graphs
  - Erg1 nuclear FRAP grap
  - Transform of Erg1 nucl
  - Data 2 graph
  - Nonlin fit of Erg1 nucle
  - Nonlin fit of Erg1 nucle
- Layouts

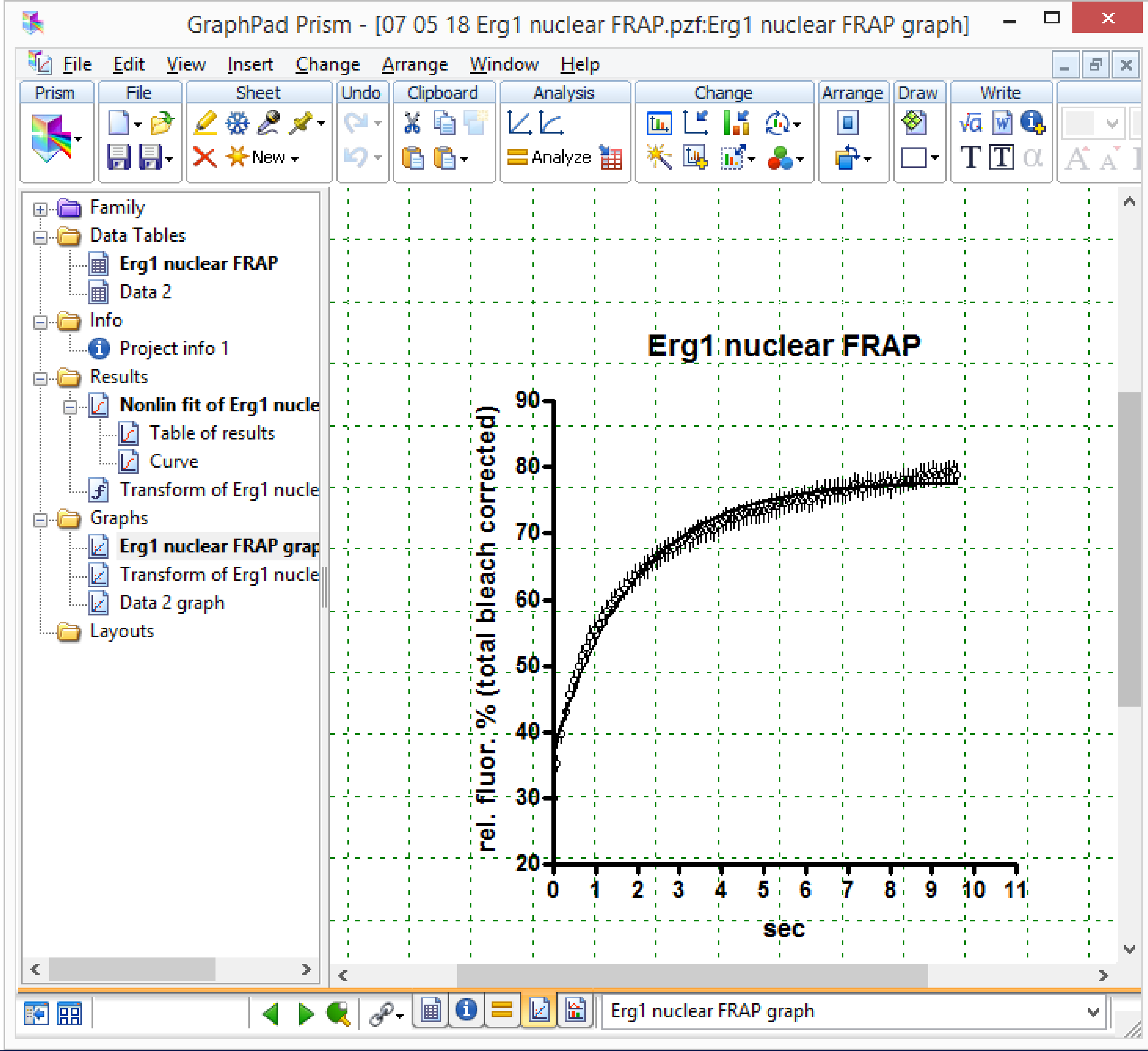
		X	A		
		sec	Data Set-A		
		X	Mean	SEM	N
1	Title	0.000000	29.894630	1.056593	8
2	Title	0.097964*	35.196740*	1.255644*	8
3	Title	0.195929*	39.657630*	1.266771*	8
4	Title	0.293894	43.070250	1.300055	8
5	Title	0.391859	45.766480	1.371448	8
6	Title	0.489823	47.726010	1.407843	8
7	Title	0.587789	49.890150	1.455766	8
8	Title	0.685753	51.565900	1.327831	8
9	Title	0.783717	52.864690	1.359461	8
10	Title	0.881683	54.396440	1.578336	8
11	Title	0.979648	55.411980	1.514497	8
12	Title	1.077612	56.396240	1.454878	8
13	Title	1.175577	57.476650	1.440859	8
14	Title	1.273541	58.300830	1.490501	8
15	Title	1.371506	59.408350	1.630551	8
16	Title	1.469471	59.918250	1.629962	8

Complete toolbar (Tab-structure)

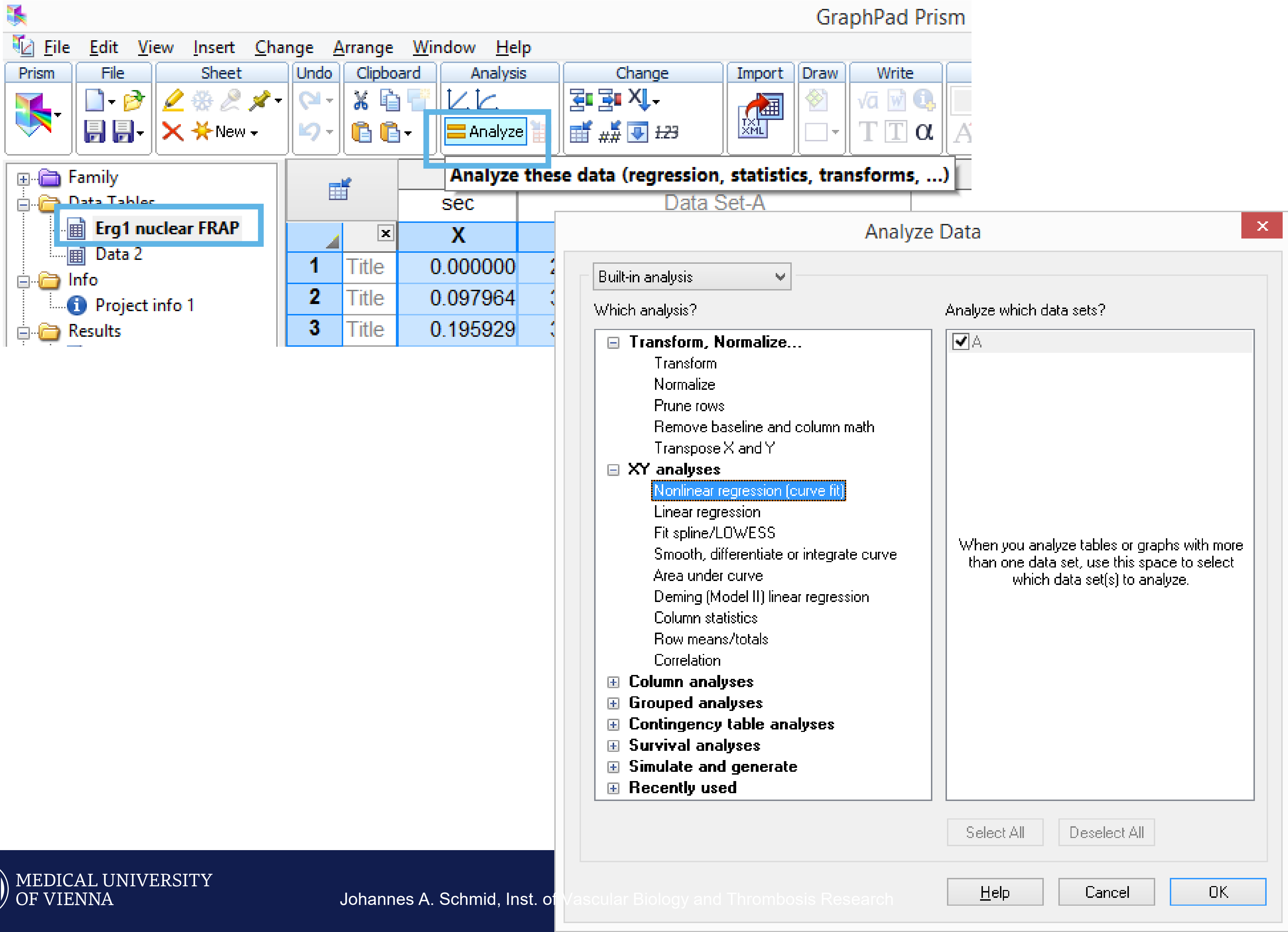


GraphPad Graphs

- error bars are drawn automatically
- graphs and results belonging to the same data sheet are shown in bold in the navigation pane



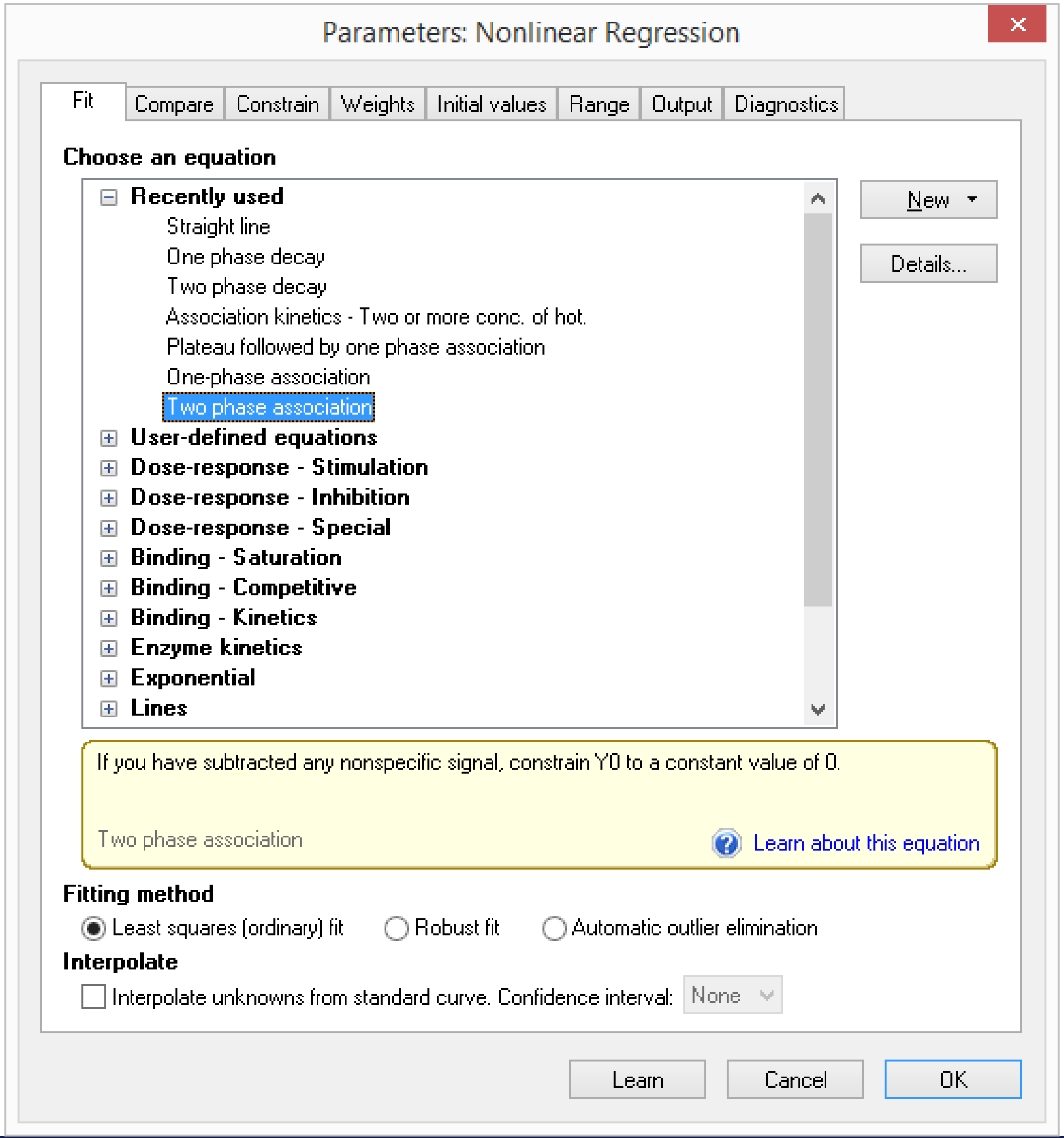
Analyzing data (curve fitting)



Analyze these data (regression, statistics, transforms, ...)

When you analyze tables or graphs with more than one data set, use this space to select which data set(s) to analyze.

Analysis options



Choose an equation

- **Recently used**
  - Straight line
  - One phase decay
  - Two phase decay
  - Association kinetics - Two or more conc. of hot.
  - Plateau followed by one phase association
  - One-phase association
  - Two phase association
- **User-defined equations**
- **Dose-response - Stimulation**
- **Dose-response - Inhibition**
- **Dose-response - Special**
- **Binding - Saturation**
- **Binding - Competitive**
- **Binding - Kinetics**
- **Enzyme kinetics**
- **Exponential**
- **Lines**

If you have subtracted any nonspecific signal, constrain Y0 to a constant value of 0.

Two phase association

Learn about this equation

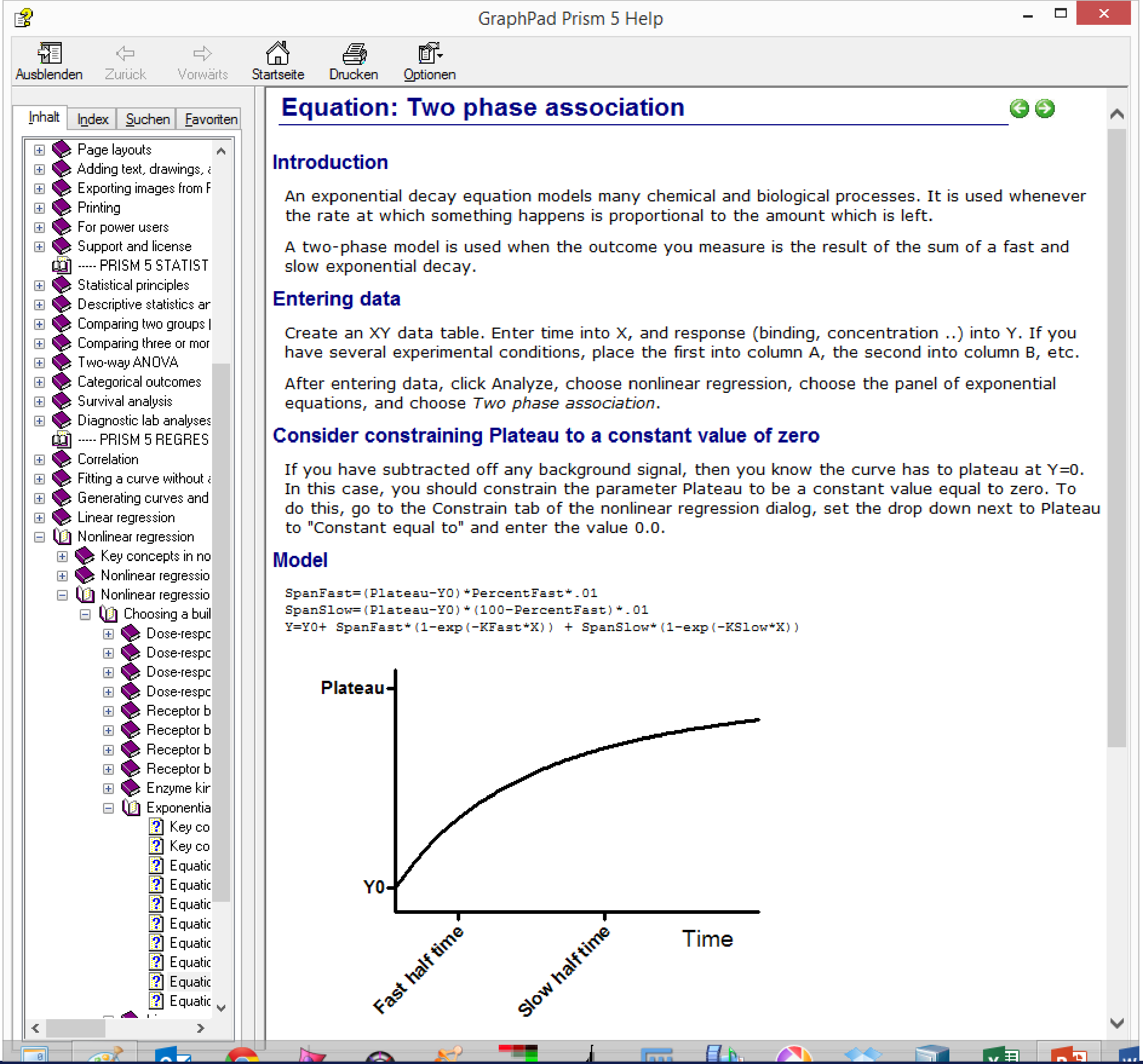
Fitting method

● Least squares (ordinary) fit ○ Robust fit ○ Automatic outlier elimination

Interpolate

☐ Interpolate unknowns from standard curve. Confidence interval: None

- One can choose a fitting algorithm from a large set of equations
- If you are not sure about the correct option you can click on "Learn about this equation"



Equation: Two phase association

Introduction

An exponential decay equation models many chemical and biological processes. It is used whenever the rate at which something happens is proportional to the amount which is left.

A two-phase model is used when the outcome you measure is the result of the sum of a fast and slow exponential decay.

Entering data

Create an XY data table. Enter time into X, and response (binding, concentration ..) into Y. If you have several experimental conditions, place the first into column A, the second into column B, etc.

After entering data, click Analyze, choose nonlinear regression, choose the panel of exponential equations, and choose *Two phase association*.

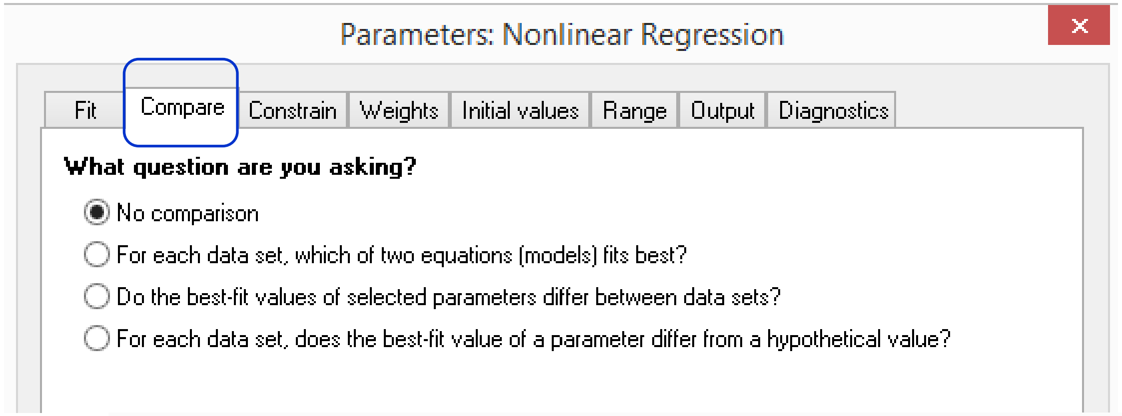
Consider constraining Plateau to a constant value of zero

If you have subtracted off any background signal, then you know the curve has to plateau at Y=0. In this case, you should constrain the parameter Plateau to be a constant value equal to zero. To do this, go to the Constrain tab of the nonlinear regression dialog, set the drop down next to Plateau to "Constant equal to" and enter the value 0.0.

Model

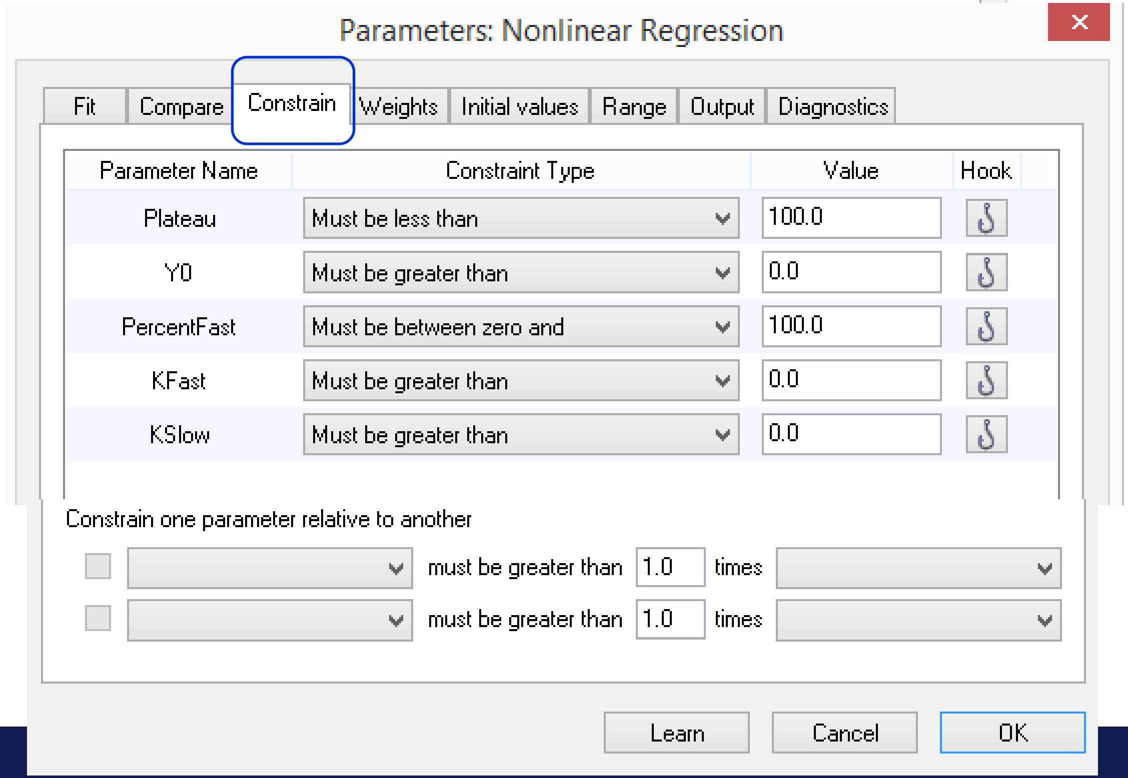
```
SpanFast=(Plateau-Y0)*PercentFast*.01
SpanSlow=(Plateau-Y0)*(100-PercentFast)*.01
Y=Y0+ SpanFast*(1-exp(-KFast*X)) + SpanSlow*(1-exp(-KSlow*X))
```

Fitting parameters I



What question are you asking?

- ● No comparison
- ○ For each data set, which of two equations (models) fits best?
- ○ Do the best-fit values of selected parameters differ between data sets?
- ○ For each data set, does the best-fit value of a parameter differ from a hypothetical value?

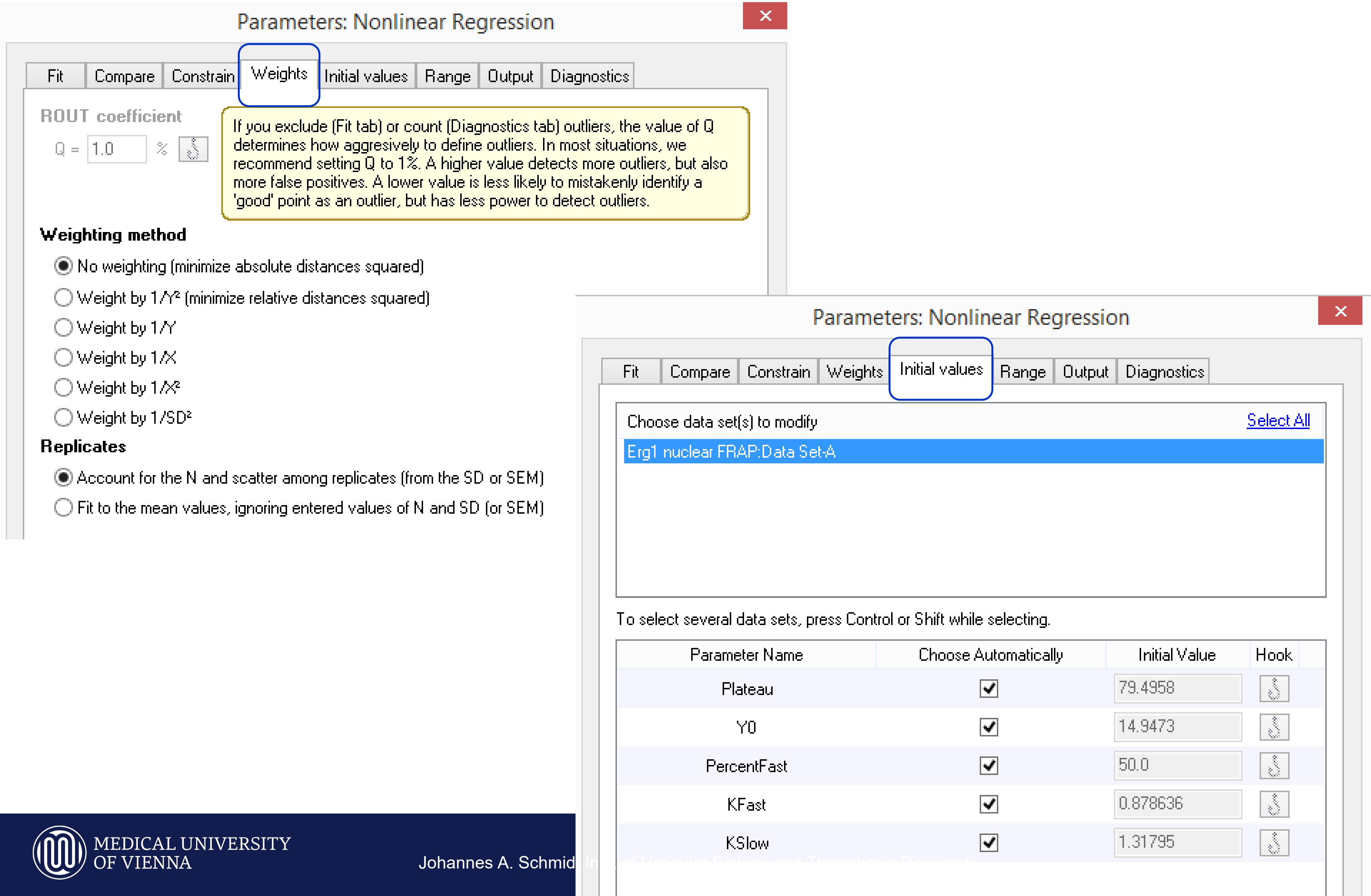


Parameter Name	Constraint Type	Value	Hook
Plateau	Must be less than	100.0	
Y0	Must be greater than	0.0	
PercentFast	Must be between zero and	100.0	
KFast	Must be greater than	0.0	
KSlow	Must be greater than	0.0	

Constrain one parameter relative to another

☐ must be greater than 1.0 times
☐ must be greater than 1.0 times

Fitting parameters II



ROUT coefficient

Q = 1.0 %

If you exclude (Fit tab) or count (Diagnostics tab) outliers, the value of Q determines how aggresively to define outliers. In most situations, we recommend setting Q to 1%. A higher value detects more outliers, but also more false positives. A lower value is less likely to mistakenly identify a 'good' point as an outlier, but has less power to detect outliers.

Weighting method

- ● No weighting (minimize absolute distances squared)
- ○ Weight by 1/Y² (minimize relative distances squared)
- ○ Weight by 1/Y
- ○ Weight by 1/X
- ○ Weight by 1/X²
- ○ Weight by 1/SD²

Replicates

- ● Account for the N and scatter among replicates (from the SD or SEM)
- ○ Fit to the mean values, ignoring entered values of N and SD (or SEM)

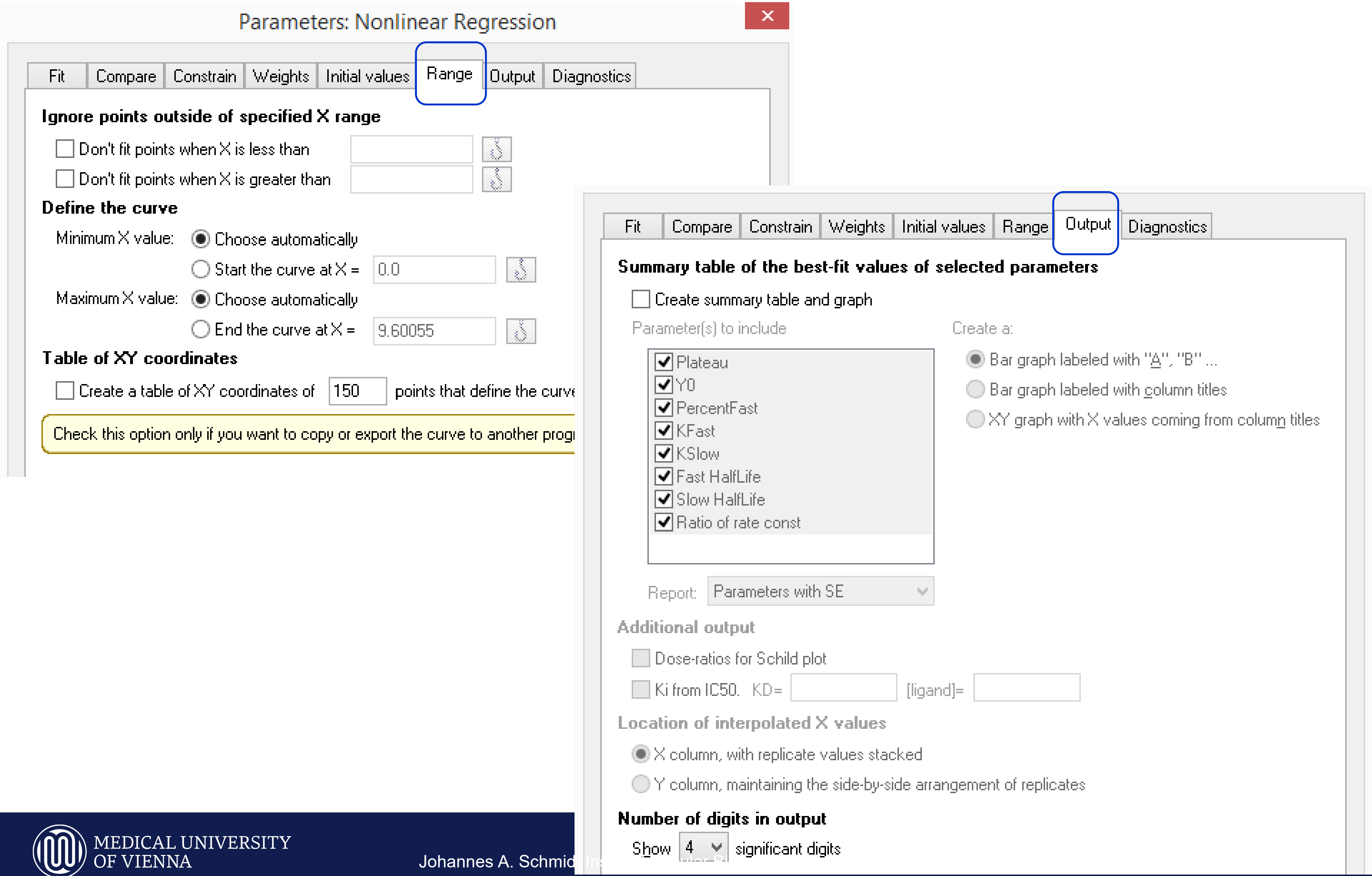
Choose data set(s) to modify

Erg1 nuclear FRAP:Data Set-A

To select several data sets, press Control or Shift while selecting.

Parameter Name	Choose Automatically	Initial Value	Hook
Plateau	☑	79.4958	
Y0	☑	14.9473	
PercentFast	☑	50.0	
KFast	☑	0.878636	
KSlow	☑	1.31795	

Fitting parameters III



Parameters: Nonlinear Regression

Ignore points outside of specified X range

☐ Don't fit points when X is less than

☐ Don't fit points when X is greater than

Define the curve

Minimum X value: ● Choose automatically

○ Start the curve at X = 0.0

Maximum X value: ● Choose automatically

○ End the curve at X = 9.60055

Table of XY coordinates

☐ Create a table of XY coordinates of 150 points that define the curv

Check this option only if you want to copy or export the curve to another prog

Summary table of the best-fit values of selected parameters

☐ Create summary table and graph

Parameter(s) to include

☑ Plateau
☑ Y0
☑ PercentFast
☑ KFast
☑ KSlow
☑ Fast HalfLife
☑ Slow HalfLife
☑ Ratio of rate const

Create a:

● Bar graph labeled with "A", "B" ...
○ Bar graph labeled with column titles
○ XY graph with X values coming from column titles

Report: Parameters with SE

Additional output

☐ Dose-ratios for Schild plot

☐ Ki from IC50. KD= [ligand]=

Location of interpolated X values

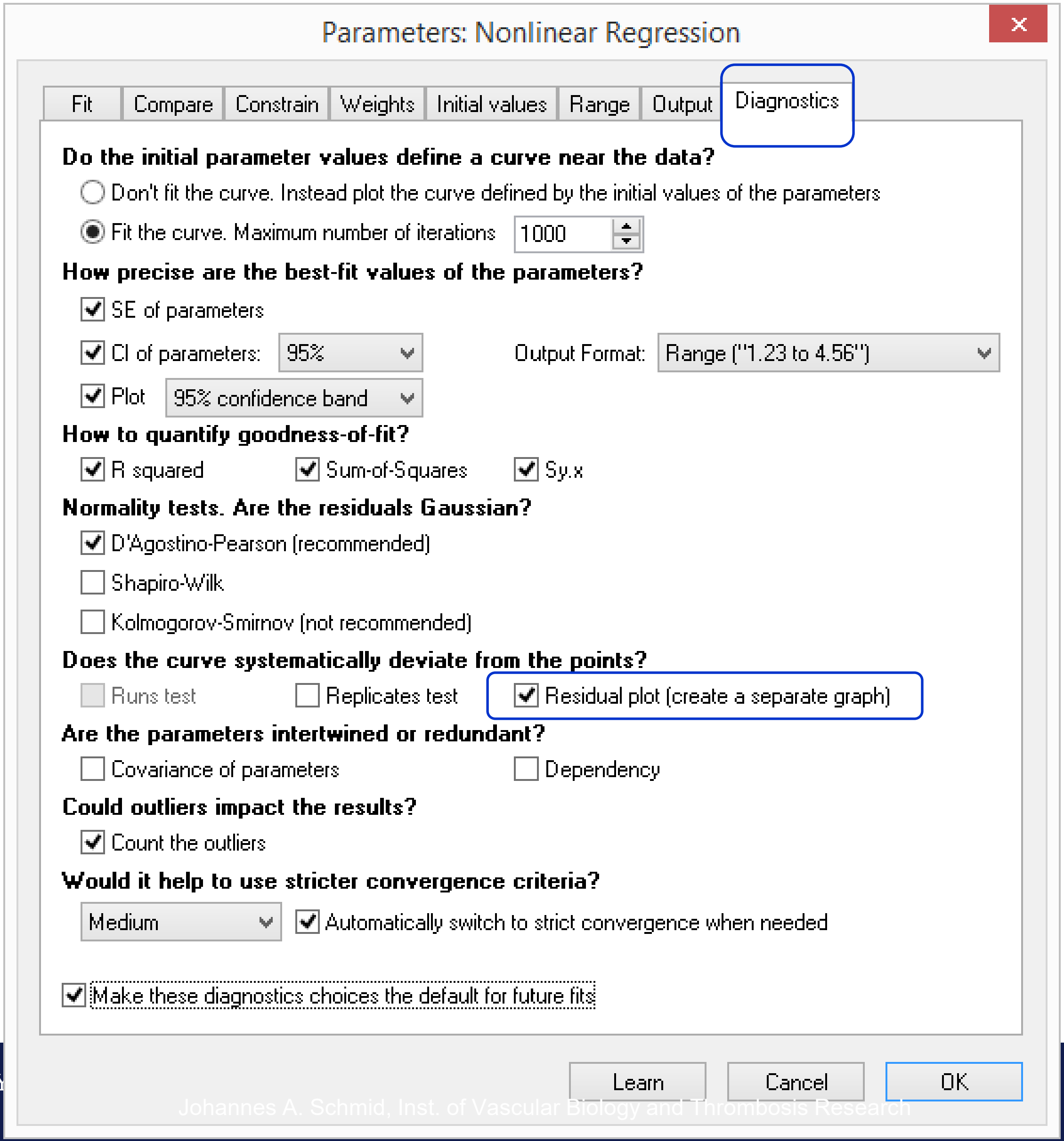
● X column, with replicate values stacked

○ Y column, maintaining the side-by-side arrangement of replicates

Number of digits in output

Show 4 significant digits

Diagnostics of curve fitting



Do the initial parameter values define a curve near the data?

○ Don't fit the curve. Instead plot the curve defined by the initial values of the parameters

● Fit the curve. Maximum number of iterations: 1000

How precise are the best-fit values of the parameters?

☑ SE of parameters

☑ CI of parameters: 95%   Output Format: Range ("1.23 to 4.56")

☑ Plot 95% confidence band

How to quantify goodness-of-fit?

☑ R squared   ☑ Sum-of-Squares   ☑ Sy.x

Normality tests. Are the residuals Gaussian?

☑ D'Agostino-Pearson (recommended)

☐ Shapiro-Wilk

☐ Kolmogorov-Smirnov (not recommended)

Does the curve systematically deviate from the points?

☐ Runs test   ☐ Replicates test   ☑ Residual plot (create a separate graph)

Are the parameters intertwined or redundant?

☐ Covariance of parameters   ☐ Dependency

Could outliers impact the results?

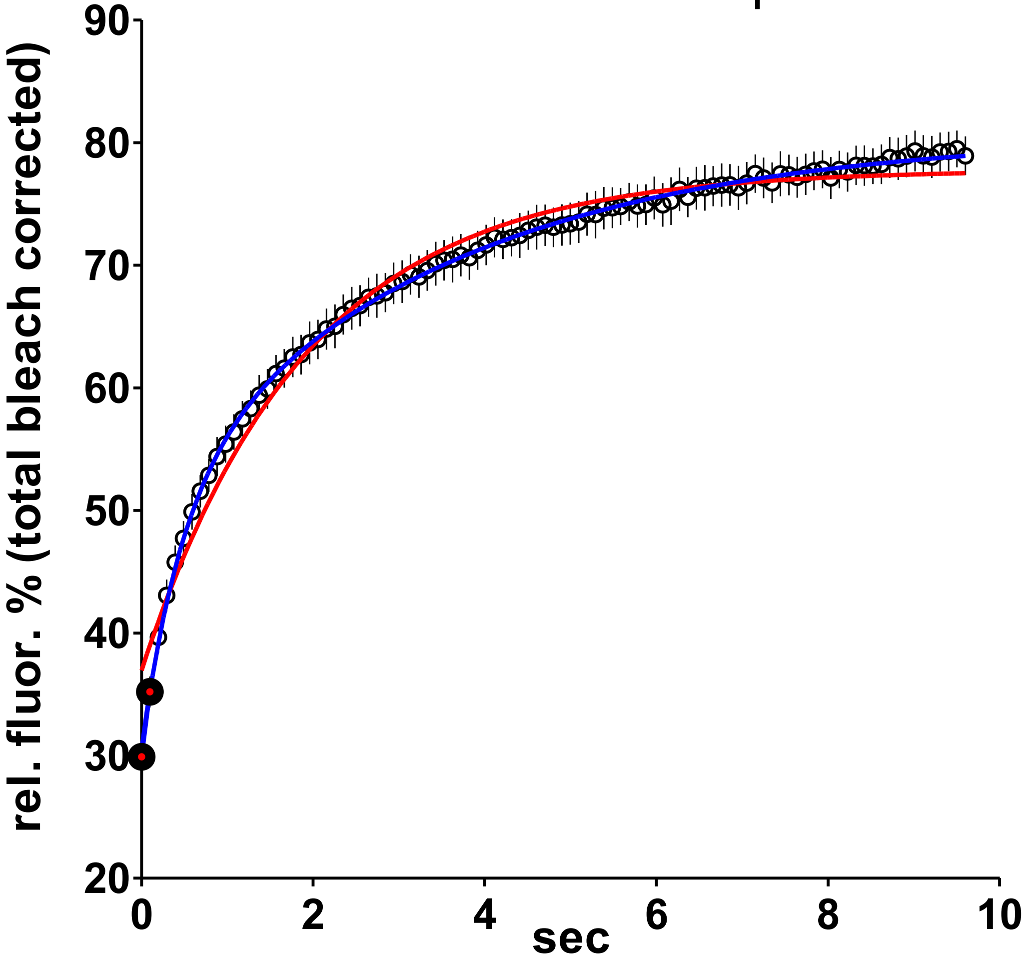
☑ Count the outliers

Would it help to use stricter convergence criteria?

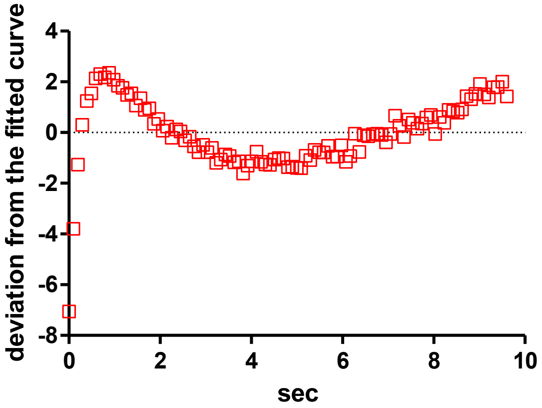
Medium   ☑ Automatically switch to strict convergence when needed

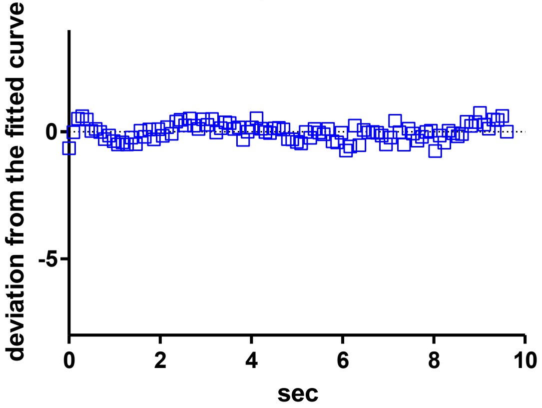
☑ Make these diagnostics choices the default for future fits

The **fitted curve** is shown in the graph; if the same data set is fitted with different equations, all fitted curves can be plotted

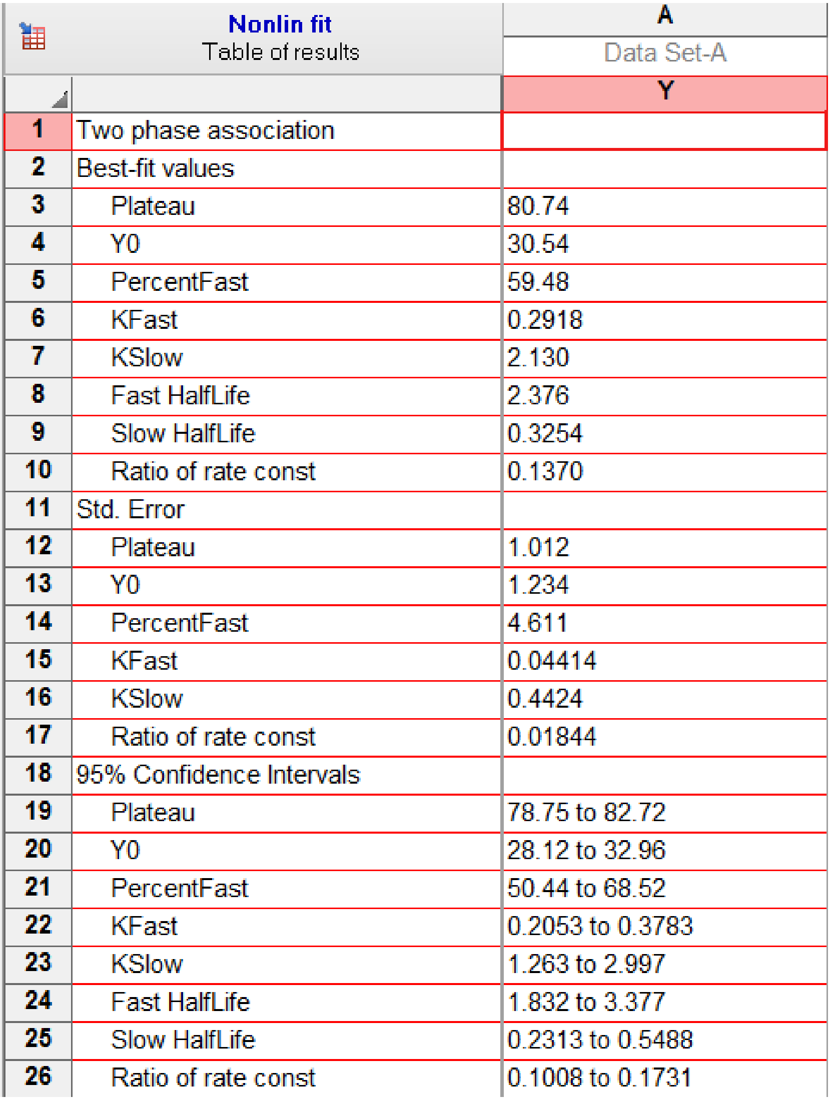


Plot of Residuals


single exp. fit:Residuals

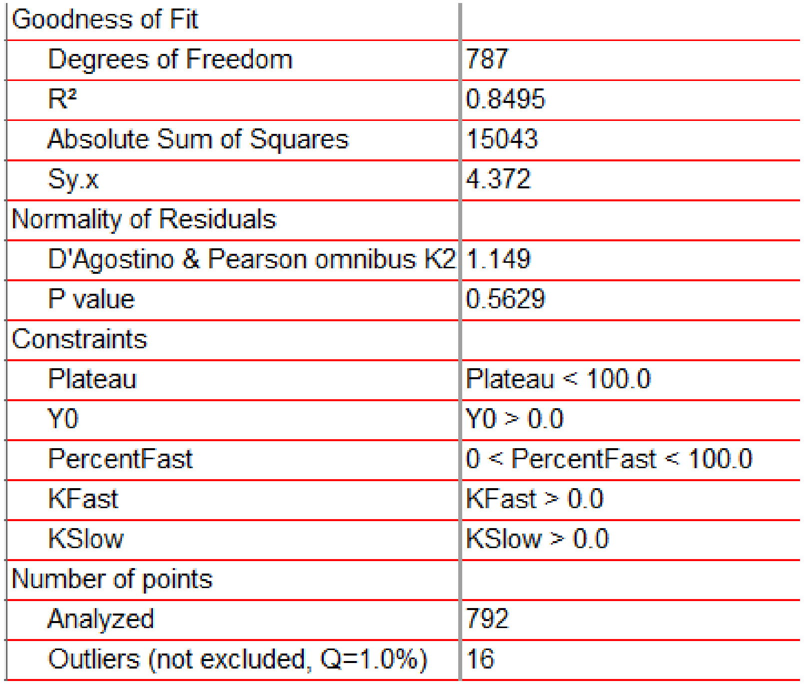

double exp. fit: Residuals

Results Window



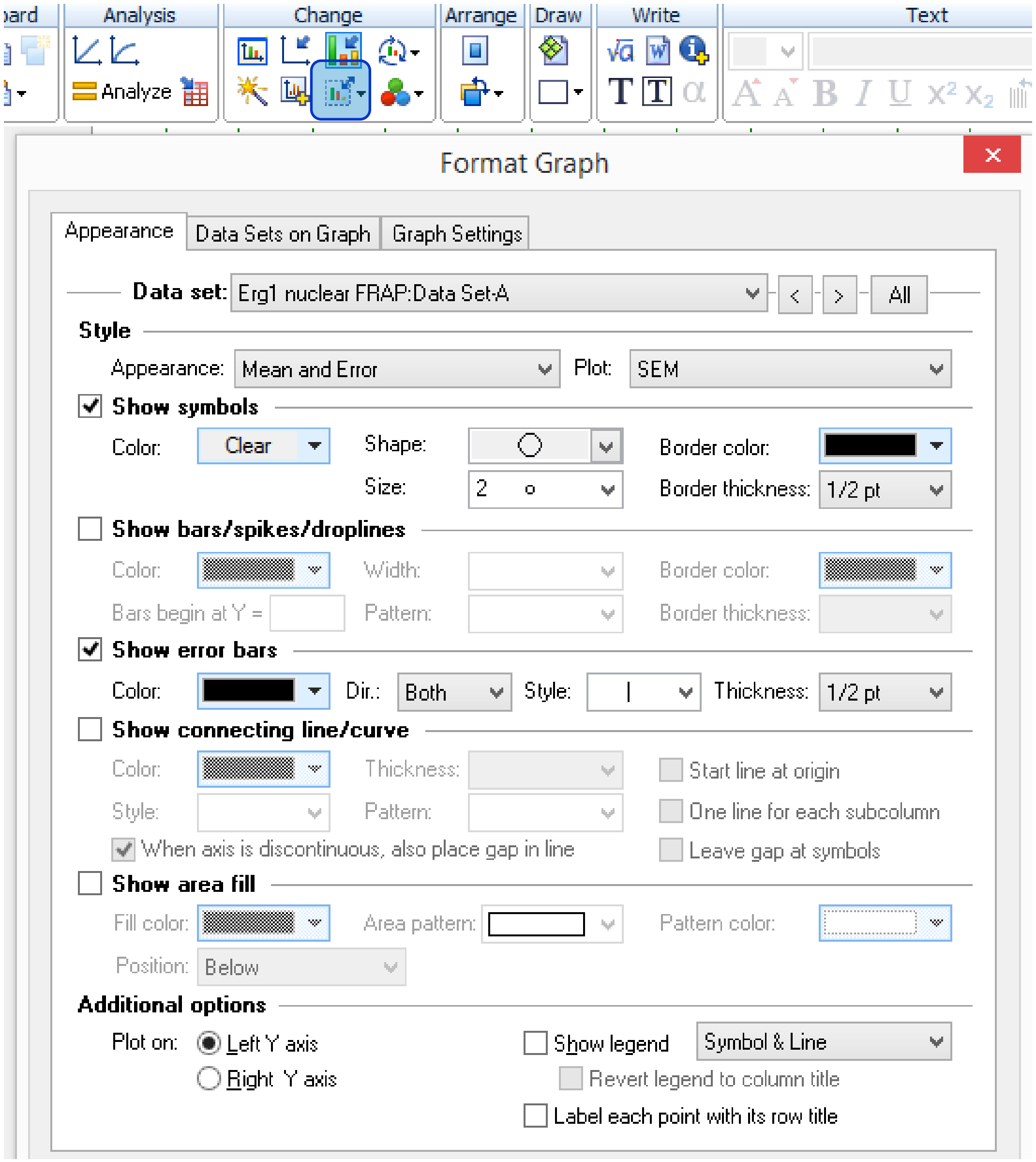
	Nonlin fit Table of results	A Data Set-A Y
1	Two phase association	
2	Best-fit values	
3	Plateau	80.74
4	Y0	30.54
5	PercentFast	59.48
6	KFast	0.2918
7	KSlow	2.130
8	Fast HalfLife	2.376
9	Slow HalfLife	0.3254
10	Ratio of rate const	0.1370
11	Std. Error	
12	Plateau	1.012
13	Y0	1.234
14	PercentFast	4.611
15	KFast	0.04414
16	KSlow	0.4424
17	Ratio of rate const	0.01844
18	95% Confidence Intervals	
19	Plateau	78.75 to 82.72
20	Y0	28.12 to 32.96
21	PercentFast	50.44 to 68.52
22	KFast	0.2053 to 0.3783
23	KSlow	1.263 to 2.997
24	Fast HalfLife	1.832 to 3.377
25	Slow HalfLife	0.2313 to 0.5488
26	Ratio of rate const	0.1008 to 0.1731

- gives the fitted values for equation variables, their standard error, 95% confidence intervals, the goodness of fit (R^2) and diagnostic parameters



Goodness of Fit	
Degrees of Freedom	787
R²	0.8495
Absolute Sum of Squares	15043
Sy.x	4.372
Normality of Residuals	
D'Agostino & Pearson omnibus K2	1.149
P value	0.5629
Constraints	
Plateau	Plateau < 100.0
Y0	Y0 > 0.0
PercentFast	0 < PercentFast < 100.0
KFast	KFast > 0.0
KSlow	KSlow > 0.0
Number of points	
Analyzed	792
Outliers (not excluded, Q=1.0%)	16

Changing of graph elements



Data set: Erg1 nuclear FRAP:Data Set-A

Style

Appearance: Mean and Error
Plot: SEM

☑ **Show symbols**

Color: Clear
Shape: ○
Border color: ■
Size: 2
Border thickness: 1/2 pt

☐ **Show bars/spikes/droplines**

Color: ▨
Width:
Border color: ▨
Bars begin at Y =
Pattern:
Border thickness:

☑ **Show error bars**

Color: ■
Dir.: Both
Style: |
Thickness: 1/2 pt

☐ **Show connecting line/curve**

Color: ▨
Thickness:
☐ Start line at origin
Style:
Pattern:
☐ One line for each subcolumn
☑ When axis is discontinuous, also place gap in line
☐ Leave gap at symbols

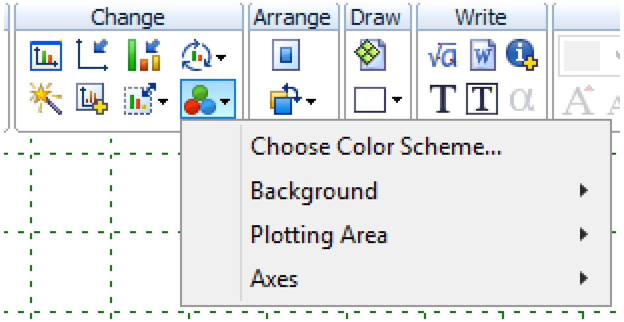
☐ **Show area fill**

Fill color: ▨
Area pattern:
Pattern color:
Position: Below

Additional options

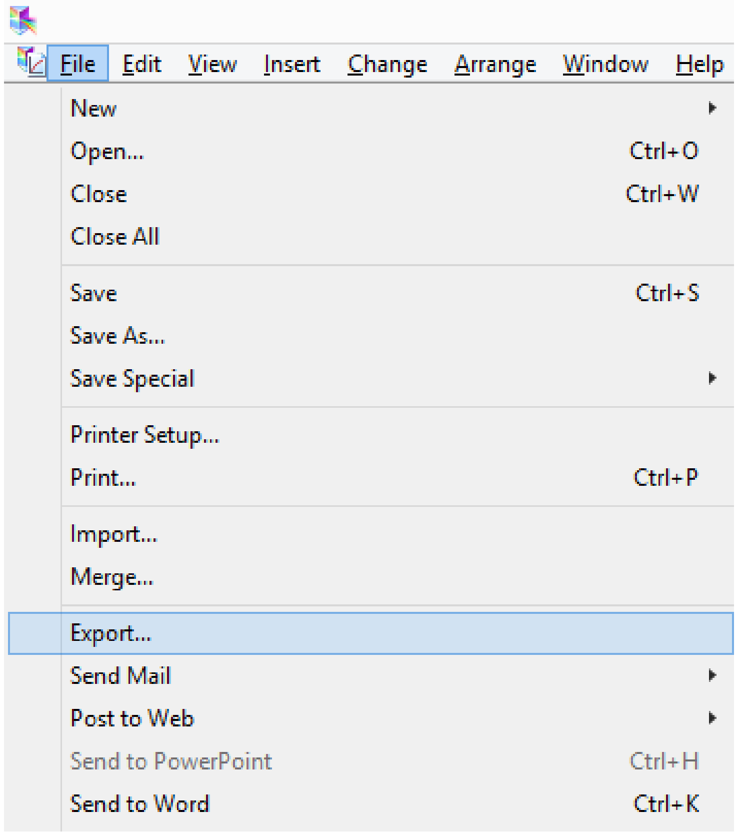
Plot on: ● Left Y axis
○ Right Y axis
☐ Show legend: Symbol & Line
☐ Revert legend to column title
☐ Label each point with its row title

< the appearance of individual datasets can be changed (or all at once)
< plotting of SEM or SD error bars can be set
< symbols, borders, lines, error bars and legends can be defined

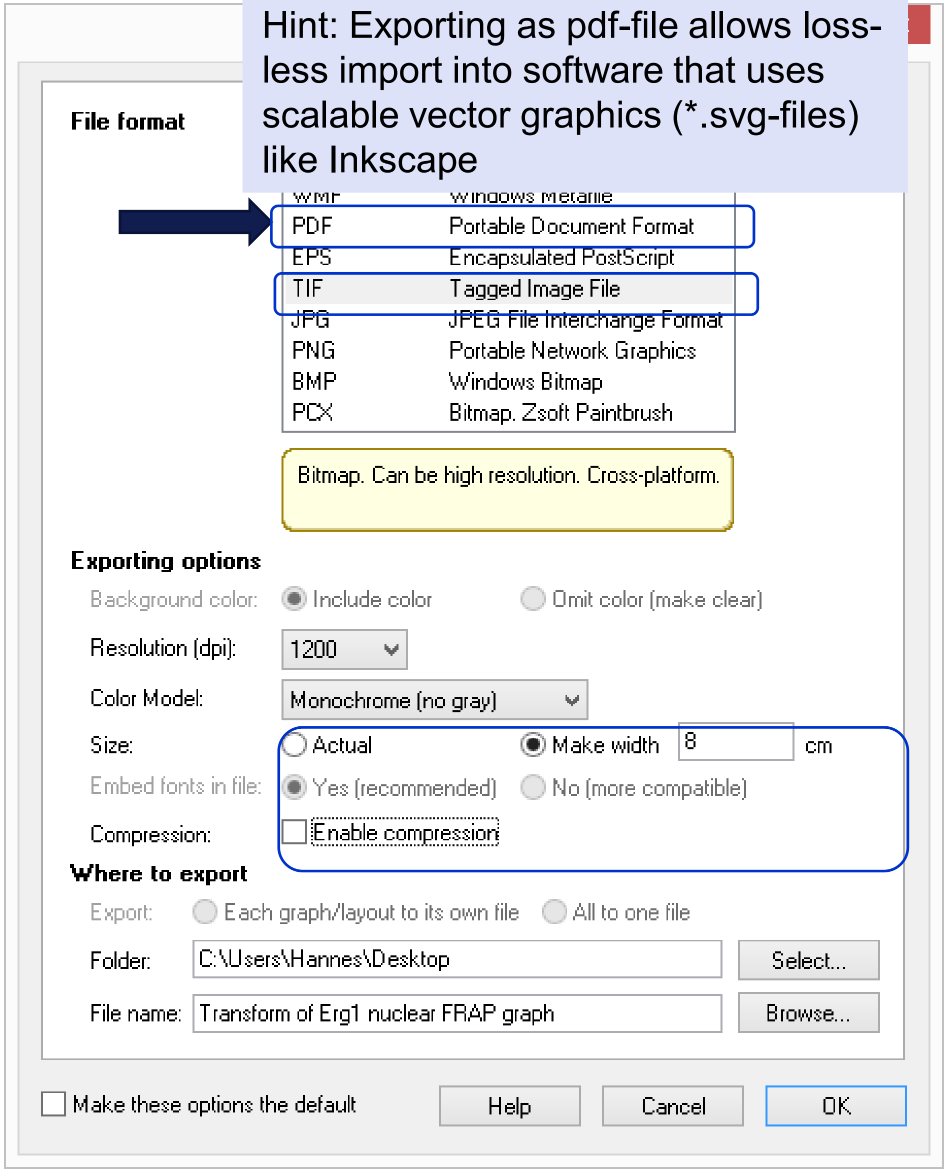


Exporting of high resolution graphs

You can either copy/paste the graph (e.g. into Word as GraphPad object) or export it with defined specifications (e.g. at high resolution for publication: monochrome, TIF, 1200 dpi)



Hint: Exporting as pdf-file allows loss-less import into software that uses scalable vector graphics (*.svg-files) like Inkscape



File format

WMF	Windows Metafile
PDF	Portable Document Format
EPS	Encapsulated PostScript
TIF	Tagged Image File
JPG	JPEG File Interchange Format
PNG	Portable Network Graphics
BMP	Windows Bitmap
PCX	Bitmap. Zsoft Paintbrush

Bitmap. Can be high resolution. Cross-platform.

Exporting options

Background color: ● Include color ○ Omit color (make clear)

Resolution (dpi): 1200

Color Model: Monochrome (no gray)

Size: ○ Actual ● Make width 8 cm

Embed fonts in file: ● Yes (recommended) ○ No (more compatible)

Compression: ☐ Enable compression

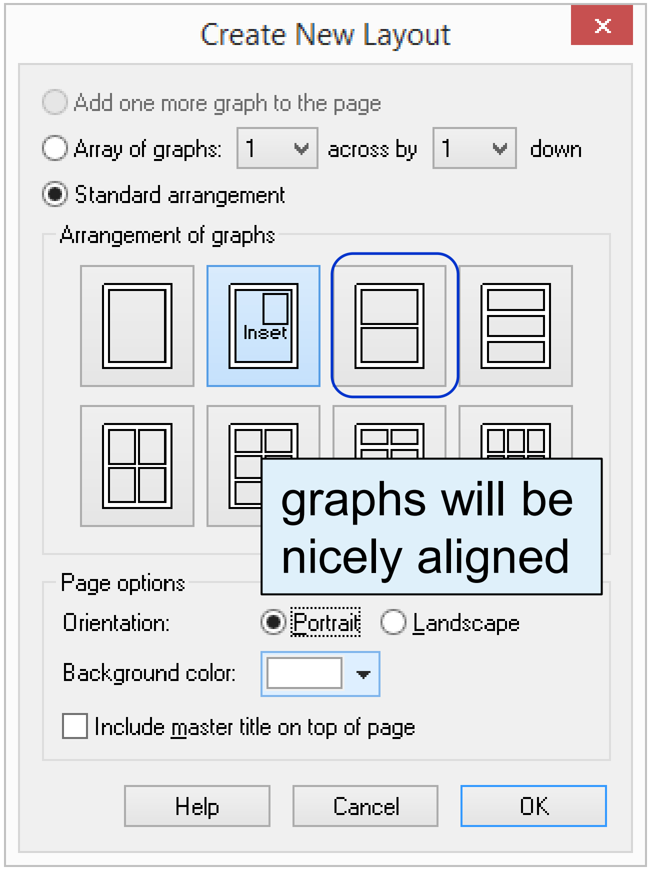
Where to export

Export: ○ Each graph/layout to its own file ○ All to one file

Folder: C:\Users\Hannes\Desktop

File name: Transform of Erg1 nuclear FRAP graph

Creating layouts of several graphs



Create New Layout

○ Add one more graph to the page

○ Array of graphs: 1 across by 1 down

● Standard arrangement

Arrangement of graphs

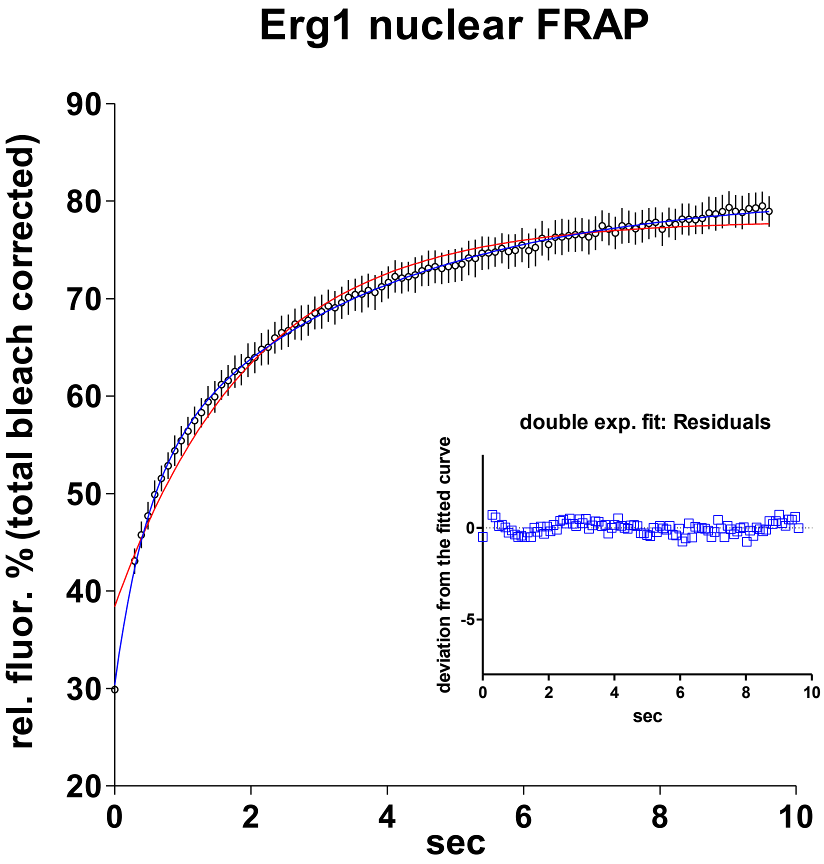
Page options

Orientation: ● Portrait ○ Landscape

Background color:

☐ Include master title on top of page

graphs will be nicely aligned



Calculating values from a standard curve (after non-linear regression). Example: dose-response

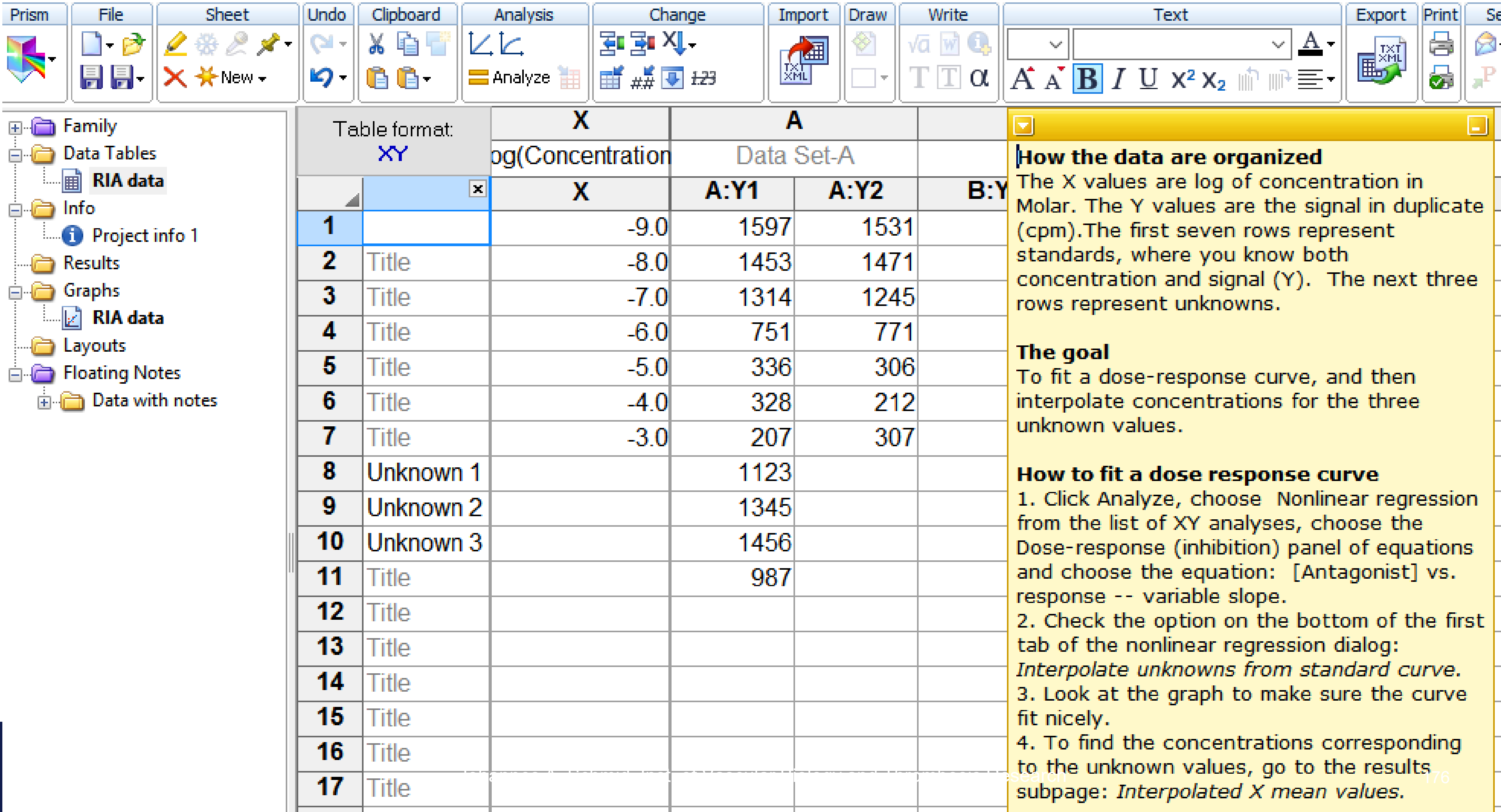


Table format: XY

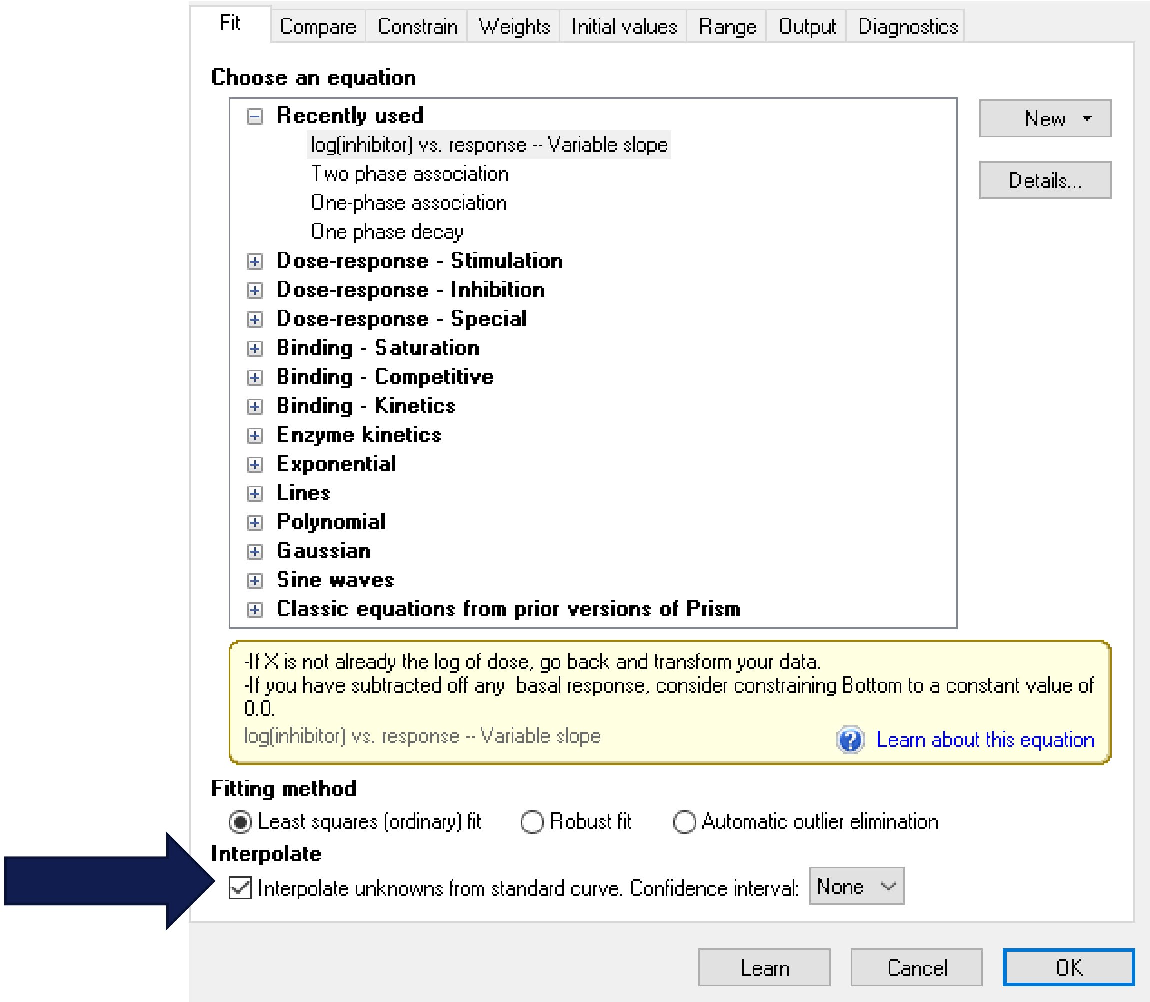
		X	A		B:Y
		og(Concentration	Data Set-A		
		X	A:Y1	A:Y2	B:Y
1		-9.0	1597	1531	
2	Title	-8.0	1453	1471	
3	Title	-7.0	1314	1245	
4	Title	-6.0	751	771	
5	Title	-5.0	336	306	
6	Title	-4.0	328	212	
7	Title	-3.0	207	307	
8	Unknown 1		1123		
9	Unknown 2		1345		
10	Unknown 3		1456		
11	Title		987		
12	Title				
13	Title				
14	Title				
15	Title				
16	Title				
17	Title				

How the data are organized
The X values are log of concentration in Molar. The Y values are the signal in duplicate (cpm).The first seven rows represent standards, where you know both concentration and signal (Y). The next three rows represent unknowns.

The goal
To fit a dose-response curve, and then interpolate concentrations for the three unknown values.

How to fit a dose response curve
1. Click Analyze, choose Nonlinear regression from the list of XY analyses, choose the Dose-response (inhibition) panel of equations and choose the equation: [Antagonist] vs. response -- variable slope.
2. Check the option on the bottom of the first tab of the nonlinear regression dialog: *Interpolate unknowns from standard curve.*
3. Look at the graph to make sure the curve fit nicely.
4. To find the concentrations corresponding to the unknown values, go to the results subpage: *Interpolated X mean values.*

Calculating values from a standard curve (after non-linear regression). Example: dose-response



Choose an equation

- ⊟ **Recently used**
  - log(inhibitor) vs. response -- Variable slope
  - Two phase association
  - One-phase association
  - One phase decay
- ⊞ **Dose-response - Stimulation**
- ⊞ **Dose-response - Inhibition**
- ⊞ **Dose-response - Special**
- ⊞ **Binding - Saturation**
- ⊞ **Binding - Competitive**
- ⊞ **Binding - Kinetics**
- ⊞ **Enzyme kinetics**
- ⊞ **Exponential**
- ⊞ **Lines**
- ⊞ **Polynomial**
- ⊞ **Gaussian**
- ⊞ **Sine waves**
- ⊞ **Classic equations from prior versions of Prism**

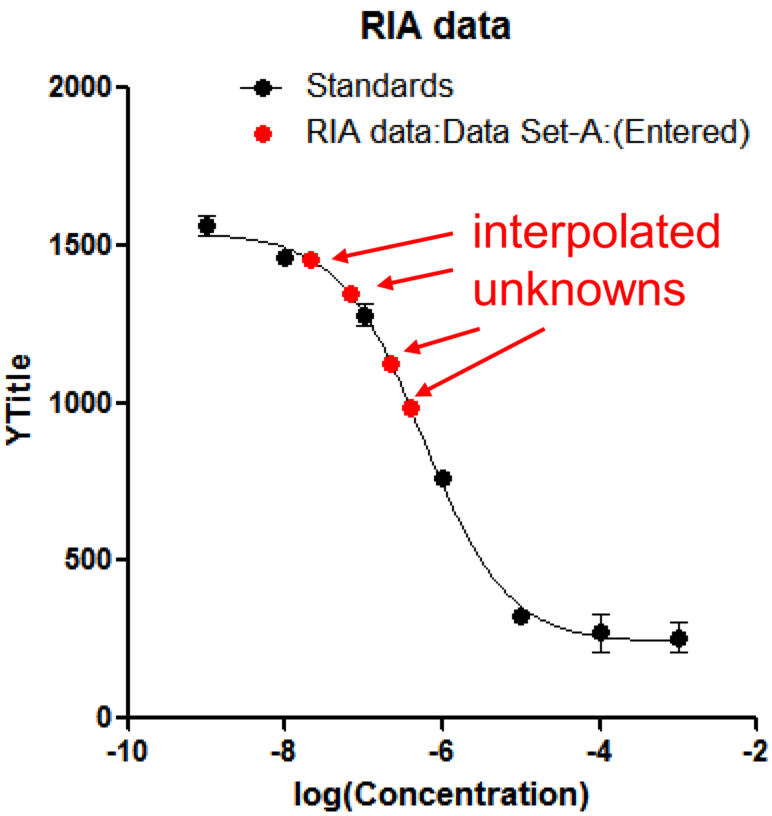
-If X is not already the log of dose, go back and transform your data.
-If you have subtracted off any basal response, consider constraining Bottom to a constant value of 0.0.
log(inhibitor) vs. response -- Variable slope
Learn about this equation

Fitting method

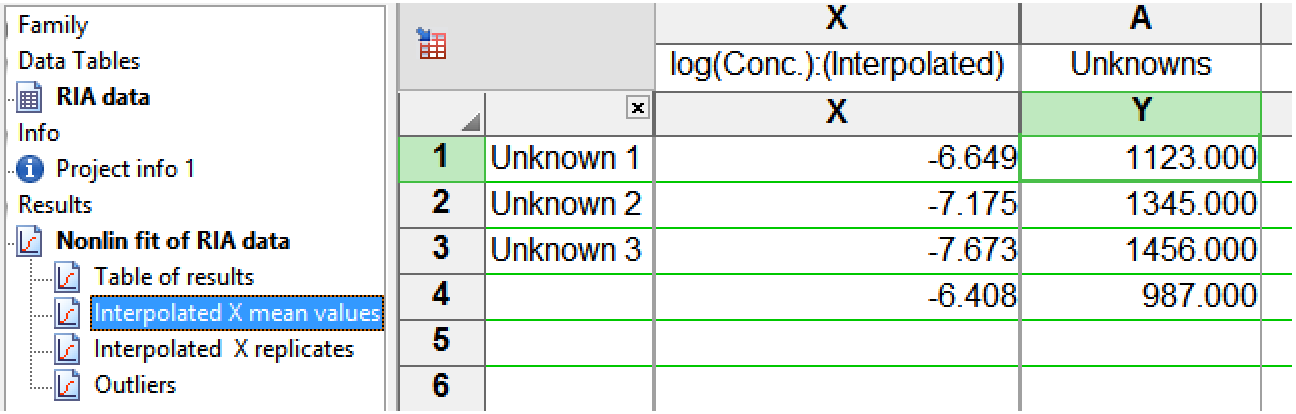
● Least squares (ordinary) fit ○ Robust fit ○ Automatic outlier elimination

Interpolate

☑ Interpolate unknowns from standard curve. Confidence interval: None



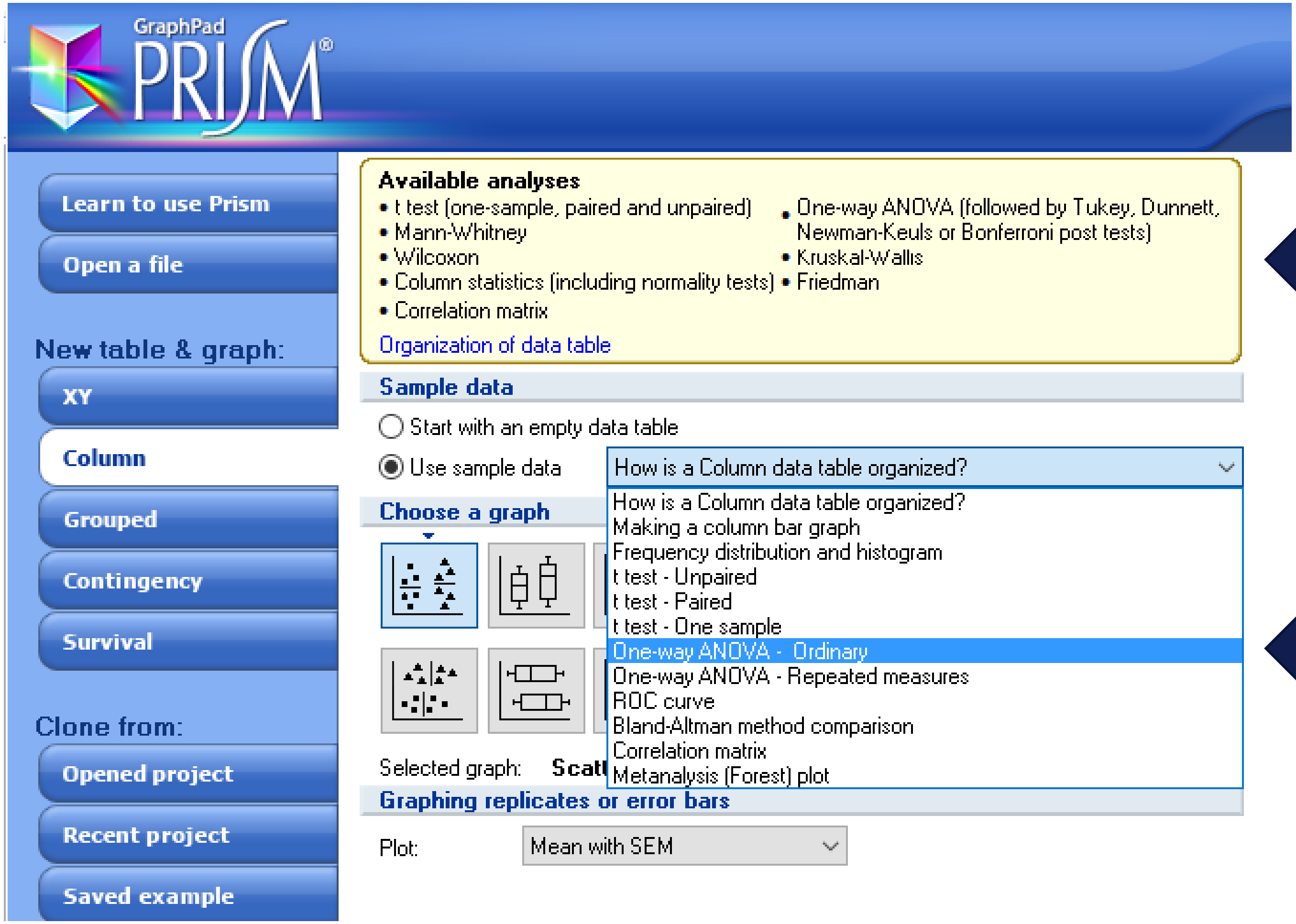
interpolated unknowns



		X	A
		log(Conc.):(Interpolated)	Unknowns
		X	Y
1	Unknown 1	-6.649	1123.000
2	Unknown 2	-7.175	1345.000
3	Unknown 3	-7.673	1456.000
4		-6.408	987.000
5			
6			

Statistics with GraphPad-Prism

http://cdn.graphpad.com/docs/prism/6/Prism-6-Statistics-Guide.pdf
Excellent Statistics Guide! (402 pages).



Available analyses

- t test (one-sample, paired and unpaired)
- Mann-Whitney
- Wilcoxon
- Column statistics (including normality tests)
- Correlation matrix
- One-way ANOVA (followed by Tukey, Dunnett, Newman-Keuls or Bonferroni post tests)
- Kruskal-Wallis
- Friedman

Organization of data table

Sample data

○ Start with an empty data table

● Use sample data: How is a Column data table organized?

- How is a Column data table organized?
- Making a column bar graph
- Frequency distribution and histogram
- t test - Unpaired
- t test - Paired
- t test - One sample
- One-way ANOVA - Ordinary
- One-way ANOVA - Repeated measures
- ROC curve
- Bland-Altman method comparison
- Correlation matrix
- Metanalysis (Forest) plot

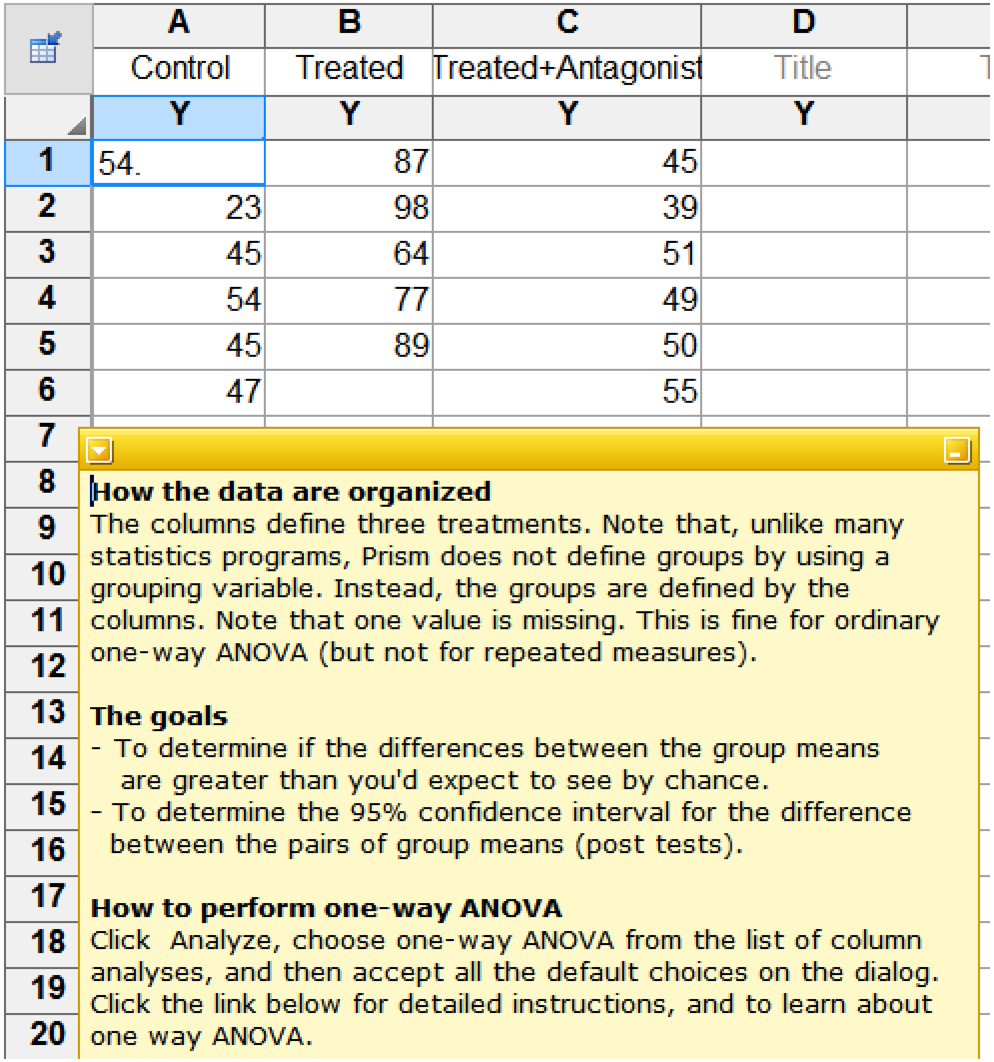
Choose a graph

Selected graph: Scatt

Graphing replicates or error bars

Plot: Mean with SEM

ANOVA (Analysis of Variances)



	A	B	C	D
	Control	Treated	Treated+Antagonist	Title
	Y	Y	Y	Y
1	54.	87	45	
2	23	98	39	
3	45	64	51	
4	54	77	49	
5	45	89	50	
6	47		55	

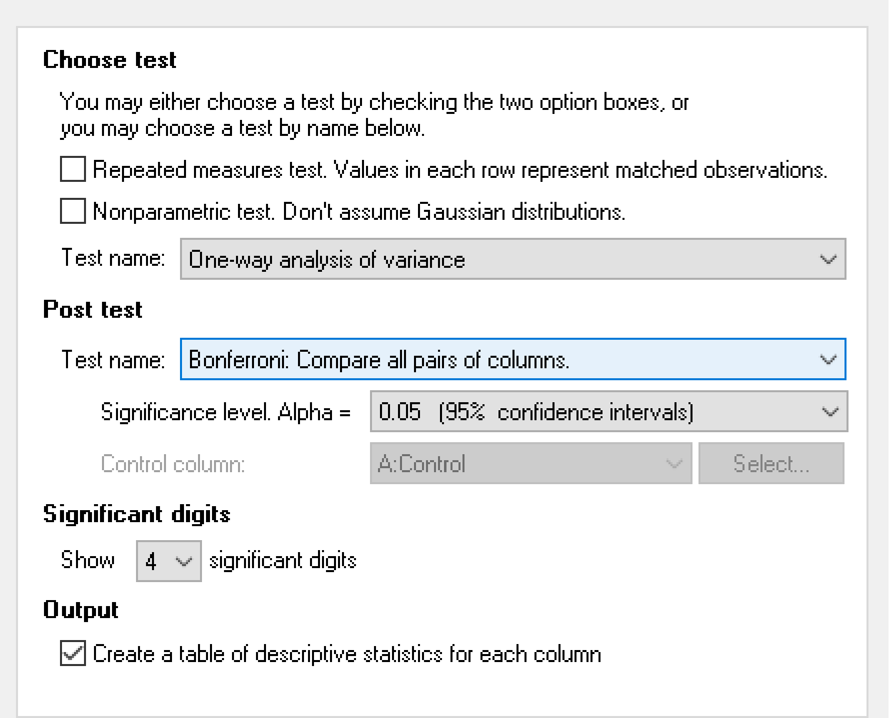
How the data are organized
The columns define three treatments. Note that, unlike many statistics programs, Prism does not define groups by using a grouping variable. Instead, the groups are defined by the columns. Note that one value is missing. This is fine for ordinary one-way ANOVA (but not for repeated measures).

The goals

- To determine if the differences between the group means are greater than you'd expect to see by chance.
- To determine the 95% confidence interval for the difference between the pairs of group means (post tests).

How to perform one-way ANOVA
Click Analyze, choose one-way ANOVA from the list of column analyses, and then accept all the default choices on the dialog. Click the link below for detailed instructions, and to learn about one way ANOVA.

ANOVA



Choose test

You may either choose a test by checking the two option boxes, or you may choose a test by name below.

☐ Repeated measures test. Values in each row represent matched observations.

☐ Nonparametric test. Don't assume Gaussian distributions.

Test name: One-way analysis of variance

Post test

Test name: Bonferroni: Compare all pairs of columns.

Significance level. Alpha = 0.05 (95% confidence intervals)

Control column: A:Control

Significant digits

Show 4 significant digits

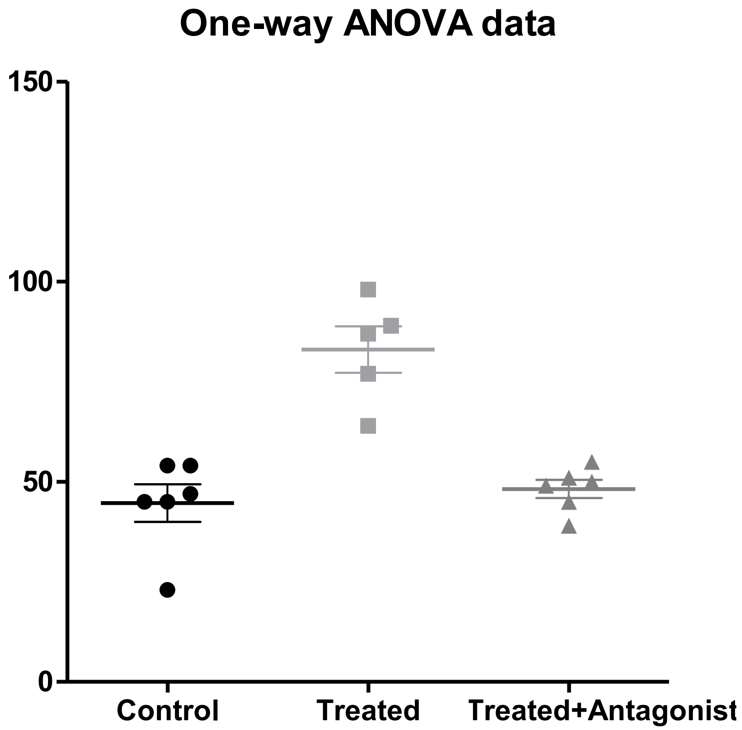
Output

☑ Create a table of descriptive statistics for each column

ANOVA alone just tells you, whether the columns (groups) are the same or not; it does not tell you, which groups differ significantly from each other. The latter question can be answered with a „Post test“ such as Bonferroni

ANOVA Results

Table Analyzed	One-way ANOVA data
One-way analysis of variance	
P value	< 0.0001
P value summary	***
Are means signif. different? (P < 0.05)	Yes
Number of groups	3
F	22.57
R squared	0.7633
Bartlett's test for equal variances	
Bartlett's statistic (corrected)	2.986
P value	0.2247
P value summary	ns
Do the variances differ signif. (P < 0.05)	No



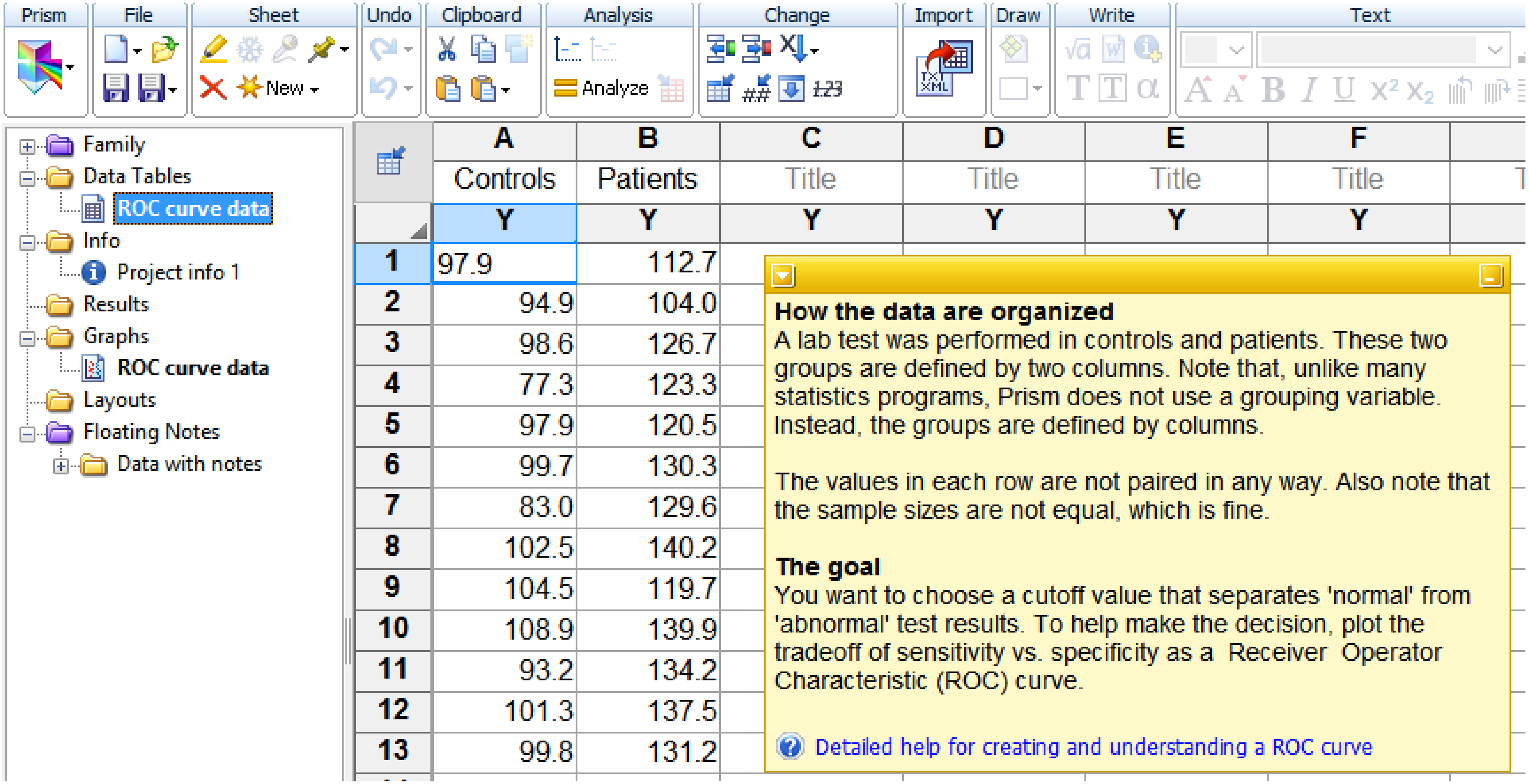
ANOVA Table	SS	df	MS
Treatment (between columns)	4760	2	2380
Residual (within columns)	1476	14	105.4
Total	6236	16	

Results of the Post-test (Bonferroni) to detect, which groups differ from each other

Bonferroni's Multiple Comparison Test	Mean Diff.	t	Significant? P < 0.05?	Summary	95% CI of diff
Control vs Treated	-38.33	6.165	Yes	***	-55.23 to -21.43
Control vs Treated+Antagonist	-3.500	0.5904	No	ns	-19.61 to 12.61
Treated vs Treated+Antagonist	34.83	5.602	Yes	***	17.93 to 51.73

ROC curves in GraphPad Prism

(Receiver Operator Characteristics – to choose a cut-off value that separates for instance normal from disease



	A	B
	Controls	Patients
	Y	Y
1	97.9	112.7
2	94.9	104.0
3	98.6	126.7
4	77.3	123.3
5	97.9	120.5
6	99.7	130.3
7	83.0	129.6
8	102.5	140.2
9	104.5	119.7
10	108.9	139.9
11	93.2	134.2
12	101.3	137.5
13	99.8	131.2

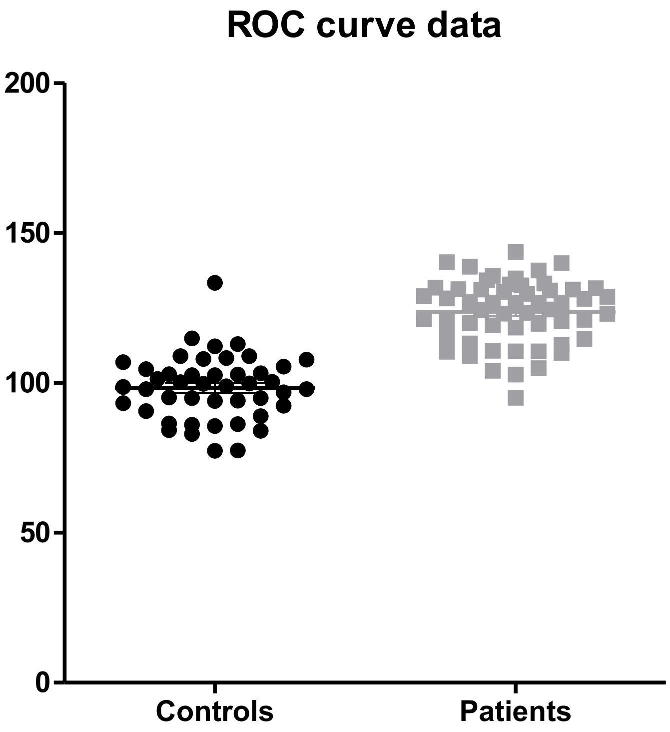
How the data are organized
A lab test was performed in controls and patients. These two groups are defined by two columns. Note that, unlike many statistics programs, Prism does not use a grouping variable. Instead, the groups are defined by columns.

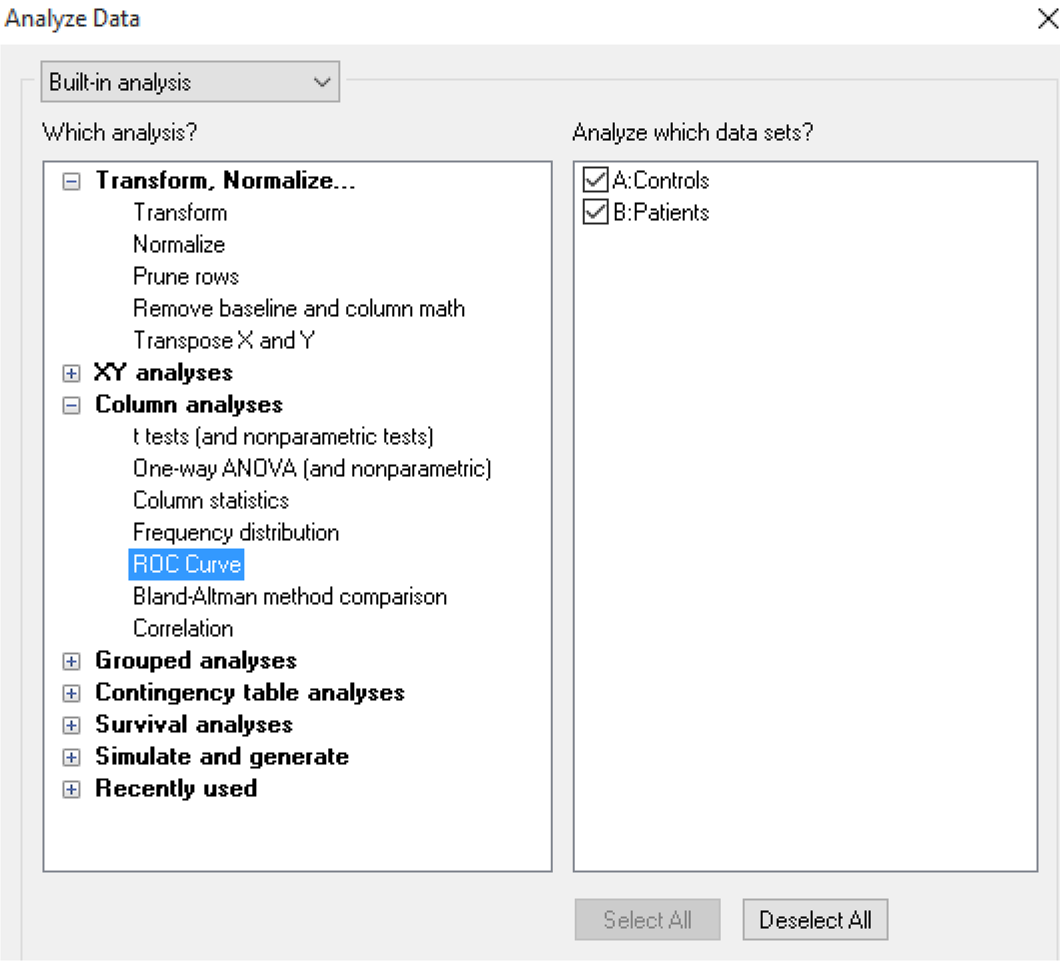
The values in each row are not paired in any way. Also note that the sample sizes are not equal, which is fine.

The goal
You want to choose a cutoff value that separates 'normal' from 'abnormal' test results. To help make the decision, plot the tradeoff of sensitivity vs. specificity as a Receiver Operator Characteristic (ROC) curve.

Detailed help for creating and understanding a ROC curve

Analyze > column analysis > ROC





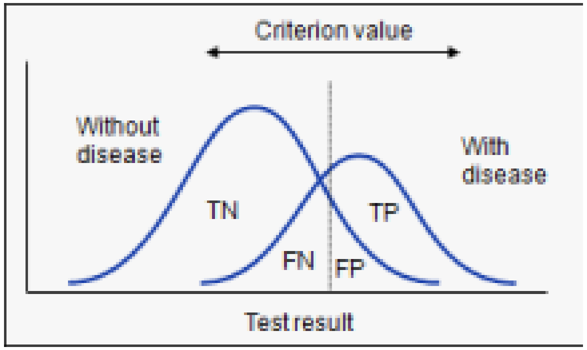
Analyze which data sets?

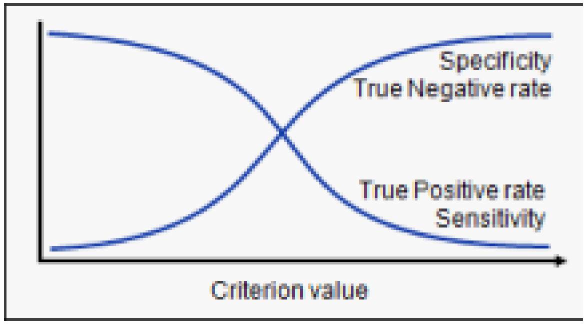
☑ A:Controls

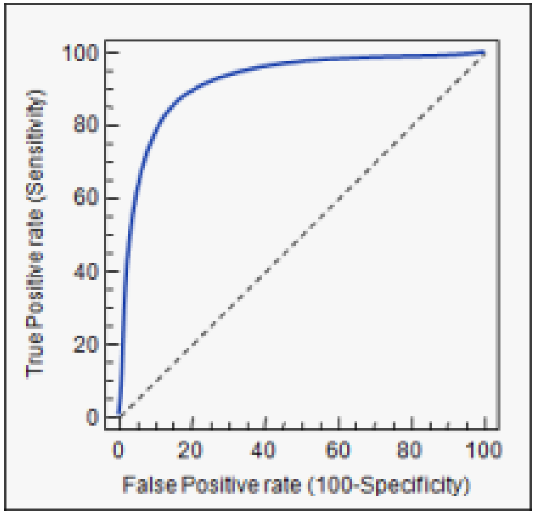
☑ B:Patients

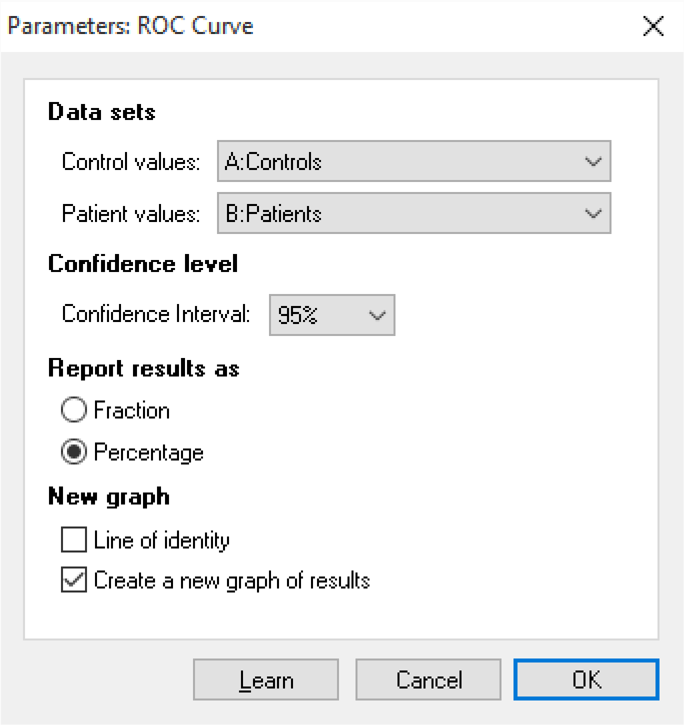
ROC curve concept

In a Receiver Operating Characteristic (ROC) curve the true positive rate (Sensitivity) is plotted in function of the false positive rate (100-Specificity) for different cut-off points. Each point on the ROC plot represents a sensitivity/specificity pair corresponding to a particular decision threshold. A test with perfect discrimination (no overlap in the two distributions) has a ROC plot that passes through the upper left corner (100% sensitivity, 100% specificity). Therefore the closer the ROC plot is to the upper left corner, the higher the overall accuracy of the test (Zweig & Campbell, 1993).









Parameters: ROC Curve

Data sets

Control values: A:Controls

Patient values: B:Patients

Confidence level

Confidence Interval: 95%

Report results as

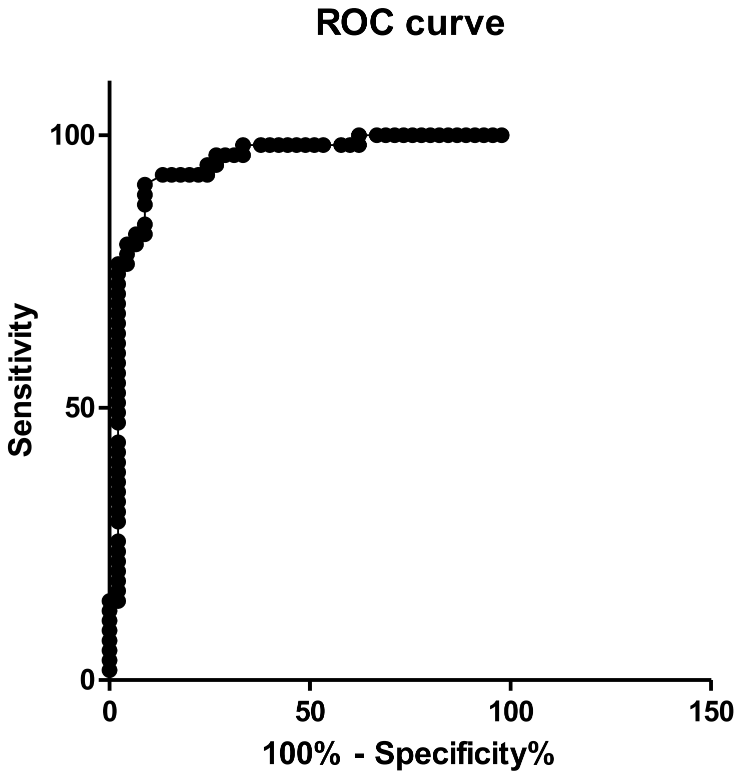
○ Fraction

● Percentage

New graph

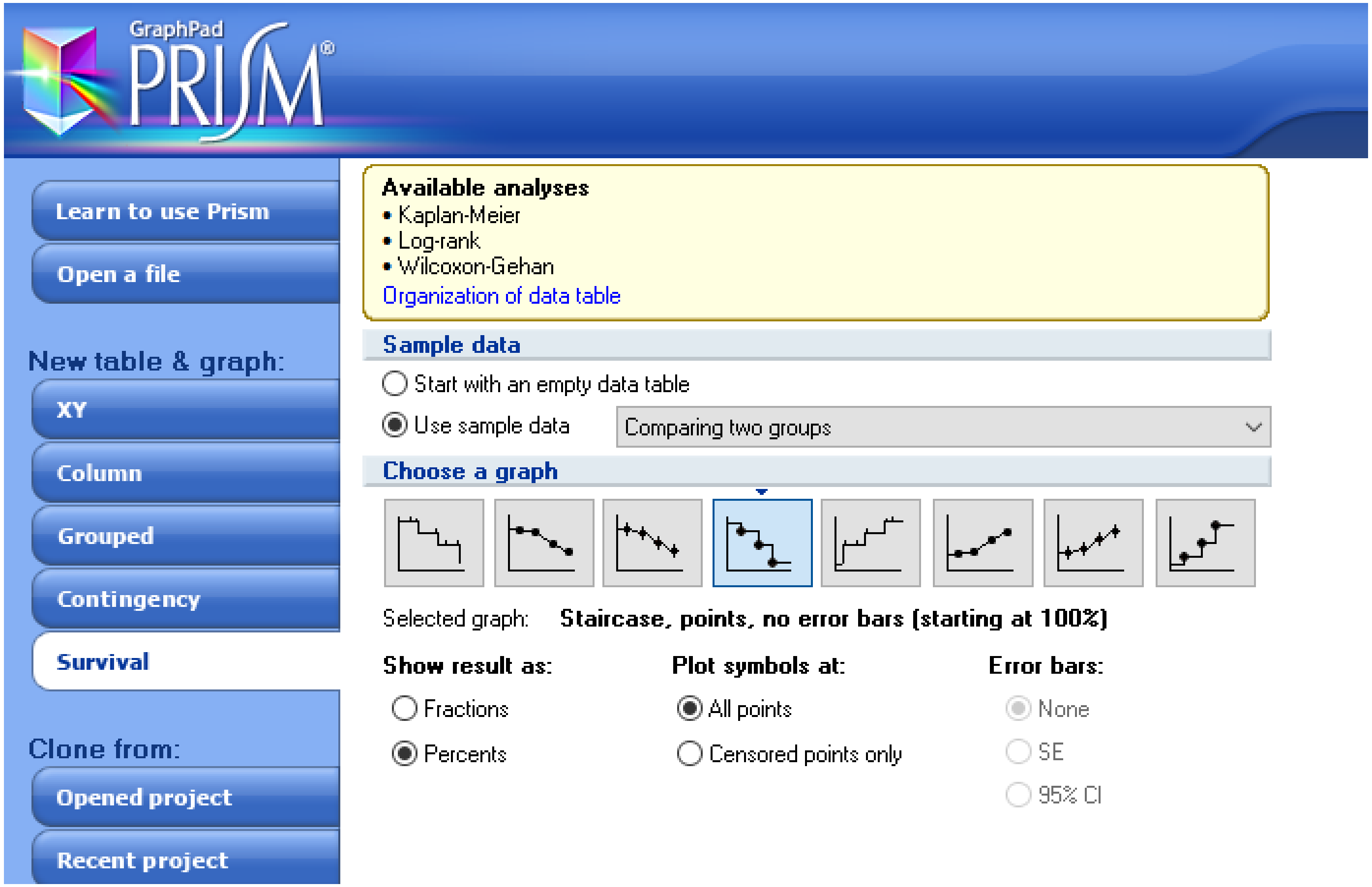
☐ Line of identity

☑ Create a new graph of results



Area under the ROC curve	
Area	0.9467
Std. Error	0.02403
95% confidence interval	0.8996 to 0.9938
P value	< 0.0001
Data	
Control	45
Patient	55
Missing Controls	0
Missing Patients	0

Kaplan Meier analysis (survival curves)



Available analyses
- Kaplan-Meier
- Log-rank
- Wilcoxon-Gehan

Organization of data table

Sample data

○ Start with an empty data table

● Use sample data — Comparing two groups

Choose a graph

Selected graph: **Staircase, points, no error bars (starting at 100%)**

Show result as:
- ○ Fractions
- ● Percents

Plot symbols at:
- ● All points
- ○ Censored points only

Error bars:
- ● None
- ○ SE
- ○ 95% CI

The data table structure of Kaplan Meier analysis

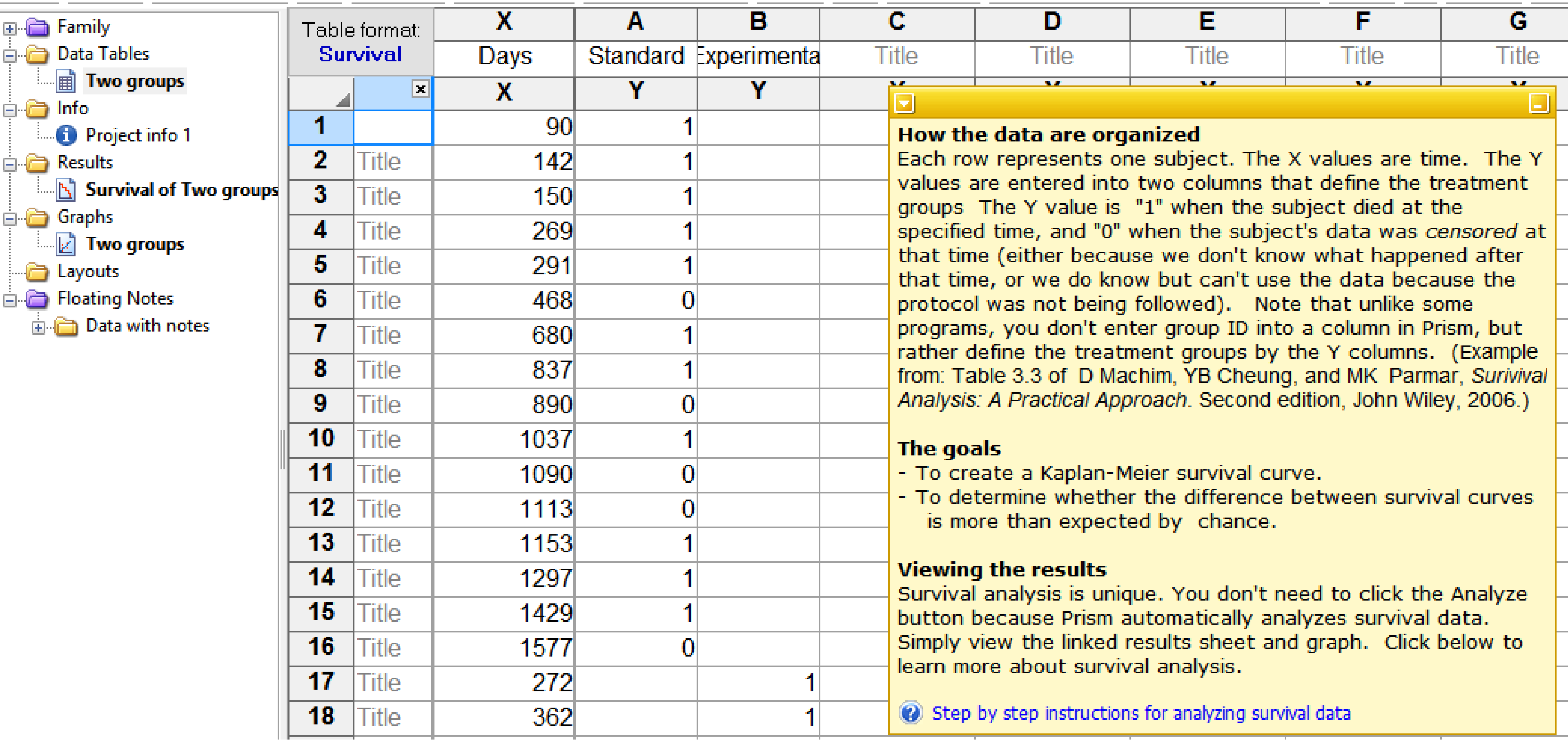


Table format: Survival		X	A	B	C	D	E	F	G
		Days	Standard	Experimenta	Title	Title	Title	Title	Title
		X	Y	Y					
1		90	1						
2	Title	142	1						
3	Title	150	1						
4	Title	269	1						
5	Title	291	1						
6	Title	468	0						
7	Title	680	1						
8	Title	837	1						
9	Title	890	0						
10	Title	1037	1						
11	Title	1090	0						
12	Title	1113	0						
13	Title	1153	1						
14	Title	1297	1						
15	Title	1429	1						
16	Title	1577	0						
17	Title	272		1					
18	Title	362		1					

How the data are organized
Each row represents one subject. The X values are time. The Y values are entered into two columns that define the treatment groups The Y value is "1" when the subject died at the specified time, and "0" when the subject's data was *censored* at that time (either because we don't know what happened after that time, or we do know but can't use the data because the protocol was not being followed). Note that unlike some programs, you don't enter group ID into a column in Prism, but rather define the treatment groups by the Y columns. (Example from: Table 3.3 of D Machim, YB Cheung, and MK Parmar, *Surivival Analysis: A Practical Approach*. Second edition, John Wiley, 2006.)

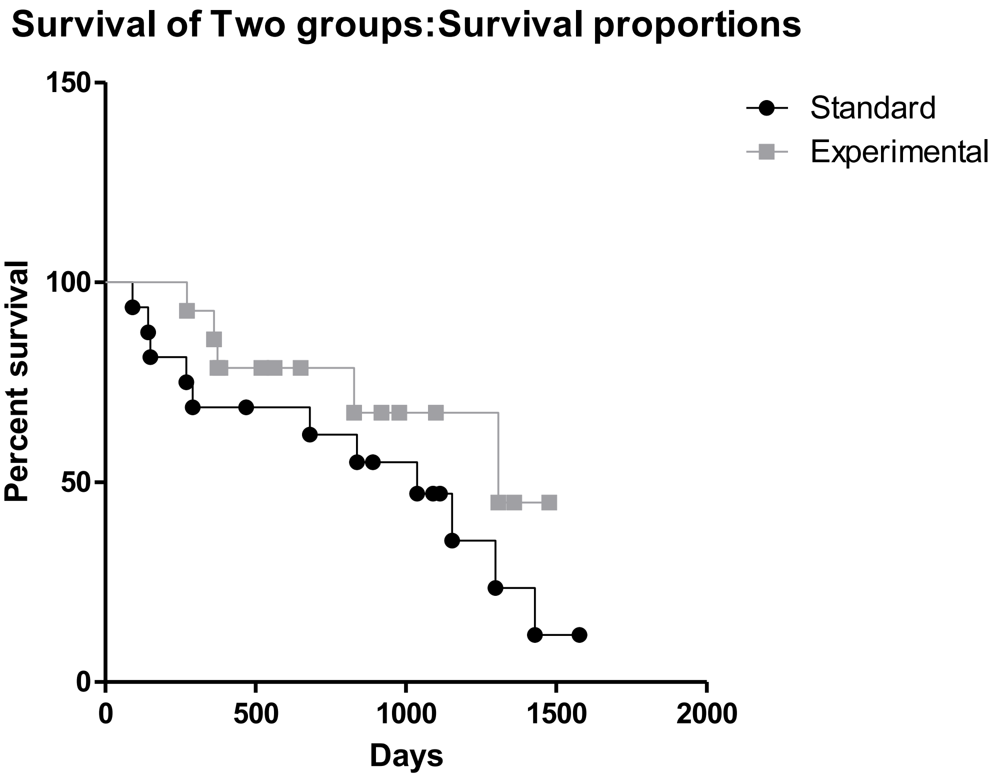
The goals
- To create a Kaplan-Meier survival curve.
- To determine whether the difference between survival curves is more than expected by chance.

Viewing the results
Survival analysis is unique. You don't need to click the Analyze button because Prism automatically analyzes survival data. Simply view the linked results sheet and graph. Click below to learn more about survival analysis.

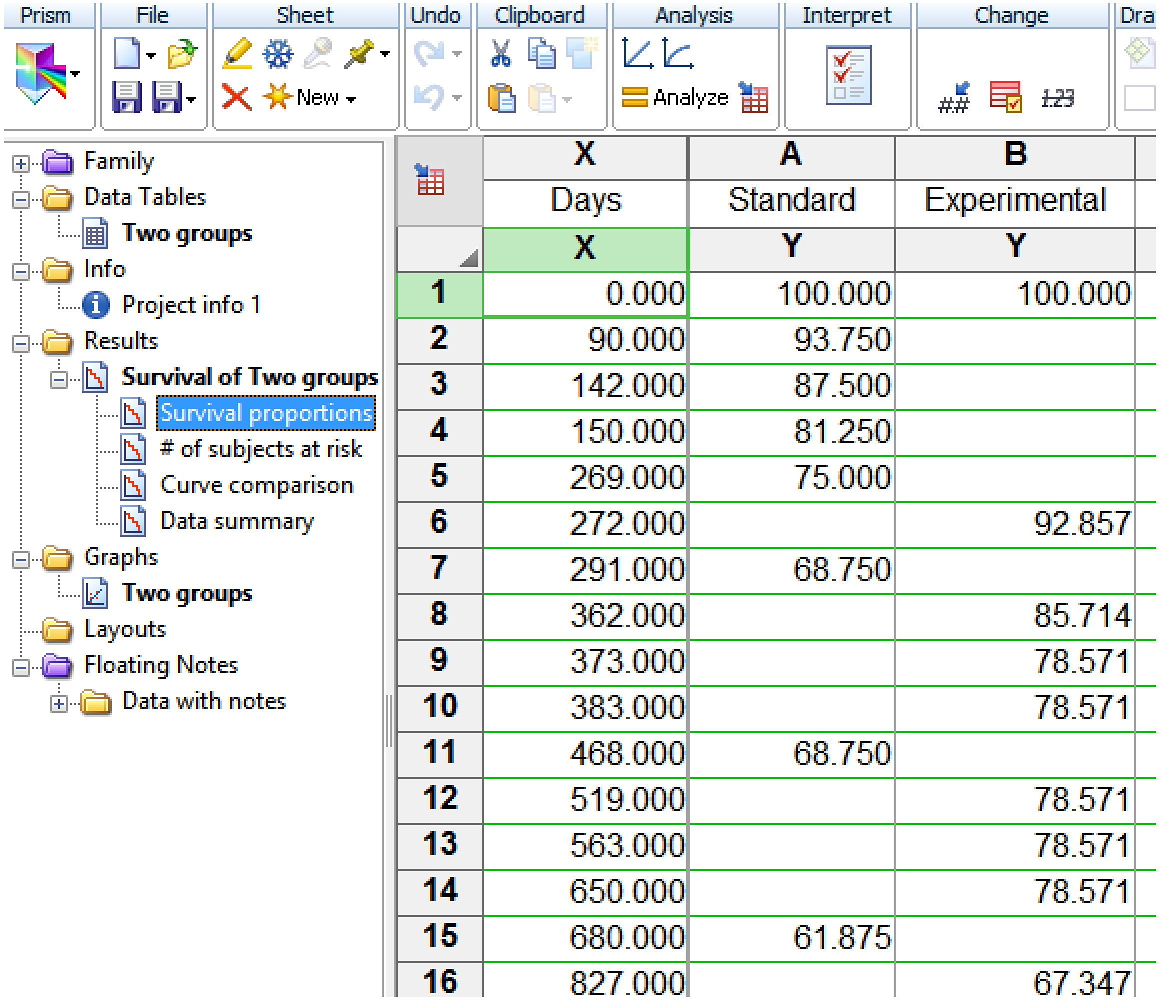
Step by step instructions for analyzing survival data

Data is automatically analyzed; you don‘t need to press the „Analyze“ button !

Kaplan-Meier curve

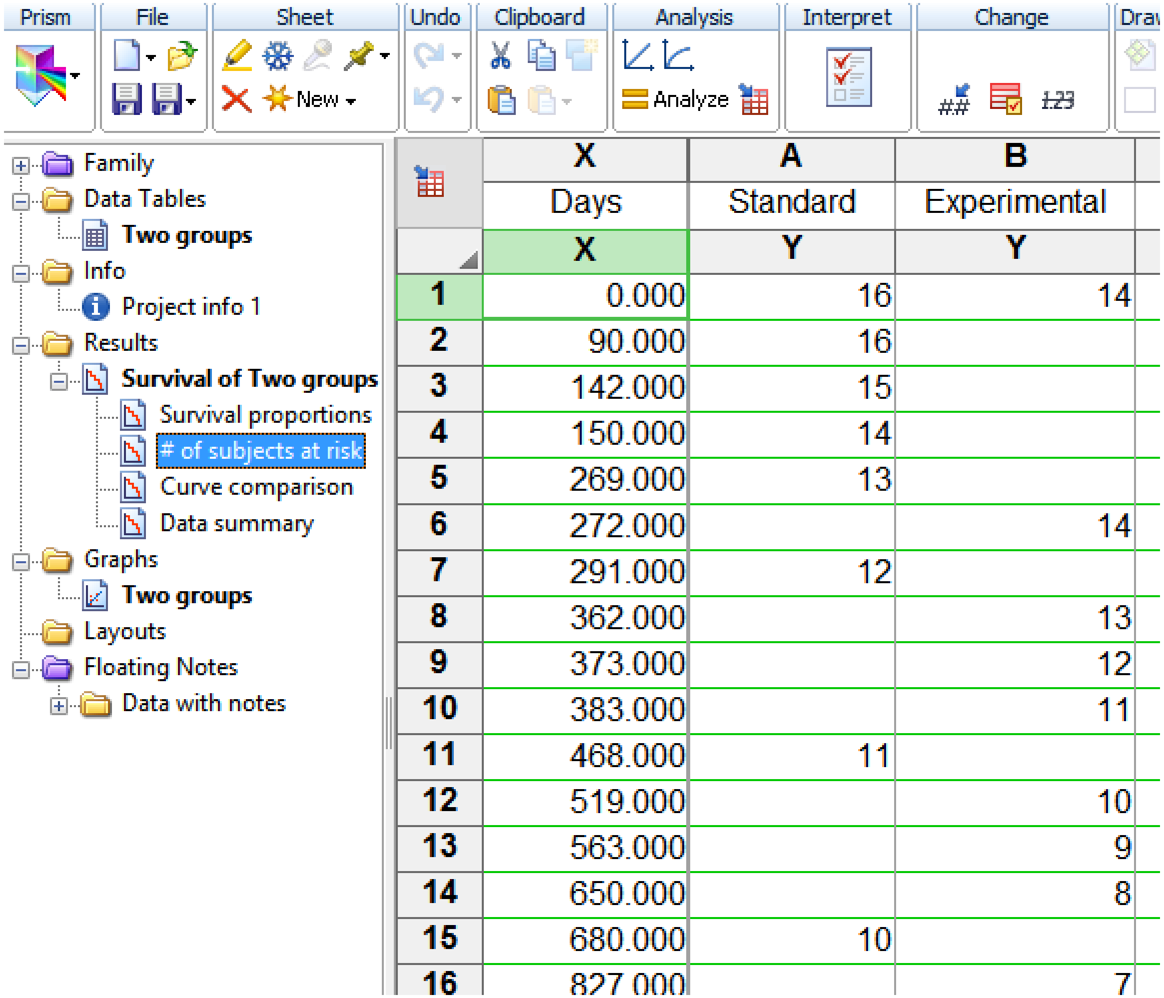


Results tables: Survival Proportions



	X	A	B
	Days	Standard	Experimental
	X	Y	Y
1	0.000	100.000	100.000
2	90.000	93.750	
3	142.000	87.500	
4	150.000	81.250	
5	269.000	75.000	
6	272.000		92.857
7	291.000	68.750	
8	362.000		85.714
9	373.000		78.571
10	383.000		78.571
11	468.000	68.750	
12	519.000		78.571
13	563.000		78.571
14	650.000		78.571
15	680.000	61.875	
16	827.000		67.347

Results tables: Nr. of subjects at risk



- Family
- Data Tables
  - **Two groups**
- Info
  - Project info 1
- Results
  - **Survival of Two groups**
    - Survival proportions
    - # of subjects at risk
    - Curve comparison
    - Data summary
- Graphs
  - **Two groups**
- Layouts
- Floating Notes
  - Data with notes

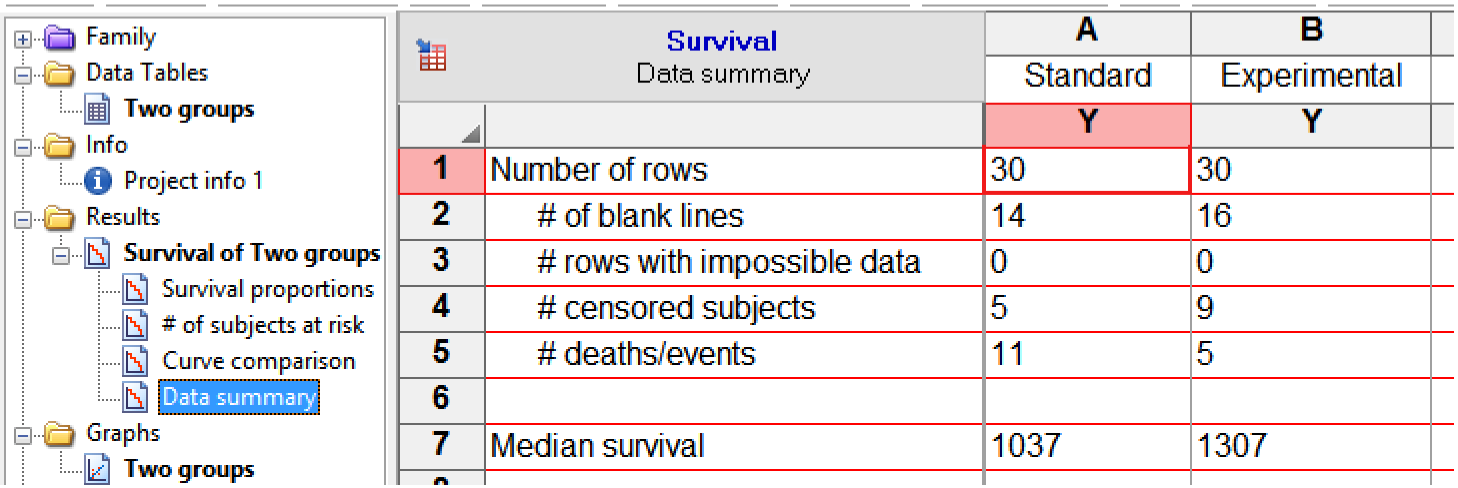
	X	A	B
	Days	Standard	Experimental
	X	Y	Y
1	0.000	16	14
2	90.000	16	
3	142.000	15	
4	150.000	14	
5	269.000	13	
6	272.000		14
7	291.000	12	
8	362.000		13
9	373.000		12
10	383.000		11
11	468.000	11	
12	519.000		10
13	563.000		9
14	650.000		8
15	680.000	10	
16	827.000		7

Results tables: Curve comparison

Comparison of Survival Curves

Log-rank (Mantel-Cox) Test	
Chi square	**1.682**
df	**1**
P value	**0.1947**
P value summary	**ns**
Are the survival curves sig different?	**No**
Gehan-Breslow-Wilcoxon Test	
Chi square	**1.392**
df	**1**
P value	**0.2380**
P value summary	**ns**
Are the survival curves sig different?	**No**
Median survival	
Standard	**1037**
Experimental	**1307**
Ratio	**0.7934**
95% CI of ratio	**0.4460 to 1.141**
Hazard Ratio	
Ratio	**1.927**
95% CI of ratio	**0.7151 to 5.191**

Results tables: Data summary

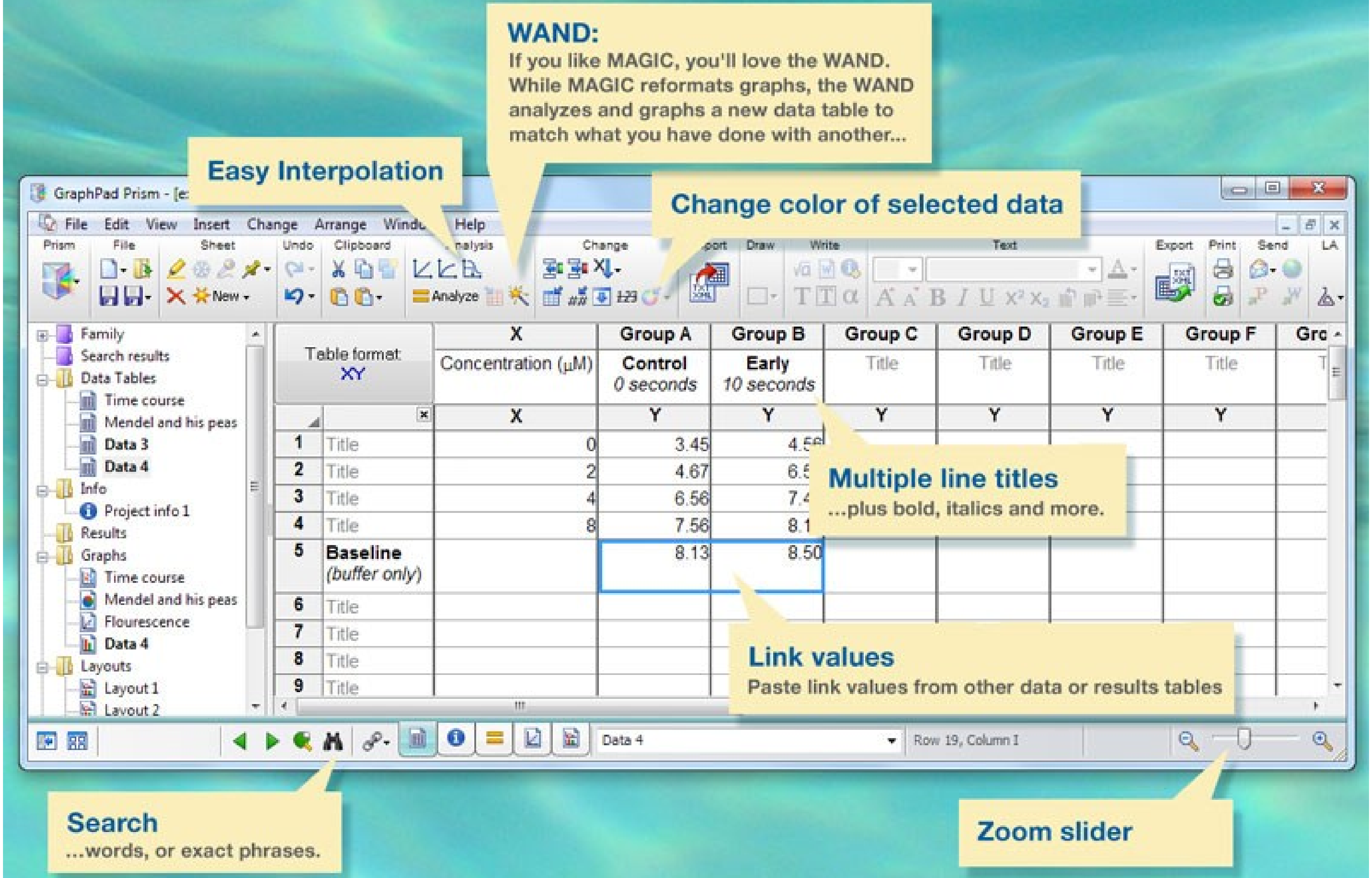


Survival
Data summary

		A	B
		Standard	Experimental
		Y	Y
1	Number of rows	30	30
2	# of blank lines	14	16
3	# rows with impossible data	0	0
4	# censored subjects	5	9
5	# deaths/events	11	5
6			
7	Median survival	1037	1307

GraphPad Prism 6: New features

- Sharing concept: LabArchives
- Improved sample data sets
- More statistical analyses (e.g. adjusted P-values for multiple comparisons; new post tests…)
- More graph types (Pie charts, superimposing of individual points and columns or box/whiskers…)
- New curve fitting modes (implicit and differential)



WAND:

If you like MAGIC, you'll love the WAND. While MAGIC reformats graphs, the WAND analyzes and graphs a new data table to match what you have done with another...

Easy Interpolation

Change color of selected data

Table format: XY	X	Group A	Group B	Group C	Group D	Group E	Group F
	Concentration (µM)	**Control** *0 seconds*	**Early** *10 seconds*	Title	Title	Title	Title
	X	Y	Y	Y	Y	Y	Y
1 Title	0	3.45	4.5				
2 Title	2	4.67	6.5				
3 Title	4	6.56	7.4				
4 Title	8	7.56	8.1				
5 **Baseline** *(buffer only)*		8.13	8.50				
6 Title							
7 Title							
8 Title							
9 Title							

Multiple line titles

...plus bold, italics and more.

Link values

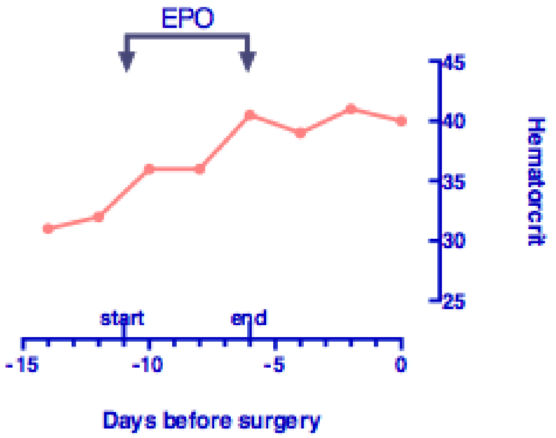
Paste link values from other data or results tables

Search

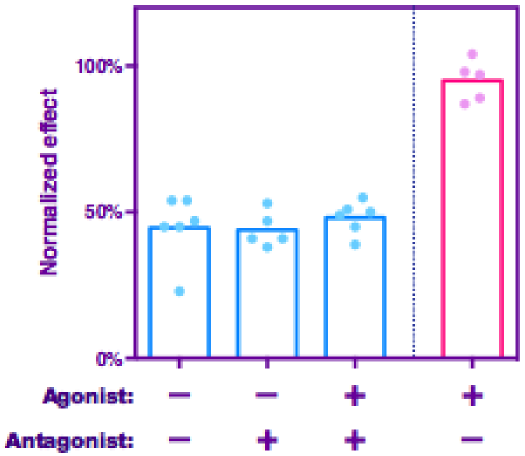
...words, or exact phrases.

Zoom slider

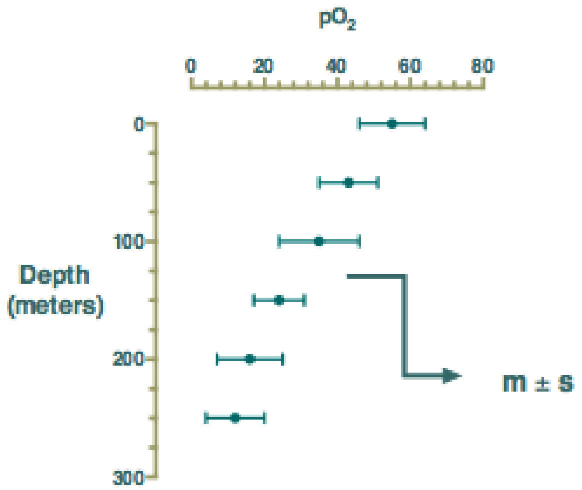
Examples for customized graphs



- Draw zig-zag and elbow lines
- Show ticks above and below axis
- Show right axis only



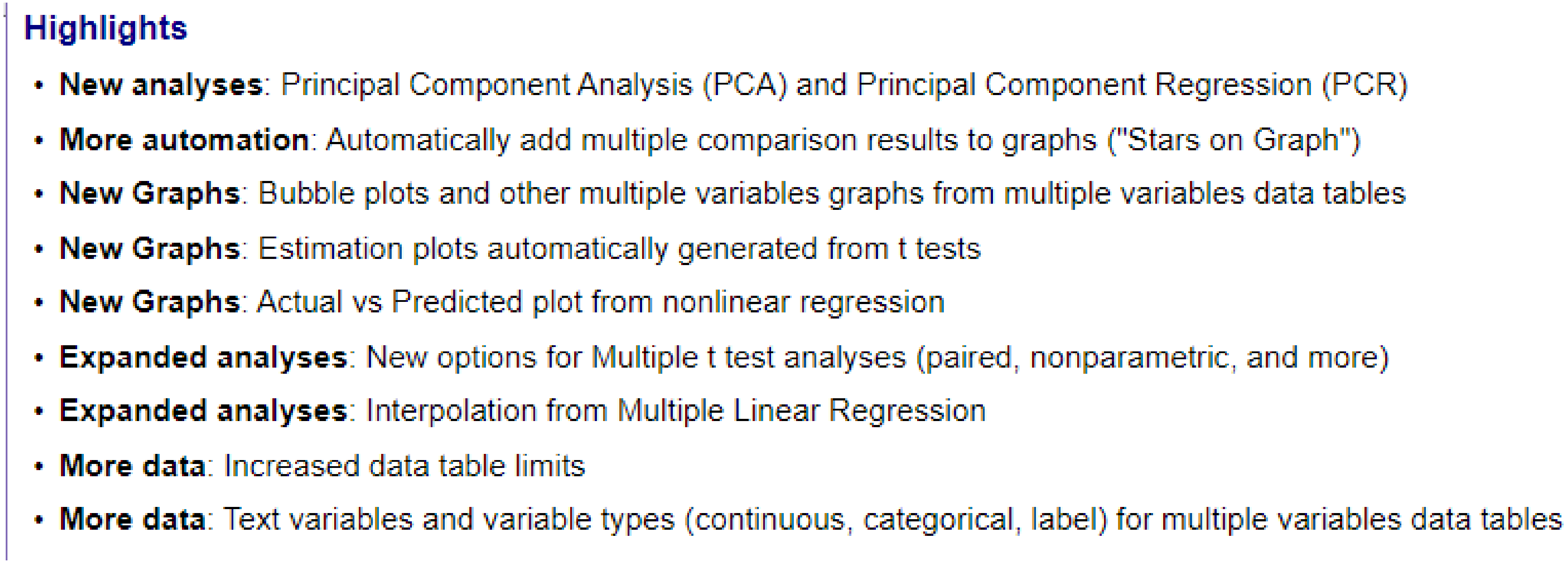
- Plot line to divide groups of bars
- Superimpose individual points with bars (or box-whiskers)
- Show two line column titles



- Plot depth charts
- Draw zig-zag and elbow lines

Newest version: GraphPad 9.0

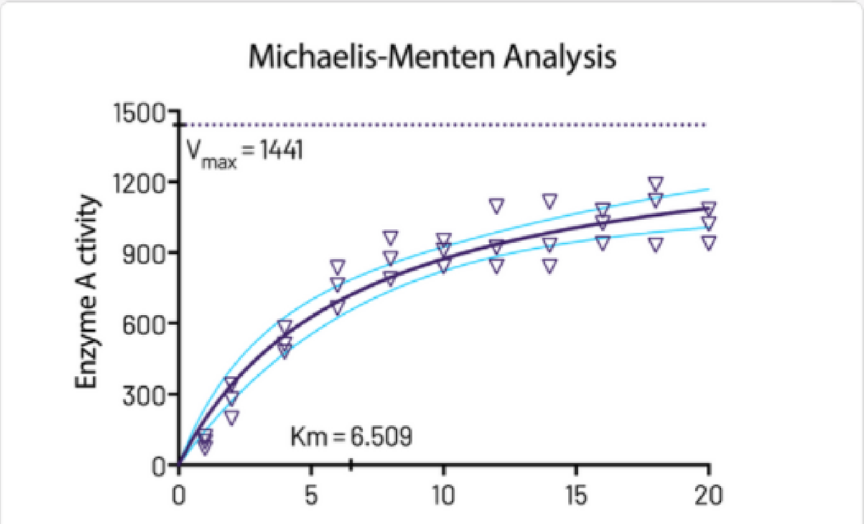
(annual rental license at our Univ. 84€/year)



Highlights

- **New analyses**: Principal Component Analysis (PCA) and Principal Component Regression (PCR)
- **More automation**: Automatically add multiple comparison results to graphs ("Stars on Graph")
- **New Graphs**: Bubble plots and other multiple variables graphs from multiple variables data tables
- **New Graphs**: Estimation plots automatically generated from t tests
- **New Graphs**: Actual vs Predicted plot from nonlinear regression
- **Expanded analyses**: New options for Multiple t test analyses (paired, nonparametric, and more)
- **Expanded analyses**: Interpolation from Multiple Linear Regression
- **More data**: Increased data table limits
- **More data**: Text variables and variable types (continuous, categorical, label) for multiple variables data tables

Newest version: GraphPad 9.0



One-Click Regression Analysis

No other program simplifies curve fitting like Prism. Select an equation and Prism does the rest—fits the curve, displays a table of results and function parameters, draws the curve on the graph, and interpolates unknown values.

Start a Free Trial

Display options

○ P values (numbers)

● Asterisks representing P value classification

P value threshold

Display asterisks/values and lines for which P values?

● All P values (including "ns")

○ P values less than or equal to: 0.05

Line/bracket and text options

Plot:

Thickness: 1/2 pt

Color:

Style:

Asterisks or value: Font... Arial, 9 pt

Automate Your Work Without Programming

Automatically add multiple pairwise comparisons to your analysis with a single click. For customization options of these lines and asterisks, simply click the toolbar button again. Make adjustments to the data or the analysis, and the results displayed on the graph will update automatically.

Start a Free Trial

Newest version: GraphPad 9.0

Countless Ways to Customize Your Graphs

Focus on the story in your data, not manipulating your software. Prism makes it easy to create the graphs you want. Choose the type of graph, and customize any part—how the data is arranged, the style of your data points, labels, fonts, colors, and much more. The customization options are endless.

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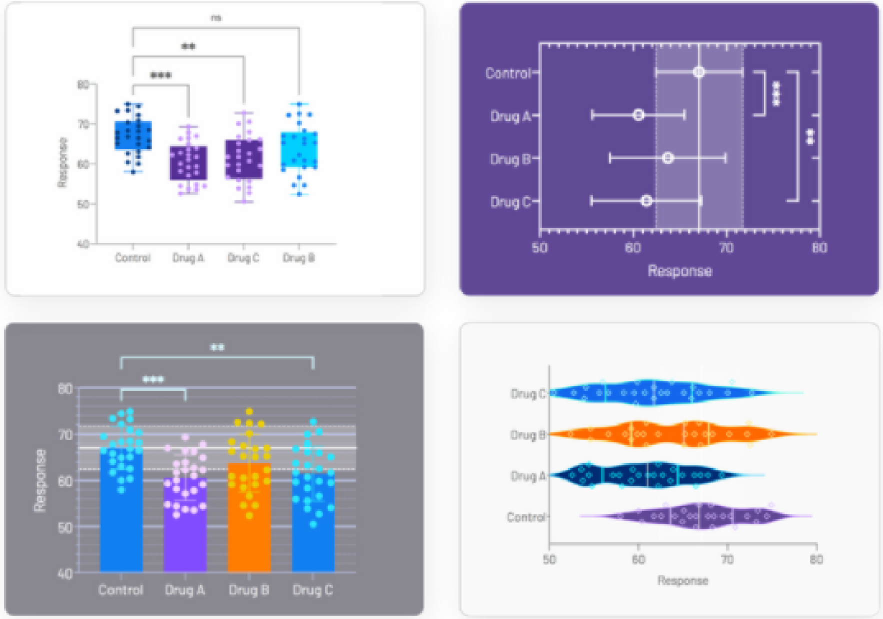
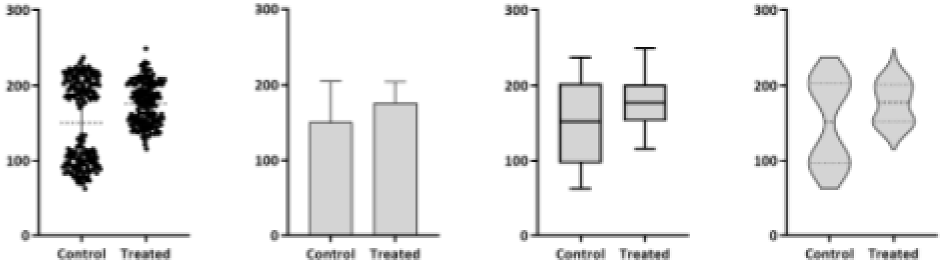
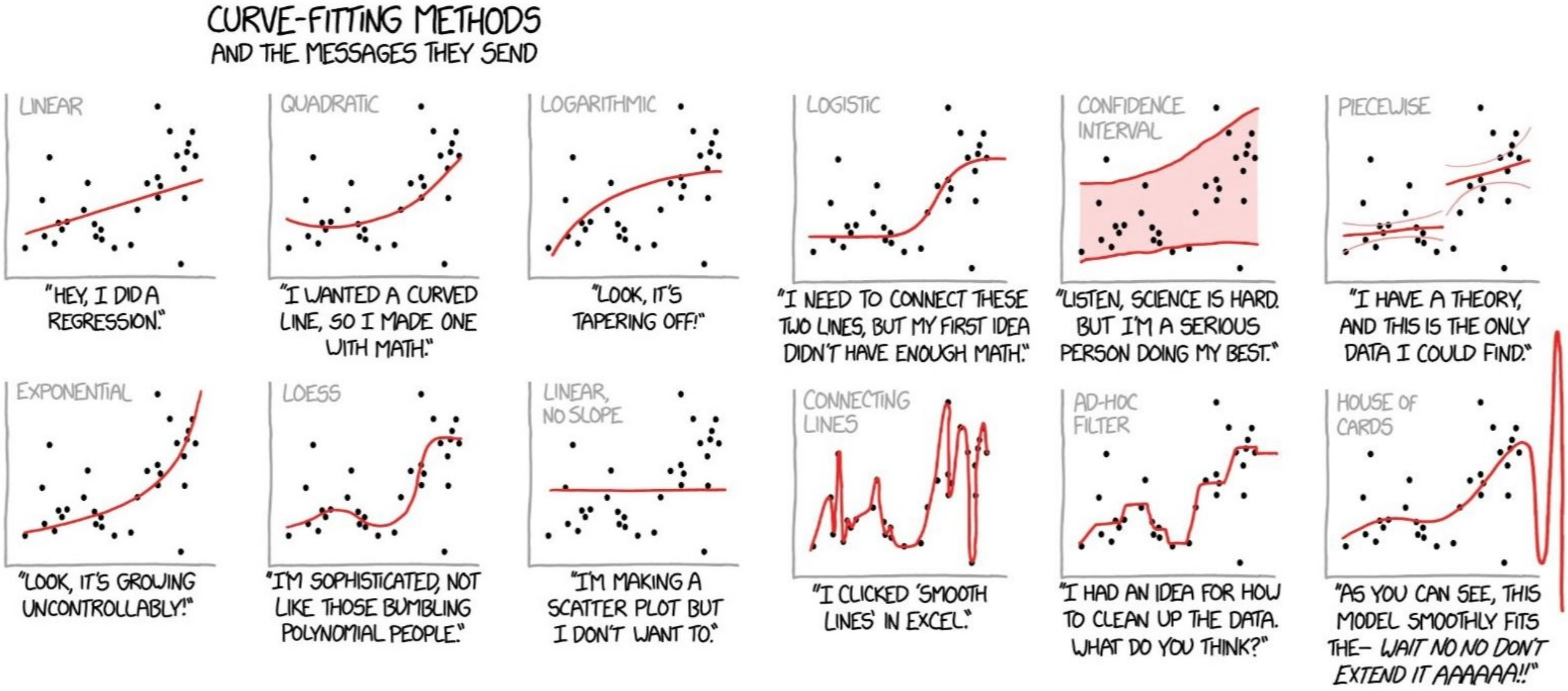


Violin plots

Violin plots show data distributions much more clearly than do box-whisker or bar graphs.




CURVE-FITTING METHODS
AND THE MESSAGES THEY SEND
LINEAR
"HEY, I DID A REGRESSION."
QUADRATIC
"I WANTED A CURVED LINE, SO I MADE ONE WITH MATH."
LOGARITHMIC
"LOOK, IT'S TAPERING OFF!"
LOGISTIC
"I NEED TO CONNECT THESE TWO LINES, BUT MY FIRST IDEA DIDN'T HAVE ENOUGH MATH."
CONFIDENCE INTERVAL
"LISTEN, SCIENCE IS HARD. BUT I'M A SERIOUS PERSON DOING MY BEST."
PIECEWISE
"I HAVE A THEORY, AND THIS IS THE ONLY DATA I COULD FIND."
EXPONENTIAL
"LOOK, IT'S GROWING UNCONTROLLABLY!"
LOESS
"I'M SOPHISTICATED, NOT LIKE THOSE BUMBLING POLYNOMIAL PEOPLE."
LINEAR, NO SLOPE
"I'M MAKING A SCATTER PLOT BUT I DON'T WANT TO."
CONNECTING LINES
"I CLICKED 'SMOOTH LINES' IN EXCEL."
AD-HOC FILTER
"I HAD AN IDEA FOR HOW TO CLEAN UP THE DATA. WHAT DO YOU THINK?"
HOUSE OF CARDS
"AS YOU CAN SEE, THIS MODEL SMOOTHLY FITS THE- WAIT NO NO DON'T EXTEND IT AAAAAA!!"

Curve Fitting Software: SigmaPlot

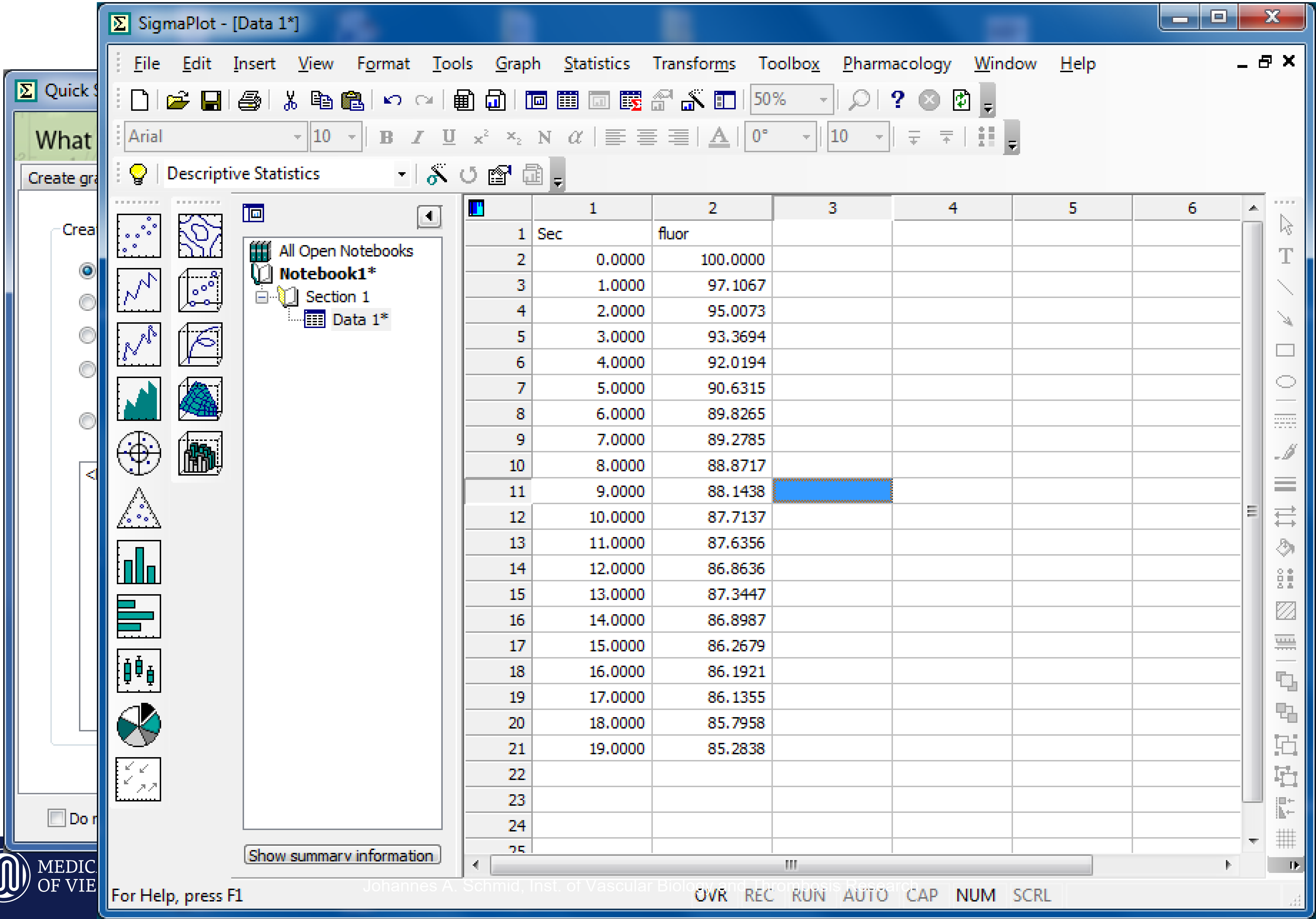
SIGMAPLOT®
Exact Graphs and Data Analysis

Rental license: 21€/year at our university

Features:

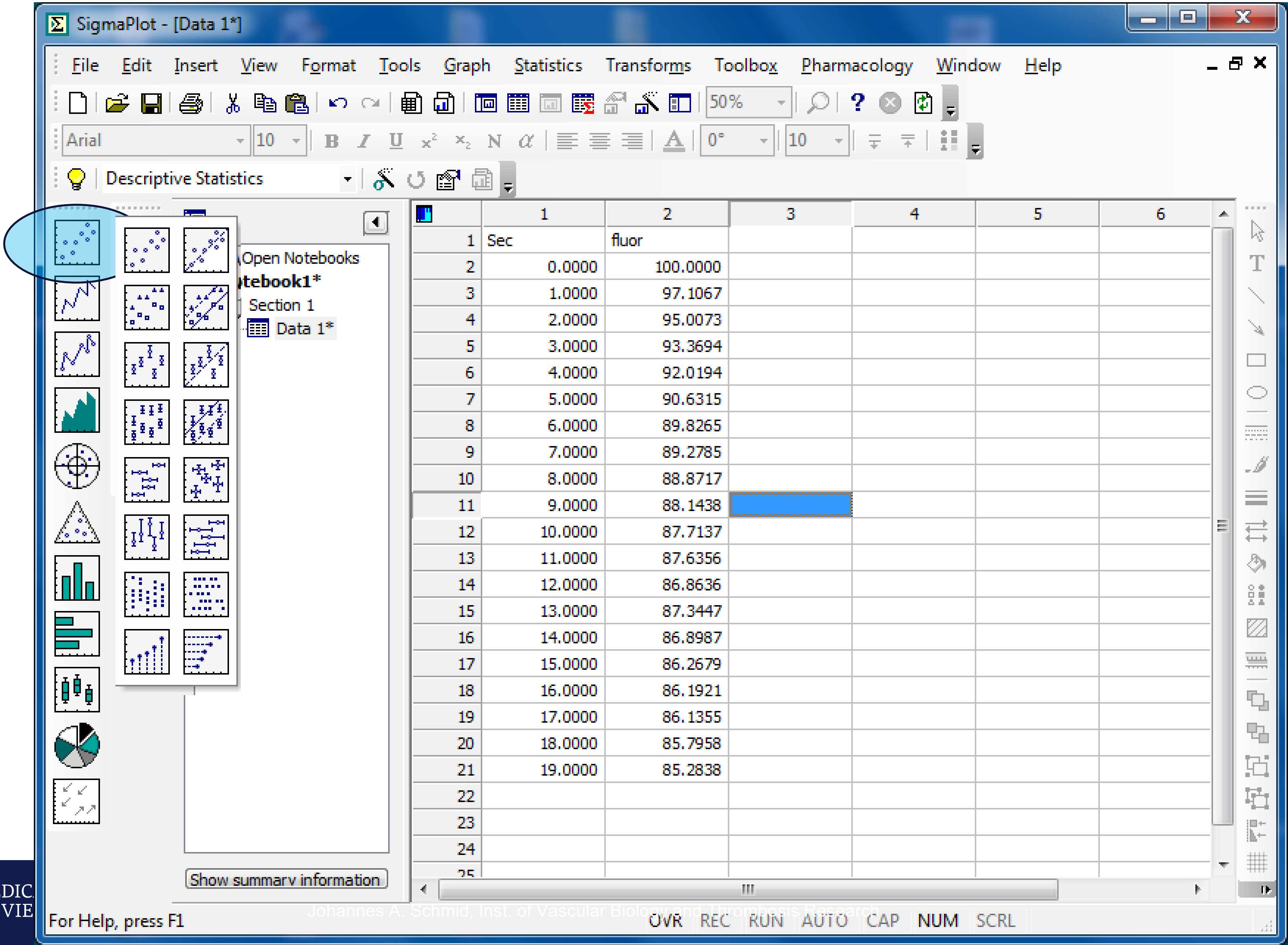
- Creating Exact Graphs
- Data Visualization
- More than 100 2-D and 3-D Graph Types
- Customizing Details of Charts and Graphs
- Plotting Data from Existing Graph Templates
- Publishing Charts and Graphs
- Sharing Graphs on the Web
- Data analysis tools
  - Integration into Microsoft Excel
  - Regression Wizard to fit data easily
  - Plotting Mathematical Functions
- Macros: Automation

Start Window (older version)



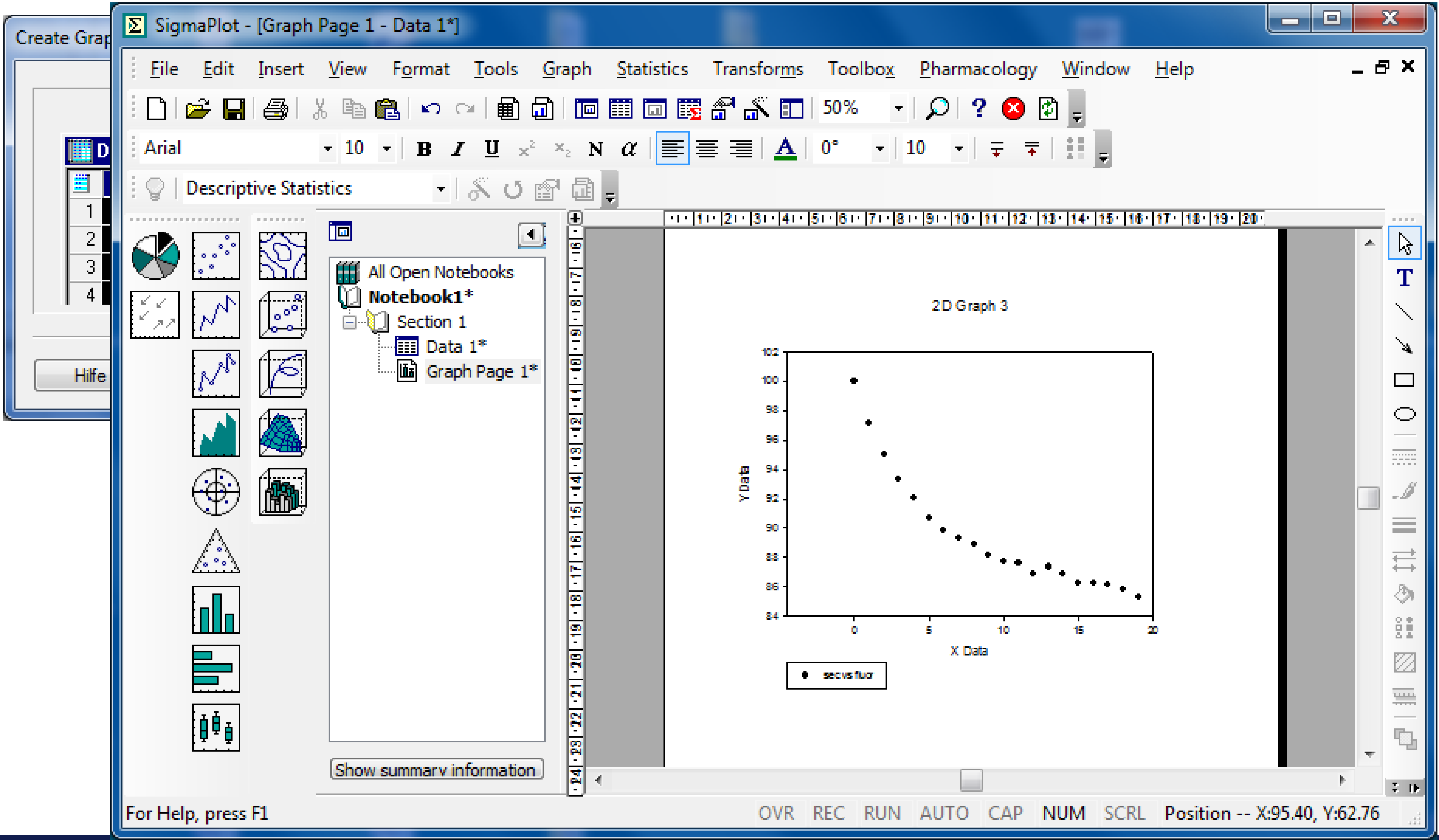
	1	2	3	4	5	6
1	Sec	fluor				
2	0.0000	100.0000				
3	1.0000	97.1067				
4	2.0000	95.0073				
5	3.0000	93.3694				
6	4.0000	92.0194				
7	5.0000	90.6315				
8	6.0000	89.8265				
9	7.0000	89.2785				
10	8.0000	88.8717				
11	9.0000	88.1438				
12	10.0000	87.7137				
13	11.0000	87.6356				
14	12.0000	86.8636				
15	13.0000	87.3447				
16	14.0000	86.8987				
17	15.0000	86.2679				
18	16.0000	86.1921				
19	17.0000	86.1355				
20	18.0000	85.7958				
21	19.0000	85.2838				
22						
23						
24						

Generating graphs

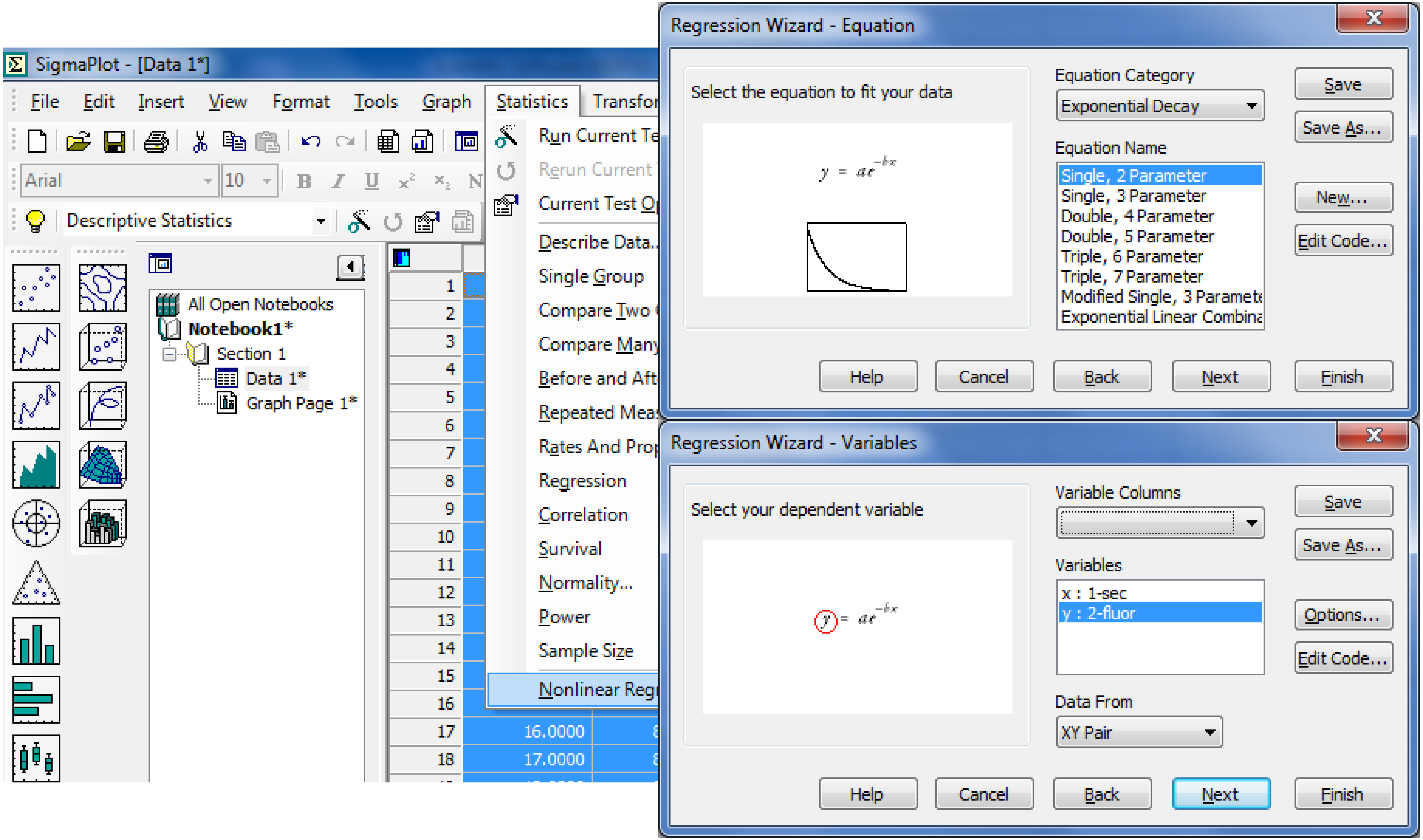


	1	2	3	4	5	6
1	Sec	fluor				
2	0.0000	100.0000				
3	1.0000	97.1067				
4	2.0000	95.0073				
5	3.0000	93.3694				
6	4.0000	92.0194				
7	5.0000	90.6315				
8	6.0000	89.8265				
9	7.0000	89.2785				
10	8.0000	88.8717				
11	9.0000	88.1438				
12	10.0000	87.7137				
13	11.0000	87.6356				
14	12.0000	86.8636				
15	13.0000	87.3447				
16	14.0000	86.8987				
17	15.0000	86.2679				
18	16.0000	86.1921				
19	17.0000	86.1355				
20	18.0000	85.7958				
21	19.0000	85.2838				
22						
23						
24						

Generating graphs II



Statistics and non-linear Regression



Regression Wizard - Equation

Select the equation to fit your data

$y = ae^{-bx}$

Equation Category: Exponential Decay

Equation Name:
- Single, 2 Parameter
- Single, 3 Parameter
- Double, 4 Parameter
- Double, 5 Parameter
- Triple, 6 Parameter
- Triple, 7 Parameter
- Modified Single, 3 Paramete
- Exponential Linear Combina

Regression Wizard - Variables

Select your dependent variable

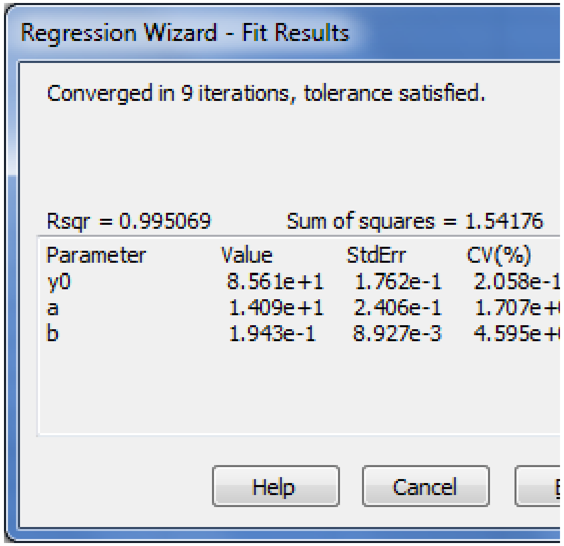
$y = ae^{-bx}$

Variable Columns:

Variables:
- x : 1-sec
- y : 2-fluor

Data From: XY Pair

Non-linear Regression

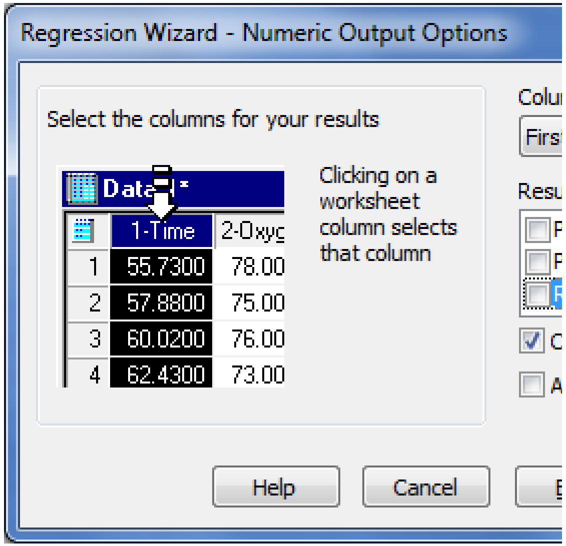


Regression Wizard - Fit Results

Converged in 9 iterations, tolerance satisfied.

Rsqr = 0.995069 Sum of squares = 1.54176

Parameter	Value	StdErr	CV(%)
y0	8.561e+1	1.762e-1	2.058e-1
a	1.409e+1	2.406e-1	1.707e+
b	1.943e-1	8.927e-3	4.595e+

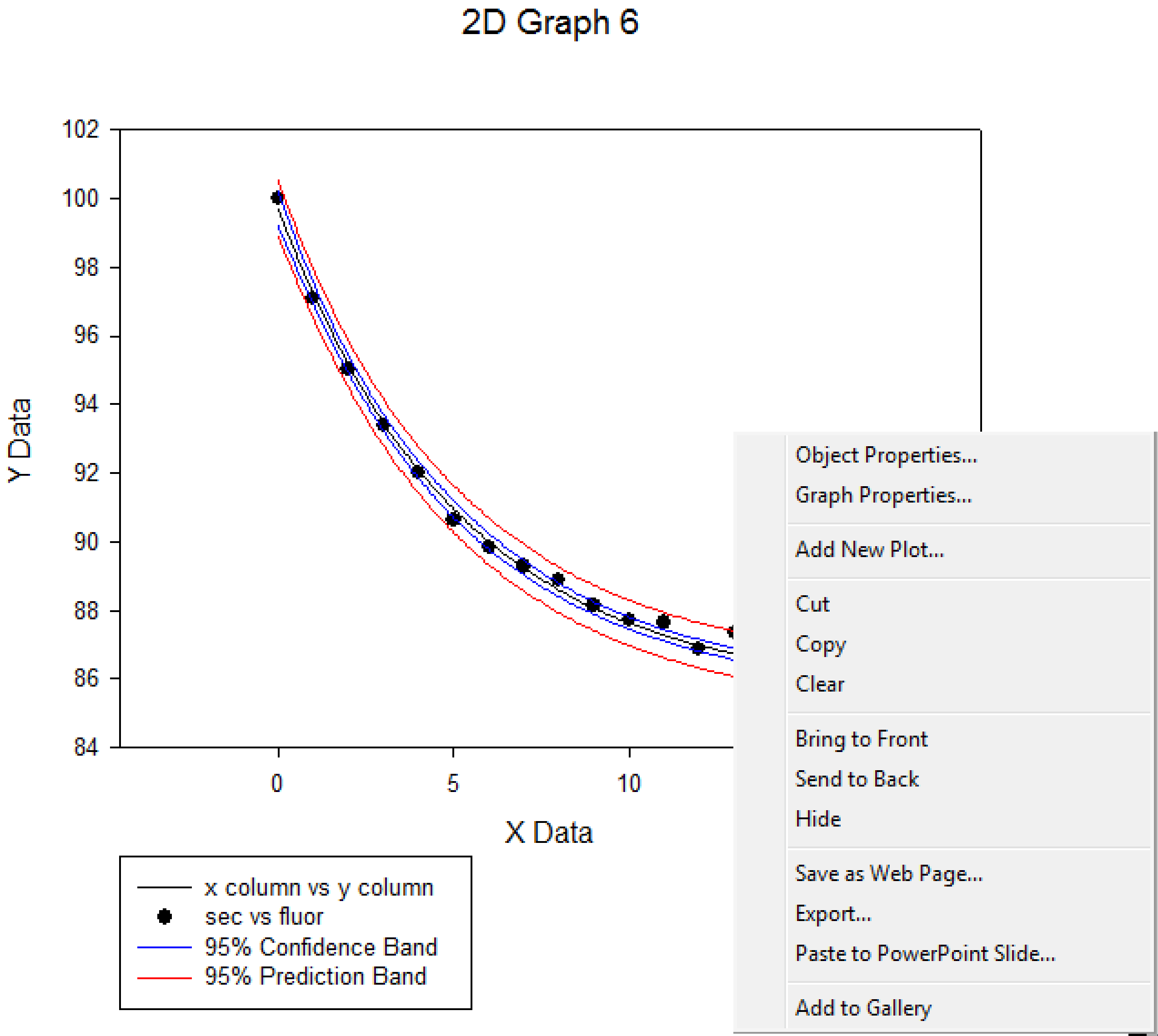


Regression Wizard - Numeric Output Options

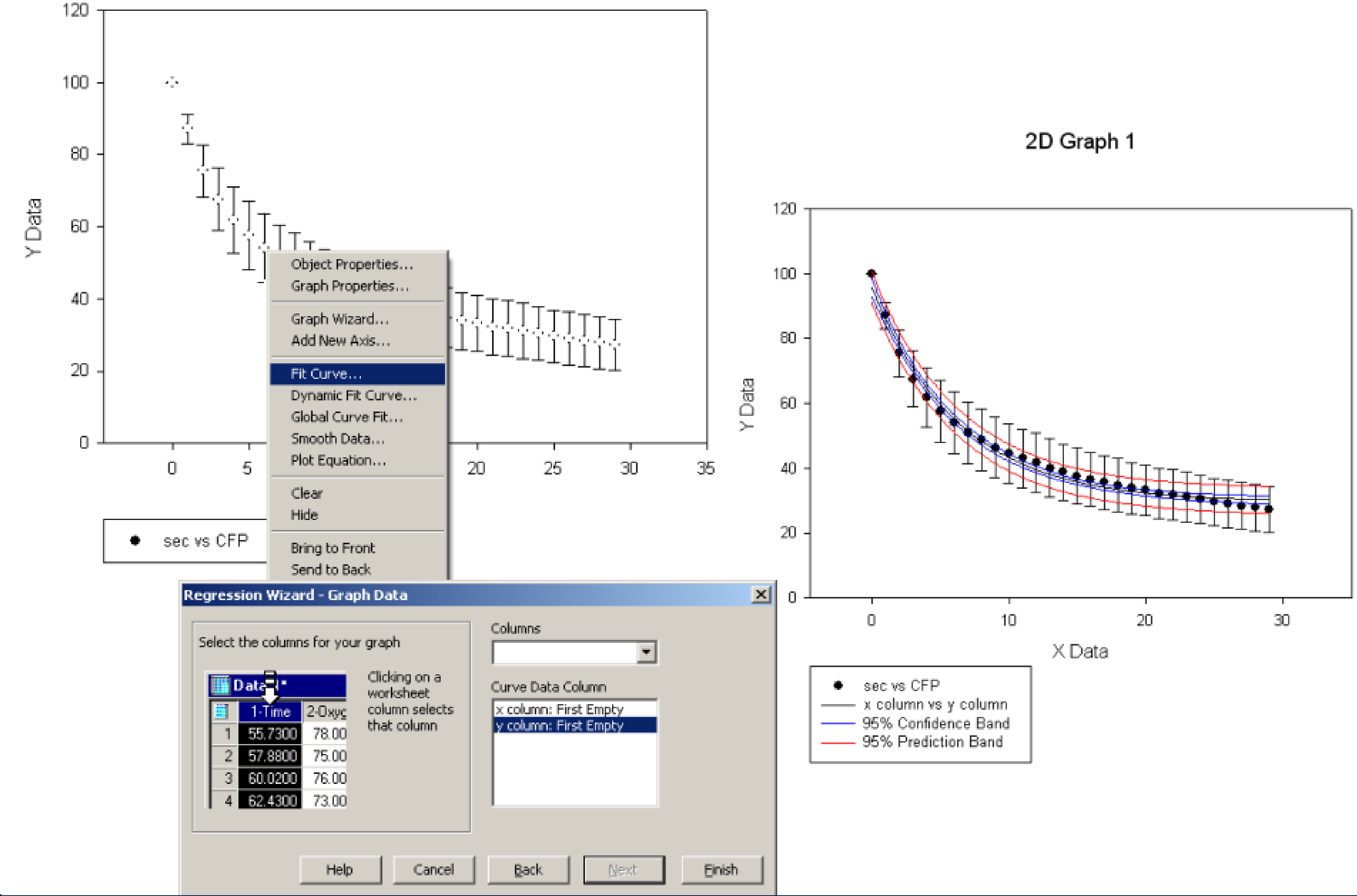
Select the columns for your results

	1-Time	2-Oxyg
1	55.7300	78.00
2	57.8800	75.00
3	60.0200	76.00
4	62.4300	73.00

Clicking on a worksheet column selects that column



Curve fitting by right-clicking on the curve



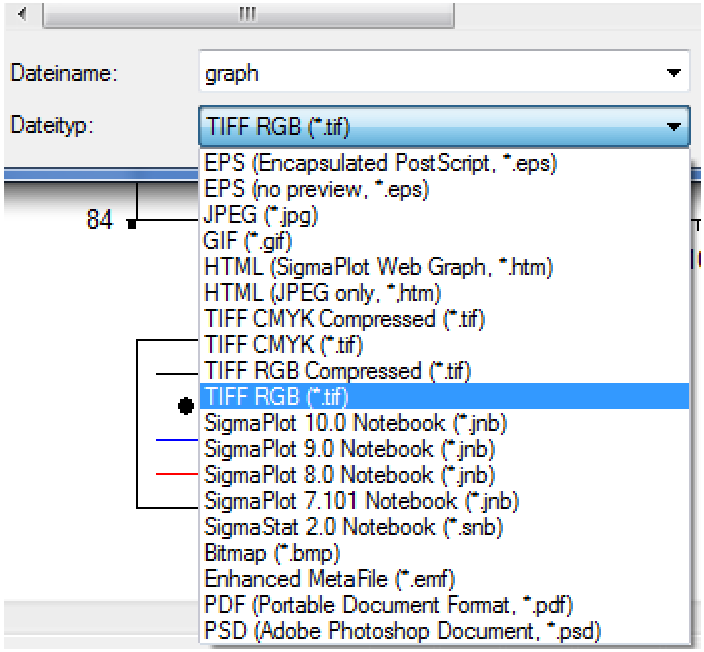
Select the columns for your graph

Clicking on a worksheet column selects that column

	1-Time	2-Oxyg
1	55.7300	78.00
2	57.8800	75.00
3	60.0200	76.00
4	62.4300	73.00

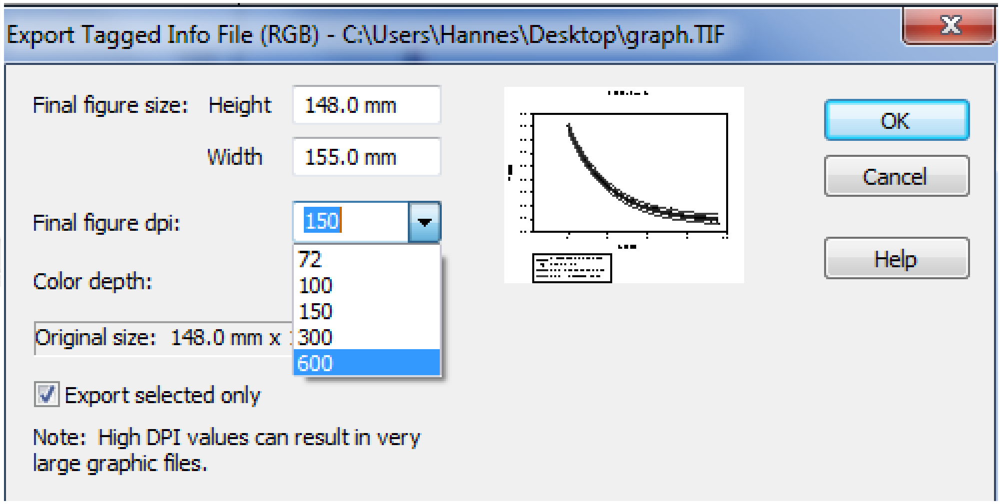
x column: First Empty
y column: First Empty

Graph Export Functions



Dateiname: graph

Dateityp: TIFF RGB (*.tif)



Export Tagged Info File (RGB) - C:\Users\Hannes\Desktop\graph.TIF

Final figure size: Height 148.0 mm

Width 155.0 mm

Final figure dpi: 150

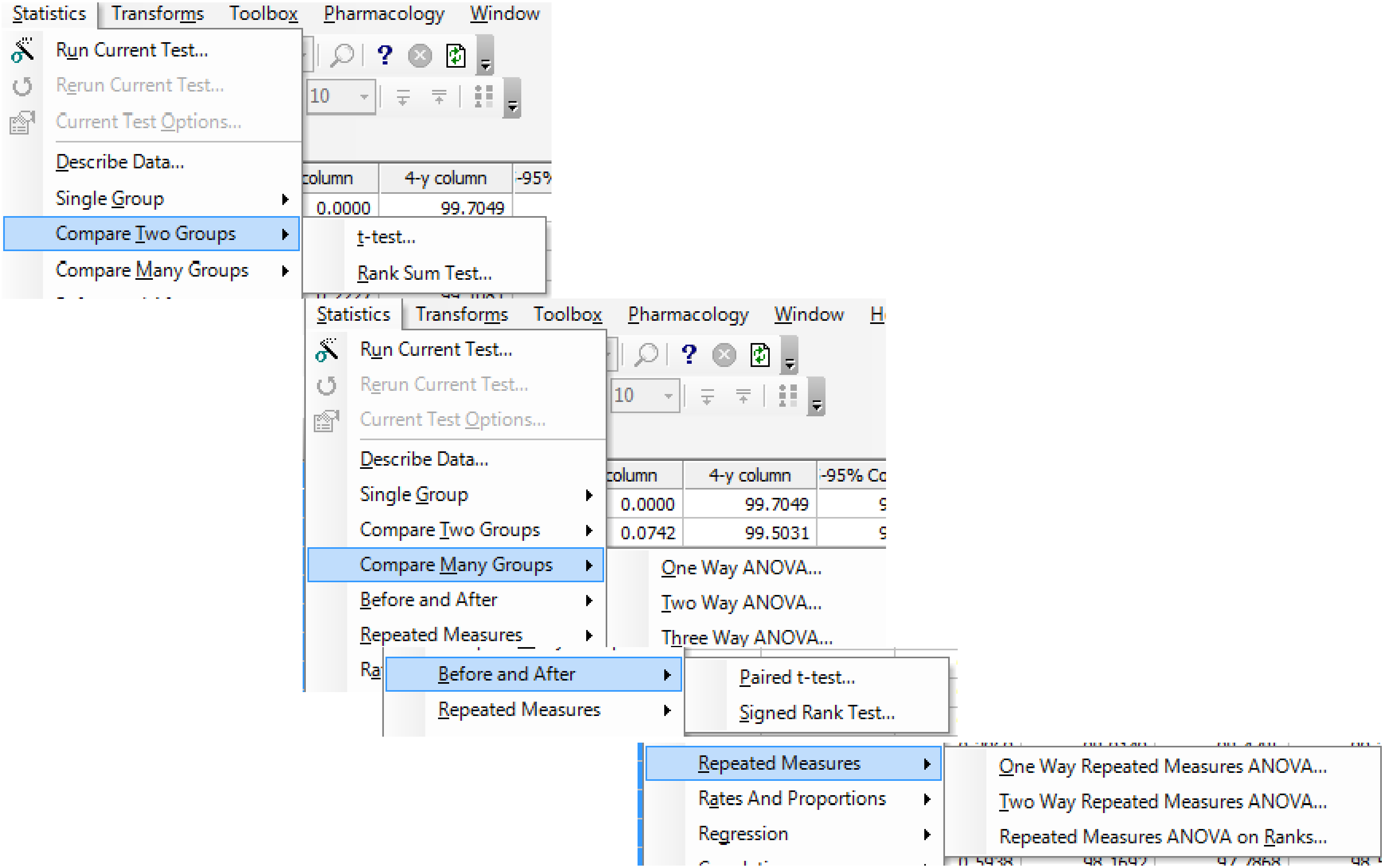
Color depth:

Original size: 148.0 mm x

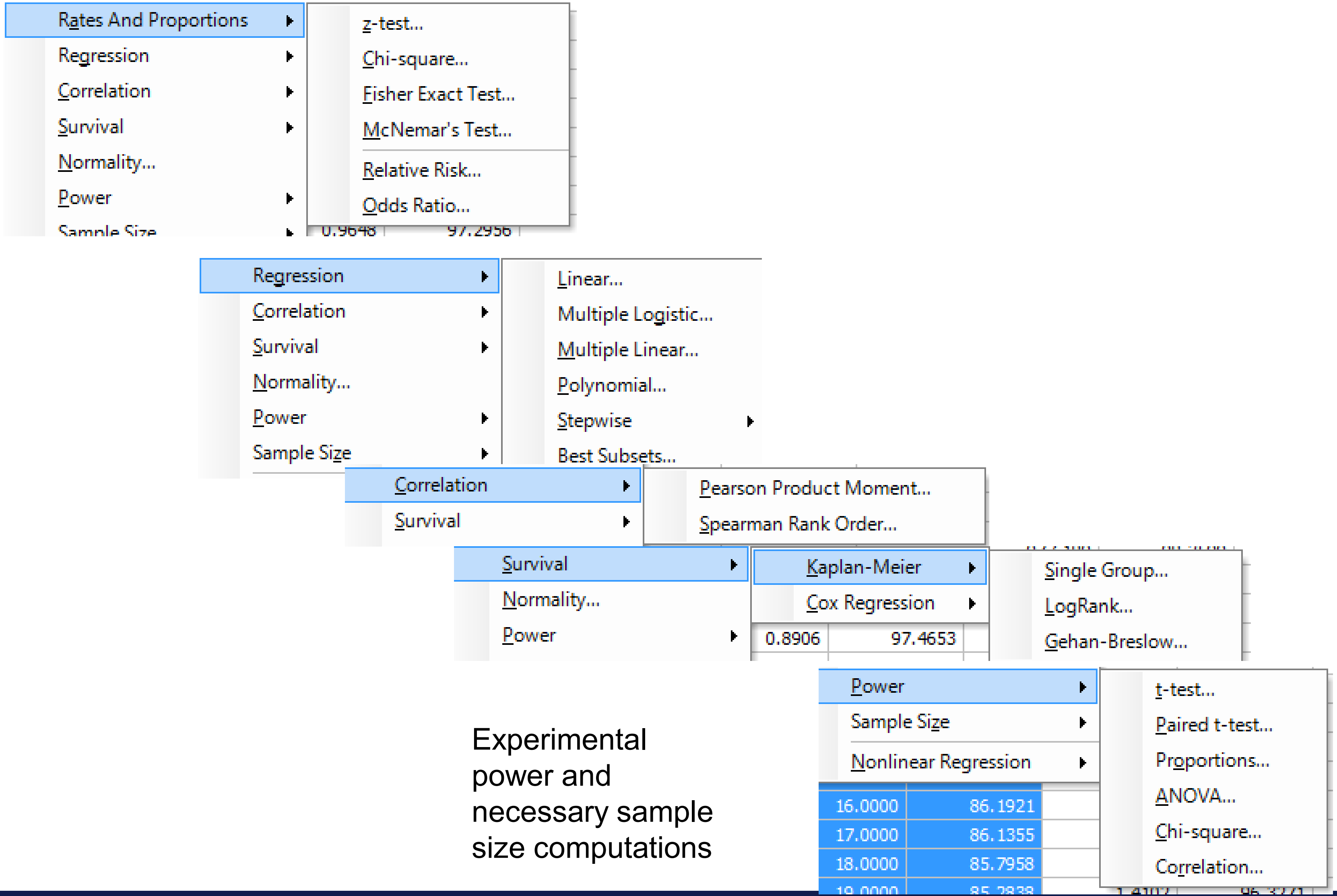
☑ Export selected only

Note: High DPI values can result in very large graphic files.

Statistics Features

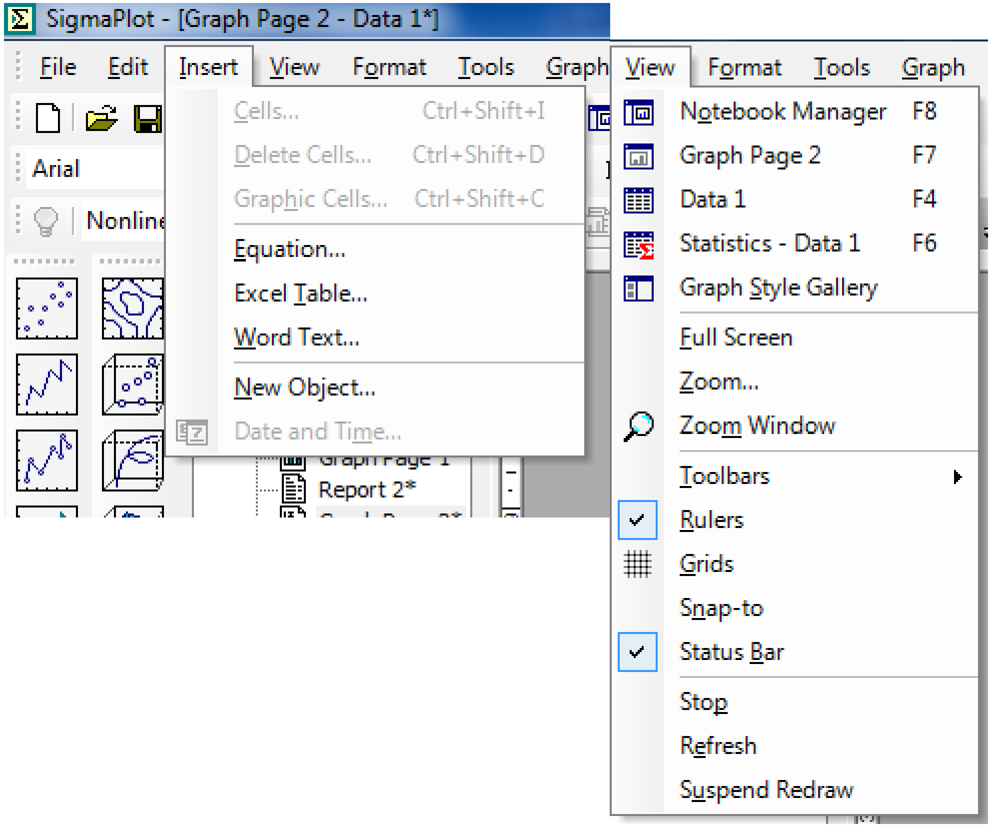


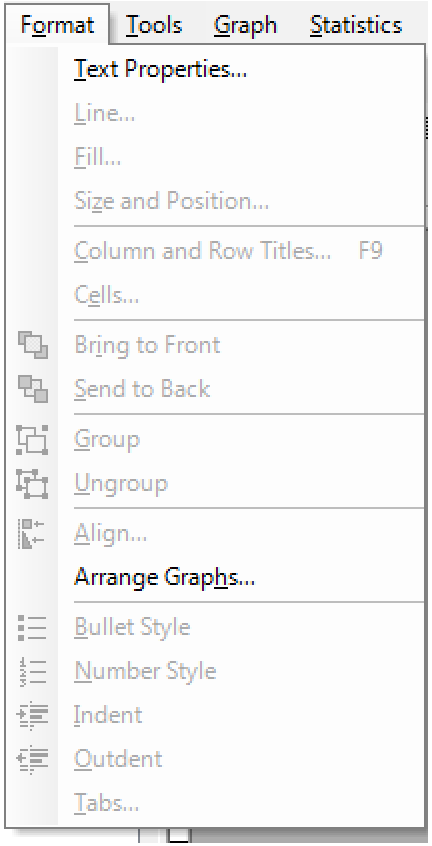
Statistics Features II

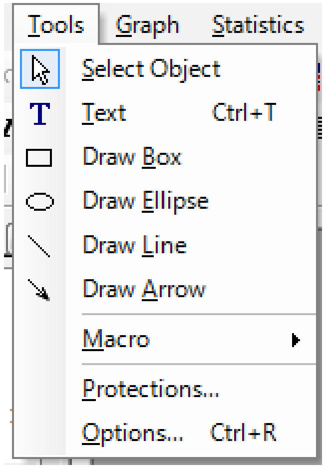


Experimental power and necessary sample size computations

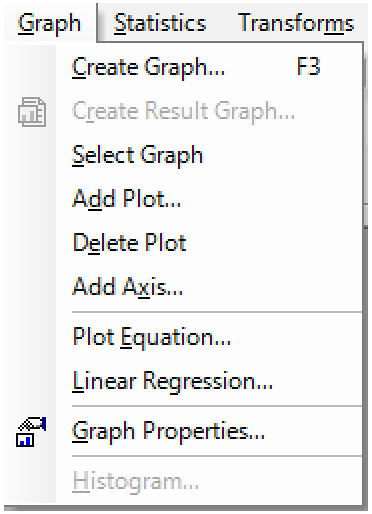
Other Features

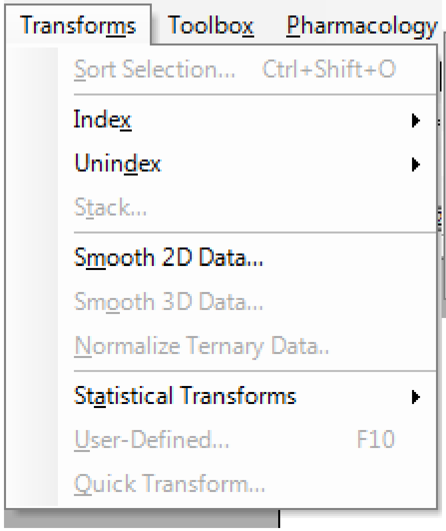


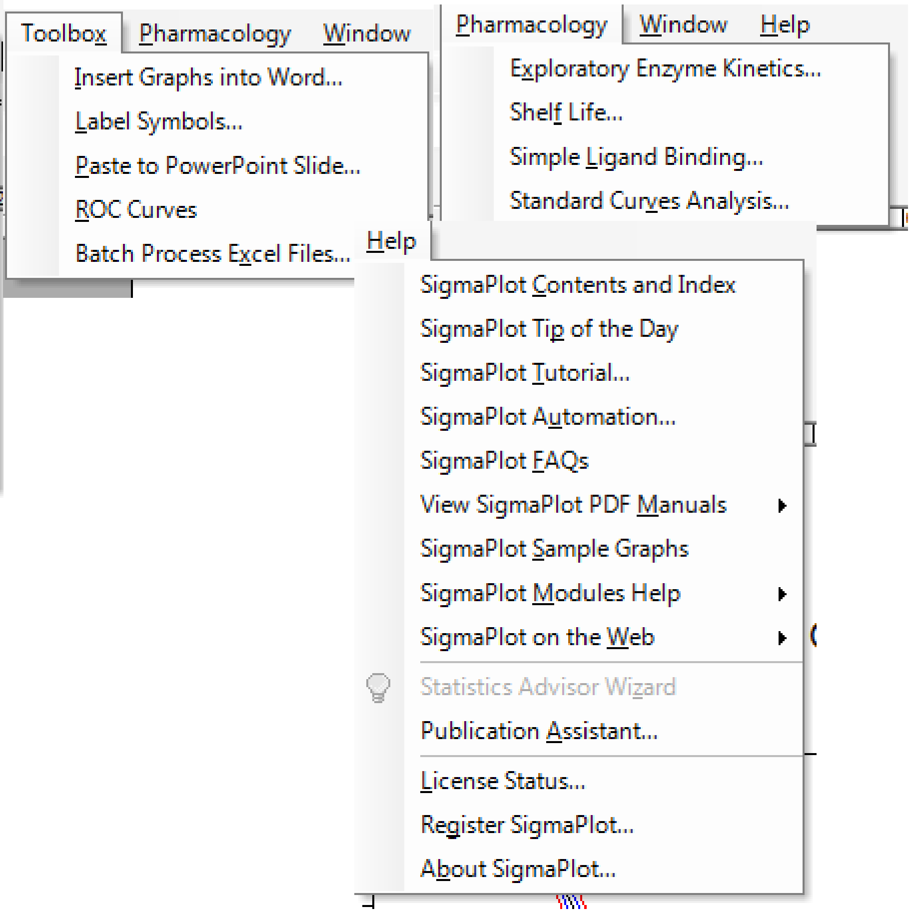




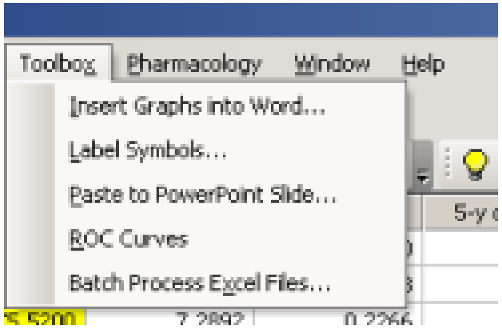
Further Menus





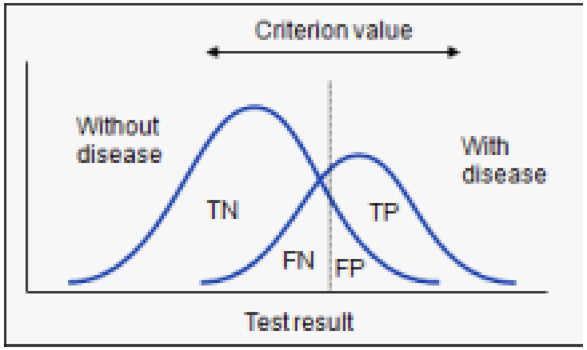


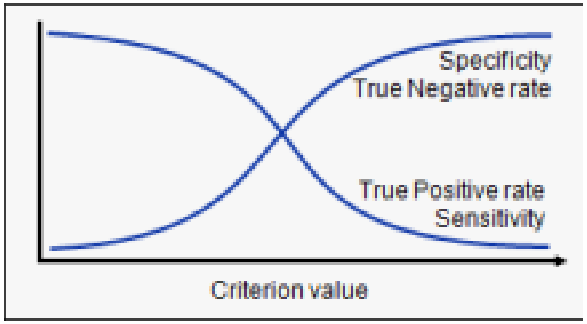
Additional functions

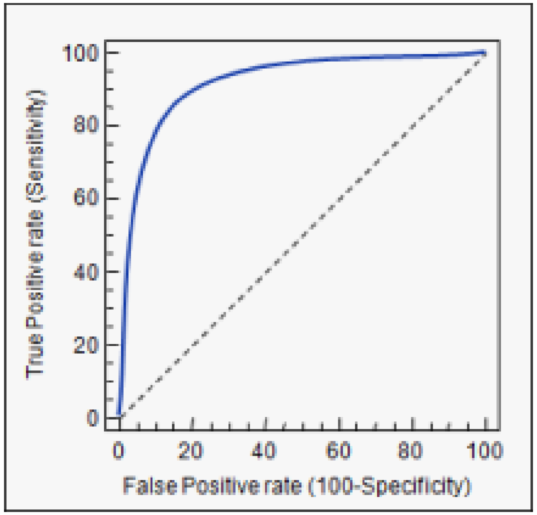


- Inserting graphs into Word or Powerpoint
- Batch processing of Excel file
- ROC curves (Receiver Operating Characteristics); e.g. diseased versus healthy)

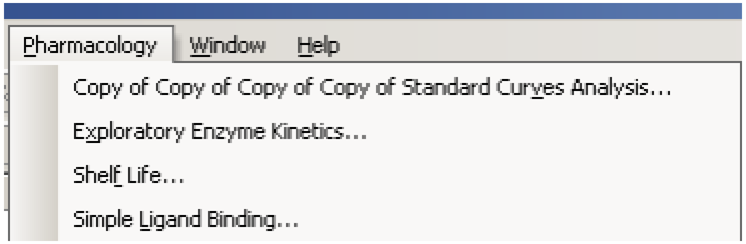
In a Receiver Operating Characteristic (ROC) curve the true positive rate (Sensitivity) is plotted in function of the false positive rate (100-Specificity) for different cut-off points. Each point on the ROC plot represents a sensitivity/specificity pair corresponding to a particular decision threshold. A test with perfect discrimination (no overlap in the two distributions) has a ROC plot that passes through the upper left corner (100% sensitivity, 100% specificity). Therefore the closer the ROC plot is to the upper left corner, the higher the overall accuracy of the test (Zweig & Campbell, 1993).

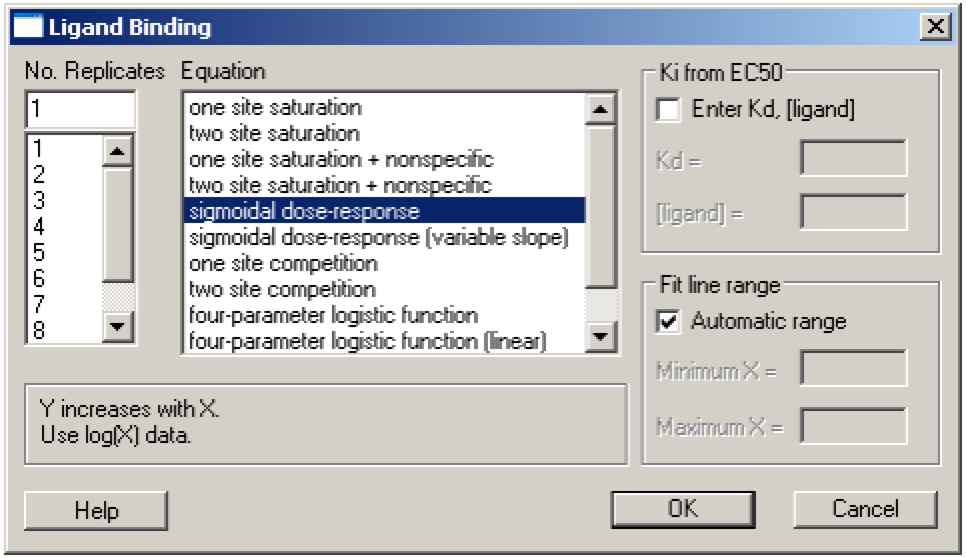






Pharmacology functions





No. Replicates: 1

Equation: sigmoidal dose-response

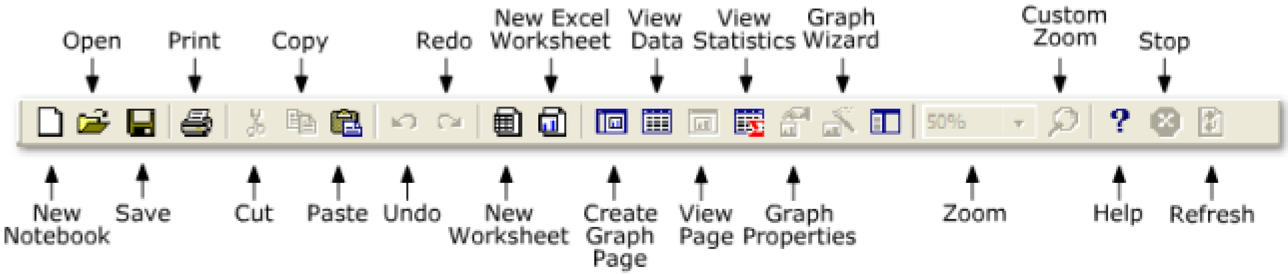
☐ Enter Kd, [ligand]

☑ Automatic range

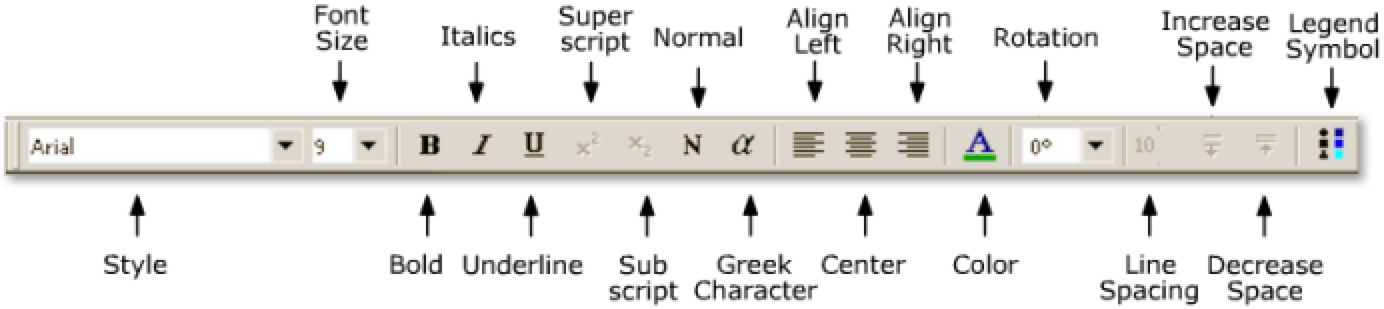
Y increases with X.
Use log(X) data.

Toolbars

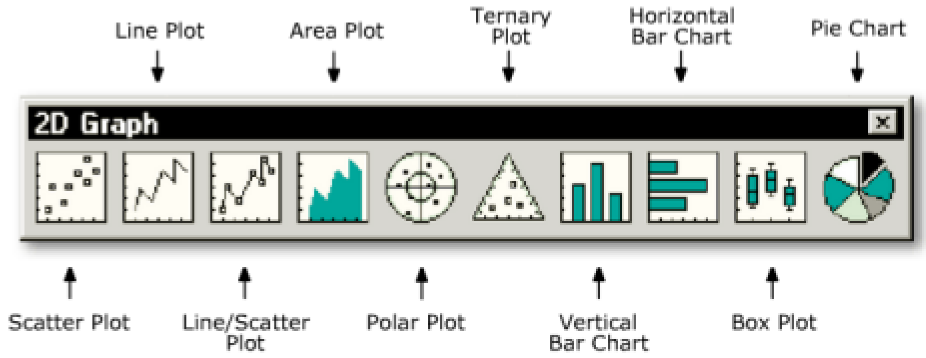
The Standard Toolbar



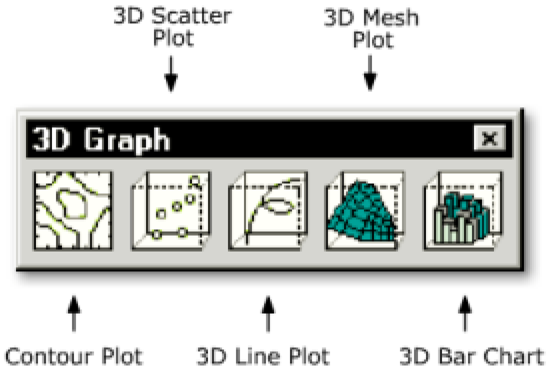
The Formatting Toolbar



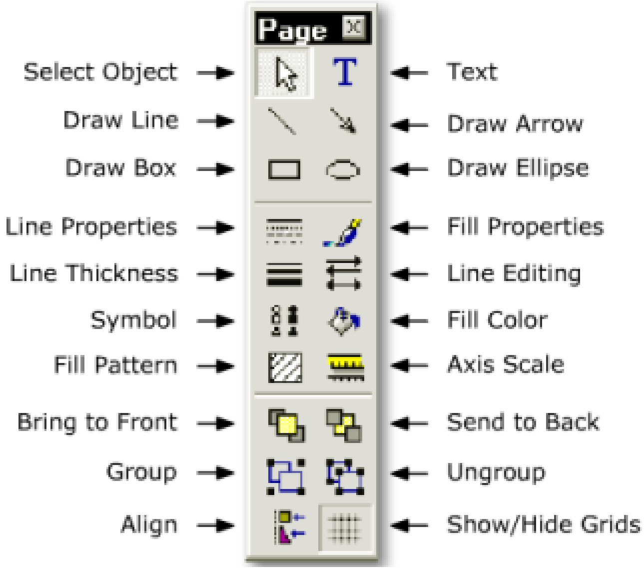
2D Graph Toolbar



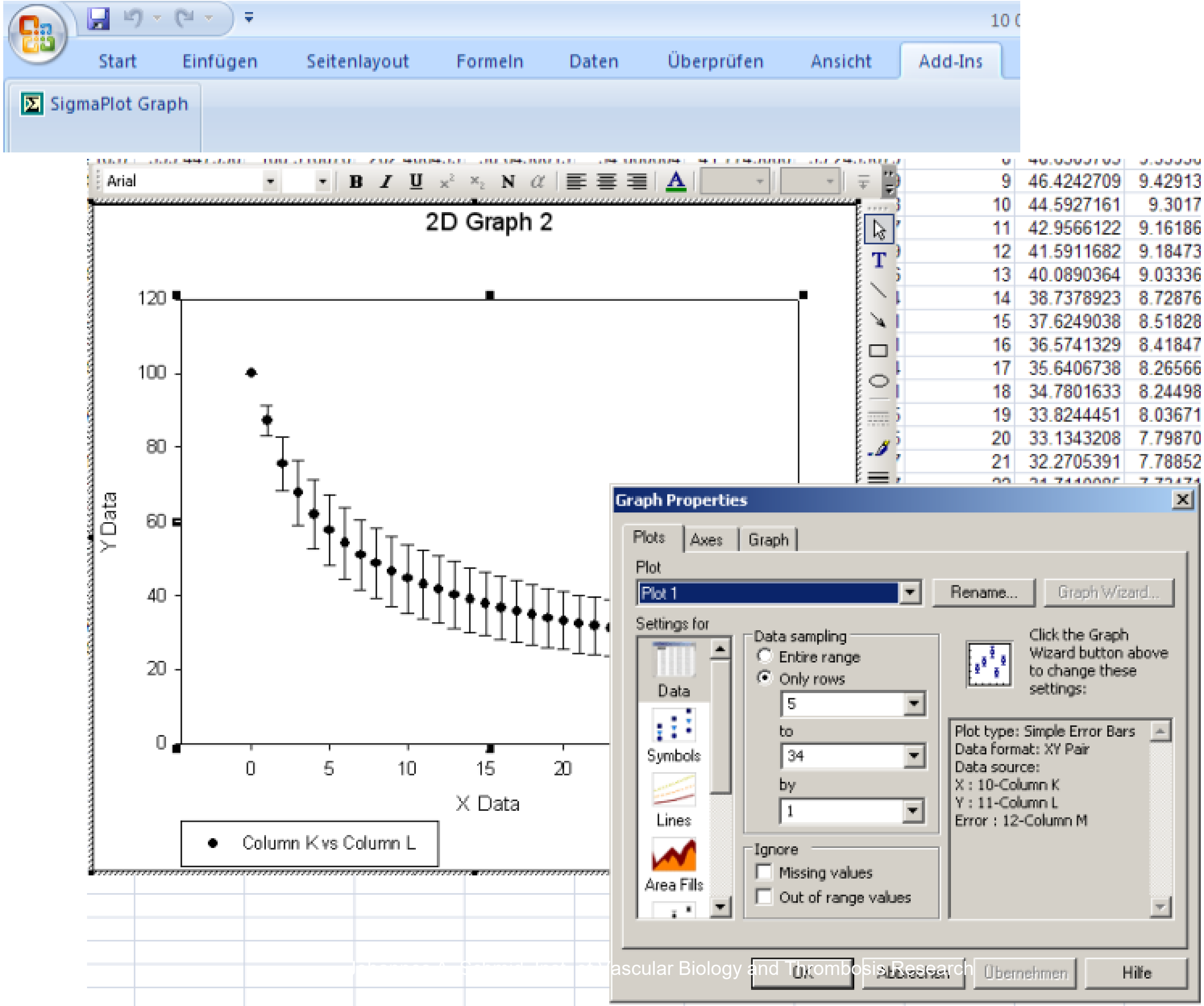
3D Graph Toolbar



Page Toolbar



Integration of Sigmaplot into Excel



9	46.4242709	9.42913
10	44.5927161	9.3017
11	42.9566122	9.16186
12	41.5911682	9.18473
13	40.0890364	9.03336
14	38.7378923	8.72876
15	37.6249038	8.51828
16	36.5741329	8.41847
17	35.6406738	8.26566
18	34.7801633	8.24498
19	33.8244451	8.03671
20	33.1343208	7.79870
21	32.2705391	7.78852

Plot: Plot 1

Data sampling
○ Entire range
● Only rows
5
to
34
by
1

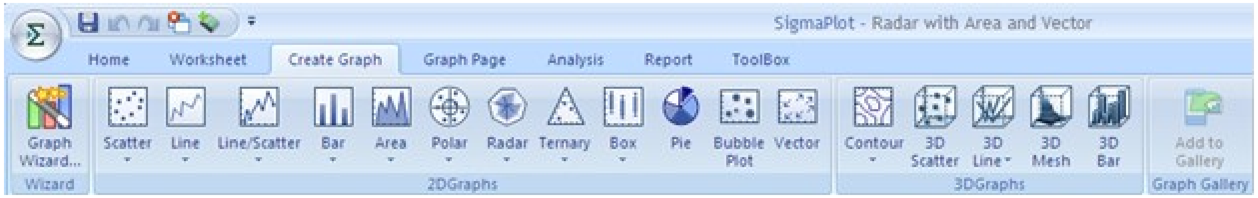
Ignore
☐ Missing values
☐ Out of range values

Click the Graph Wizard button above to change these settings:

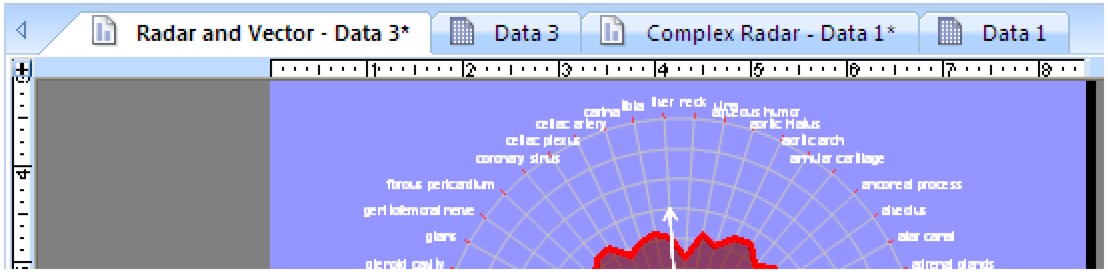
Plot type: Simple Error Bars
Data format: XY Pair
Data source:
X : 10-Column K
Y : 11-Column L
Error : 12-Column M

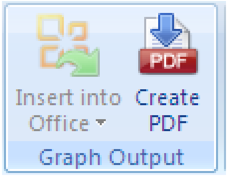
Sigmaplot 12.0 –Features

Office 2007-like ribbon user interface including a quick access toolbar



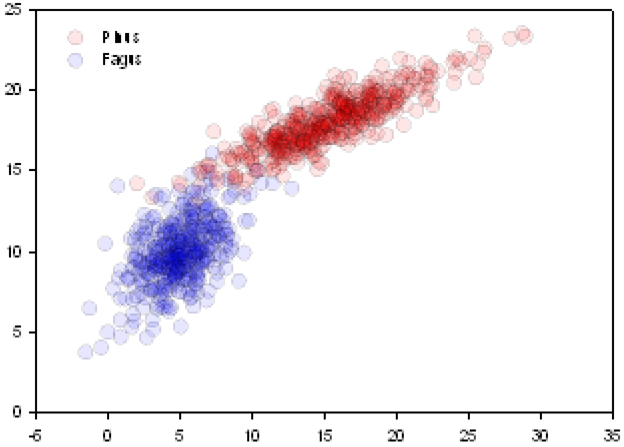
New Tabbed Window Views





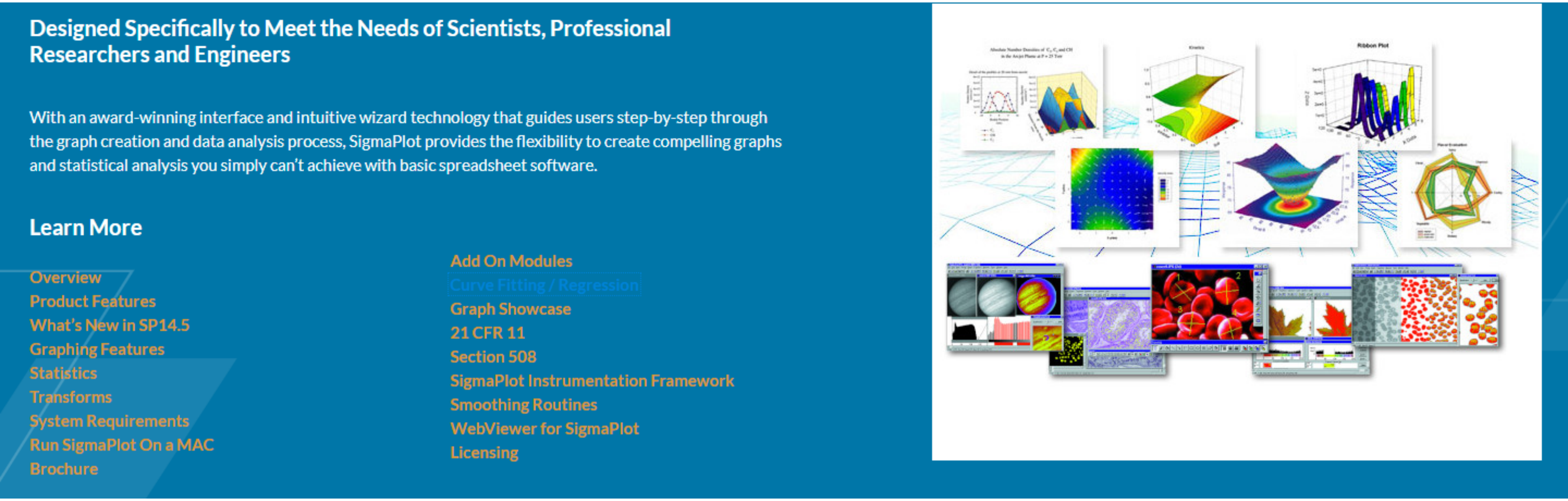
Create pdf-button added

- New curve fitting features (including: implicit function curve fitting, when the equation is not known)
- New statistics functions (e.g. normal distribution comparison)
- New analysis features (e.g. enzyme kinetics)
- New graphing features (including transparent graph objects such as symbols)



Current version: Sigmaplot 14

- https://systatsoftware.com/sigmaplot/



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- Overview
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- Graphing Features
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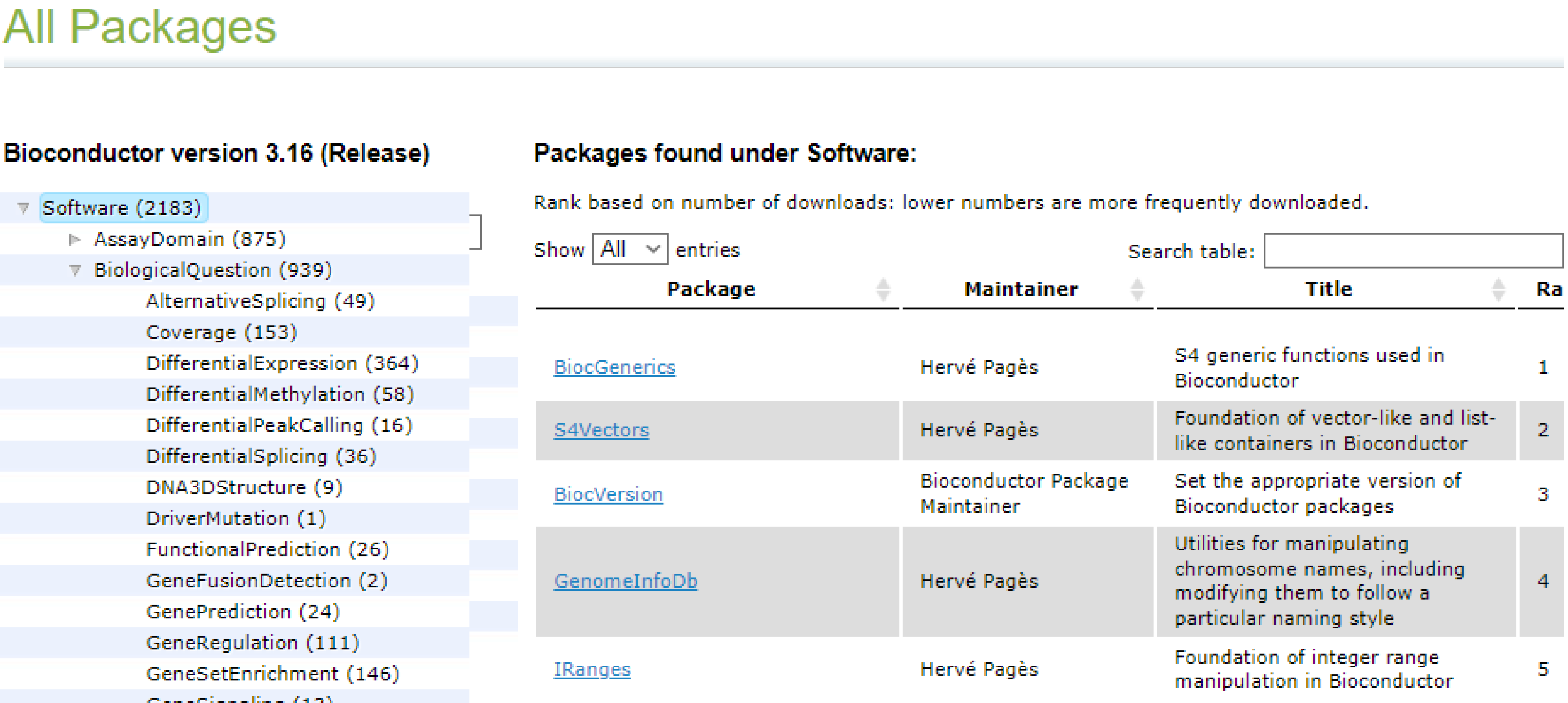
- Run SigmaPlot On a MAC
- Brochure
- Add On Modules
- Curve Fitting / Regression
- Graph Showcase
- 21 CFR 11
- Section 508
- SigmaPlot Instrumentation Framework
- Smoothing Routines
- WebViewer for SigmaPlot
- Licensing

GNU R - Bioconductor

- Introduction by Alexander Tolios

Bioconductor *R* additional slides

- R is a language and environment for statistical computing and graphics: Programming environment for many different applications in life sciences including biostatistics, data analysis, sophisticated plotting, etc. (https://cran.r-project.org/manuals.html)
- https://bioconductor.org – searching something: https://rseek.org
- Many packages available for tailored tasks:



All Packages

Bioconductor version 3.16 (Release)

- Software (2183)
  - AssayDomain (875)
  - BiologicalQuestion (939)
    - AlternativeSplicing (49)
    - Coverage (153)
    - DifferentialExpression (364)
    - DifferentialMethylation (58)
    - DifferentialPeakCalling (16)
    - DifferentialSplicing (36)
    - DNA3DStructure (9)
    - DriverMutation (1)
    - FunctionalPrediction (26)
    - GeneFusionDetection (2)
    - GenePrediction (24)
    - GeneRegulation (111)
    - GeneSetEnrichment (146)

Packages found under Software:

Rank based on number of downloads: lower numbers are more frequently downloaded.

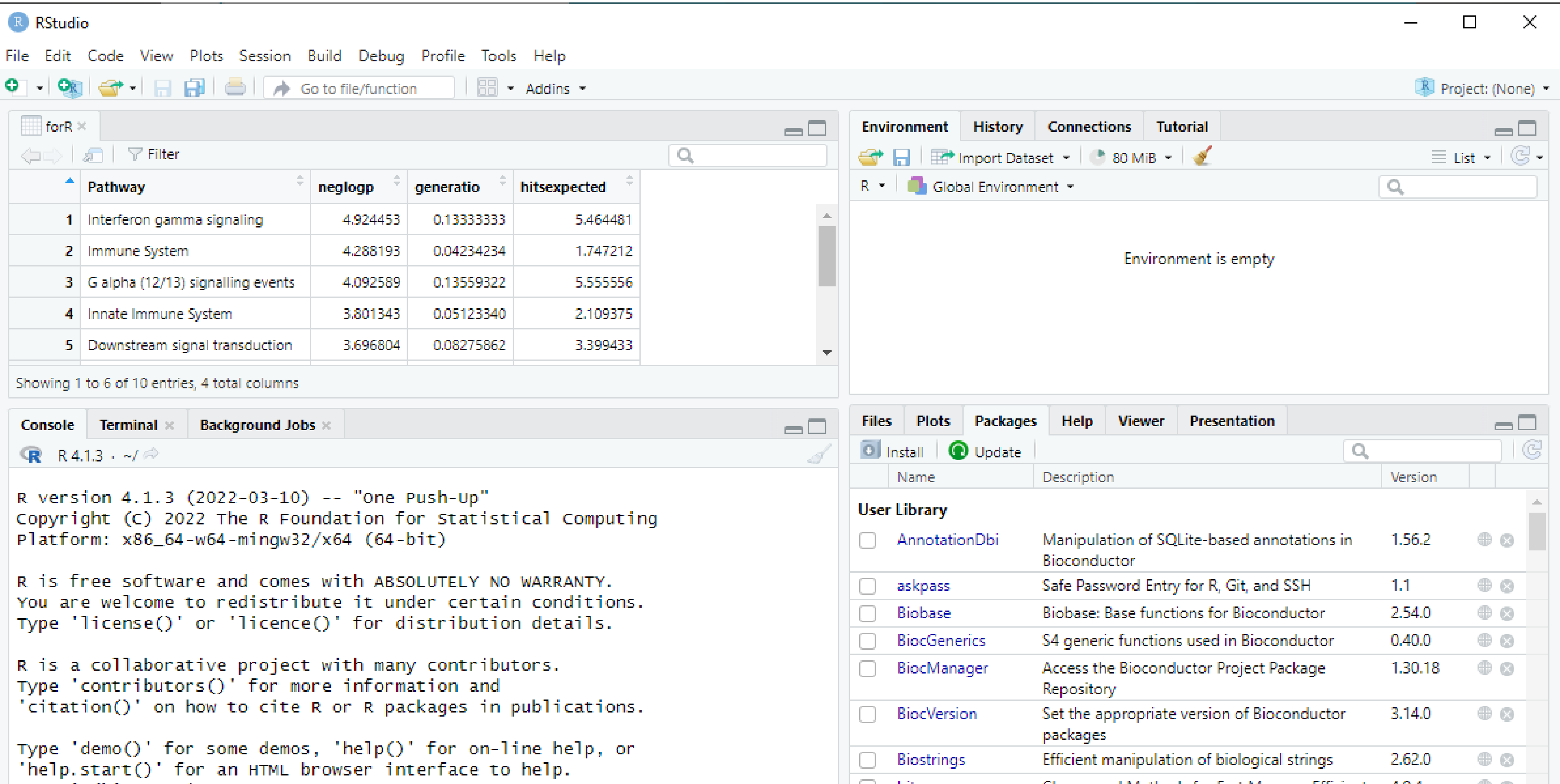
Show All entries

Search table:

Package	Maintainer	Title	Ra
BiocGenerics	Hervé Pagès	S4 generic functions used in Bioconductor	1
S4Vectors	Hervé Pagès	Foundation of vector-like and list-like containers in Bioconductor	2
BiocVersion	Bioconductor Package Maintainer	Set the appropriate version of Bioconductor packages	3
GenomeInfoDb	Hervé Pagès	Utilities for manipulating chromosome names, including modifying them to follow a particular naming style	4
IRanges	Hervé Pagès	Foundation of integer range manipulation in Bioconductor	5

RStudio – now: *Posit* *(https://posit.co)*

- Graphical user interface for Windows:
- https://posit.co/download/rstudio-desktop/ - requires R install.
- https://rstudio-conf-2020.github.io/r-for-excel/



	Pathway	neglogp	generatio	hitsexpected
1	Interferon gamma signaling	4.924453	0.13333333	5.464481
2	Immune System	4.288193	0.04234234	1.747212
3	G alpha (12/13) signalling events	4.092589	0.13559322	5.555556
4	Innate Immune System	3.801343	0.05123340	2.109375
5	Downstream signal transduction	3.696804	0.08275862	3.399433

Showing 1 to 6 of 10 entries, 4 total columns

```
R version 4.1.3 (2022-03-10) -- "One Push-Up"
Copyright (C) 2022 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

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'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
```
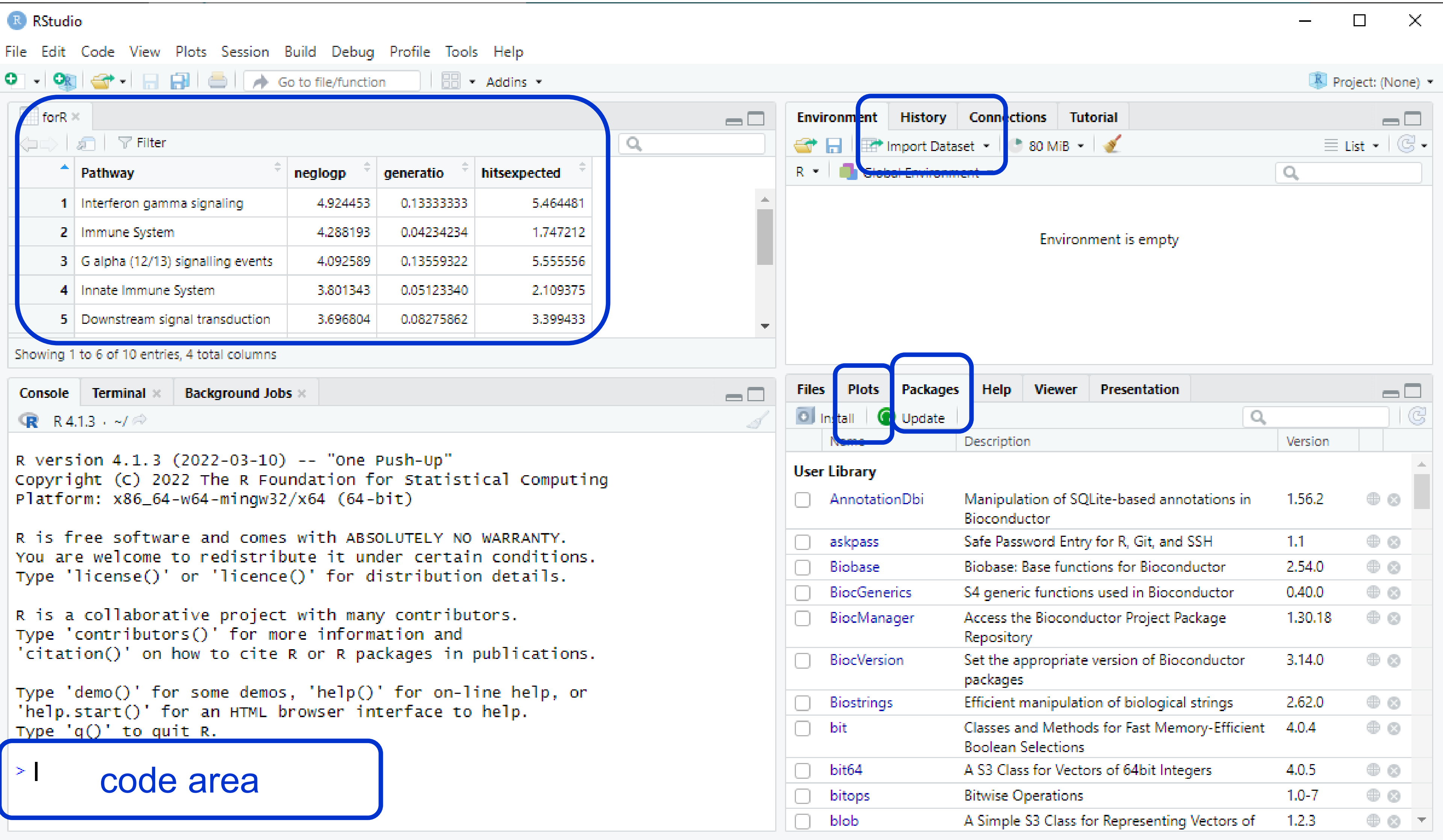

	Name	Description	Version
	User Library		
☐	AnnotationDbi	Manipulation of SQLite-based annotations in Bioconductor	1.56.2
☐	askpass	Safe Password Entry for R, Git, and SSH	1.1
☐	Biobase	Biobase: Base functions for Bioconductor	2.54.0
☐	BiocGenerics	S4 generic functions used in Bioconductor	0.40.0
☐	BiocManager	Access the Bioconductor Project Package Repository	1.30.18
☐	BiocVersion	Set the appropriate version of Bioconductor packages	3.14.0
☐	Biostrings	Efficient manipulation of biological strings	2.62.0



	Pathway	neglogp	generatio	hitsexpected
1	Interferon gamma signaling	4.924453	0.13333333	5.464481
2	Immune System	4.288193	0.04234234	1.747212
3	G alpha (12/13) signalling events	4.092589	0.13559322	5.555556
4	Innate Immune System	3.801343	0.05123340	2.109375
5	Downstream signal transduction	3.696804	0.08275862	3.399433

Showing 1 to 6 of 10 entries, 4 total columns

```
R version 4.1.3 (2022-03-10) -- "One Push-Up"
Copyright (C) 2022 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> |
```

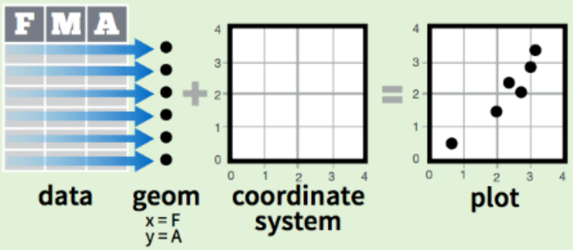
User Library

	Name	Description	Version
☐	AnnotationDbi	Manipulation of SQLite-based annotations in Bioconductor	1.56.2
☐	askpass	Safe Password Entry for R, Git, and SSH	1.1
☐	Biobase	Biobase: Base functions for Bioconductor	2.54.0
☐	BiocGenerics	S4 generic functions used in Bioconductor	0.40.0
☐	BiocManager	Access the Bioconductor Project Package Repository	1.30.18
☐	BiocVersion	Set the appropriate version of Bioconductor packages	3.14.0
☐	Biostrings	Efficient manipulation of biological strings	2.62.0
☐	bit	Classes and Methods for Fast Memory-Efficient Boolean Selections	4.0.4
☐	bit64	A S3 Class for Vectors of 64bit Integers	4.0.5
☐	bitops	Bitwise Operations	1.0-7
☐	blob	A Simple S3 Class for Representing Vectors of	1.2.3

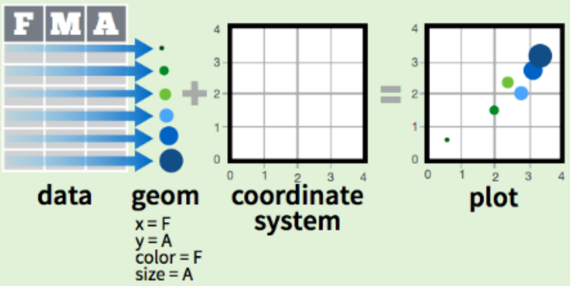
GGPLOT2 – a professional graph package

Basics

ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same few components: a **data** set, a set of **geoms**—visual marks that represent data points, and a **coordinate system.**



To display data values, map variables in the data set to aesthetic properties of the geom like **size**, **color**, and **x** and **y** locations.



Complete the template below to build a graph.

required

ggplot (data = <DATA>) +
<GEOM_FUNCTION>(mapping = aes(<MAPPINGS>),
stat = <STAT>, position = <POSITION>) +
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>

Not required, sensible defaults supplied

ggplot(data = mpg, **aes(**x = cty, y = hwy**))** Begins a plot that you finish by adding layers to. Add one geom function per layer.

aesthetic mappings · data · geom

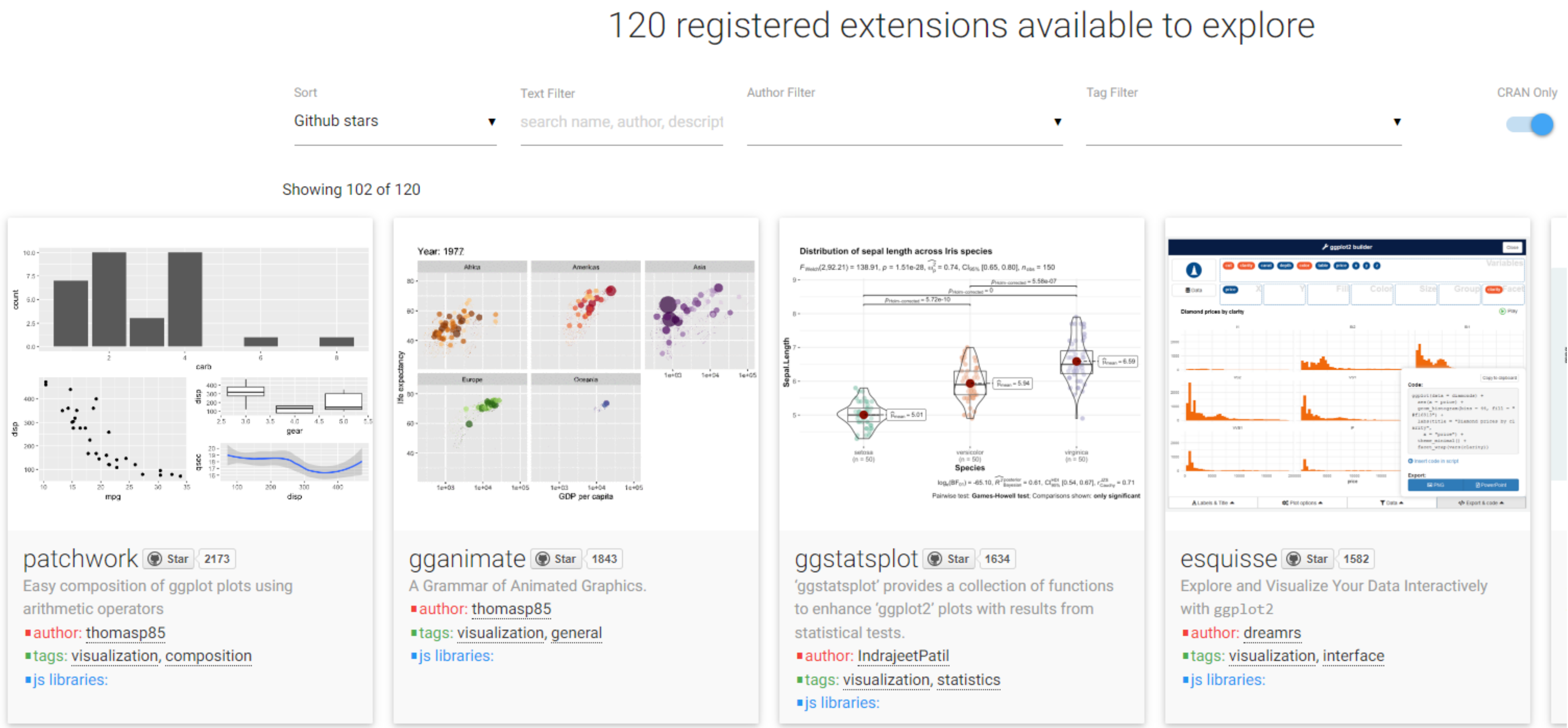
qplot(x = cty, y = hwy, data = mpg, geom = “point"**)** Creates a complete plot with given data, geom, and mappings. Supplies many useful defaults.

last_plot() Returns the last plot

ggsave("plot.png", width = 5, height = 5) Saves last plot as 5’ x 5’ file named "plot.png" in working directory. Matches file type to file extension.

GGPLOT2 – a professional graph package

- https://exts.ggplot2.tidyverse.org/gallery/



120 registered extensions available to explore

Sort: Github stars ▾

Text Filter: search name, author, descript

Author Filter: ▾

Tag Filter: ▾

CRAN Only: ●

Showing 102 of 120

patchwork Star 2173

Easy composition of ggplot plots using arithmetic operators

- author: thomasp85
- tags: visualization, composition
- js libraries:

gganimate Star 1843

A Grammar of Animated Graphics.

- author: thomasp85
- tags: visualization, general
- js libraries:

ggstatsplot Star 1634

'ggstatsplot' provides a collection of functions to enhance 'ggplot2' plots with results from statistical tests.

- author: IndrajeetPatil
- tags: visualization, statistics
- js libraries:

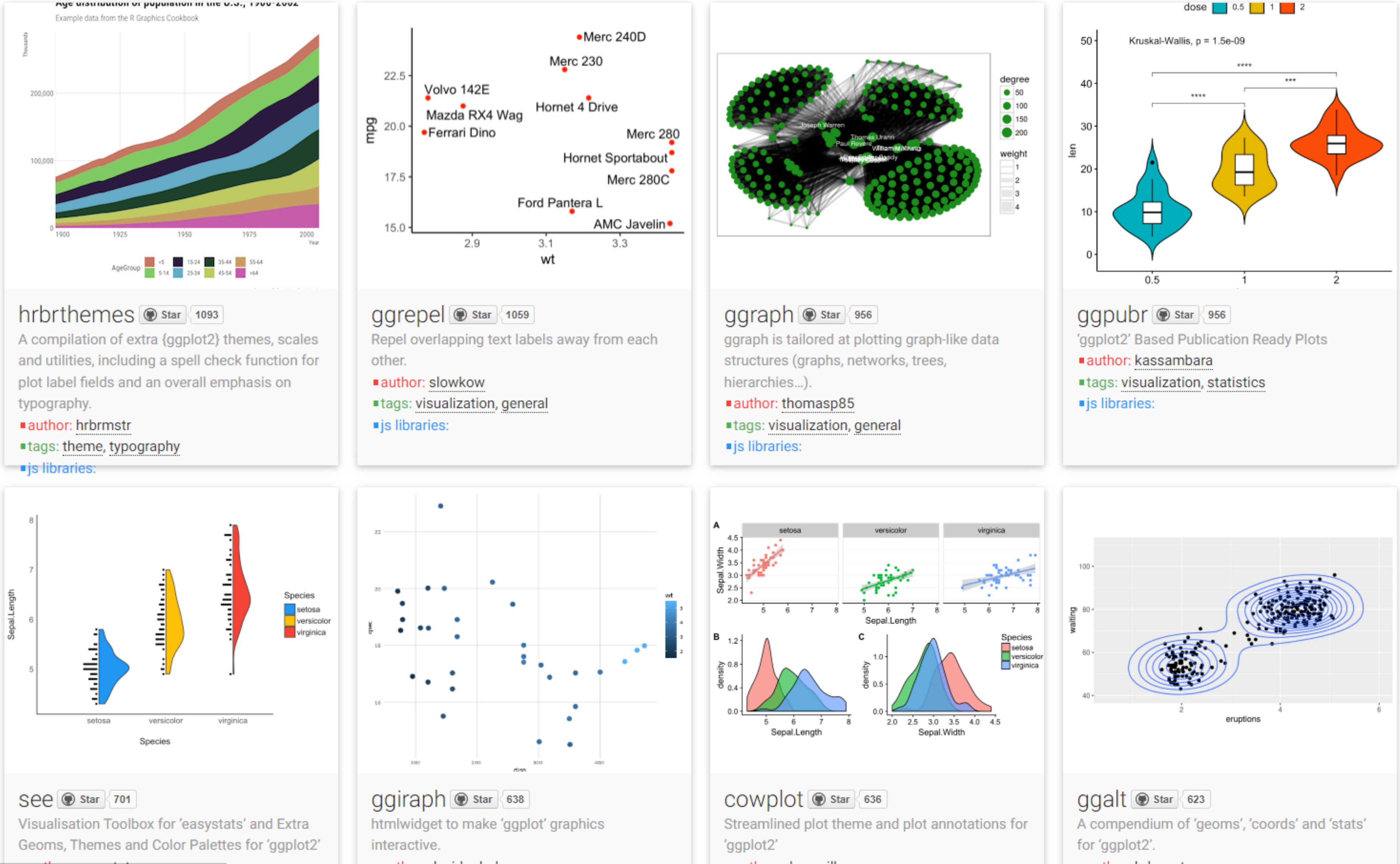
esquisse Star 1582

Explore and Visualize Your Data Interactively with `ggplot2`

- author: dreamrs
- tags: visualization, interface
- js libraries:

GGPLOT2 – a professional graph package

- https://exts.ggplot2.tidyverse.org/gallery/



hrbrthemes ☆ Star 1093

A compilation of extra {ggplot2} themes, scales and utilities, including a spell check function for plot label fields and an overall emphasis on typography.

- author: hrbrmstr
- tags: theme, typography
- js libraries:

ggrepel ☆ Star 1059

Repel overlapping text labels away from each other.

- author: slowkow
- tags: visualization, general
- js libraries:

ggraph ☆ Star 956

ggraph is tailored at plotting graph-like data structures (graphs, networks, trees, hierarchies...).

- author: thomasp85
- tags: visualization, general
- js libraries:

ggpubr ☆ Star 956

'ggplot2' Based Publication Ready Plots

- author: kassambara
- tags: visualization, statistics
- js libraries:

see ☆ Star 701

Visualisation Toolbox for 'easystats' and Extra Geoms, Themes and Color Palettes for 'ggplot2'

ggiraph ☆ Star 638

htmlwidget to make 'ggplot' graphics interactive.

cowplot ☆ Star 636

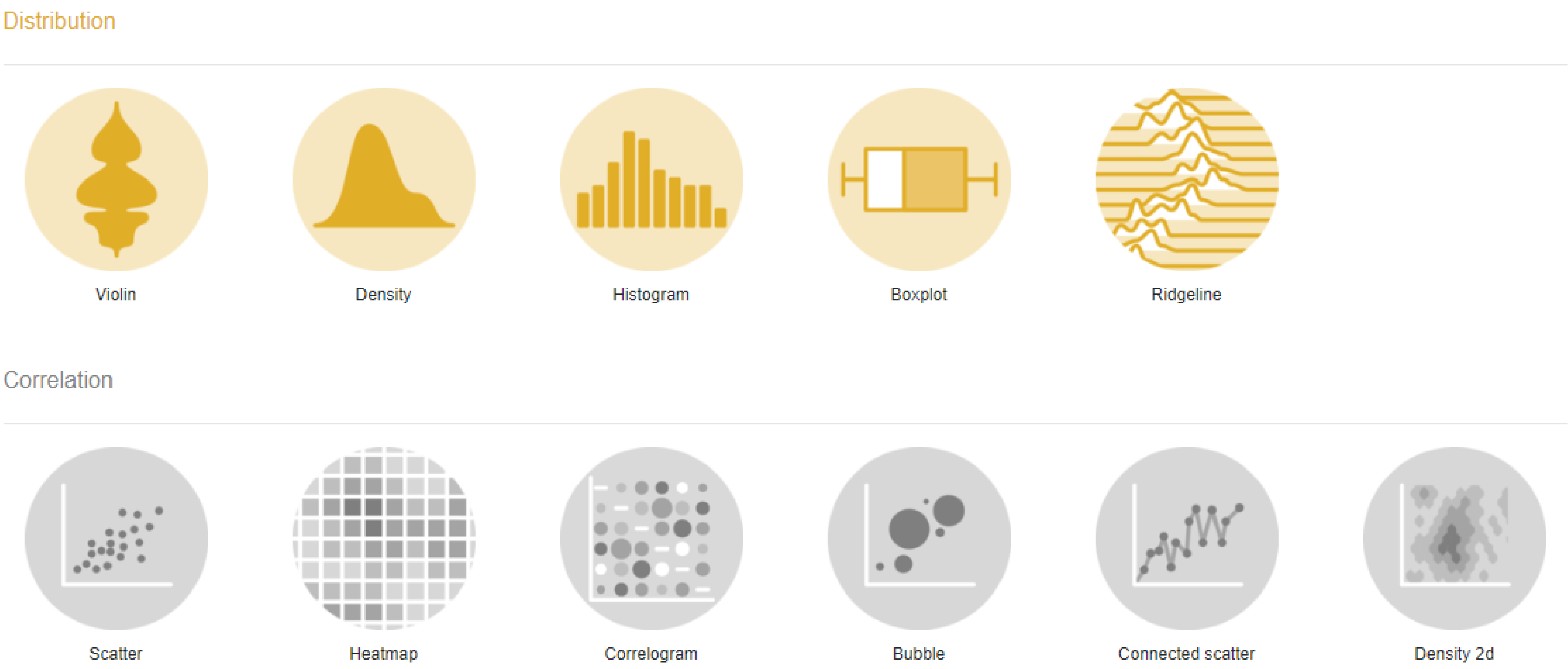
Streamlined plot theme and plot annotations for 'ggplot2'

ggalt ☆ Star 623

A compendium of 'geoms', 'coords' and 'stats' for 'ggplot2'.

GGPLOT2 – a professional graph package

- http://r-statistics.co/Top50-Ggplot2-Visualizations-MasterList-R-Code.html
- https://r-graph-gallery.com



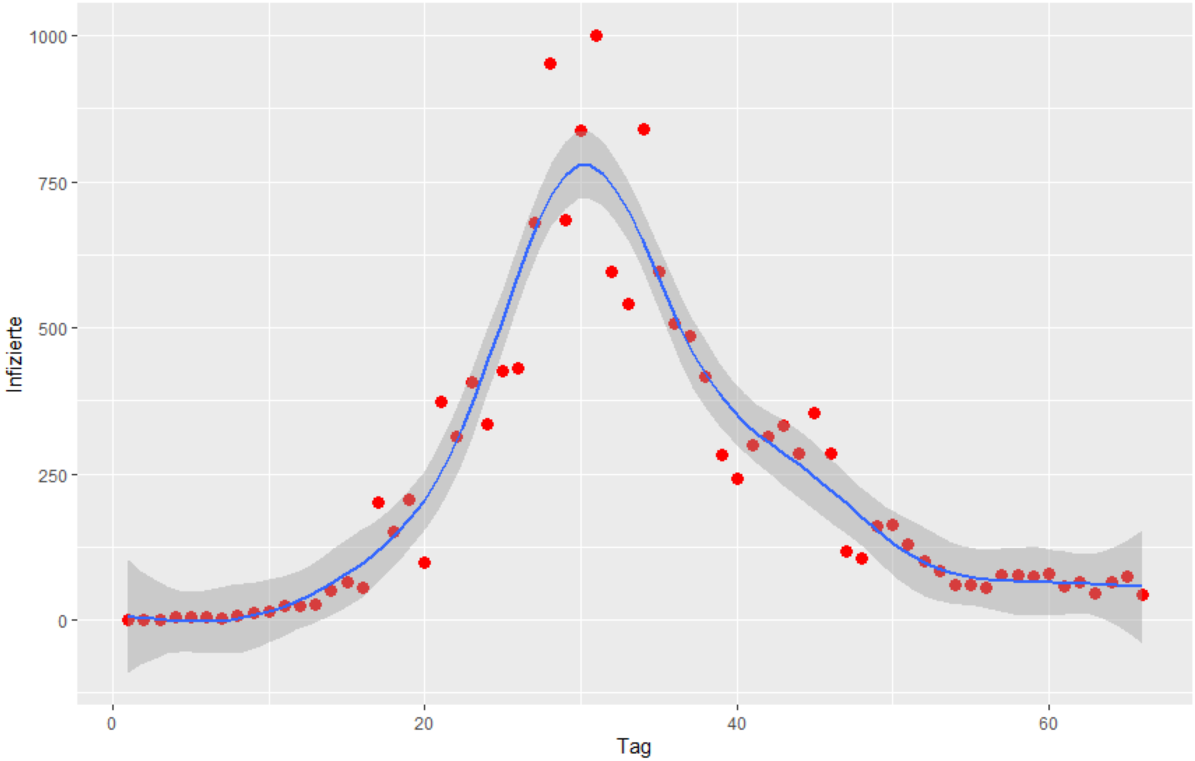
GGPLOT2 – some own examples

Scattergram in ggplot2:

Data: COVIDexample (Tag, Infizierte)

Code for scatter with smoothing:

```
ggplot(COVIDexample,aes(x=Tag, y=Infizierte))+geom_point(size=3,colour="red")+geom_smooth(method="gam")
```

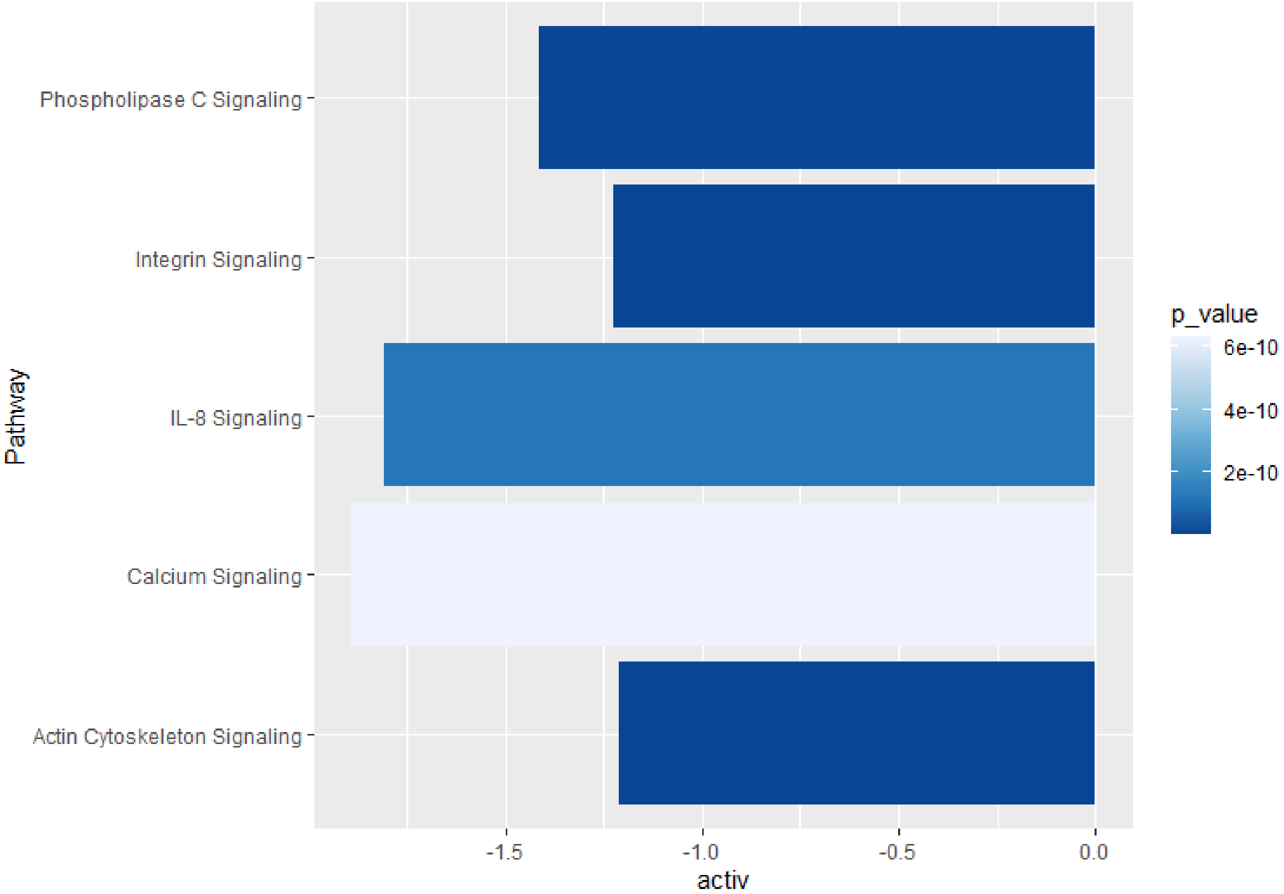


Bar graphs with colors depending on values

Pathway	activ	p_value	Ratio
Integrin Signaling	-1.225	5.01E-20	1.09E-01
Actin Cytoskeleton Signaling	-1.213	3.98E-13	8.12E-02
Phospholipase C Signaling	-1.414	2.51E-12	7.39E-02
IL-8 Signaling	-1.807	1.20E-10	7.44E-02
Calcium Signaling	-1.89	6.31E-10	7.28E-02

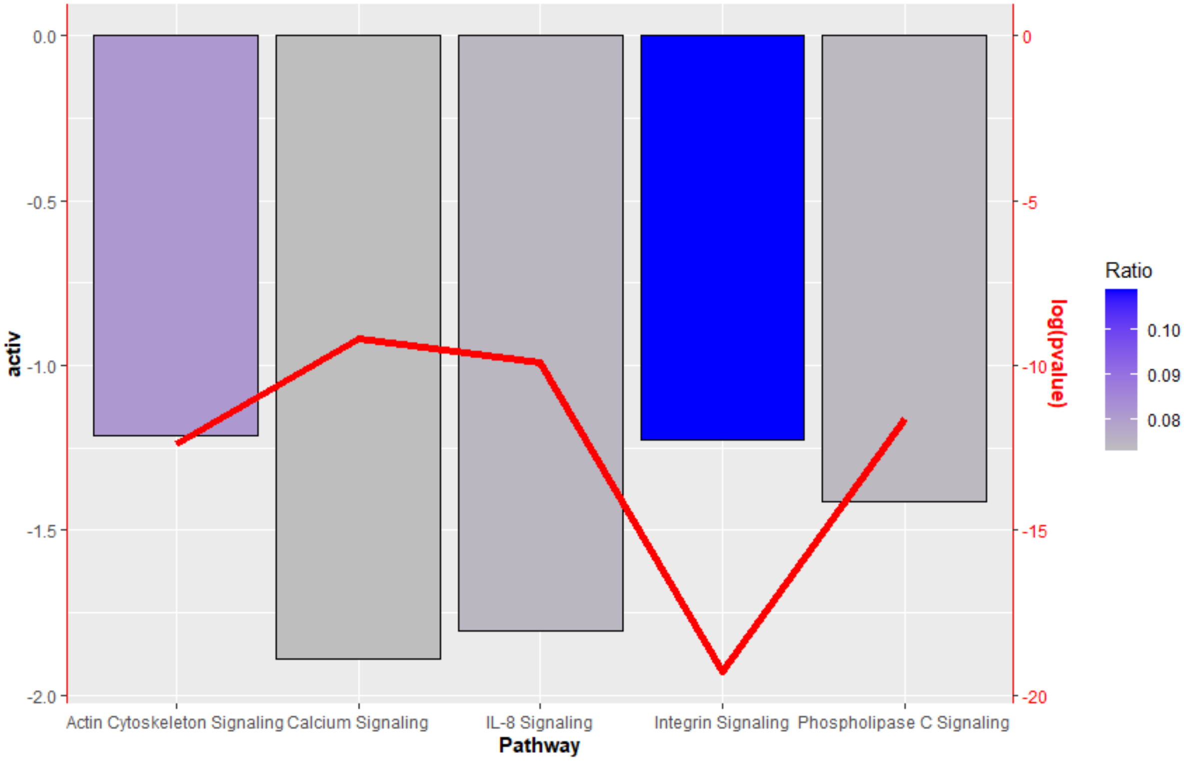
forR: Excel table

```
ggplot (forR,aes(x=Pathway,y=activ,fill=p_value)) +
geom_bar(stat="identity") +
coord_flip() +
scale_fill_distiller(palette = "Blues")
```



Column + line-graph + gradient

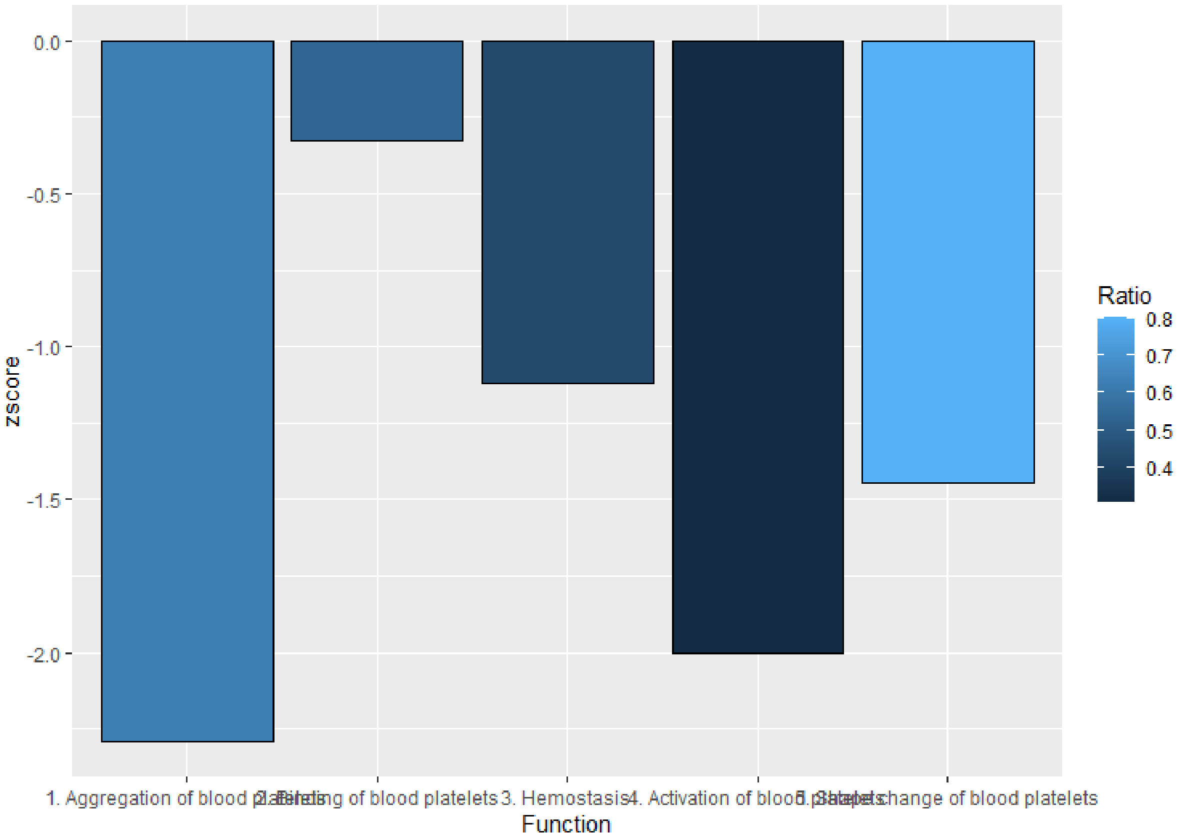
```
ggplot(data=data) +
#erste Dimension: column + 2. Dimension: Fuellung nach Parameter2
geom_col(aes(x=Pathway,y=activ,fill=Ratio),colour="black")+
scale_fill_gradient2(low="blue",mid="green",high="red",midpoint=0.09)+
#dritte Dimension: log-pvalue als Linie
geom_line(aes(x=Pathway,y=-minuslogp/10),color="red", size=2,group=1)+
scale_y_continuous(name="activ",sec.axis = sec_axis(~.*10, name = "log(pvalue)"))+
#rechte y-Achse + Beschriftung in Rot, alles in Bold
theme(axis.title=element_text(face="bold"),axis.line.y = element_line(color = "red"),axis.text.y.right = element_text(color = "red"), axis.title.y.right = element_text(color = "red"))
ggsave(file="Columngraph.svg")
```



Define global parameter first

```
>p=ggplot(forR, aes(x=Function,y=zscore,fill=Ratio))
#Defines that "p" is the variable for a ggplot with "forR" as data and x, y, and fill-values defined as global aesthetics
# x=Function,y=zscore,fill=Ratio > afterwards, x and y and fill don't have to be defined again.
```

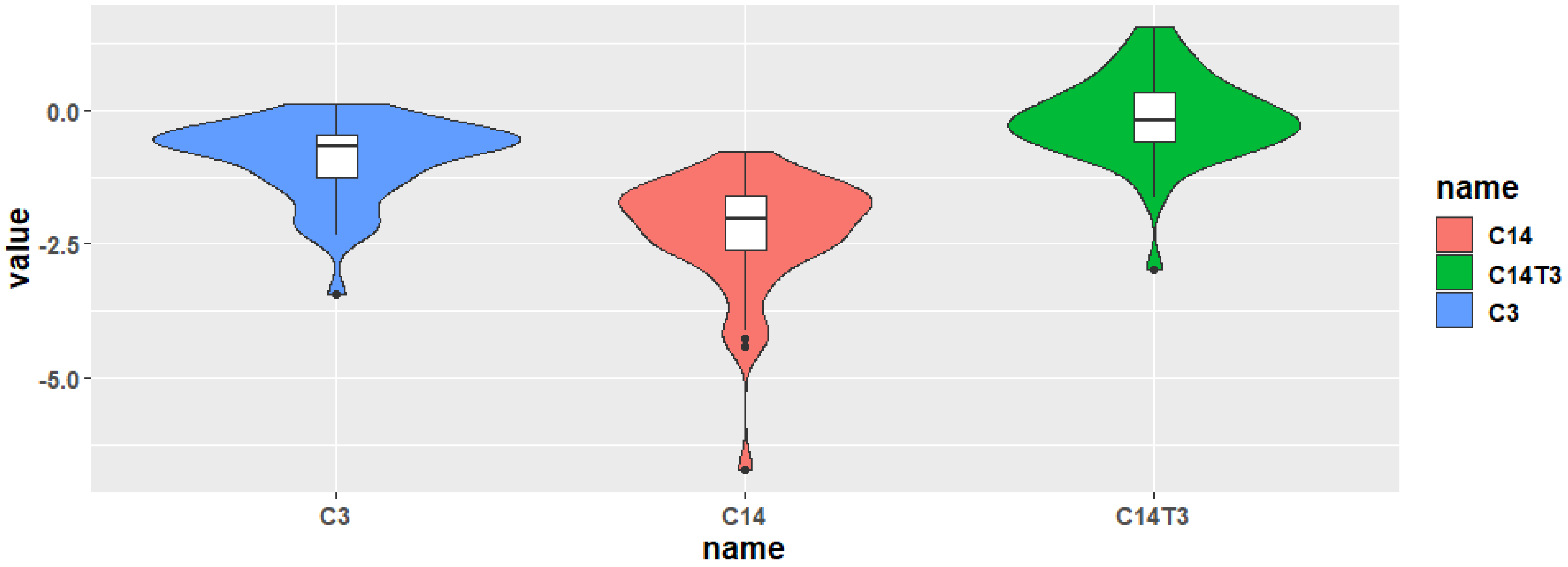
```
>p+geom_col(color="black")
#is all what is needed then to plot that:
```



Violin plots with box plot inset

```
ggplot(pivot,aes(name,value)) + geom_violin(aes(fill=name)) + scale_x_discrete(limits=c("C3", "C14", "C14T3")) + theme(text = element_text(size = 14,face="bold")) + geom_boxplot(width=0.1)
```

… if you want to plot several datasets on the same x-axis you have to use the pivot function



Parallel coordinate plots

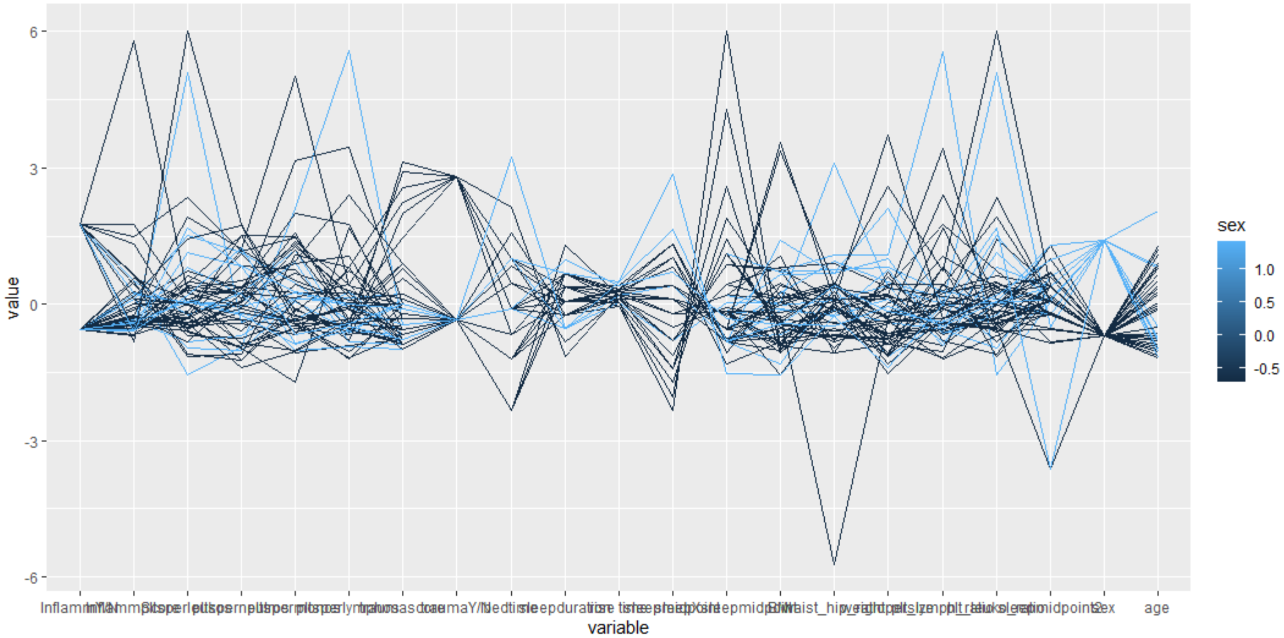
- Different possibilities: a) ggplot2 and ggally or b) plotly (interactive)

a) ggplot2/ggally:

- ggparcoord function - RDocumentation
- # loading of the necessary packages
- library(GGally)
- library(ggplot2)
- library(svglite)

ggparcoord(data, columns=1:21,groupColumn = "sex")

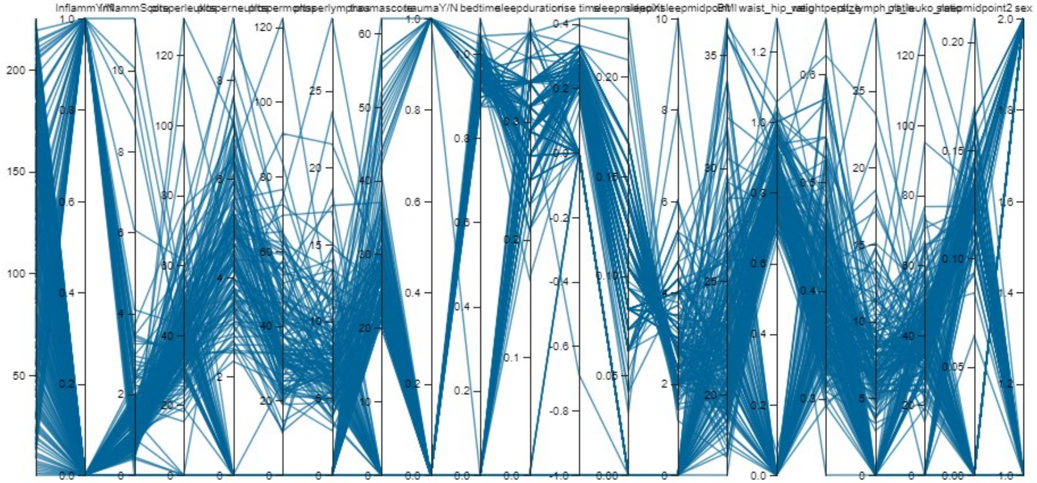
In contrast to parcoord from plotly; ggparcoord can plot more than 21 axes (but it is not interactive)



Interactive parallel coordinate plots

```
packages = c('GGally', 'plotly', 'parcoords', 'tidyverse')
for(p in packages){
  if(!require(p, character.only = T)){
    install.packages(p)
  }
}
parcoords(
 data[,1:20],
 reorderable = T,
 brushMode = '1D-axes')
```

```
# data[,1:20] means: all rows, columns 1 – 20
# data[1:10,1:20] would mean rows 1-10 and columns 1- 20 are plotted
# reorderable = T (True), means that the axes can be dragged for re-ordering
# the parcoords package can handle only a maximum of 21 columns
```



Interactive parallel coordinate plots: gating

Gates for several parameters can be defined to select the corresponding lines

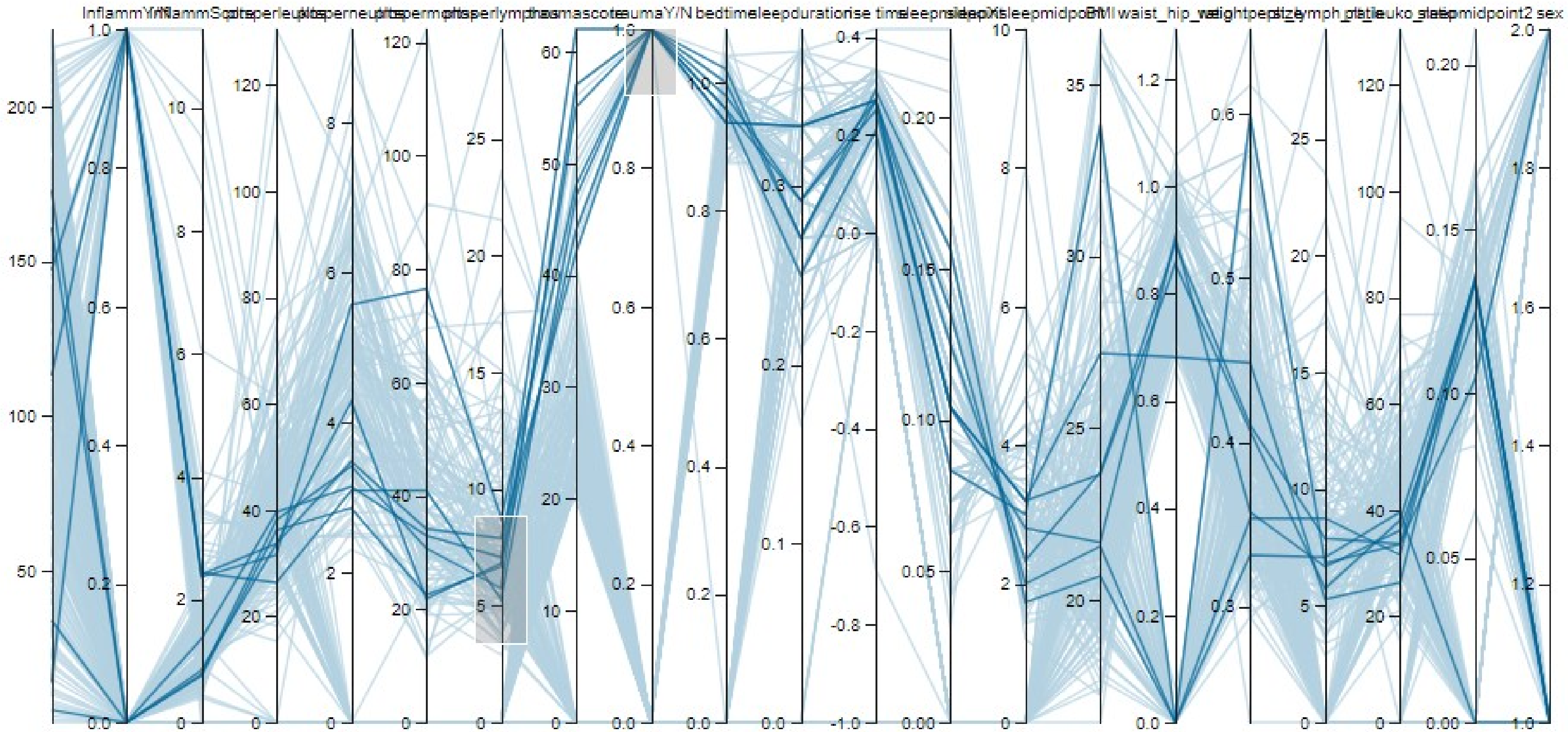
(by hovering with the mouse over a range on an axis).

Gates are by default combined with AND operand

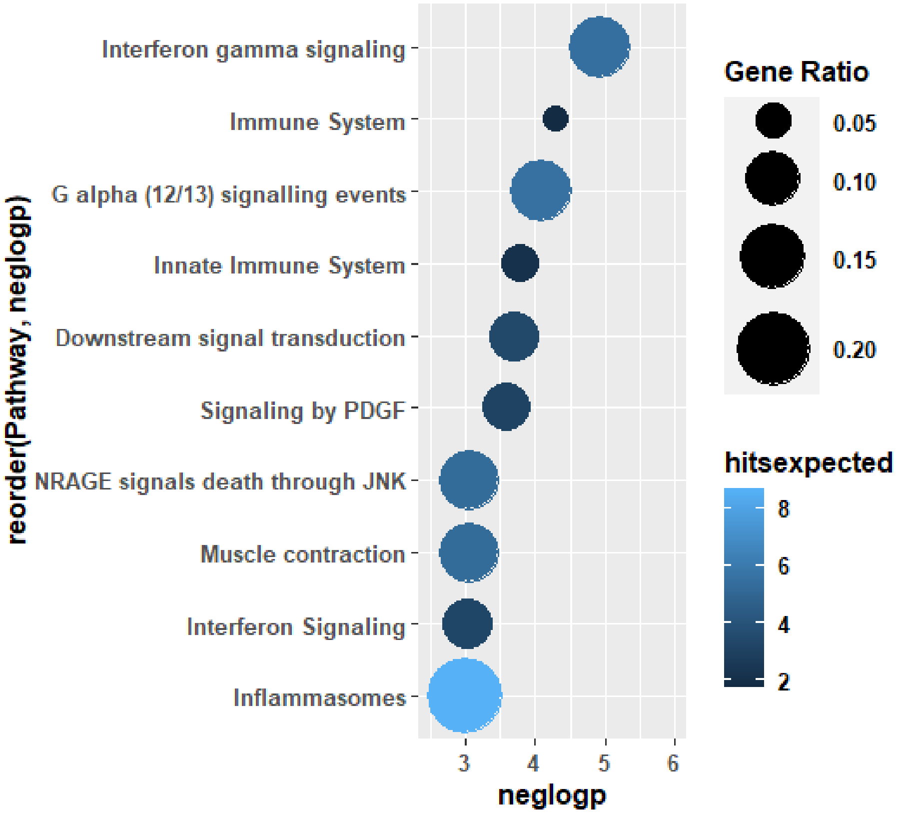
using an alphaOnBrushed command, the non-chosen lines have and alpha-density reduction

while the chosen lines are shown with full density (alpha=1)

parcoords(data[,1:20], reorderable = T, brushMode = '1D-axes', alphaOnBrushed = 0.3)



Bubble chart + Color + reordered

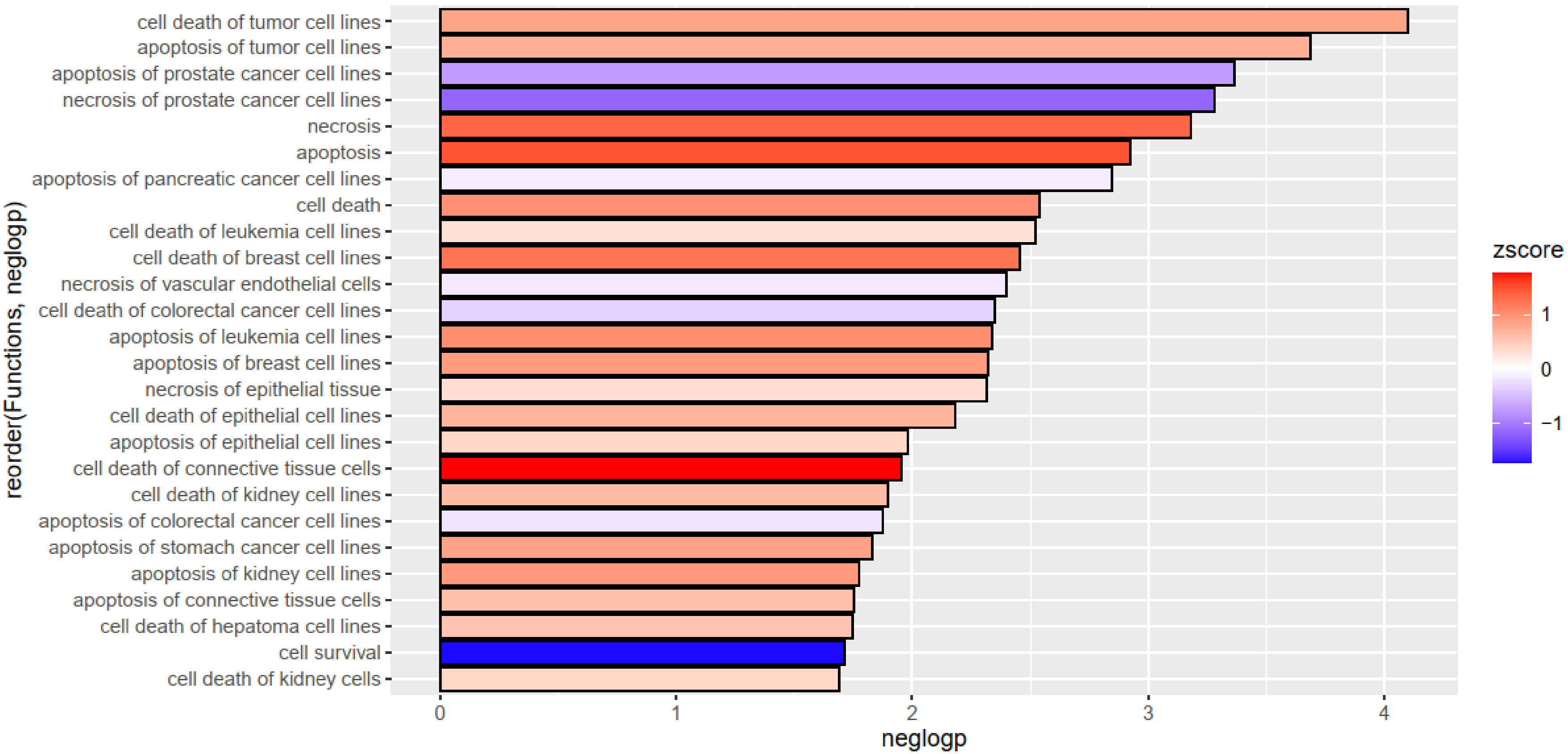


```
ggplot(data = forR,
       mapping = aes(x = neglogp,
                     y = reorder(Pathway, neglogp),
                     size = generatio,
                     colour = hitsexpected)) +
  geom_point() + scale_size(range = c(5, 15), name = "Gene Ratio") +
xlim(2.5,6) +
theme(text = element_text(size = 12,face="bold"))
```

Bar graph colored

library(ggplot2)

```
ggplot(IPA,aes(y=reorder(Functions,neglogp),x=neglogp,fill=zscore)) +
geom_col(colour="black")+ scale_fill_gradient2(low="blue",high ="red")
```



SVG-graphs with ggplot

Svg-Export > to Inkscape: to consider:

Font in Inkscape do not work, if svg-file was exported from ggplot2.

Workaround: `install.packages("svglite")`

- Save Plot extra :

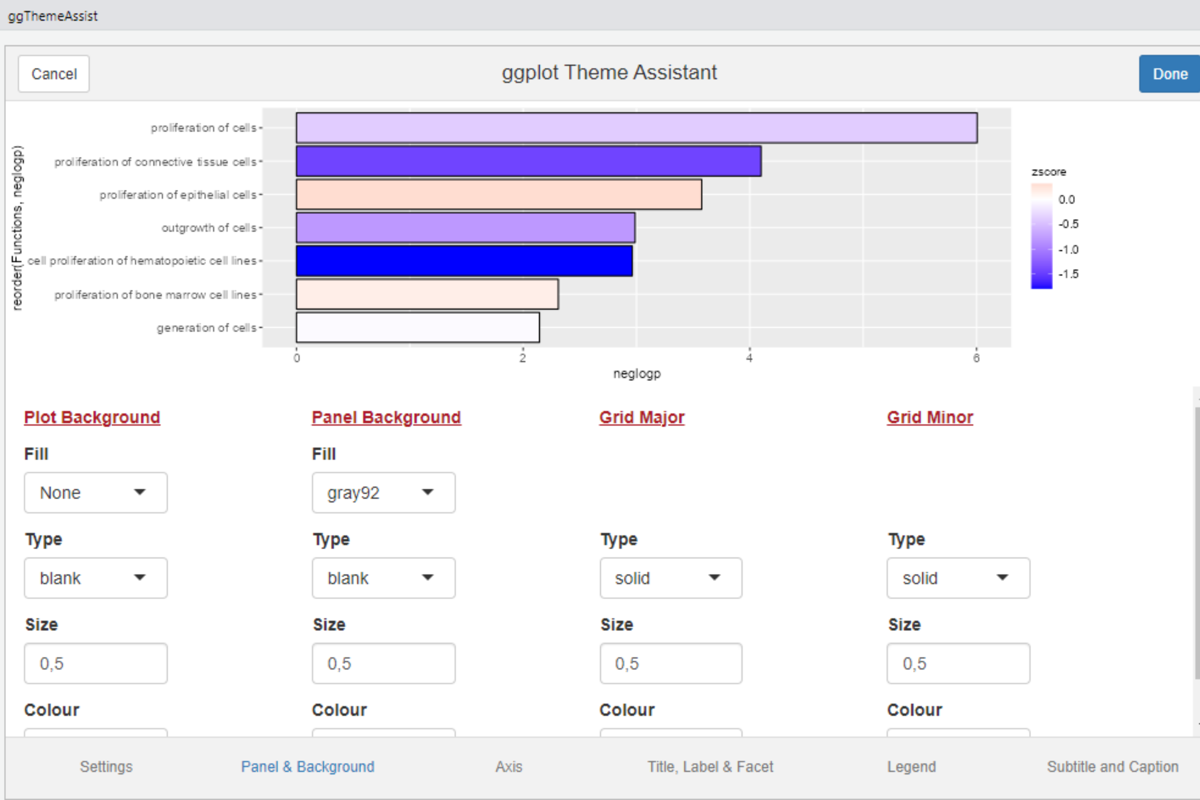
```
> plot=ggplot(Rcourse,aes(x=Tag, y=Infizierte))+geom_point(size=3,colour="red")
> ggsave(file="Scatter.svg", plot=plot, width=10, height=10)
```

The svg-file will be in the standard folder (Documents); in Inkscape it is possible to change the font and type.

Work around 2: export as pdf file and open the pdf file with Inkscape

Customizing ggplot2 Visualizations With ggThemeAssist

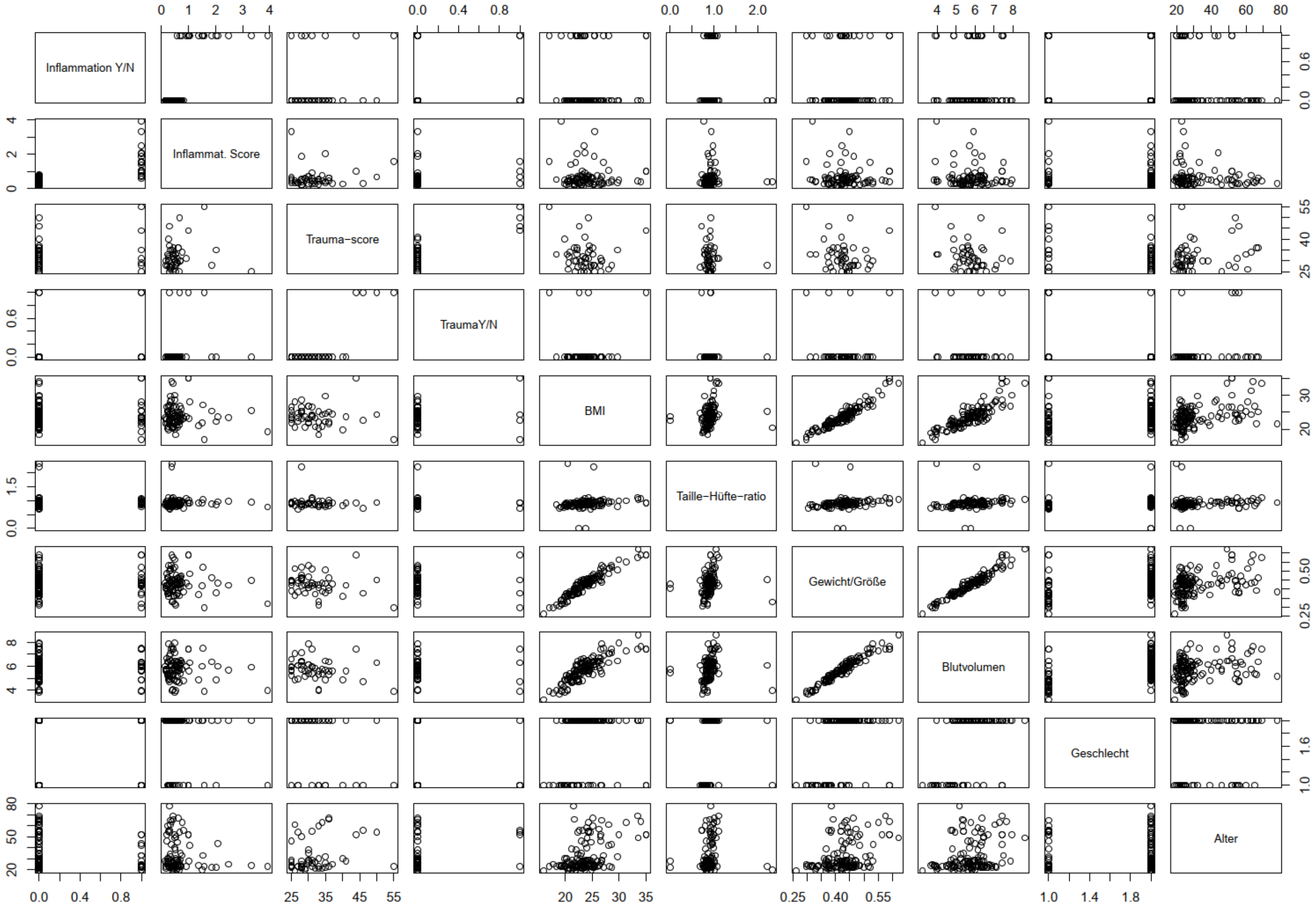
```
install.packages("ggThemeAssist")
library(ggThemeAssist)
library(ggplot2)
#Example:
plot=ggplot(IPA,aes(y=reorder(Functions,neglogp),x=neglogp,fill=zscore)) +
geom_col(colour="black")+ scale_fill_gradient2(low="blue",high ="red")
ggThemeAssistGadget(plot)
```



	Plot Background	Panel Background	Grid Major	Grid Minor
Fill	None	gray92		
Type	blank	blank	solid	solid
Size	0,5	0,5	0,5	0,5
Colour				

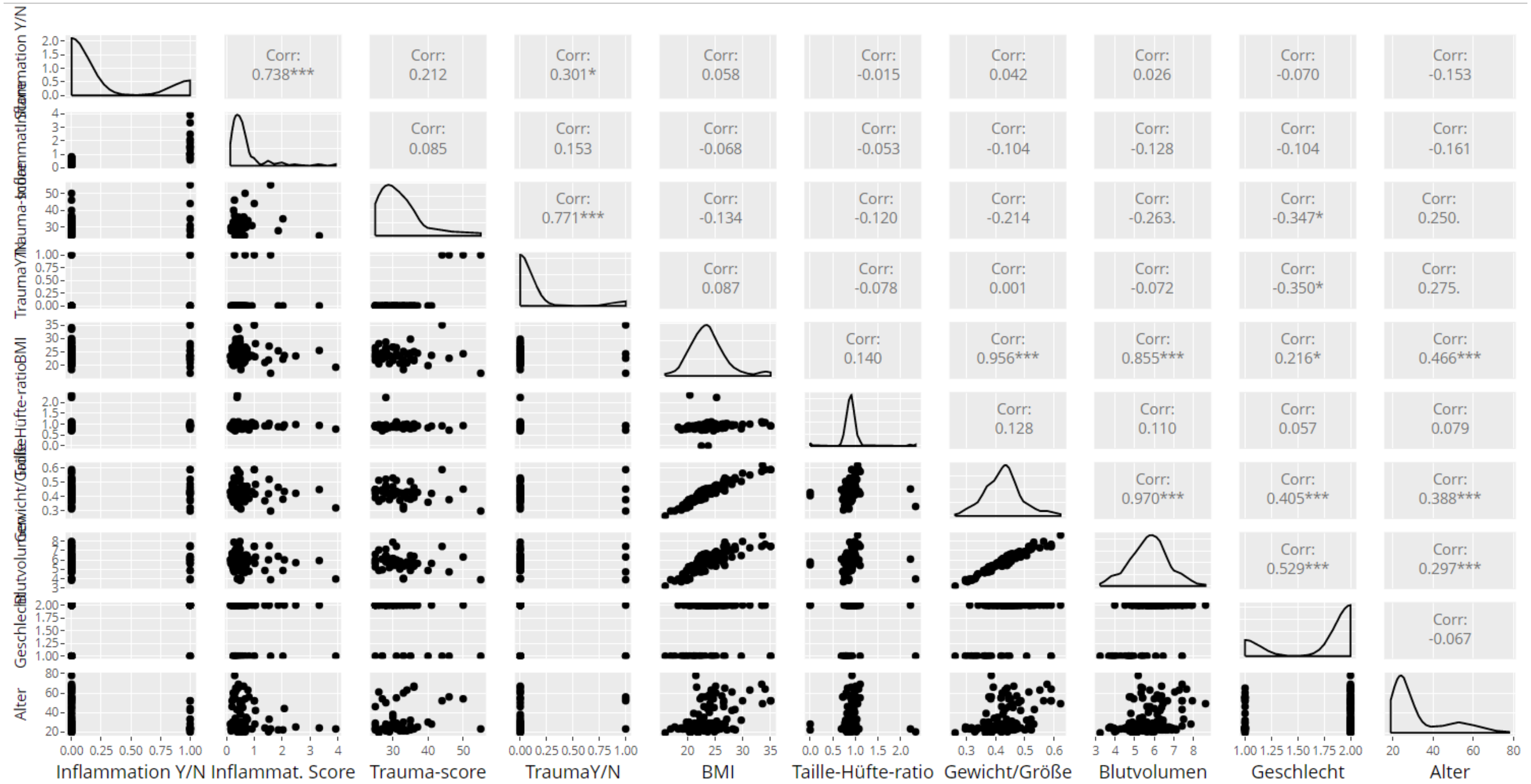
Scatterplot matrix

- Command:
- pairs(forR[1:10])



Scatterplot matrix with ggally

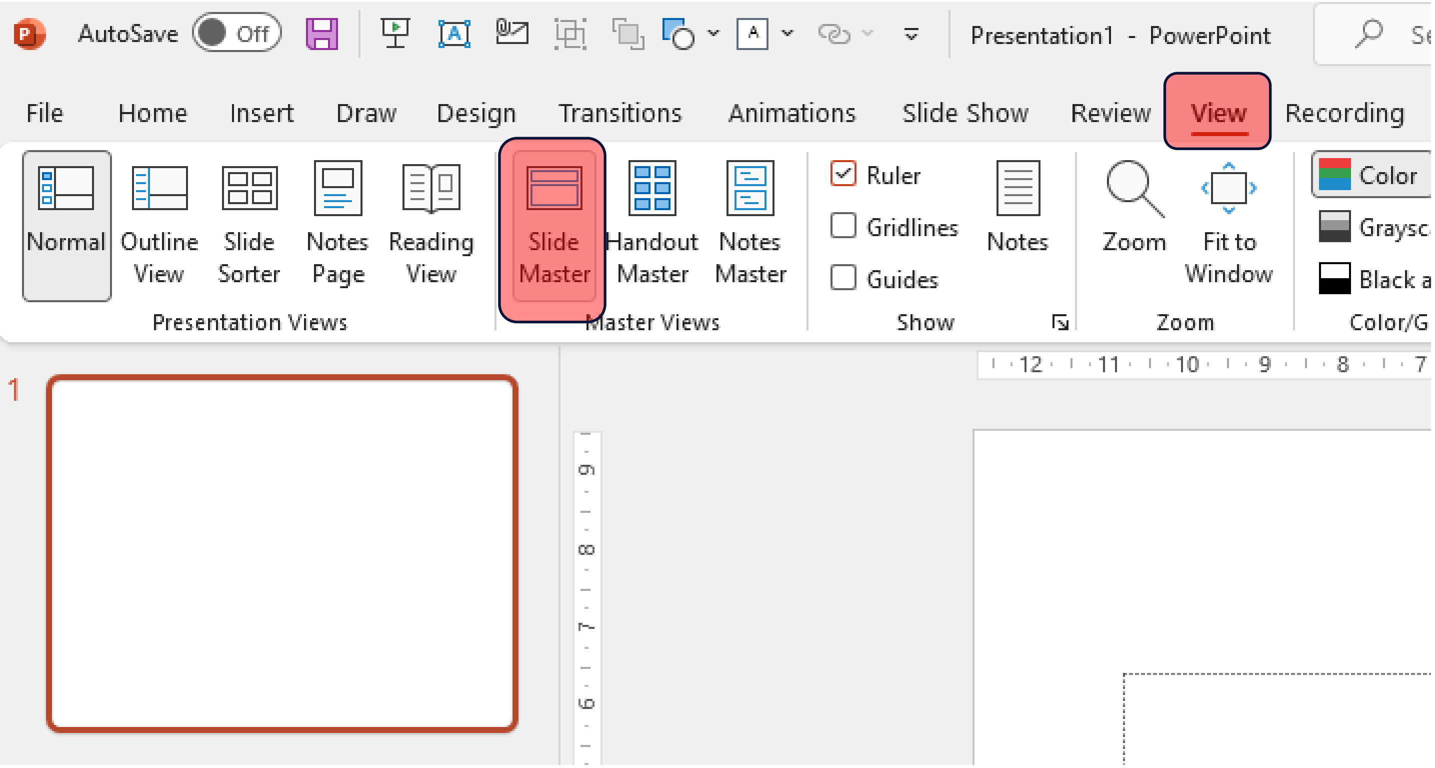
```
install.packages("plotly")
library(plotly)
library(devtools)
install_github("ggobi/ggally")
install.packages("GGally")
library(GGally)
p <- ggpairs(forR[1:10])
ggplotly(p)
```



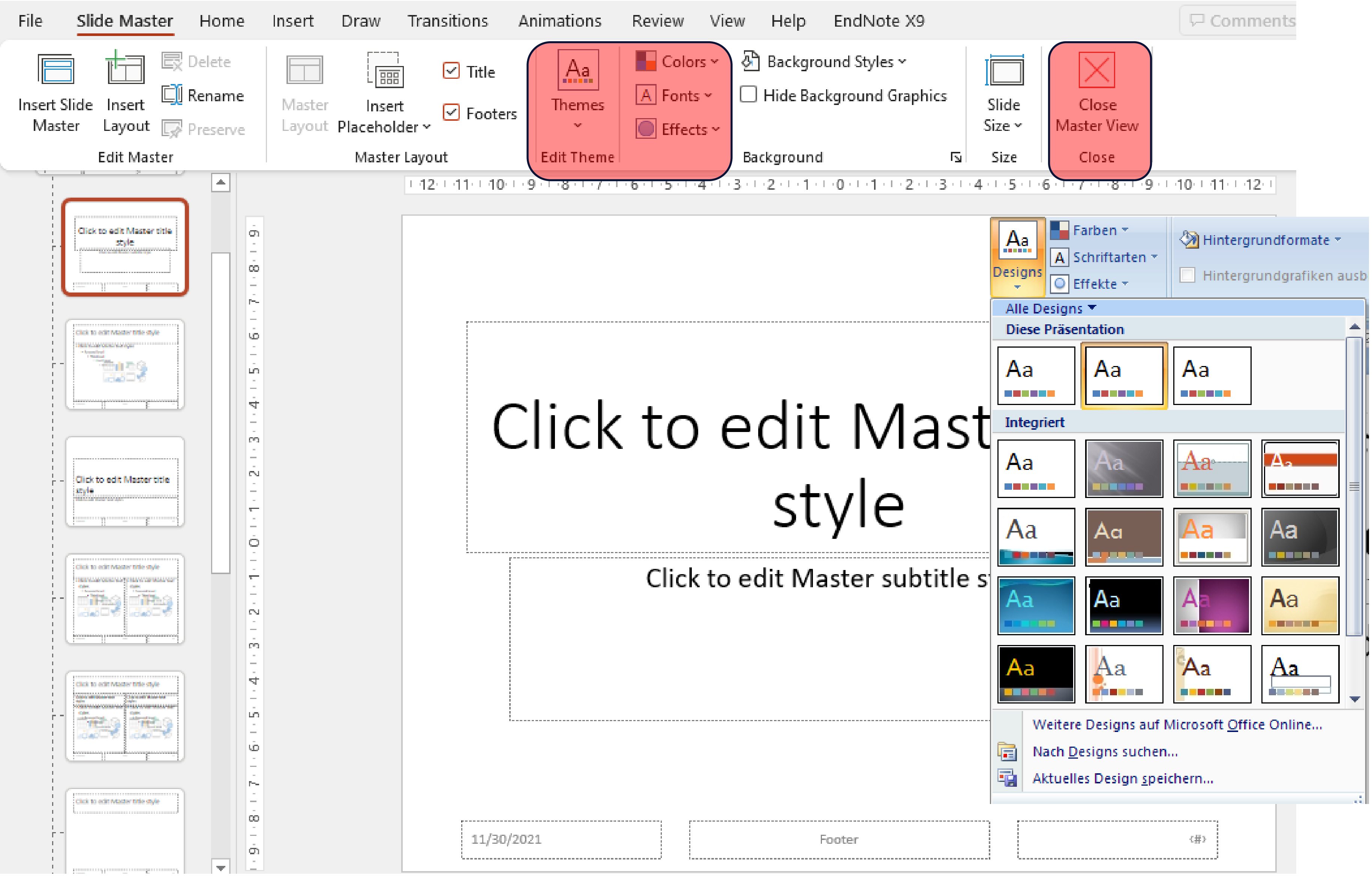
MS-Powerpoint

Master view: to change general settings

- Font type and size can be adjusted
- Footnotes or icons can be customized
- Background and Layout
- at the end the Master view has to be closed again

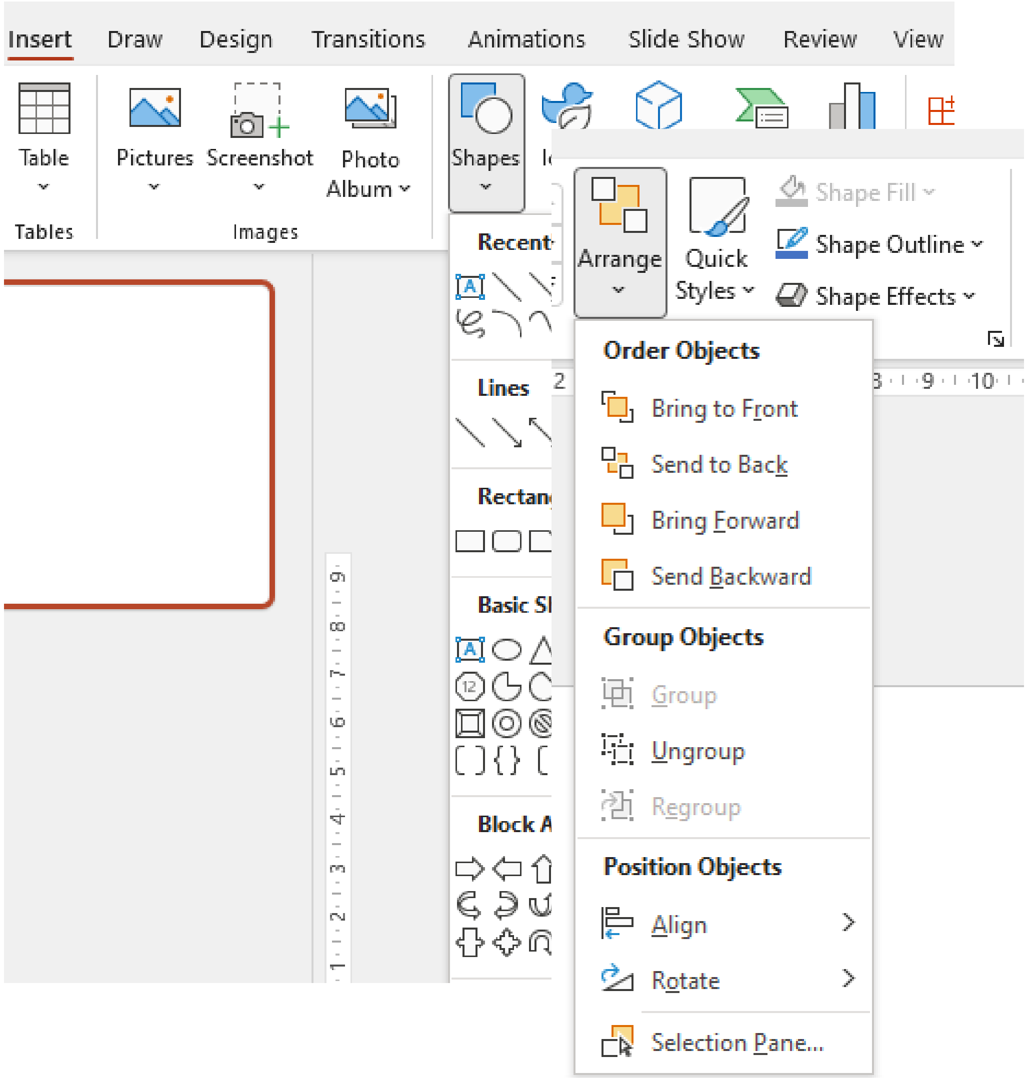


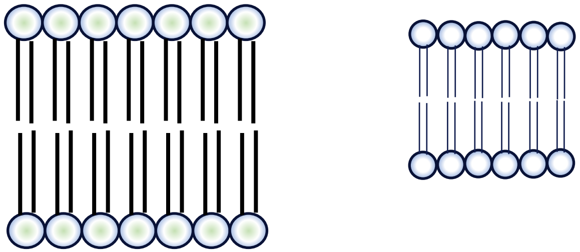
MS-Powerpoint



Some Powerpoint Hints

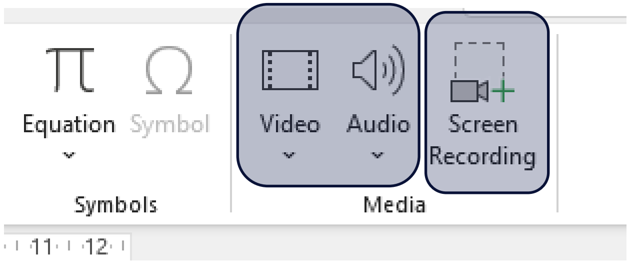
- Exact positioning of objects and exact drawing: when you press the „Alt“ Key, while you are dragging or drawing
- Pixel-wise shifting of objects: „Strg“ (Ctrl) + arrow keys
- Drawing: „Start“ tab > Drawing
- Arrange button (Anordnen): contains buttons for grouping of objects, flipping and mirroring of, positioning forward or backward….
- usefull short cuts: Ctrl-D: Duplicate Ctrl-C, Ctrl-V for copy/paste

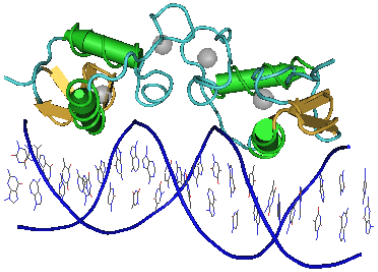




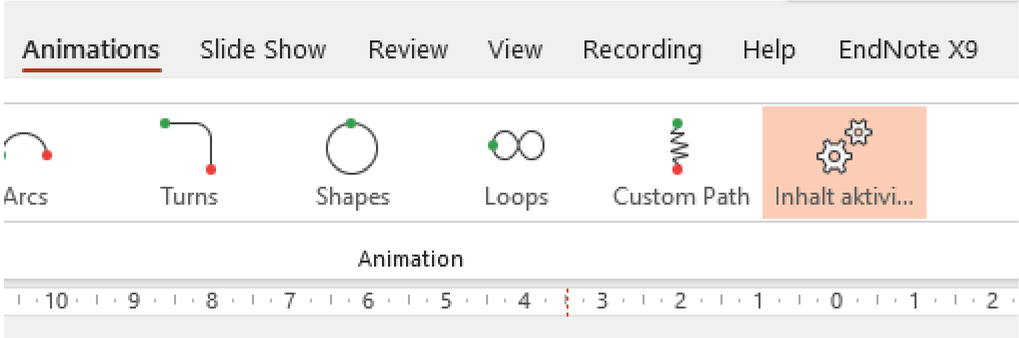
Some Powerpoint Hints

- insertion of more sophisticated objects: movies (*.avi-files, later versions: mp4-files); pictures, equations…
- Screen recording if you want to record part of a screen (e.g. a movie running on the 2nd screen – or recording your own presentation)
- objects that can be activated: select an object > add a user-defined animation (object action > activate content): You can use this to activate „foreign“ programs (e.g. crystal structure program, when you want to show a molecule at a presentation)





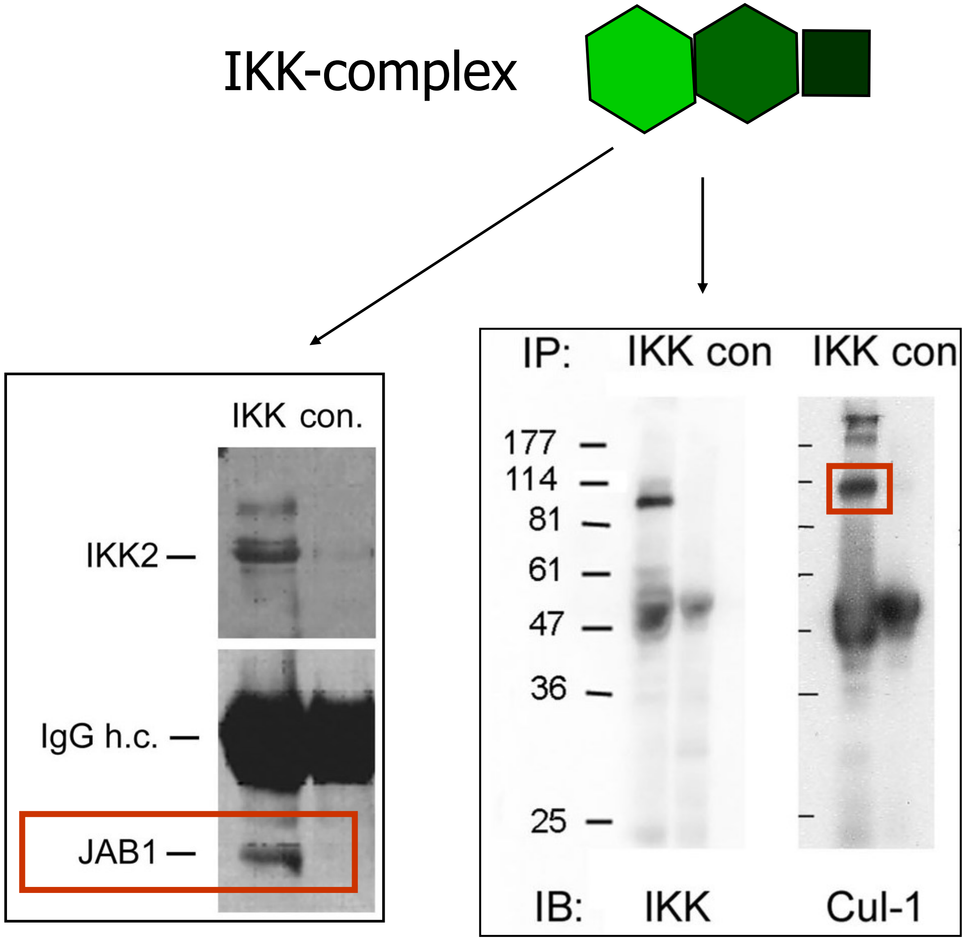
AR DNA-BD.cn3



Hints for using Animations

- You can use animated bulleted lists to guide the auditory through list text parts
- Use animations just when it is suited to improve the presentation (not just for fun, and not too much)
- you can use animations for instance to build up a complicated slide step by step
- you can use animations to emphasize important data
- You can use animations in drawings to illustrate „reactions“ or movements.

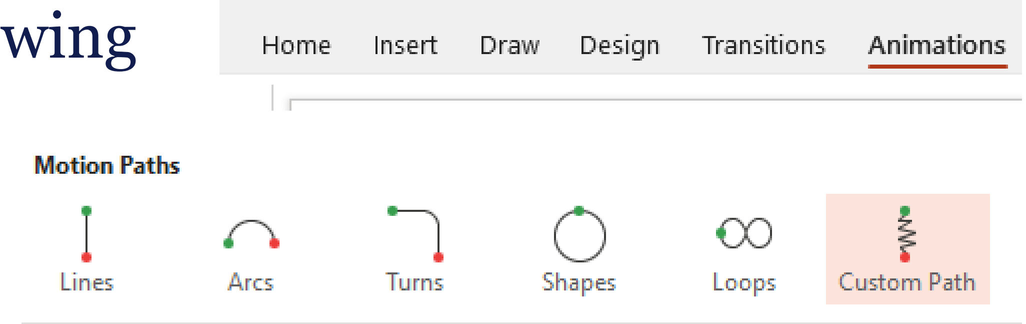
IKK-complex



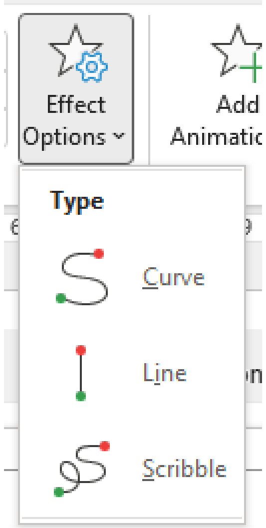
CSN complex

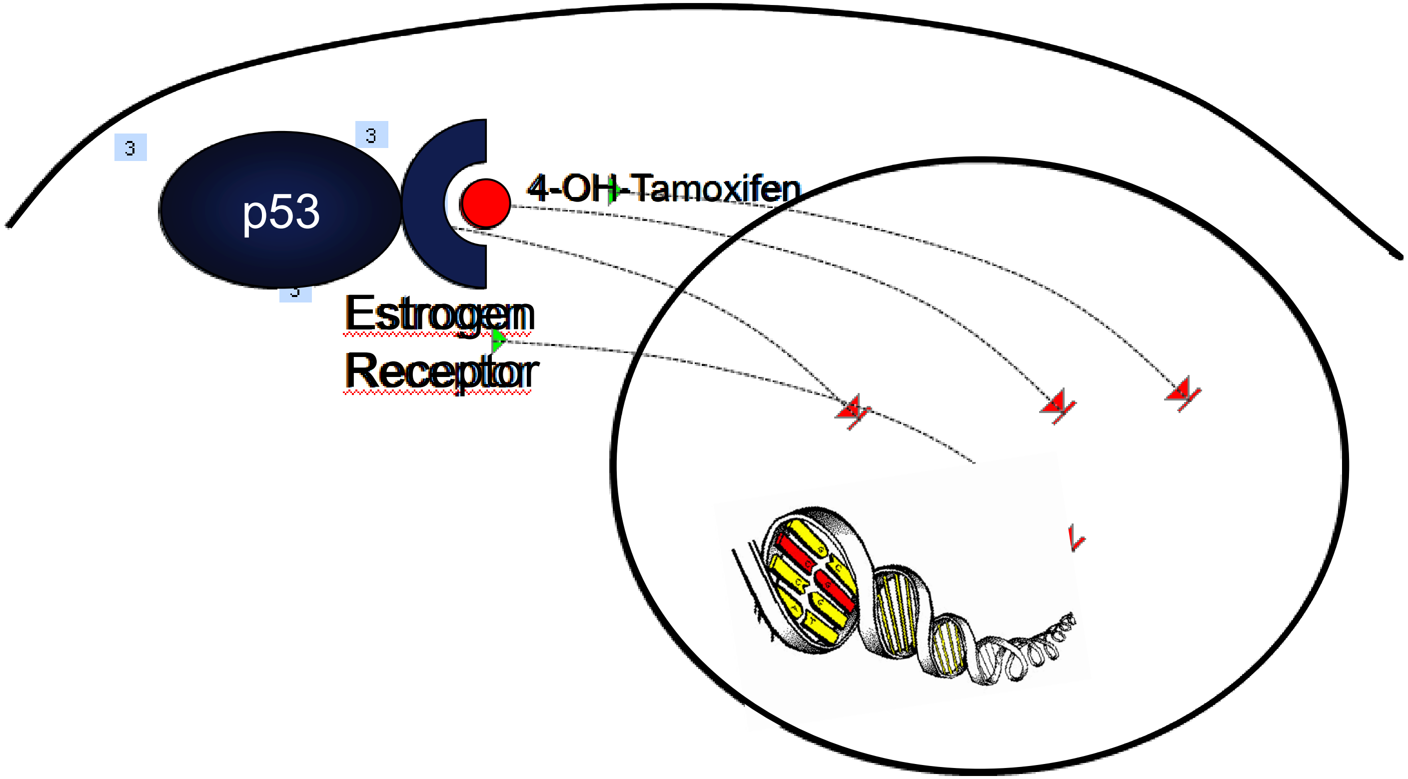
SCF complex

Example for an animated drawing



- select the objects
- add a user-defined animation path





Hints from the San Francisco Edit Company

http://www.sfedit.net

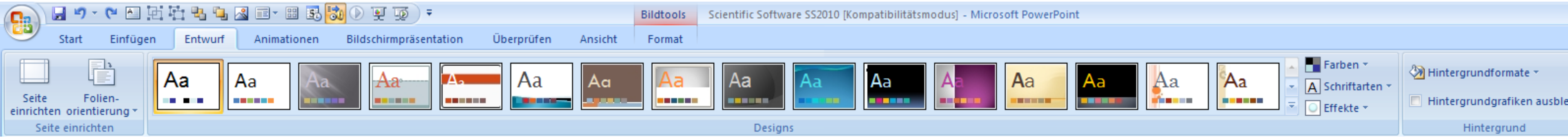
Many communication experts agree that there is a right and a wrong way to use presentation software like PowerPoint or Keynote. If used correctly, the software can greatly enhance your presentation. Here are some technical tips to assist you in developing an appropriate presentation.

1. Learn to use the software. Use the software's defaults for font size, margins, and placement.
2. Keep the layout and style as consistent as possible.
3. Choose colors with care. The text and background colors should contrast, dark letters on a light background for small rooms, light letters on a dark background for large rooms. The background should be a solid color, no fading, photos, etc. Avoid red-green combinations because a significant fraction of the human population is red-green colorblind.
4. Use animated features in moderation. Overuse of these effects, such as slide transitions and custom animations, can be distracting. Focus should be on the content.
5. Strive for simplicity and visibility. Eliminate any words, lines, and diagrams that do not add essential information to the slide.

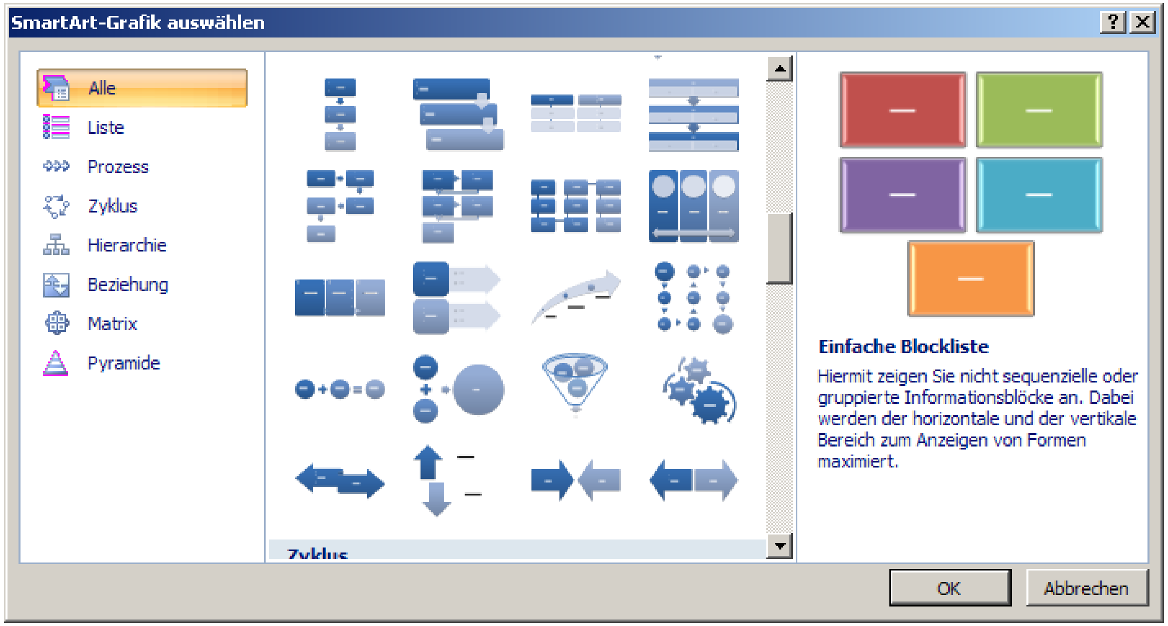
6. Display data using diagrams and figures instead of tables; they are easier for the audience to comprehend.
7. Keep tables simple. There should only be one table per slide. The font size for the data should not be smaller than 22 point. If you need to decrease the font size to have the table fit on the slide, eliminate some of the data or do not use the table.
8. Use fonts at least 36 point in size for titles, 28 point for main bullets, and 24 point for sub-bullets. If it can't be, read it's a waste.
9. Limit text blocks to no more than two lines each. Do not have large text blocks containing paragraphs; the audience will spend time reading the text and ignore what you are saying.
10. Use a heading on every slide.
11. Limit the number of items on each slide. Each slide should make just one or two points using 7-9 lines maximum.
12. Avoid using too many words in bold, italics, or capital letters.
13. Use the same font throughout to avoid distraction. Sans serif fonts (e.g., Arial) are easier to read and more attractive than fonts with serifs (e.g., Times New Roman).
14. Using "builds" in diagrams and text slides can be very useful. Text builds can be made even more effective if you darken previous text as new material is added.
15. Control the number of slides. Budget 2-3 minutes per slide (e.g. 30 minute talk = 10-15 slides).
16. Practice with feedback and then practice some more.

Some other features

… various design options



… SmartArts:

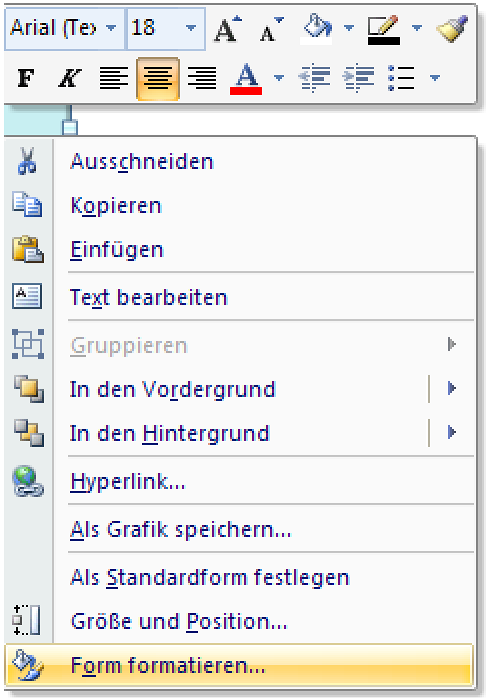


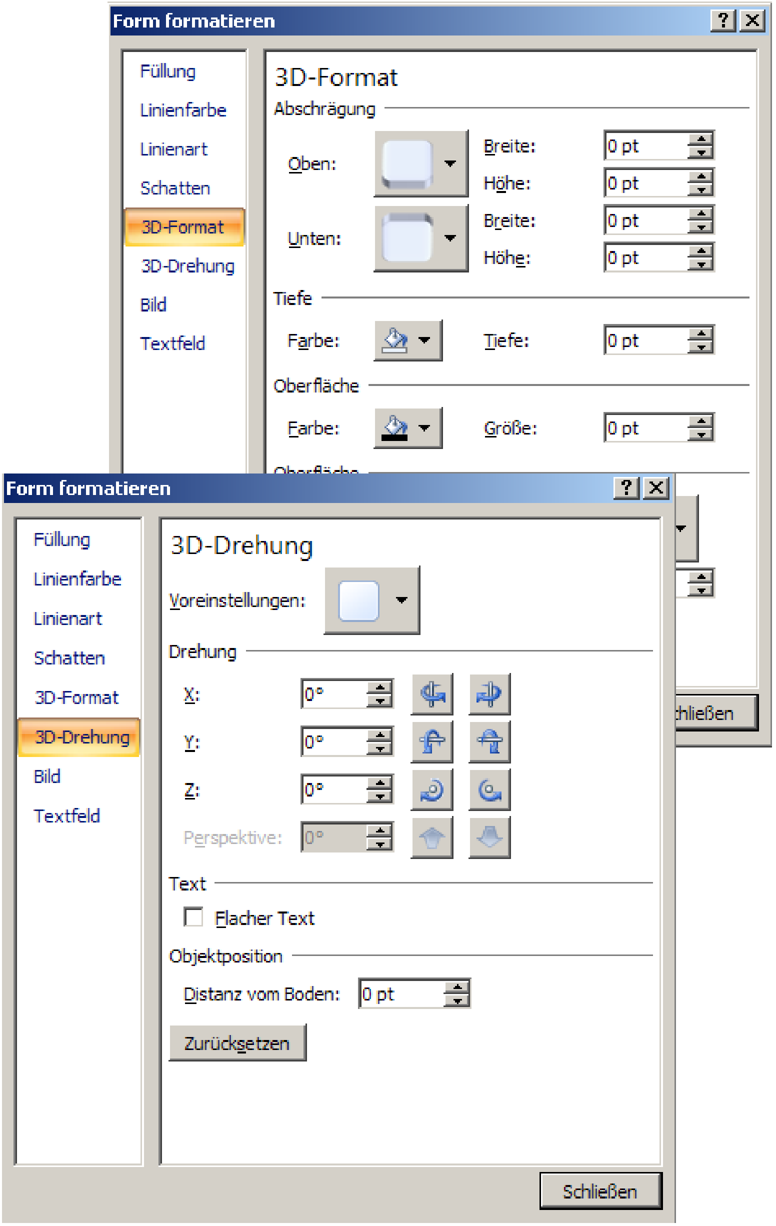
Einfache Blockliste

Hiermit zeigen Sie nicht sequenzielle oder gruppierte Informationsblöcke an. Dabei werden der horizontale und der vertikale Bereich zum Anzeigen von Formen maximiert.

3D Options

Right click on the form:





3D-Format

Abschrägung

Oben: Breite: 0 pt Höhe: 0 pt

Unten: Breite: 0 pt Höhe: 0 pt

Tiefe

Farbe: Tiefe: 0 pt

Oberfläche

Farbe: Größe: 0 pt

3D-Drehung

Voreinstellungen:

Drehung

X: 0°

Y: 0°

Z: 0°

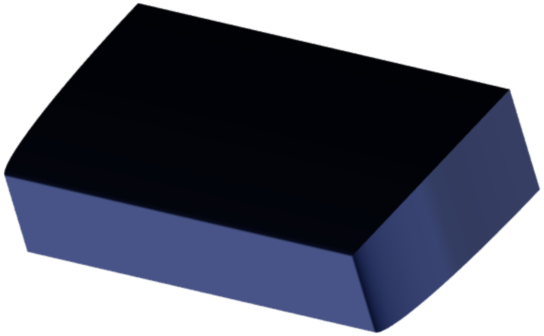
Perspektive: 0°

Text

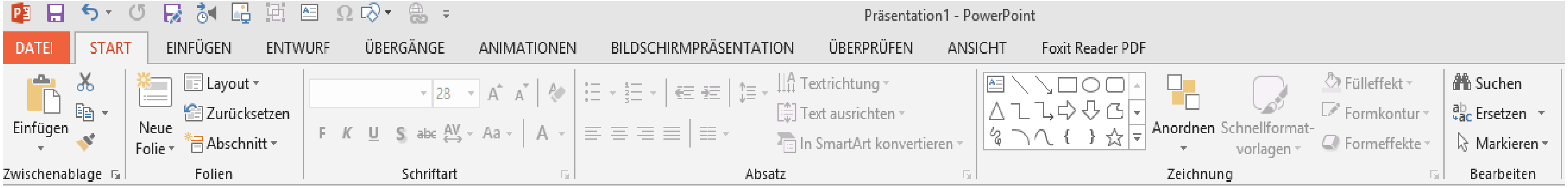
☐ Flacher Text

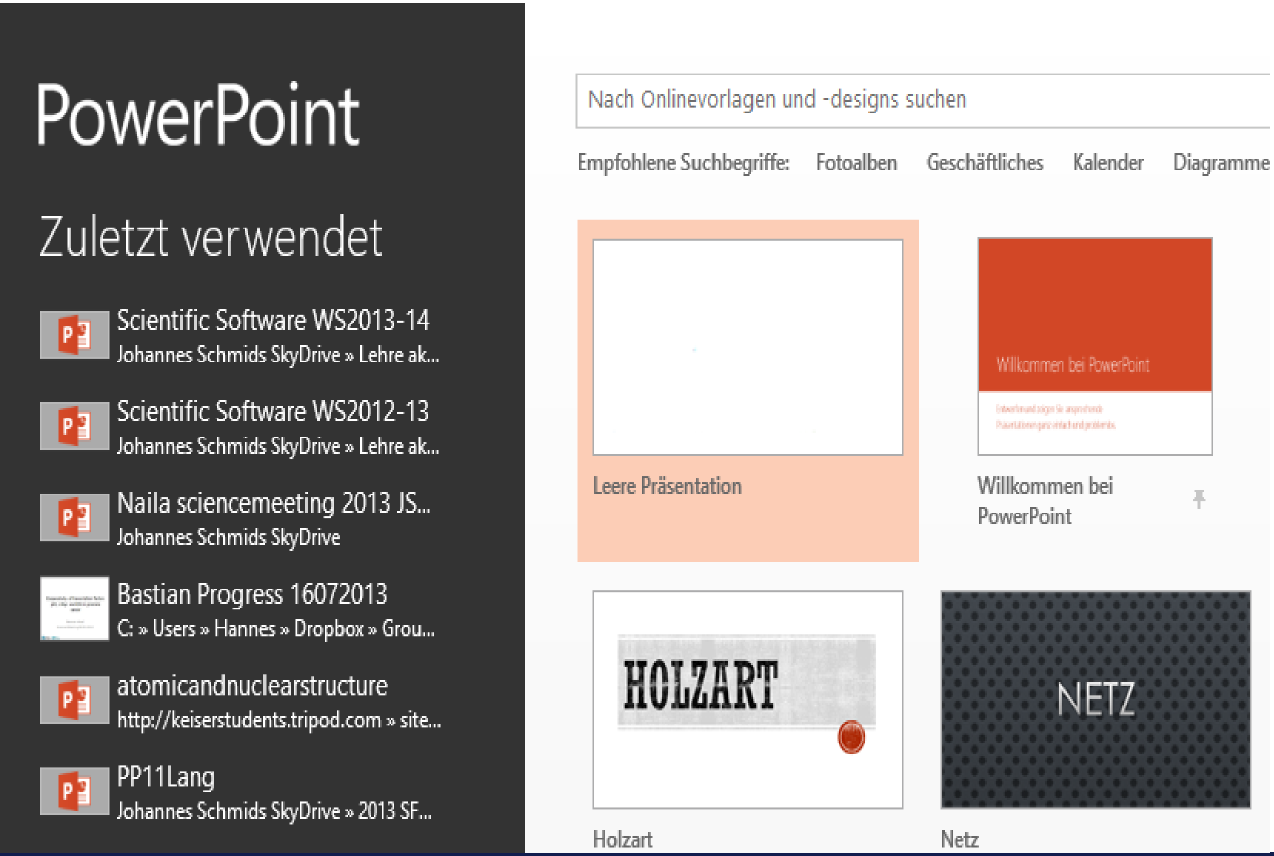
Objektposition

Distanz vom Boden: 0 pt



MS-Powerpoint 2013 and later…





Scientific Software WS2013-14
Johannes Schmids SkyDrive » Lehre ak...

Scientific Software WS2012-13
Johannes Schmids SkyDrive » Lehre ak...

Naila sciencemeeting 2013 JS...
Johannes Schmids SkyDrive

Bastian Progress 16072013
C: » Users » Hannes » Dropbox » Grou...

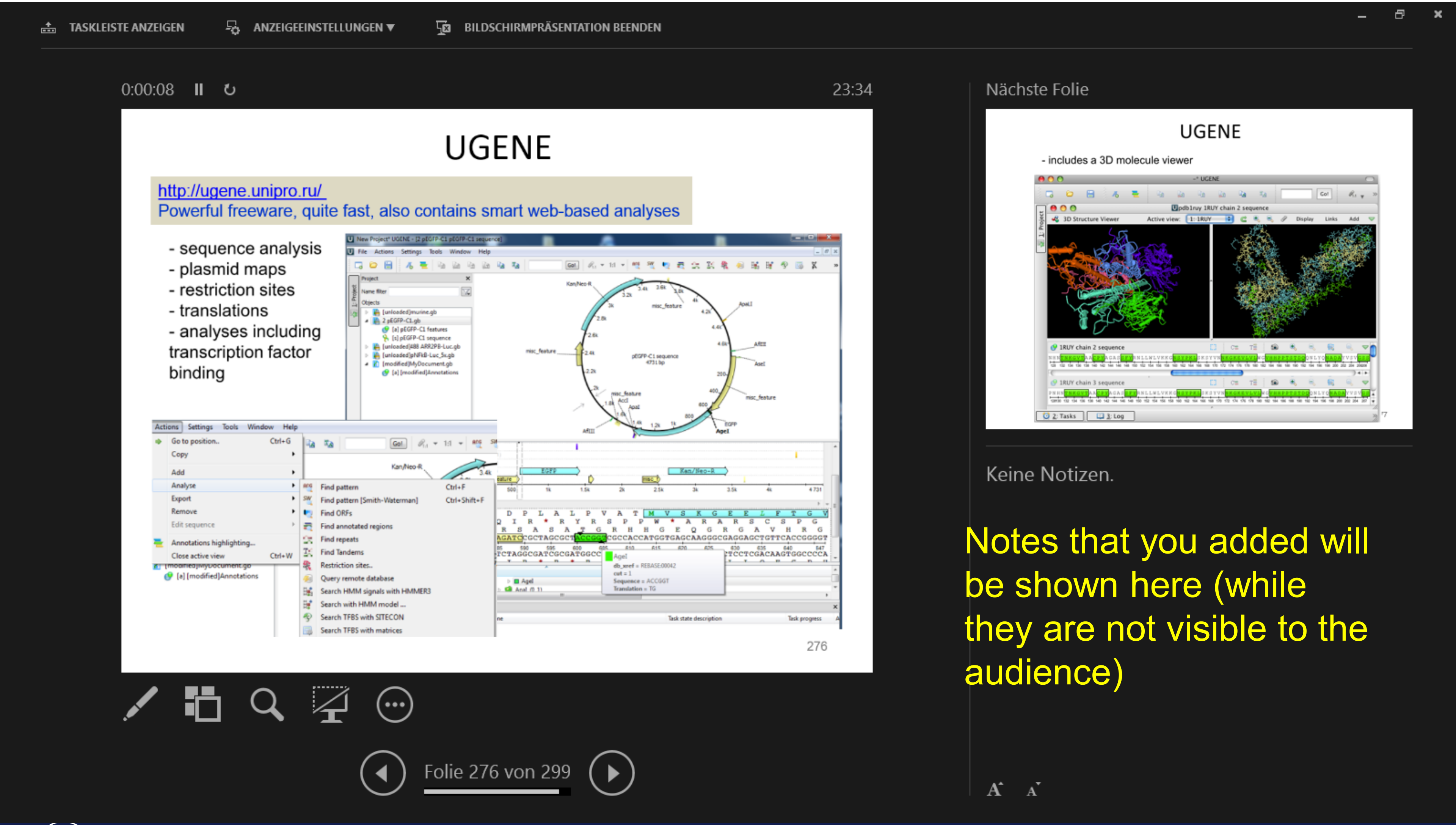
atomicandnuclearstructure
http://keiserstudents.tripod.com » site...

PP11Lang
Johannes Schmids SkyDrive » 2013 SF...

- Better speaker mode
- also suited for 16:9 screens
- Improved video- and audio features (also plays mp4- or flash-videos)
- new designs
- etc. etc.

Speaker Mode

The speaker sees the speaker mode screen, the audience only the presentation. Laser point can be activated, a zoom function can be used, etc.



UGENE

http://ugene.unipro.ru/
Powerful freeware, quite fast, also contains smart web-based analyses

- sequence analysis
- plasmid maps
- restriction sites
- translations
- analyses including transcription factor binding

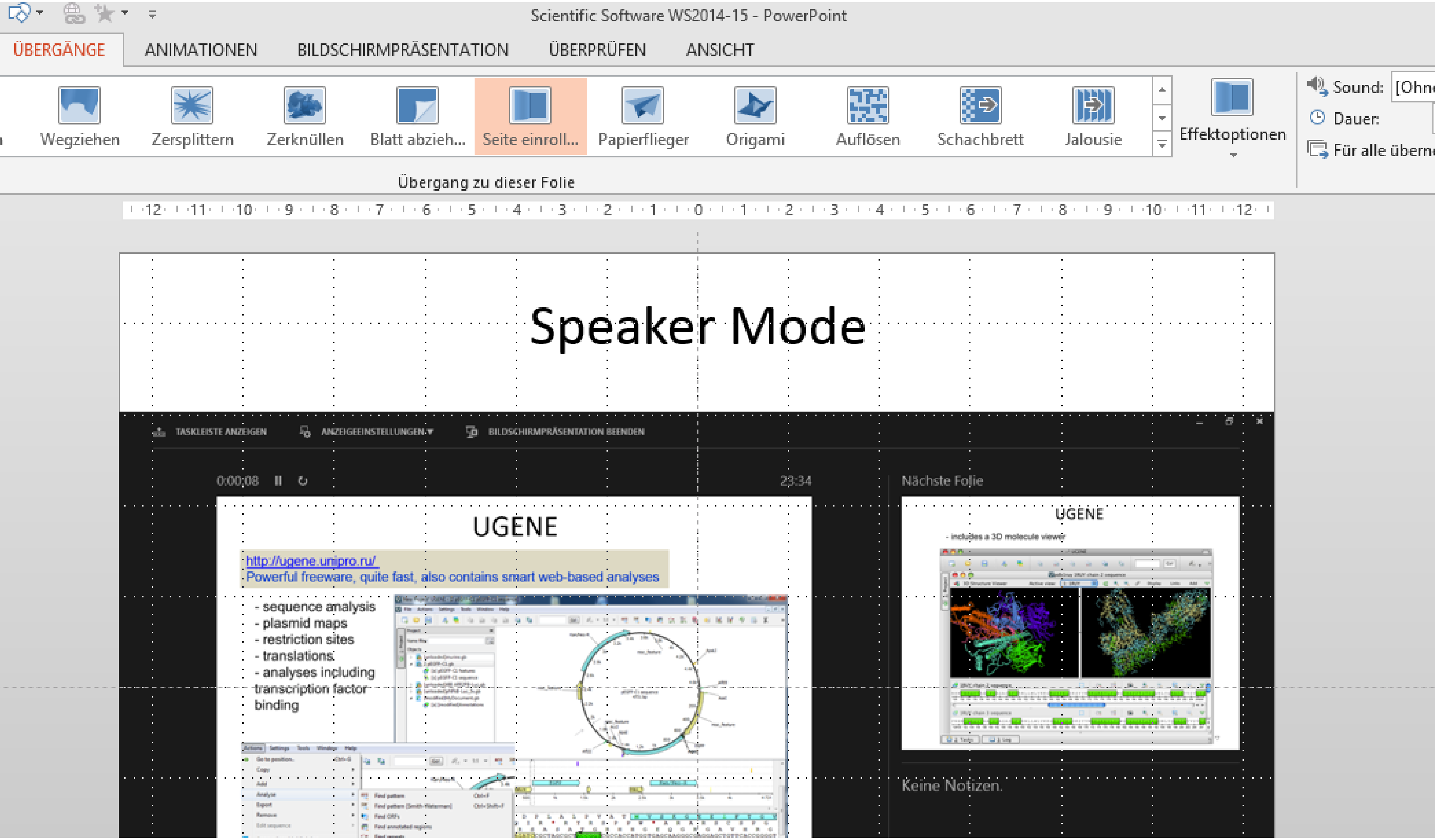
276

UGENE

- includes a 3D molecule viewer

Keine Notizen.

Notes that you added will be shown here (while they are not visible to the audience)



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- sequence analysis
- plasmid maps
- restriction sites
- translations
- analyses including transcription factor binding

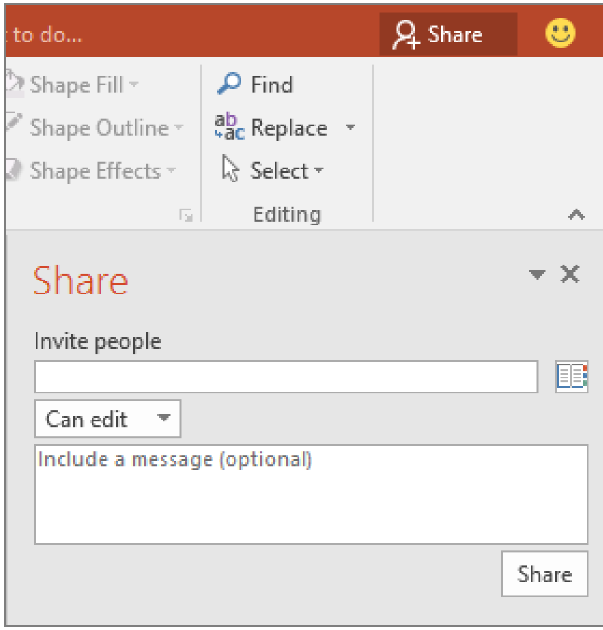
UGENE

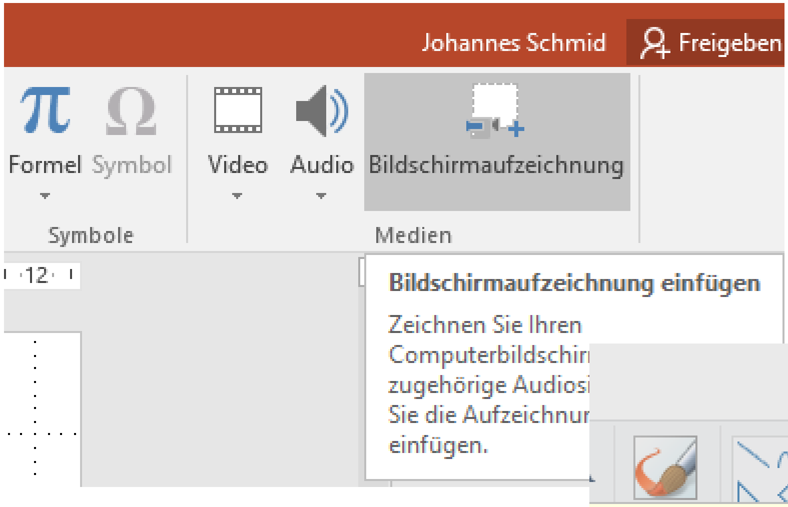
- includes a 3D molecule viewer

Keine Notizen.

Powerpoint 2016

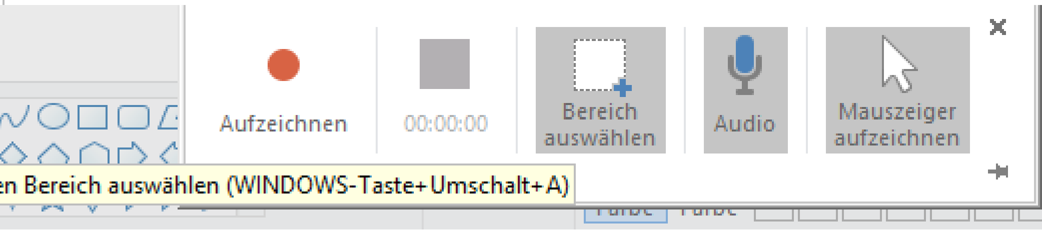
- Tell me… function (to access functions quickly)
- Smart Look-up (Wikipedia…)
- Ink Equations (Hand-written equations are converted to proper math)
- Sharing with others, including „conflict resolution“)
- Insert Screen recording function





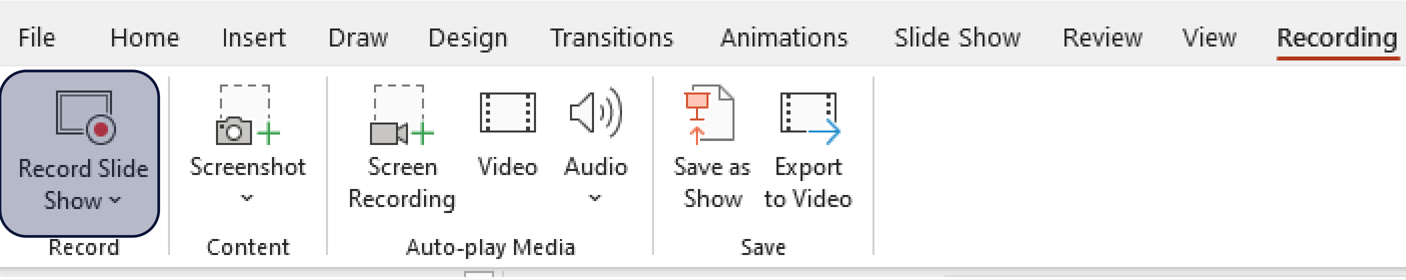
Bildschirmaufzeichnung einfügen

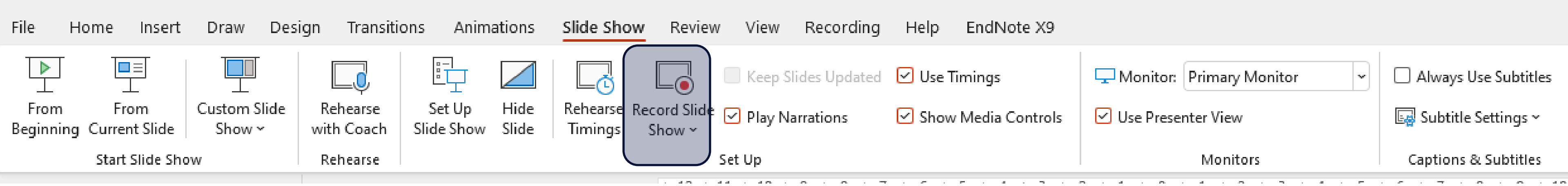
Zeichnen Sie Ihren Computerbildschir zugehörige Audiosi Sie die Aufzeichnur einfügen.



Benutzerdefinierten Bereich auswählen (WINDOWS-Taste+Umschalt+A)

New recording functions





☐ Keep Slides Updated
☑ Use Timings
☑ Play Narrations
☑ Show Media Controls
Monitor: Primary Monitor
☑ Use Presenter View
☐ Always Use Subtitles

If you want to record your presentation (e.g. for online talks)
Settings: +/- microphone and camera (to record the video of the speaker)

Microphone
Mikrofon (2- USB Audio Device)
Camera
USB Camera

✓ USB Camera

PROPEDEUTICS Seminar

Scientific Software and Databases

Johannes A. Schmid

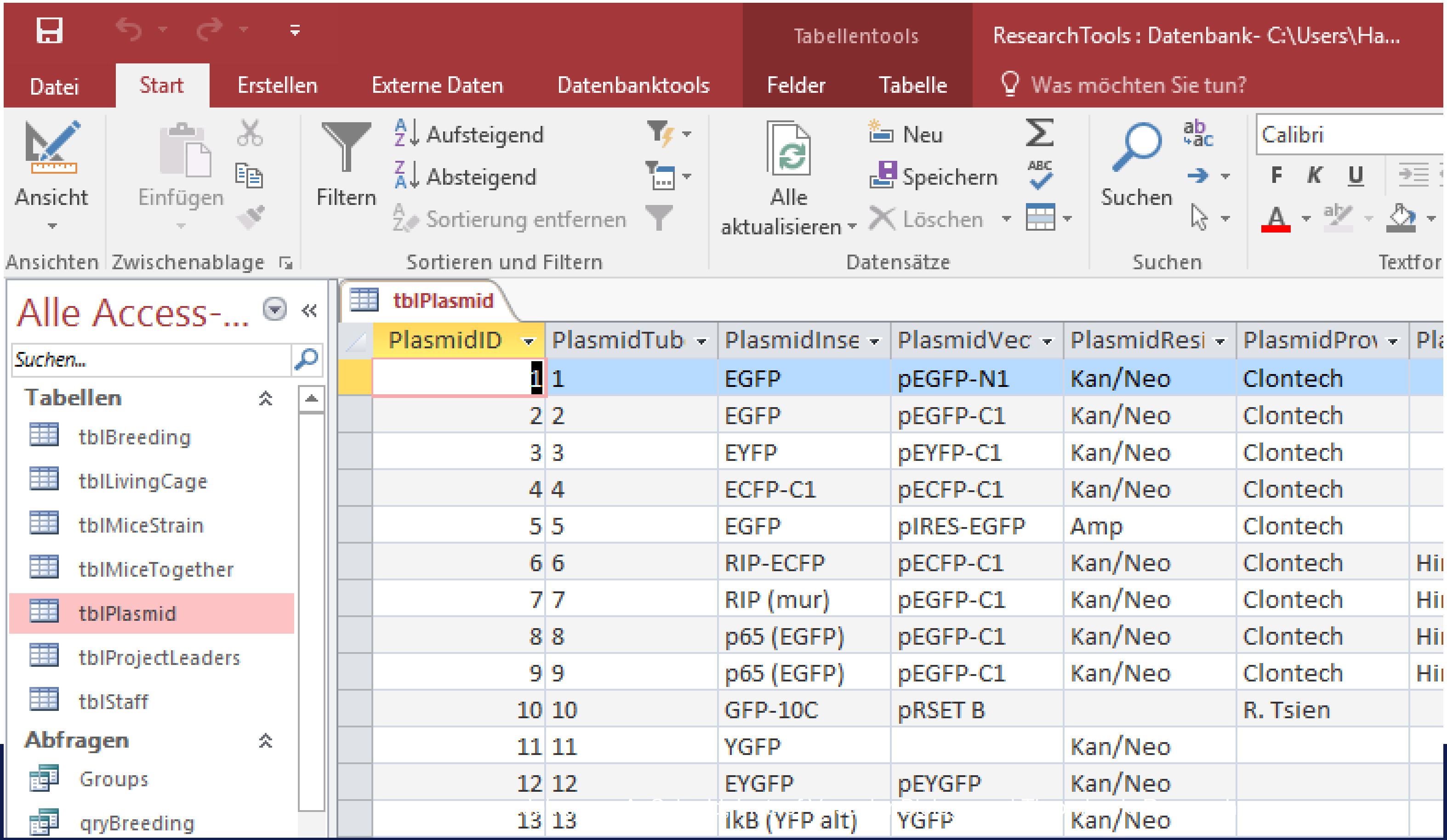
MEDICAL UNIVERSITY OF VIENNA

Johannes A. Schmid, Inst. of Vascular Biology and Thrombosis

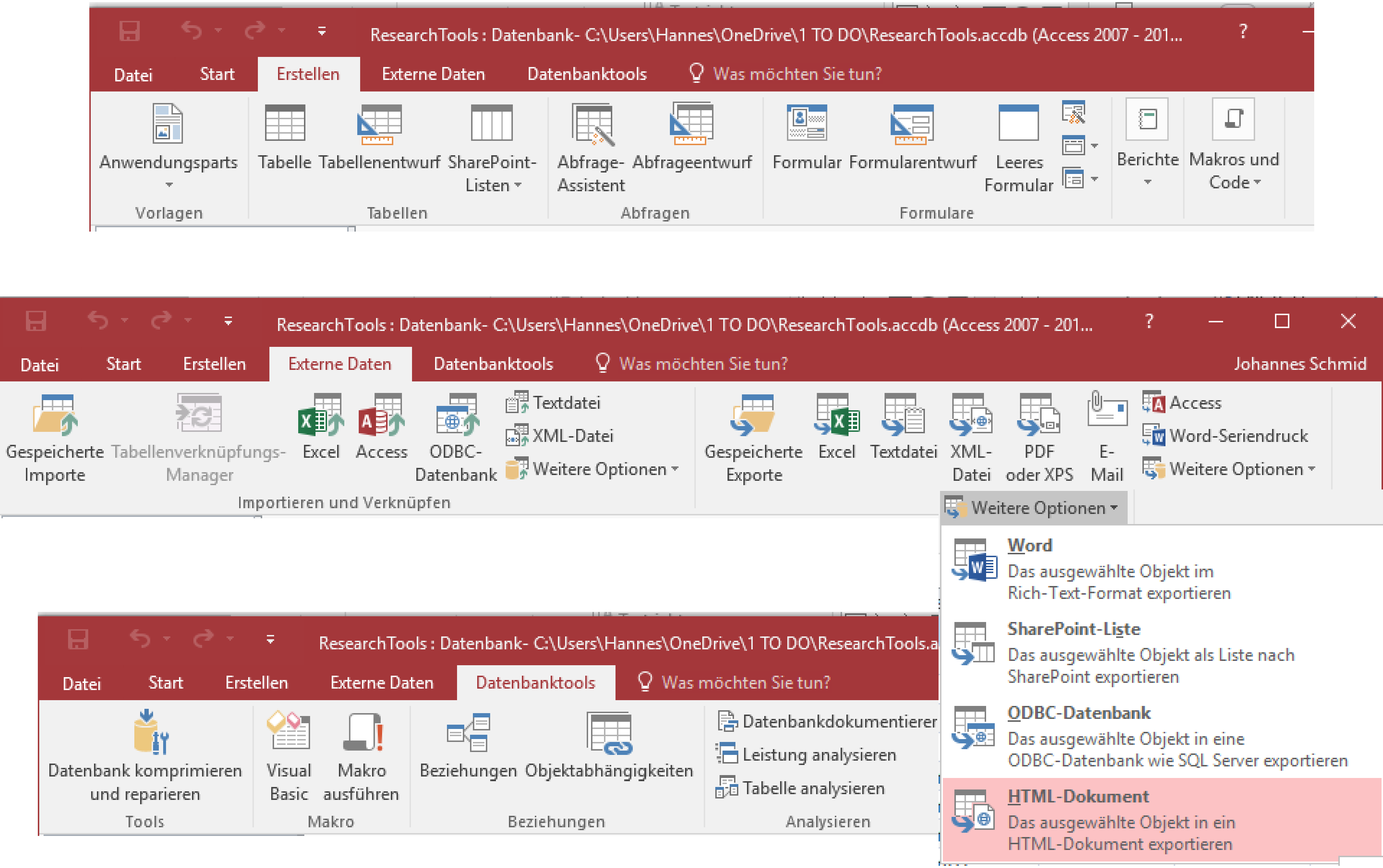
00:00,00

Microsoft Access 2016

- Relational database management system
- You can generate tables, queries, forms, reports …
  to access data in a professional manner – so that the relations between data features are maintained



PlasmidID	PlasmidTub	PlasmidInse	PlasmidVec	PlasmidResi	PlasmidPro	Pla
1	1	EGFP	pEGFP-N1	Kan/Neo	Clontech	
2	2	EGFP	pEGFP-C1	Kan/Neo	Clontech	
3	3	EYFP	pEYFP-C1	Kan/Neo	Clontech	
4	4	ECFP-C1	pECFP-C1	Kan/Neo	Clontech	
5	5	EGFP	pIRES-EGFP	Amp	Clontech	
6	6	RIP-ECFP	pECFP-C1	Kan/Neo	Clontech	Hi
7	7	RIP (mur)	pEGFP-C1	Kan/Neo	Clontech	Hi
8	8	p65 (EGFP)	pEGFP-C1	Kan/Neo	Clontech	Hi
9	9	p65 (EGFP)	pEGFP-C1	Kan/Neo	Clontech	Hi
10	10	GFP-10C	pRSET B		R. Tsien	
11	11	YGFP		Kan/Neo		
12	12	EYGFP	pEYGFP	Kan/Neo		
13	13	IkB (YFP alt)	YGFP	Kan/Neo		

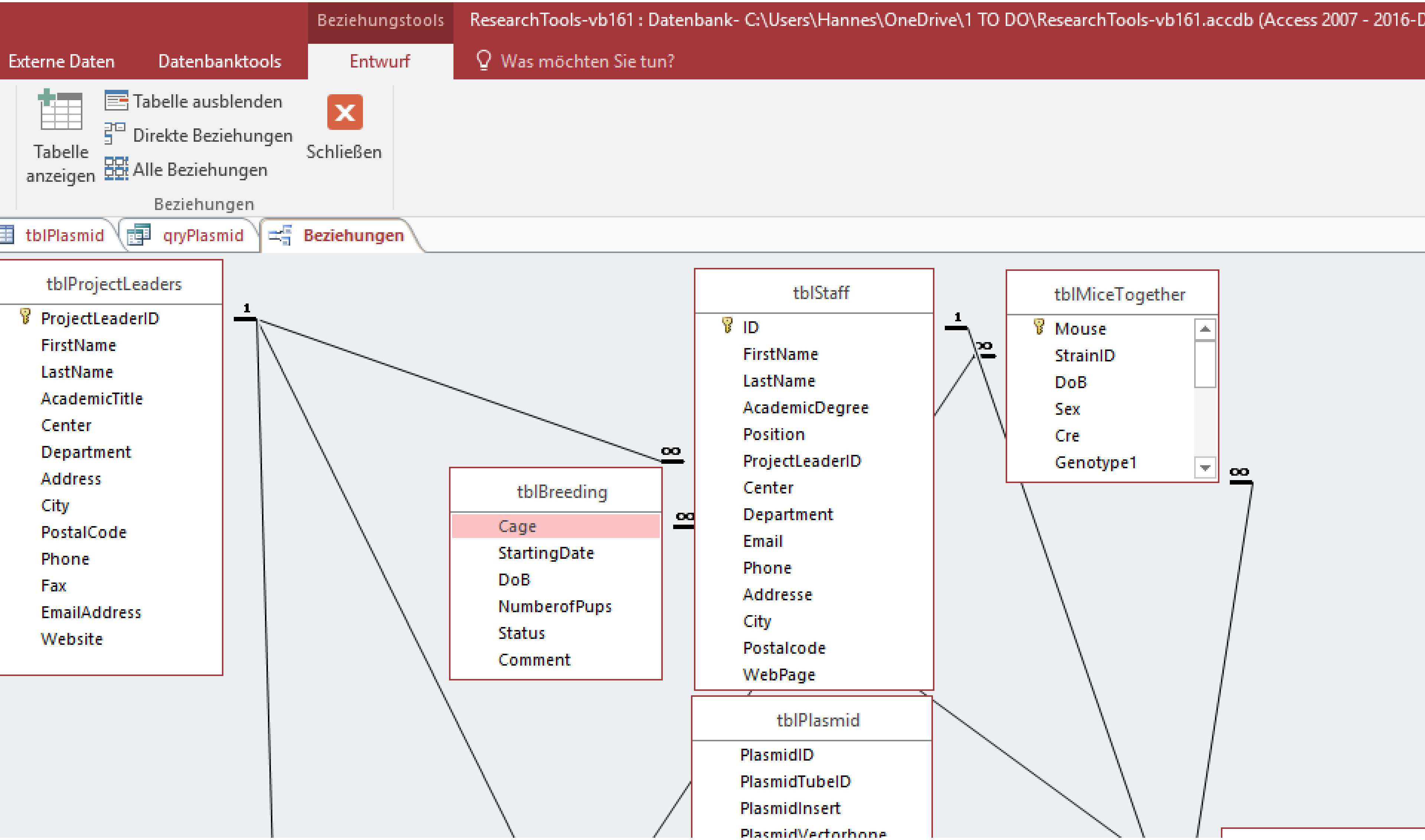


Word
Das ausgewählte Objekt im Rich-Text-Format exportieren

SharePoint-Liste
Das ausgewählte Objekt als Liste nach SharePoint exportieren

ODBC-Datenbank
Das ausgewählte Objekt in eine ODBC-Datenbank wie SQL Server exportieren

HTML-Dokument
Das ausgewählte Objekt in ein HTML-Dokument exportieren



ResearchTools-vb161 : Datenbank- C:\Users\Hannes\OneDrive\1 TO DO\ResearchTools-vb161.accdb (Access 2007 - 2016-D

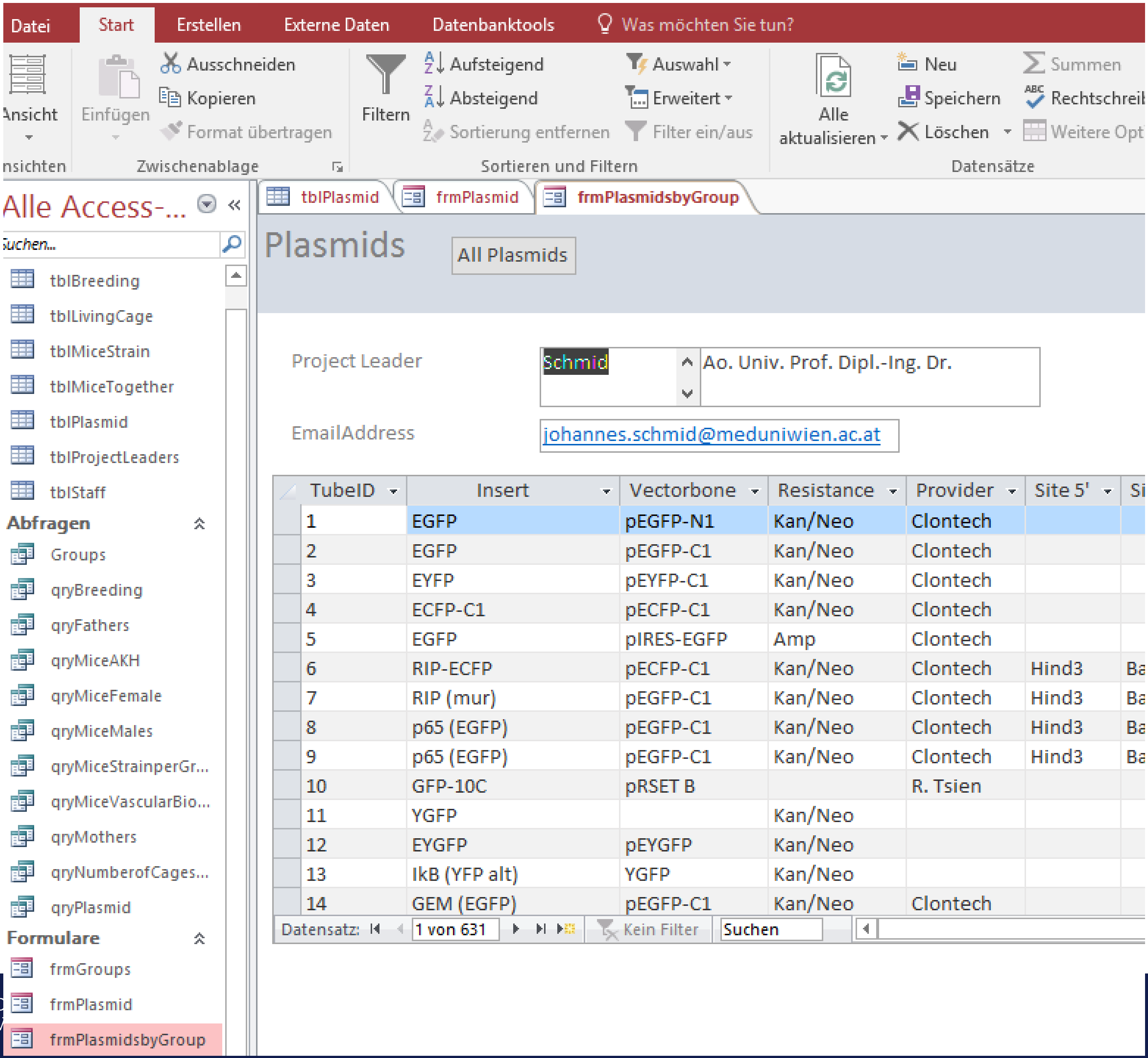
tblProjectLeaders
ProjectLeaderID
FirstName
LastName
AcademicTitle
Center
Department
Address
City
PostalCode
Phone
Fax
EmailAddress
Website

tblBreeding
Cage
StartingDate
DoB
NumberofPups
Status
Comment

tblStaff
ID
FirstName
LastName
AcademicDegree
Position
ProjectLeaderID
Center
Department
Email
Phone
Addresse
City
Postalcode
WebPage

tblMiceTogether
Mouse
StrainID
DoB
Sex
Cre
Genotype1

tblPlasmid
PlasmidID
PlasmidTubeID
PlasmidInsert
PlasmidVectorbone



Plasmids

Project Leader: Schmid | Ao. Univ. Prof. Dipl.-Ing. Dr.

EmailAddress: johannes.schmid@meduniwien.ac.at

TubeID	Insert	Vectorbone	Resistance	Provider	Site 5'	Si
1	EGFP	pEGFP-N1	Kan/Neo	Clontech		
2	EGFP	pEGFP-C1	Kan/Neo	Clontech		
3	EYFP	pEYFP-C1	Kan/Neo	Clontech		
4	ECFP-C1	pECFP-C1	Kan/Neo	Clontech		
5	EGFP	pIRES-EGFP	Amp	Clontech		
6	RIP-ECFP	pECFP-C1	Kan/Neo	Clontech	Hind3	Ba
7	RIP (mur)	pEGFP-C1	Kan/Neo	Clontech	Hind3	Ba
8	p65 (EGFP)	pEGFP-C1	Kan/Neo	Clontech	Hind3	Ba
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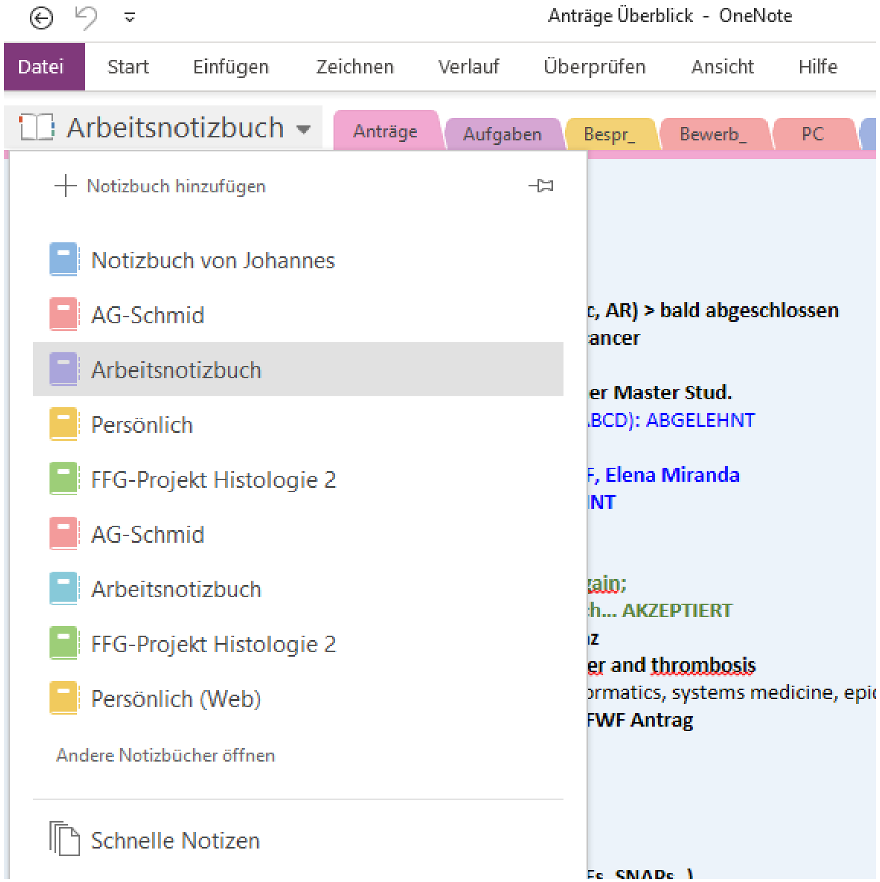
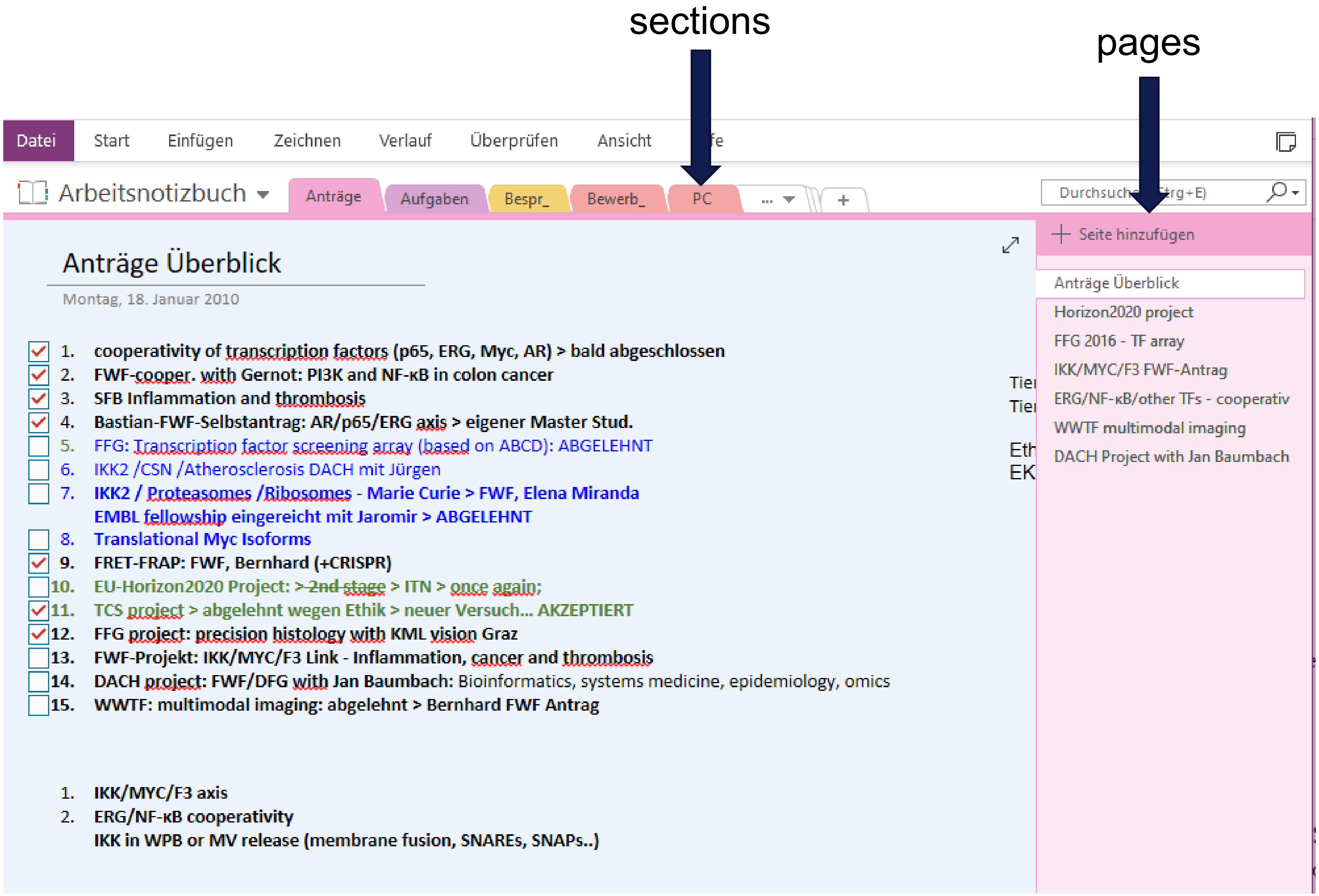
10	GFP-10C	pRSET B		R. Tsien		
11	YGFP		Kan/Neo			
12	EYGFP	pEYGFP	Kan/Neo			
13	IkB (YFP alt)	YGFP	Kan/Neo			
14	GEM (EGFP)	pEGFP-C1	Kan/Neo	Clontech		

Microsoft Onenote

- Notebook platform
- works best with a Microsoft account (Hotmail or Outlook)
- There is a desktop version, a free Windows10-version, an online version – and also versions for Android and iPad
- You can have several notebooks
- you can create sections and pages



Microsoft Onenote



Anträge Überblick

Montag, 18. Januar 2010

☑ 1. cooperativity of transcription factors (p65, ERG, Myc, AR) > bald abgeschlossen
☑ 2. FWF-cooper. with Gernot: PI3K and NF-κB in colon cancer
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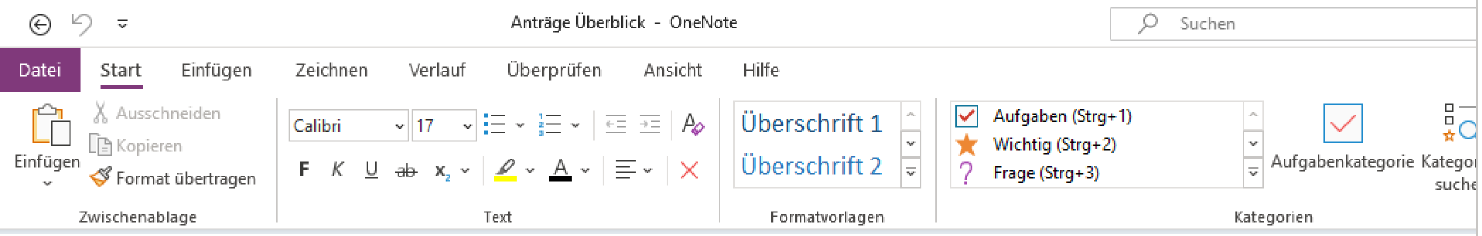
☐ 15. WWTF: multimodal imaging: abgelehnt > Bernhard FWF Antrag

1. IKK/MYC/F3 axis
2. ERG/NF-κB cooperativity
IKK in WPB or MV release (membrane fusion, SNAREs, SNAPs..)

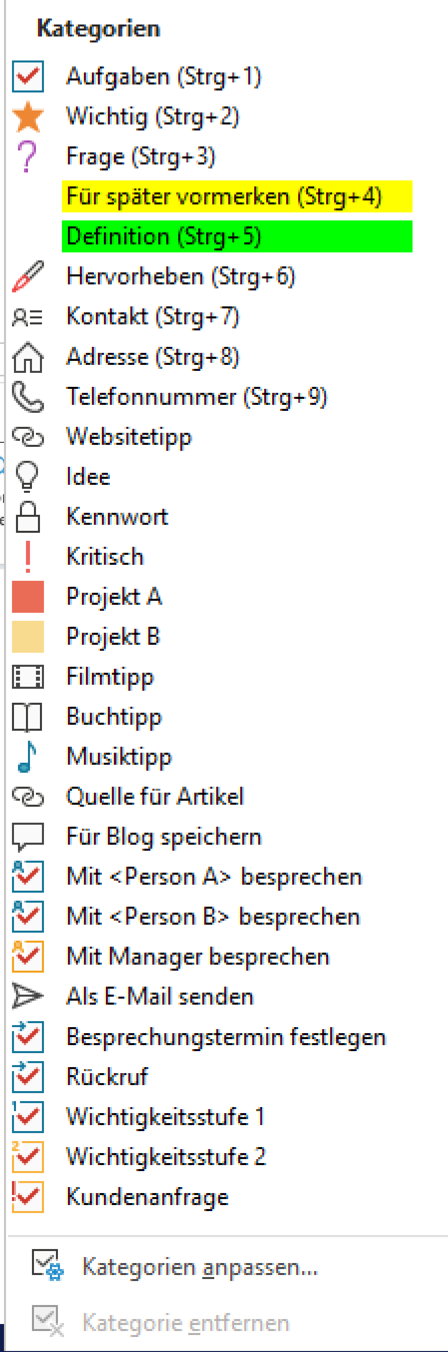
Microsoft Onenote

search function (searches in all notebooks)

rich formatting options similar to Word:



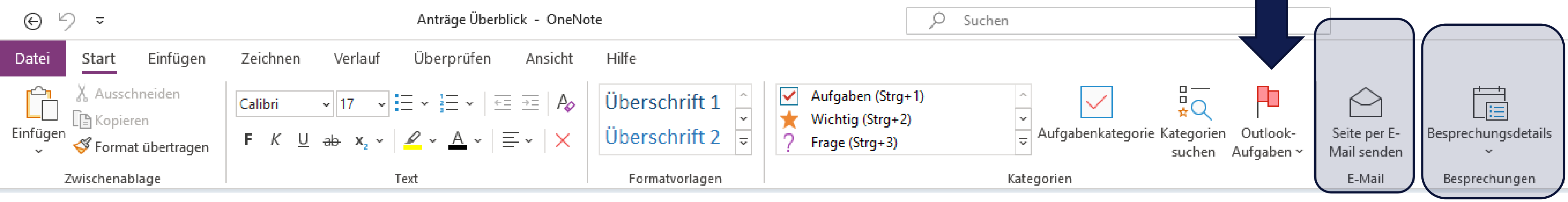
specific categories and task options

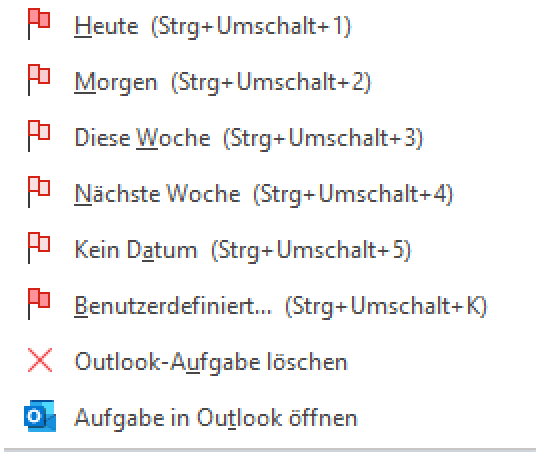


Microsoft Onenote

you can send a section as task to Outlook

rich formatting options similar to Word:

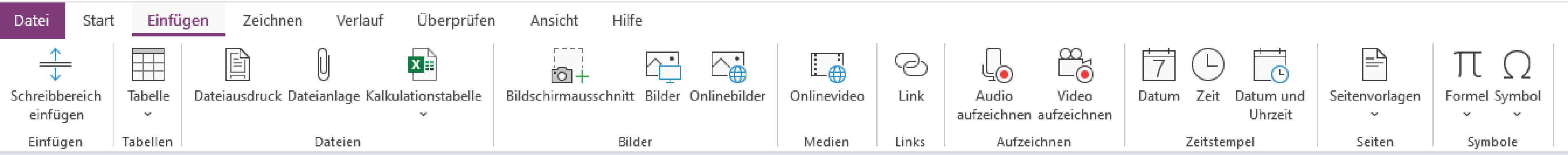




you can send the page via mail

You can add a calendar event to the page

Microsoft Onenote

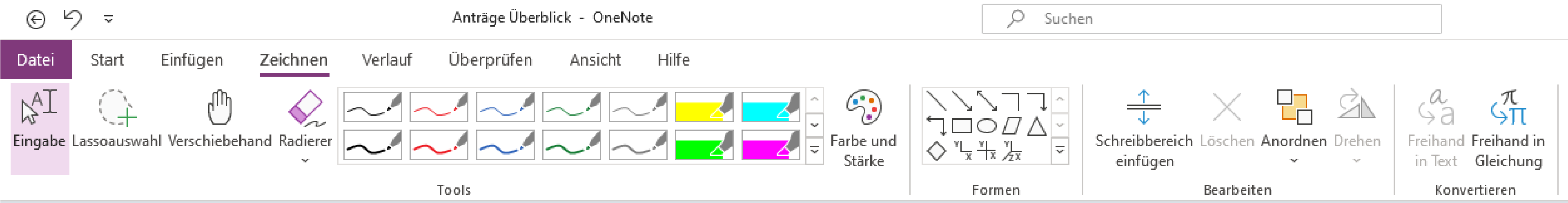


You can insert many elements:

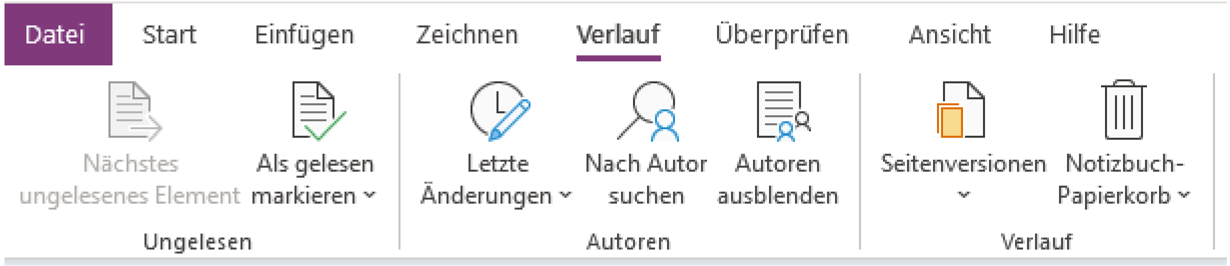
- attachments
- Excel spreadsheets
- images or screenshots
- videos
- Hyperlinks to websites
- you can record audio or video
- you can insert time stamps
- equations
- symbols

Microsoft Onenote

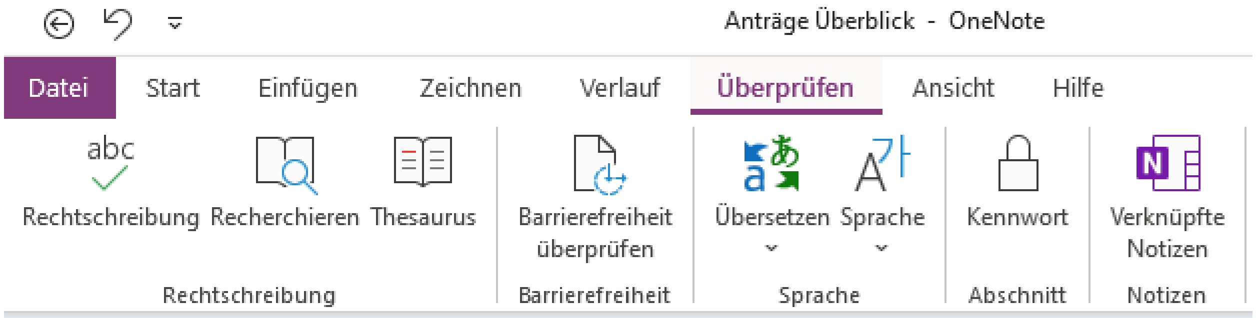
Many drawing features
(particularly useful with graphics tablets)



version history of changes

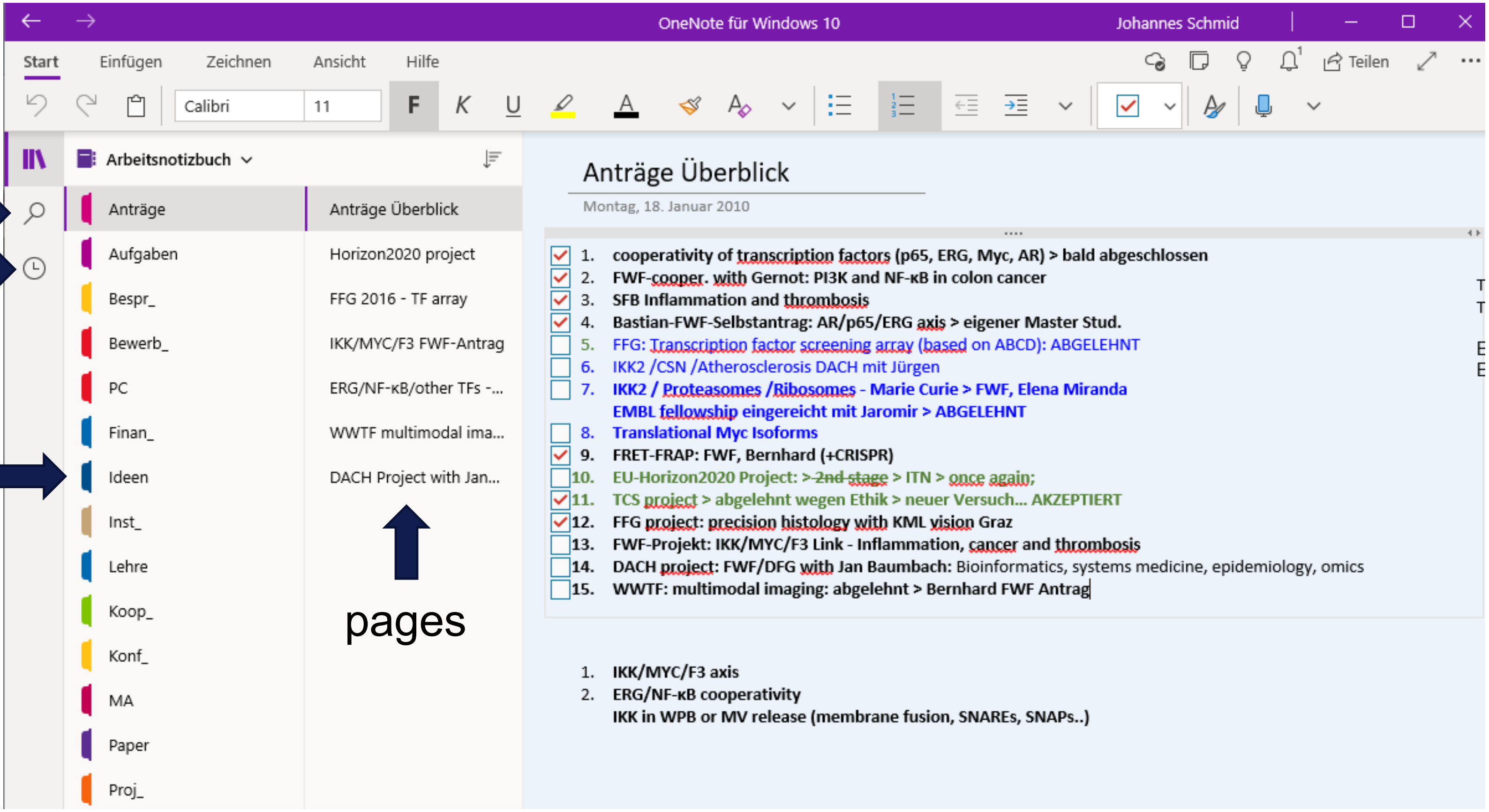


reviewing: spell check, search, thesaurus, translation…



Microsoft Onenote for Windows 10

Has the same basic features (but less), slightly different appearance



notebooks

search

history

sections

pages

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2. ERG/NF-κB cooperativity
IKK in WPB or MV release (membrane fusion, SNAREs, SNAPs..)

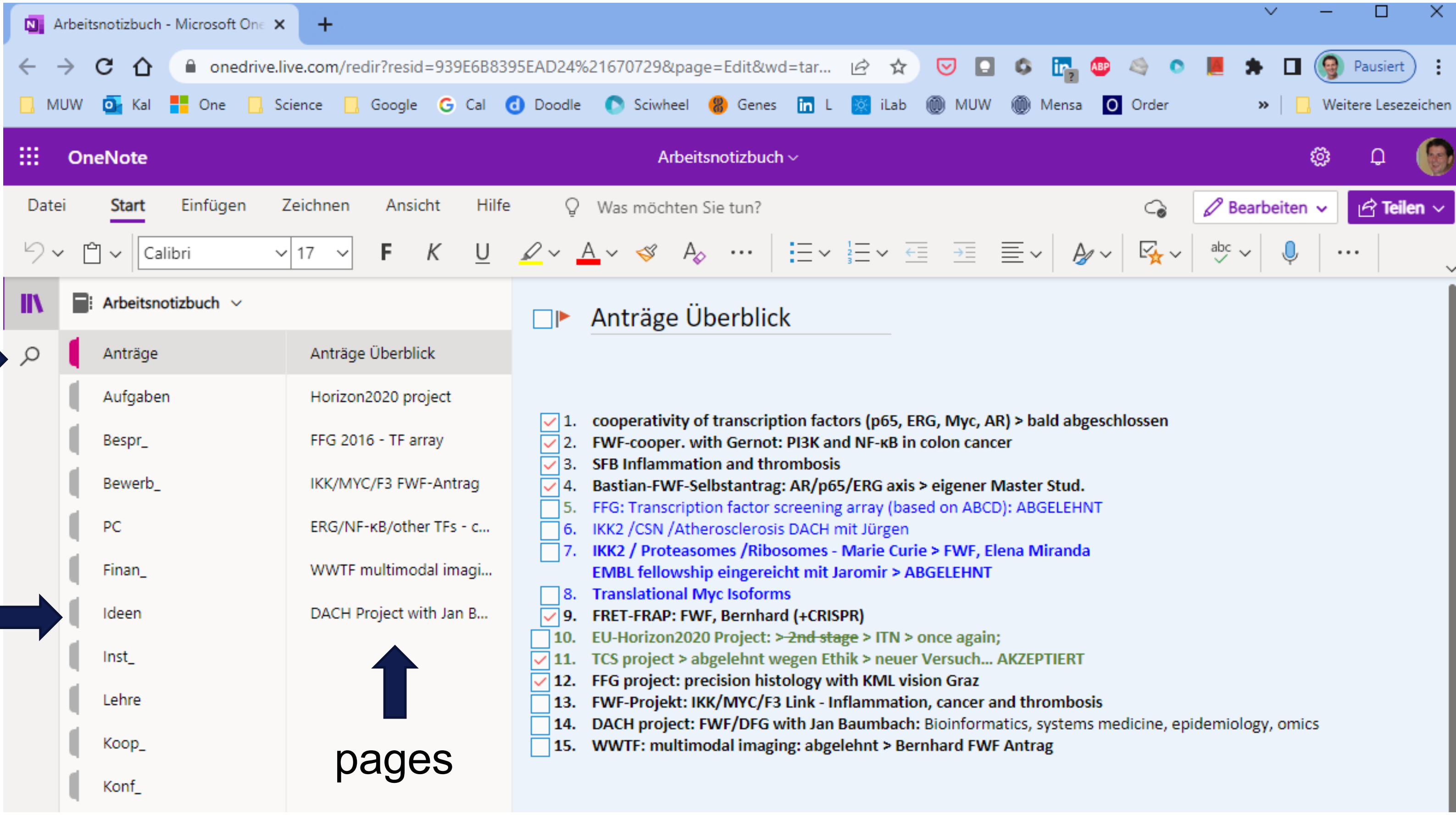
Microsoft Onenote Browser-Version

notebooks

search

sections

pages



Antrāge
Aufgaben
Bespr_
Bewerb_
PC
Finan_
Ideen
Inst_
Lehre
Koop_
Konf_

Anträge Überblick
Horizon2020 project
FFG 2016 - TF array
IKK/MYC/F3 FWF-Antrag
ERG/NF-κB/other TFs - c...
WWTF multimodal imagi...
DACH Project with Jan B...

Anträge Überblick

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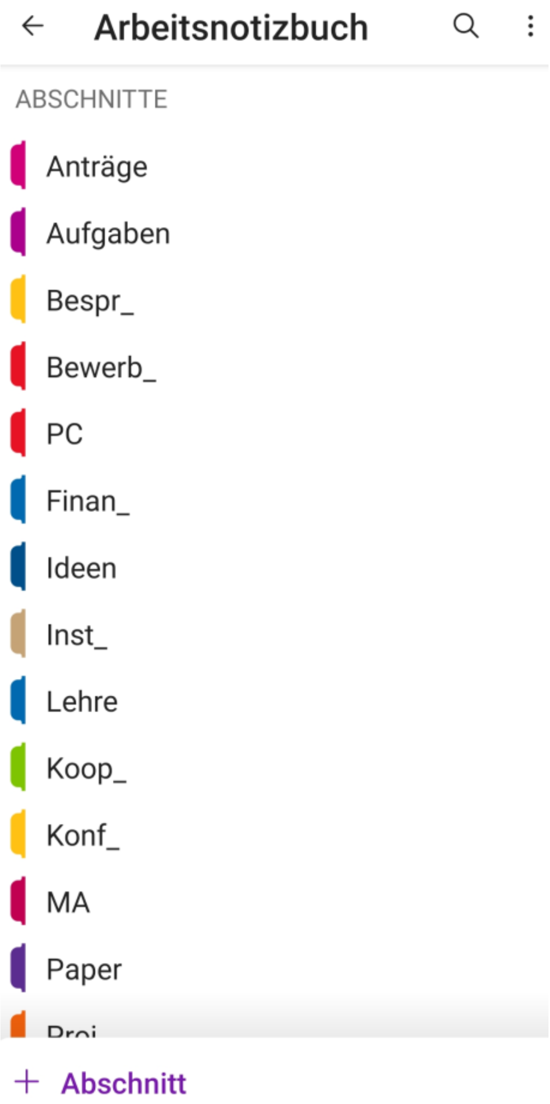
Microsoft Onenote

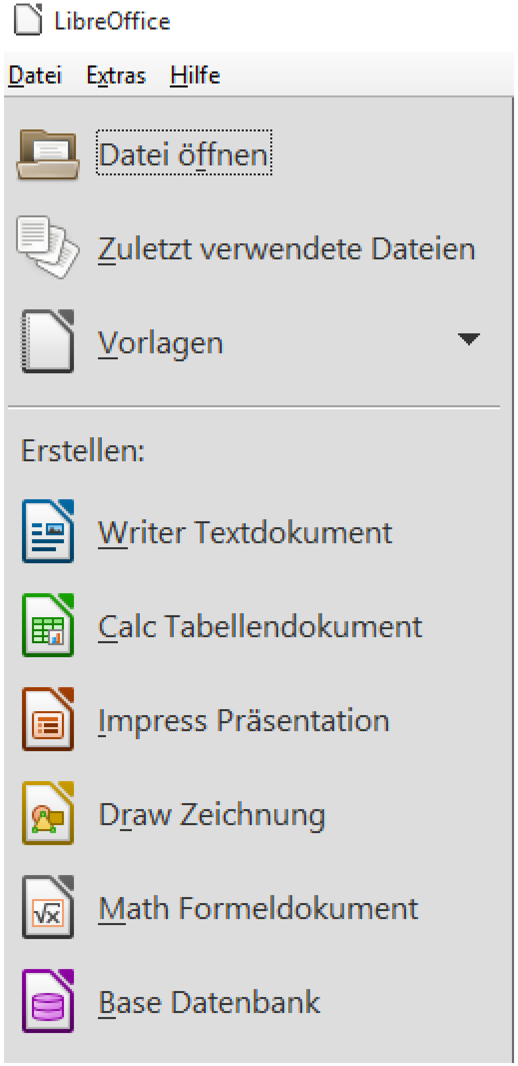
Cell phone version (Android)



OpenOffice and LibreOffice: Alternatives to MS-Office

https://www.libreoffice.org/

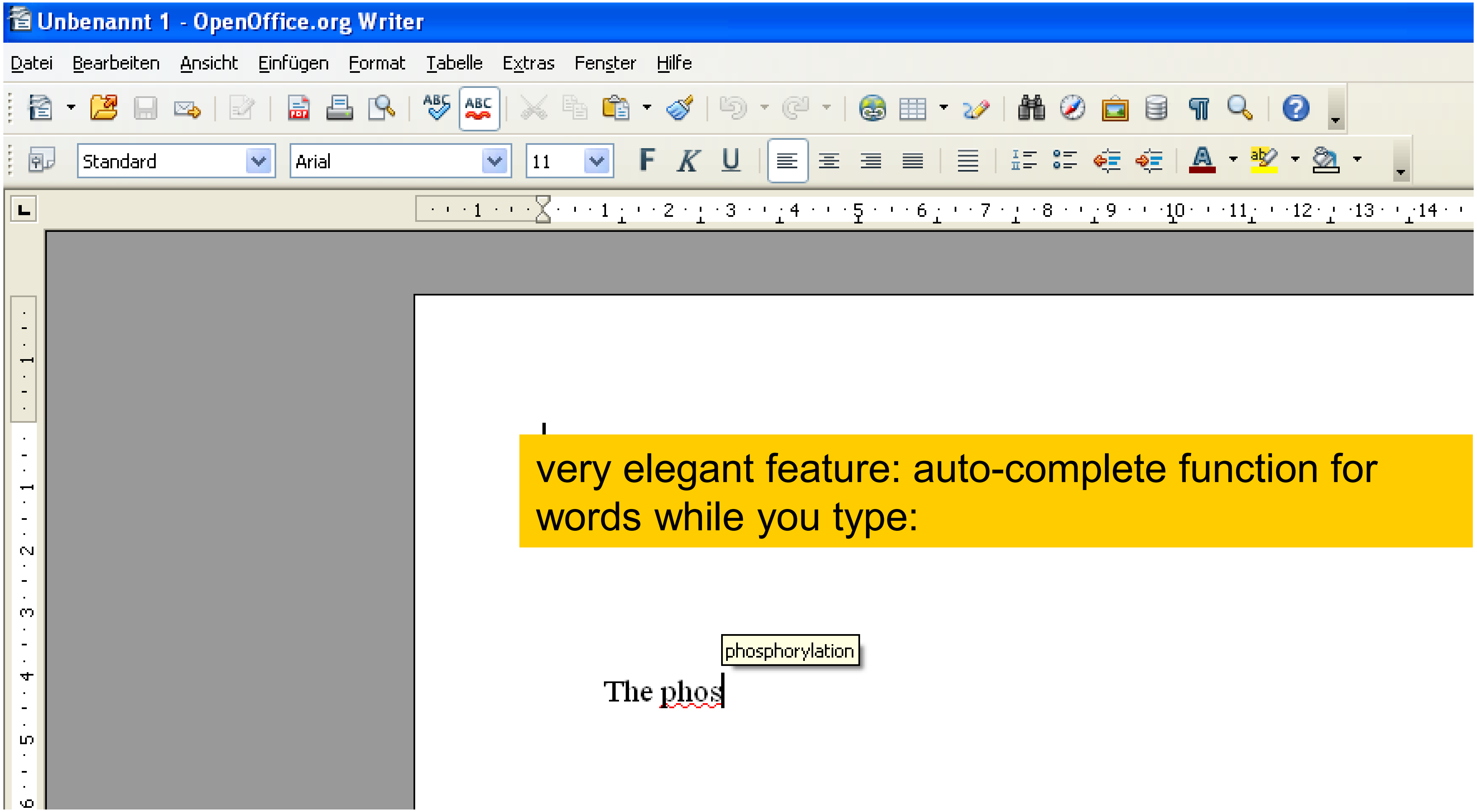
http://www.openoffice.org/
driven by Apache



OpenOffice Features

- Look a bit like MS-Office 2003 (Button appearance)
- OpenOffice applications can read MS-Office files (and also save in MS-Office format- although the later with some restrictions: some formatings might be lost)
- OpenOffice is available for many languages and platforms (including Macintosh and Linux)
- Bibliography support (similar to Endnote Plug-In) possible via www.zotero.org (free extension for Firefox) – and more recently also with Mendeley and Endnote

OpenOffice-Writer



very elegant feature: auto-complete function for words while you type:

The phos

Pdf-Viewers / Editors and generating of pdf‘s

Viewing and editing

- PDF-Xchange Viewer:
  small (about 40 MB), very fast, files can be edited (highlighting, comments, stamps…)
- Follow-up: **PDF-xchange editor** (340 MB)
- **pdf24**: extract pages or combine files to a joint pdf…
- (Acrobat Professional Commercial): huge file, slow
  \- but can extract and delete pages

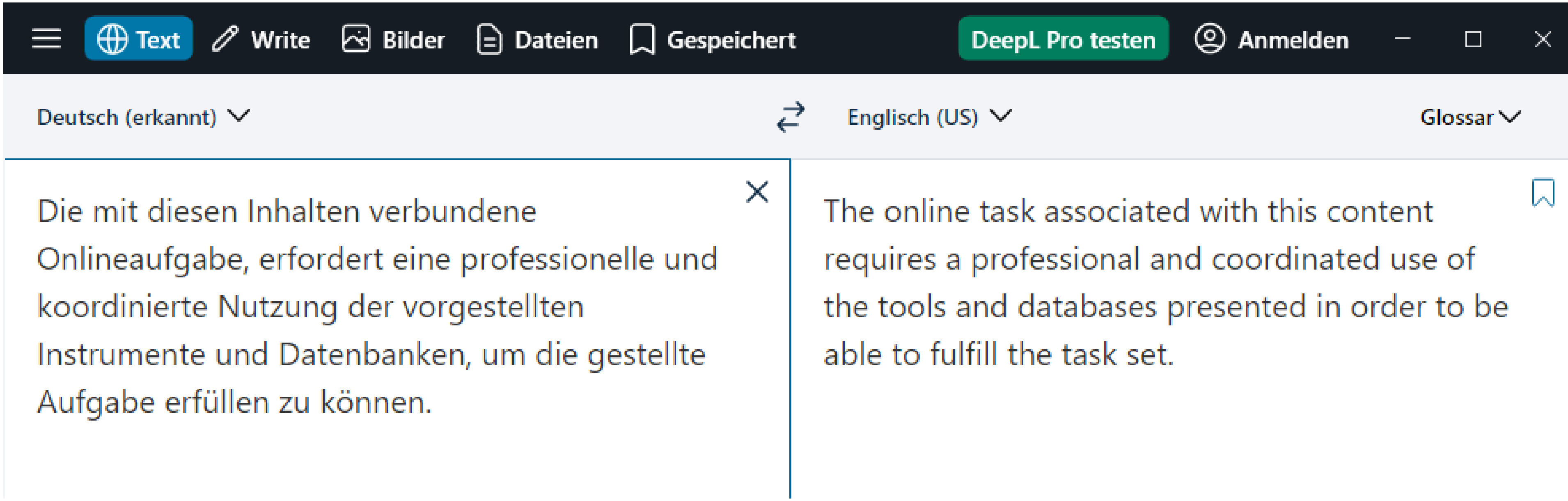
Generating pdf-files

- Office 2007 and later
- OpenOffice
- DoPDF: installs a pdf-printer driver (printer command in any software > choose DoPDF as printer > pdf-file is generated instead of a print-out)
- Foxit pdf-viewer also installs a pdf-printer driver

Translation of Text

Online Services
- LEO: http://dict.leo.org/
- Google: http://translate.google.at

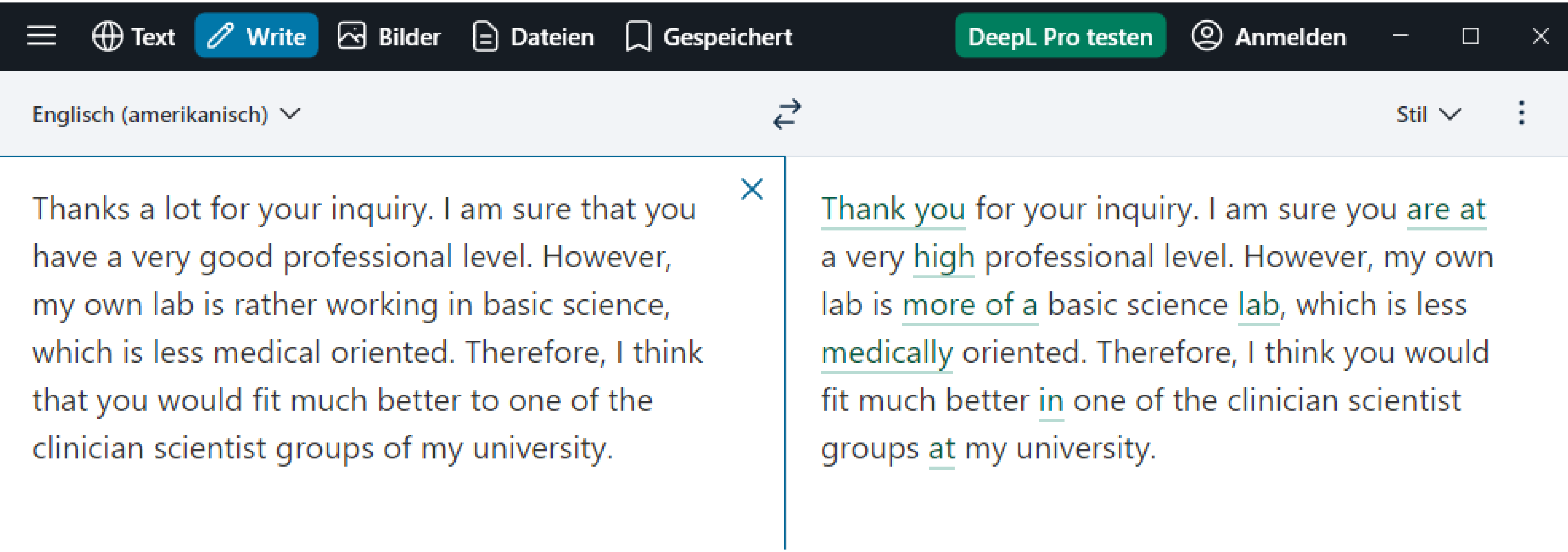
Translation of phrases: DeepL https://www.deepl.com/
(when desktop program is installed: Ctrl+CC translates selected text in all programs



Die mit diesen Inhalten verbundene Onlineaufgabe, erfordert eine professionelle und koordinierte Nutzung der vorgestellten Instrumente und Datenbanken, um die gestellte Aufgabe erfüllen zu können.

The online task associated with this content requires a professional and coordinated use of the tools and databases presented in order to be able to fulfill the task set.

Improving English text with DeepL Write

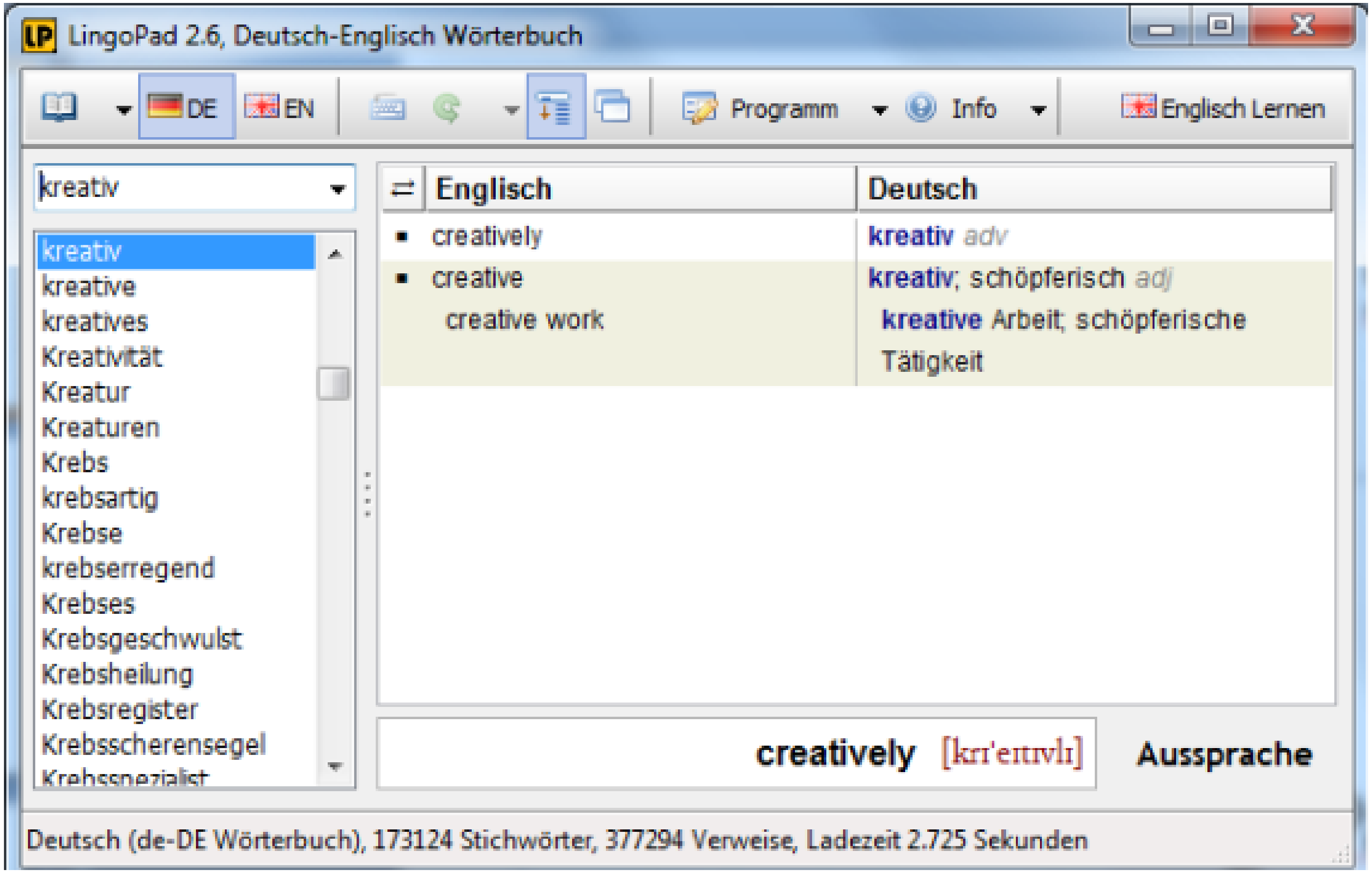


Thanks a lot for your inquiry. I am sure that you have a very good professional level. However, my own lab is rather working in basic science, which is less medical oriented. Therefore, I think that you would fit much better to one of the clinician scientist groups of my university.

Thank you for your inquiry. I am sure you are at a very high professional level. However, my own lab is more of a basic science lab, which is less medically oriented. Therefore, I think you would fit much better in one of the clinician scientist groups at my university.

Translation of Text offline

Offline program: LingoPad: http://www.ego4u.de/de/lingopad
Installs a dictionary locally



kreativ

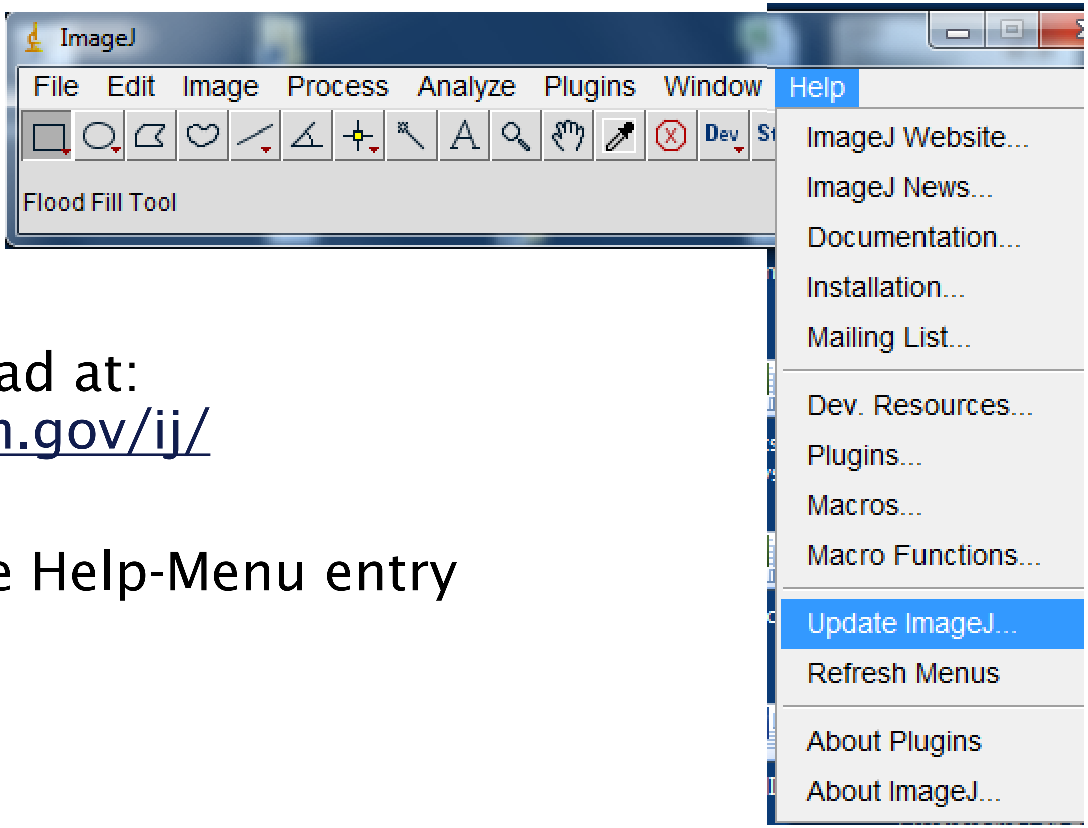
- kreativ
- kreative
- kreatives
- Kreativität
- Kreatur
- Kreaturen
- Krebs
- krebsartig
- Krebse
- krebserregend
- Krebses
- Krebsgeschwulst
- Krebsheilung
- Krebsregister
- Krebsscherensegel
- Krebsspezialist

Englisch	Deutsch
creatively	kreativ *adv*
creative	kreativ; schöpferisch *adj*
creative work	kreative Arbeit; schöpferische Tätigkeit

creatively [krɪ'eɪtɪvlɪ]

Deutsch (de-DE Wörterbuch), 173124 Stichwörter, 377294 Verweise, Ladezeit 2.725 Sekunden

ImageJ



- Freeware: download at: http://rsb.info.nih.gov/ij/
- Update-Link in the Help-Menu entry

ImageJ Plugins and Macros – and new ImageJ: Fiji

- Many plugins and macros available:

  [Acquisition]
  [Analysis]
  [Collections]
  [Color]
  [Filters]
  [Graphics]
  [Input/Output]
  [Programming Examples]
  [Stacks]
  [Utilities]

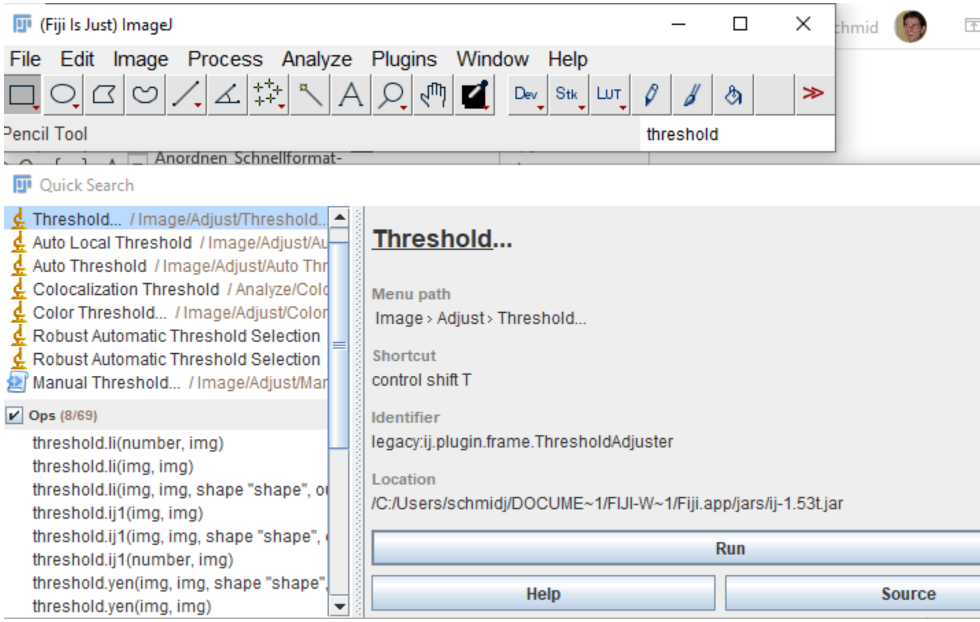
- **Improved version with additional built-in plugins and automated updates**:

  - **Fiji**: **https://fiji.sc**

  With an integrated search field

  List of extensions:

  https://imagej.net/list-of-extensions



Threshold... / Image/Adjust/Threshold..
Auto Local Threshold / Image/Adjust/Au
Auto Threshold / Image/Adjust/Auto Thr
Colocalization Threshold / Analyze/Colo
Color Threshold... / Image/Adjust/Color
Robust Automatic Threshold Selection
Robust Automatic Threshold Selection
Manual Threshold... / Image/Adjust/Mar

☑ Ops (8/69)

threshold.li(number, img)
threshold.li(img, img)
threshold.li(img, img, shape "shape", o
threshold.ij1(img, img)
threshold.ij1(img, img, shape "shape",
threshold.ij1(number, img)
threshold.yen(img, img, shape "shape",
threshold.yen(img, img)

Threshold...

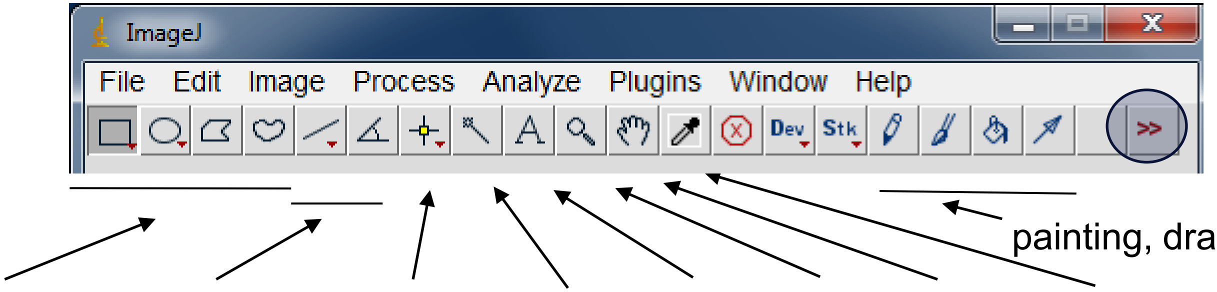
Menu path
Image › Adjust › Threshold...

Shortcut
control shift T

Identifier
legacy:ij.plugin.frame.ThresholdAdjuster

Location
/C:/Users/schmidj/DOCUME~1/FIJI-W~1/Fiji.app/jars/ij-1.53t.jar

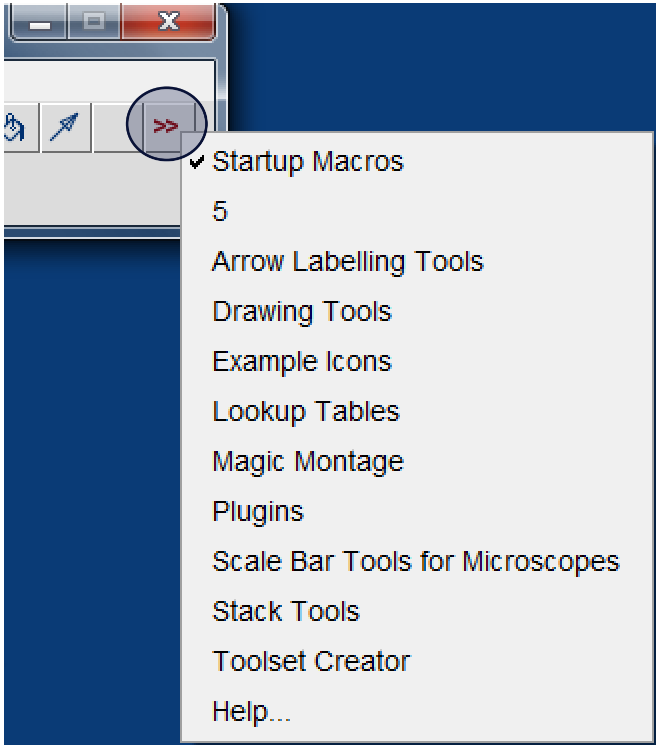
Main Menu

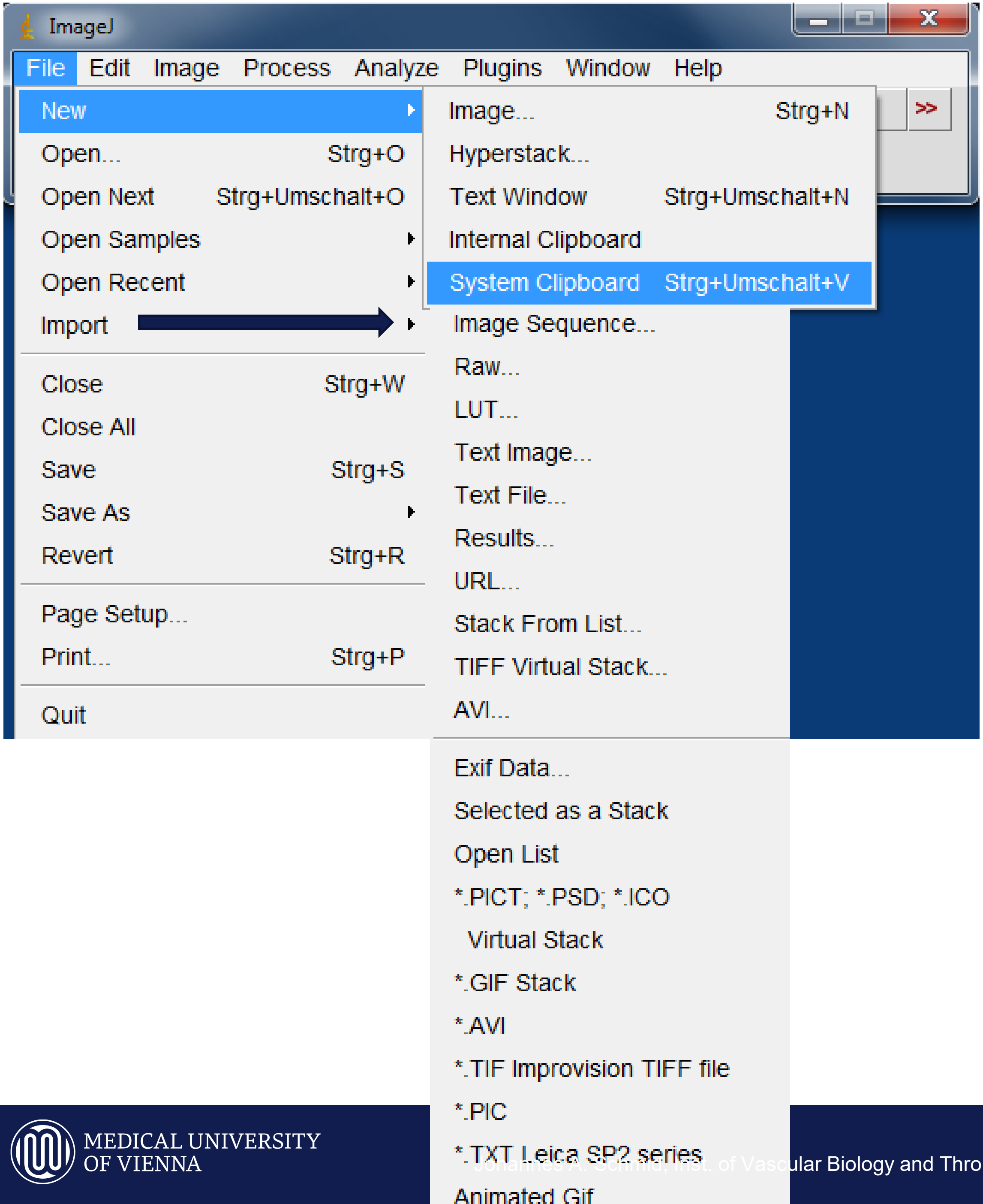


painting, drawing

selction tools line tools crosshair wand text tool zoom scrolling colour picker

additional toolsets

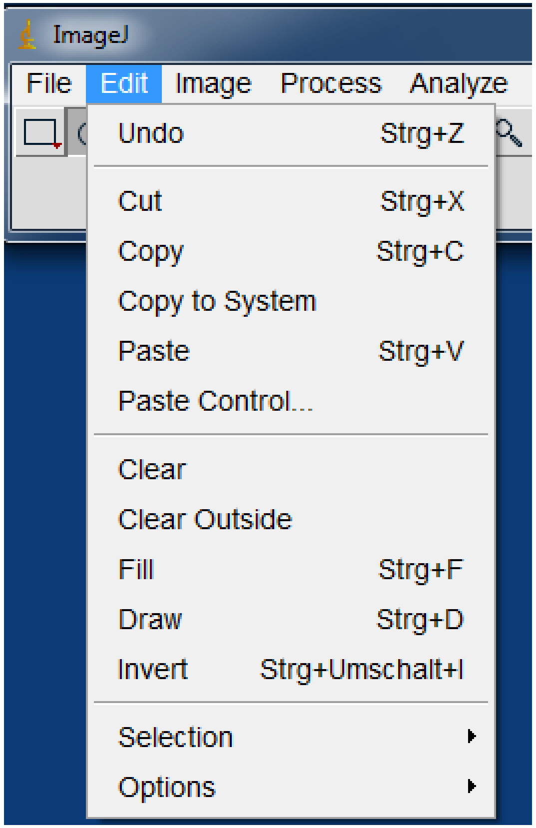




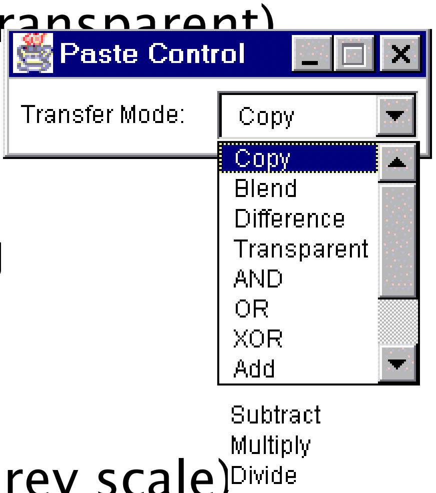
The File Menu

- New images (e.g. pasting from the Clipboard)
- Opening of images
- Importing of images: Many different file formats
- Saving
- Reverting: opening the last saved version of an image
- Page setup and printing

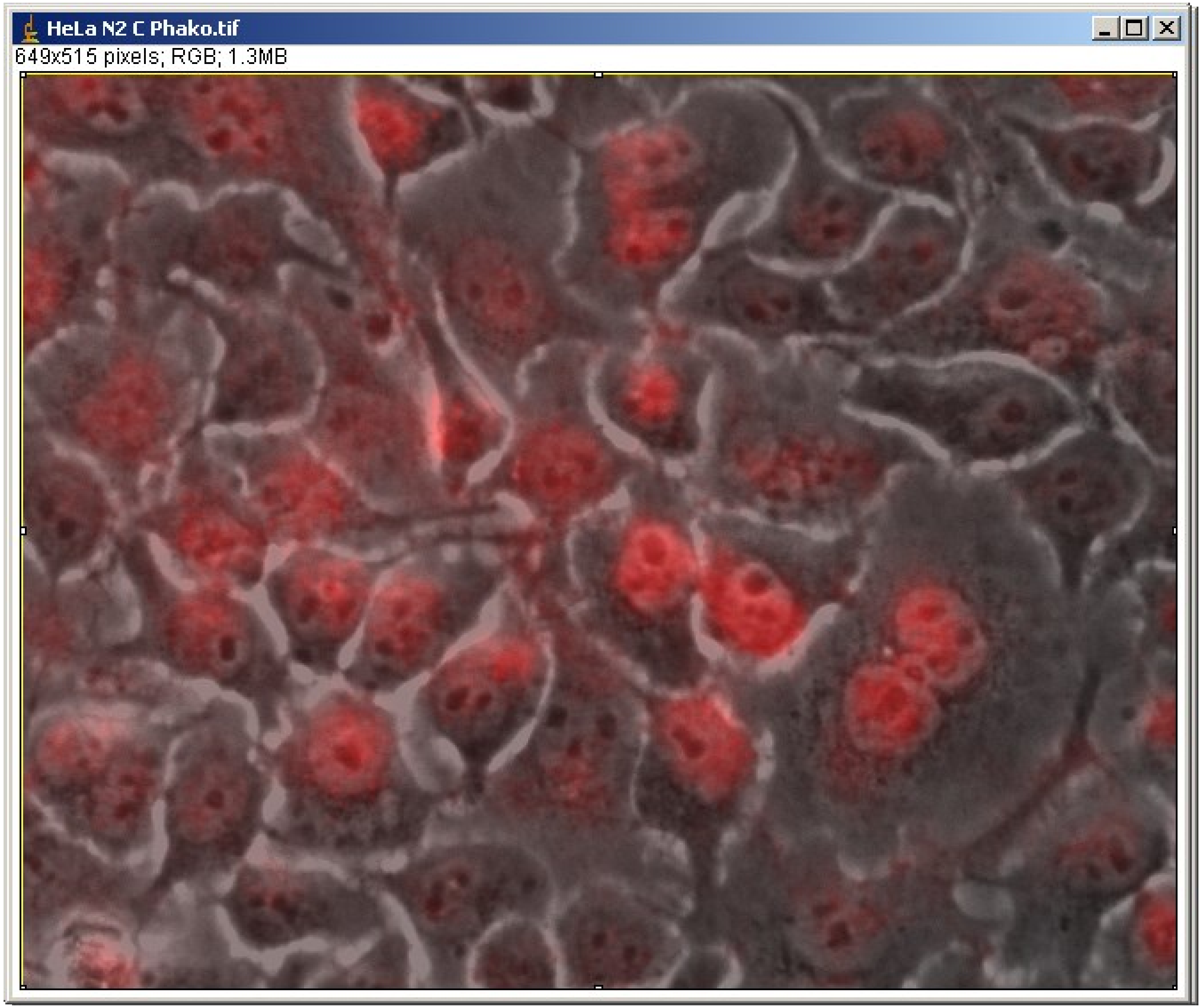
The Edit Menu



- Copy/Paste, Undo comand (also: *Copy to System*)
- Paste control: allows pasting with additional operations: blending, transparent (white pixels copied as transparent) logical operations difference..
- Draw (a line along selection)
- Invert the image (also inverts the grey scale)



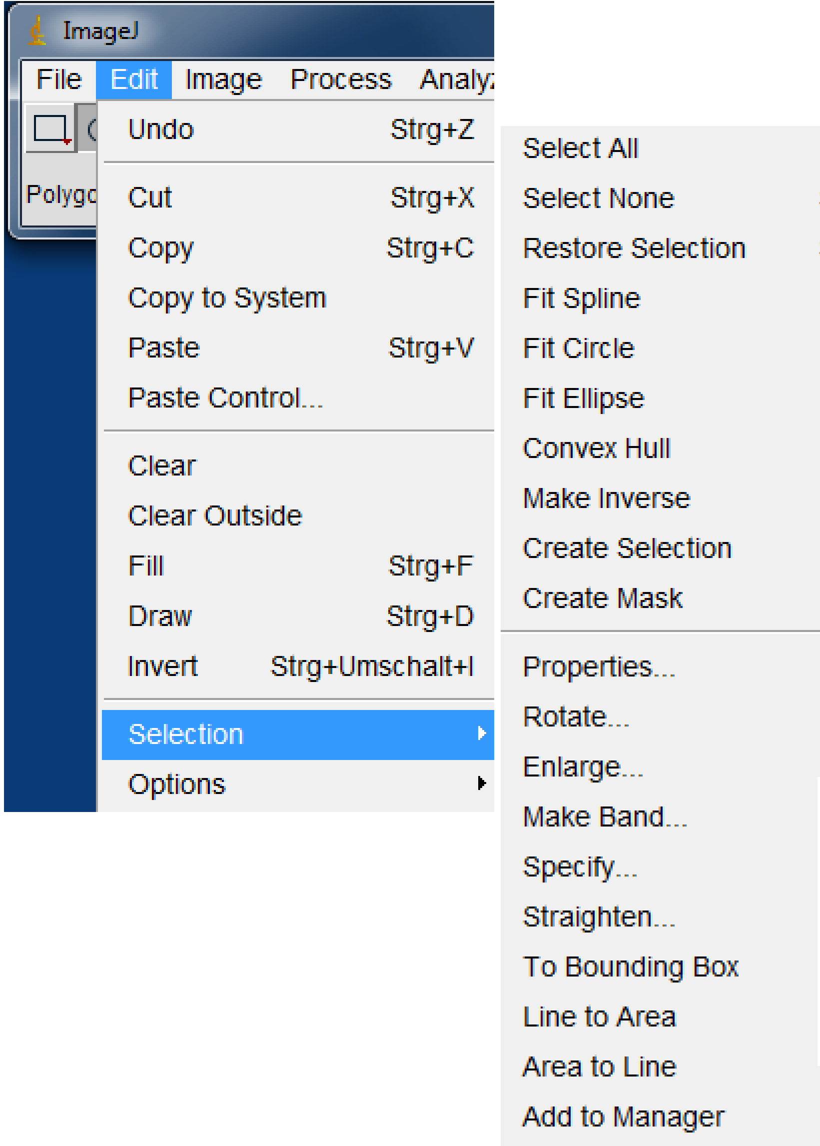
„Blending“of fluorescence and phase contrast



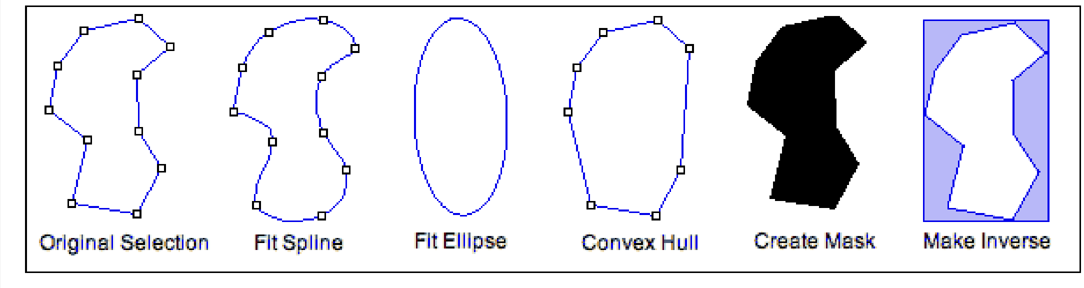
649x515 pixels; RGB; 1.3MB

Transfer Mode: Blend

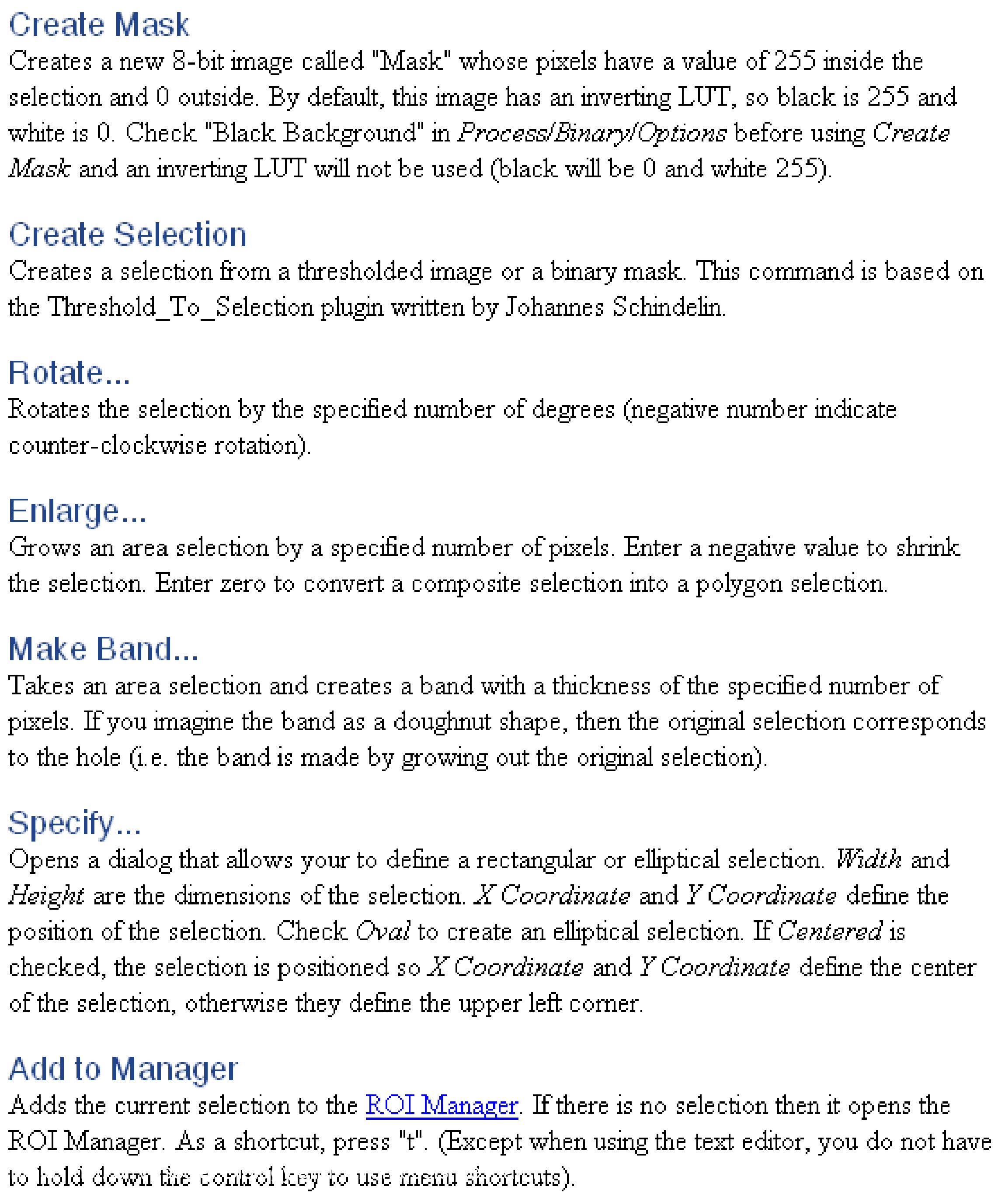
Selection tools



- Restore selection: places a selection at exactly the same position in a different image (Strg+Shift E)
- Fitting of selections: modifies a freehand or polygonal selection with different criteria



Editing of selections



Create Mask

Creates a new 8-bit image called "Mask" whose pixels have a value of 255 inside the selection and 0 outside. By default, this image has an inverting LUT, so black is 255 and white is 0. Check "Black Background" in *Process/Binary/Options* before using *Create Mask* and an inverting LUT will not be used (black will be 0 and white 255).

Create Selection

Creates a selection from a thresholded image or a binary mask. This command is based on the Threshold_To_Selection plugin written by Johannes Schindelin.

Rotate...

Rotates the selection by the specified number of degrees (negative number indicate counter-clockwise rotation).

Enlarge...

Grows an area selection by a specified number of pixels. Enter a negative value to shrink the selection. Enter zero to convert a composite selection into a polygon selection.

Make Band...

Takes an area selection and creates a band with a thickness of the specified number of pixels. If you imagine the band as a doughnut shape, then the original selection corresponds to the hole (i.e. the band is made by growing out the original selection).

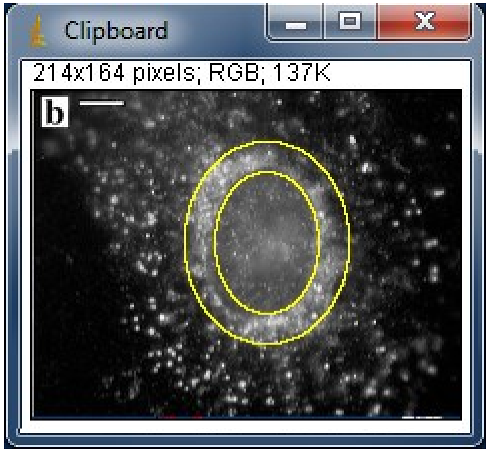
Specify...

Opens a dialog that allows your to define a rectangular or elliptical selection. *Width* and *Height* are the dimensions of the selection. *X Coordinate* and *Y Coordinate* define the position of the selection. Check *Oval* to create an elliptical selection. If *Centered* is checked, the selection is positioned so *X Coordinate* and *Y Coordinate* define the center of the selection, otherwise they define the upper left corner.

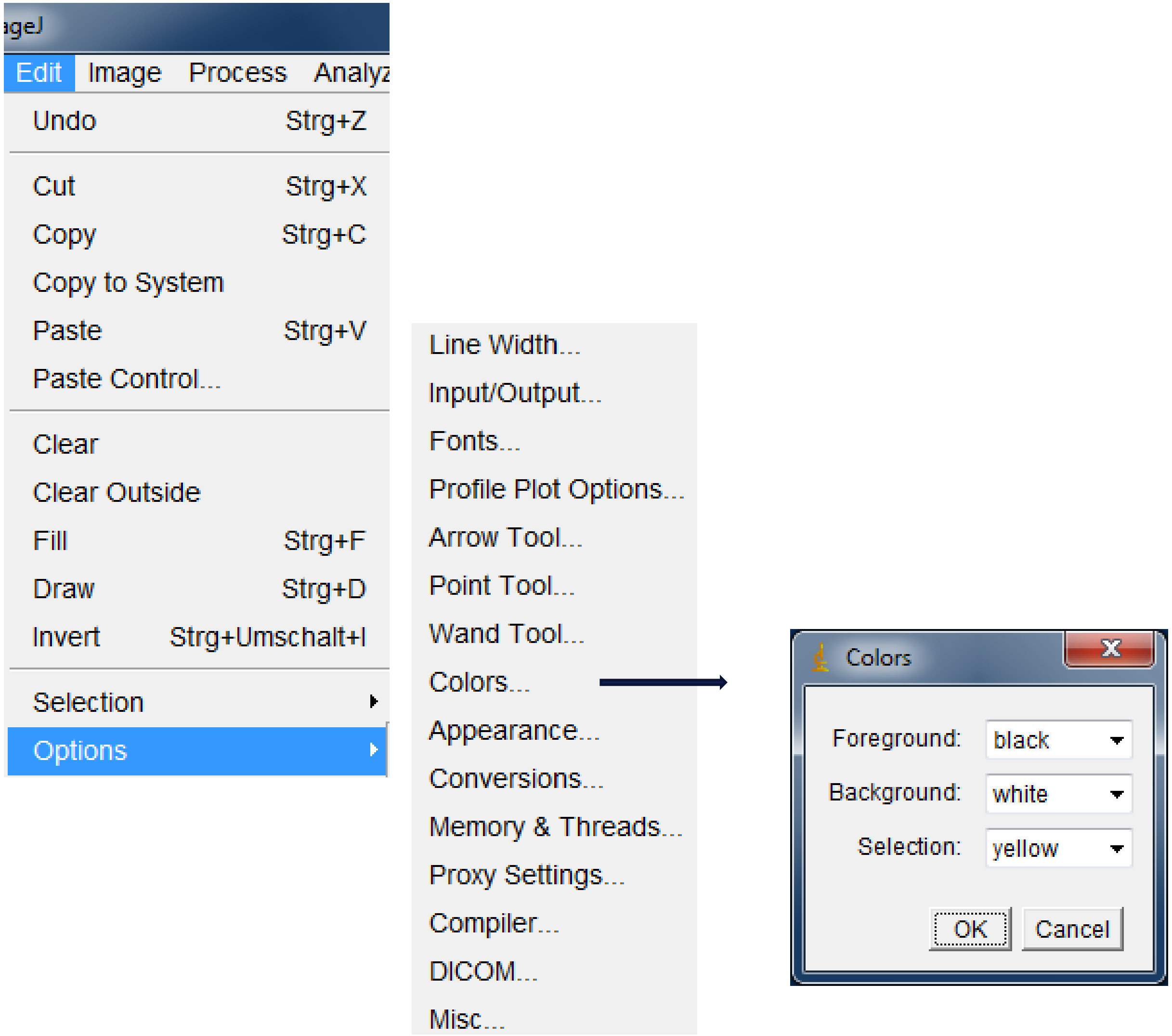
Add to Manager

Adds the current selection to the ROI Manager. If there is no selection then it opens the ROI Manager. As a shortcut, press "t". (Except when using the text editor, you do not have to hold down the control key to use menu shortcuts).

example: make band around nucleus to measure perinuclear area



General Options of ImageJ

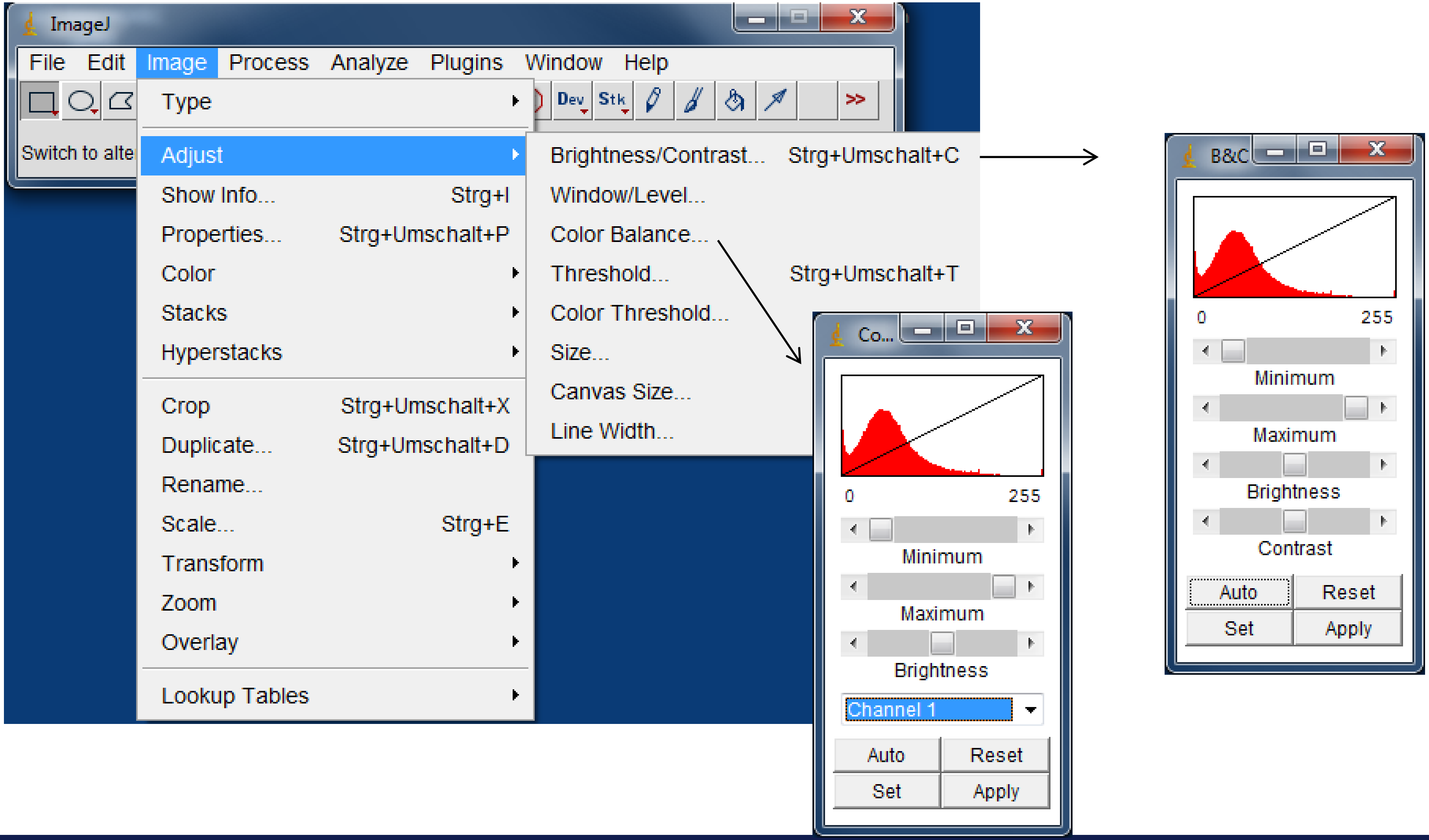


Foreground: black

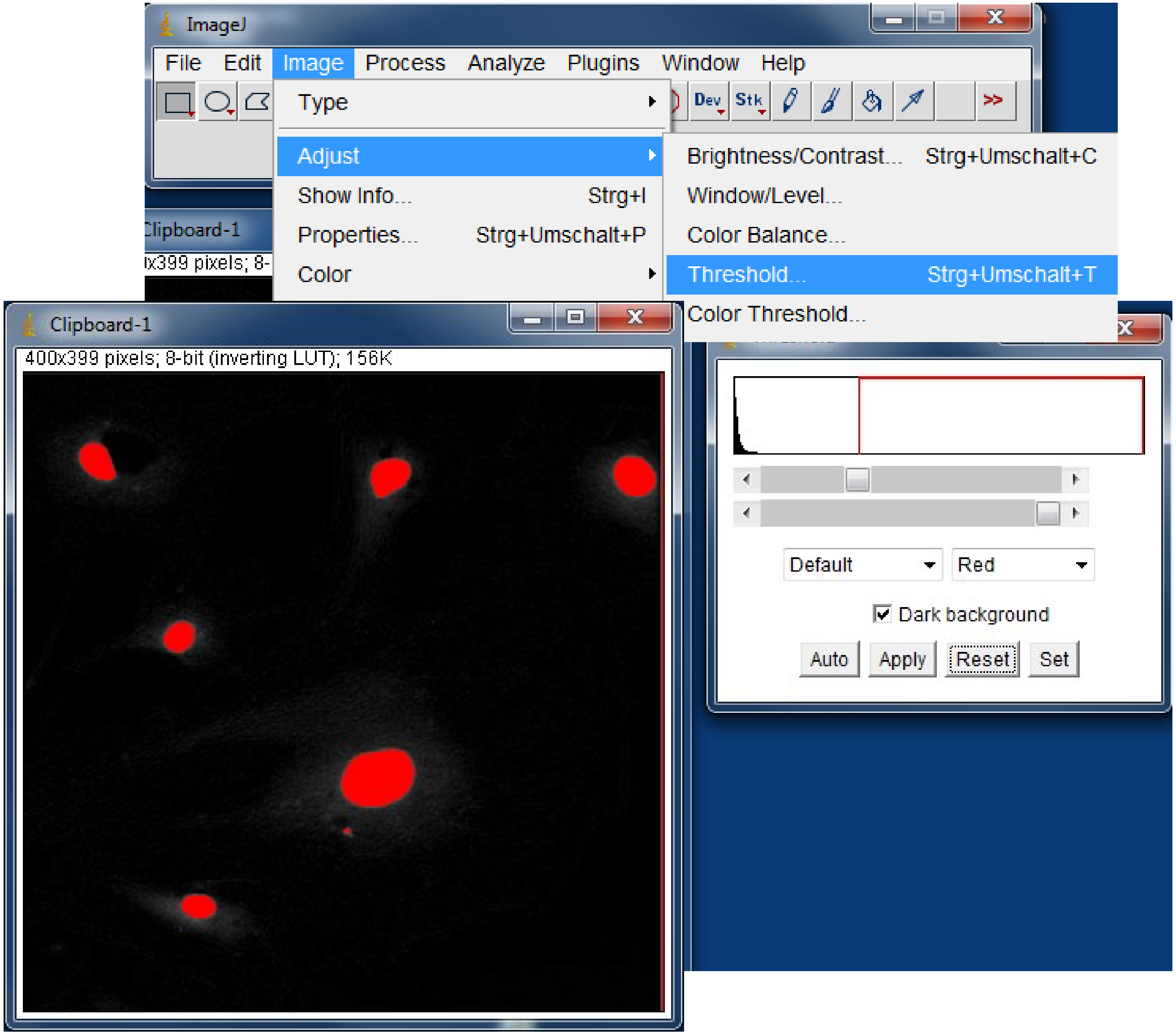
Background: white

Selection: yellow

The Image Menu > Brightness/Contrast



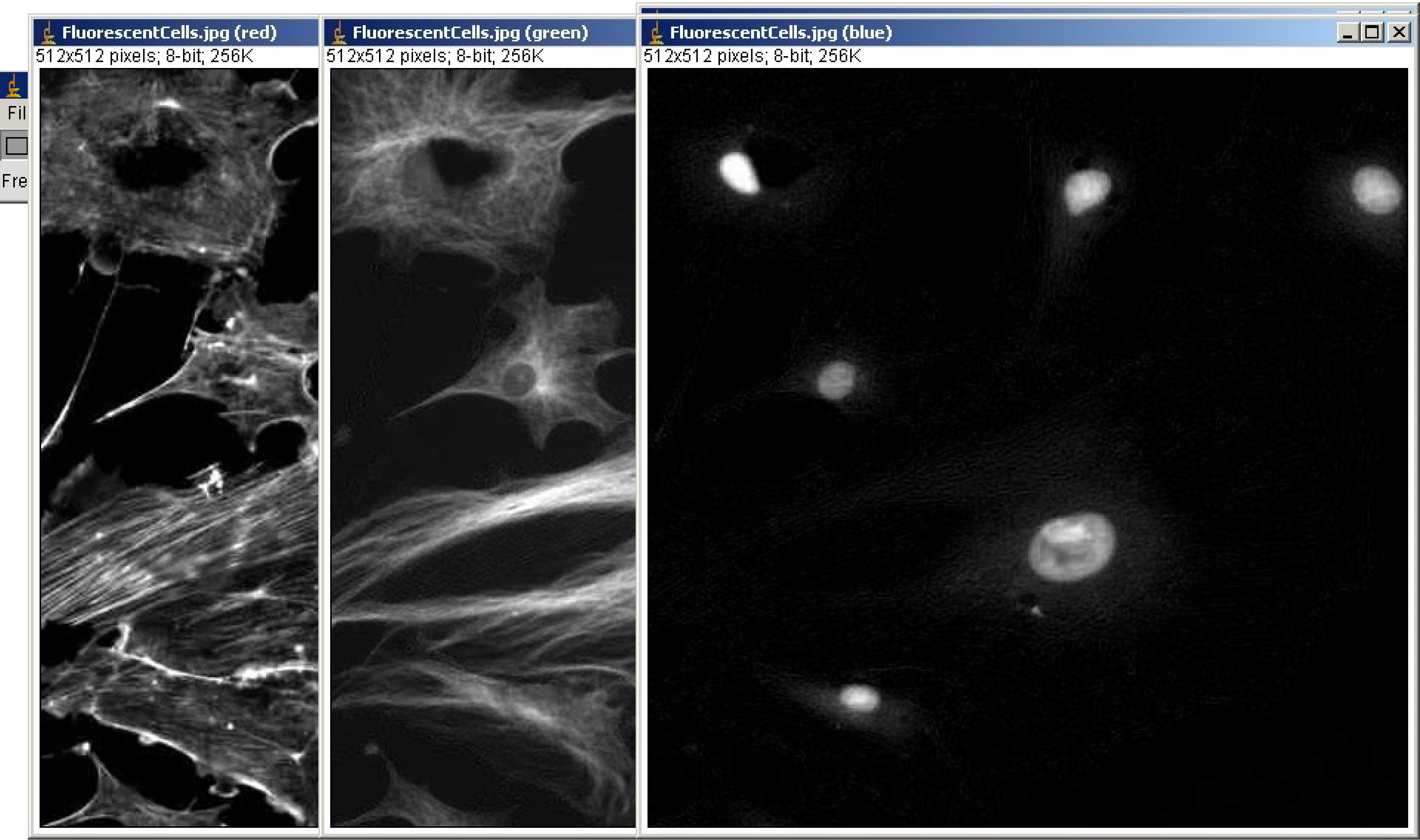
The Image Menu > Threshold



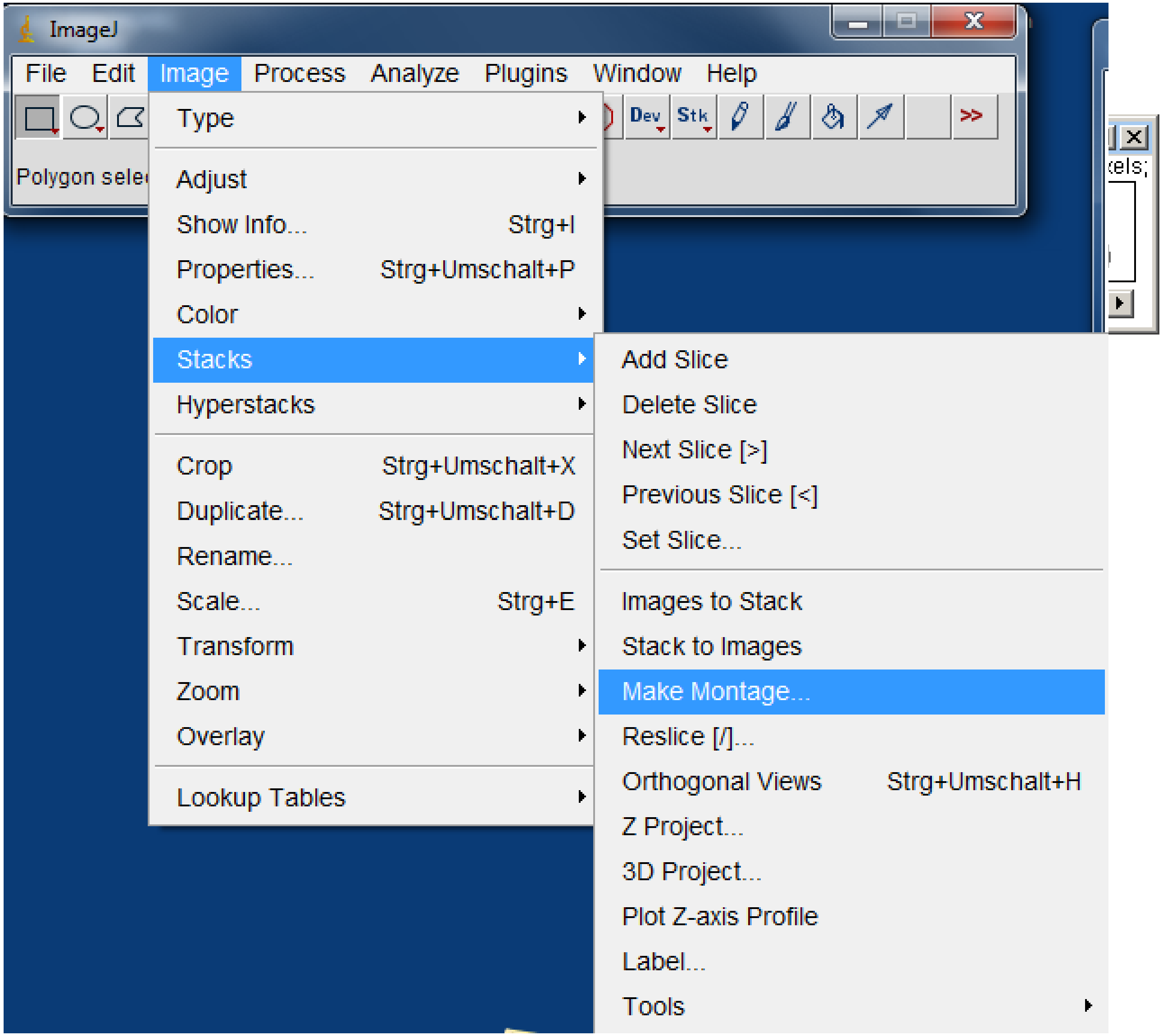
400x399 pixels; 8-bit (inverting LUT); 156K

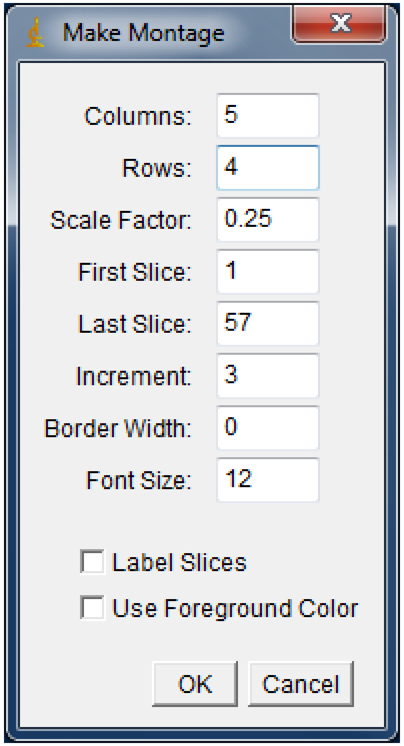
☑ Dark background

Splitting of colour of an RGB image



Working with image stacks

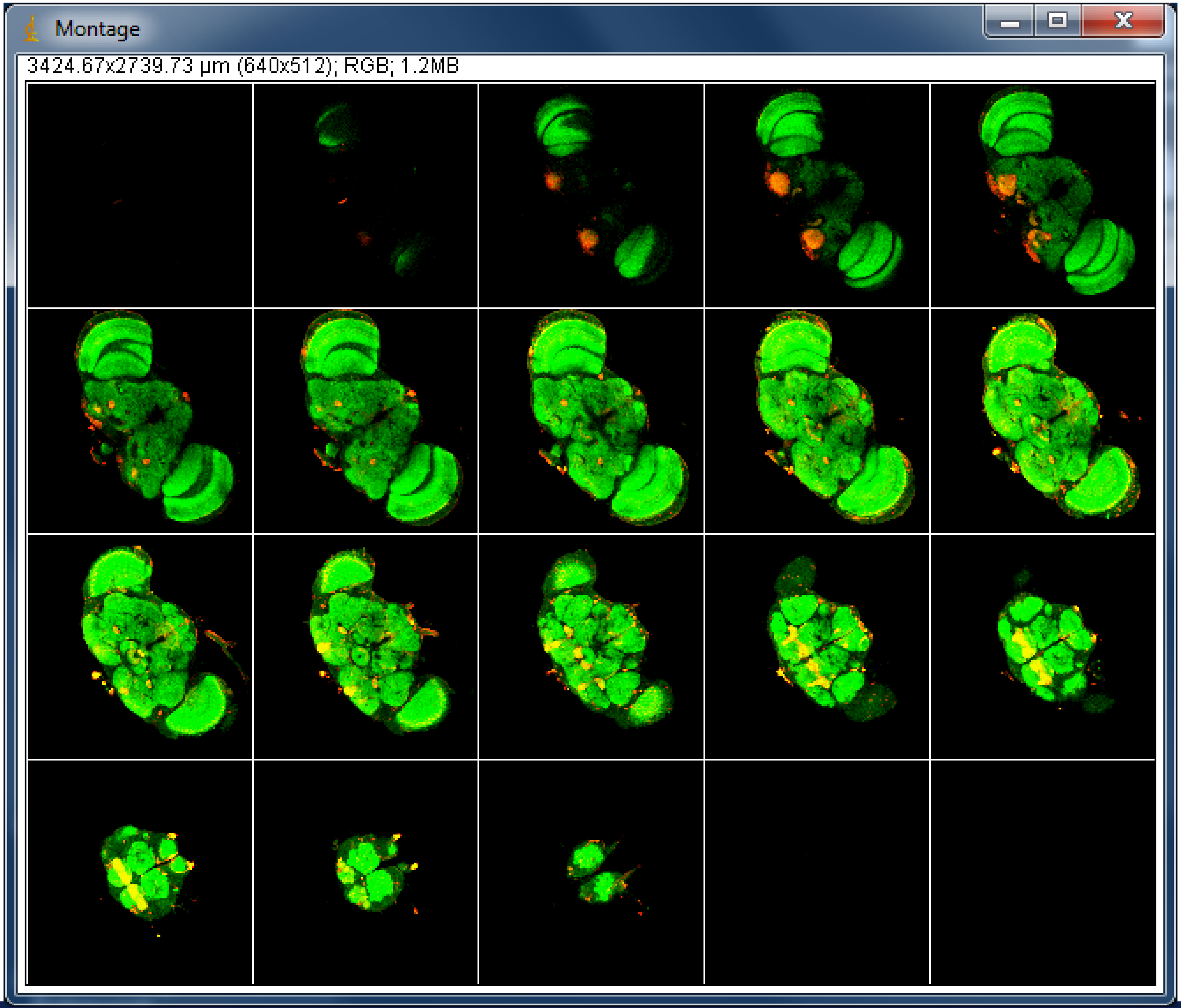



Make Montage

Columns: 5
Rows: 4
Scale Factor: 0.25
First Slice: 1
Last Slice: 57
Increment: 3
Border Width: 0
Font Size: 12

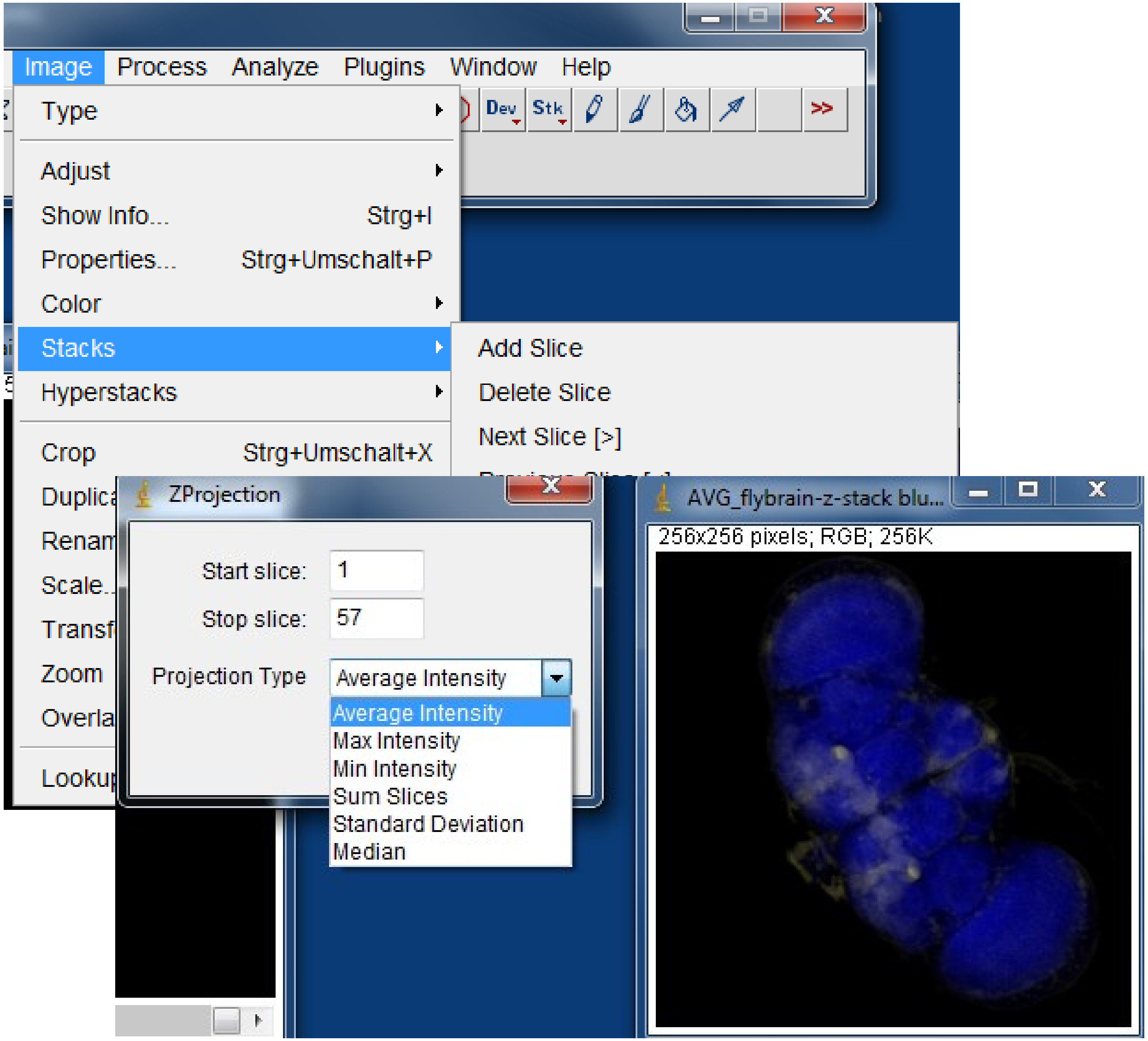
☐ Label Slices
☐ Use Foreground Color

Image stack montage



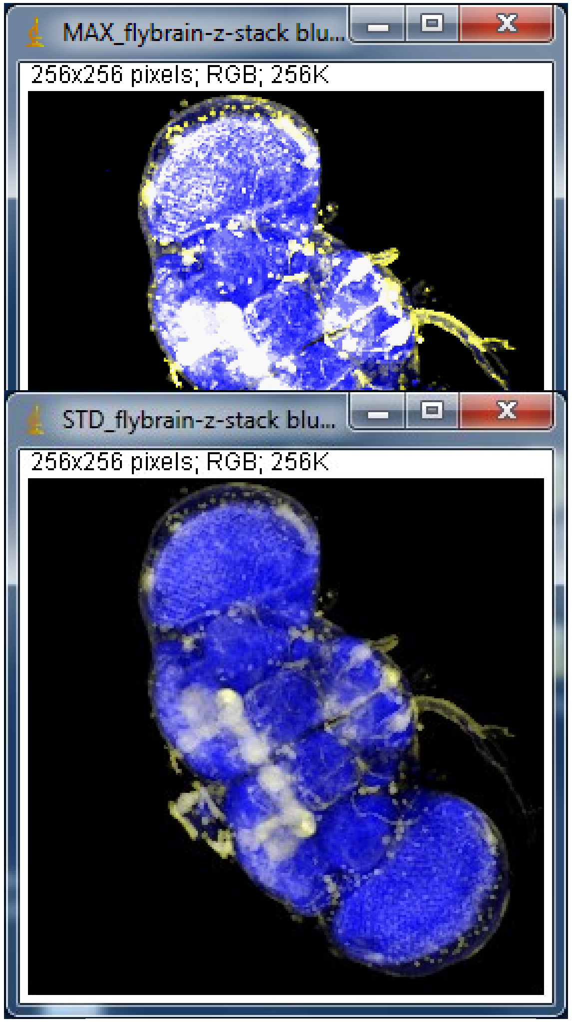
3424.67x2739.73 µm (640x512); RGB; 1.2MB

Z-stacks: maximum projections



Start slice: 1
Stop slice: 57
Projection Type: Average Intensity

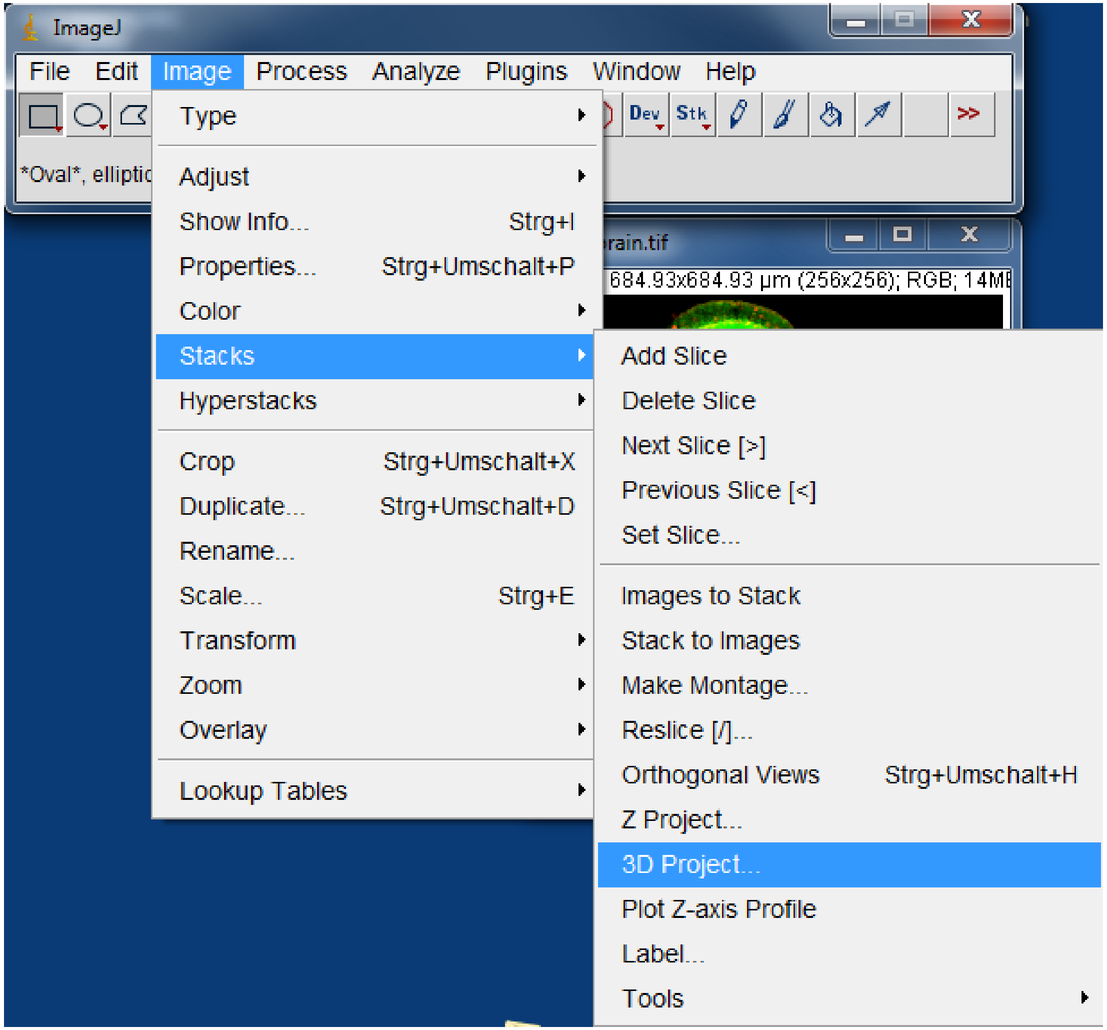
Max Intensity

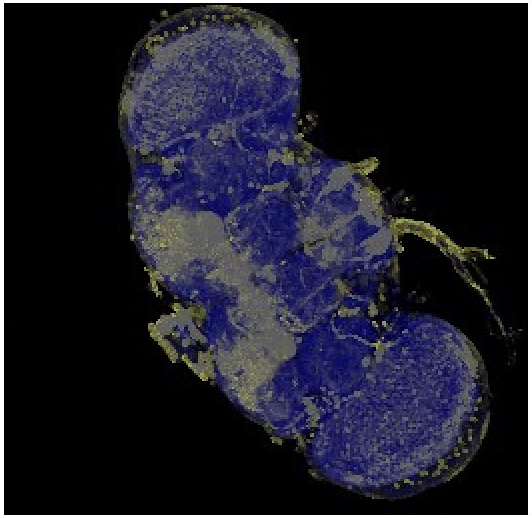


Standard Deviation

Average Intensity

3D projections of z-stacks

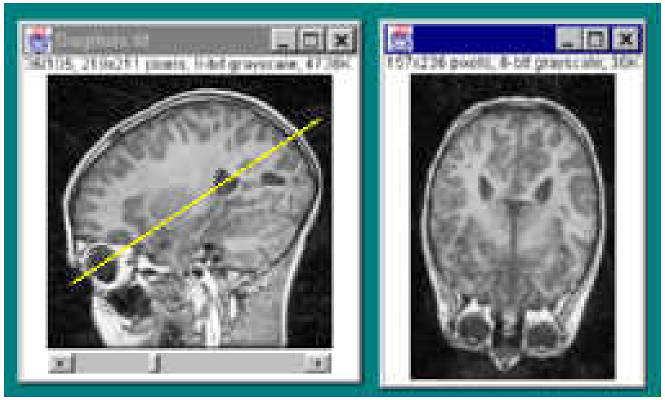




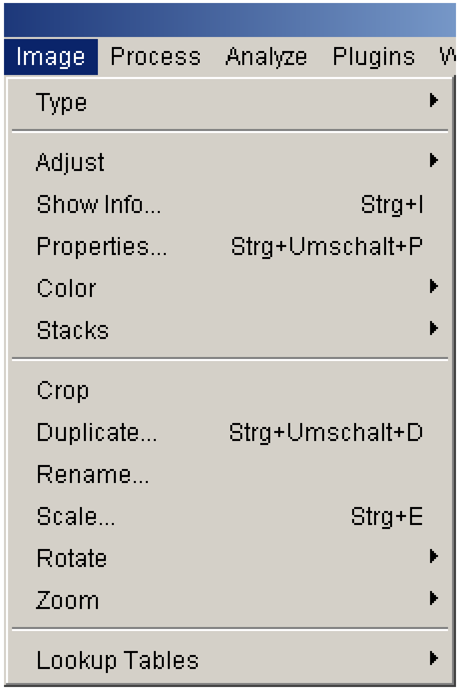
Reslicing of image stacks

Reslice...

Reconstructs one or more orthogonal slices through the image volume represented by the current stack. Before using this command, create a straight line or rectangular selection to specify were the reconstructions will be done. A dialog box allows you the specify the *Z-Spacing* (displacement between slices) of the source volume. Multiple slices are reconstructed and saved as a stack if you create a rectangular selection or set *Slice Width* greater than one.

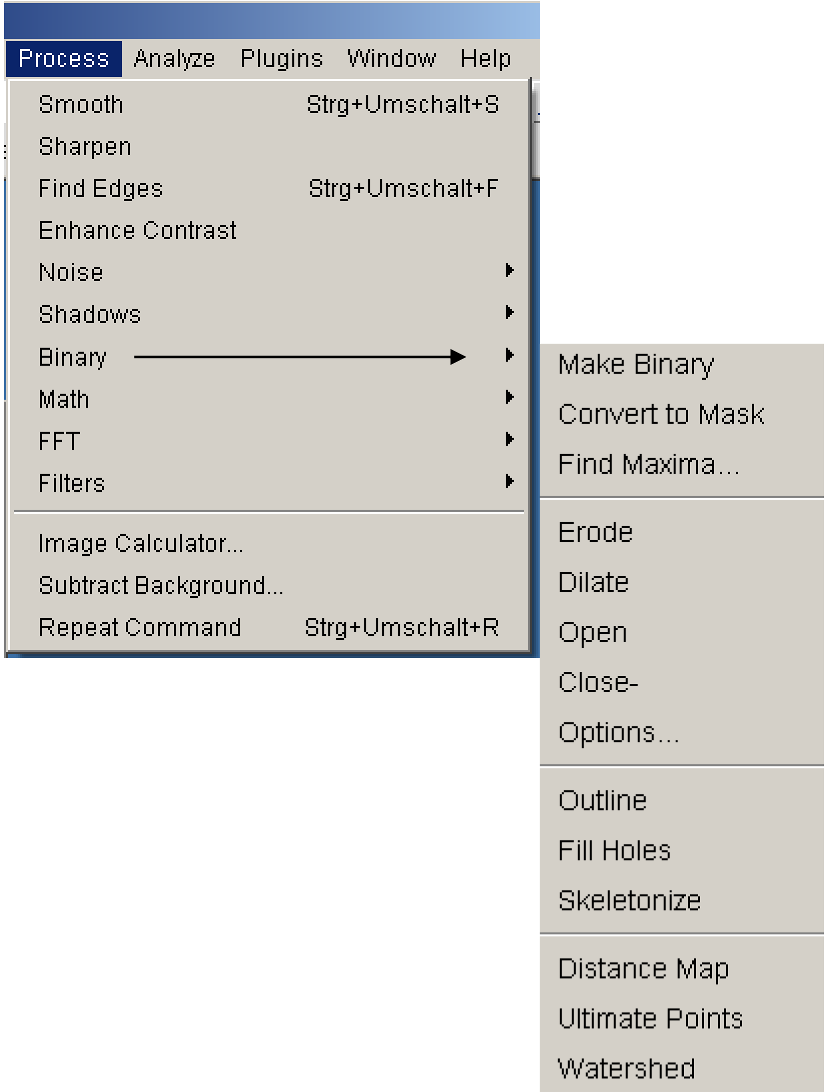


Additional Image Menu Options



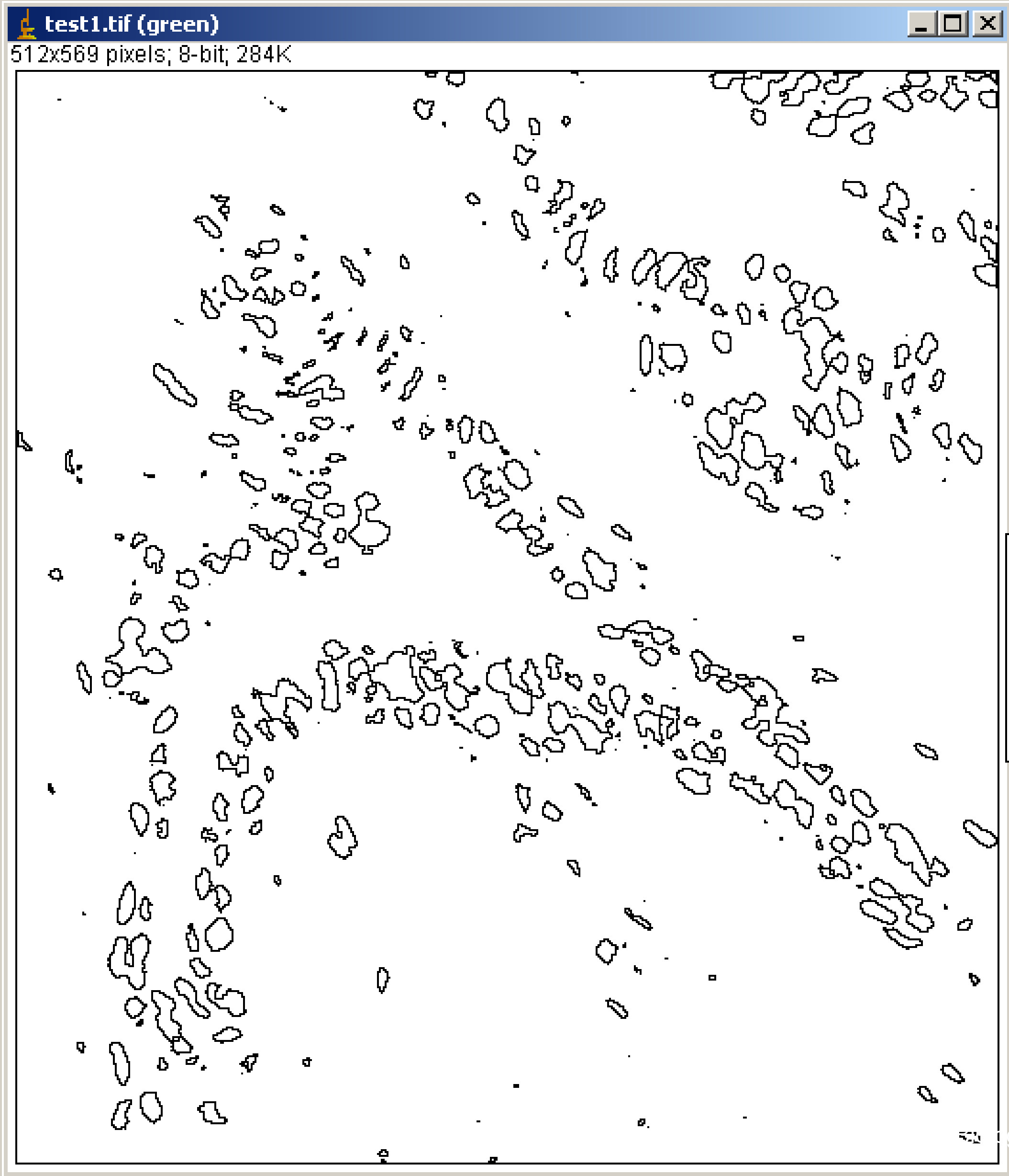
- Cropping: Cut out relevant part of the image
- Duplicate image
- Rename image
- Scaling: enlarge or reduce (changes the resolution)
- Rotate: flipping, 90˚ or arbitrary
- Zoom: enlarge or reduce without changing the resolution
- Lookup-Tables: Gray-Values, Pseudo-Colours

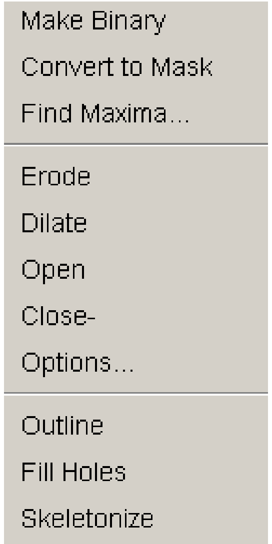
The Process Menu

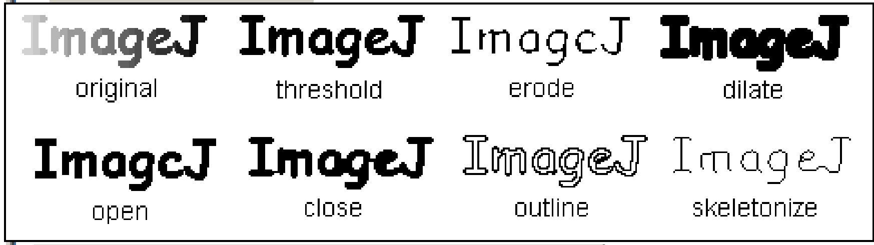


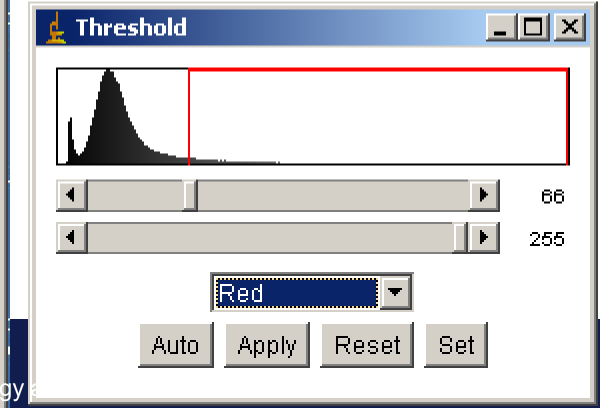
- Smooting, Sharpening
- Find edges: areas of significant contrast change
- Enhance contrast
- Add noise or shadows
- Binary: Thresholded images can be adjusted and modified

Options with Binary images (after thresholding)

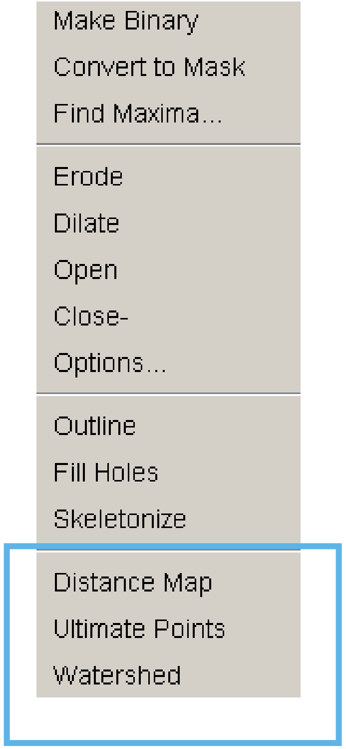


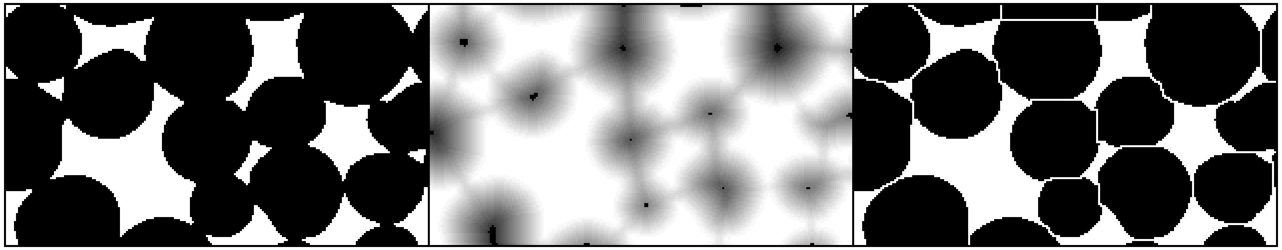






Segmentation of thresholded binarized image

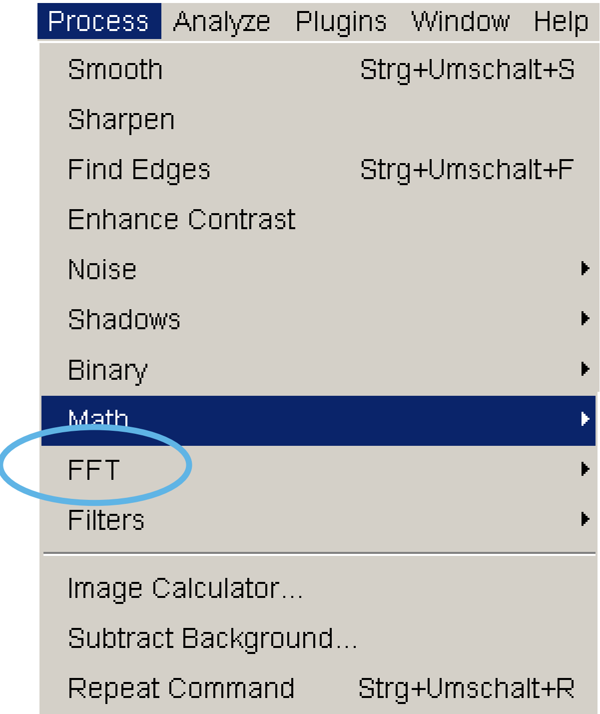




Thresholded Cells　EDM and UEPs　After Watershed Segmentation

- <u>EDM: Euklidian Distance Map</u>: Each foreground pixel in the binary image is replaced with a gray value equal to that pixel's distance from the nearest background pixel.
- <u>Ultimate Points:</u> Generates the ultimate eroded points (UEPs) of the EDM. Requires a binary image as input. The UEPs represent the centers of particles that would be separated by segmentation.
- <u>Watershed</u>: automatically separating or cutting apart particles that touch. It first calculates the Euclidian distance map (EDM) and finds the ultimate eroded points (UEPs). It then dilates each of the UEPs (the peaks or local maxima of the EDM) as far as possible - either until the edge of the particle is reached, or the edge of the region of another (growing) UEP.

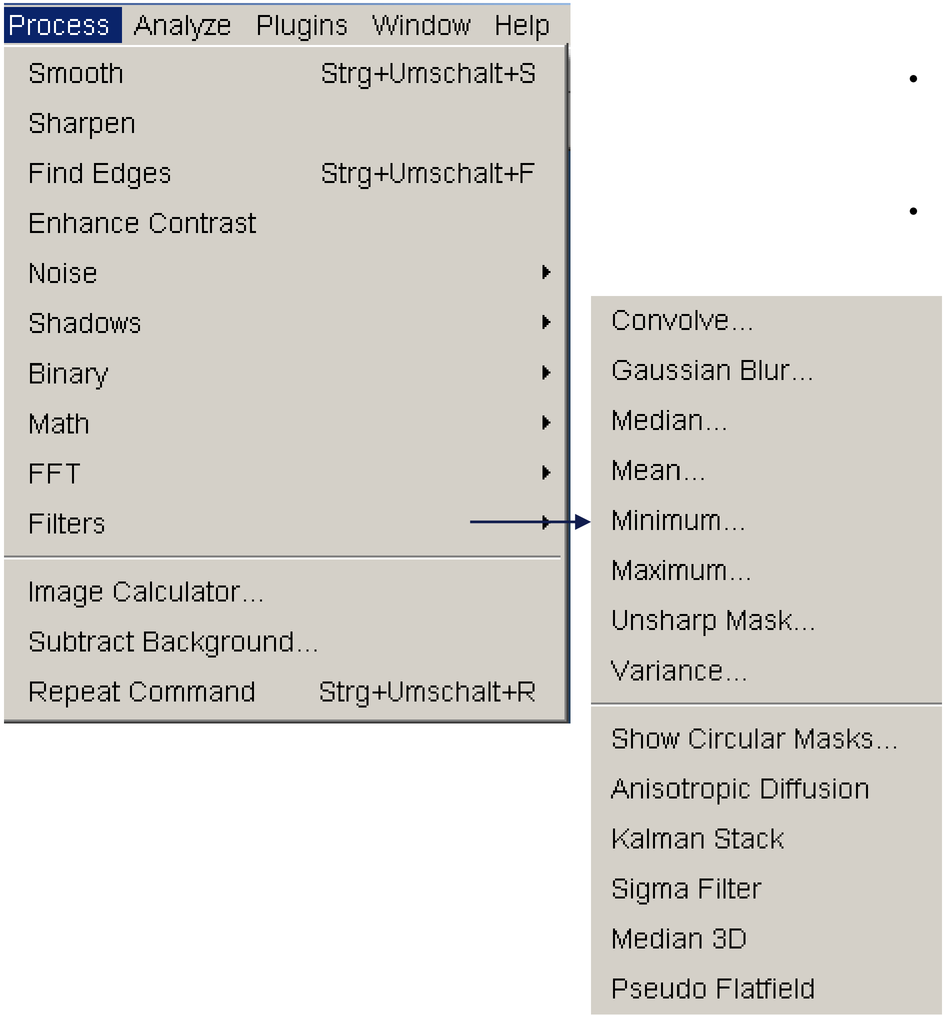
Image Mathematics (with Constants)



Fourier Transformation - can be applied to reduce noise and other more specific applications

- Add... Adds a constant to the image. With 8-bit images, results greater than 255 are set to 255. With 16-bit signed images, results greater than 65,535 are set to 65,535.
- Subtract...Subtracts a constant from the image. With 8-bit and 16-bit images, results less than 0 are set to 0.
- Multiply.. Multiplies the image by the specified real constant. With 8-bit images, results greater than 255 are set to 255. With 16-bit signed images, results greater than 65,535 are set to 65,535.
- Divide...Divides the image by the specified real constant. Attempts to divide by zero will be ignored.
- AND...Does a bitwise AND of the image and the specified binary constant.
- Min..Pixels in the image with a value less than the specified constant are replaced by the constant.
- Max...Pixels in the image with a value greater than the specified constant are replaced by the constant.
- Gamma...Applies the function f(p) = (p/255)^gamma*255 to each pixel (p) in the image or selection, where 0.1 <= gamma <= 5.0. For RGB images, this function is applied to all three color channels. For 16-bit images, the image min and max are used for scaling instead of 255.
- Log..For 8-bit images, applies the function f(p) = log(p) * 255/log(255) to each pixel (p) in the image or selection. For RGB images, this function is applied to all three color channels. For 16-bit images, the image min and max are used for scaling instead of 255. For float images, no scaling is done. To calculate log10 of the image, multiply the result of this operation by 0.4343 (1/log(10).
- Reciprocal: Generates the reciprocal of the active image or selection. Only works with 32-bit float images.
- NaN Background: Sets non-thresholded pixels in 32-bit float images to the NaN (Not a Number) value. For float images, the "Apply" option in Image/Adjust Threshold runs this command. Pixels with a value of Float.NaN (0f/0f), Float.POSITIVE_INFINITY (1f/0f) or Float.NEGATIVE_INFINITY (-1f/0f) are ignored when making measurements on 32-bit float images
- Abs: Generates the absolute value of the active image or selection. Only works with 32-bit float images.

Process > Filters



- **Gaussian Blur...**Smooths the current image by doing a convolution using a square, Gaussian (bell-shaped) kernel. The width of the kernel, in pixels, is 2**radius*+1, where *radius* is entered into a dialog box.
- **Median...**Reduces noise in the active image by replacing each pixel with the median of the neighboring pixel values.
- **Mean...**Smooths the current image by replacing each pixel with the neighborhood mean. The size of the neighborhood is specified by entering its radius in a dialog box.
- **Minimum...**This filter does grayscale erosion by replacing each pixel in the image with the smallest pixel value in that pixel's neighborhood.

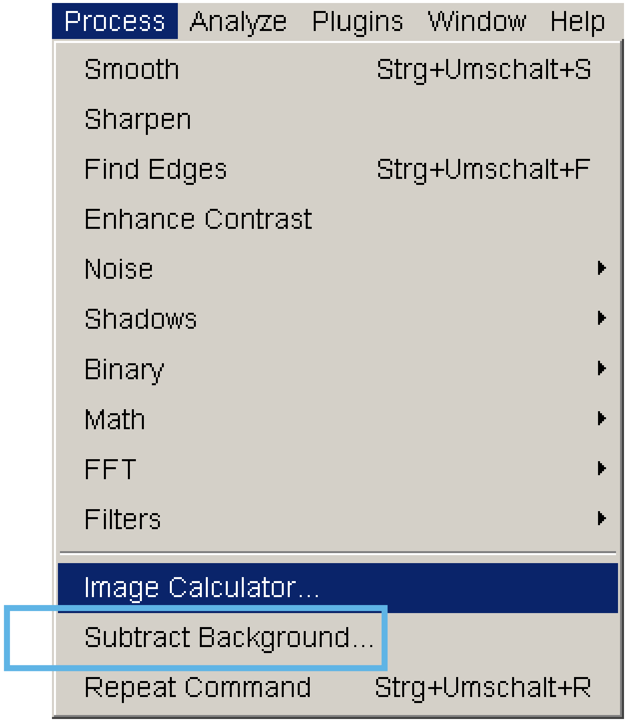
Maximum... This filter does grayscale dilation by replacing each pixel in the image with the largest pixel value in that pixel's neighborhood.

Unsharp Mask... Sharpens and enhances edges by subtracting a blurred version of the image (the unsharp mask) from the original. The unsharp mask is created by Gaussian blurring the original image and then multiplying by the "Mask Weight" parameter. Increase the Guassian blur radius to increase contrast and increase the "Mask Weight" value for additional edge enhancement.

Variance... Highlights edges in the image by replacing each pixel with the neighborhood variance.

Show Circular Masks: Generates a stack containing examples of the circular masks used by the *Median*, *Mean*, *Minimum*, *Maximum* and *Variance* filters for various neighborhood sizes.

Image Mathematics (with 2 Images)



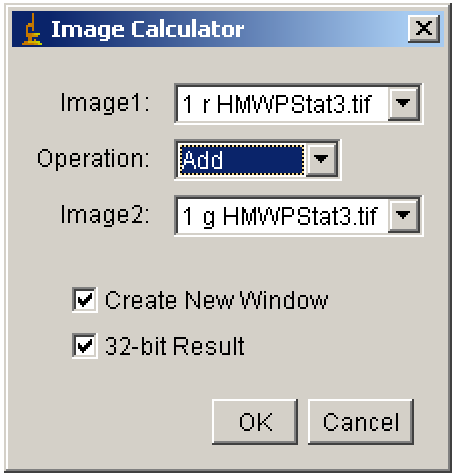


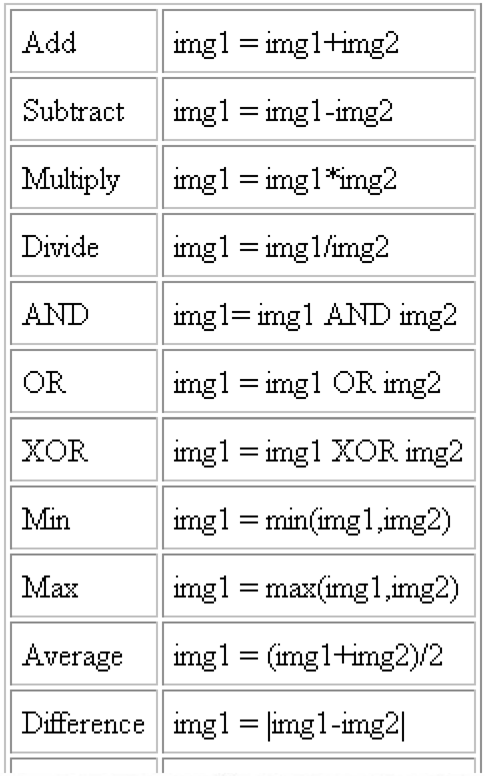
Image1: 1 r HMWPStat3.tif

Operation: Add

Image2: 1 g HMWPStat3.tif

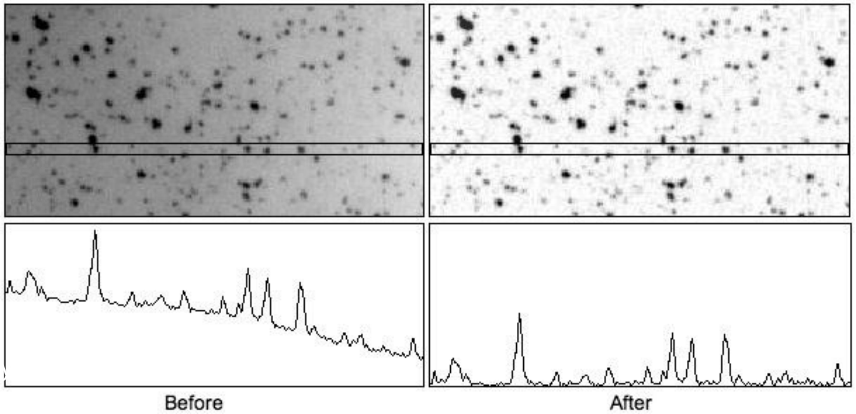
☑ Create New Window

☑ 32-bit Result

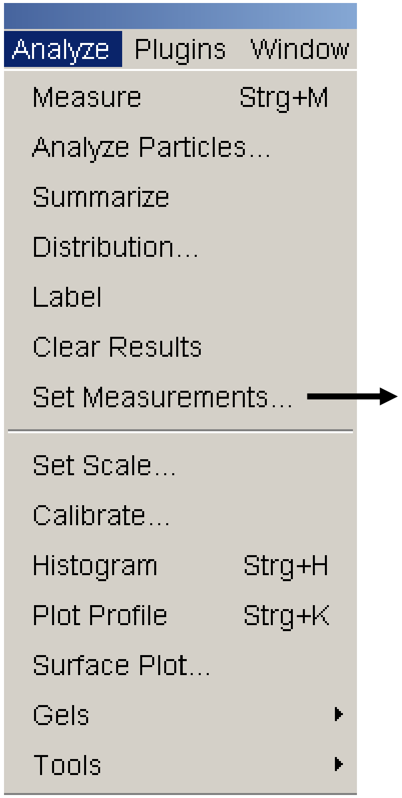


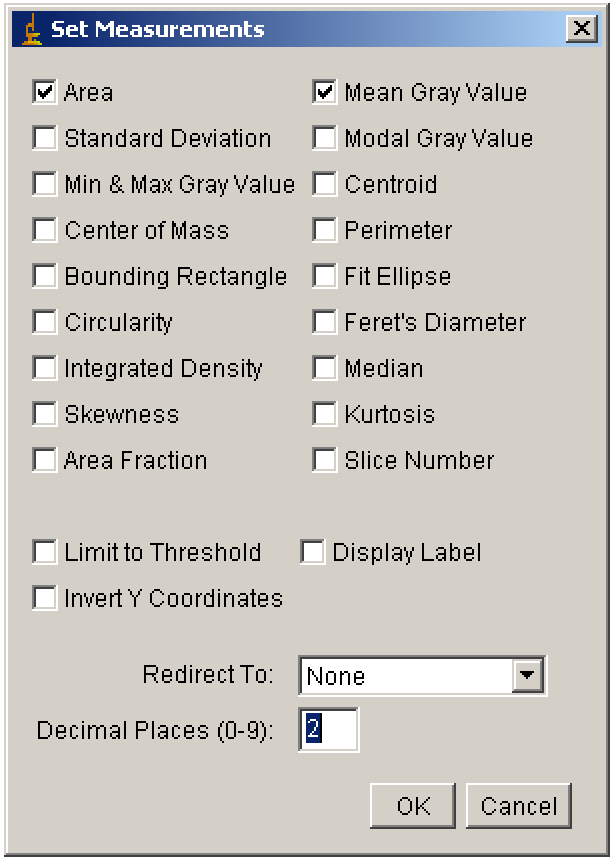
Add	img1 = img1+img2
Subtract	img1 = img1-img2
Multiply	img1 = img1*img2
Divide	img1 = img1/img2
AND	img1= img1 AND img2
OR	img1 = img1 OR img2
XOR	img1 = img1 XOR img2
Min	img1 = min(img1,img2)
Max	img1 = max(img1,img2)
Average	img1 = (img1+img2)/2
Difference	img1 = |img1-img2|

Subtract Background...(dark objects on bright background)
Removes smooth continuous backgrounds from gels and other images. Uses a rolling ball algorithm inspired by Stanley Sternberg's article, "Biomedical Image Processing", IEEE Computer, January 1983. The Rolling Ball Radius should be at least as large as the radius of the largest object in the image that is not part of the background



The Analyze Menu: Measuring





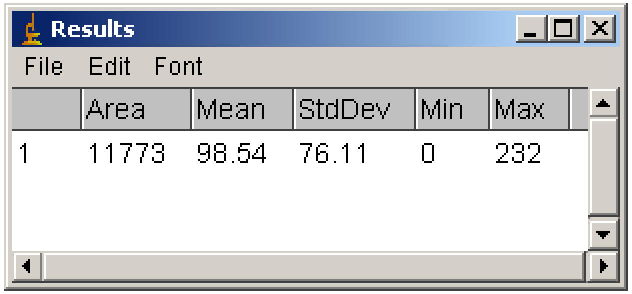
☑ Area
☑ Mean Gray Value
☐ Standard Deviation
☐ Modal Gray Value
☐ Min & Max Gray Value
☐ Centroid
☐ Center of Mass
☐ Perimeter
☐ Bounding Rectangle
☐ Fit Ellipse
☐ Circularity
☐ Feret's Diameter
☐ Integrated Density
☐ Median
☐ Skewness
☐ Kurtosis
☐ Area Fraction
☐ Slice Number

☐ Limit to Threshold
☐ Display Label
☐ Invert Y Coordinates

Redirect To: None

Decimal Places (0-9): 2

- Based on the options checked in the „Set Measurement“ menu, different values of the selected regions can be measured (by clicking „Measure“ or Strg-M)
- > a Results window is opened, showing the data – these can be copied into MS-Excel or other programs (or saved as .xls file)



	Area	Mean	StdDev	Min	Max
1	11773	98.54	76.11	0	232

Measurement Options I

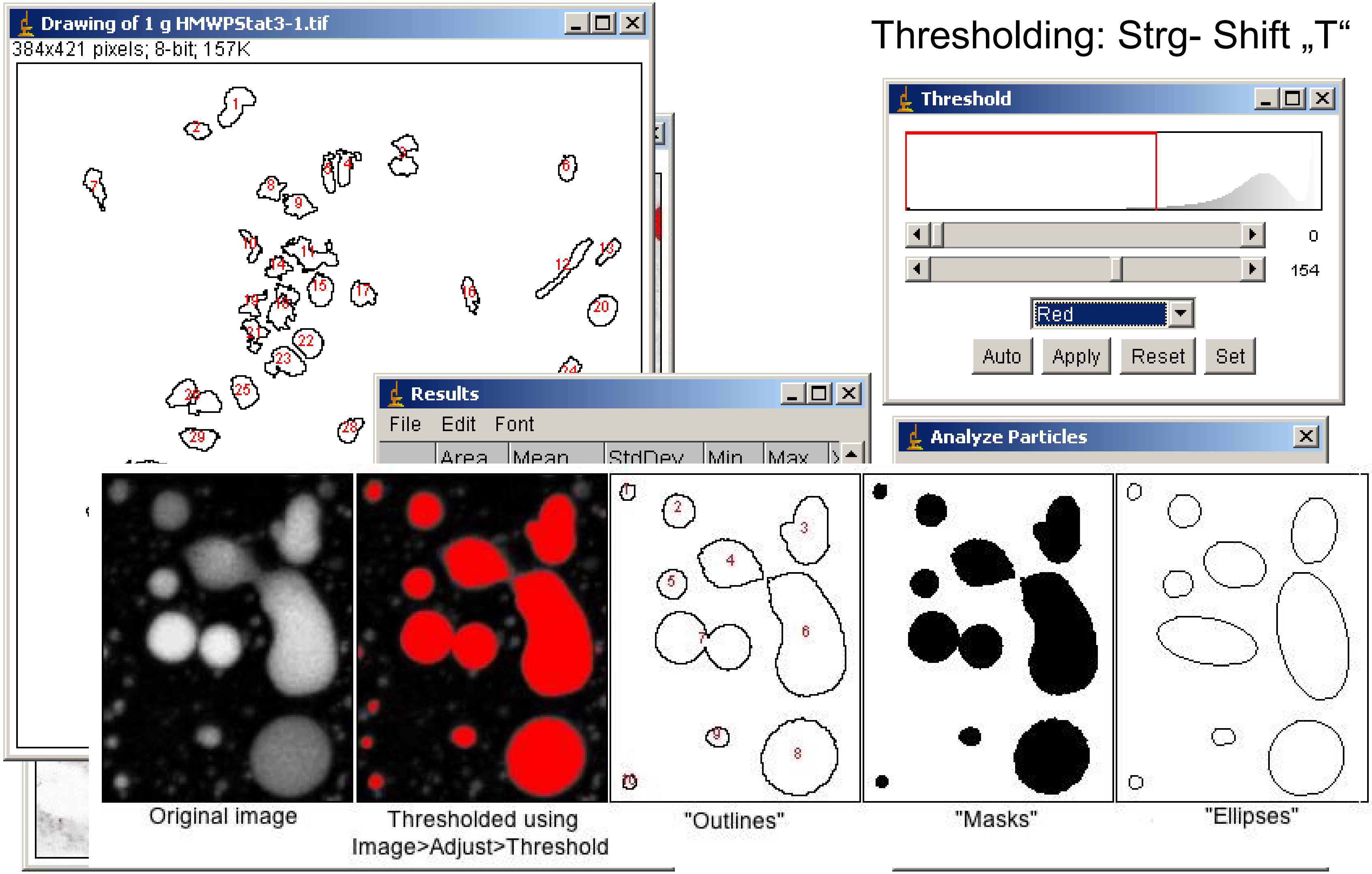
- Area - Area of selection in square pixels. Area is in calibrated units, such as square millimeters, if Analyze/Set Scale was used to spatially calibrate the image.
- Mean Gray Value - Average gray value within the selection. This is the sum of the gray values of all the pixels in the selection divided by the number of pixels. Reported in calibrated units (e.g., optical density) if Analyze/Calibrate was used to calibrate the image. For RGB images, the mean is calulated by converting each pixel to grayscale using the formula gray=0.299red+0.587green+0.114blue or the formula gray=(red+green+blue)/3 if "Unweighted RGB to Grayscale Conversion" is checked in Edit/Options/Conversions.
- Standard Deviation- Standard deviation of the gray values used to generate the mean gray value.
- Modal Gray Value - Most frequently occurring gray value within the selection. Corresponds to the highest peak in the histogram.
- Min & Max Gray Level - Minimum and maximum gray values within the selection.
- Centroid - The center point of the selection. This is the average of the x and y coordinates of all of the pixels in the image or selection. Uses the X and Y Results table headings.
- Center of Mass - This is the brightness-weighted average of the x and y coordinates all pixels in the image or selection. Uses the XM and YM headings. These coordinates are the first order spatial moments.
- Perimeter - The length of the outside boundary of the selection.
- Bounding Rectangle - The smallest rectangle enclosing the selection. Uses the headings BX, BY, Width and Height, where BX and BY are the coordinates of the upper left corner of the rectangle

Measurement Options II

- **Fit Ellipse** - Fit an ellipse to the selection. Uses the headings Major, Minor and Angle. Major and Minor are the primary and seconday axis of the best fitting ellipse. Angle is the angle between the primary axis and a line parallel to the x-axis of the image. Note that ImageJ cannot calculate the major and minor axis lengths if Pixel Aspect Ratio in the Set Scale dialog is not 1.0.
- **Circularity** - 4pi(area/perimeter^2). A value of 1.0 indicates a perfect circle. As the value approaches 0.0, it indicates an increasingly elongated polygon. Values may not be valid for very small particles.
- **Feret's Diameter** - The longest distance between any two points along the selection boundary. Also known as the caliper length. The Feret's Diameter macro will draw the Feret's Diameter of the current selection on the image.
- **Integrated Density** - The sum of the values of the pixels in the image or selection. This is equavalent to the product of Area and Mean Gray Value.
- **Median**- The median value of the pixels in the image or selection.
- **Skewness**- The third order moment about the mean.
- **Kurtosis**- The fourth order moment about the mean.
- **Area Fraction**- The percentage of pixels in the image or selection that have been highlighted in red using Image/Adjust/Threshold. For non-thresholded images, the percentage of non-zero pixels.
- **Limit to Threshold** - If checked, only thresholded pixels are included in measurement calculations. Use Image/Adjust/Threshold to set the threshold limits.
- Display Label - If checked, the image name and slice number (for stacks) are recoded in the first column of the results table.
- Invert Y Coordinates - If checked, the XY origin is assumed to be the lower left corner of the image window instead of the upper left corner.
- Redirect To - The image selected from this popup menu will be used as the target for statistical calculations done by the Measure and Analyze Particles commands. The Redirect To feature allows you to outline a structure on one image and measure the intensity of the corresponding region in another image. With ImageJ 1.35d or later this feature also works with stacks.
- **Decimal Places** - This is the number of digits to the right of the decimal point in real numbers displayed in the results table and in histogram windows

Analyze Particles (or objects of interest)

Thresholding: Strg- Shift „T“



Original image

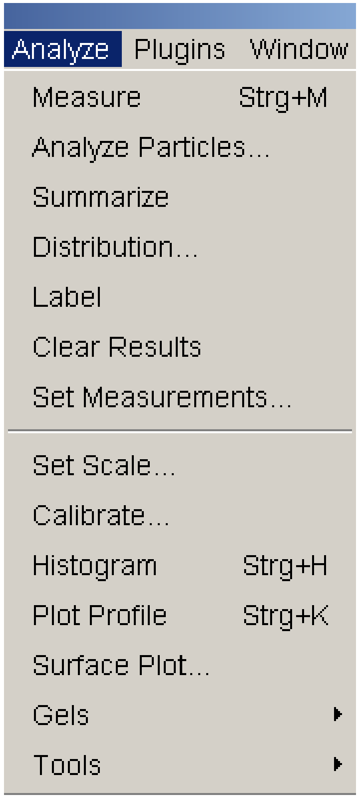
Thresholded using Image>Adjust>Threshold

"Outlines"

"Masks"

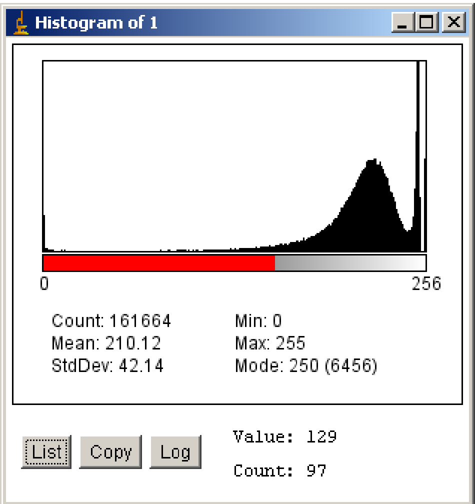
"Ellipses"

Additional Analyze Options



- Summarize: For each column in the results table, calculates and displays the mean, standard deviation, minimum and maximum of the values in that column
- Distribution: Calculates a binary distribution (histogram) for a list of results
- Label: labels the analyzed objects in the image ("Centroid" option has to be checked in "Set Measurements" options)

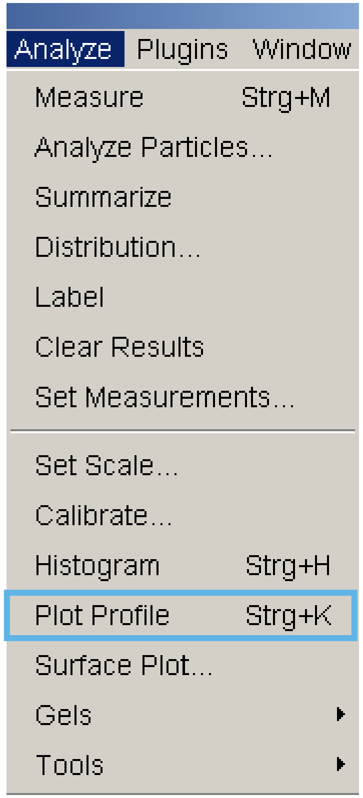
- Set Scale: Can be used to convert a distance in pixel (specified with the line tool) into a known distance in *mm* or similar
- Calibrate: Can be used to calibrate an image to a set of density standards, for example radioactive isotope standards
- Histogram: Calculates and displays a histogram of the distribution of gray values in the active image or selection



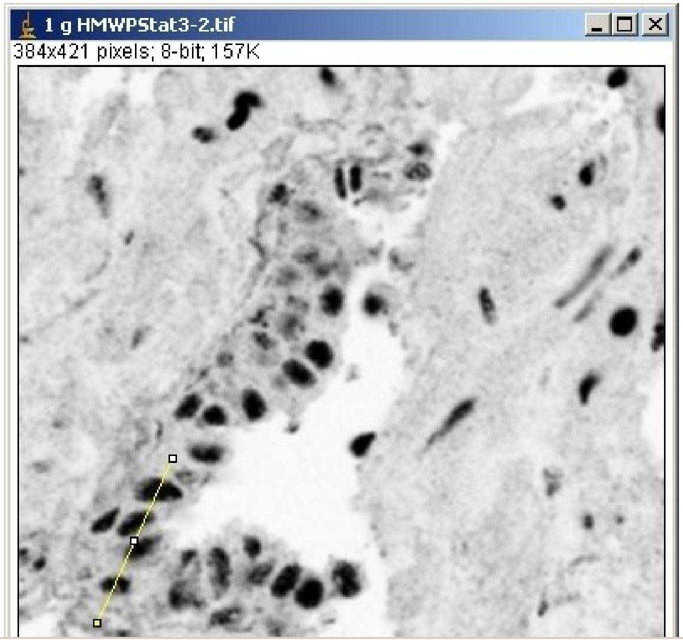
Count: 161664
Mean: 210.12
StdDev: 42.14
Min: 0
Max: 255
Mode: 250 (6456)

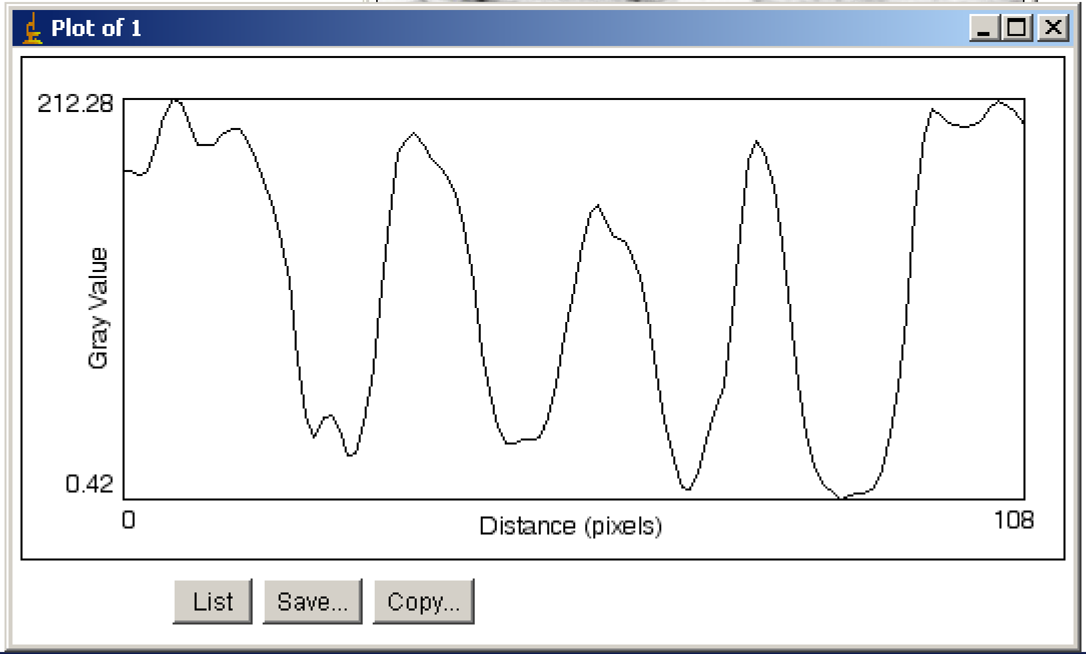
Value: 129
Count: 97

Plot Profiles

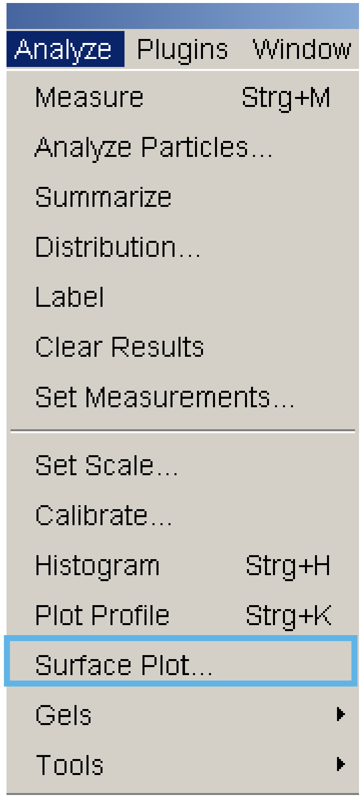


- Plot Profile: For each column in the results table, calculates and displays the mean, standard deviation, minimum and maximum of the values in that column

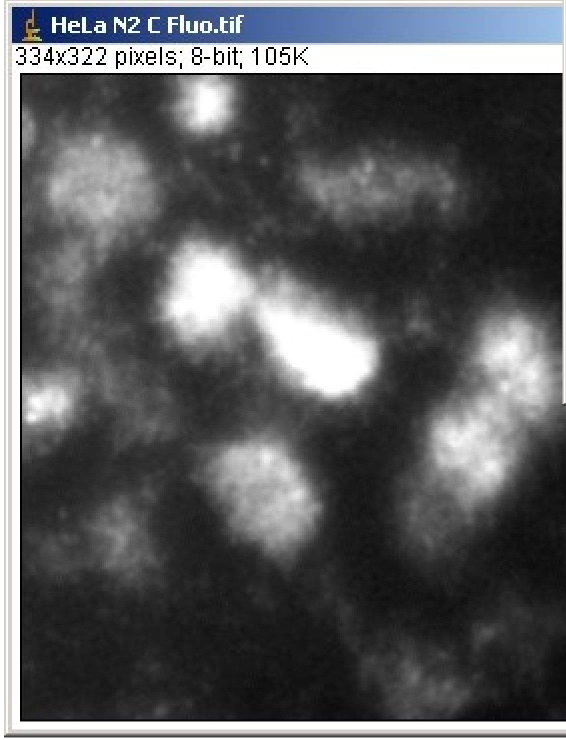


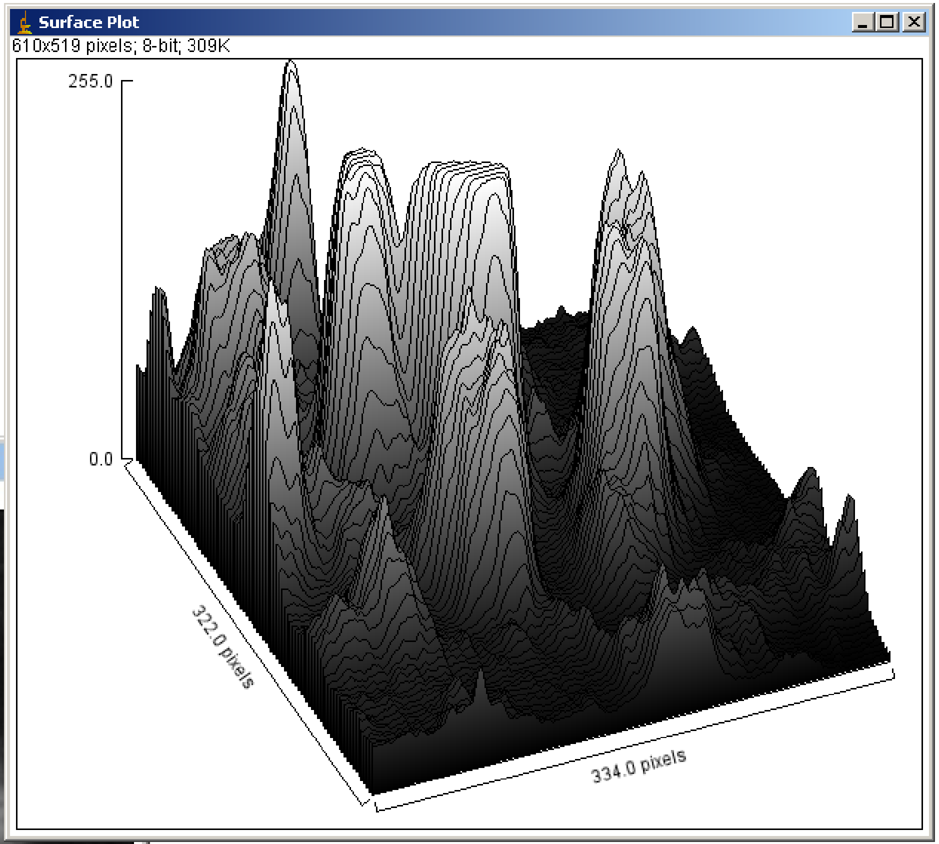


Surface Plots

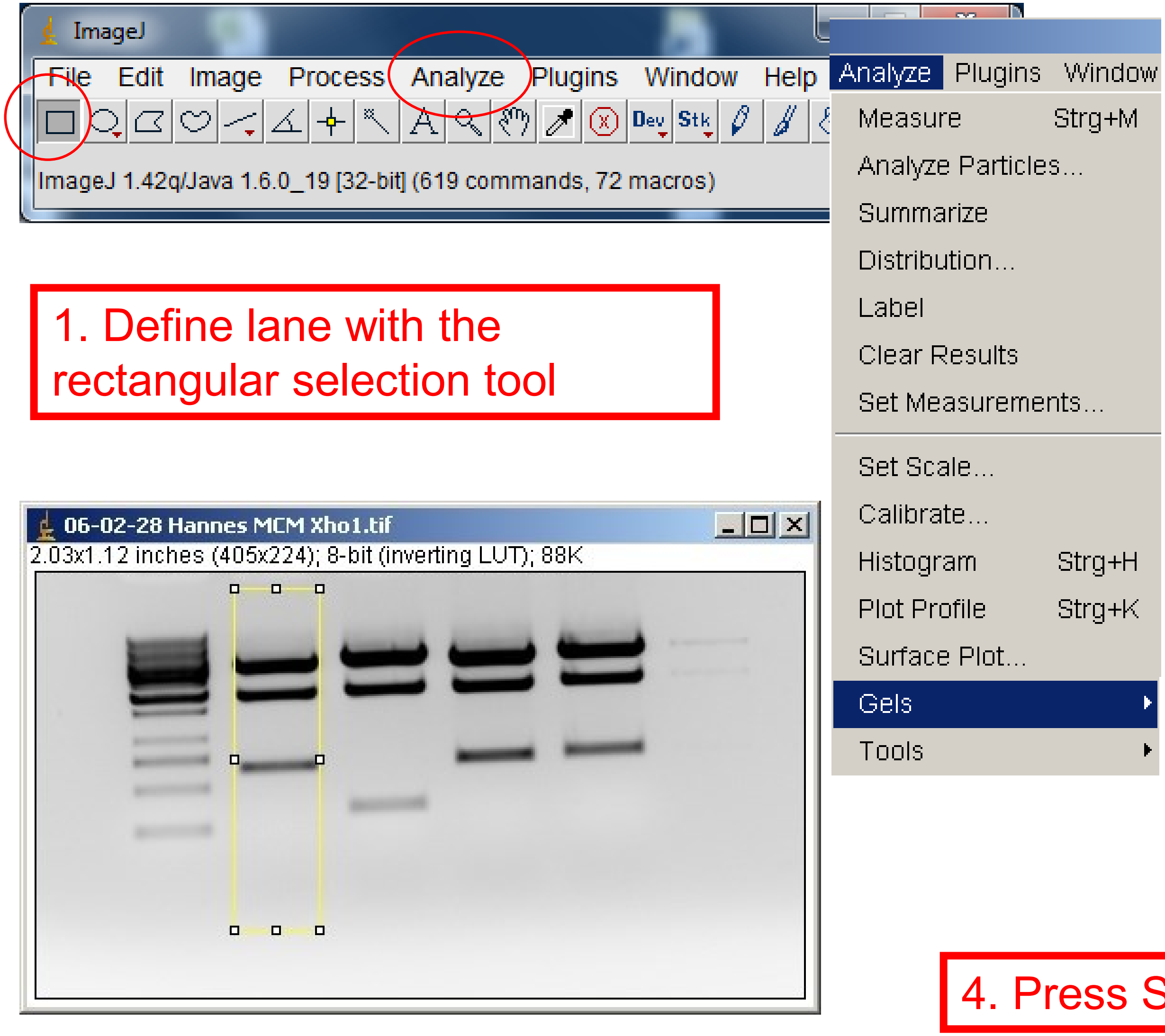


- **Surface Plot**: Displays a three-dimensional graph of the intensities of pixels in a grayscale or pseudo color image





Analyzing Gels

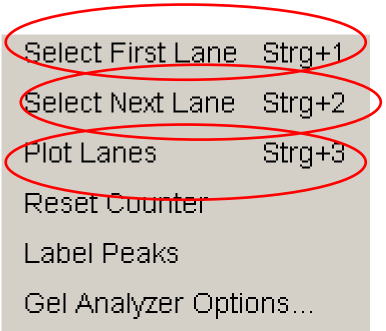


ImageJ 1.42q/Java 1.6.0_19 [32-bit] (619 commands, 72 macros)

2.03x1.12 inches (405x224); 8-bit (inverting LUT); 88K

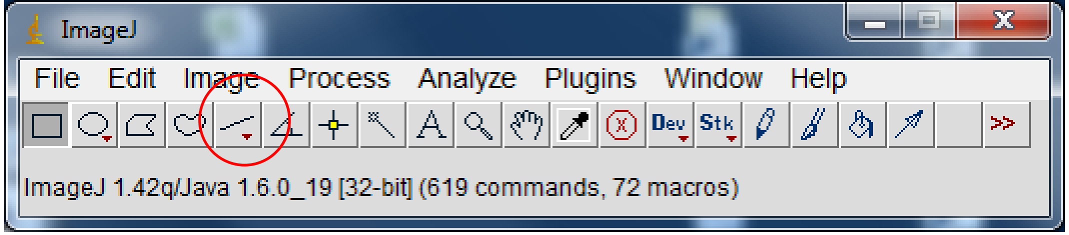
1. Define lane with the rectangular selection tool

2. Press Strg+1 (or menu: analyze > Gels > select first lane)



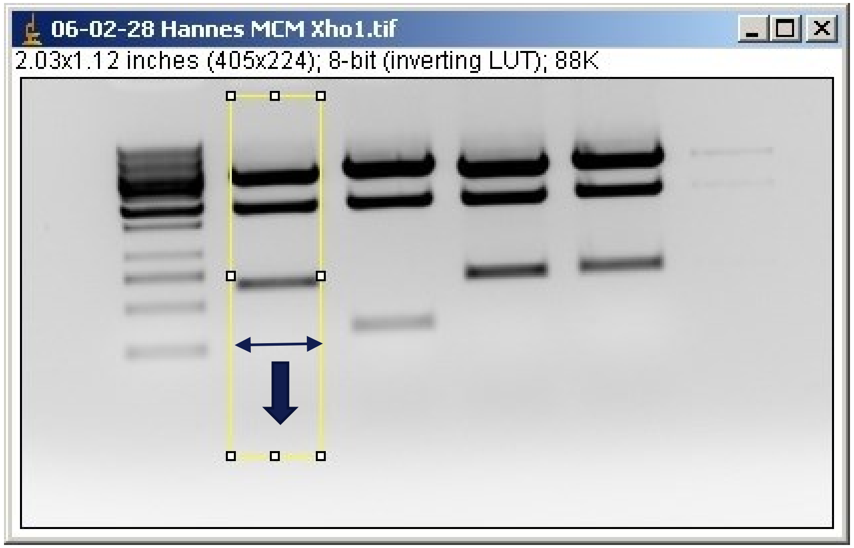
3. Move the rectangle over the second lane and press Strg.+2; Repeat that for all lanes

4. Press Strg.+3 to plot the profiles

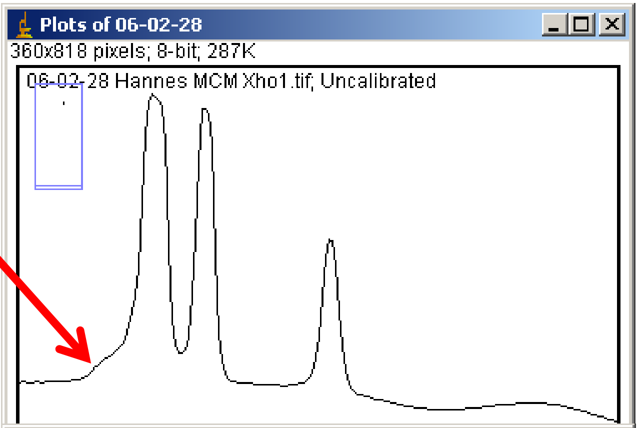


ImageJ 1.42q/Java 1.6.0_19 [32-bit] (619 commands, 72 macros)

5. Use the line tool to define the background line

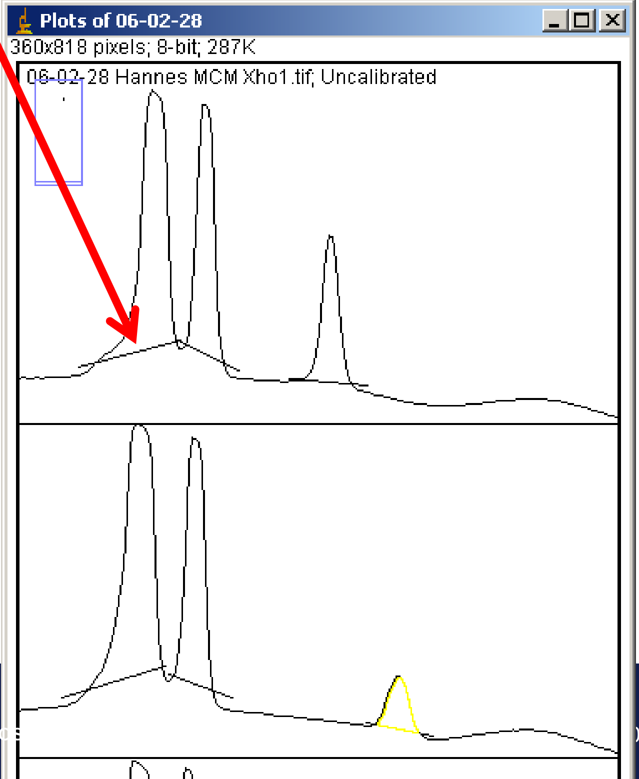


2.03x1.12 inches (405x224); 8-bit (inverting LUT); 88K



360x818 pixels; 8-bit; 287K

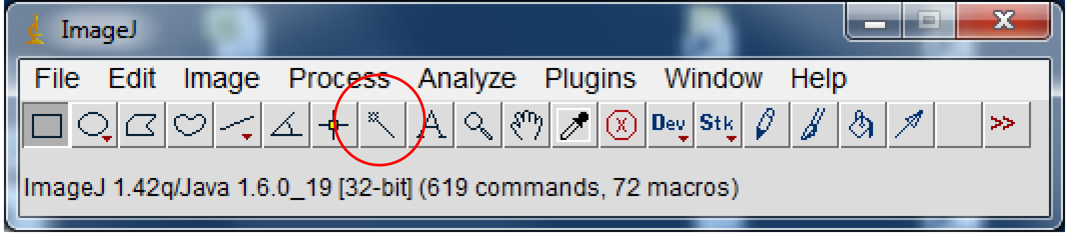
06-02-28 Hannes MCM Xho1.tif, Uncalibrated



360x818 pixels; 8-bit; 287K

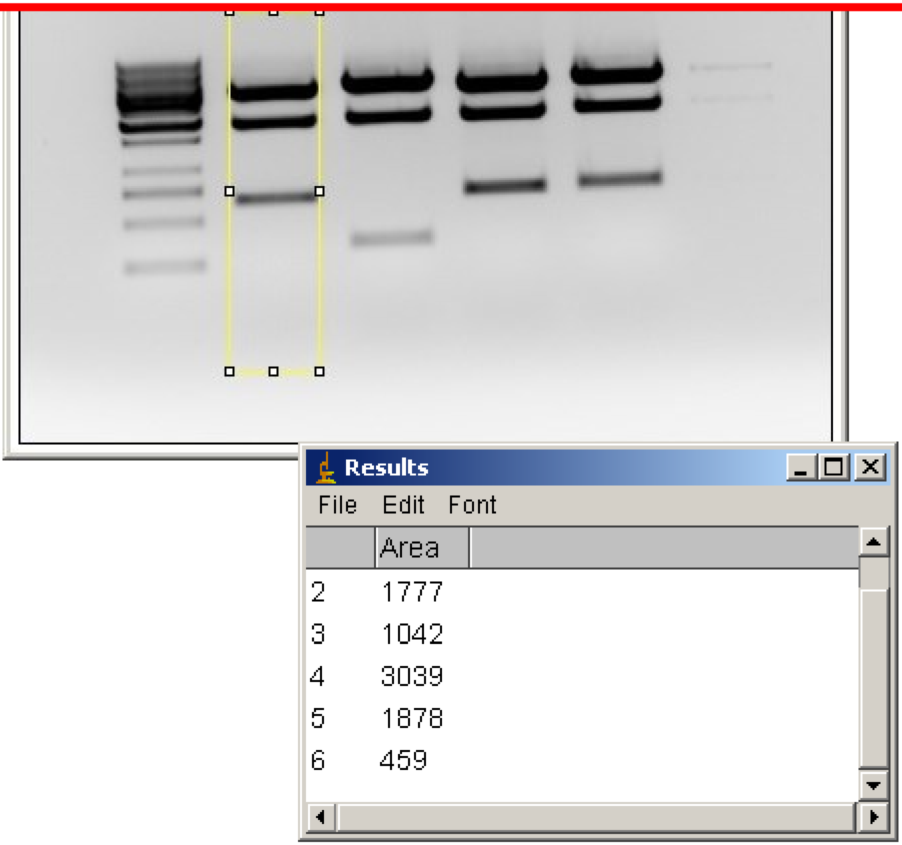
06-02-28 Hannes MCM Xho1.tif, Uncalibrated

The average intensity is calculated over the lane width and that value is plotted over the lane length > usually a Gauss-like curve with the peak in the center of the band.

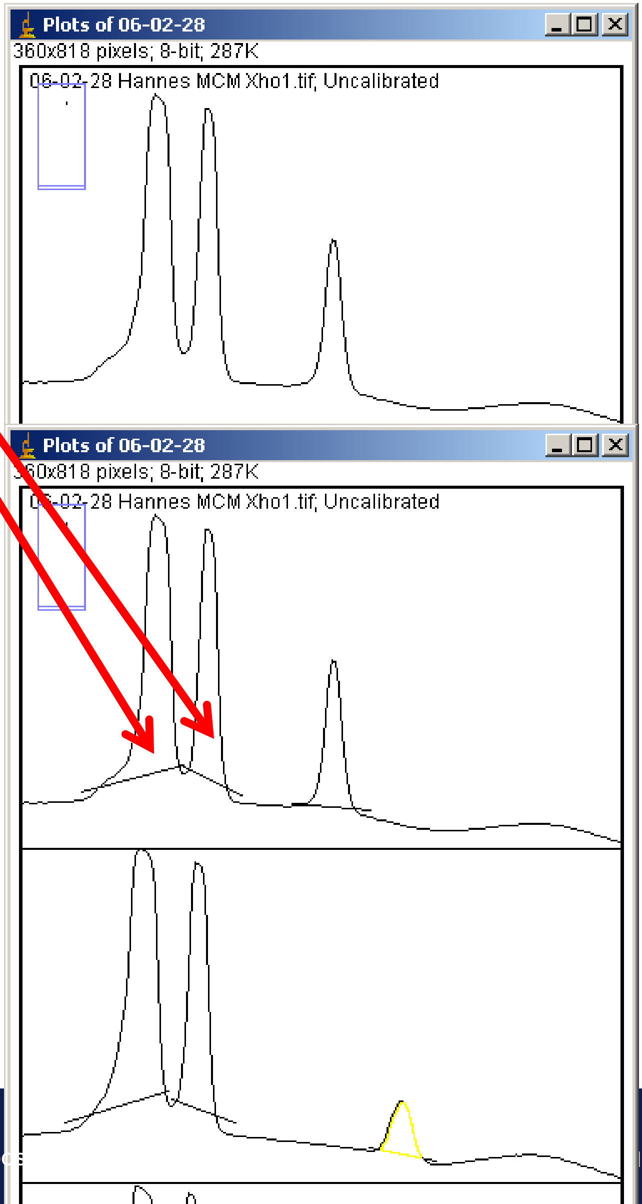


ImageJ 1.42q/Java 1.6.0_19 [32-bit] (619 commands, 72 macros)

6. Click the magic stick tool and click on the different peaks > this generates a result window with the peak areas = quantification.



	Area
2	1777
3	1042
4	3039
5	1878
6	459



Method 1

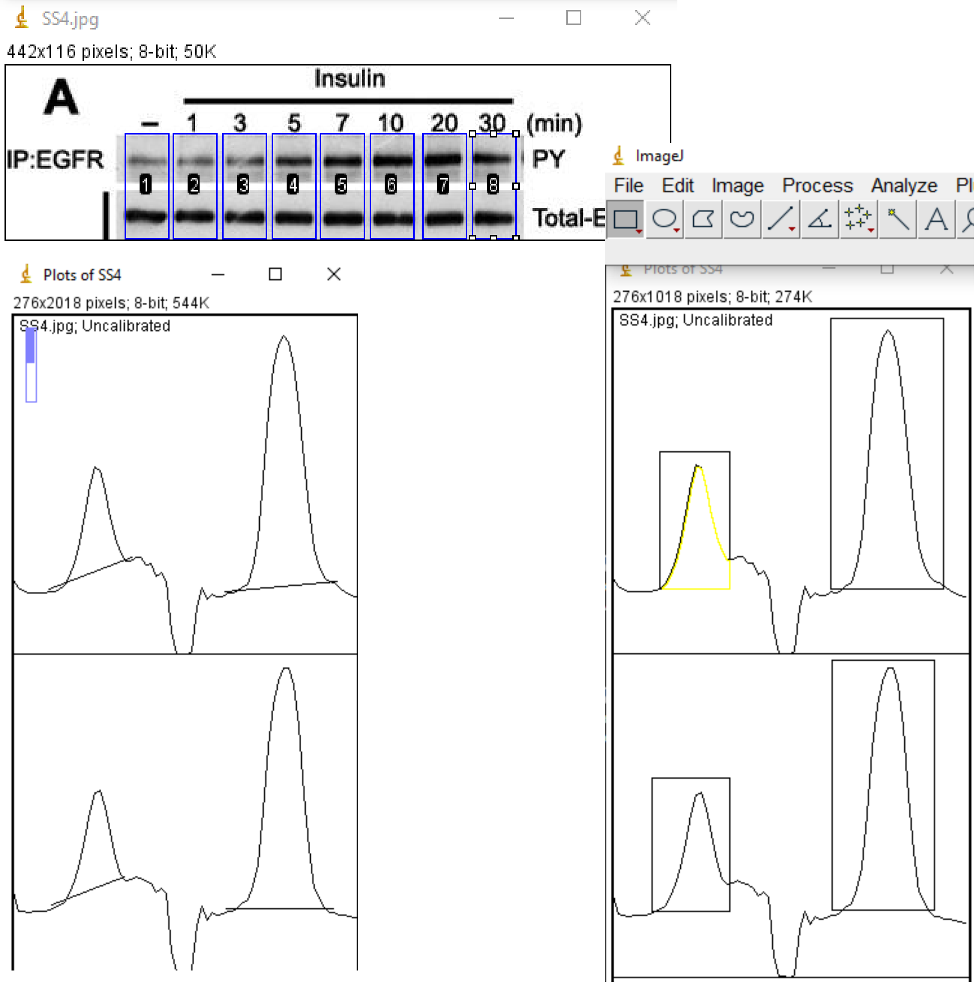
(line background connecting “valleys”)

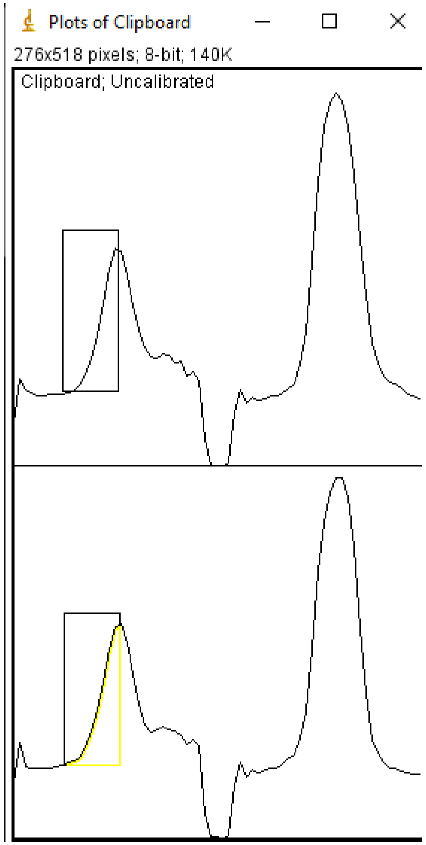
Method 2

(rectangle + draw Ctrl+D better quantification)

Method 3

(rectangle over the half of the peak, which goes down to the correct background + draw Ctrl+D > measure area with the magic stick > multiply by 2: best quantification of the band)



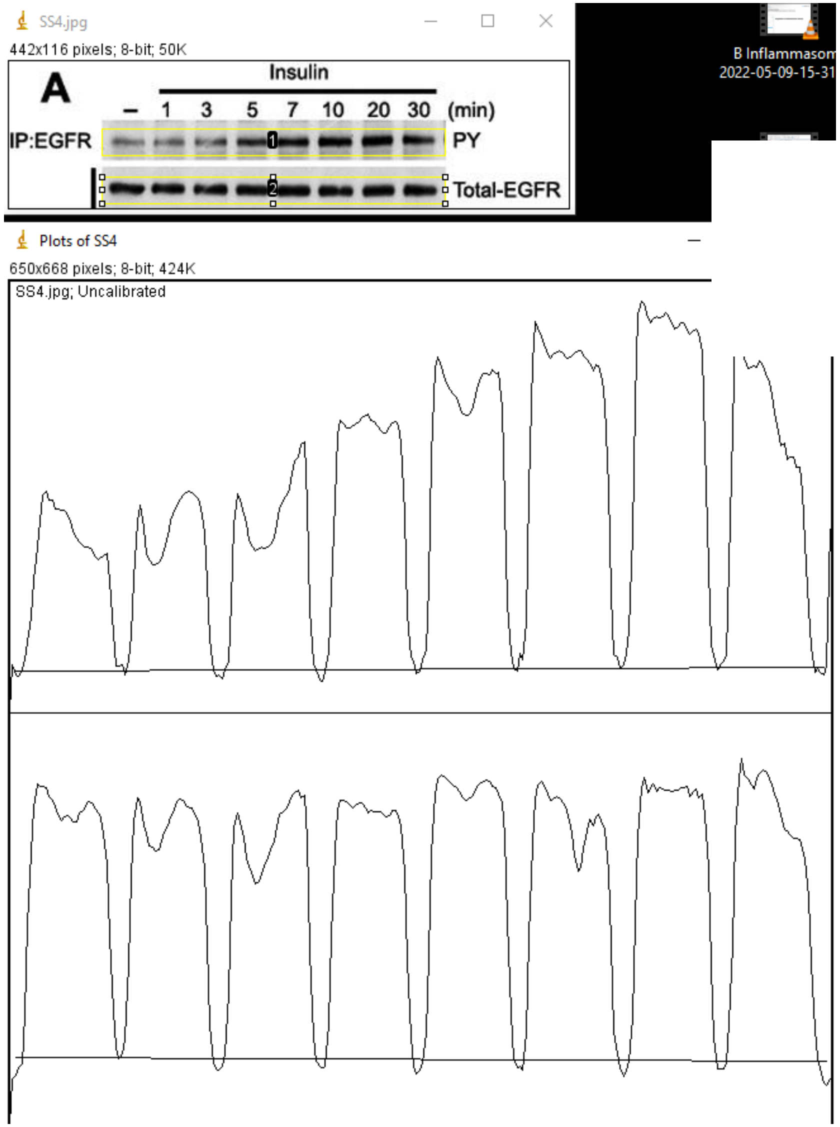


(correct averaging of the intensities over the lane width > peaks)

Method 4

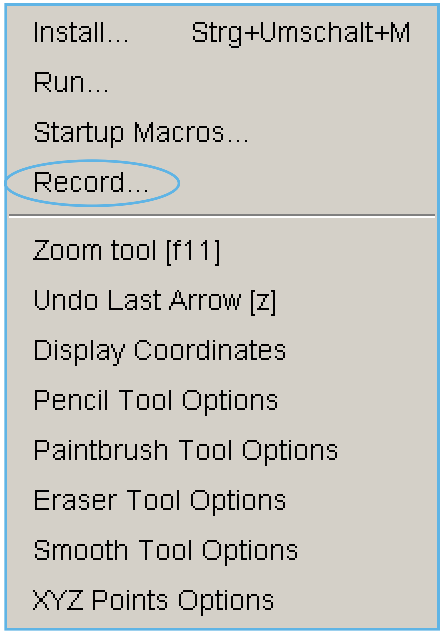
(horizontal measurement lane,
fast method, but not completely correct,
quantification still quite good)

(averaging perpendicular to the lane
> not showing proper peaks, but the
lateral heterogeneity of the bands)



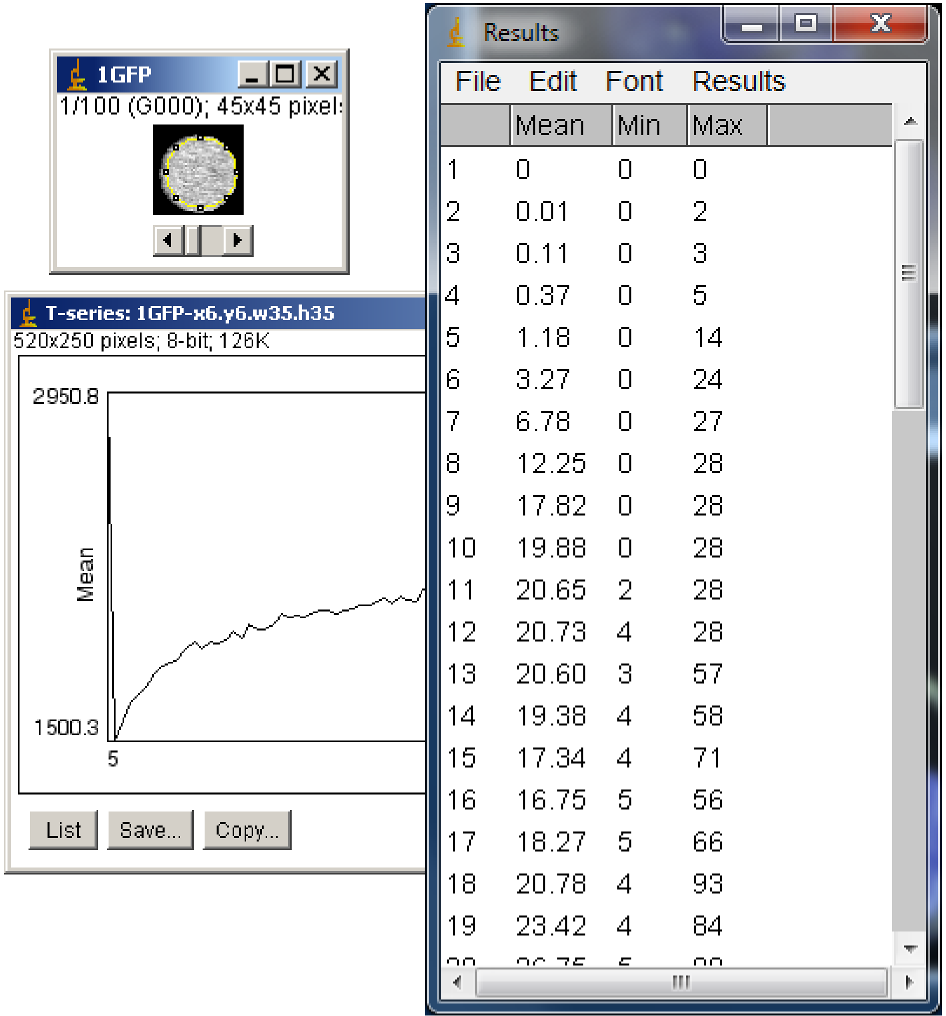
The Plugins Menu

- Many freely available plugins can be loaded into ImageJ, which appear in this menu
  for a list see:
  http://rsb.info.nih.gov/ij/plugins/index.html



- Macros can be recorded to automatize frequently used commands

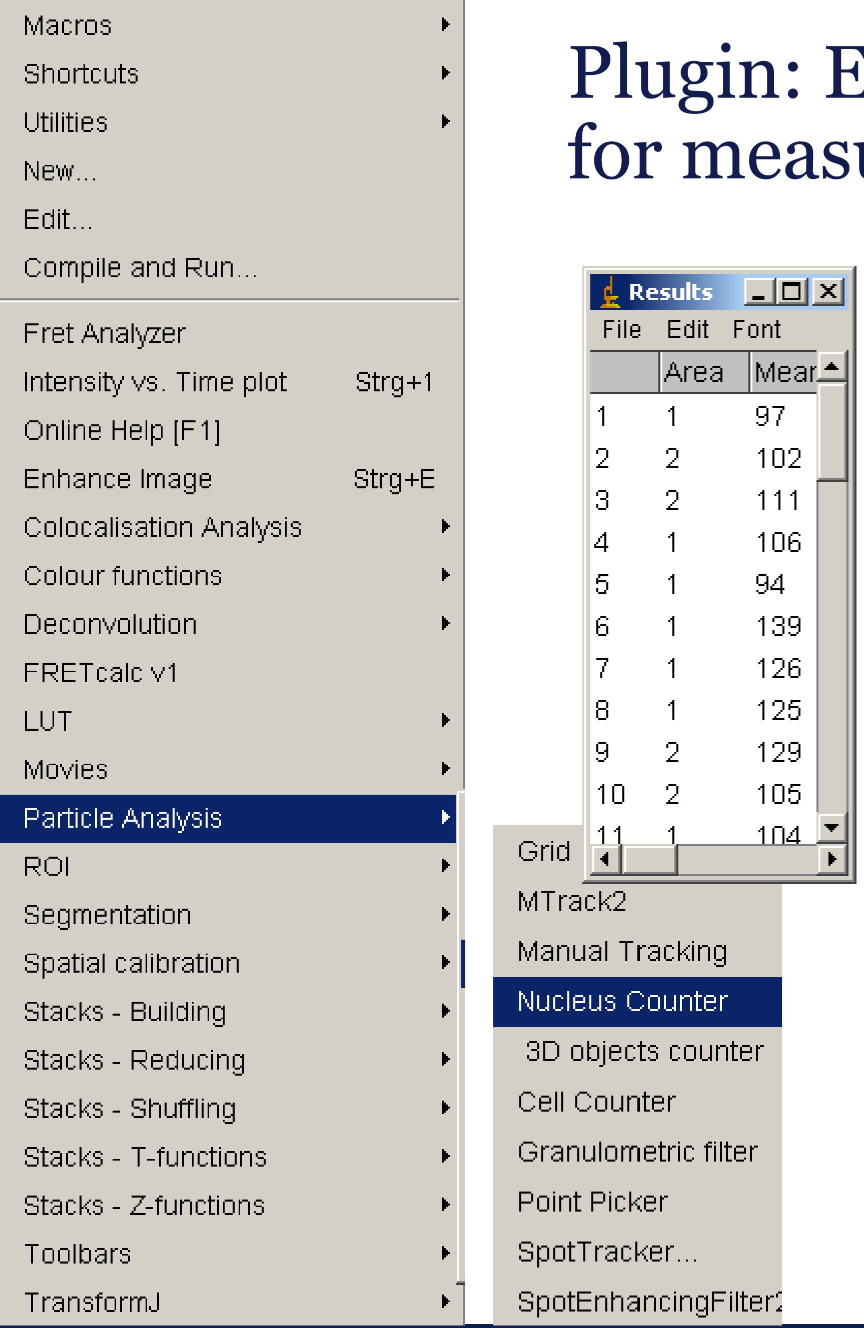
Plugin Example: FRAP Analysis by Intensity vs. Time Plot or Plugin: Stacks > measure stack



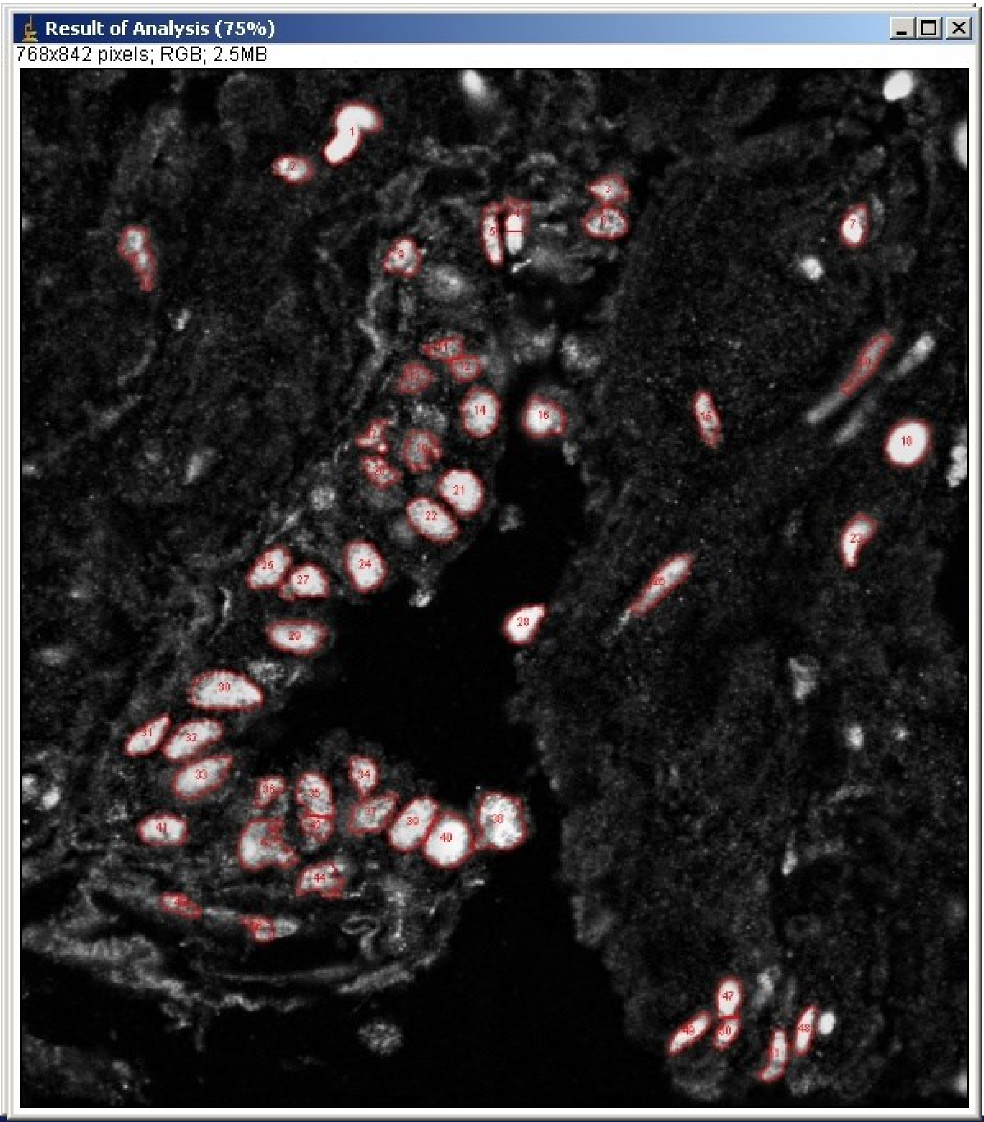
	Mean	Min	Max
1	0	0	0
2	0.01	0	2
3	0.11	0	3
4	0.37	0	5
5	1.18	0	14
6	3.27	0	24
7	6.78	0	27
8	12.25	0	28
9	17.82	0	28
10	19.88	0	28
11	20.65	2	28
12	20.73	4	28
13	20.60	3	57
14	19.38	4	58
15	17.34	4	71
16	16.75	5	56
17	18.27	5	66
18	20.78	4	93
19	23.42	4	84

- Images recorded with LSM510: time stack of bleached area
- circle selected for quantification
- click Strg.1 (Intensity vs. Time Plot) in the Plugin menu > graph appears
- Click „List“ in the graph > List of results appears
- The results can be copied into MS-Excel > into curve fitting software (e.g. Graphpad Prism)

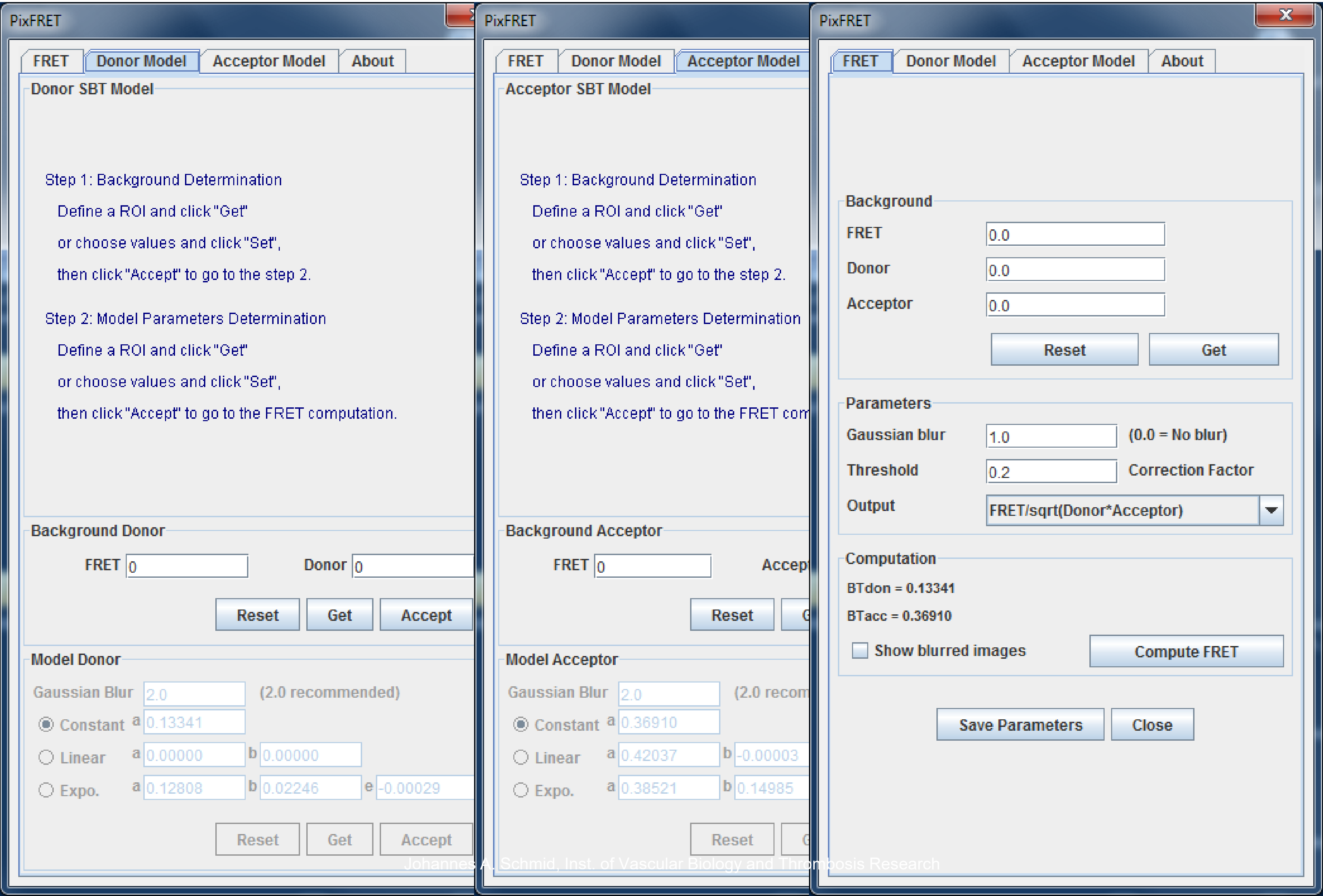
Plugin: Example 2: Nucleus Counter for measuring multiple cells



	Area	Mear
1	1	97
2	2	102
3	2	111
4	1	106
5	1	94
6	1	139
7	1	126
8	1	125
9	2	129
10	2	105
11	1	104



Example 3: FRET analysis with PixFRET



Donor SBT Model

Step 1: Background Determination

Define a ROI and click "Get"

or choose values and click "Set",

then click "Accept" to go to the step 2.

Step 2: Model Parameters Determination

Define a ROI and click "Get"

or choose values and click "Set",

then click "Accept" to go to the FRET computation.

Background Donor

FRET 0 Donor 0

Model Donor

Gaussian Blur 2.0 (2.0 recommended)

● Constant a 0.13341

○ Linear a 0.00000 b 0.00000

○ Expo. a 0.12808 b 0.02246 e -0.00029

Acceptor SBT Model

Step 1: Background Determination

Define a ROI and click "Get"

or choose values and click "Set",

then click "Accept" to go to the step 2.

Step 2: Model Parameters Determination

Define a ROI and click "Get"

or choose values and click "Set",

then click "Accept" to go to the FRET com

Background Acceptor

FRET 0 Accep

Model Acceptor

Gaussian Blur 2.0 (2.0 recom

● Constant a 0.36910

○ Linear a 0.42037 b -0.00003

○ Expo. a 0.38521 b 0.14985

Background

FRET 0.0

Donor 0.0

Acceptor 0.0

Parameters

Gaussian blur 1.0 (0.0 = No blur)

Threshold 0.2 Correction Factor

Output FRET/sqrt(Donor*Acceptor)

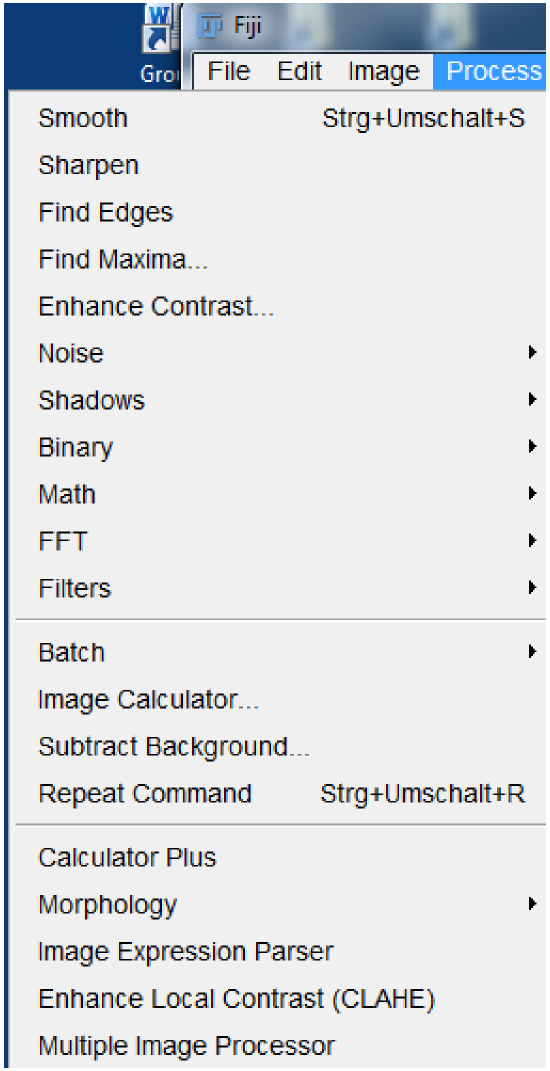
Computation

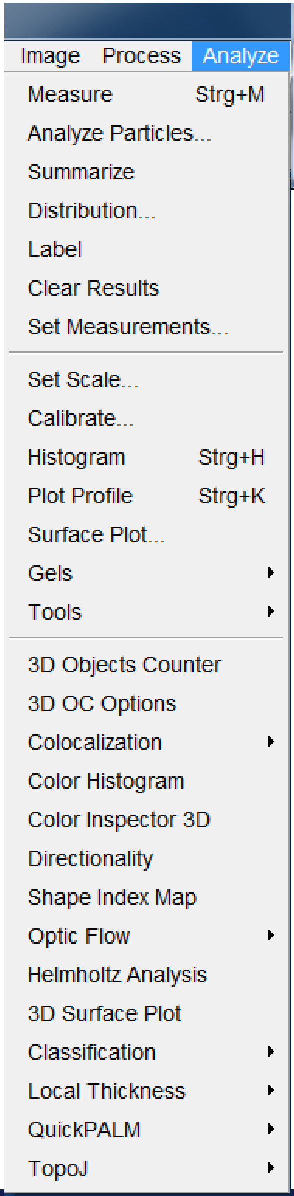
BTdon = 0.13341

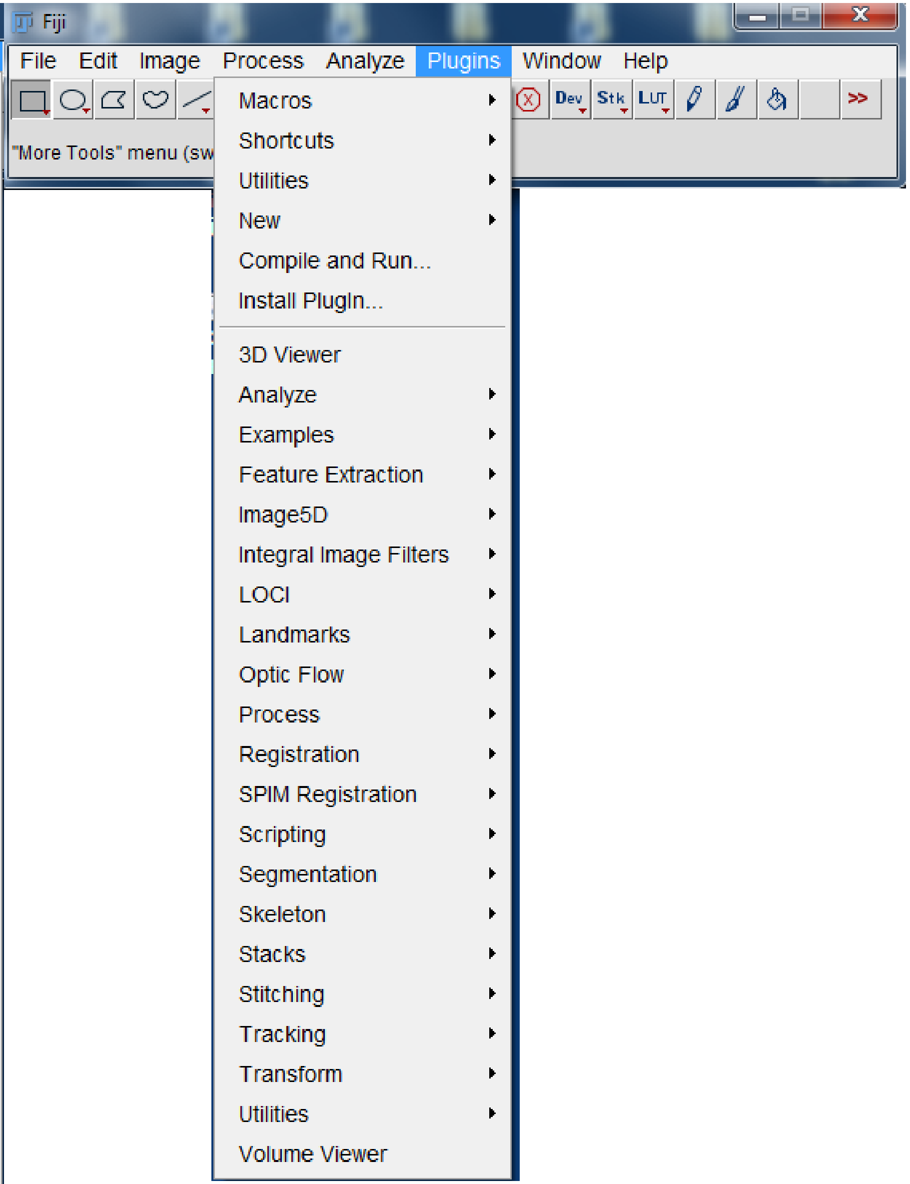
BTacc = 0.36910

☐ Show blurred images

Fiji: „Fiji Is Just ImageJ“







Task 3a (curve fitting)

1. Download CurveExpert Pro from https://www.curveexpert.net/
2. Download data from here: https://www.meduniwien.ac.at/user/johannes.schmid/2023Task3a.xlsx and copy days (as x) and accumulated cases (as y) into CurveExpert
3. Search for the best equations using the Curve finder tool (checking only the built-in non-linear regressions)
4. Choose the result with the highest score and check the equation by double clicking on this result.
5. In the original Excel file: Define the variables of this equation (with name manager); type in the correct equation and perform a curve fit in Excel using the Solver function and minimizing the sum of residuals squared
6. Type the expected number of accumulated cases at day 100 into the online text field of the task – and upload your Excel file

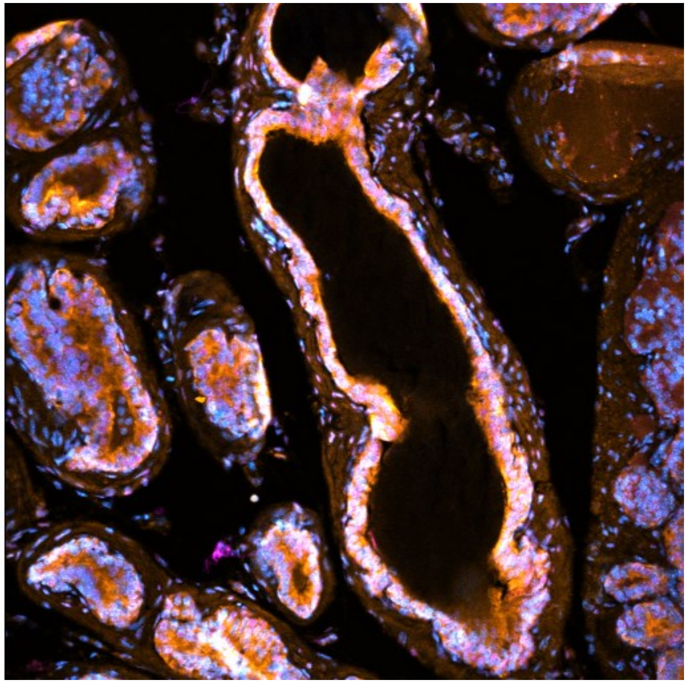
Task 3b Professional graphs with R-ggplot2

- Download and install R
- Download and install R-Studio
- Download the Excel file pathwaysR.xlsx
- Create a ggplot2 bubble graph with pathway names on y-axis, neglogp on x-axis, color gradient of bubbles defined by zscore (with positive in red, zero=white and negative in blue) and size of bubble=Ratio)

Example Macro for ImageJ

- Record macro to define nuclei via the DAPI channel and measure fluorescence of the nuclei in another channel for a composite image

```
rename("test.tif");
run("Split Channels");
selectWindow("C1-test.tif");
setAutoThreshold("Default dark no-reset");
//run("Threshold...");
setOption("BlackBackground", false);
run("Convert to Mask");
run("Watershed");
setAutoThreshold("Default no-reset");
run("Analyze Particles...", "size=10 pixel show=Outlines
display exclude clear include summarize add");
selectWindow("C2-test.tif");
selectWindow("ROI Manager");
roiManager("Measure");
selectWindow("Results");
```



CellProfiler

www.cellprofiler.org

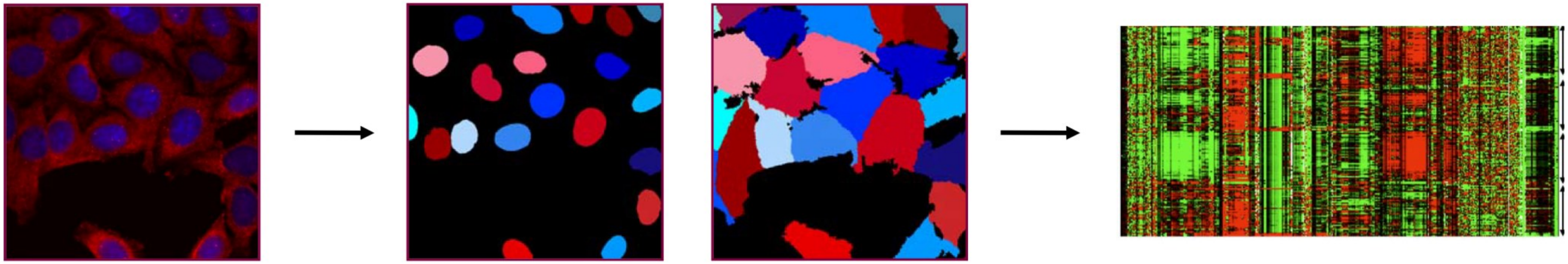
CellProfiler™
cell image analysis software

Image Analysis & Quantification

CellProfiler™ Analyst
data exploration software

Image-centric Data Analysis

- **Process** large sets of images
- **Identifies and measures** objects
- **Export** data for further analysis



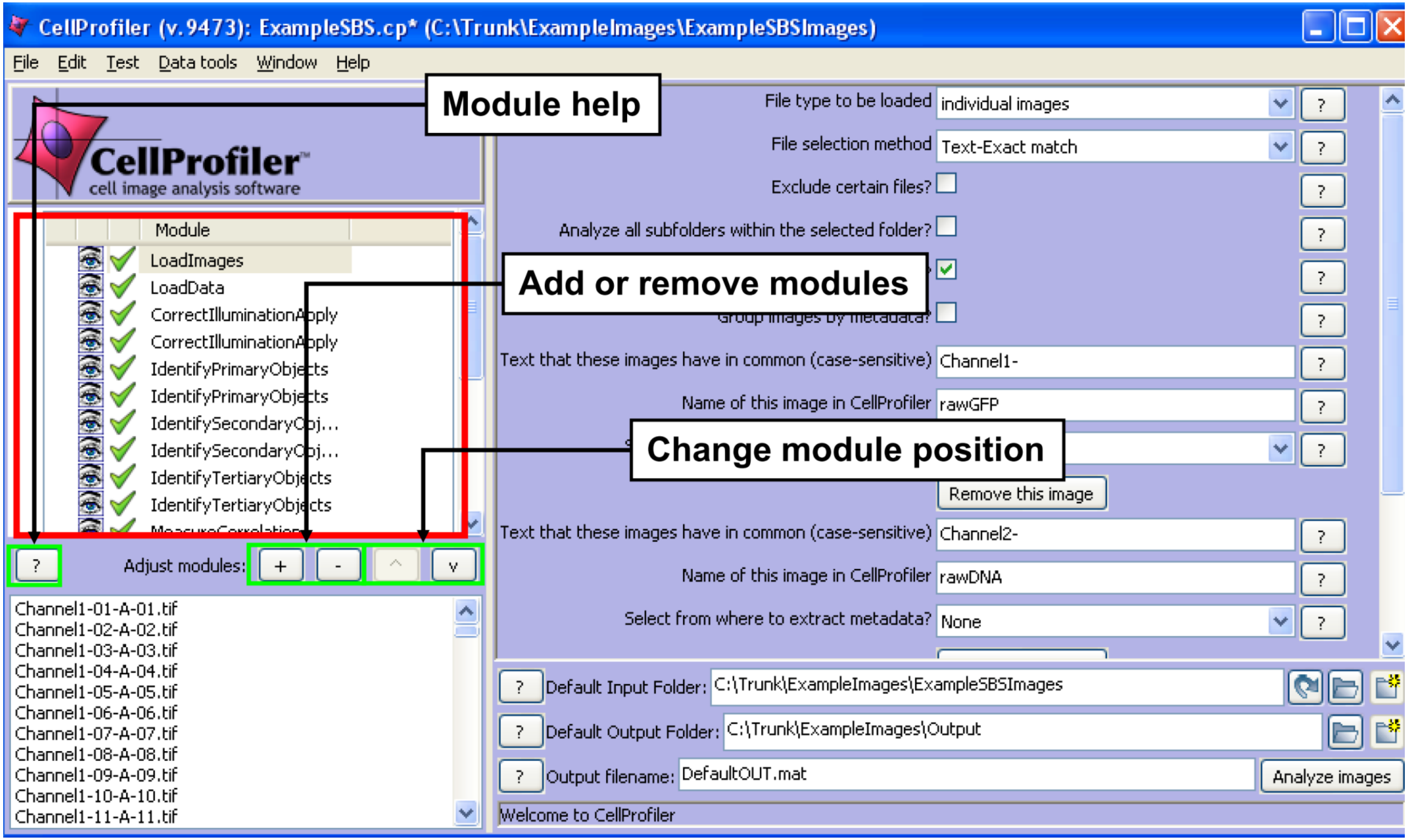
CellProfiler - Basics

Establish a „Pipeline“ of a predefined workflow:

- **Load images**: based on parts of the file name…
- **Improve images** if necessary (brightness, contrast, background subtraction…)
- **Identify objects** (primary, secondary, tertiary objects)
- **Measure** object features (mean intensity, shape factors: diameter, perimeter…)
- **Visualize data** (e.g. density plots…)
- **Export** data (database format, Excel-csv-format)

  – *Pipeline:* Steps of image processing in CellProfiler
  – *Module:* One step of a pipeline
  – *Primary Objects:* Key objects used to identify cells
  – *Secondary Objects:* Other parts of cells, attached to primary objects

CellProfiler-Interface



CellProfiler (v.9473): ExampleSBS.cp* (C:\Trunk\ExampleImages\ExampleSBSImages)

Module help

Add or remove modules

Change module position

Module
- LoadImages
- LoadData
- CorrectIlluminationApply
- CorrectIlluminationApply
- IdentifyPrimaryObjects
- IdentifyPrimaryObjects
- IdentifySecondaryObj...
- IdentifySecondaryObj...
- IdentifyTertiaryObjects
- IdentifyTertiaryObjects
- MeasureCorrelation

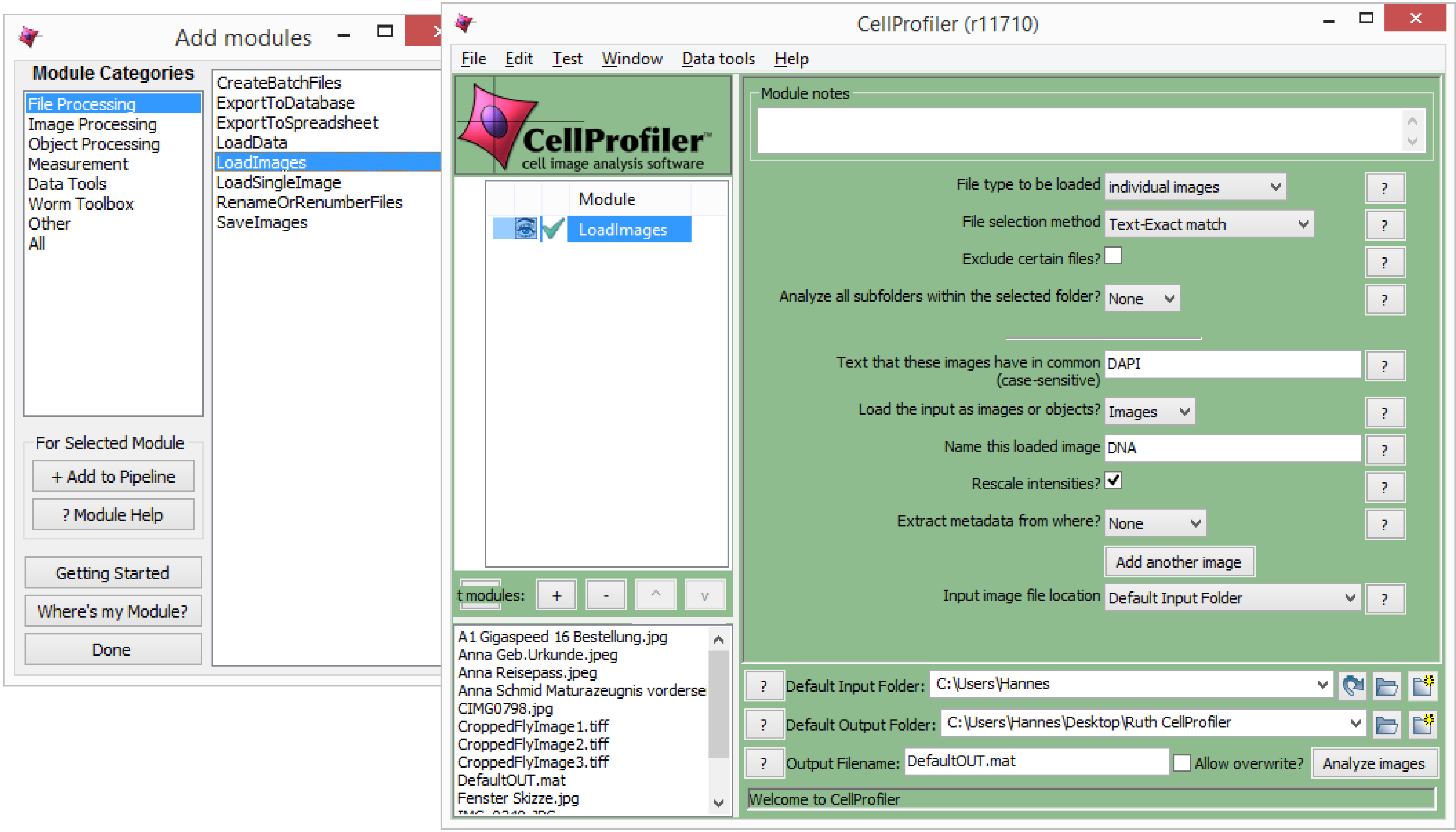
Channel1-01-A-01.tif
Channel1-02-A-02.tif
Channel1-03-A-03.tif
Channel1-04-A-04.tif
Channel1-05-A-05.tif
Channel1-06-A-06.tif
Channel1-07-A-07.tif
Channel1-08-A-08.tif
Channel1-09-A-09.tif
Channel1-10-A-10.tif
Channel1-11-A-11.tif

File type to be loaded: individual images
File selection method: Text-Exact match
Exclude certain files? ☐
Analyze all subfolders within the selected folder? ☐
☑
Group images by metadata? ☐
Text that these images have in common (case-sensitive): Channel1-
Name of this image in CellProfiler: rawGFP
Remove this image
Text that these images have in common (case-sensitive): Channel2-
Name of this image in CellProfiler: rawDNA
Select from where to extract metadata? None

Default Input Folder: C:\Trunk\ExampleImages\ExampleSBSImages
Default Output Folder: C:\Trunk\ExampleImages\Output
Output filename: DefaultOUT.mat

Welcome to CellProfiler

Module: Loading of Images



File type to be loaded: individual images

File selection method: Text-Exact match

Exclude certain files? ☐

Analyze all subfolders within the selected folder? None

Text that these images have in common (case-sensitive): DAPI

Load the input as images or objects? Images

Name this loaded image: DNA

Rescale intensities? ☑

Extract metadata from where? None

Input image file location: Default Input Folder

Default Input Folder: C:\Users\Hannes

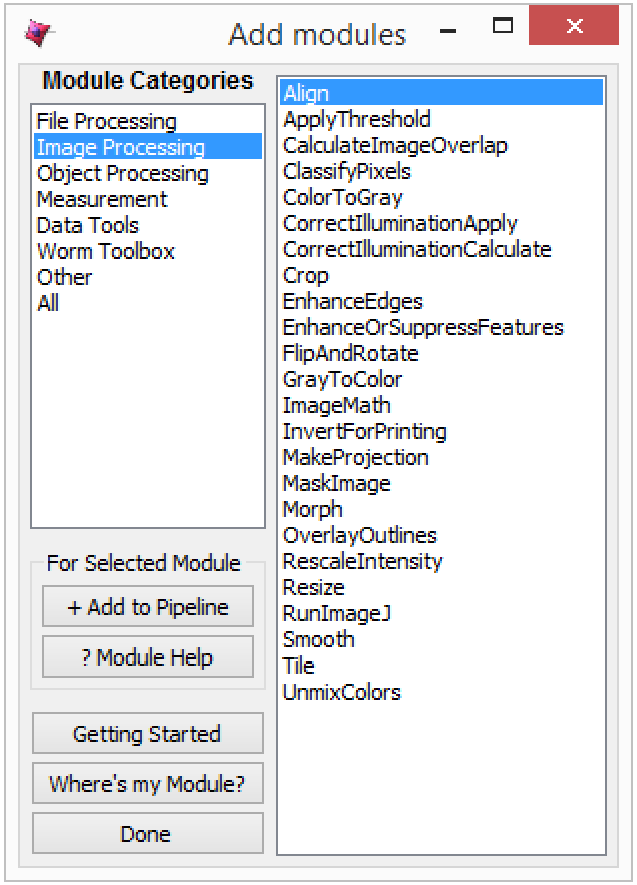
Default Output Folder: C:\Users\Hannes\Desktop\Ruth CellProfiler

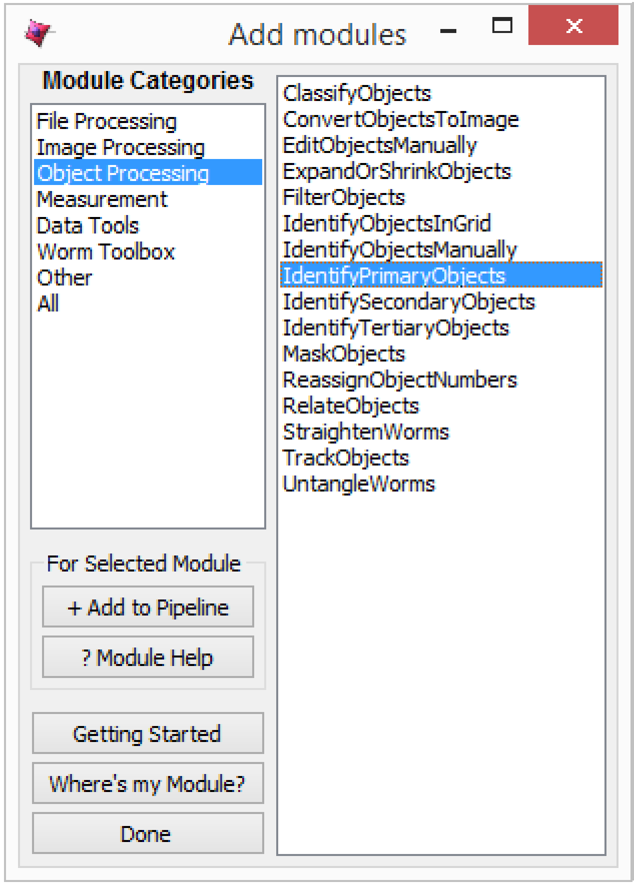
Output Filename: DefaultOUT.mat

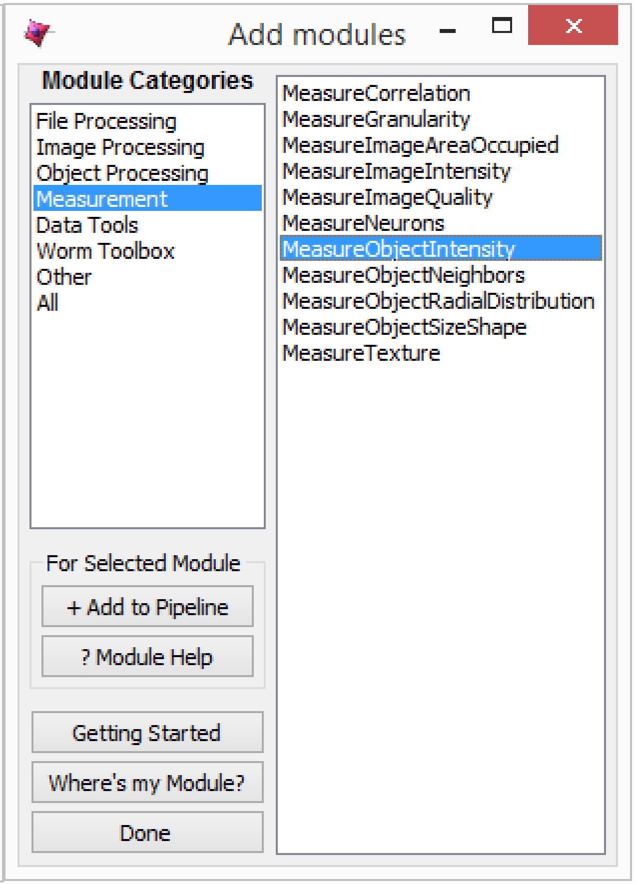
Allow overwrite? ☐

Welcome to CellProfiler

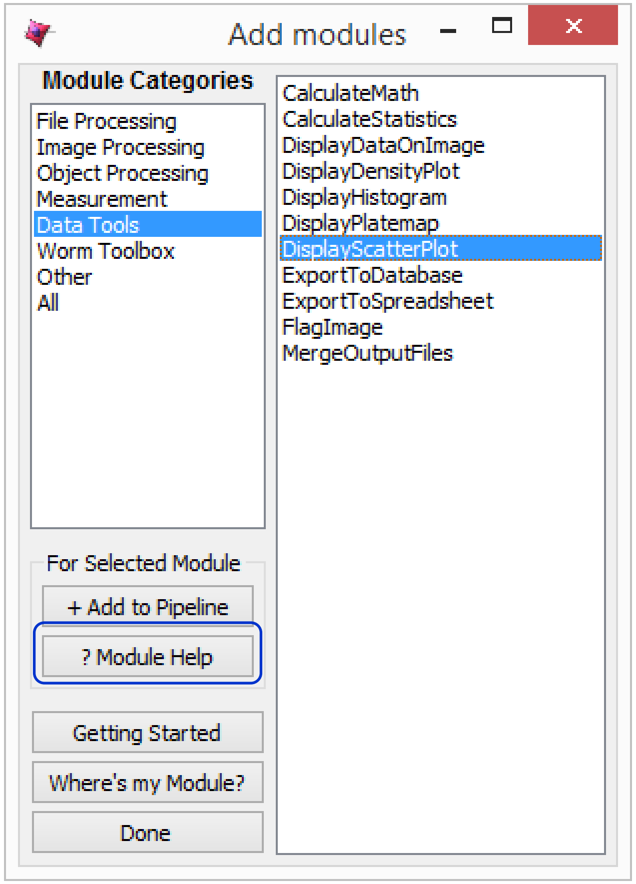
Other modules

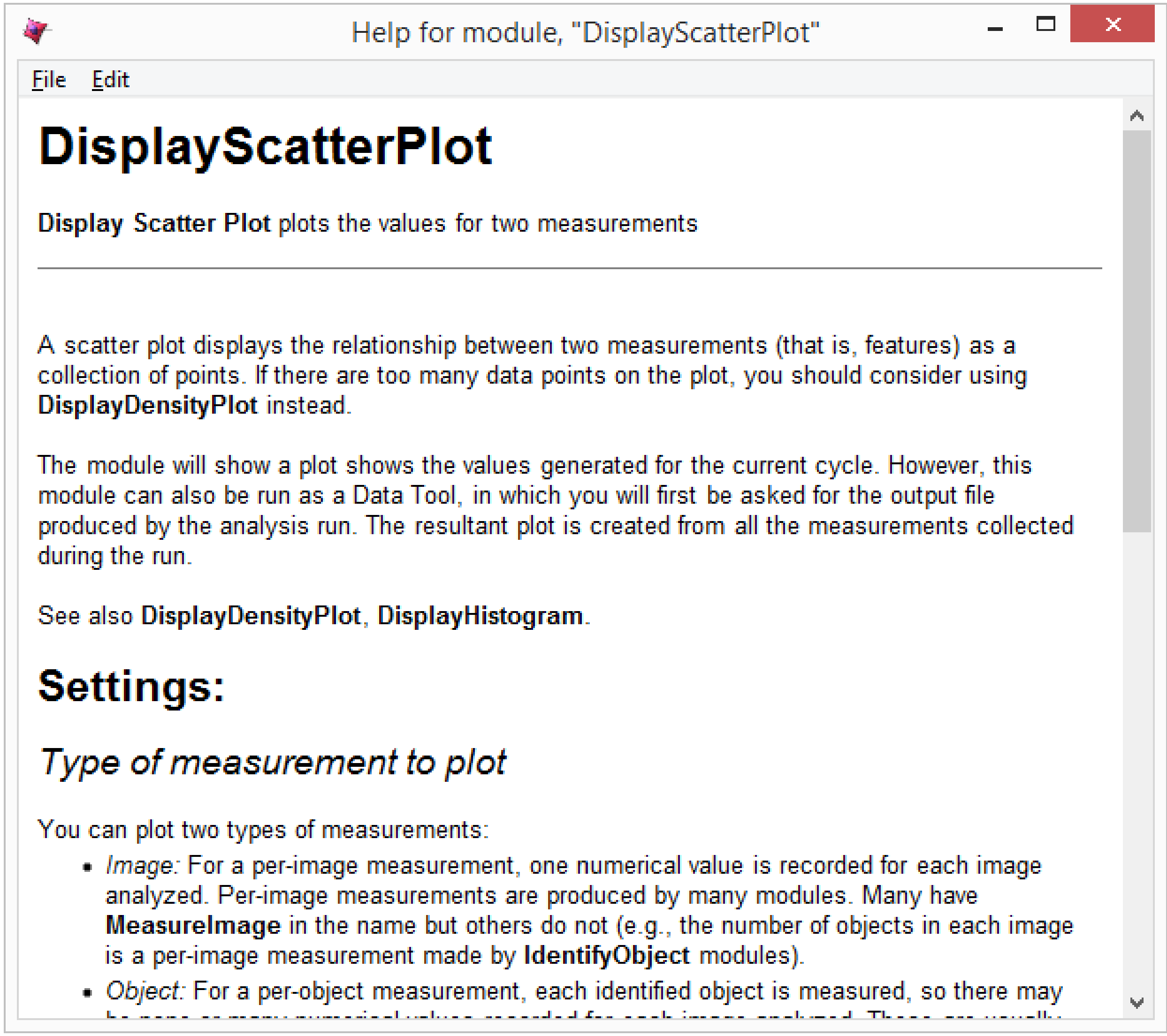






Other modules





DisplayScatterPlot

Display Scatter Plot plots the values for two measurements

A scatter plot displays the relationship between two measurements (that is, features) as a collection of points. If there are too many data points on the plot, you should consider using **DisplayDensityPlot** instead.

The module will show a plot shows the values generated for the current cycle. However, this module can also be run as a Data Tool, in which you will first be asked for the output file produced by the analysis run. The resultant plot is created from all the measurements collected during the run.

See also **DisplayDensityPlot**, **DisplayHistogram**.

Settings:

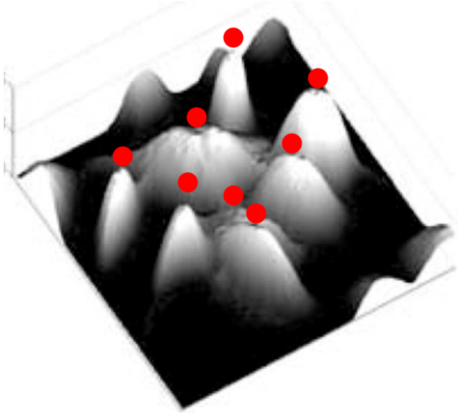
Type of measurement to plot

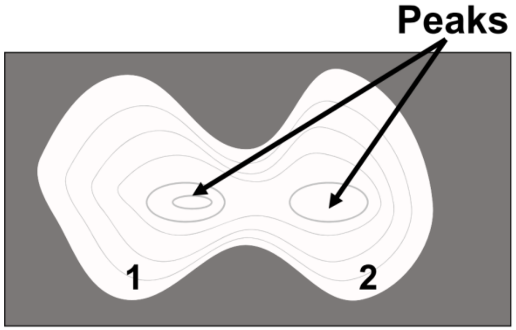
You can plot two types of measurements:

- *Image:* For a per-image measurement, one numerical value is recorded for each image analyzed. Per-image measurements are produced by many modules. Many have **MeasureImage** in the name but others do not (e.g., the number of objects in each image is a per-image measurement made by **IdentifyObject** modules).
- *Object:* For a per-object measurement, each identified object is measured, so there may

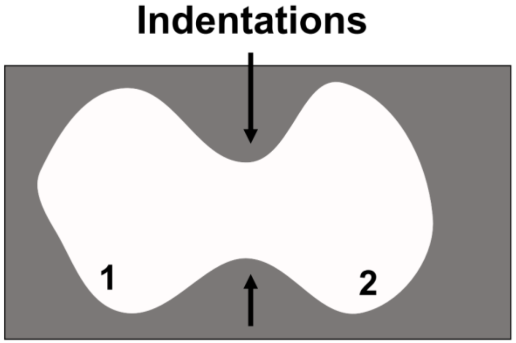
Object separation

- Clump identification: Two options





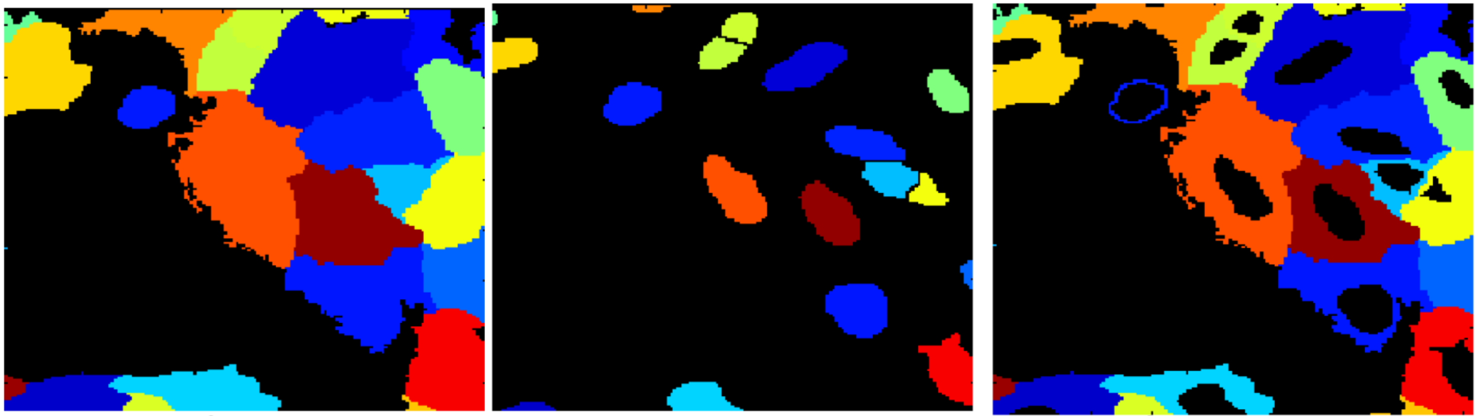
– **Intensity:** Works best if objects are brighter at center, dimmer at edges



Shape: Works best if objects have indentations where clumps touch (esp. if objects are round)

Primary, secondary and tertiary objects

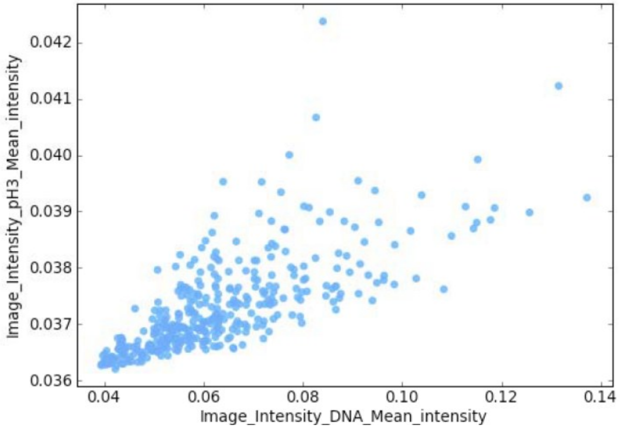
- **Goal:** Identify *tertiary objects* by removing the primary objects from secondary objects
  - "Subtract" the nuclei objects from cell objects to obtain cytoplasm

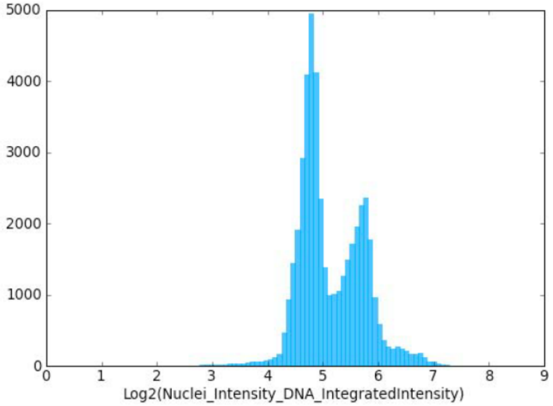


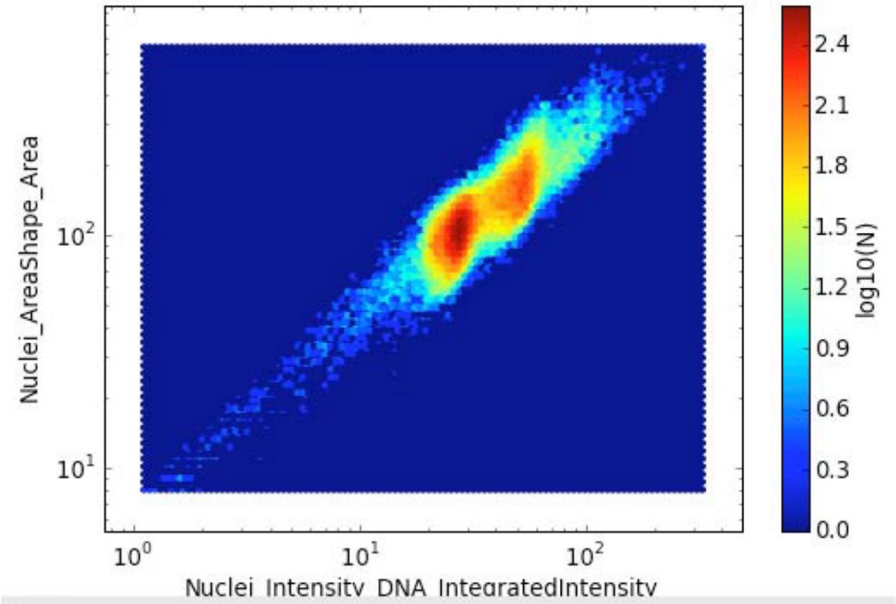
Cells — Nuclei = Cytoplasm

CellProfiler- Data visualization

Data from thousands of cells can be stored in Spreadsheet (Excel) of Database formats and visualized in different ways:







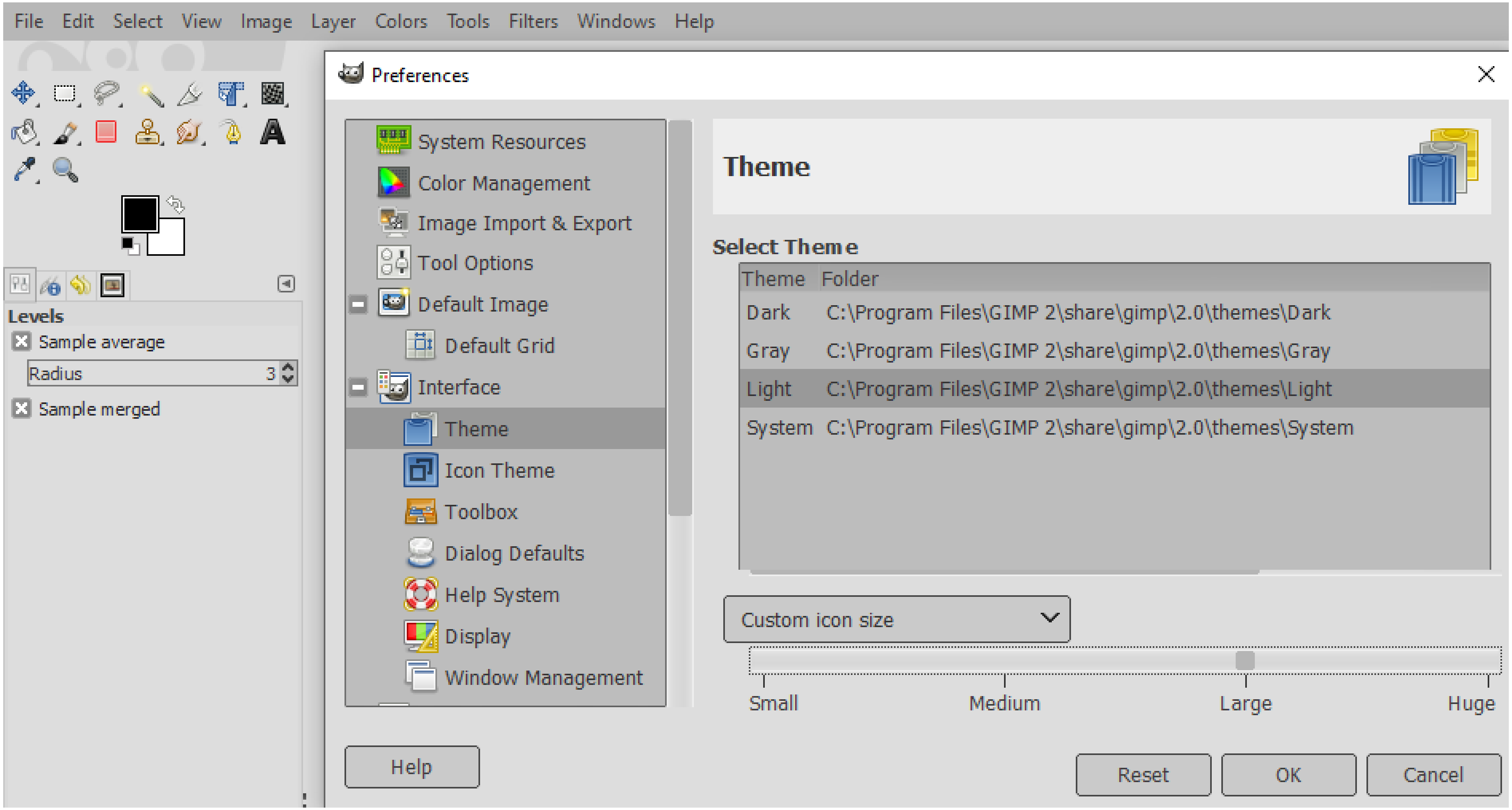
Data in csv-format can also be converted to fcs-file format, which can be read and analyzed by any flow cytometry software (TextToFCS: http://www.flowjo.com/utilities/)

GIMP (GNU Image Manipulation Program) (free alternative to Adobe Photoshop)

- **https://www.gimp.org/**: for generating publication quality figures
- to create professional images of research results (microscopy images, Western Blots…)
- Can be set to different languages (default: system language)
- Theme and icons can be set to different modes: system, light, gray, dark (under: Edit > preferences)

If you prefer Photoshop: an older version (CS2) is available at:
https://www.computerbild.de/download/Adobe-Photoshop-CS2-Vollversion-8040793.html

GIMP (GNU Image Manipulation Program) (free alternative to Adobe Photoshop)



Levels

☒ Sample average

Radius 3

☒ Sample merged

Theme

Select Theme

Theme	Folder
Dark	C:\Program Files\GIMP 2\share\gimp\2.0\themes\Dark
Gray	C:\Program Files\GIMP 2\share\gimp\2.0\themes\Gray
Light	C:\Program Files\GIMP 2\share\gimp\2.0\themes\Light
System	C:\Program Files\GIMP 2\share\gimp\2.0\themes\System

Custom icon size

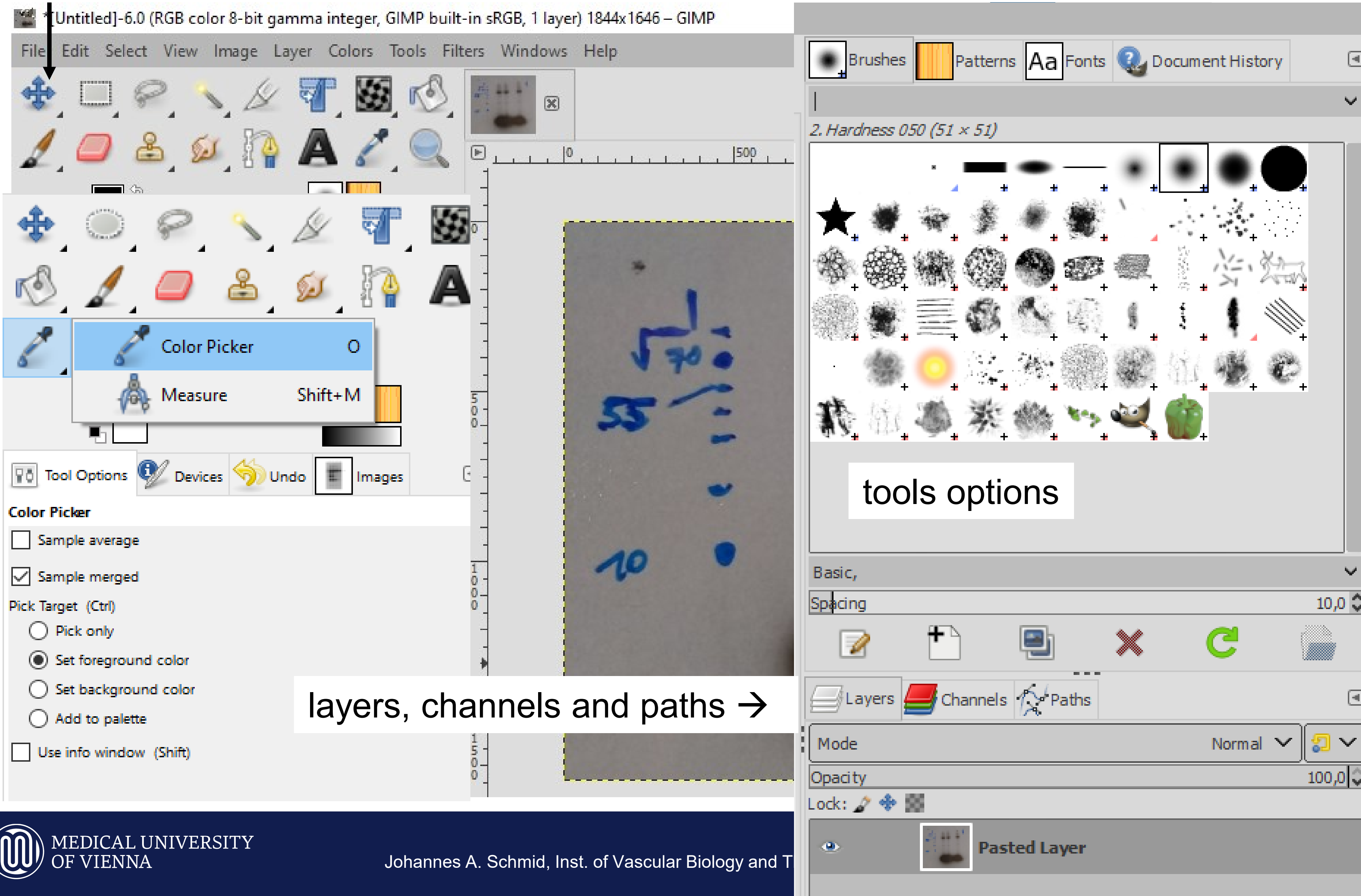
Small Medium Large Huge

Some Features

- GIMP works with layers, that means that you can change, move… just one layer (e.g. text) while leaving the others un-altered. This also includes changing of contrast and brightness.
- Colour pictures usually work in RGB mode (Red-Green-Blue) – called channels (Kanäle). You can select one channel (by highlighting it) and modify it. You can watch all channels (clicking on the eye-symbol left of RGB), while changing just one.
- You can copy/paste image data in one channel alone (> you can generate a merged colour image from monochrome microscopy images generated with different filters)

Example of an image in GIMP

Tools window



*[Untitled]-6.0 (RGB color 8-bit gamma integer, GIMP built-in sRGB, 1 layer) 1844x1646 – GIMP

Color Picker

☐ Sample average

☑ Sample merged

Pick Target (Ctrl)

- ○ Pick only
- ● Set foreground color
- ○ Set background color
- ○ Add to palette

☐ Use info window (Shift)

2. Hardness 050 (51 × 51)

Basic,

Spacing 10,0

Mode Normal

Opacity 100,0

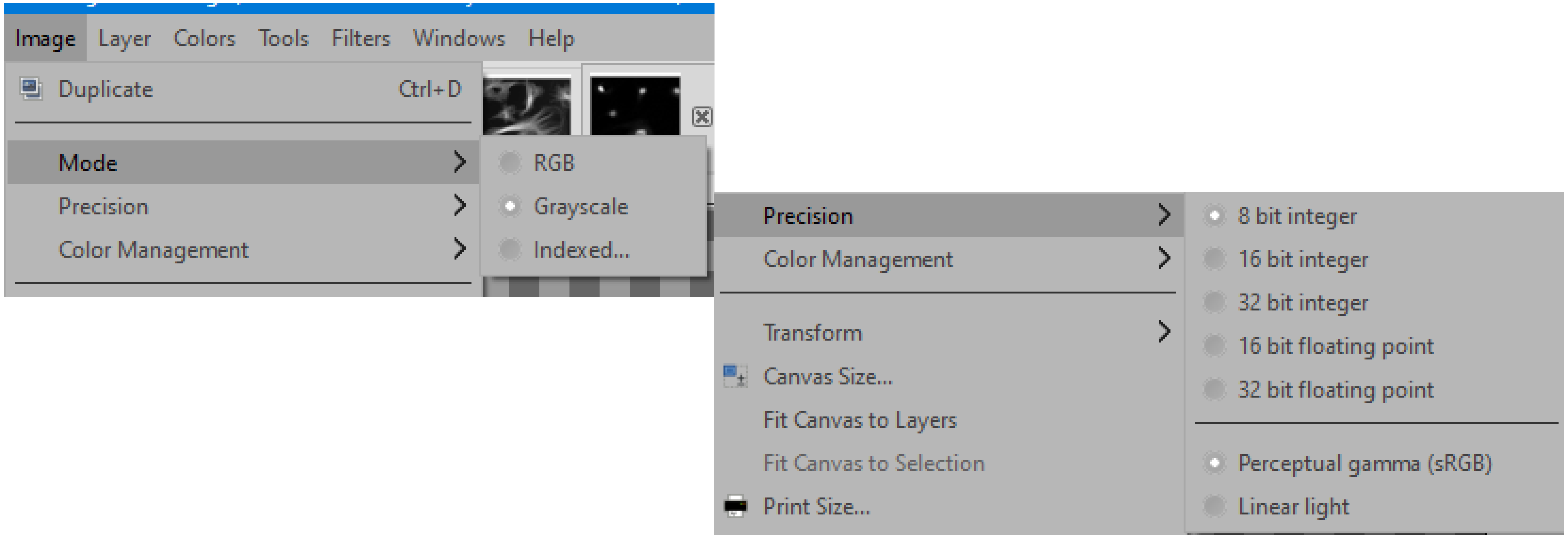
Lock:

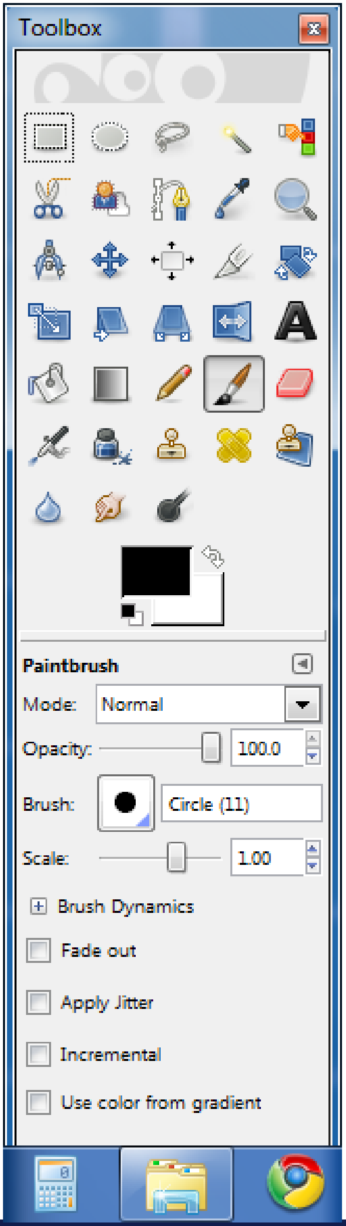
Pasted Layer

tools options

layers, channels and paths →

Image Modes: Gray, RGB, 8 bit, 16 bit…





Paintbrush

Mode: Normal

Opacity: 100.0

Brush: Circle (11)

Scale: 1.00

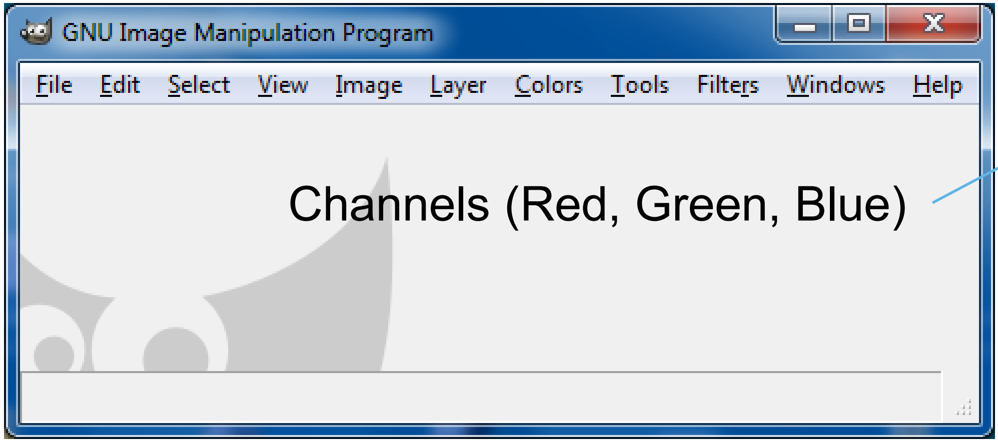
Brush Dynamics

☐ Fade out

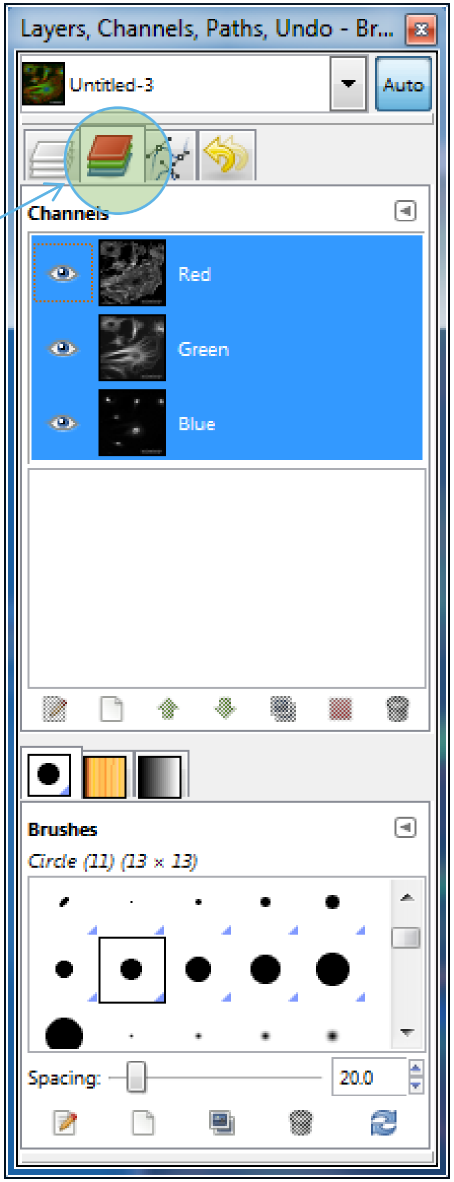
☐ Apply Jitter

☐ Incremental

☐ Use color from gradient



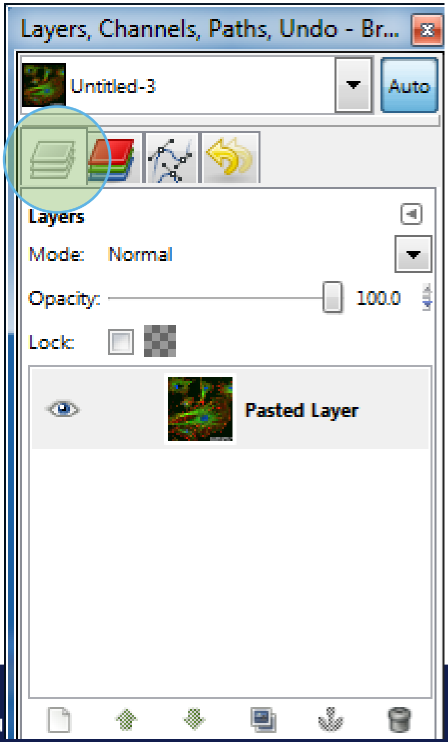
Channels (Red, Green, Blue)



Circle (11) (13 × 13)

Spacing: 20.0

Layers)

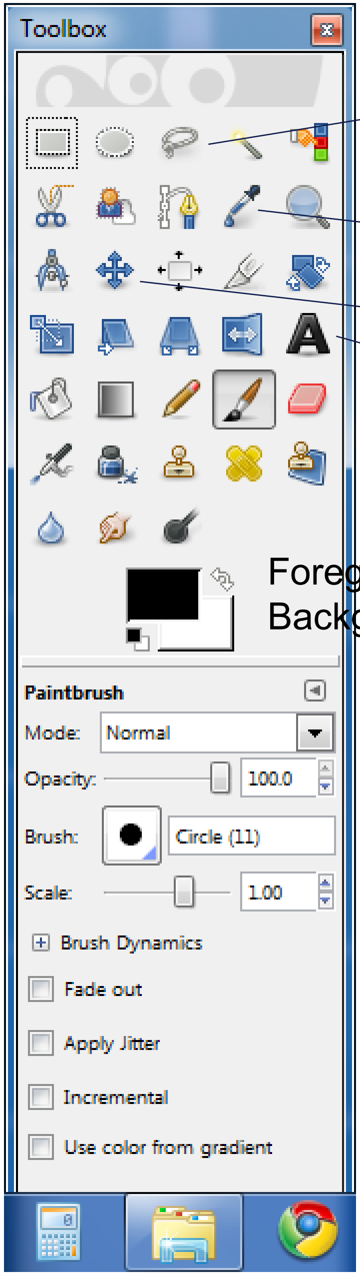


Mode: Normal

Opacity: 100.0

Lock: ☐

Pasted Layer



Paintbrush

Mode: Normal

Opacity: 100.0

Brush: Circle (11)

Scale: 1.00

Brush Dynamics

☐ Fade out

☐ Apply Jitter

☐ Incremental

☐ Use color from gradient

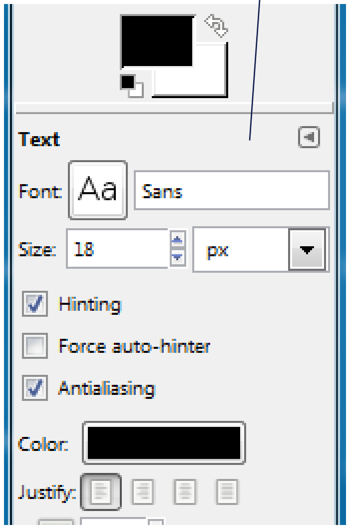
Selection tools (including magic stick selection of area of similar colour)

Colour picker

Moving tool

Text tool

Foreground/
Background colour



Text

Font: Sans

Size: 18 px

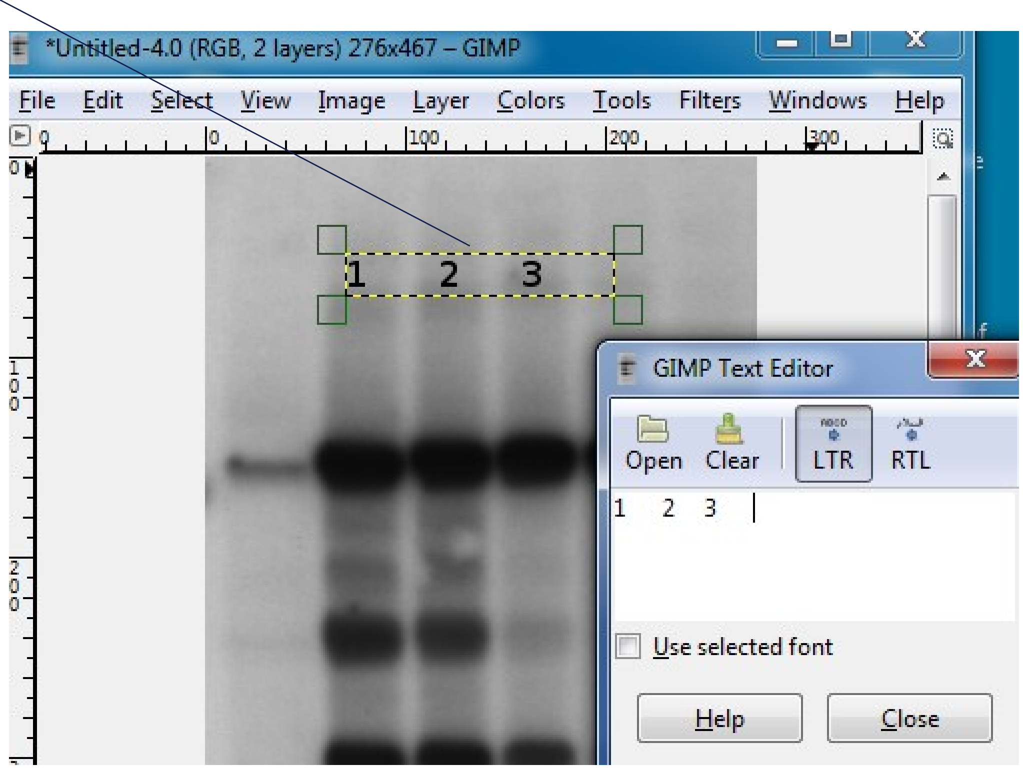
☑ Hinting

☐ Force auto-hinter

☑ Antialiasing

Color:

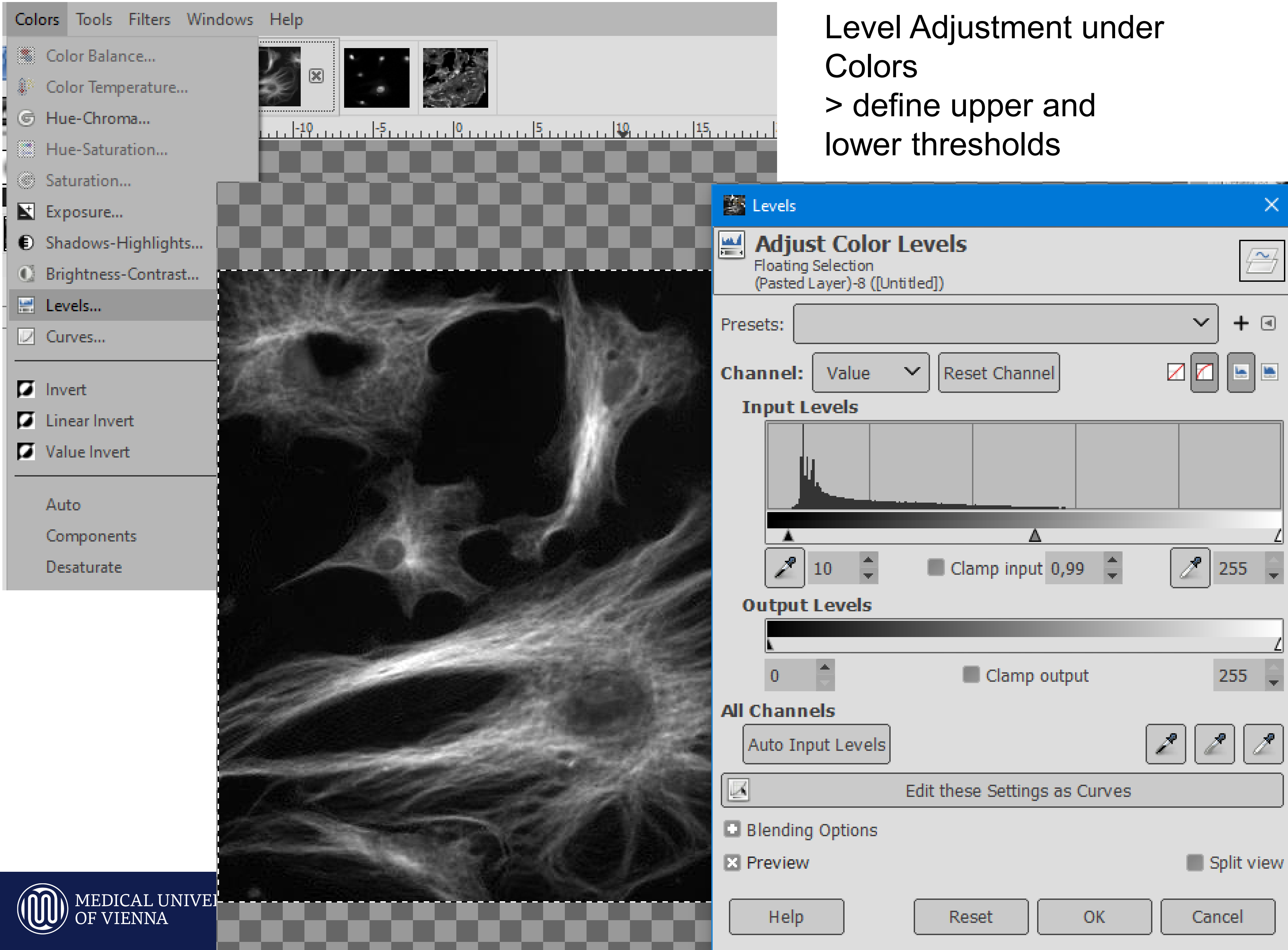
Justify:



1 2 3

☐ Use selected font

Level Adjustment under Colors
> define upper and lower thresholds



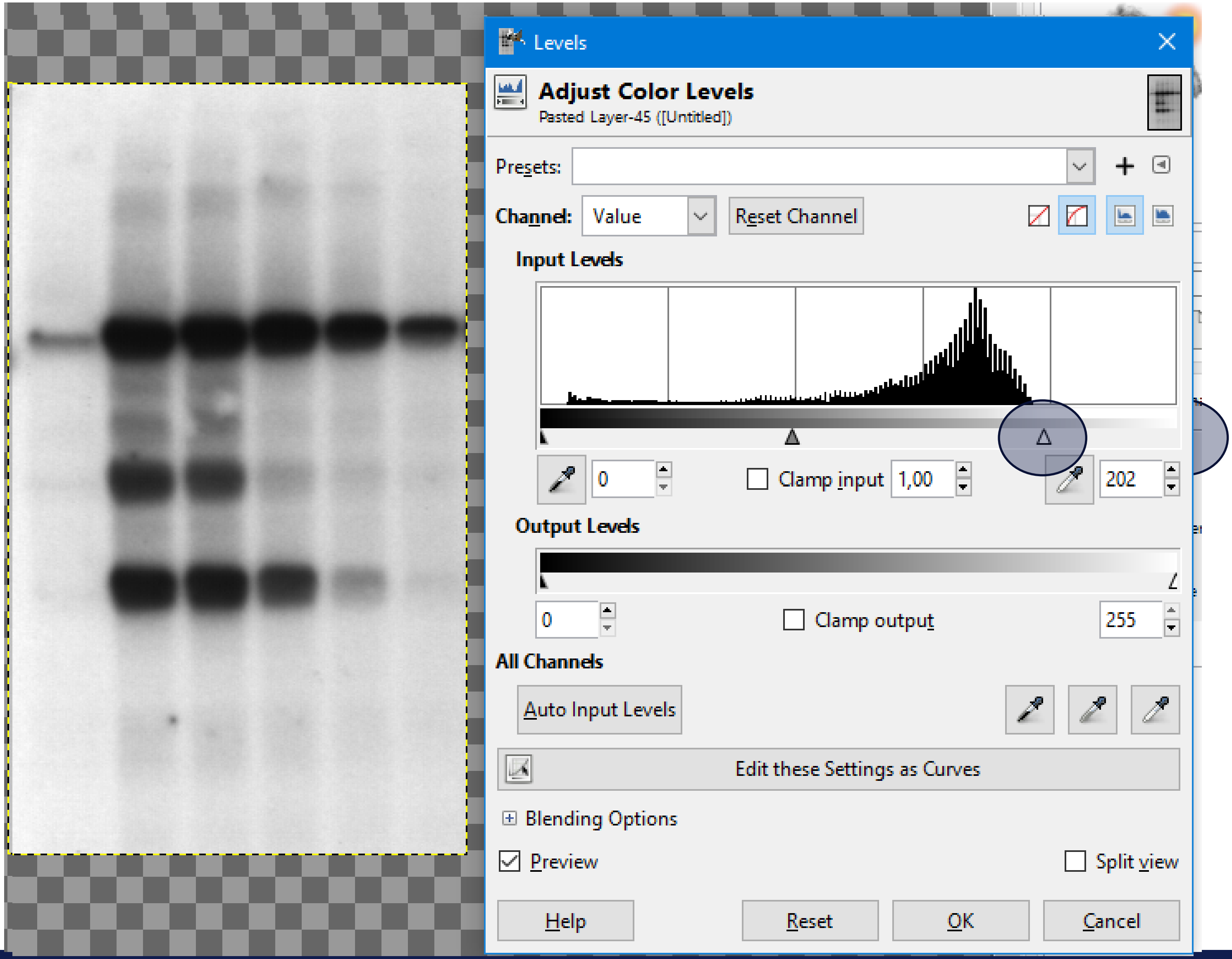
Channel: Value

Input Levels: 10 ☐ Clamp input 0,99 255

Output Levels: 0 ☐ Clamp output 255

☒ Preview ☐ Split view

Image Adjustments: intensity levels II



Levels

Adjust Color Levels

Pasted Layer-45 ([Untitled])

Presets:

Channel: Value

Reset Channel

Input Levels

0

☐ Clamp input 1,00

202

Output Levels

0

☐ Clamp output

255

All Channels

Auto Input Levels

Edit these Settings as Curves

Blending Options

☑ Preview

☐ Split view

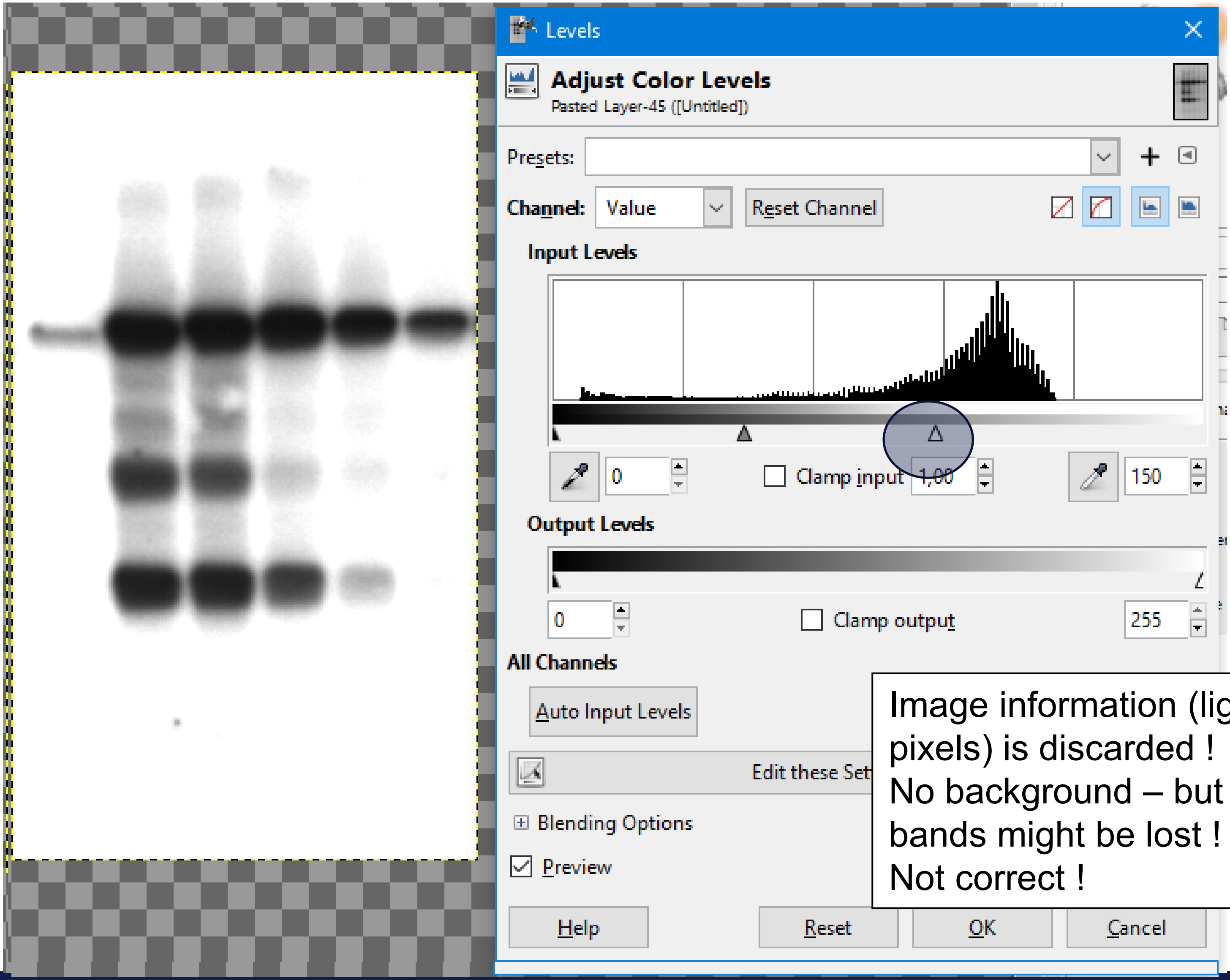
Help

Reset

OK

Cancel

Image Adjustments: intensity levels II



Levels

Adjust Color Levels

Pasted Layer-45 ([Untitled])

Presets:

Channel: Value

Input Levels: 0 ☐ Clamp input 1,00 150

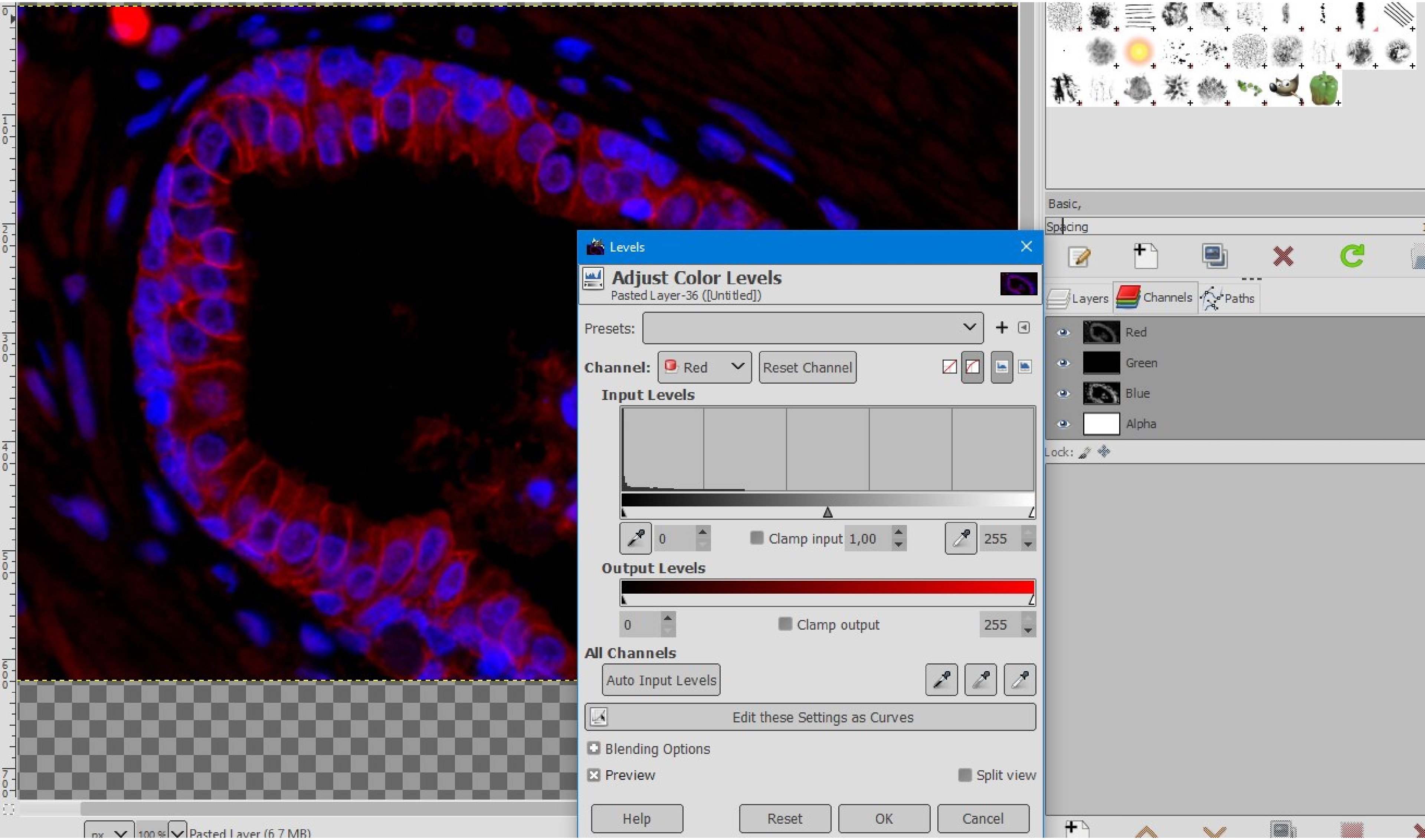
Output Levels: 0 ☐ Clamp output 255

All Channels

☑ Preview

Image information (light gray pixels) is discarded !
No background – but faint bands might be lost !
Not correct !

Image Adjustments: intensity levels of colour channels



Levels

Adjust Color Levels

Pasted Layer-36 ([Untitled])

Presets:

Channel: Red

Input Levels

0 ☐ Clamp input 1,00 255

Output Levels

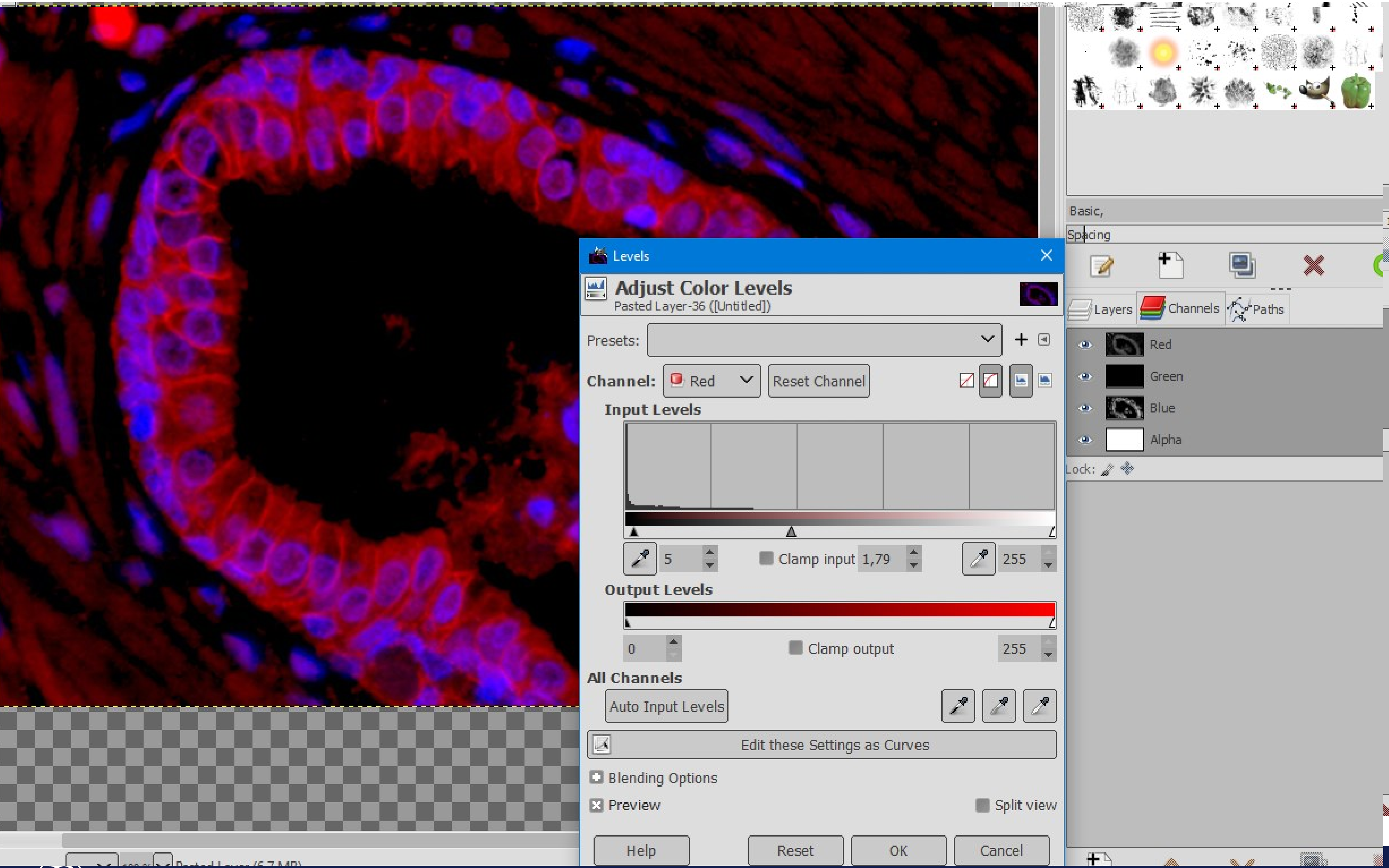
0 ☐ Clamp output 255

All Channels

☒ Preview ☐ Split view

Pasted Layer (6.7 MB)

Image Adjustments: intensity levels of colour channels



Levels

Adjust Color Levels

Pasted Layer-36 ([Untitled])

Presets:

Channel: Red

Input Levels: 5 — 1,79 — 255

☐ Clamp input

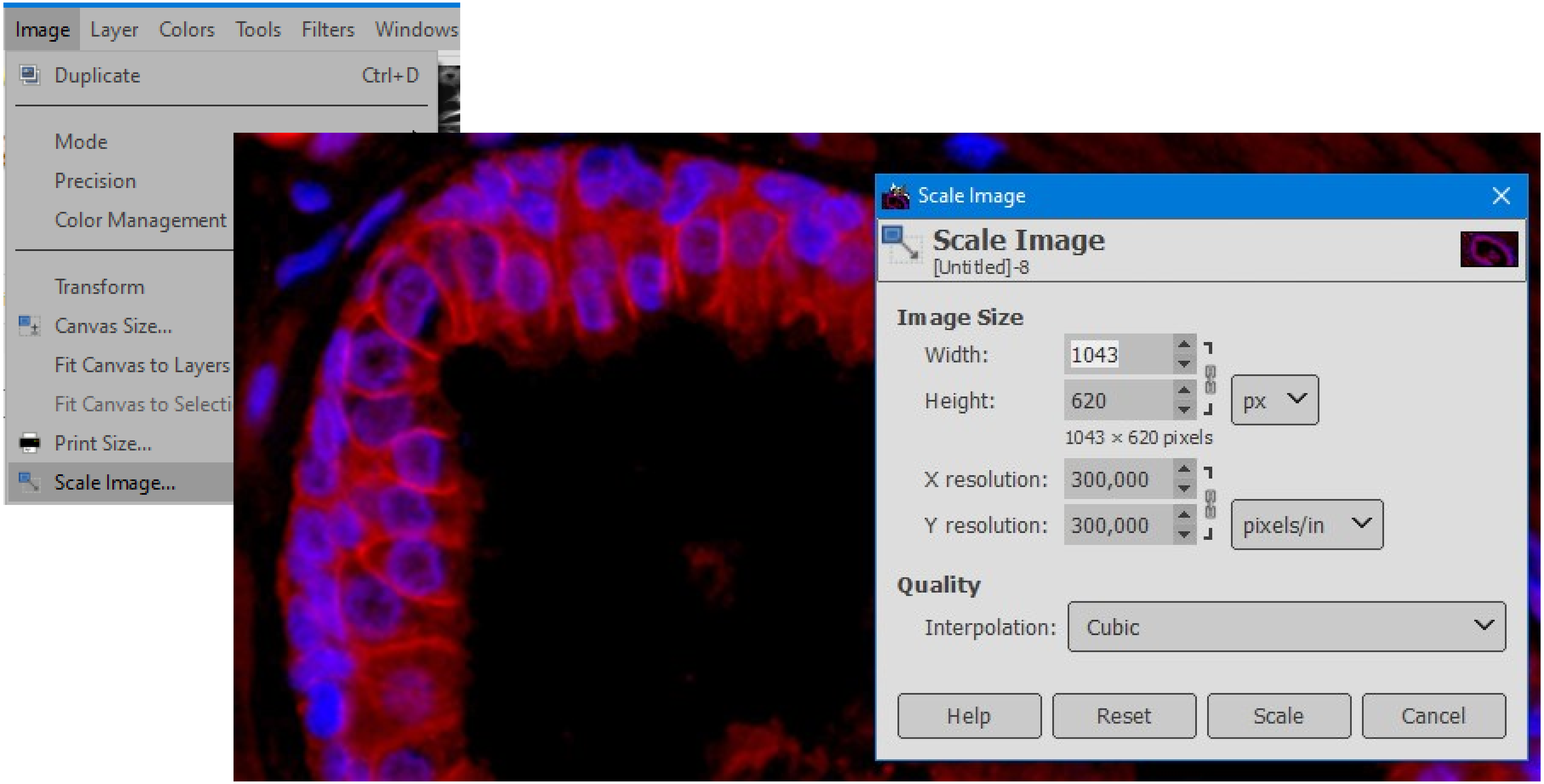
Output Levels: 0 — 255

☐ Clamp output

☒ Preview

☐ Split view

The image resolution (pixels per inch, dpi)



Scale Image
[Untitled]-8

Image Size
Width: 1043
Height: 620
px
1043 × 620 pixels
X resolution: 300,000
Y resolution: 300,000
pixels/in

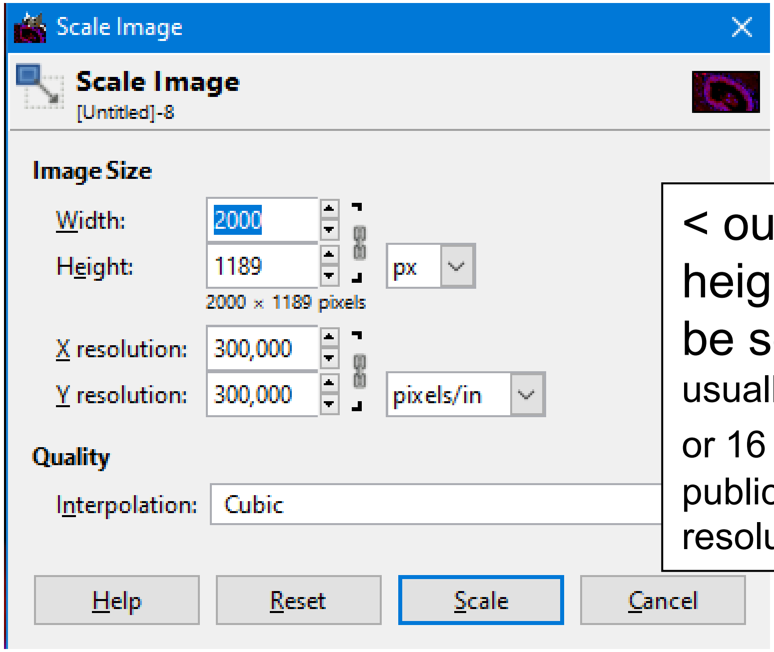
Quality
Interpolation: Cubic

Ctrl (STRG) and scroll > enlargens or shrinks the canvas

The *Scale Image* window

width and height in pixels
this defines the file size

resolution >
300 dpi is minimum for publications (for decent text quality you need at least 150 dpi)

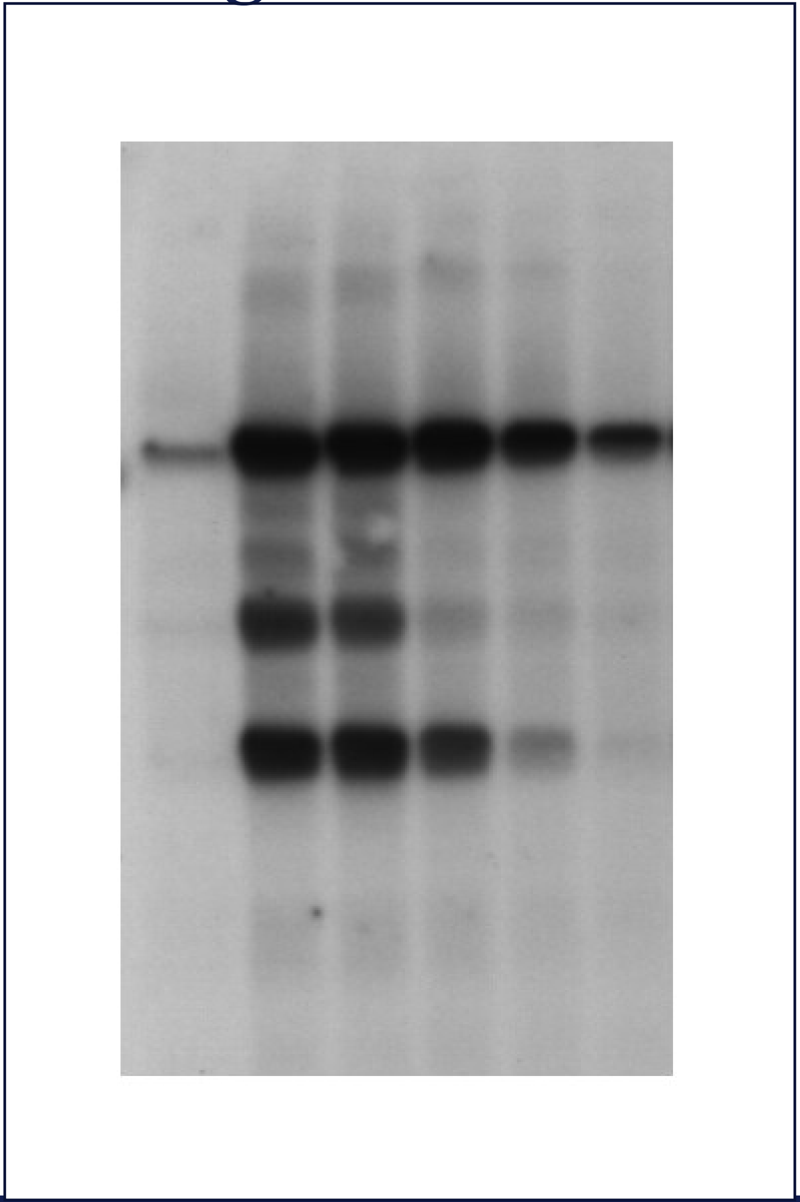


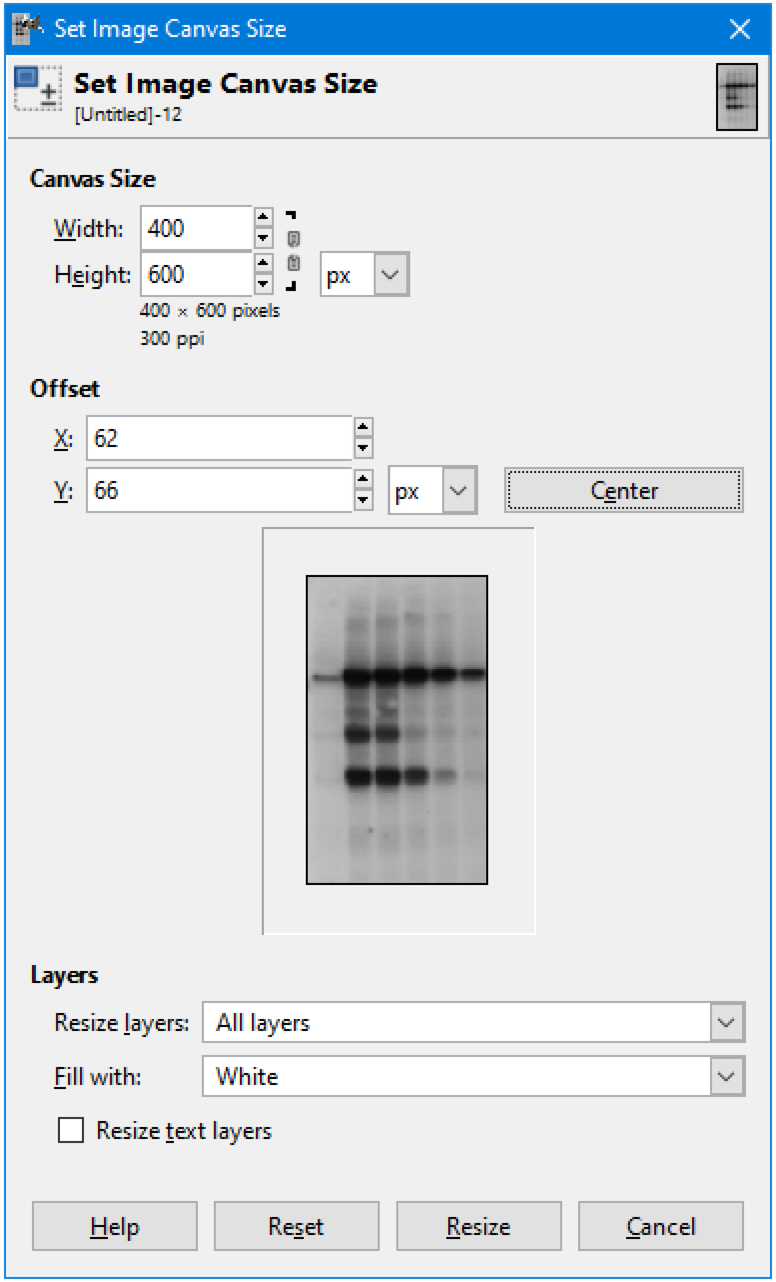
Width: 2000
Height: 1189
px
2000 × 1189 pixels
X resolution: 300,000
Y resolution: 300,000
pixels/in
Interpolation: Cubic

< output width and height (e.g. in cm) can be set
usually 8 cm (1 column), 12 cm or 16 cm (2 columns) for publications (depends on the resolution)

Scaling = re-calculation of images (intra- or extrapolation) - you can specify whether the proportions are maintained

Resizing the canvas





Set Image Canvas Size

Set Image Canvas Size

[Untitled]-12

Canvas Size

Width: 400

Height: 600 px

400 × 600 pixels

300 ppi

Offset

X: 62

Y: 66 px

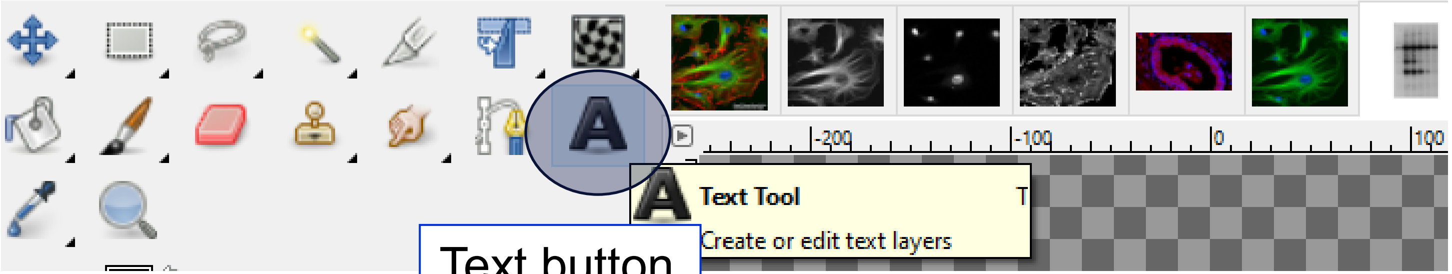
Layers

Resize layers: All layers

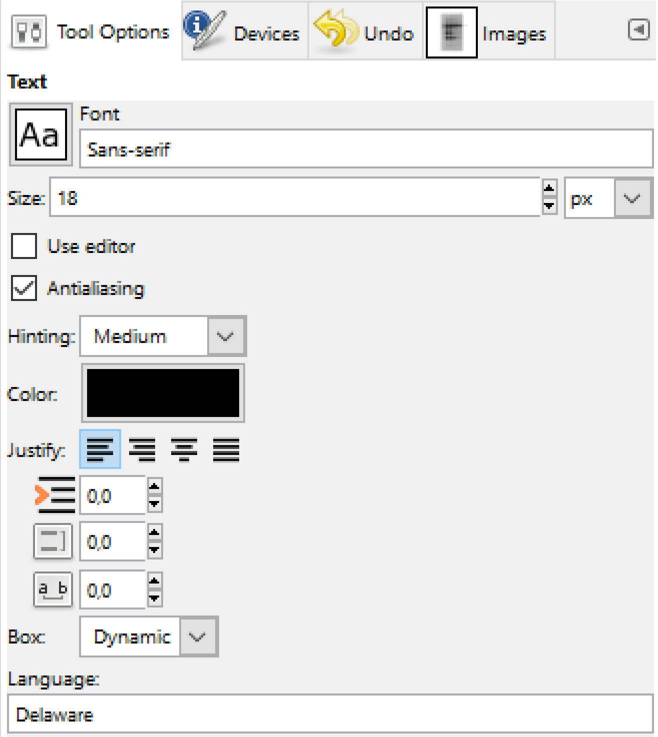
Fill with: White

☐ Resize text layers

Adding text to images



Text button



Text

Font: Sans-serif

Size: 18 px

☐ Use editor

☑ Antialiasing

Hinting: Medium

Color:

Justify:

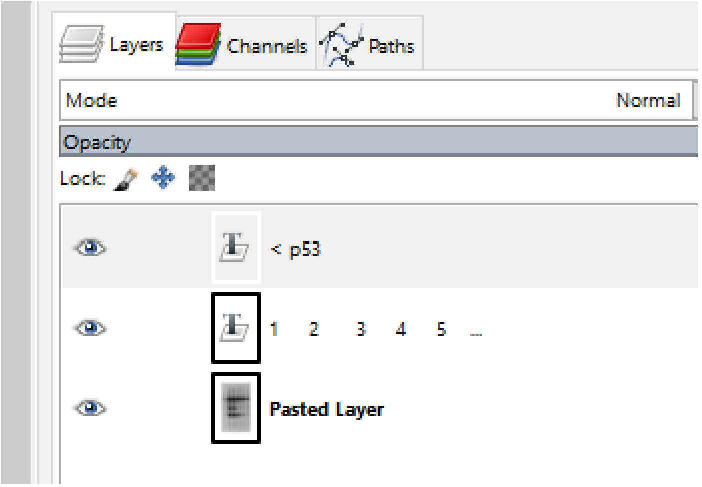
0,0

0,0

0,0

Box: Dynamic

Language: Delaware



Mode Normal

Opacity

< p53

1 2 3 4 5 ...

Pasted Layer

< Text Layer: can be moved…

Image Layers (e.g. with text)

- Layers can be modified separately
- Saving the image in GIMP or Photoshop format (*.psd) also saves the layer information (> you can later on change them again, e.g. the text of figures !)
- You can merge layers (for saving in JPG- or TIF-format)

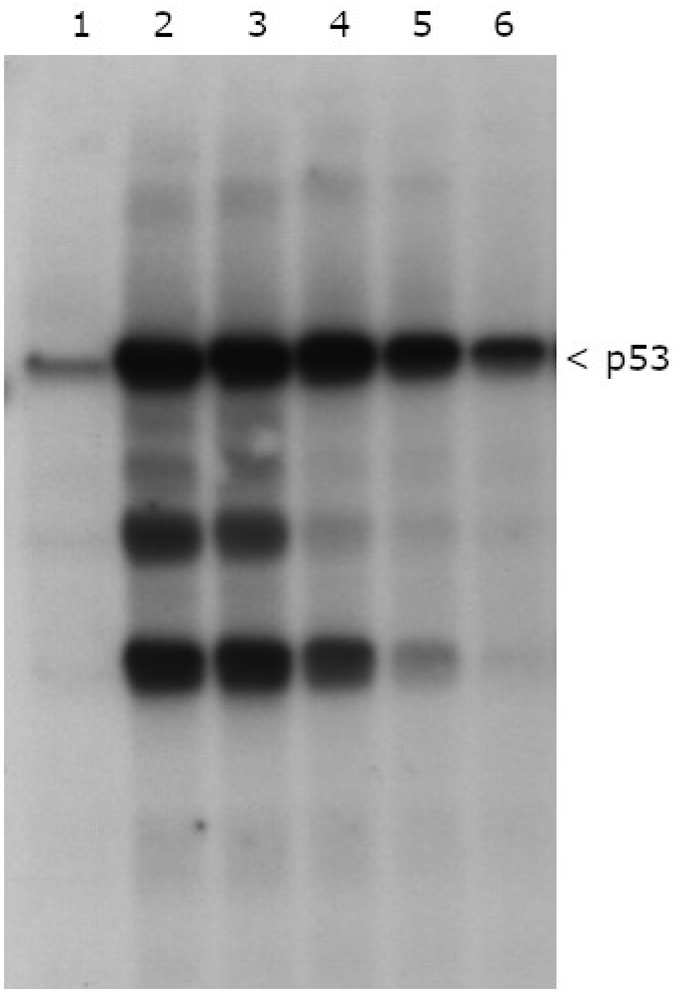
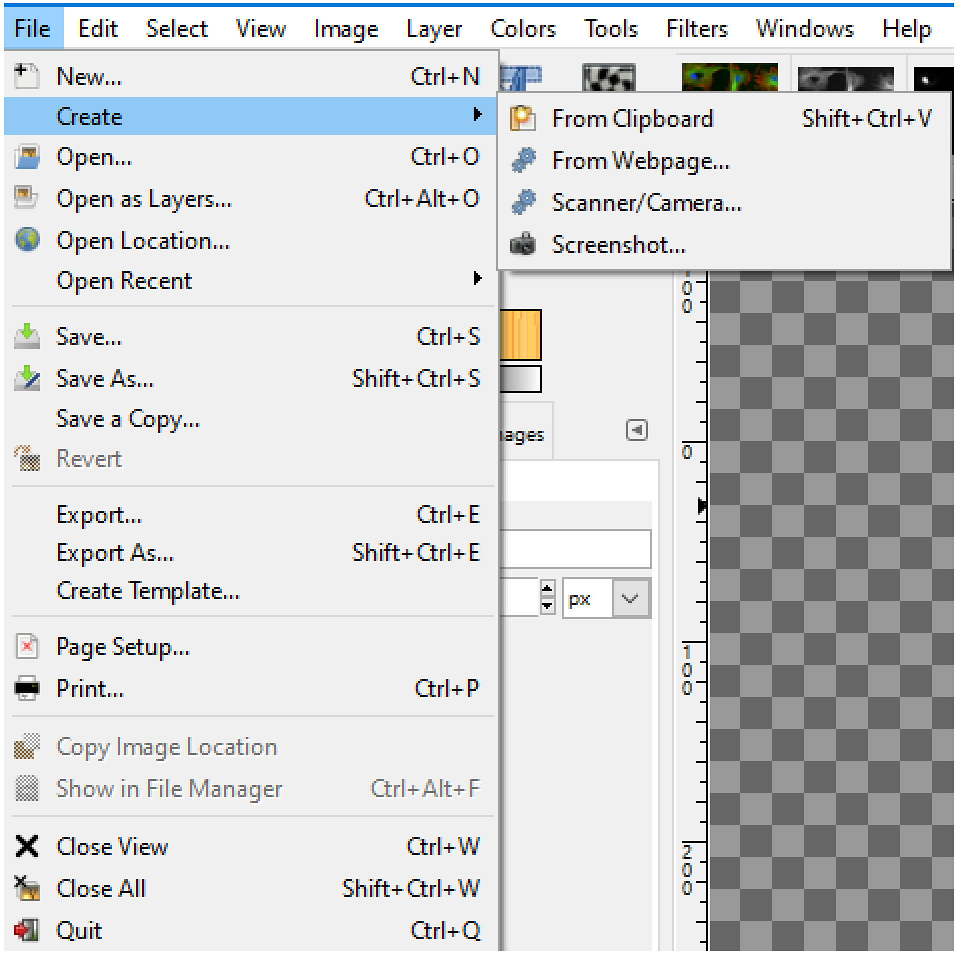


Image processing: Rules for correct usage of features

- Changes (levels, brightness, contrast) should always be made on the whole image (and not parts of it; changing parts of the image, e.g. single bands is of course not allowed)
- You should not discard any image information (e.g. the background by making it completely white)
- Computer experts can prove that something was changed – so be carefull when changing anything

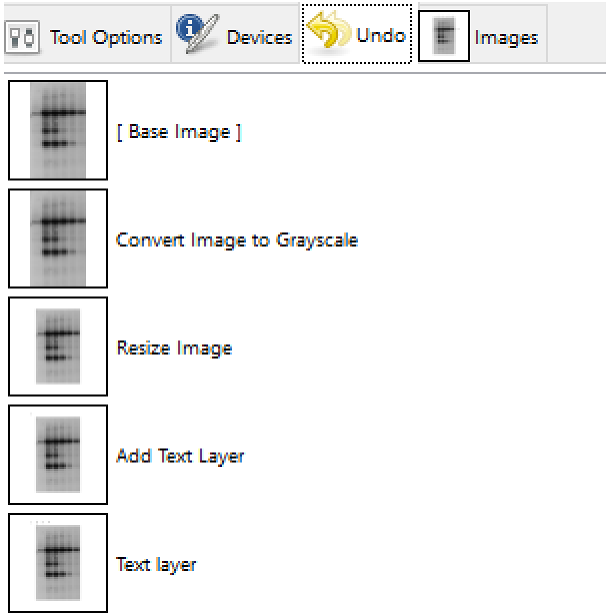
Gimp Menu: File



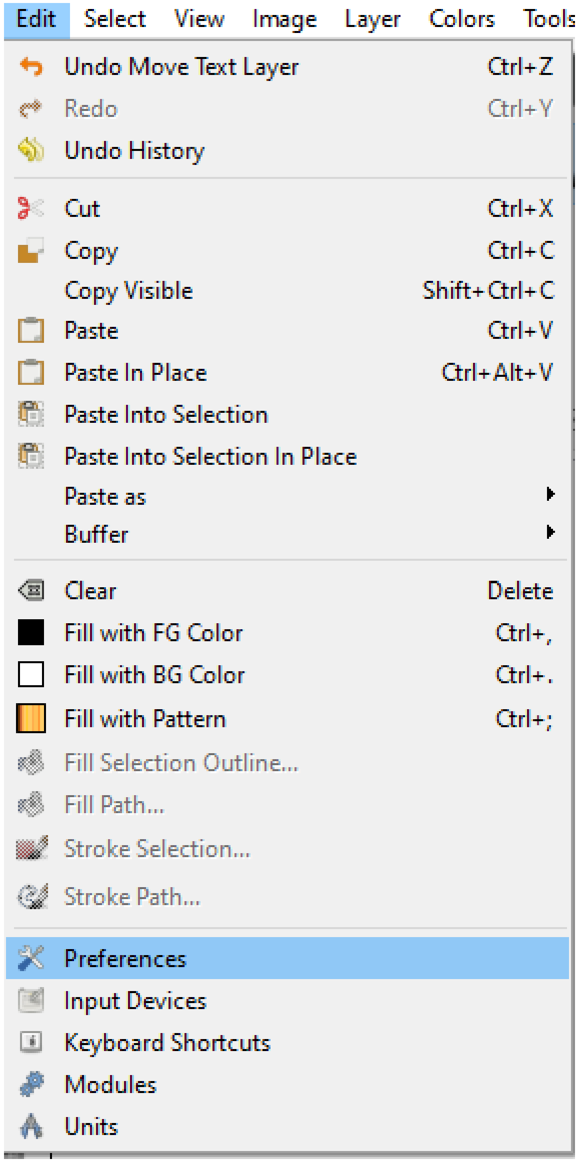
< open from clipboard

Gimp Menu: Edit

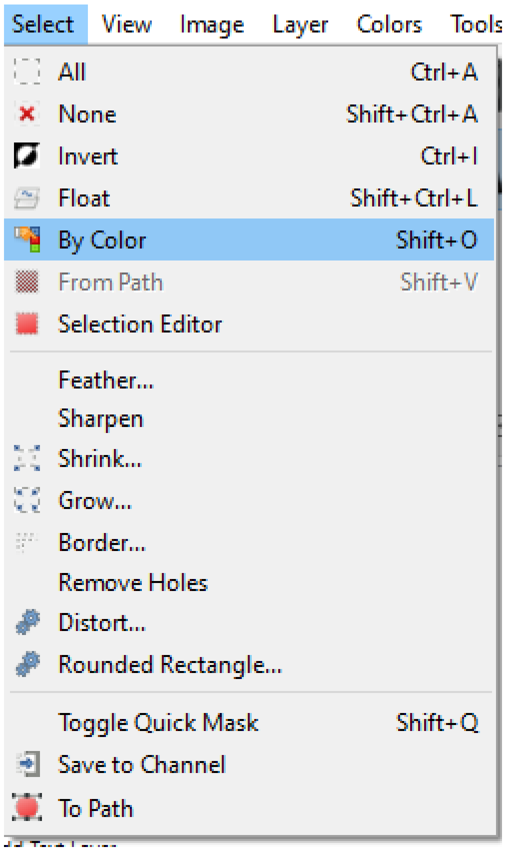
Undo history

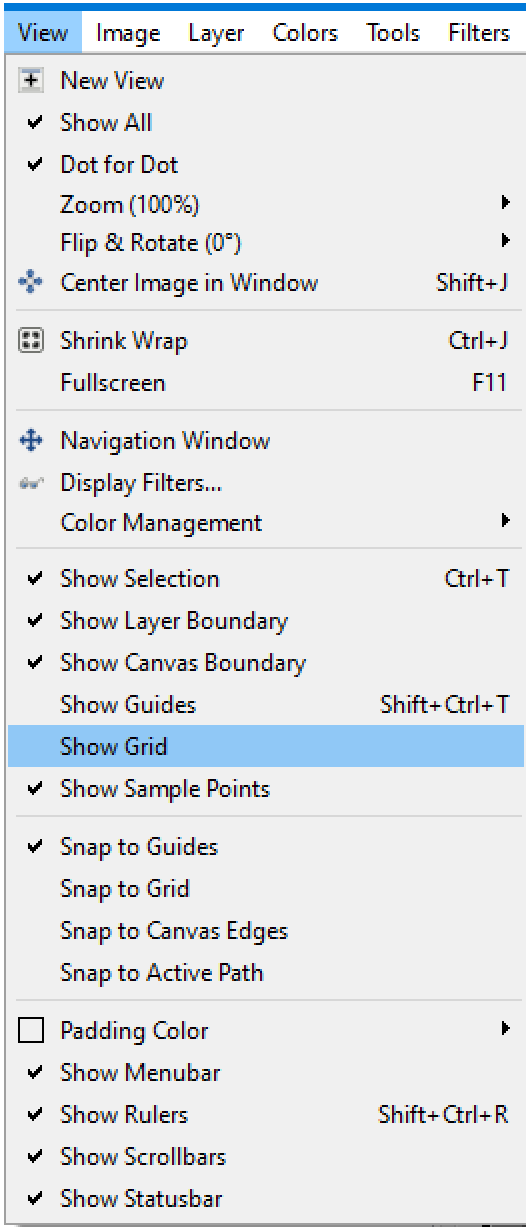


preferences >

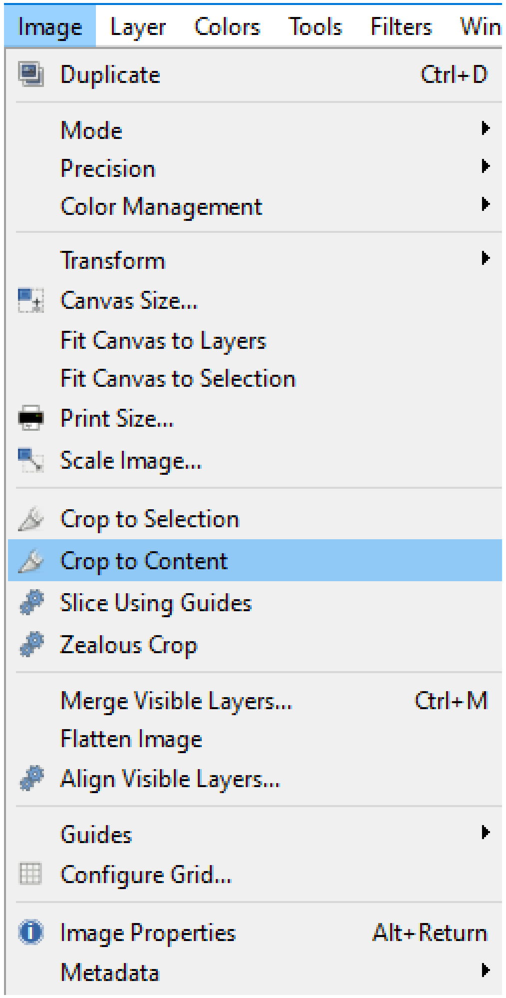


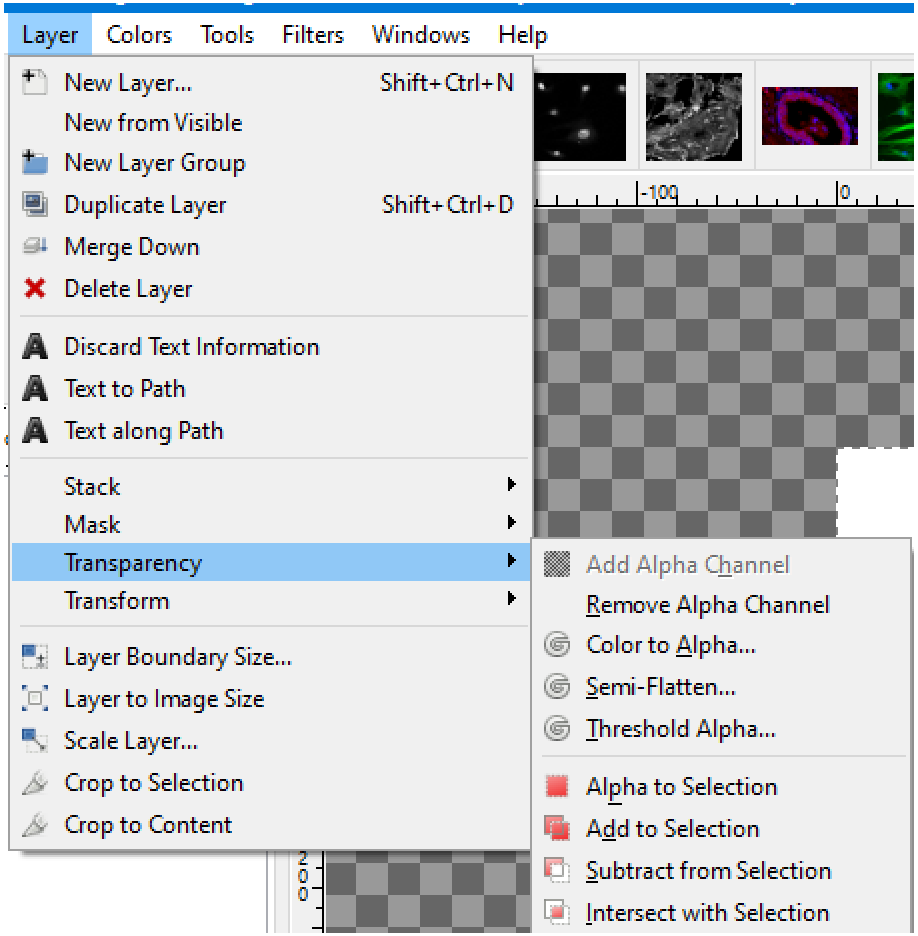
Gimp Menus: Select and View



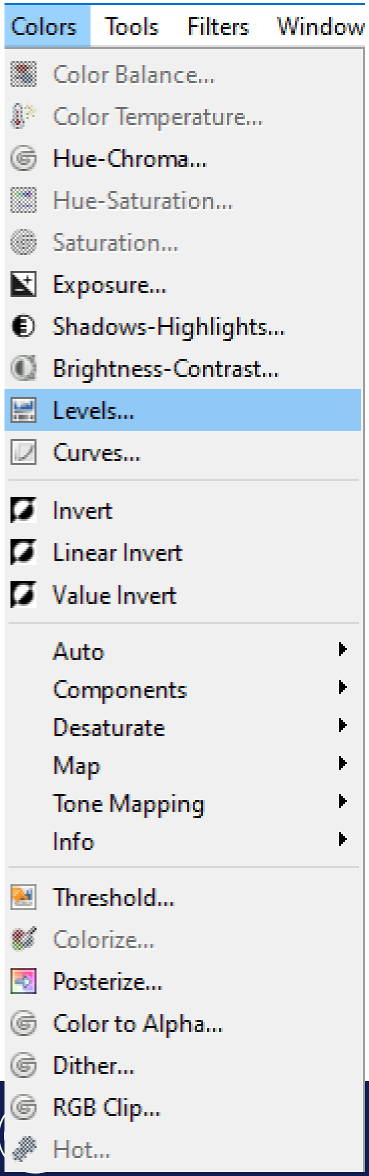


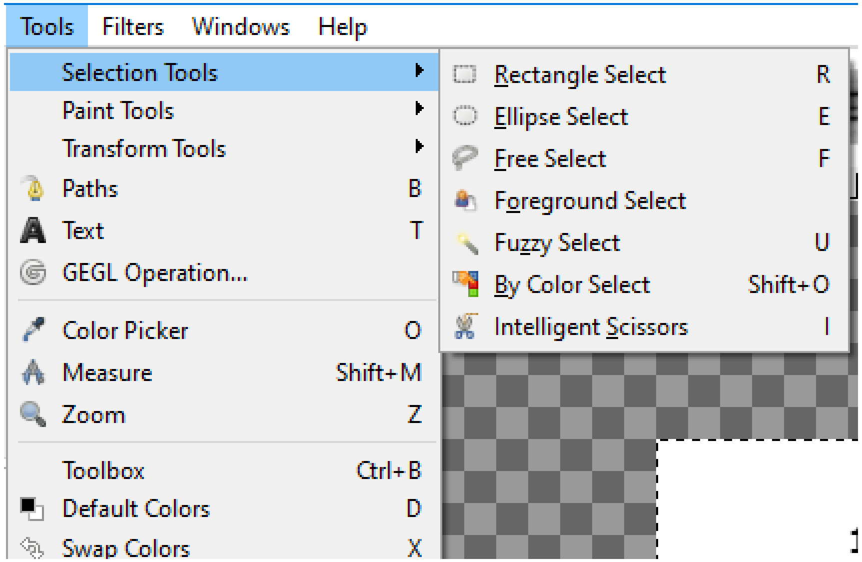
Gimp Menus: Image and Layer

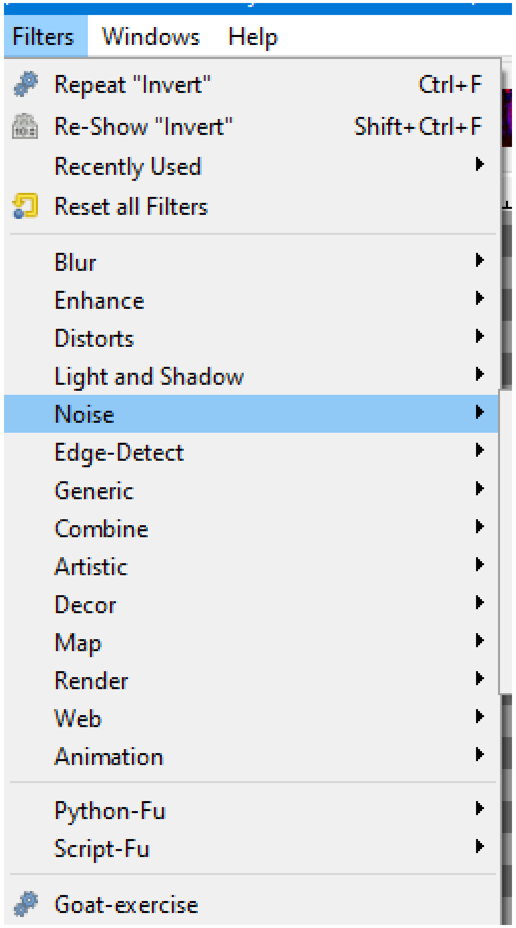




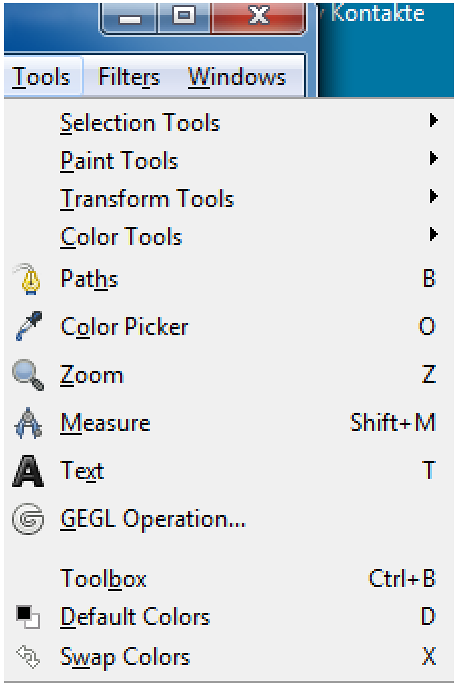
Gimp Menus: Colors, Tools and Filters

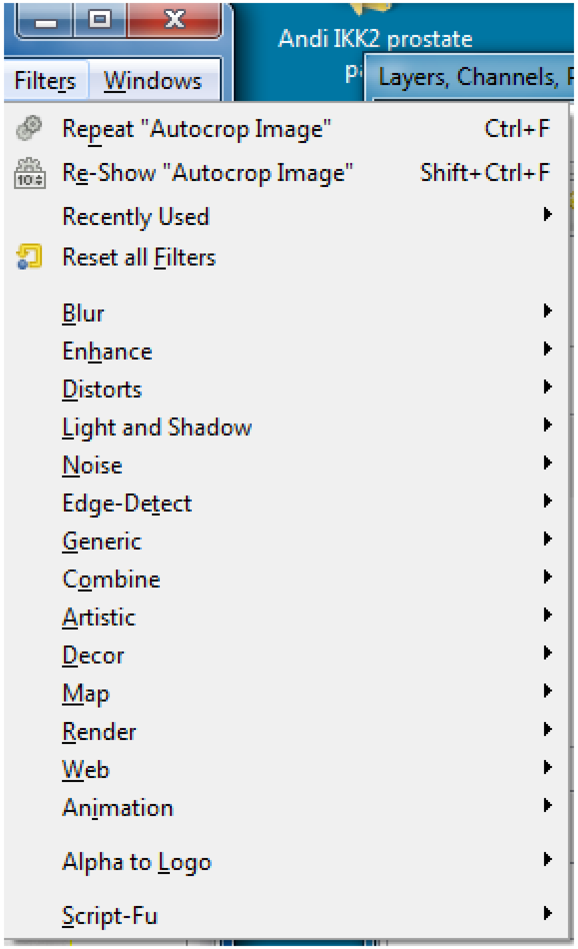


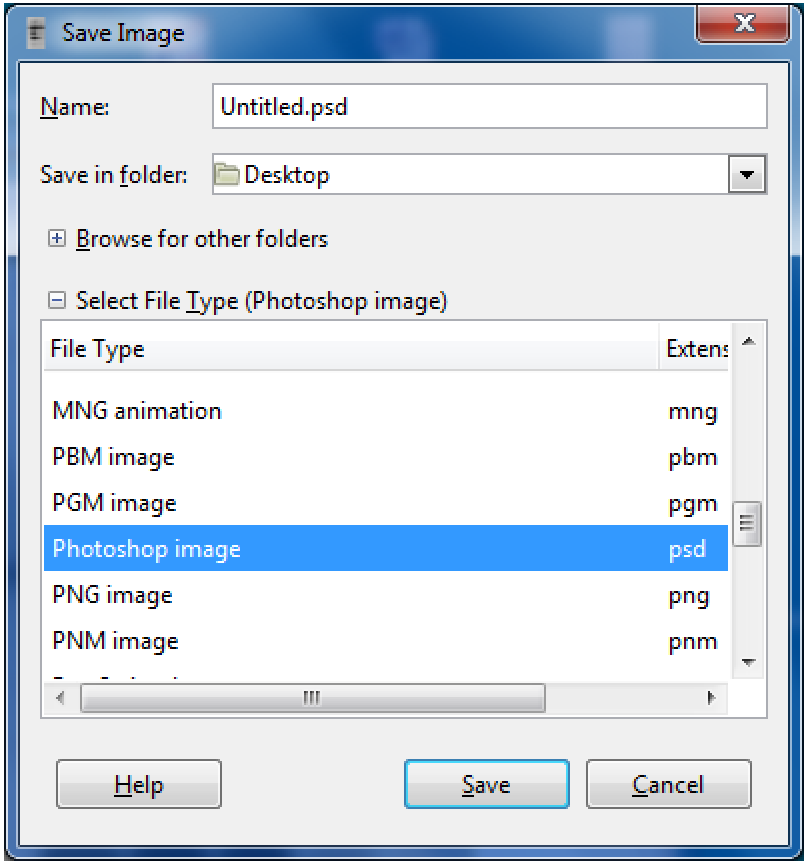




Opening of Photoshop-files and saving in Photoshop-format is possible







Name: Untitled.psd

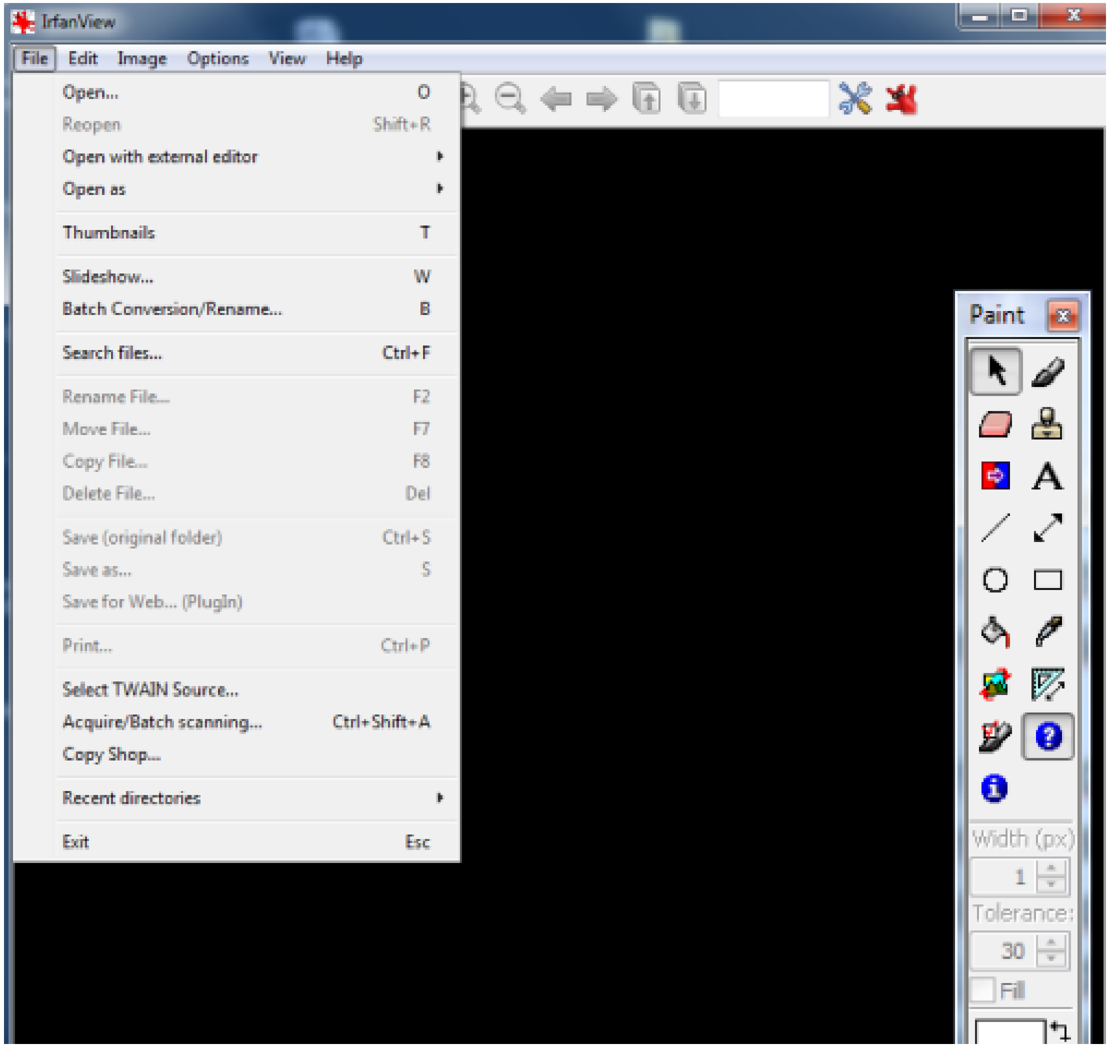
Save in folder: Desktop

Select File Type (Photoshop image)

File Type	Extens
MNG animation	mng
PBM image	pbm
PGM image	pgm
Photoshop image	psd
PNG image	png
PNM image	pnm

IrfanView

http://www.irfanview.com/



Freeware, which can handle many file types (with plugins: even flash-videos)

Some nice features:
- very fast
- batch conversion of images (e.g. to change the resolution)
- available in many languages
- slideshow option
- also contains Paint-tools and a text tool
- rotating of images
- changing canvas size or resolution ...

Inkscape
(free alternative for Adobe Illustrator)

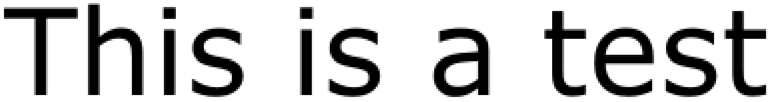
- https://inkscape.org
- for generating publication quality figures
- Creates scalable vector graphics files (svg-files) – and also other file formats, where images can be expanded without losing the resolution (e.g. perfectly suited for posters and figures to prevent pixelated images)
- Good tutorials and documentation at: https://inkscape.org/learn/
- If you prefer **Adobe Illustrator**: an older version (CS2) is available at: https://www.computerbild.de/download/Adobe-Illustrator-CS2-Vollversion-8043129.html

Difference between bitmap and vector graphics

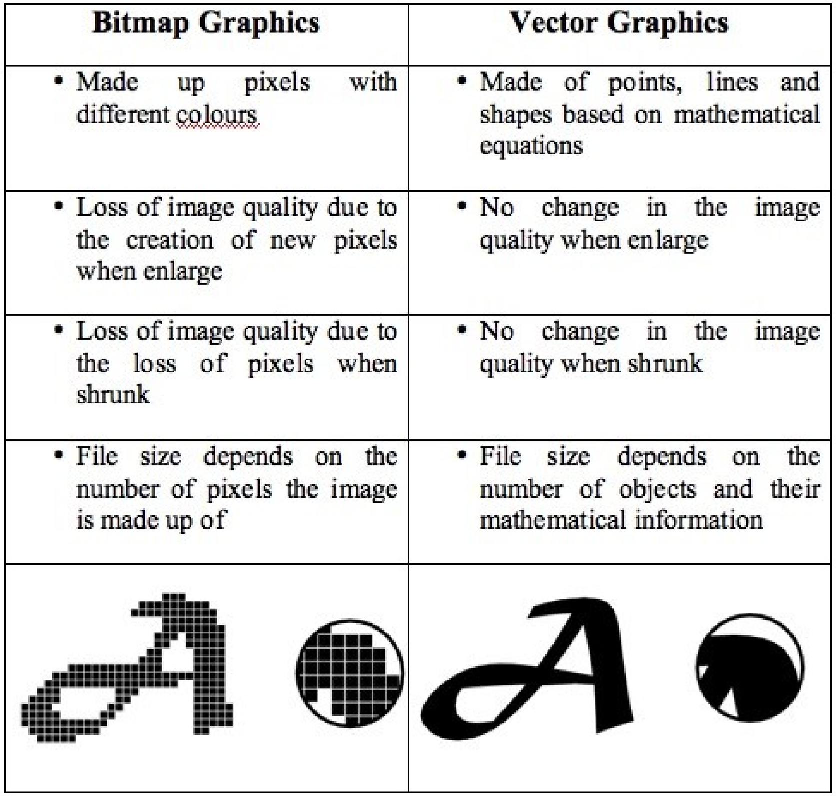
Gimp, jpg-file (enlarged):

This is a test

Inkscape:



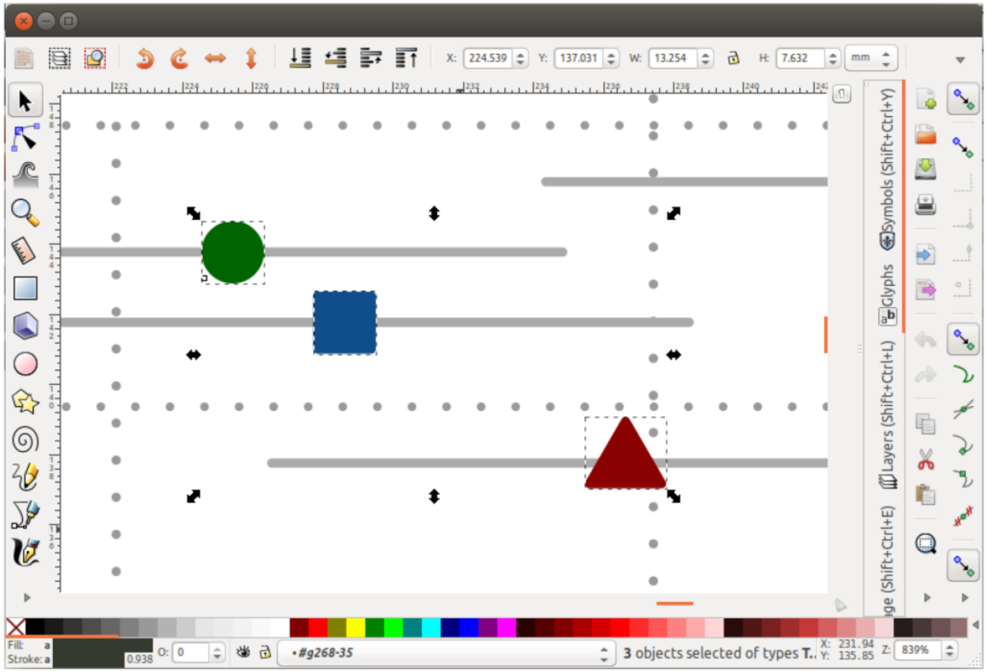
This is a test



Bitmap Graphics	**Vector Graphics**
- Made up pixels with different colours	- Made of points, lines and shapes based on mathematical equations
- Loss of image quality due to the creation of new pixels when enlarge	- No change in the image quality when enlarge
- Loss of image quality due to the loss of pixels when shrunk	- No change in the image quality when shrunk
- File size depends on the number of pixels the image is made up of	- File size depends on the number of objects and their mathematical information

What is Inkscape?

- Vector Graphics Editor
- Free Software
- Cross Platform
- Easy to use
- Good for:
  - Compositing
  - Drawing
- Not for:
  - Bitmap editing



X: 224.539 Y: 137.031 W: 13.254 H: 7.632 mm

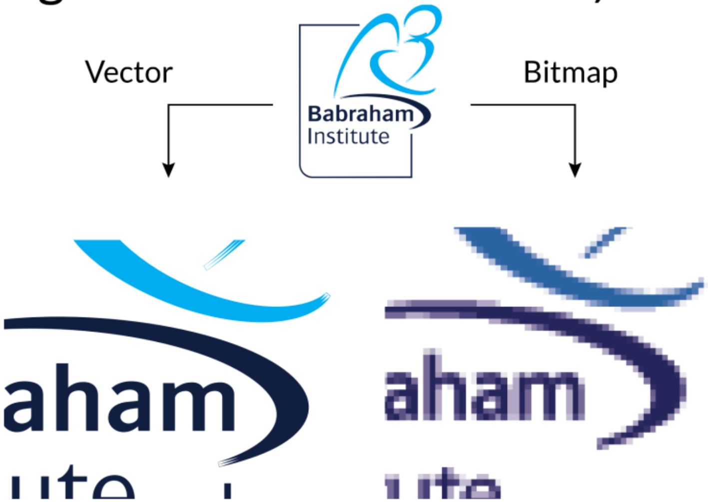
O: 0 #g268-35

3 objects selected of types T..

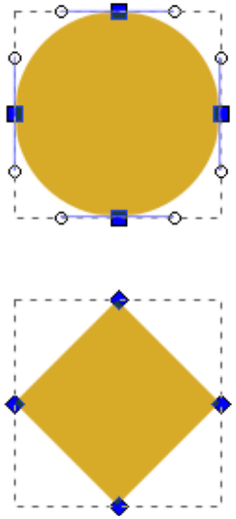
X: 231.94 Y: 135.85 Z: 839%

Scaling figures

- Vector images can be scaled freely without loss of quality
- Bitmap images can be scaled down, but not up



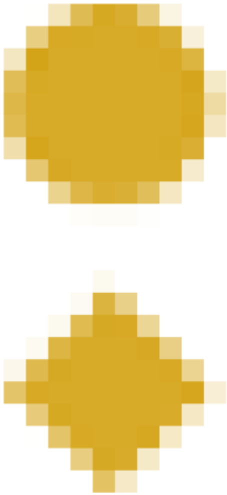
Vector images



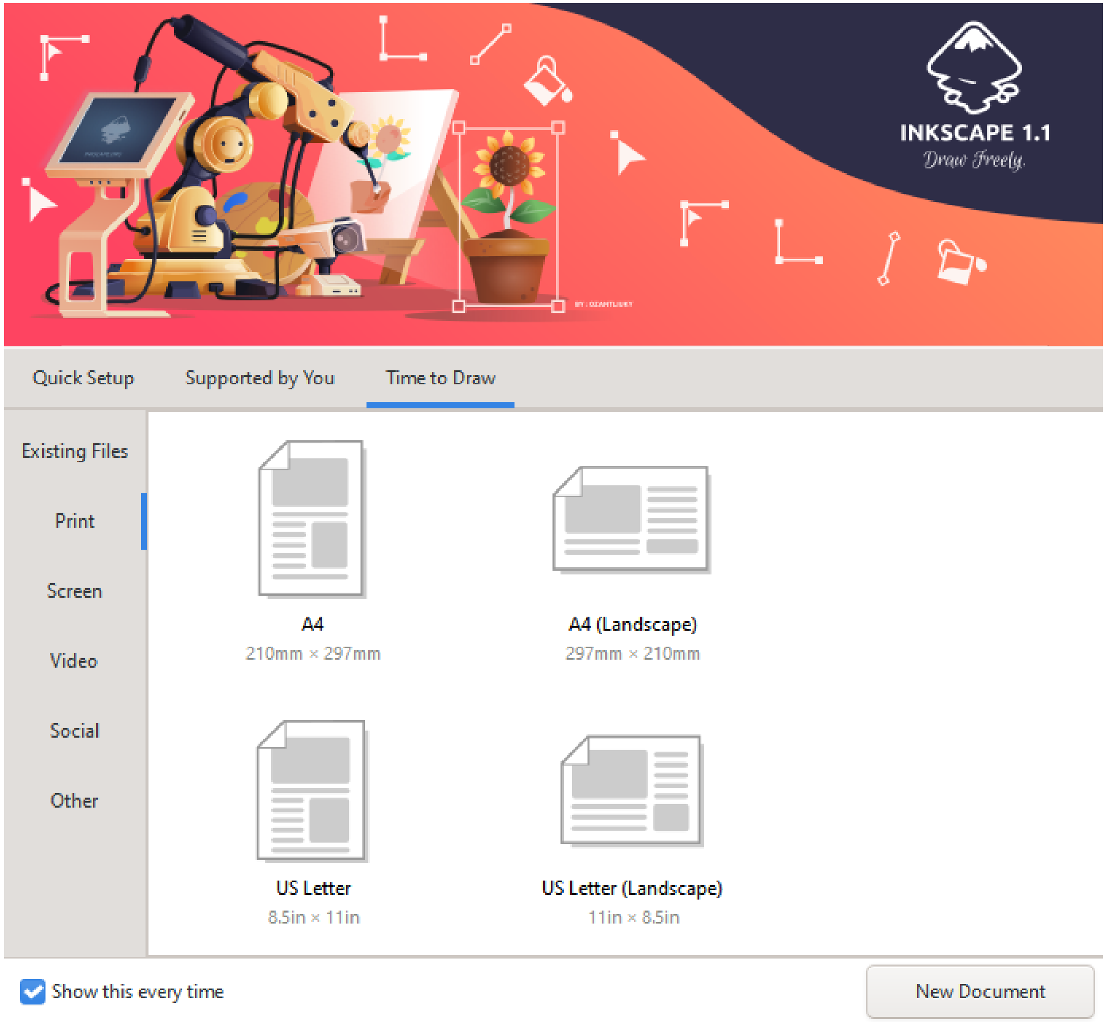
Images are made by points and their connections.
Connections can be straight or smooth

Bitmap

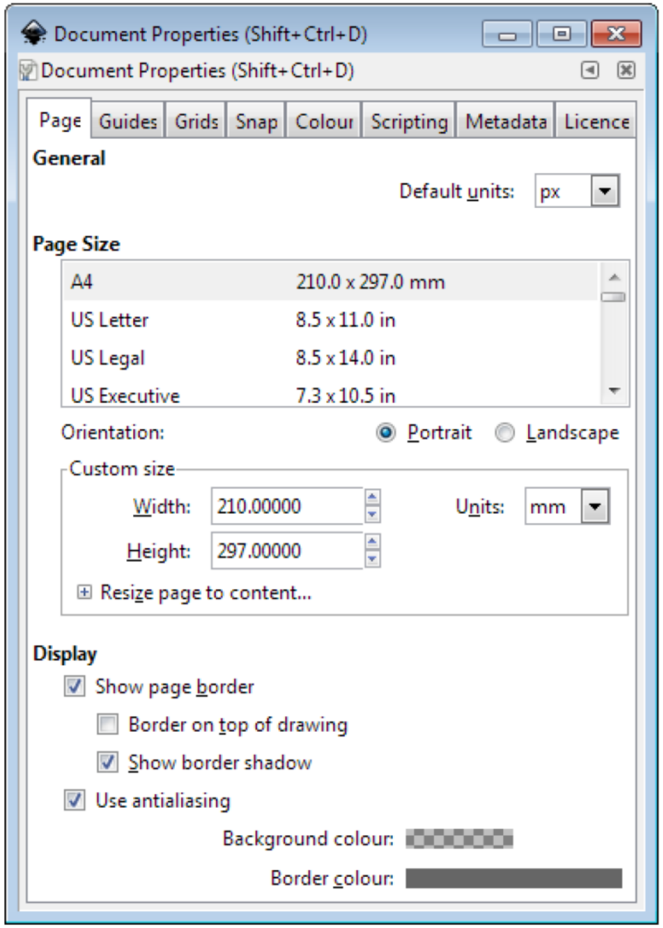
Images are made of pixels and a colour value



The start screen



Exercise 1: set up a canvas



General

Default units: px

Page Size

A4	210.0 x 297.0 mm
US Letter	8.5 x 11.0 in
US Legal	8.5 x 14.0 in
US Executive	7.3 x 10.5 in

Orientation: ● Portrait ○ Landscape

Custom size

Width: 210.00000 Units: mm

Height: 297.00000

⊞ Resize page to content...

Display

☑ Show page border

☐ Border on top of drawing

☑ Show border shadow

☑ Use antialiasing

Background colour: ▨

Border colour: ■

- ***File > Document Properties***
  - Shows page in view
  - Doesn’t restrict drawing
  - Useful as a guide
- Change background colour to white
- Change to landscape

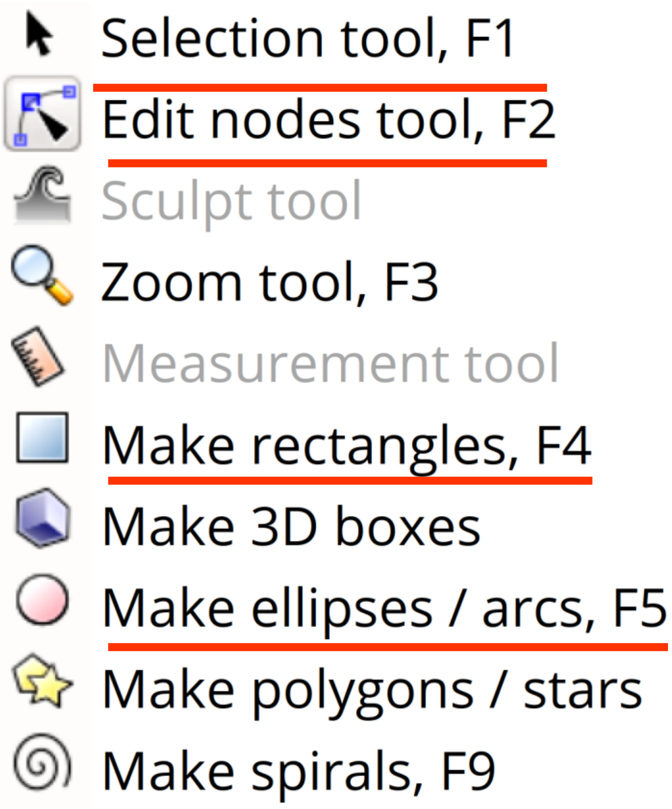
Moving around

- Panning
  - Scroll bars on bottom / right
  - Scroll up/down, Shift+scroll for left/right
- Zooming in / out
  - Click to zoom in, shift+click to zoom out
  - Control + Scroll Up/Down to zoom in/out to cursor
- Shortcuts
  - Fit page, drawing, selection in window

Create basic shapes

- Select tool from toolbar
- **Click and drag on canvas**
  - Box selects the bounds of the new shape
  - Colours are remembered from the last shape
- Basic options appear in **top toolbar**
  - Number of spokes on stars
  - Rounded corners on rectangles
  - Circle vs segment vs arc

The main toolbar



Selection tool, F1

Edit nodes tool, F2

Sculpt tool

Zoom tool, F3

Measurement tool

Make rectangles, F4

Make 3D boxes

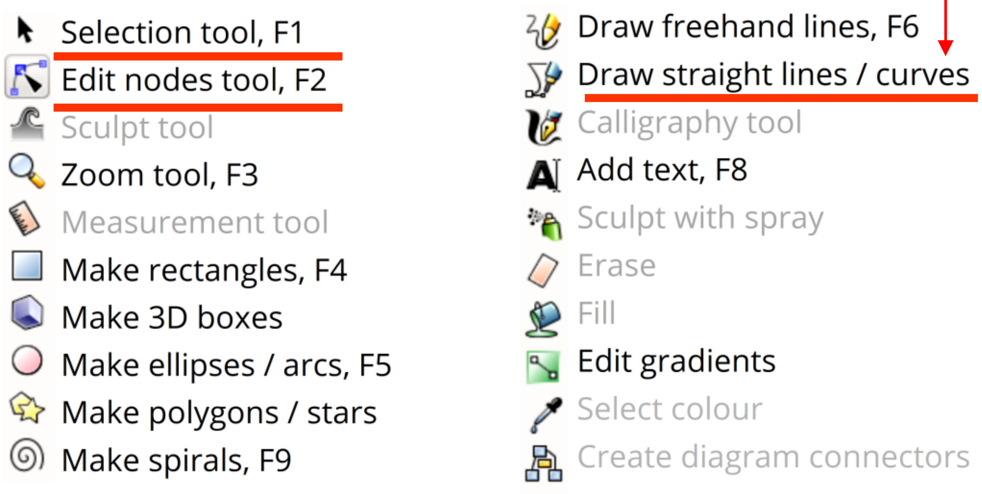
Make ellipses / arcs, F5

Make polygons / stars

Make spirals, F9

The main toolbar

press Strg (Ctrl) to force an exact horizontal/vertical line or 15° angles

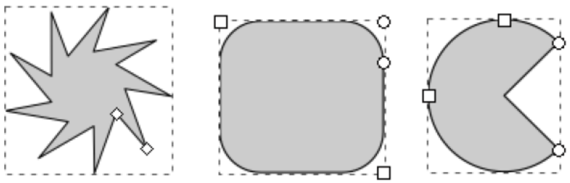


- Selection tool, F1
- Edit nodes tool, F2
- Sculpt tool
- Zoom tool, F3
- Measurement tool
- Make rectangles, F4
- Make 3D boxes
- Make ellipses / arcs, F5
- Make polygons / stars
- Make spirals, F9

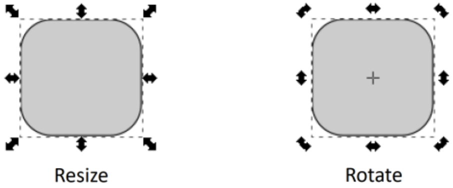
- Draw freehand lines, F6
- Draw straight lines / curves
- Calligraphy tool
- Add text, F8
- Sculpt with spray
- Erase
- Fill
- Edit gradients
- Select colour
- Create diagram connectors

Control nodes

- Use the Edit Nodes tool
- Two types of control points, squares and circles
  - Squares generally change the size of the shape
  - Circles change the appearance



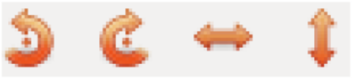
Resize / Rotate



- Can use shift/control keyboard modifiers as before
- For rotation you can move the crosshair to change the centre of rotation

Transform Shortcuts

or



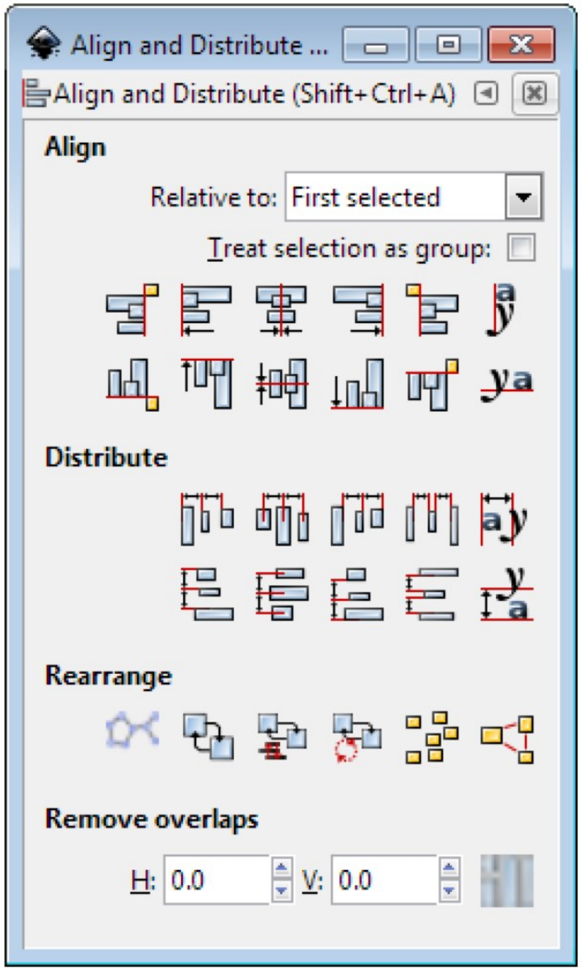
- Rotate 90 degrees anticlockwise
- Rotate 90 degrees clockwise
- Mirror object around the vertical axis
- Mirror object around the horizontal axis

Grouping

- Grouping (right click > Group or Ctrl + G)
  - Combine multiple objects into a single object
  - Reversible: Ungroup (Control+Shift+G)

Aligning and distributing

- Object > Align and Distribute
  - – Align = Give objects the same centre/edge position
  - – Distribute = Space objects evenly
- Align relative to
  - – First/Last selected object in group
  - – Largest/Smallest object in group
  - – Page
  - – Drawing
- Never align anything by eye!



Align and Distribute ...

Align and Distribute (Shift+Ctrl+A)

Align

Relative to: First selected

Treat selection as group: ☐

Distribute

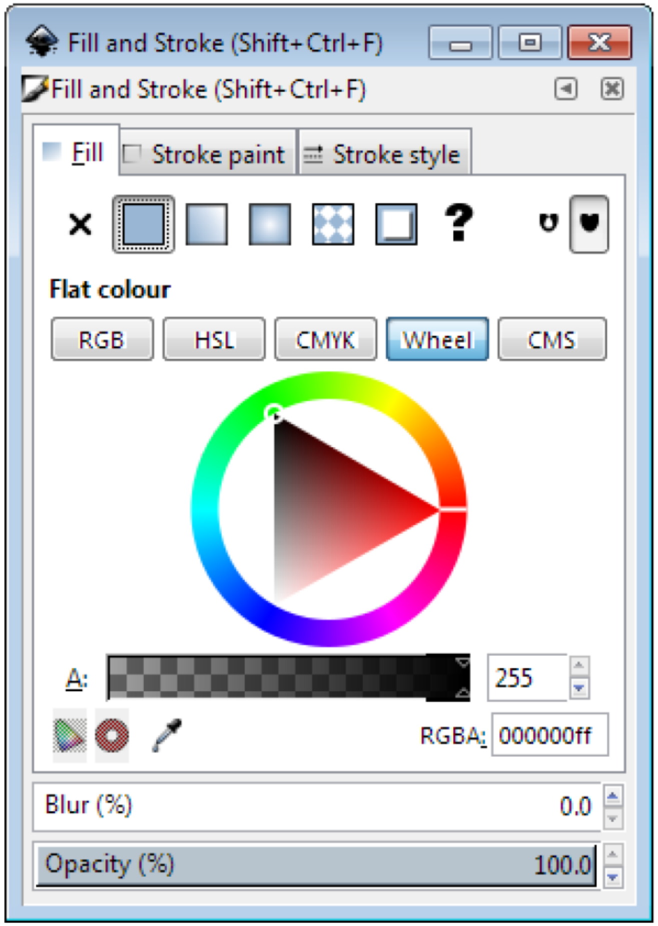
Rearrange

Remove overlaps

H: 0.0 V: 0.0

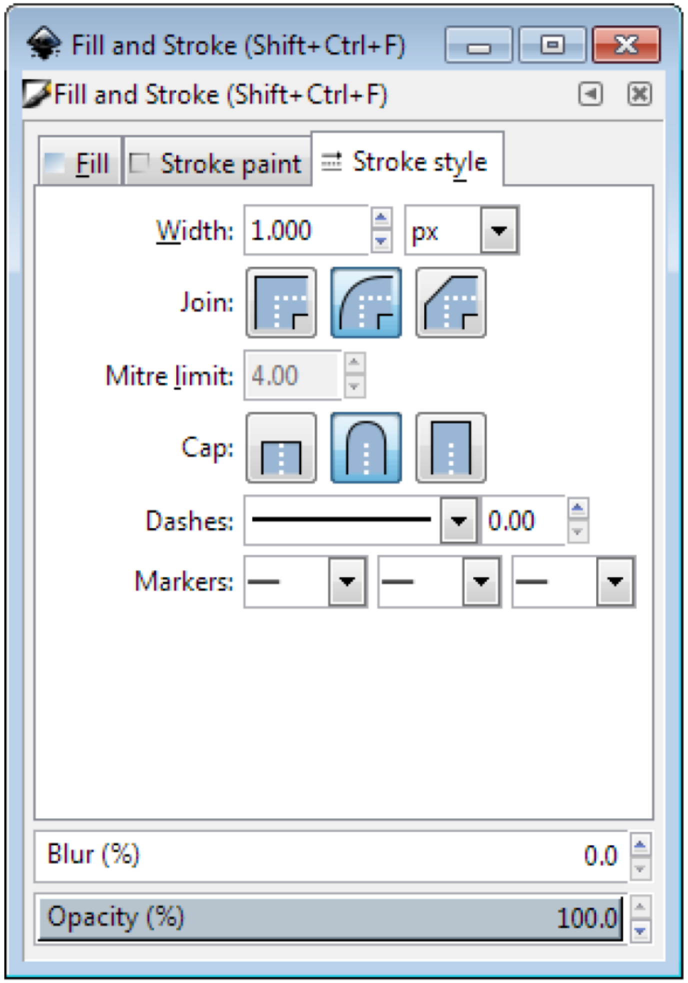
Fill and Stroke

- Fill = Colour/ Gradient/ Pattern within a shape
- Stroke = The line around a shape
- Object > Fill and Stroke (Shift+Ctrl+F)
- Edit
  - – Colours
  - – Opacity
  - – Blur



Stroke Options

- Width of line
- Shape of corners
- Shape of line ends
- Dashes
- Arrowheads



Fill and Stroke (Shift+Ctrl+F)

Fill and Stroke (Shift+Ctrl+F)

Width: 1.000 px

Mitre limit: 4.00

Dashes: 0.00

Blur (%) 0.0

Opacity (%) 100.0

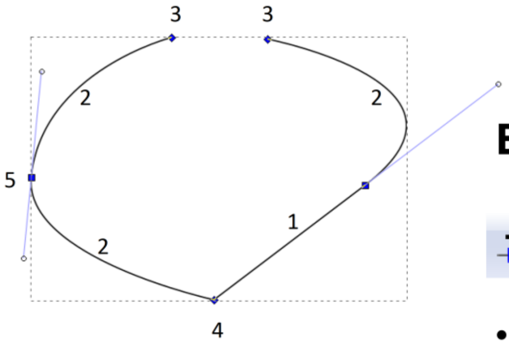
Creating and Editing Paths

- Created using freehand or line tool
- Can convert other objects to become a path

- Paths are composed of nodes and segments
- There are different types of node and segment

Nodes and Segments

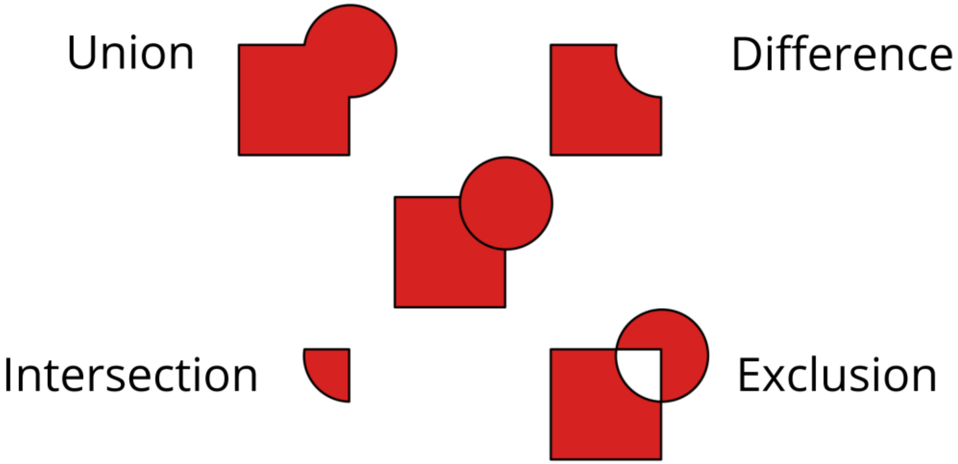
- Segment types
  - Lines (1)
  - Curves (2)
- Node types
  - End (3)
  - Corner (4)
  - Smooth (5)
    - Normal
    - Symmetric
    - Auto



Editing nodes

- Use nodes toolbar to add, remove or convert nodes or segments
- Select nodes or segments to make their handles visible
- Drag handles to change the arc of curves

Combining Paths



Union

Difference

Intersection

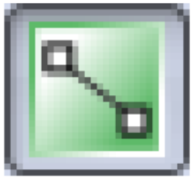
Exclusion

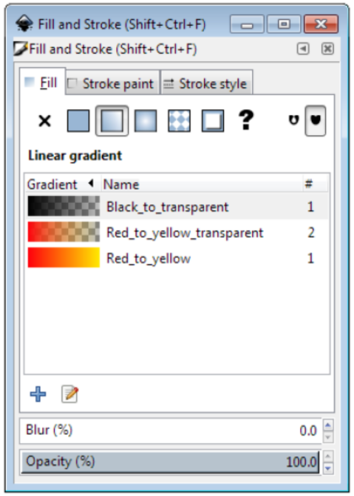
Opacity / Blur

- Applies to whole object
- Separate from alpha in colours
- Works on all Objects

Gradients

- Standard colour option
- Set multiple colours / opacities to go through
- Set the direction and extent of the gradient



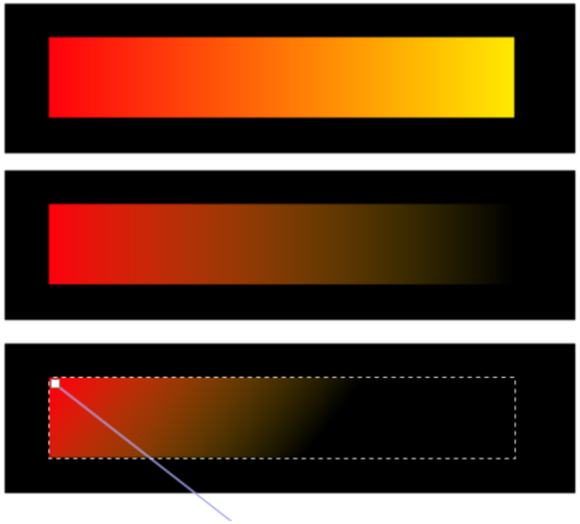


Linear gradient

Gradient	Name	#
	Black_to_transparent	1
	Red_to_yellow_transparent	2
	Red_to_yellow	1

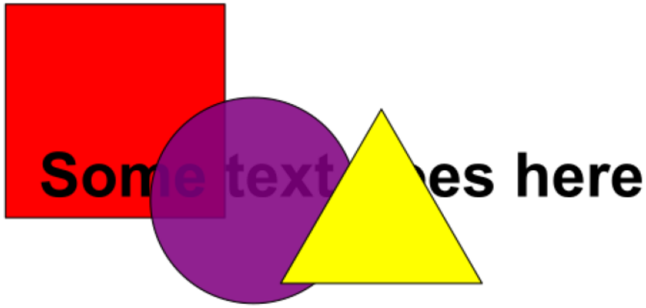
Blur (%) 0.0

Opacity (%) 100.0



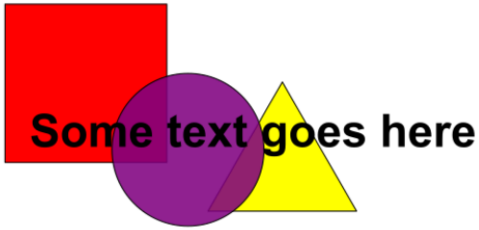
Z axis - Ordering

- New objects sit over the top of old objects
- Objects obscure those underneath them (except for transparency)



Z-axis Ordering

- Send object to bottom of z-stack
- Lower object one level
- Raise object one level
- Bring object to top



Working with bitmaps (photos)

- Inkscape can include bitmaps in images
- Appear as objects alongside vector objects
- Can’t edit the images
- Can’t increase the resolution of the image
- Transparency (from PNG etc) is preserved

- ***File > Import***
- Formats: PNG, JPEG, SVG, PDF etc.

Text toolbar

sans-serif

10

Normal

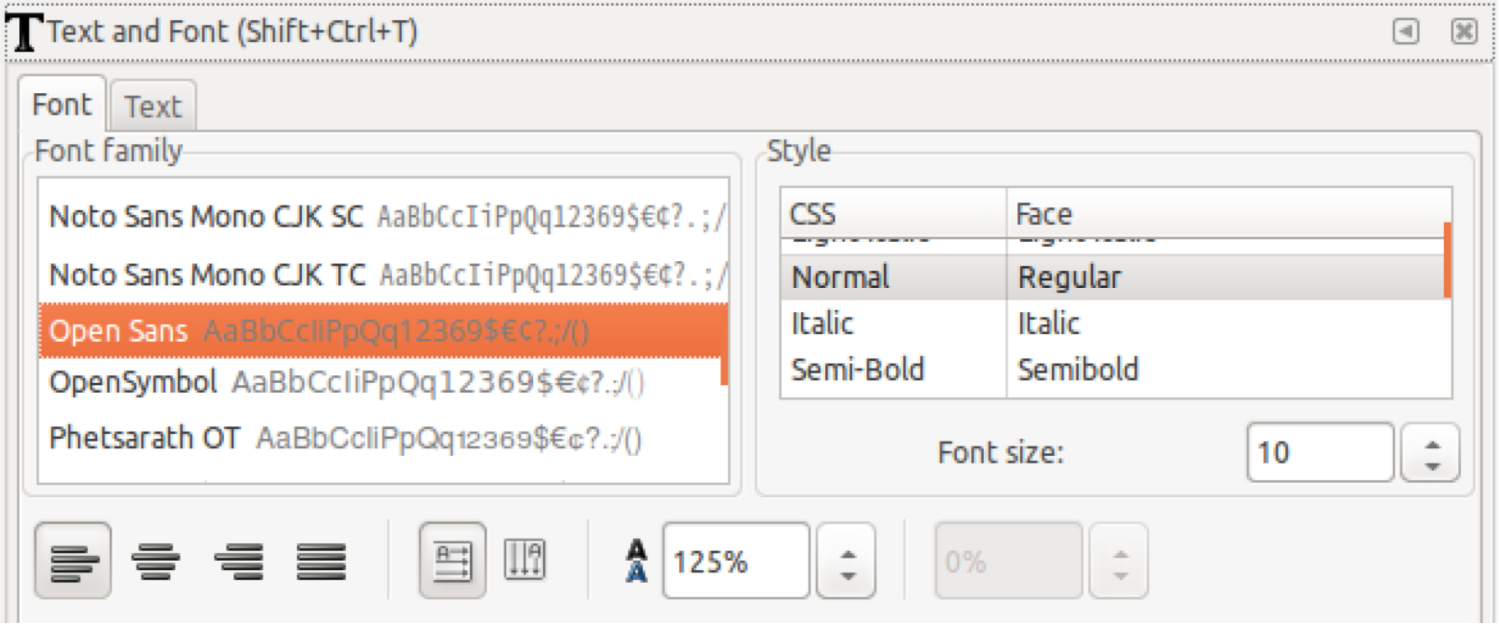
1.25

0.00

0.00

0.00

Text and font settings: font, alignment, spacing



Text and Font (Shift+Ctrl+T)

Font | Text

Font family

Noto Sans Mono CJK SC AaBbCcIiPpQq12369$€¢?.;/

Noto Sans Mono CJK TC AaBbCcIiPpQq12369$€¢?.;/

Open Sans AaBbCcIiPpQq12369$€¢?.;/()

OpenSymbol AaBbCcIiPpQq12369$€¢?.;/()

Phetsarath OT AaBbCcIiPpQq12369$€¢?.;/()

Style

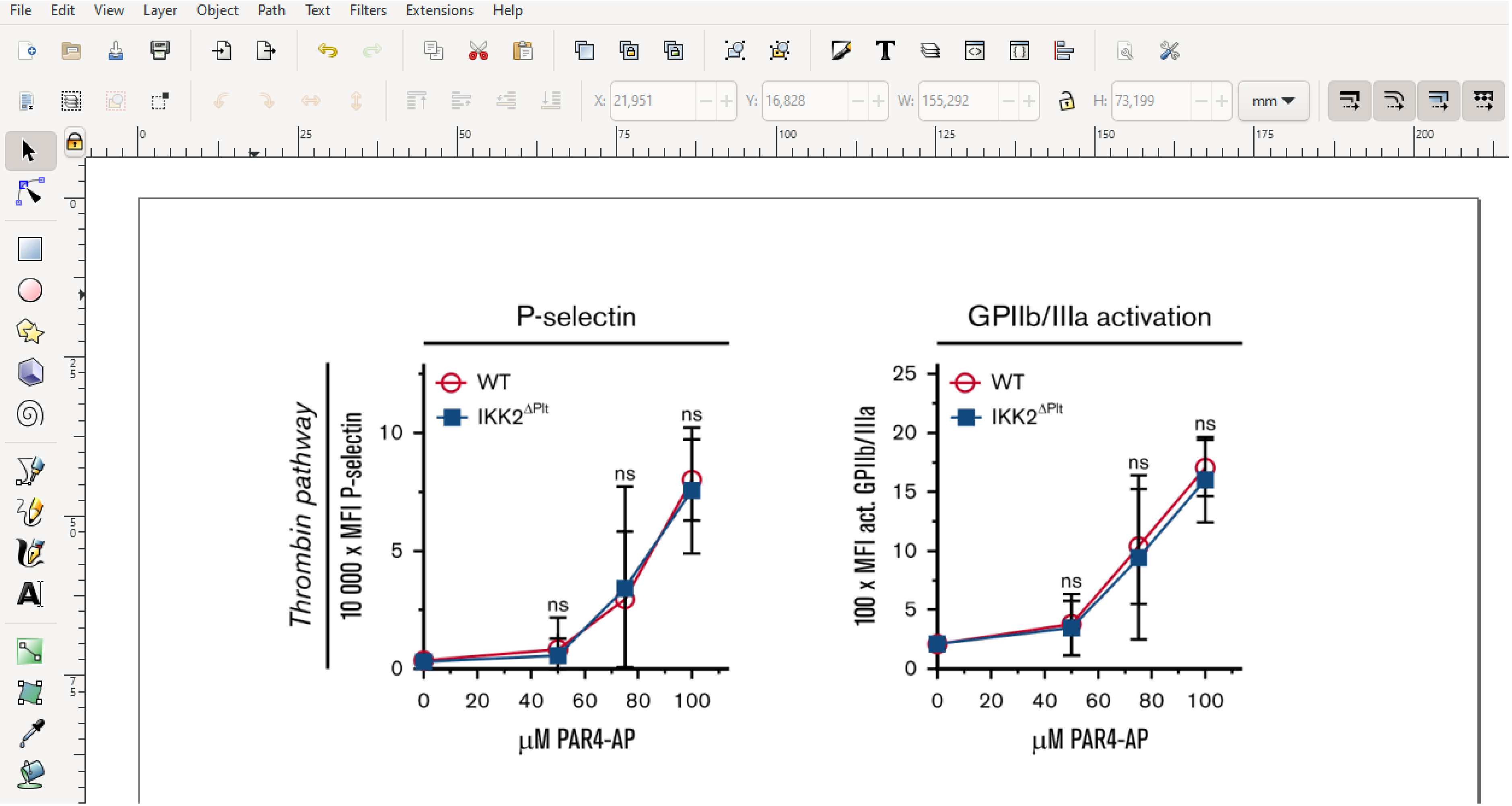
CSS	Face
Normal	Regular
Italic	Italic
Semi-Bold	Semibold

Font size: 10

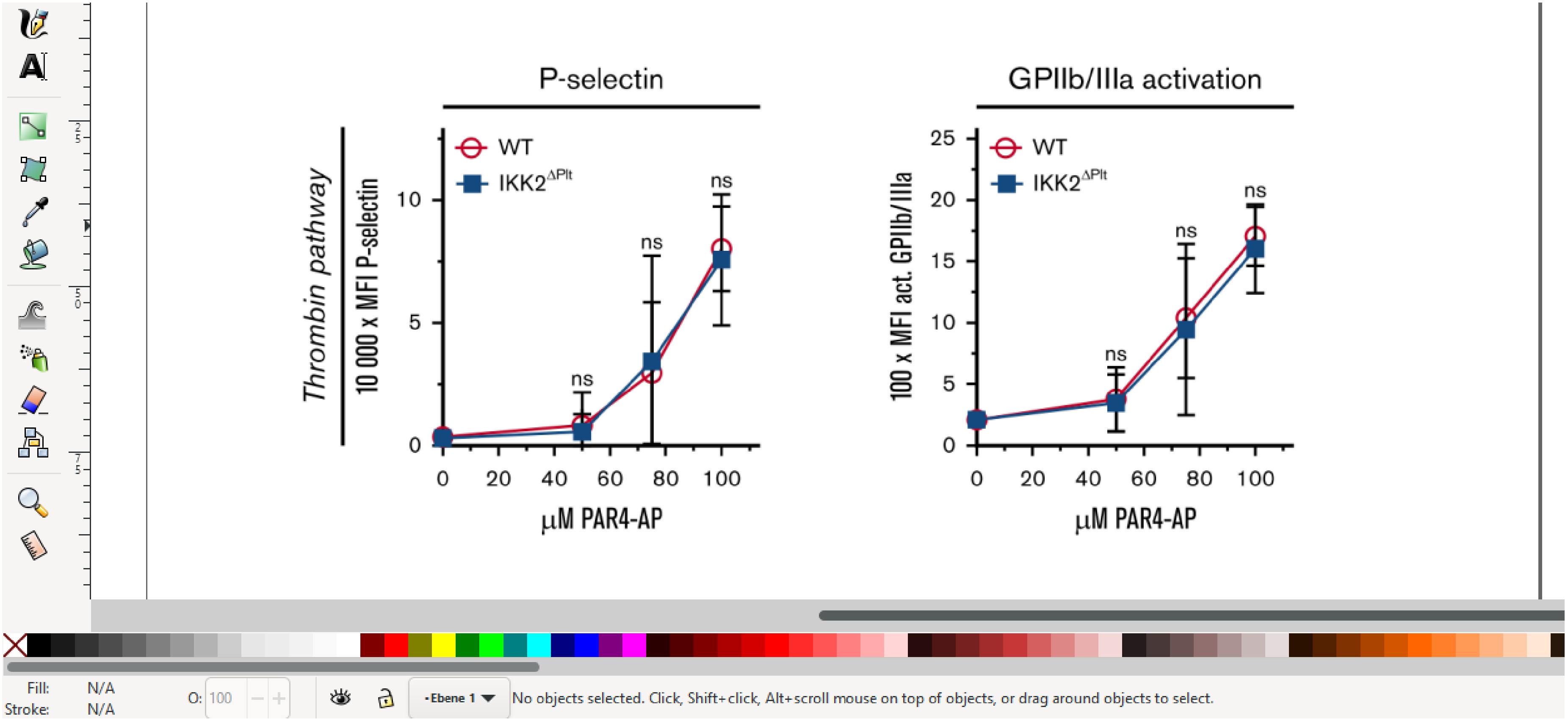
125%

0%

Example for a Figure template in Inkscape



X: 21,951 Y: 16,828 W: 155,292 H: 73,199

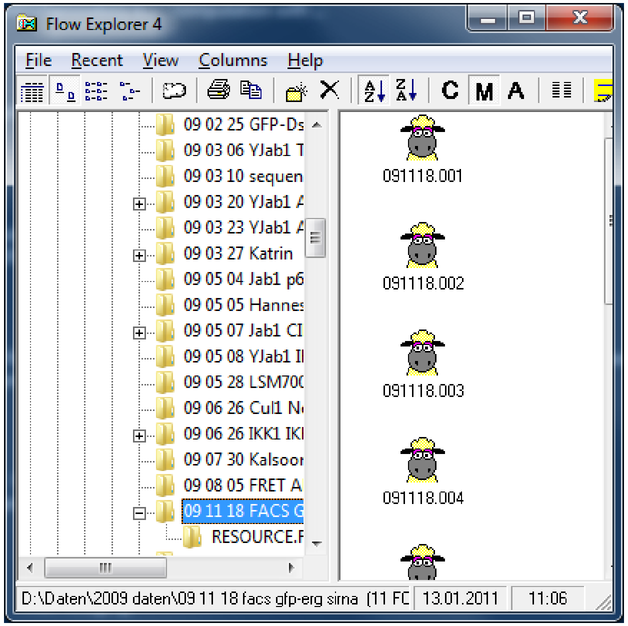


Fill: N/A
Stroke: N/A
O: 100

No objects selected. Click, Shift+click, Alt+scroll mouse on top of objects, or drag around objects to select.

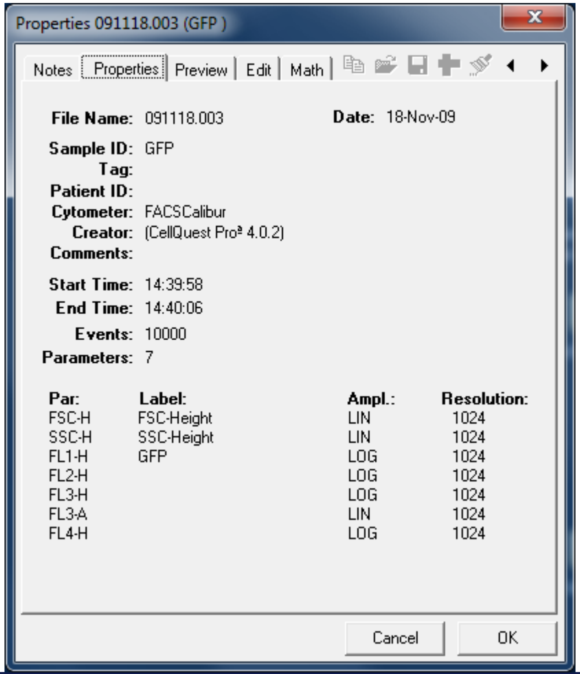
Cytometry Software: FlowExplorer - freeware

Scattergrams (Dot plots): each event is a dot



09 02 25 GFP-Ds
09 03 06 YJab1 T
09 03 10 sequen
09 03 20 YJab1 A
09 03 23 YJab1 A
09 03 27 Katrin
09 05 04 Jab1 p6
09 05 05 Hannes
09 05 07 Jab1 CI
09 05 08 YJab1 II
09 05 28 LSM70
09 06 26 Cul1 N
09 06 26 IKK1 IKI
09 07 30 Kalsoor
09 08 05 FRET A
09 11 18 FACS G
RESOURCE.F

D:\Daten\2009 daten\09 11 18 facs gfp-erg sirna (11 FC | 13.01.2011 | 11:06



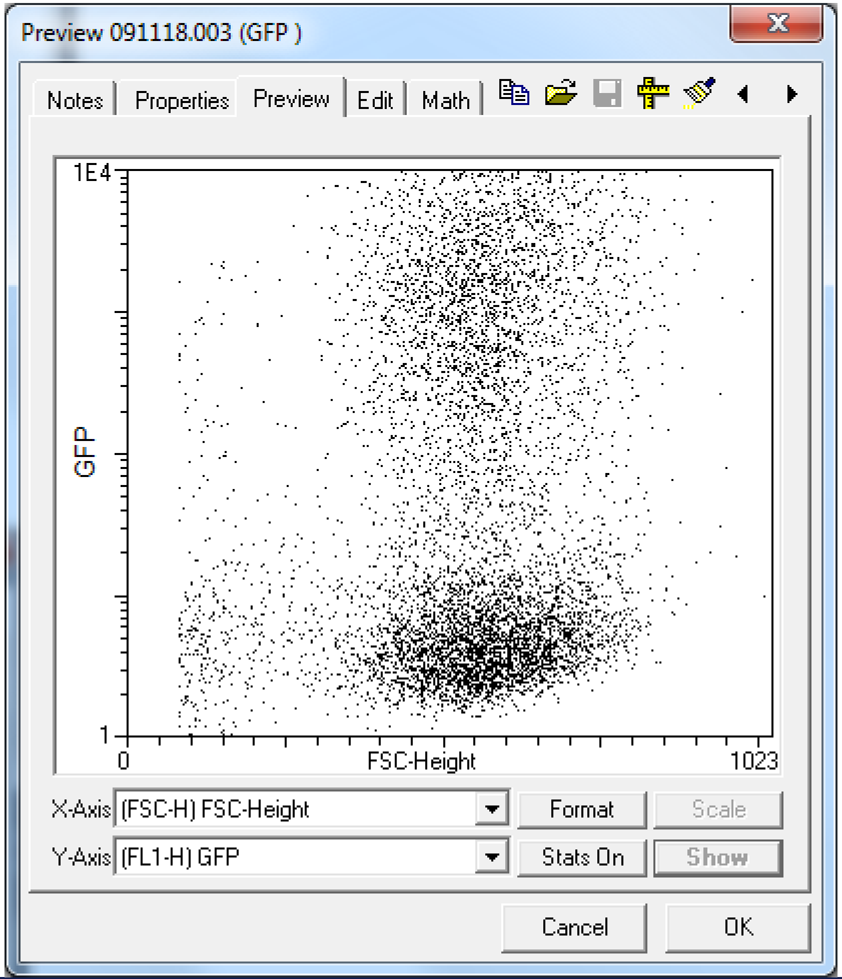
File Name: 091118.003 **Date:** 18-Nov-09

Sample ID: GFP
Tag:
Patient ID:
Cytometer: FACSCalibur
Creator: (CellQuest Pro³ 4.0.2)
Comments:

Start Time: 14:39:58
End Time: 14:40:06

Events: 10000
Parameters: 7

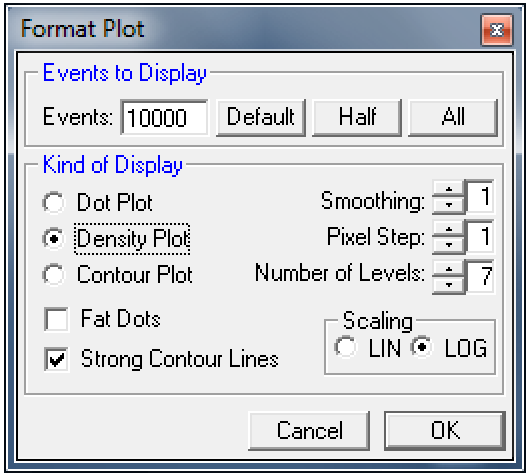
Par:	Label:	Ampl.:	Resolution:
FSC-H	FSC-Height	LIN	1024
SSC-H	SSC-Height	LIN	1024
FL1-H	GFP	LOG	1024
FL2-H		LOG	1024
FL3-H		LOG	1024
FL3-A		LIN	1024
FL4-H		LOG	1024



X-Axis (FSC-H) FSC-Height
Y-Axis (FL1-H) GFP

Contour plots and density plots

Dot plots are 2D-graphs they show values of two parameters
Density plots show a pseudocolor visualization of dot density


Format Plot

Events to Display

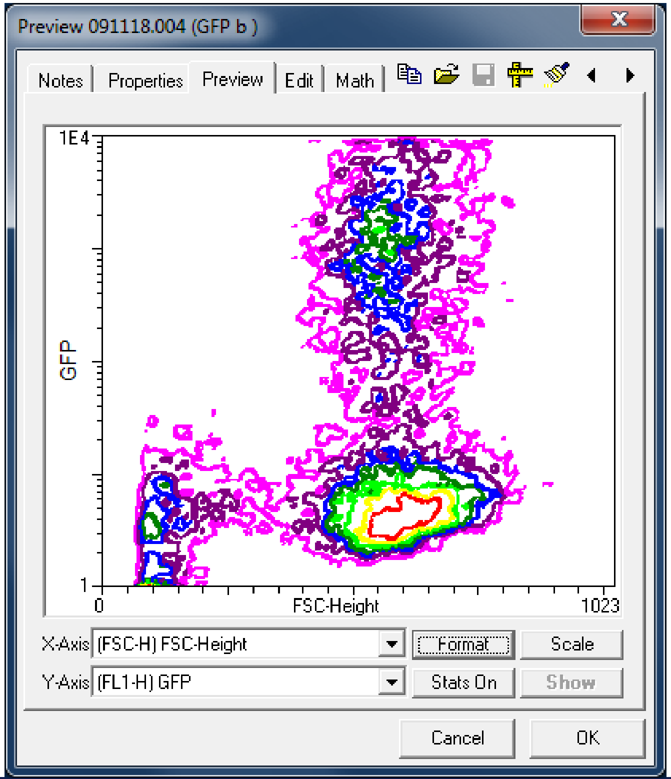
Events: 10000

Kind of Display

○ Dot Plot
● Density Plot
○ Contour Plot
☐ Fat Dots
☑ Strong Contour Lines

Smoothing: 1
Pixel Step: 1
Number of Levels: 7

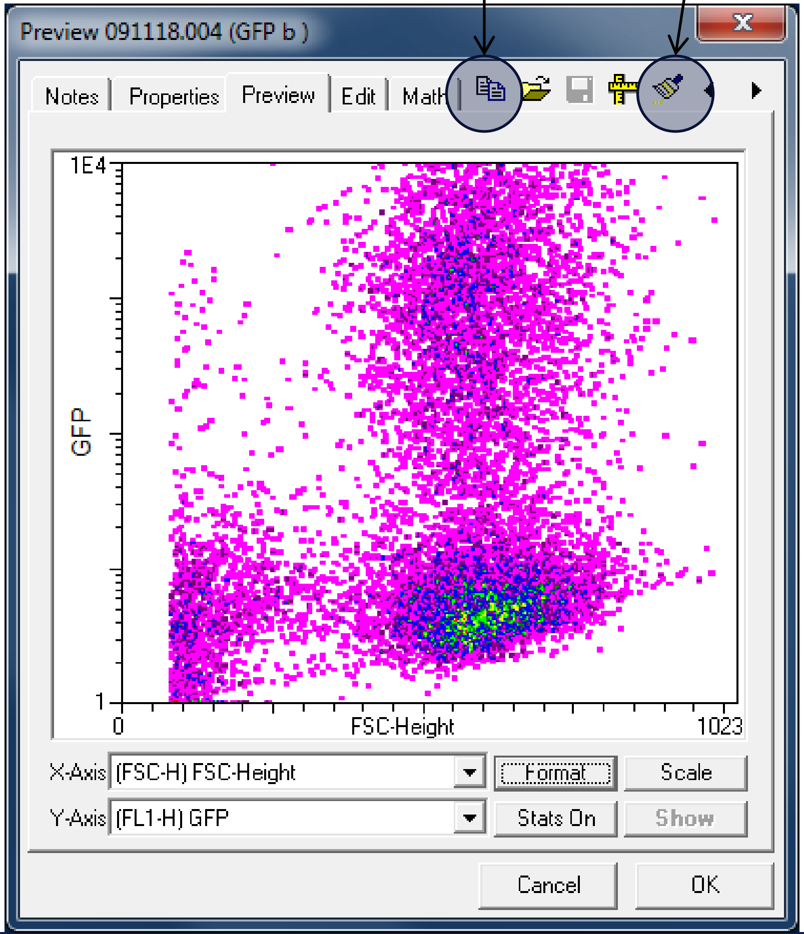
Scaling ○ LIN ● LOG


Preview 091118.004 (GFP b)

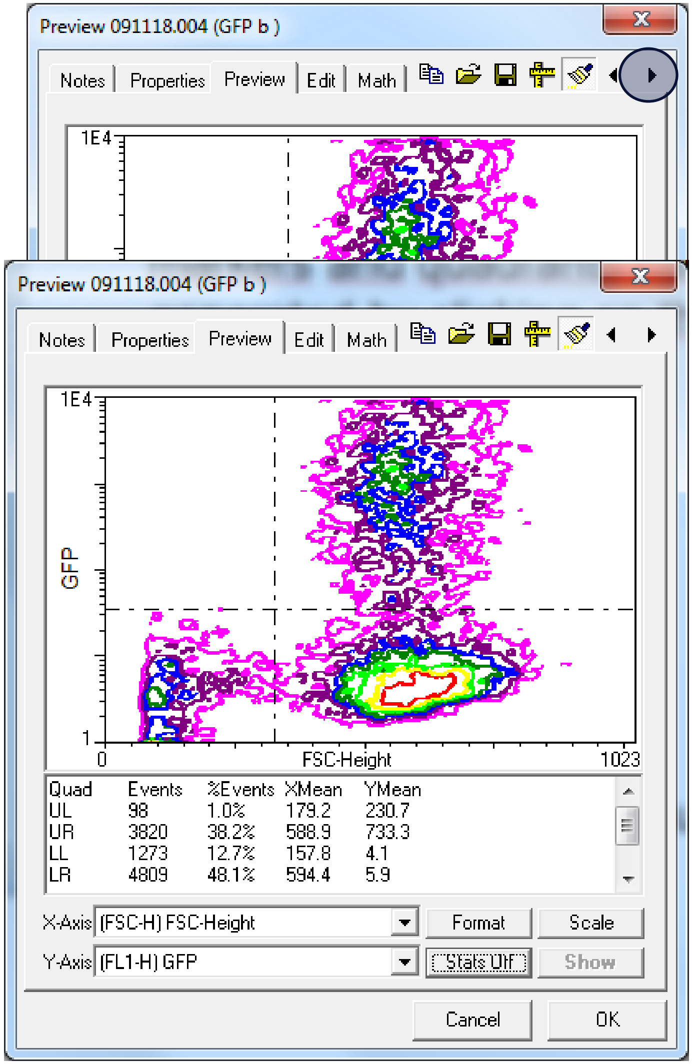
X-Axis (FSC-H) FSC-Height
Y-Axis (FL1-H) GFP

copy graph

auto-preview


Preview 091118.004 (GFP b)

X-Axis (FSC-H) FSC-Height
Y-Axis (FL1-H) GFP



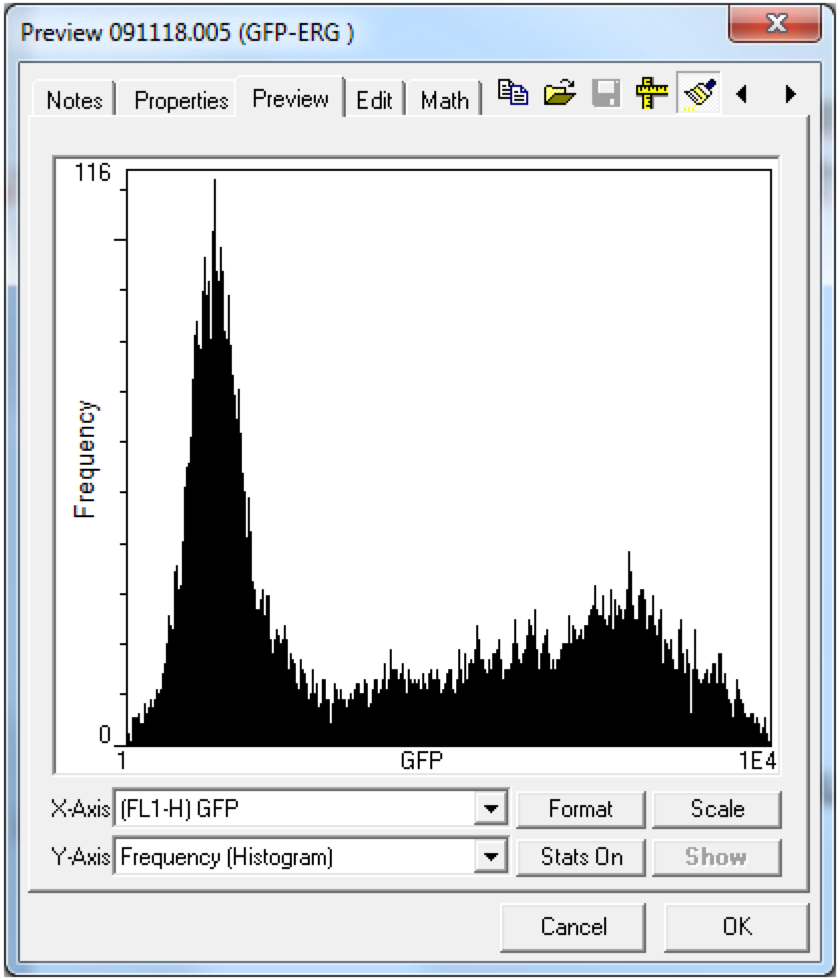
```
Quad   Events  %Events  XMean  YMean
UL     98      1.0%     179.2  230.7
UR     3820    38.2%    588.9  733.3
LL     1273    12.7%    157.8  4.1
LR     4809    48.1%    594.4  5.9
```

next file

markers and quadrants can be generated by clicking on the border and dragging into the graph

Pressing the „Stats On“ Button shows statistics

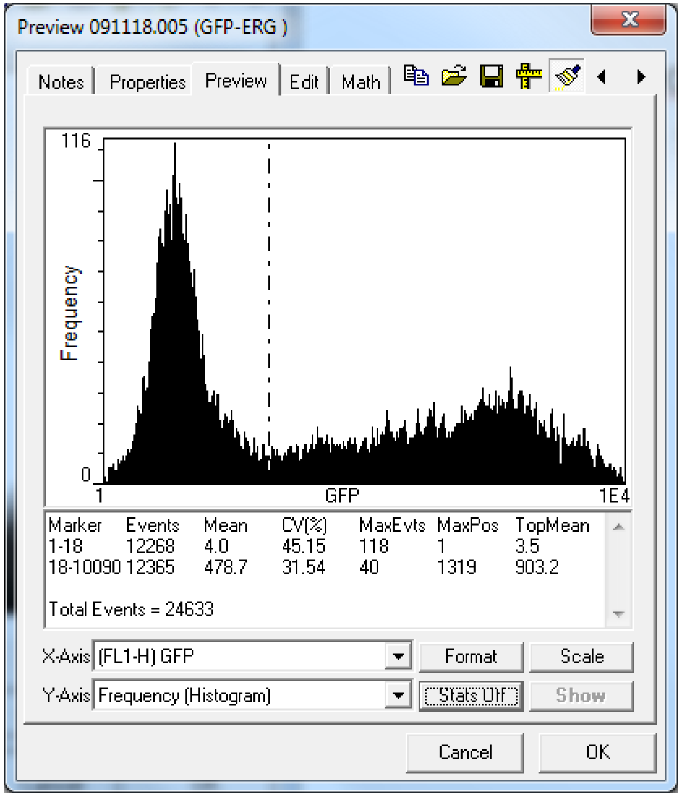
Histograms
(frequency of events for a parameter)



X-Axis (FL1-H) GFP

Y-Axis Frequency (Histogram)

choosing Frequency (Histogram) for the Y-axis generates a histogram



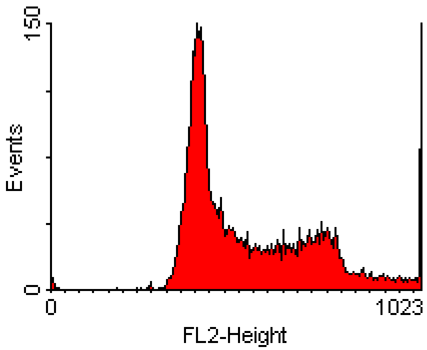
```
Marker   Events  Mean   CV(%)  MaxEvts  MaxPos  TopMean
1-18     12268   4.0    45.15  118      1       3.5
18-10090 12365   478.7  31.54  40       1319    903.2

Total Events = 24633
```

X-Axis (FL1-H) GFP

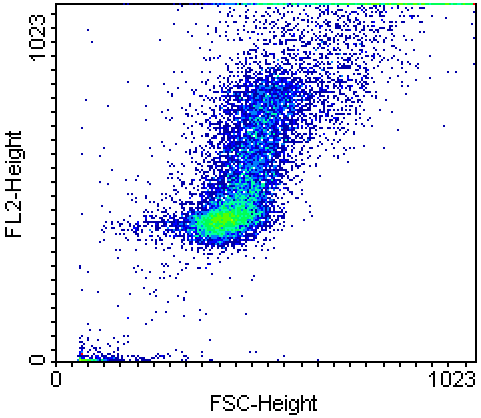
Y-Axis Frequency (Histogram)

Overview of cytometry plots

Histogram

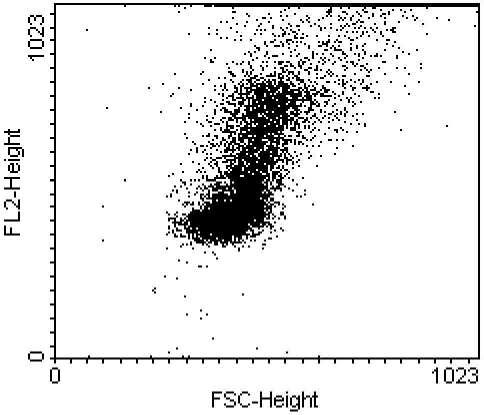


Density Plot

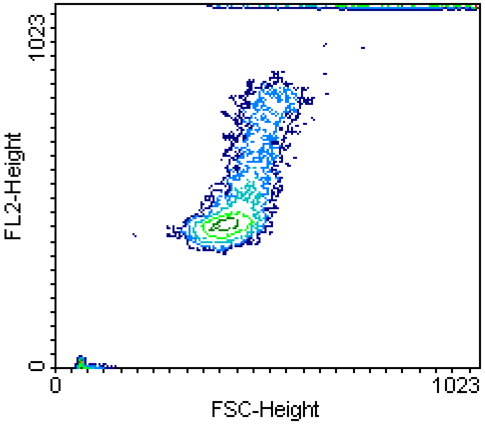


colour coding of the frequency

Dot Plot



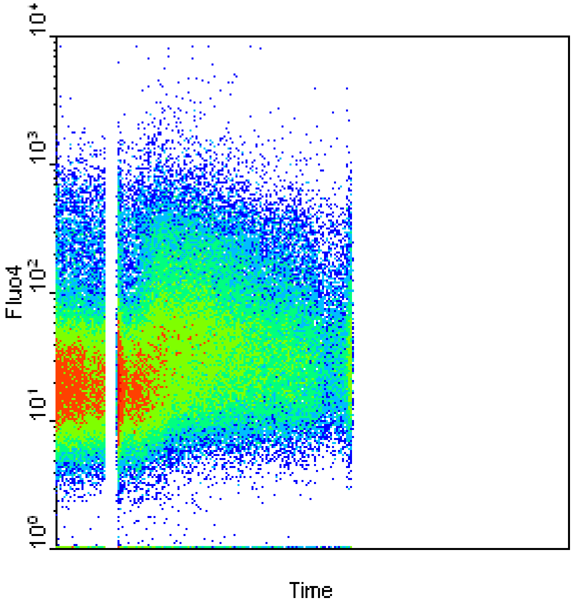
Contour Plot

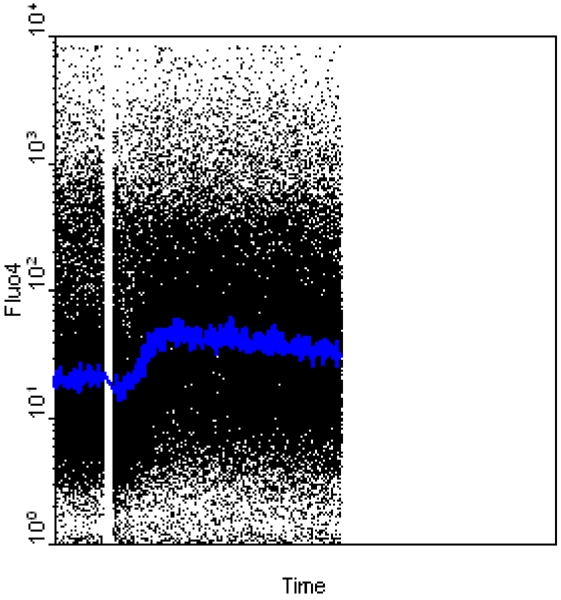


colour coded contours of the frequency (similar to the height lines in a map)

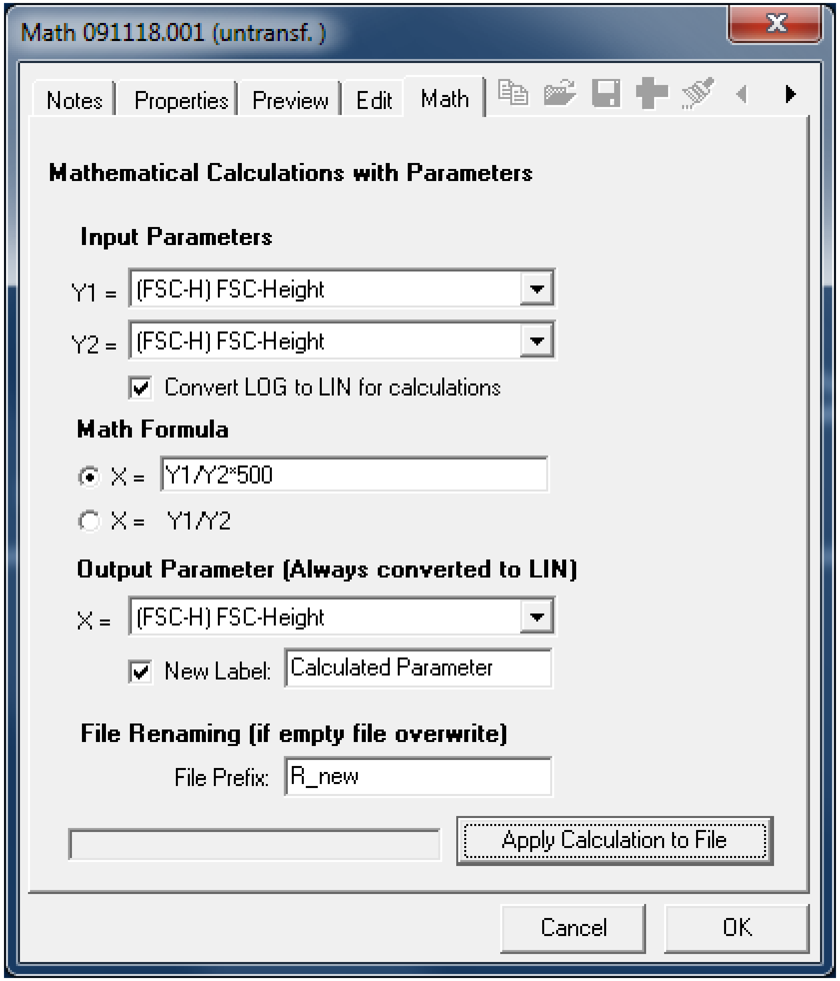
Time course of fluorescence in flow analysis

Some processes can be measured by analyzing the time course of fluorescence (e.g. calcium influx with Fluo-4 calcium sensitive fluorophores). The time parameter can be recorded at the data acquisition – and also visualized with WinMDI





Mathematical operations (e.g. ratios)



Mathematical Calculations with Parameters

Input Parameters

Y1 = (FSC-H) FSC-Height

Y2 = (FSC-H) FSC-Height

☑ Convert LOG to LIN for calculations

Math Formula

● X = Y1/Y2*500

○ X = Y1/Y2

Output Parameter (Always converted to LIN)

X = (FSC-H) FSC-Height

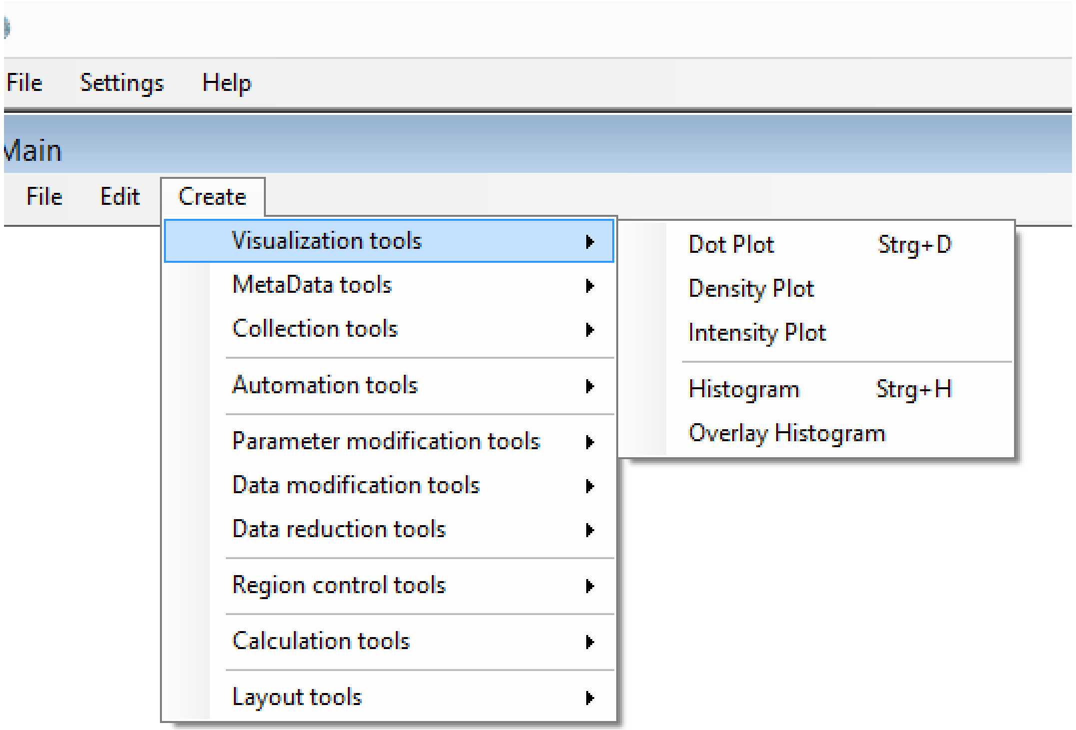
☑ New Label: Calculated Parameter

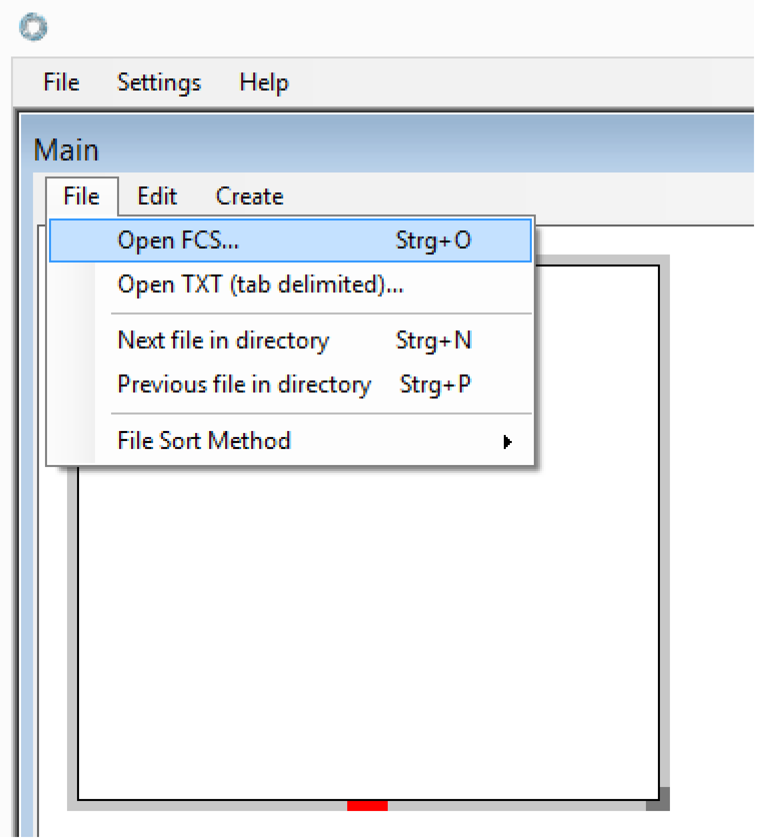
File Renaming (if empty file overwrite)

File Prefix: R_new

Cytometry software: Flowing Software 2

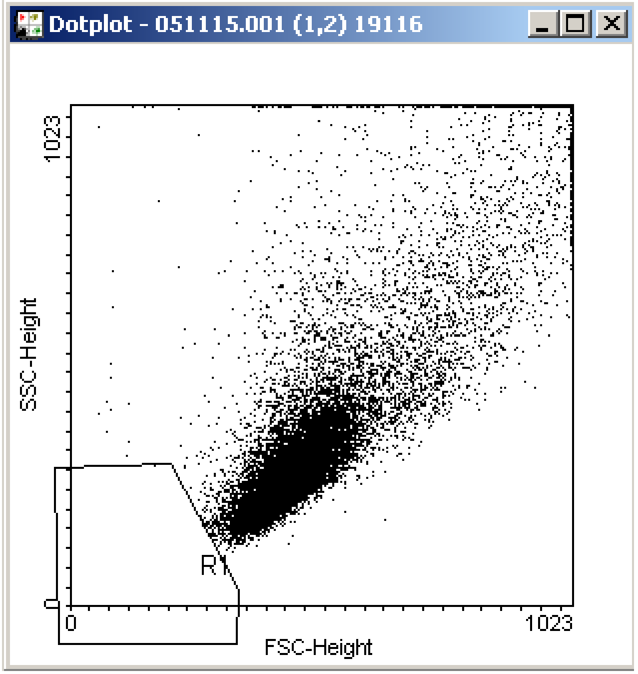
http://www.flowingsoftware.com



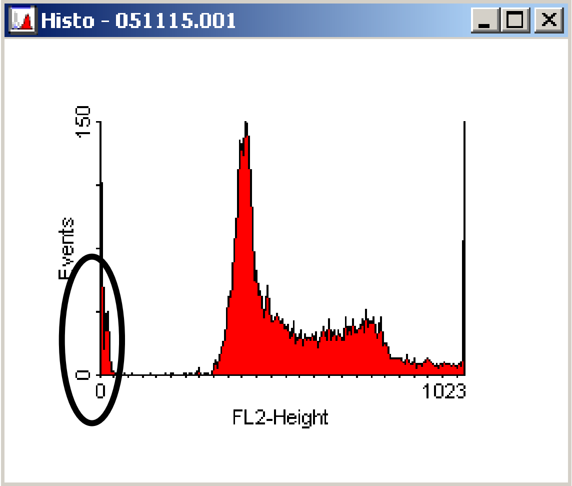


Gating can be done in different graphs than the one used for defining the region

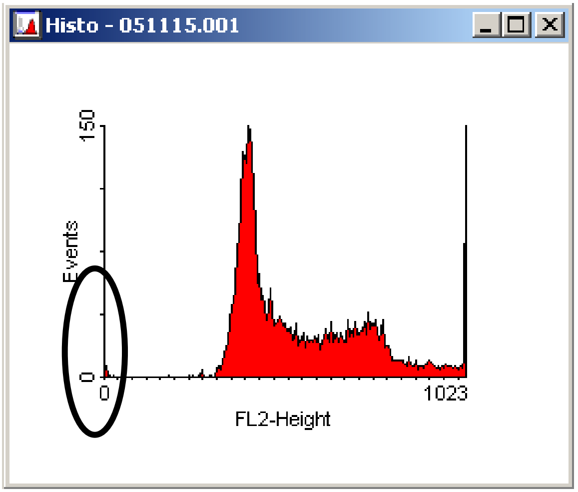
Regions can be used as locigal „Gates“ to accept or reject data (e.g. to exclude cell debris)



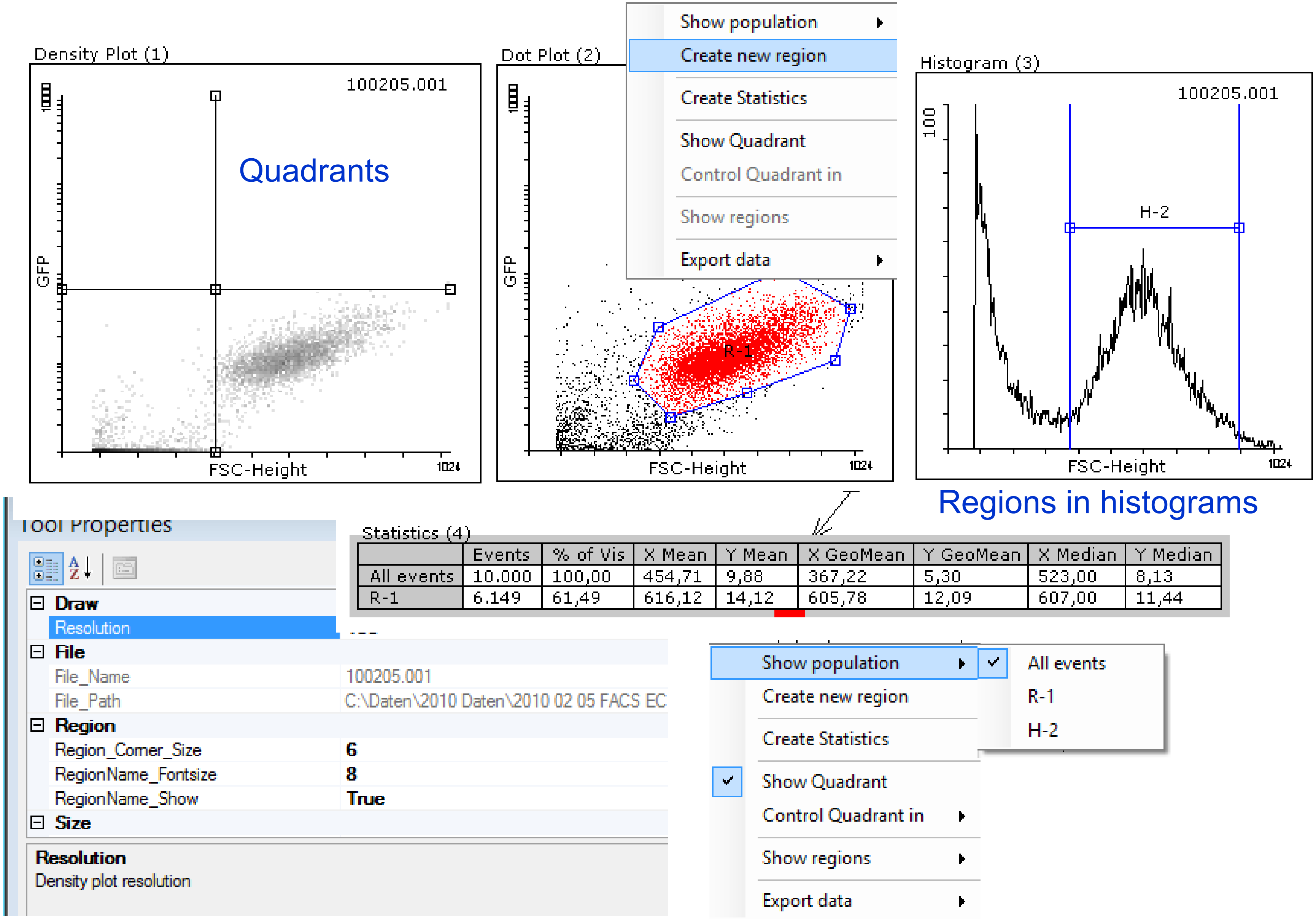
ungated



gated



Flowing Software 2 – Regions and statistics



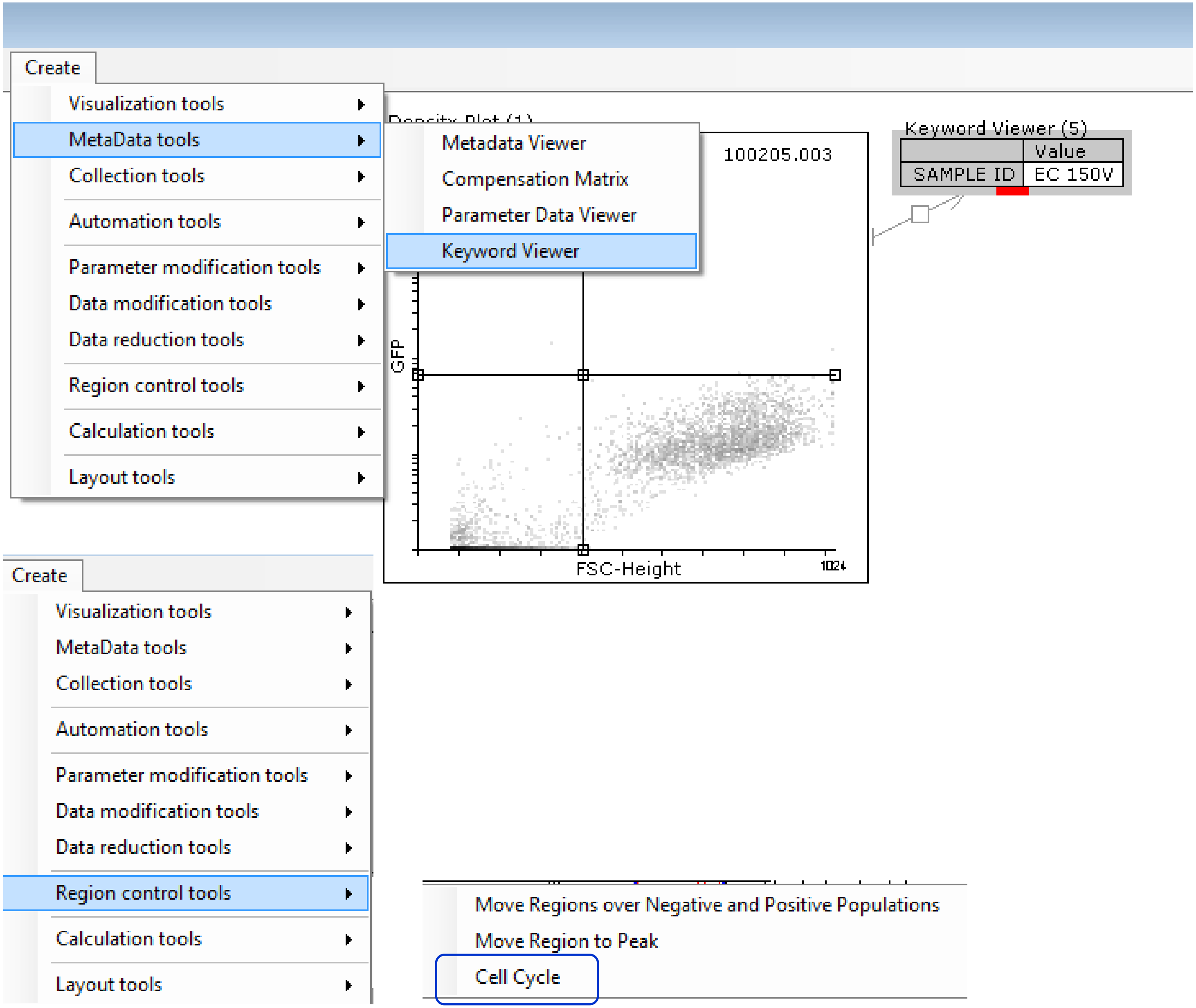
Statistics (4)

	Events	% of Vis	X Mean	Y Mean	X GeoMean	Y GeoMean	X Median	Y Median
All events	10.000	100,00	454,71	9,88	367,22	5,30	523,00	8,13
R-1	6.149	61,49	616,12	14,12	605,78	12,09	607,00	11,44

Tool Properties

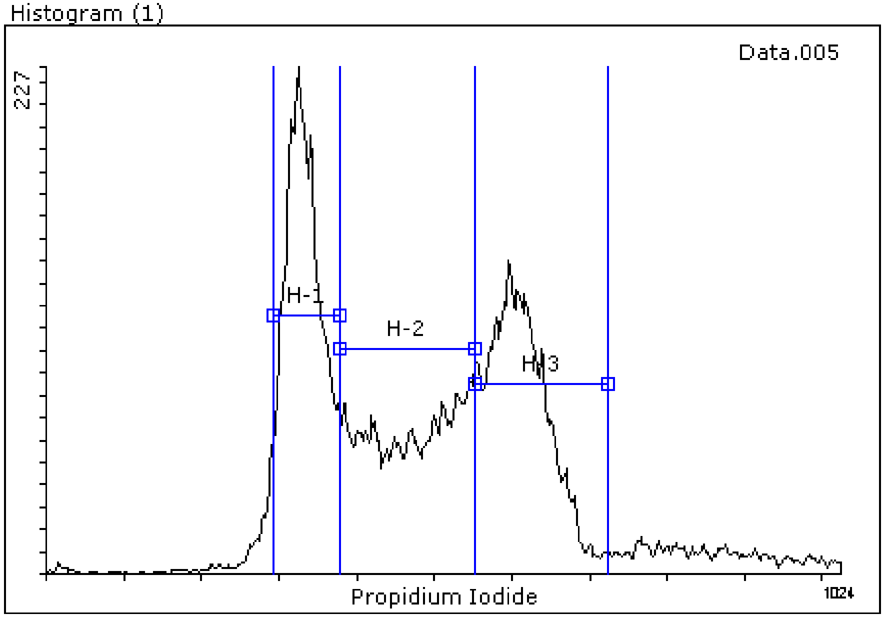
Draw	
Resolution	
File	
File_Name	100205.001
File_Path	C:\Daten\2010 Daten\2010 02 05 FACS EC
Region	
Region_Corner_Size	6
RegionName_Fontsize	8
RegionName_Show	True
Size	

Resolution
Density plot resolution

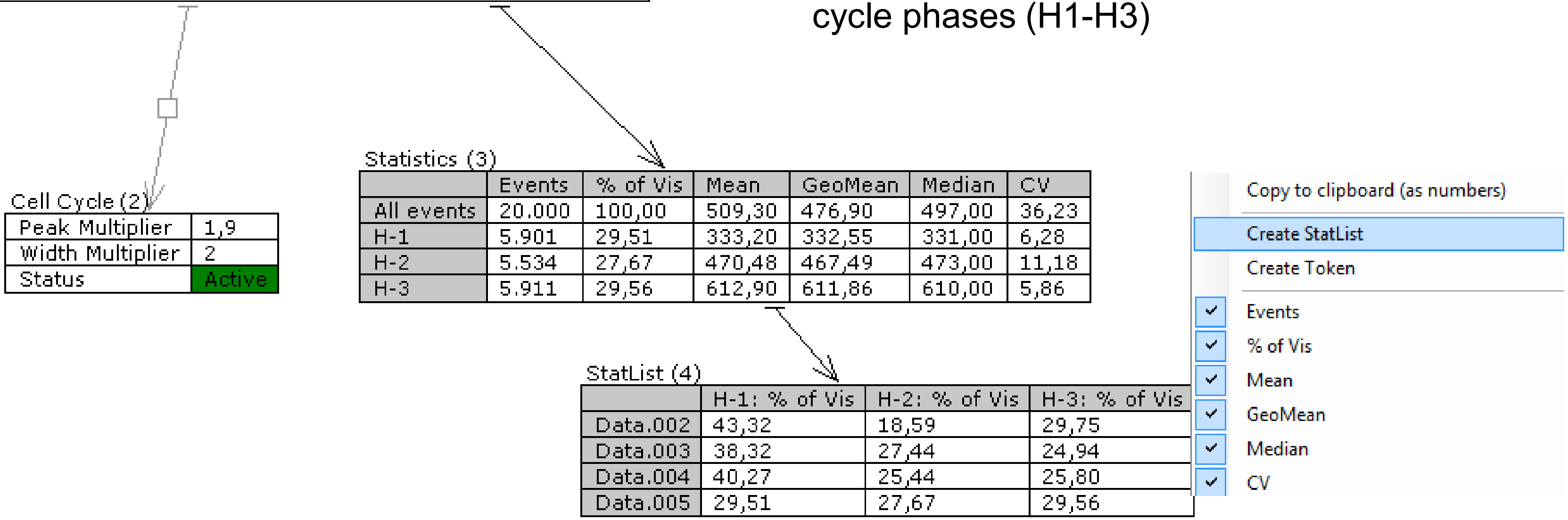


	Value
SAMPLE ID	EC 150V

Cell cycle analysis with Flowing Software



- Define 3 histogram regions (H1, H2, H3: G0/G1, S and G2/M-phase, respectively)
- Activate the region control tool: Cell Cycle
- Define the G2 peak multiplier and peak width (right click in the cell cycle window)
- Choose active control (after right clicking)
- Create statistics (by right clicking into the histogram window)
- Create a Stat.List by right-clicking into the Statistics window
- Ctrl-N loads the next file, adjusts the H1-H3 regions automatically and calculates the cell cycle phases (H1-H3)



Cell Cycle (2)

Peak Multiplier	1,9
Width Multiplier	2
Status	Active

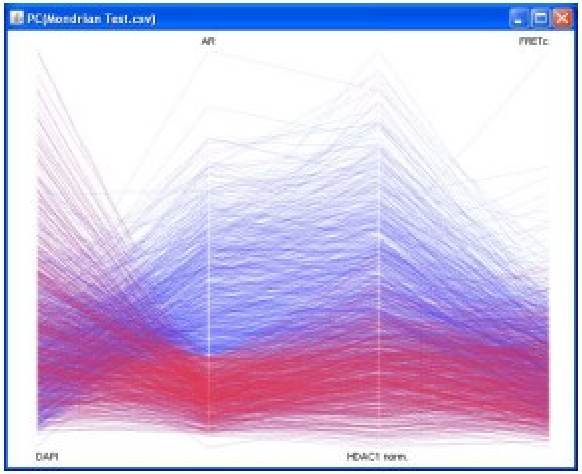
Statistics (3)

	Events	% of Vis	Mean	GeoMean	Median	CV
All events	20.000	100,00	509,30	476,90	497,00	36,23
H-1	5.901	29,51	333,20	332,55	331,00	6,28
H-2	5.534	27,67	470,48	467,49	473,00	11,18
H-3	5.911	29,56	612,90	611,86	610,00	5,86

StatList (4)

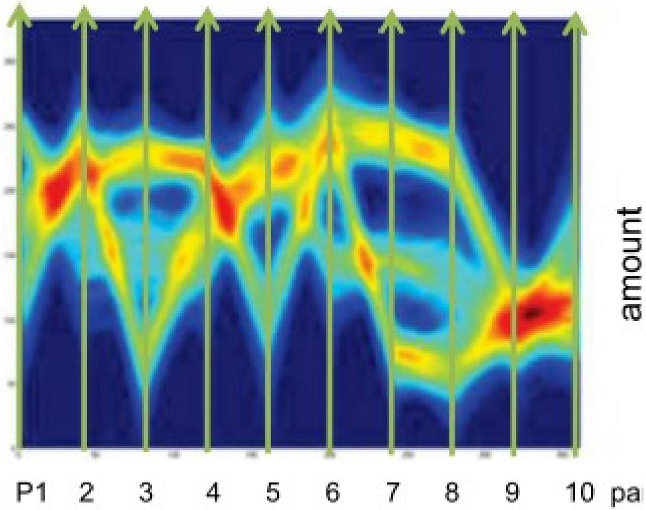
	H-1: % of Vis	H-2: % of Vis	H-3: % of Vis
Data.002	43,32	18,59	29,75
Data.003	38,32	27,44	24,94
Data.004	40,27	25,44	25,80
Data.005	29,51	27,67	29,56

Multi-parallel coordinate plots for visualization of several parameters in parallel



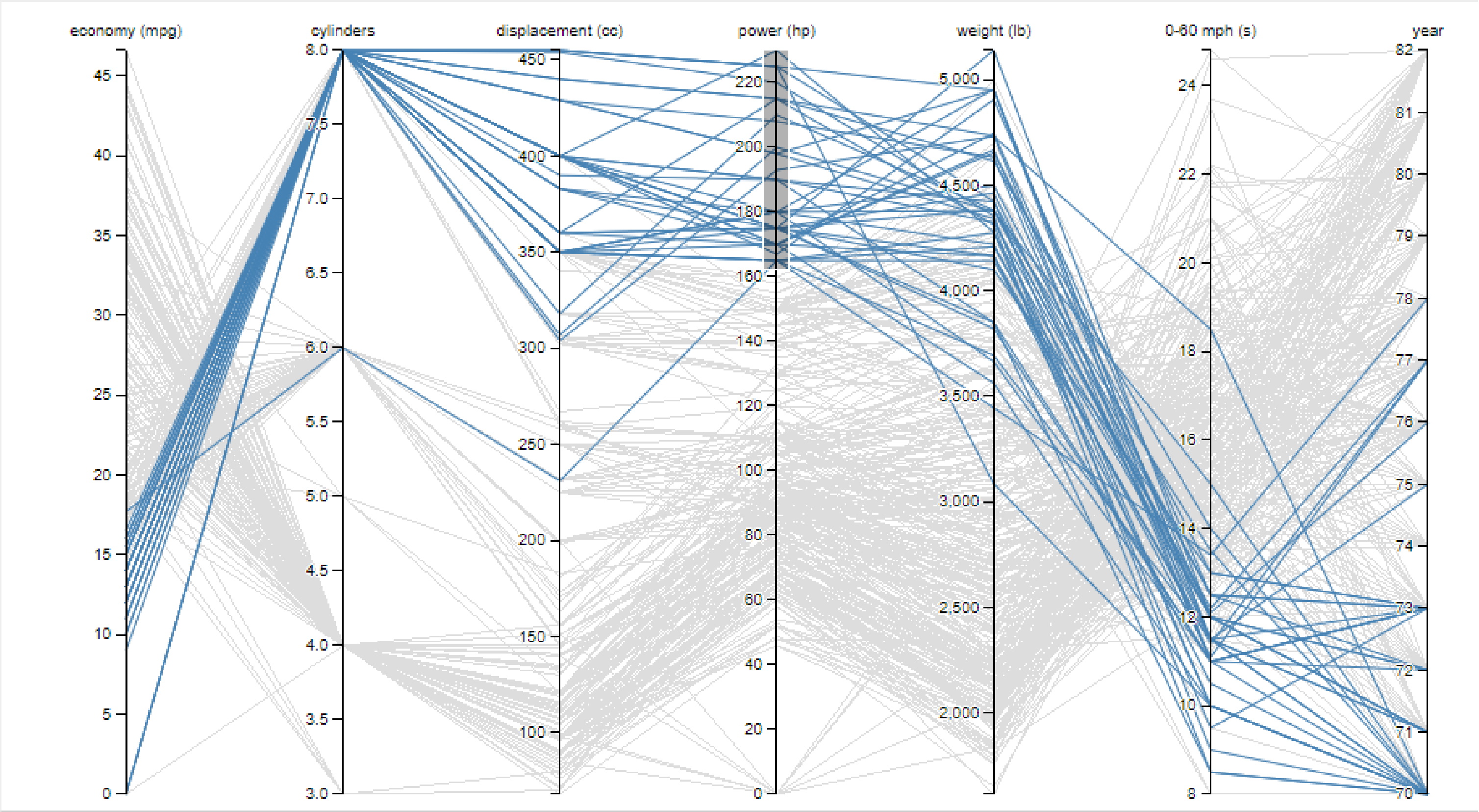
Can be done with Freeware (Mondrian: http://www.theusrus.de/Mondrian/index.html)

One event (e.g. one cell) is represented by a line linking several y-axis (for the different parameters e.g. fluorescence signals); a „population“ can be selected and is highlighted also for the other parameters. The data density can be reduced (using a so called alpha-factor) to obtain better visibility of numerous data points.



MatLab-Visualization of a parallel coordinate plot

Parallel coordinates with gating



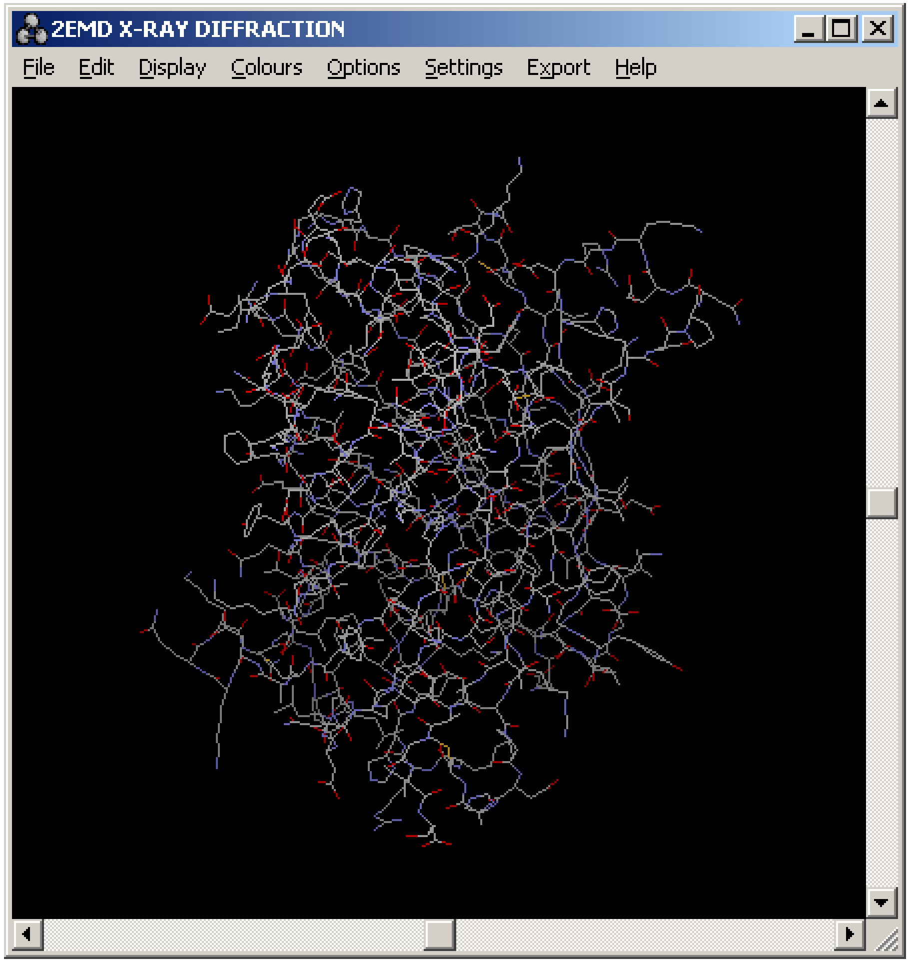
https://bl.ocks.org/jasondavies/1341281

Molecular Structure Analysis Software (Visualization and analysis of crystallographic data)

- **Chimera (UCSF):** http://www.cgl.ucsf.edu/chimera/
- Rasmol: http://www.openrasmol.org/
- RasTop: http://www.geneinfinity.org/rastop/
- Protein Explorer: http://www.umass.edu/microbio/rasmol/
- Cn3D: http://www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml
- Jmol: http://jmol.sourceforge.net/

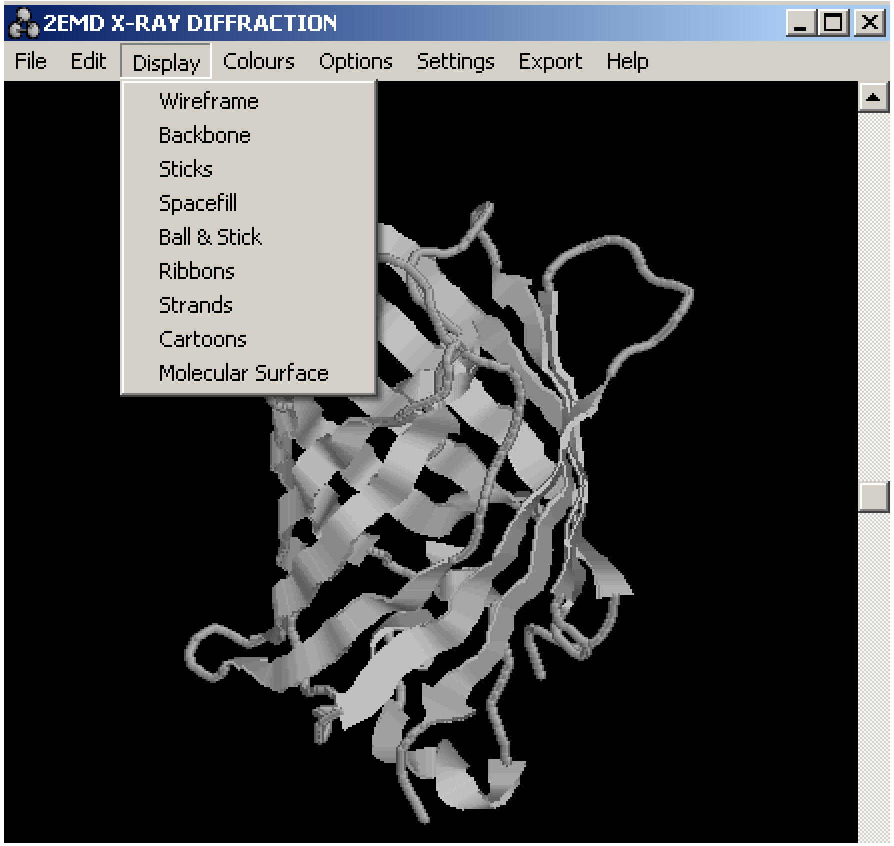
Rasmol

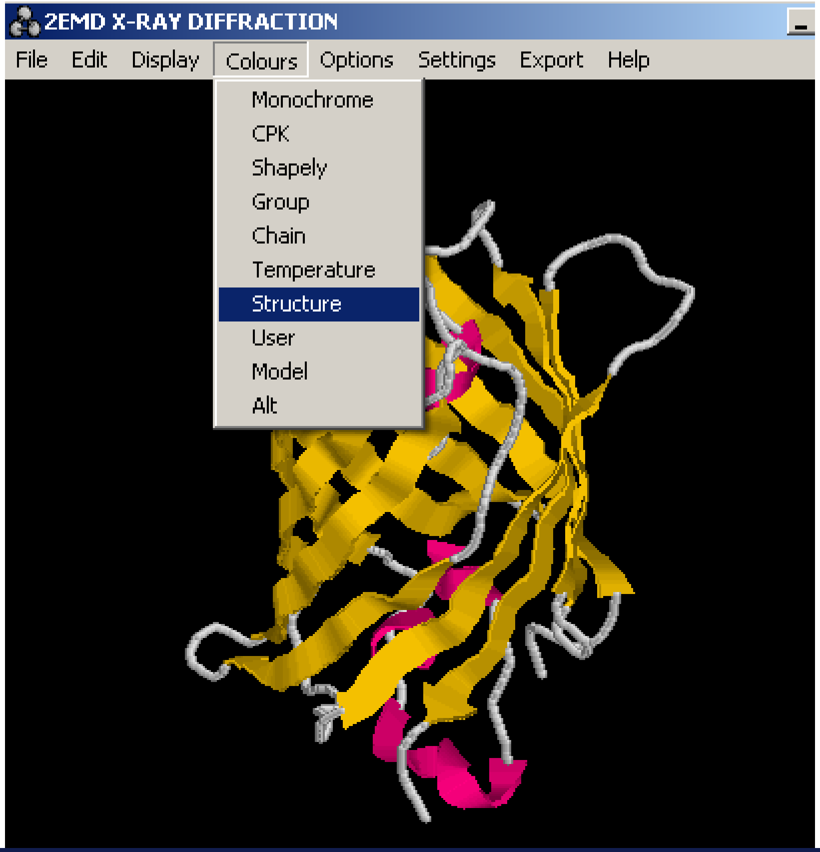
- simple small tool (400 kB) to visualize molecular structures from *.pdb files (protein data bank)
- Molecules can be moved back and forth
- Molecules can be rendered in different ways (wire, cartoon, space fill..)
- Molecules can be colored in different ways
- Distances can be measured in Angstroem
- You can also incorporate a Rasmol application into Powerpoint



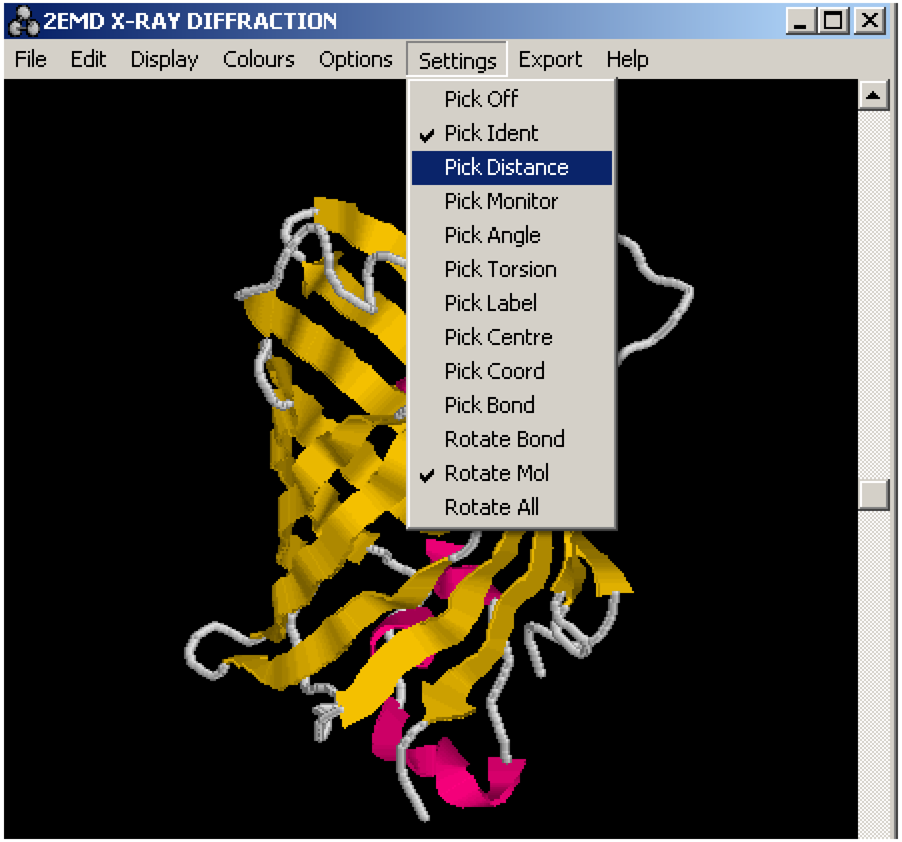
GFP structure.pdb

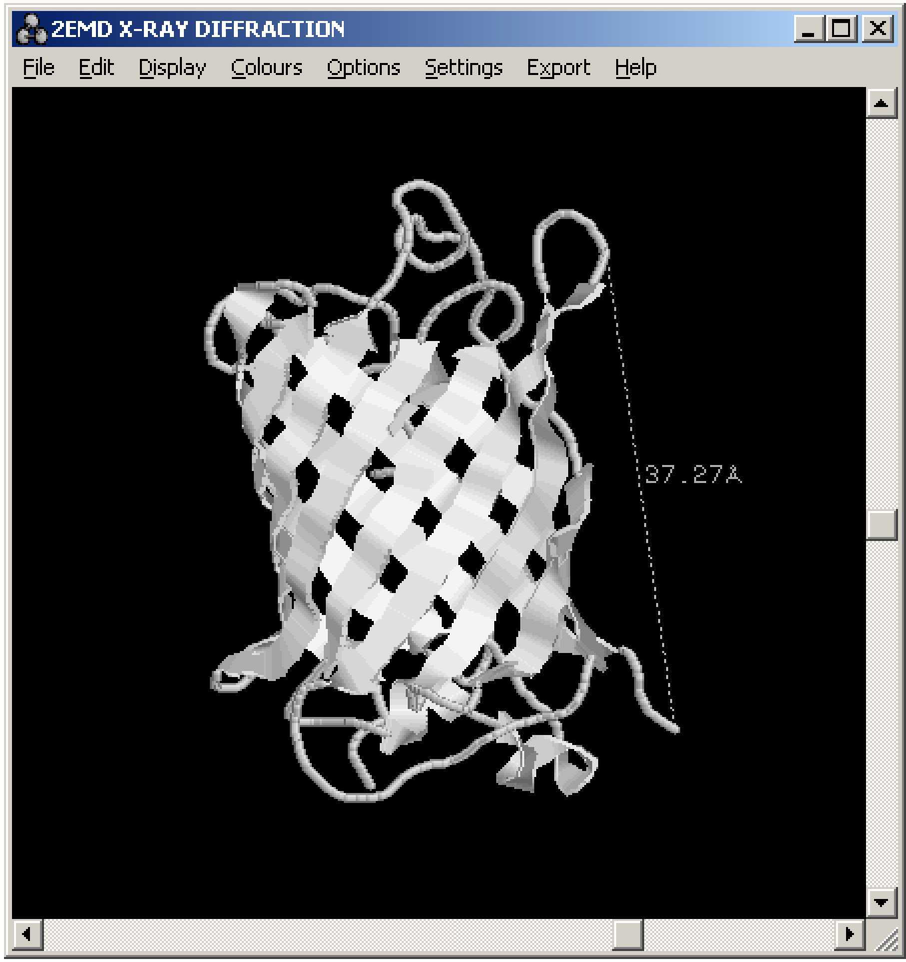
Display modes in RasMol: Rendering and colour





Measure Distances with RasMol

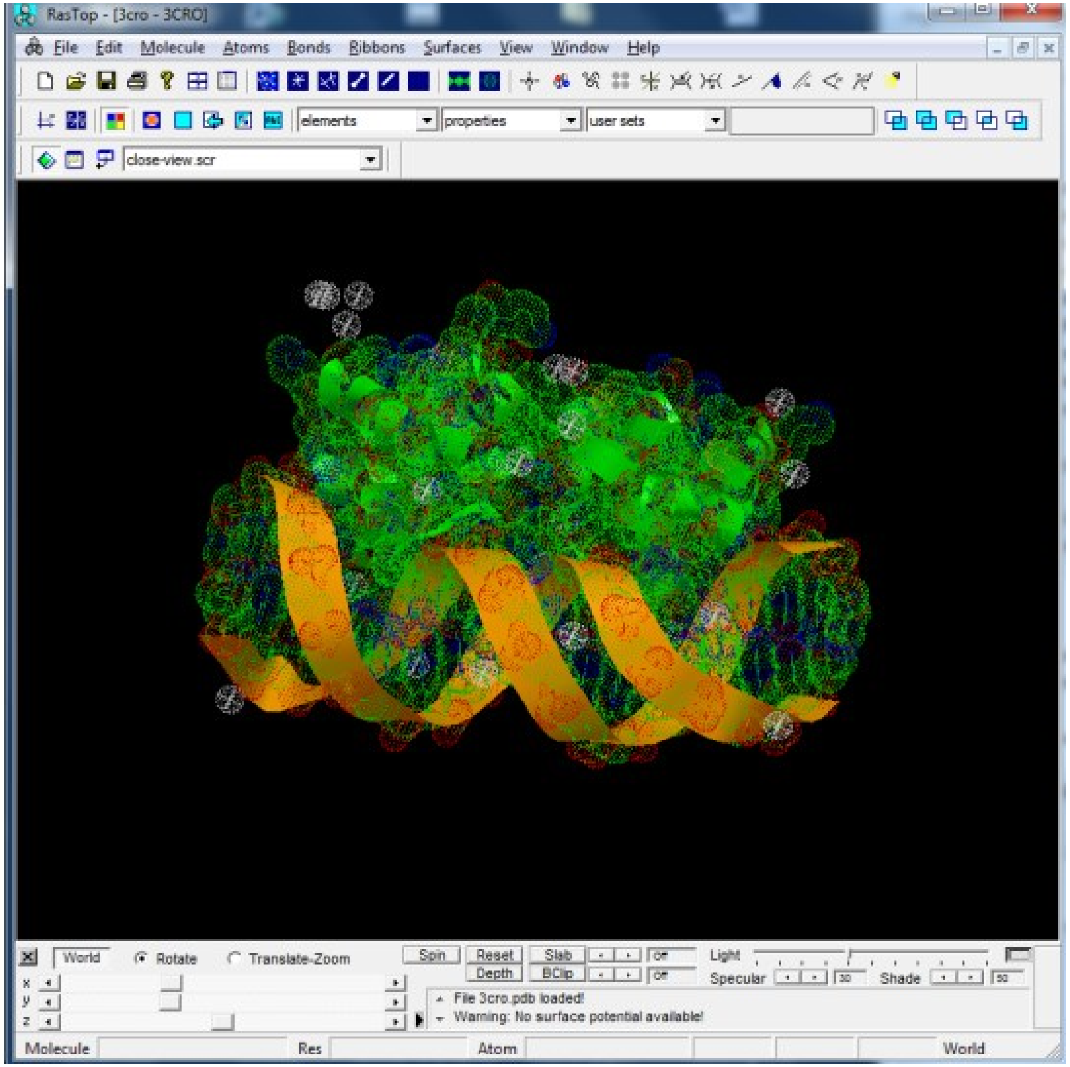




RasTop
(modern Rasmol)

http://www.geneinfinity.org/rastop/

- small (1 MB) and fast 3D molecule viewer based on Rasmol
- allows loading of more than one molecule
- allows surface views and many other features

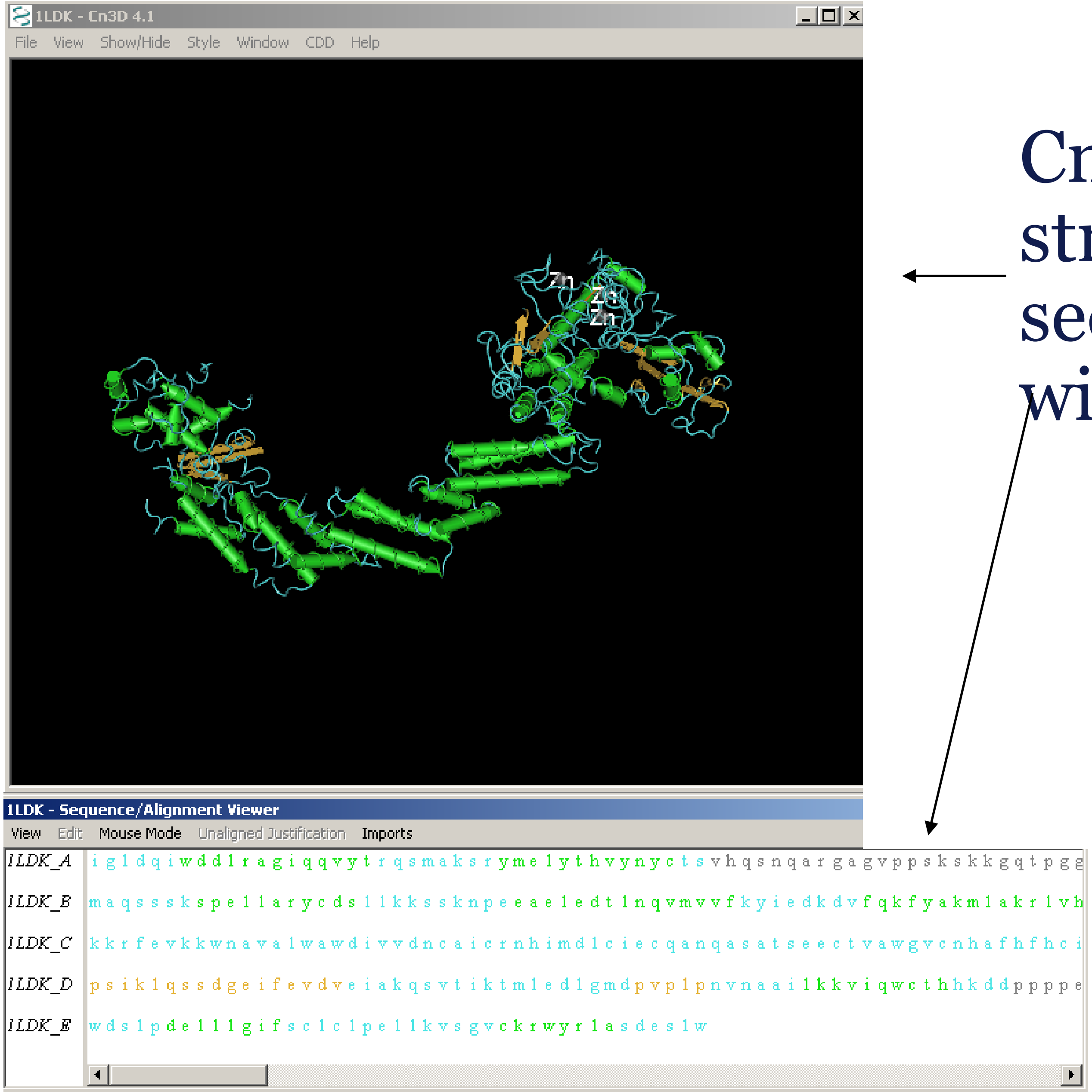


```
File 3cro.pdb loaded!
Warning: No surface potential available!
```

Cn3D Molecule Viewer (NCBI)

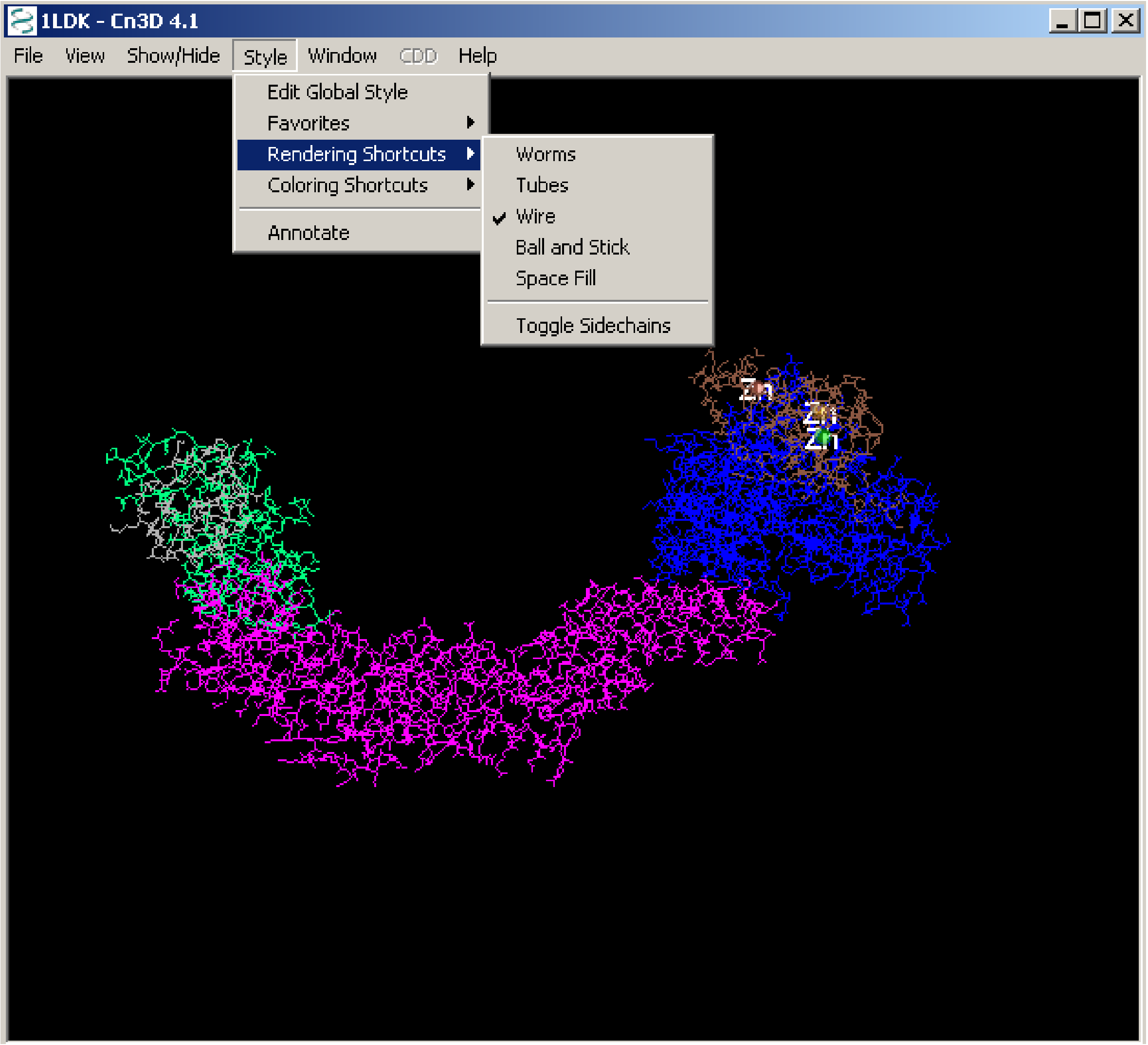
- structure window for visualization of the 3D structure of the molecule: you can turn the molecule, render it in different ways and colour it in different ways
- sequence window: shows the amino acid sequences of proteins: residues can be selected (Mouse Mode: rectangle, column or row): sequence homologies can be aligned
- Import window: activated from the sequence window: can be used to import additional molecules from NCBI

Cn3D structure and sequence window

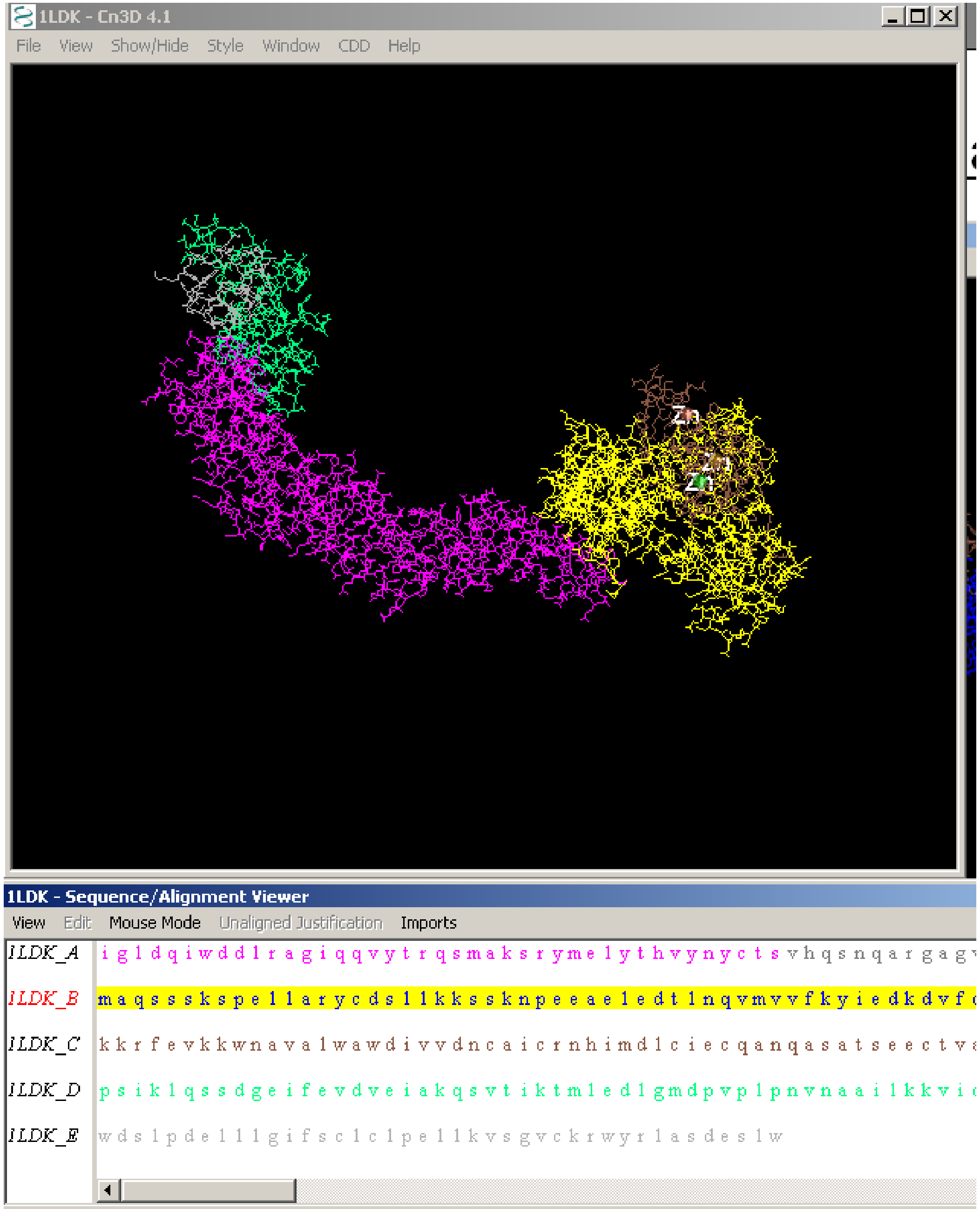


```
1LDK_A  i g l d q i w d d l r a g i q q v y t r q s m a k s r y m e l y t h v y n y c t s v h q s n q a r g a g v p p s k s k k g q t p g
1LDK_B  m a q s s s k s p e l l a r y c d s l l k k s s k n p e e a e l e d t l n q v m v v f k y i e d k d v f q k f y a k m l a k r l v h
1LDK_C  k k r f e v k k w n a v a l w a w d i v v d n c a i c r n h i m d l c i e c q a n q a s a t s e e c t v a w g v c n h a f h f h c i
1LDK_D  p s i k l q s s d g e i f e v d v e i a k q s v t i k t m l e d l g m d p v p l p n v n a a i l k k v i q w c t h h k d d p p p p e
1LDK_E  w d s l p d e l l l g i f s c l c l p e l l k v s g v c k r w y r l a s d e s l w
```

Cn3D Rendering and Colouring



- Molecules can be rendered in different ways (worms, tubes, wire, balls+sticks, space fill). The appearance can be customized („Edit Global Style)
- Colours can be adjusted to distinguish domains, molecules, secondary structures, charges and even alignements.

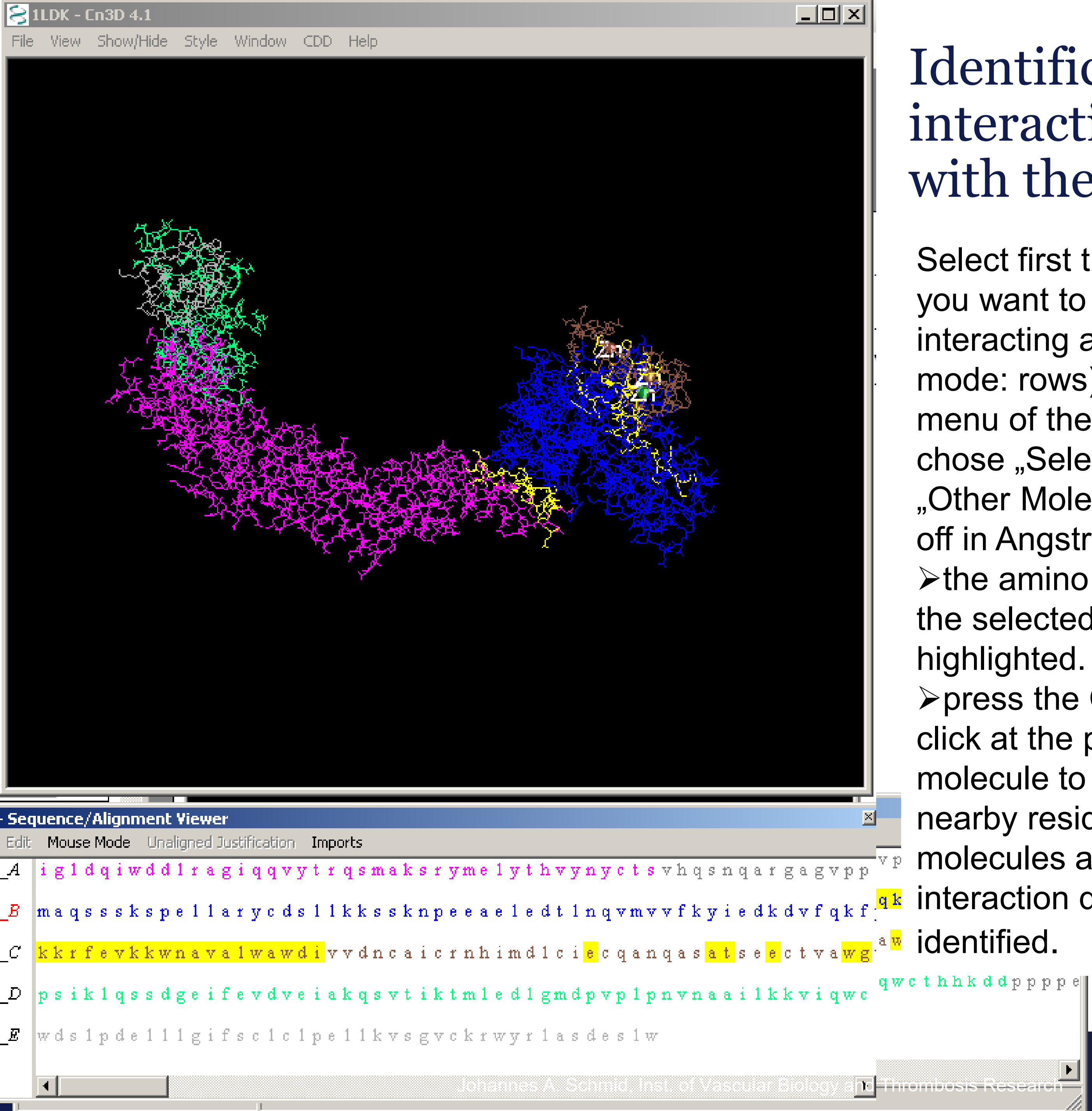


```
1LDK_A  igldqiwddlragiqqvytrqsmaksrymelythvynyctsvhqsnqargag
1LDK_B  maqssskspellarycdsllkksskn peeaeledtlnqvmvvfkyiedkdvf
1LDK_C  kkrfevkkwnavalwawdivvdncaicrnhimdlciecqanqasatseectv
1LDK_D  psiklqssdgeifevdveiakqsvtiktmledlgmdpvplpnvnaailkkvi
1LDK_E  wdslpdelllgifsclclpellkvsgvckrwyrlasdeslw
```

Selection of molecules or domains

sequences selected in the sequence window are highlighted in the structure window

Identification of interaction domains with the help of Cn3D



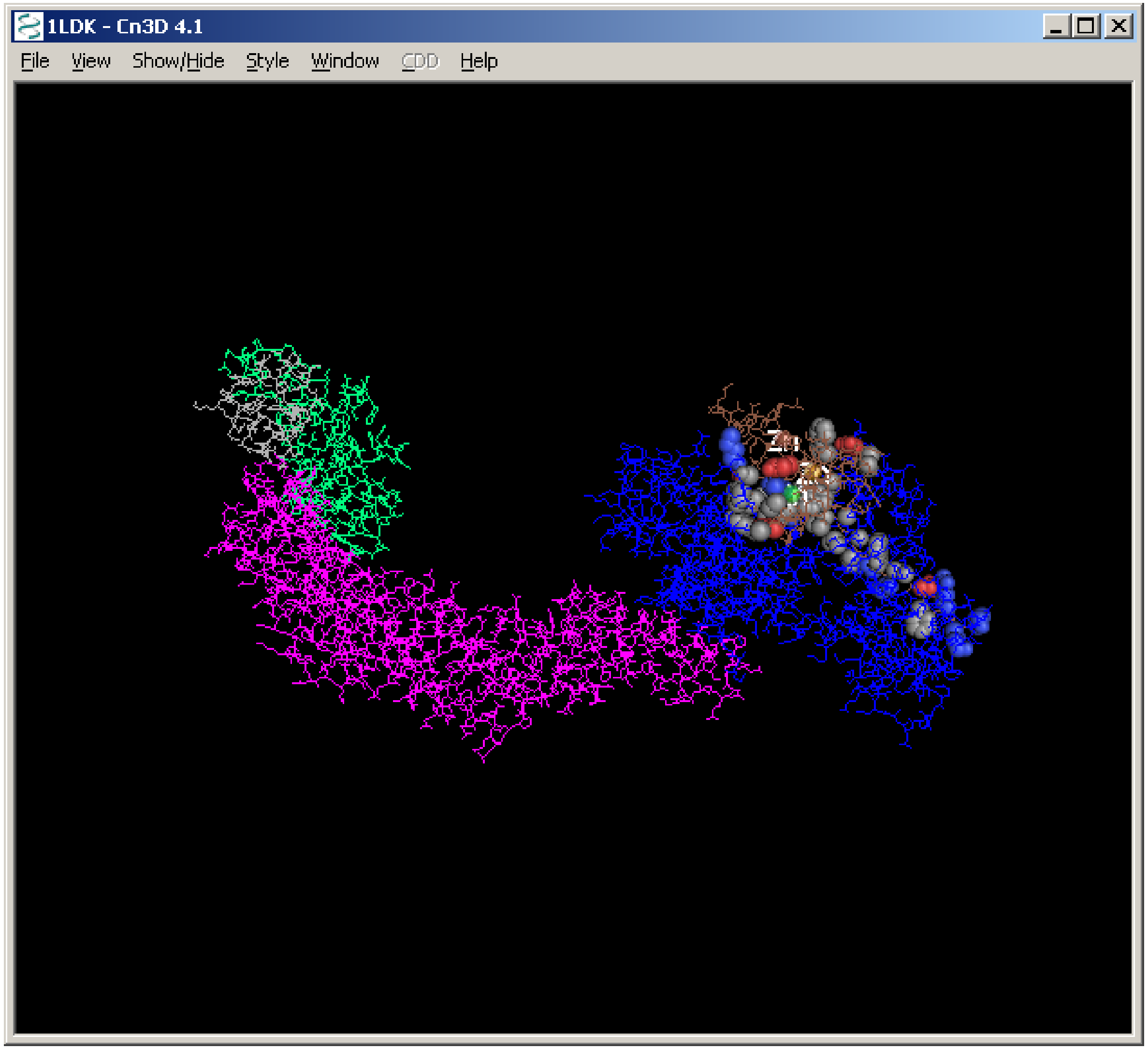
```
_A  i g l d q i w d d l r a g i q q v y t r q s m a k s r y m e l y t h v y n y c t s v h q s n q a r g a g v p p   v p
_B  m a q s s s k s p e l l a r y c d s l l k k s s k n p e e a e l e d t l n q v m v v f k y i e d k d v f q k f   q k
_C  k k r f e v k k w n a v a l w a w d i v v d n c a i c r n h i m d l c i e c q a n q a s a t s e e c t v a w g   a w
_D  p s i k l q s s d g e i f e v d v e i a k q s v t i k t m l e d l g m d p v p l p n v n a a i l k k v i q w c   q w c t h h k d d p p p p e
_E  w d s l p d e l l l g i f s c l c l p e l l k v s g v c k r w y r l a s d e s l w
```

Select first the molecule for which you want to define the potentially interacting amino acids (Mouse mode: rows). From the Show/Hide menu of the structure window chose „Select by Distance“ and „Other Molecule“ > define the cut-off in Angstroem.

➢the amino acids in the vicinity of the selected molecule will be highlighted.

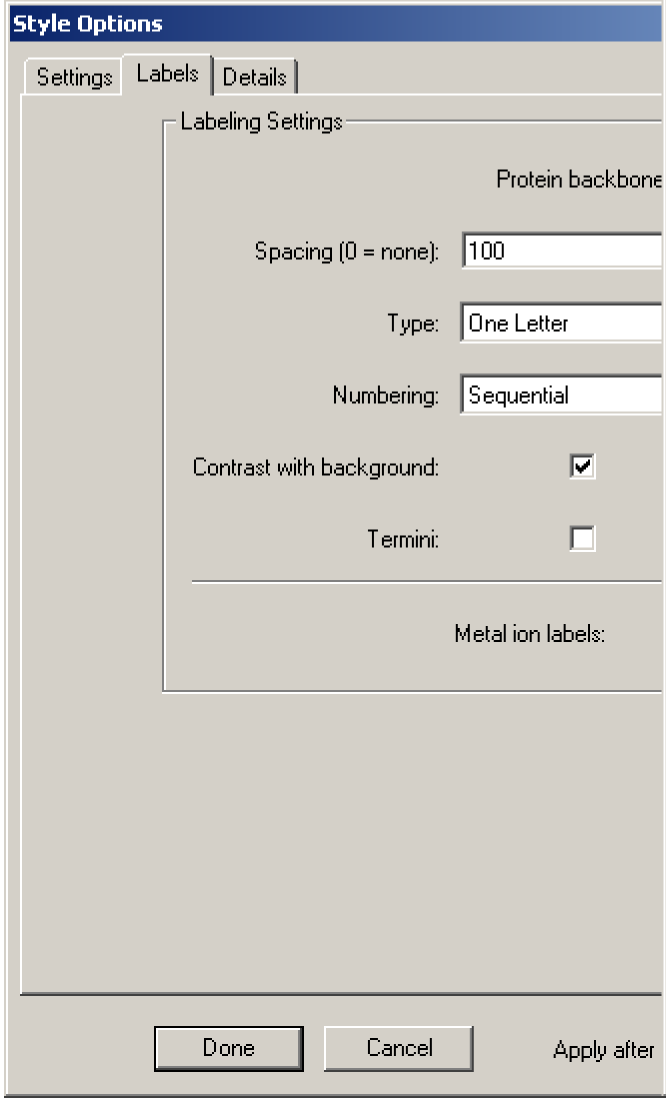
➢press the Ctrl (Strg) button and click at the previously selected molecule to de-select it > only the nearby residues of the other molecules are highlighted > interaction domains can be identified.

Customized appearance of selected residues



Selected residues can be rendered and coloured differently:
Menu „Style“ > Annotate
- ➢New > Edit Style
- ➢the appearance can be adjusted for the selected residues (e.g. space fill, colouring by charge)

Style options: adding amino acid numbers



Style Options

Labeling Settings

Protein backbone

Spacing (0 = none): 100

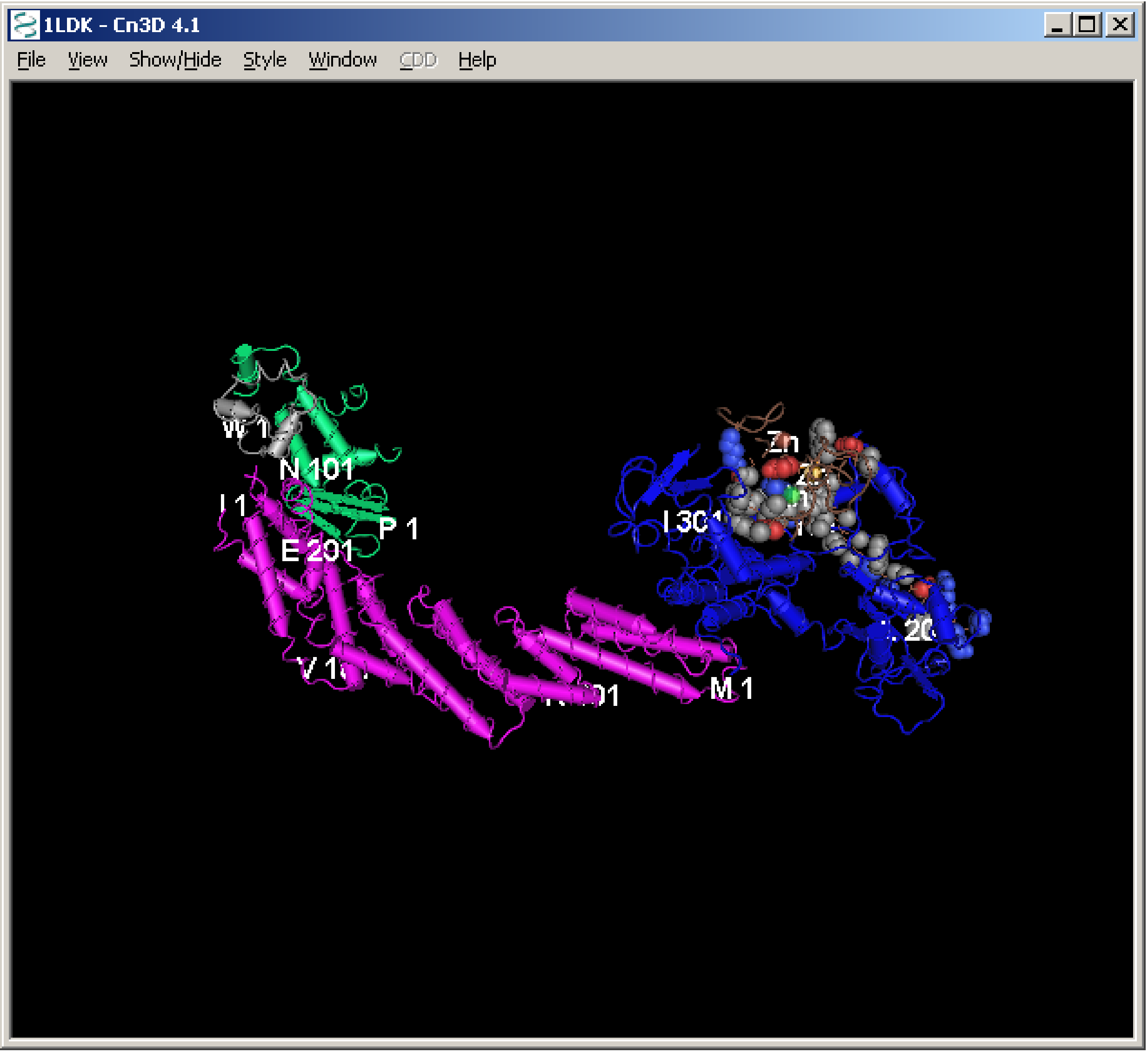
Type: One Letter

Numbering: Sequential

Contrast with background: ☑

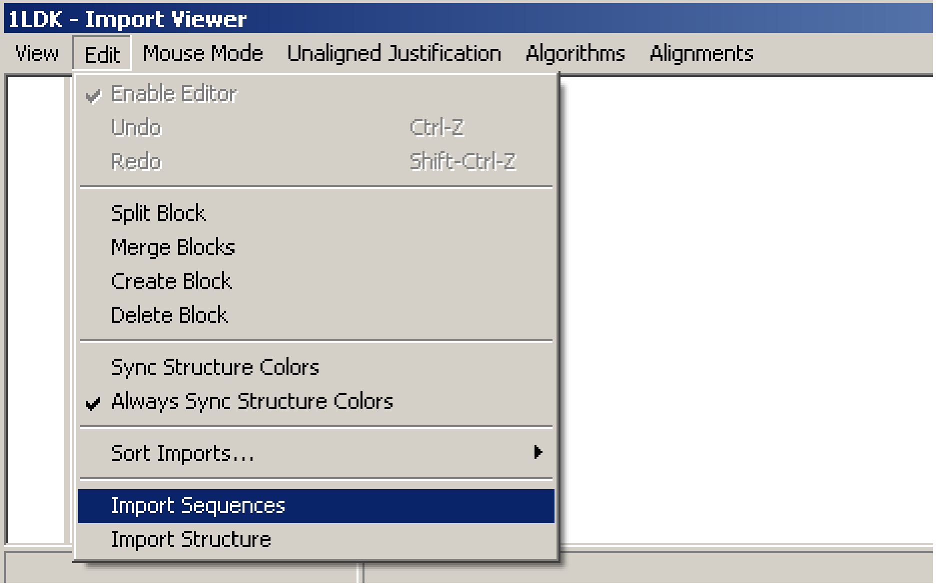
Termini: ☐

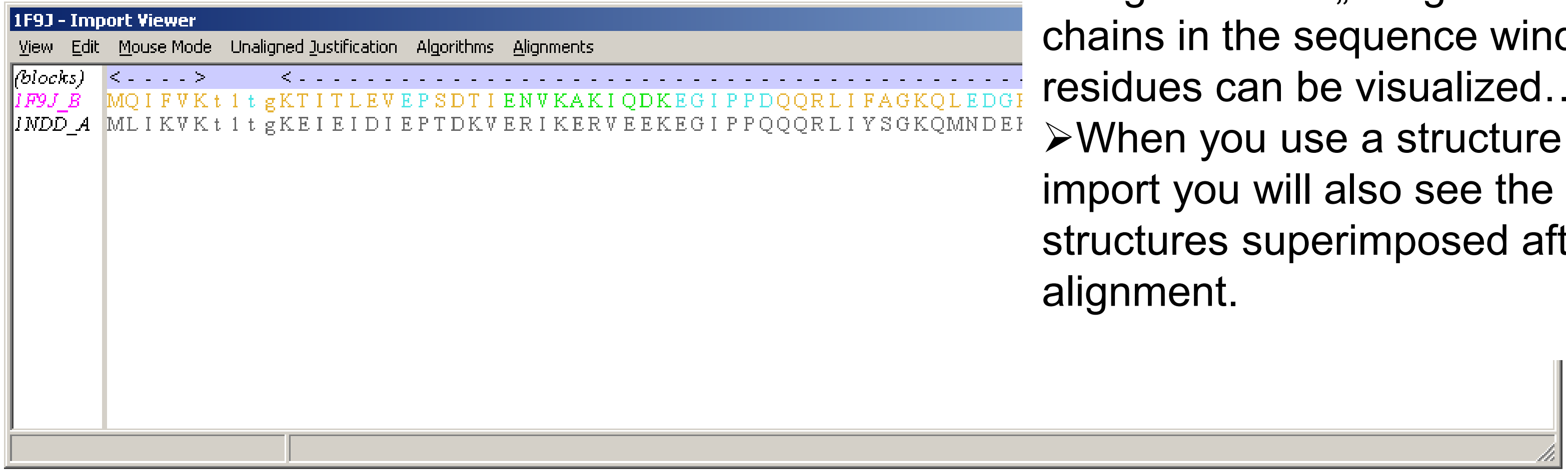
Metal ion labels:



1LDK - Cn3D 4.1

Importing sequences and aligning them



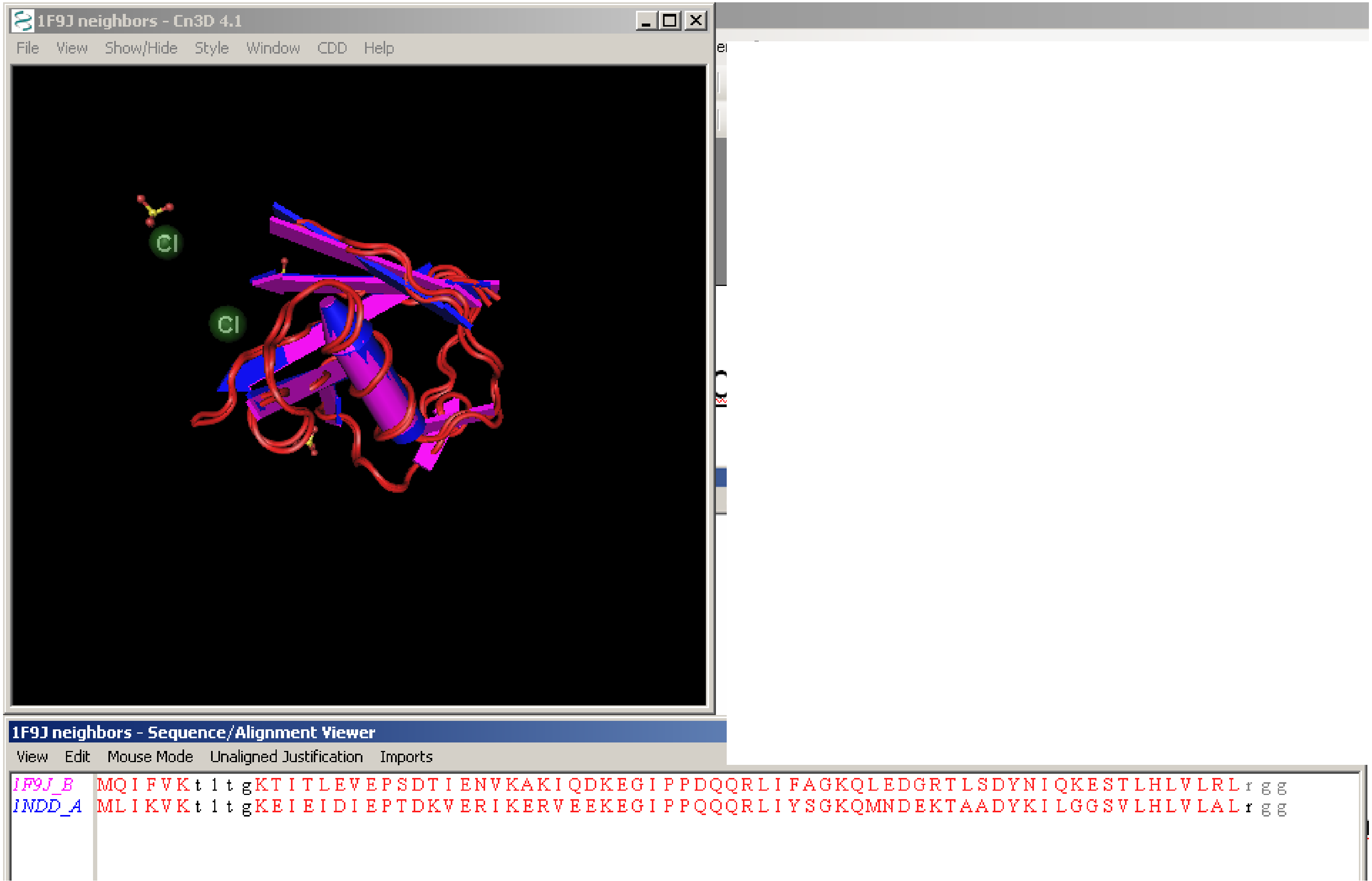


```
(blocks)  <- - - - >      <- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
1F9J_B    MQIFVKtltgKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDG
1NDD_A    MLIKVKtltgKEIEIDIEPTDKVERIKERVEEKEGIPPQQQRLIYSGKQMNDE
```

From the sequence window: click „Imports“ and „Show Imports“ -then the Import window comes up > in the menu „Edit“ select „Import Sequences“ > define with which molecule the imported sequence will be aligned > define the molecule to be imported (either by accession number or the sequence in FASTA format) > The two sequences will be shown aligned in the Import window

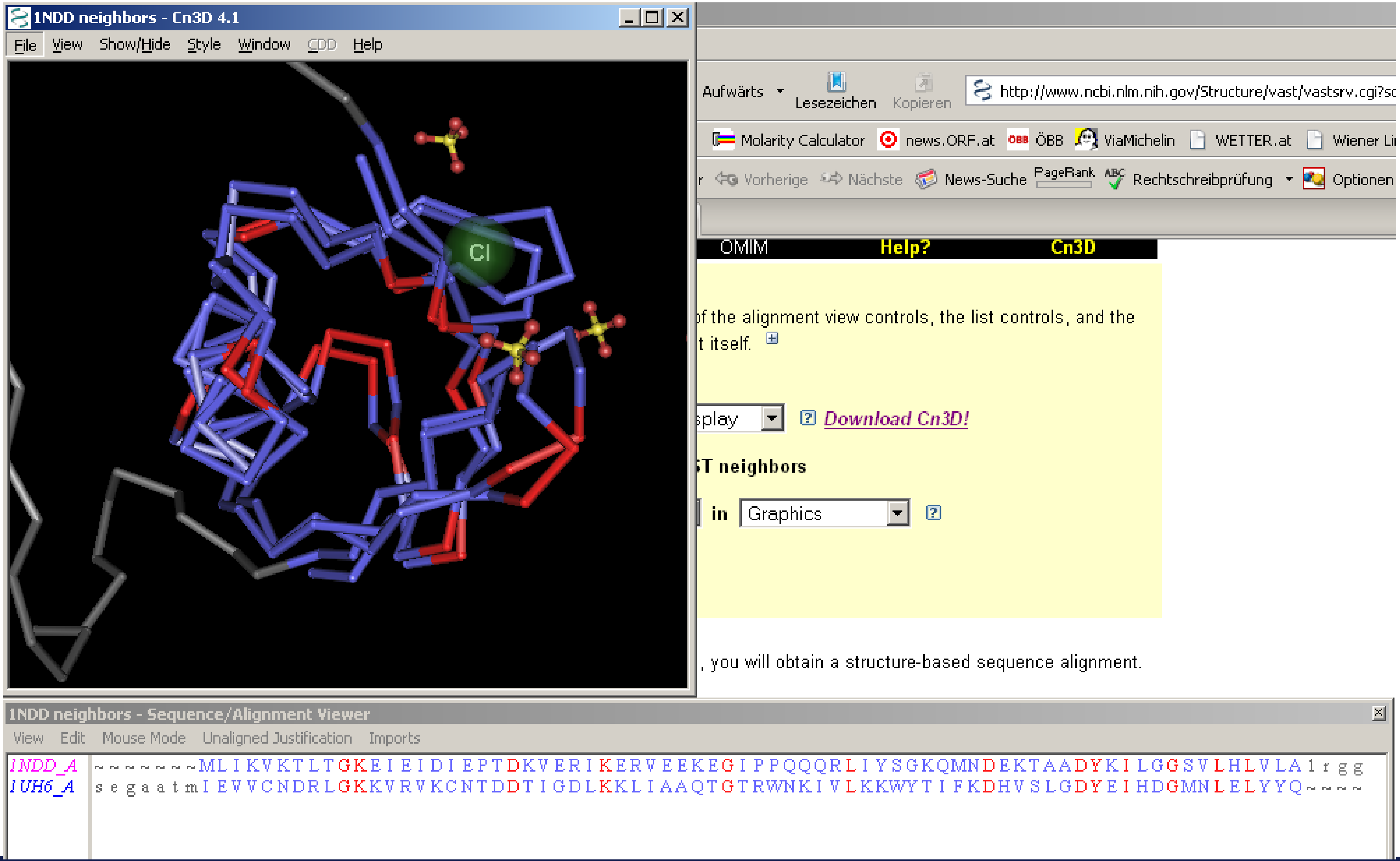
- ➢Alignments > „Merge all“ aligns the two chains in the sequence window > aligned residues can be visualized…
- ➢When you use a structure file for import you will also see the two structures superimposed after saving the alignment.

Example of two aligned structures



```
1F9J_B  MQIFVKtltgKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLrgg
1NDD_A  MLIKVKtltgKEIEIDIEPTDKVERIKERVEEKEGIPPQQQRLIYSGKQMNDEKTAADYKILGGSVLHLVLALrgg
```

VAST (Vector Alignement Search Tool) for defining structural neighbours



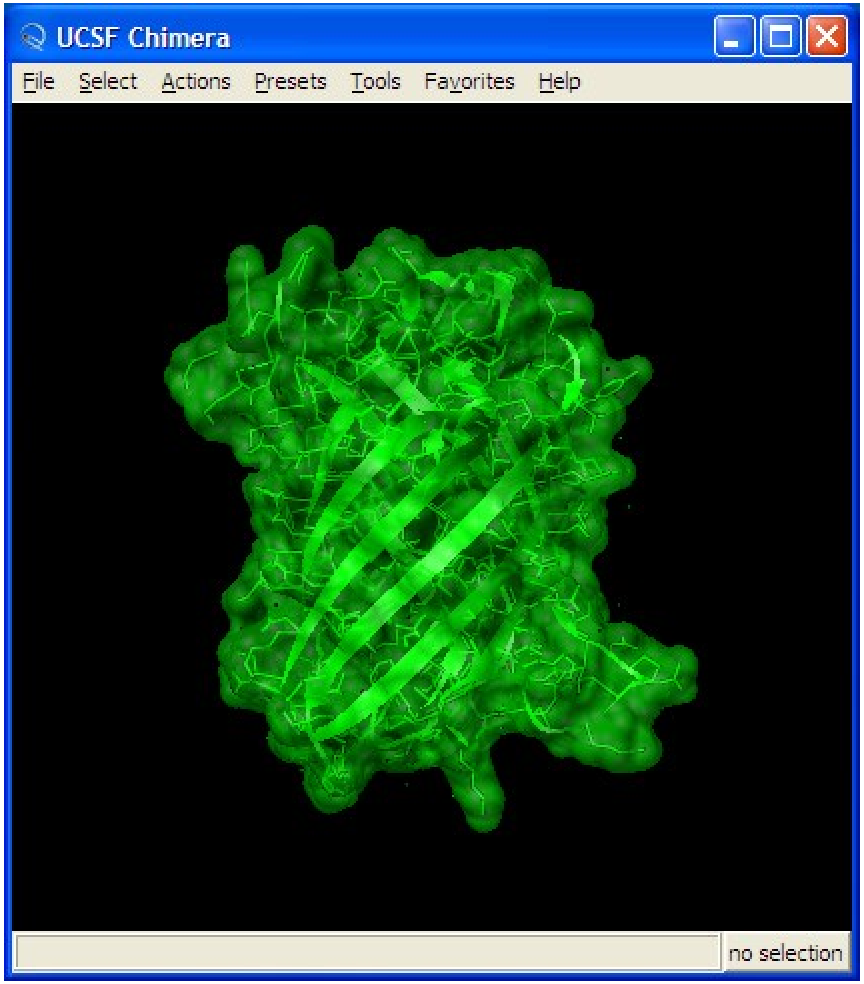
f the alignment view controls, the list controls, and the t itself.

, you will obtain a structure-based sequence alignment.

```
1NDD_A  ~~~~~~~MLIKVKTLTGKEIEIDIEPTDKVERIKERVEEKEGIPPQQQRLIYSGKQMNDEKTAADYKILGGSVLHLVLAlrgg
1UH6_A  segaatmIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYYQ~~~~
```

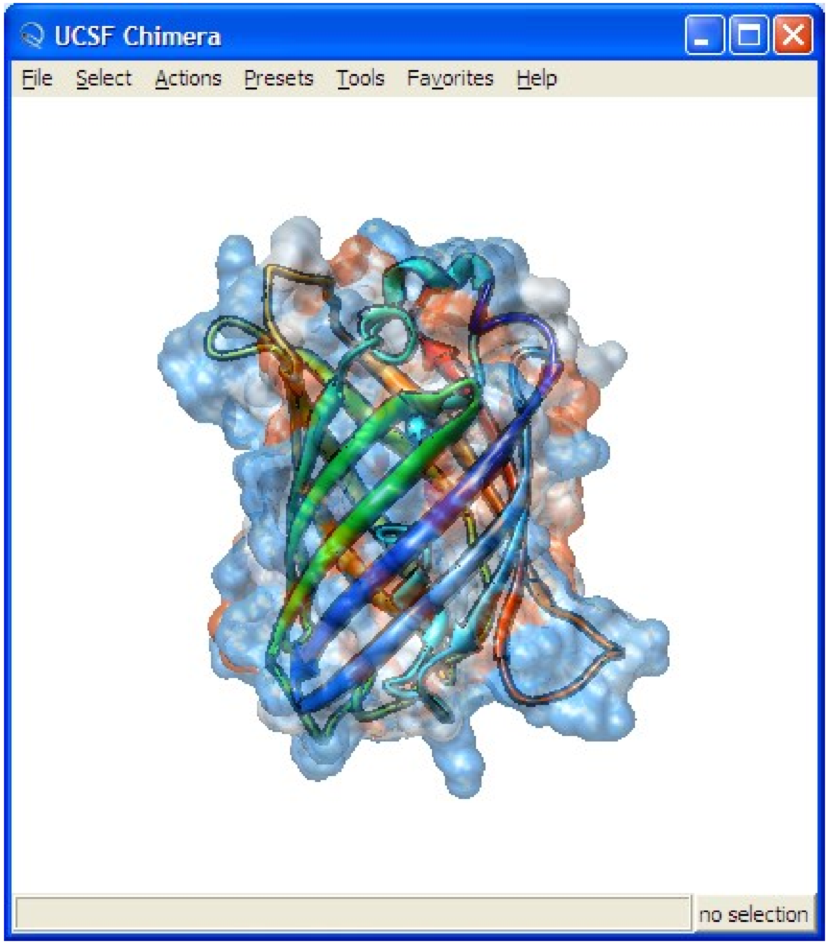
Chimera

- http://www.cgl.ucsf.edu/chimera/
- capable of showing surfaces (also in transparency mode)
- very good 3D rendering and visualization tools
- fancy preset visualization options
- several molecules can be loaded into the same window
- many tools (e.g. side view, cutting through molecules, rotation, movie recorder…)

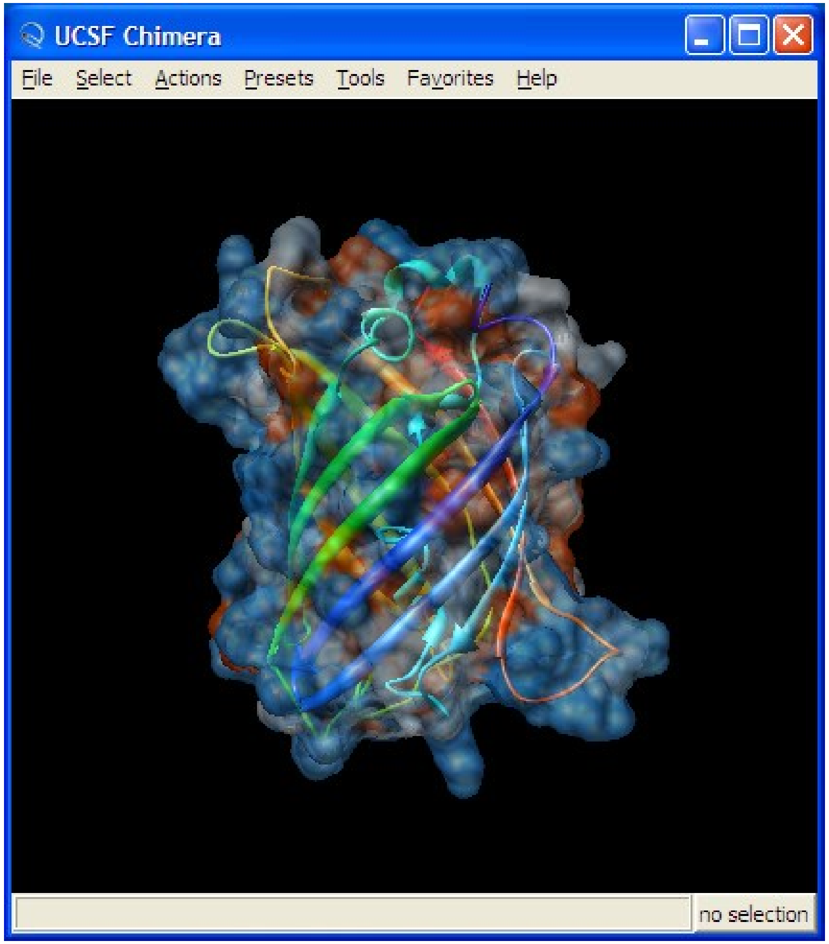


Examples

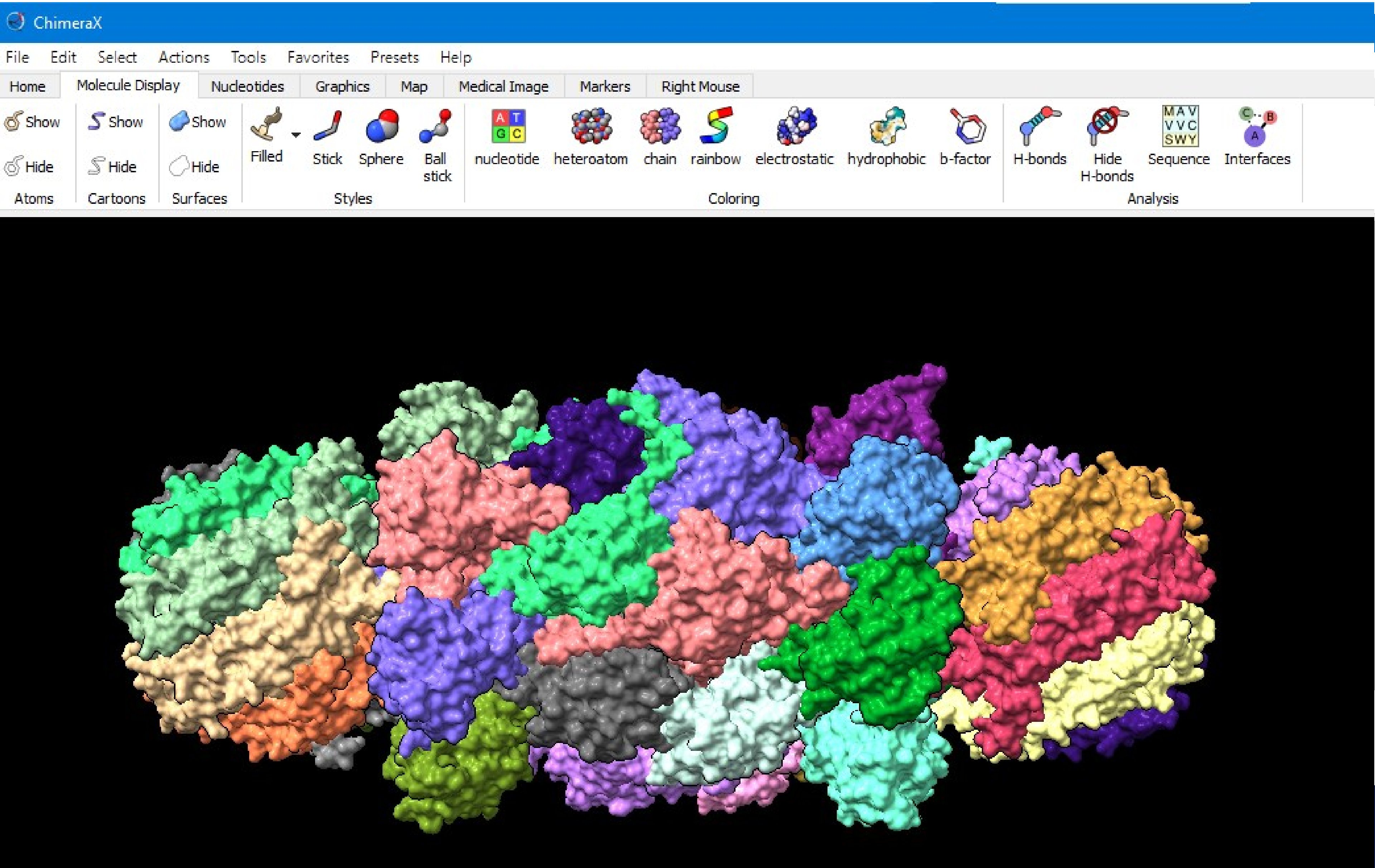
Preset: Publication1 + 60% transparent surface



Preset hydrophobicity surface view

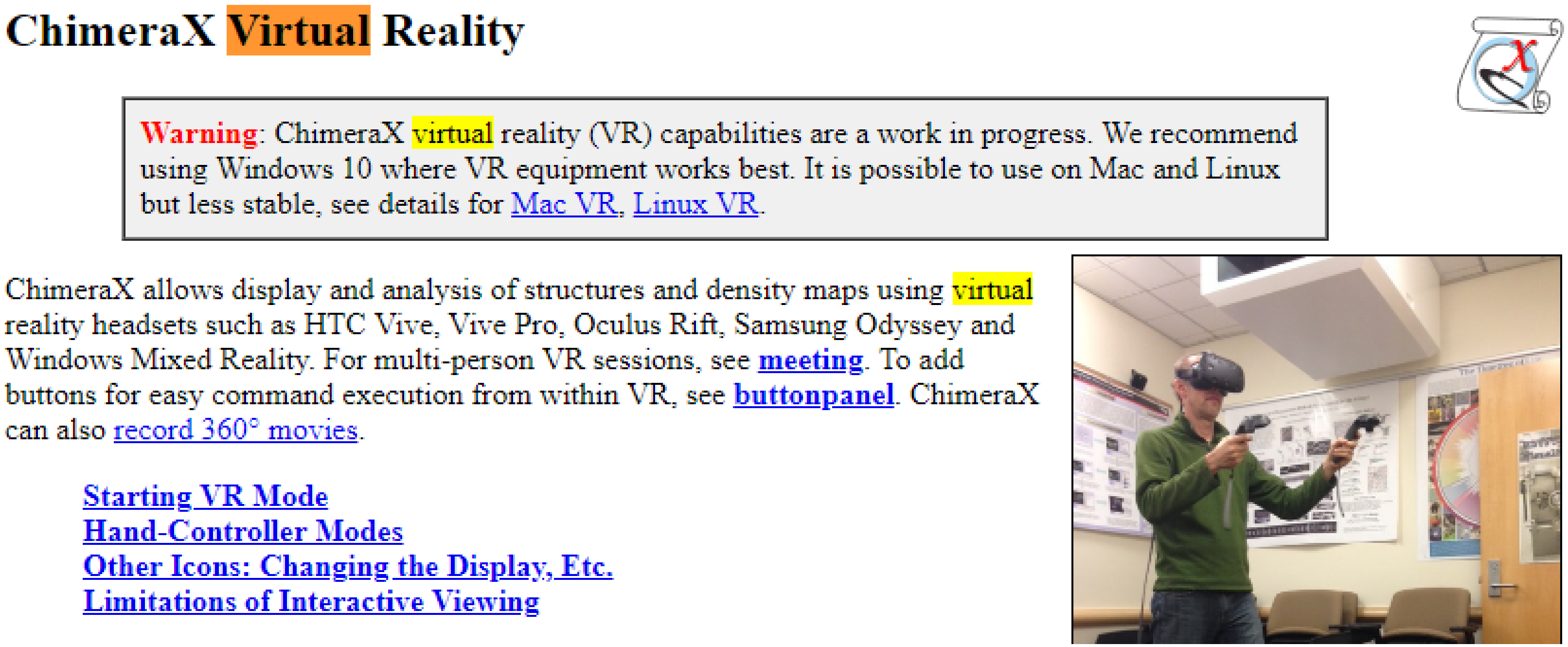


New Chimera X



New Chimera X

… allows virtual reality view of molecules with a VR headset:



ChimeraX Virtual Reality

Warning: ChimeraX virtual reality (VR) capabilities are a work in progress. We recommend using Windows 10 where VR equipment works best. It is possible to use on Mac and Linux but less stable, see details for Mac VR, Linux VR.

ChimeraX allows display and analysis of structures and density maps using virtual reality headsets such as HTC Vive, Vive Pro, Oculus Rift, Samsung Odyssey and Windows Mixed Reality. For multi-person VR sessions, see **meeting**. To add buttons for easy command execution from within VR, see **buttonpanel**. ChimeraX can also record 360° movies.

Starting VR Mode
Hand-Controller Modes
Other Icons: Changing the Display, Etc.
Limitations of Interactive Viewing

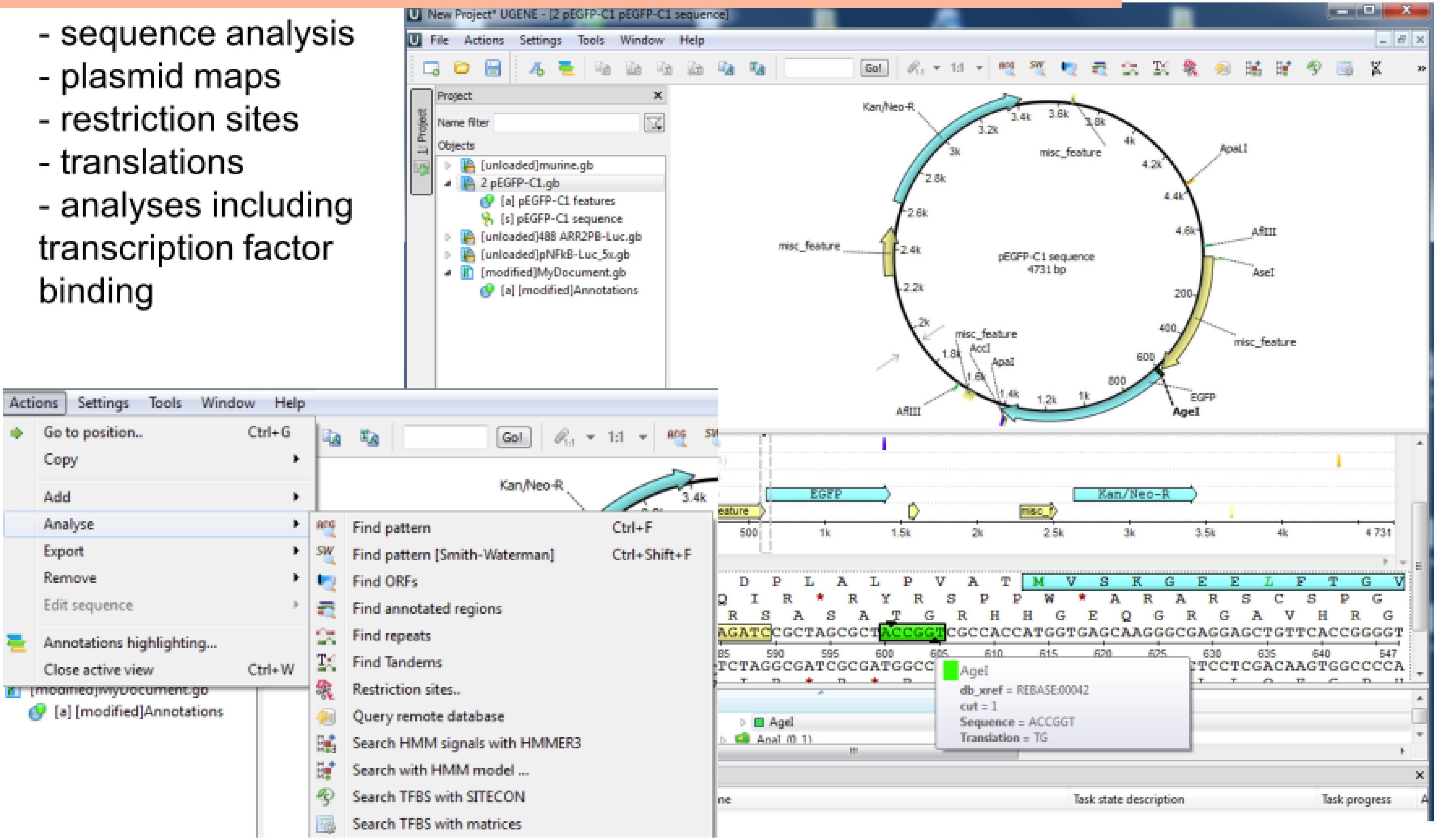
Free Molecular Biology Software

- website showing an overview of available freeware (a bit outdated): http://molbiol-tools.ca/molecular_biology_freeware.htm
- **UGENE** - http://ugene.unipro.ru/
- GenomeProfiler: obsolet: Flash-based https://designer.genomecompiler.com/app online or standalone
- Gene Designer: https://www.atum.bio/resources/tools/gene-designer - obsolet - (Adobe Air-based)
- **SnapGene Viewer:** https://www.snapgene.com/snapgene-viewer
- **SerialCloner: http://serialbasics.free.fr/Serial_Cloner.html**
- **ApE: https://jorgensen.biology.utah.edu/wayned/ape/**

UGENE

http://ugene.unipro.ru/
Powerful freeware, quite fast, also contains smart web-based analyses

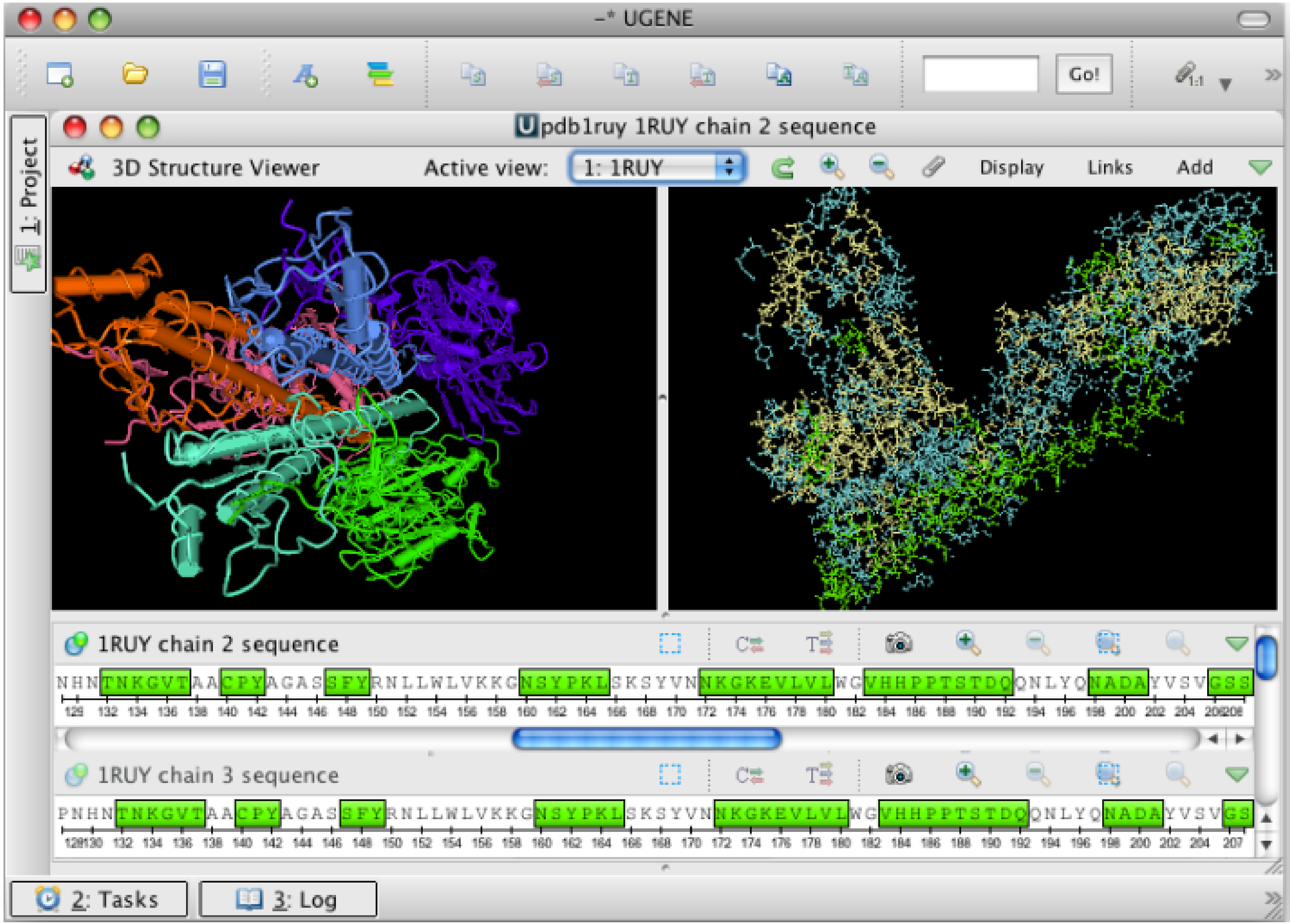
- sequence analysis
- plasmid maps
- restriction sites
- translations
- analyses including transcription factor binding



AgeI
db_xref = REBASE:00042
cut = 1
Sequence = ACCGGT
Translation = TG

UGENE

- includes a 3D molecule viewer



1RUY chain 2 sequence

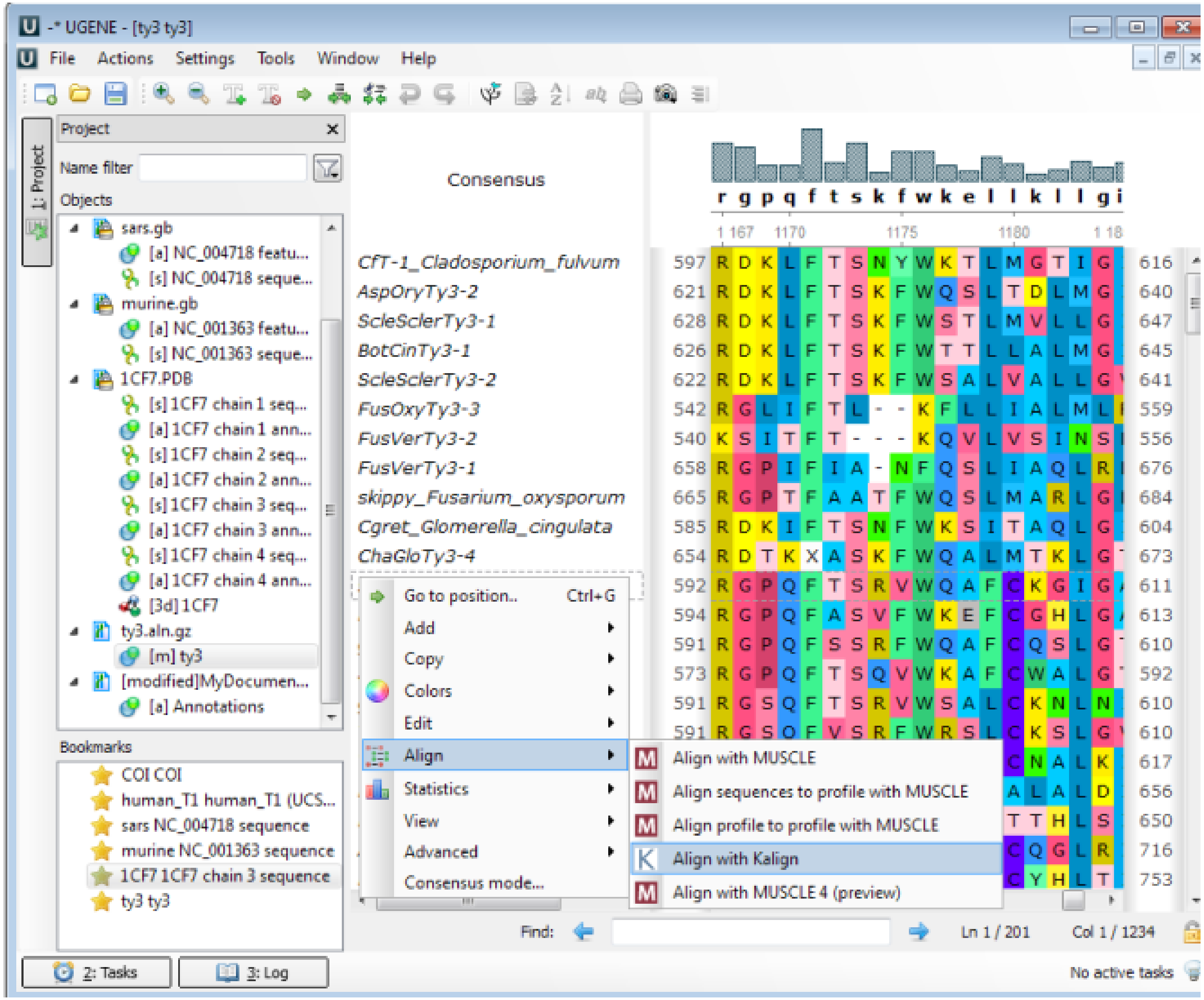
NHNTNKGVTAACPYAGASSFYRNLLWLVKKGNSYPKLSKSYVNNKGKEVLVLWGVHHPPTSTDQQNLYQNADAYVSVGSS

1RUY chain 3 sequence

PNHNTNKGVTAACPYAGASSFYRNLLWLVKKGNSYPKLSKSYVNNKGKEVLVLWGVHHPPTSTDQQNLYQNADAYVSVGS

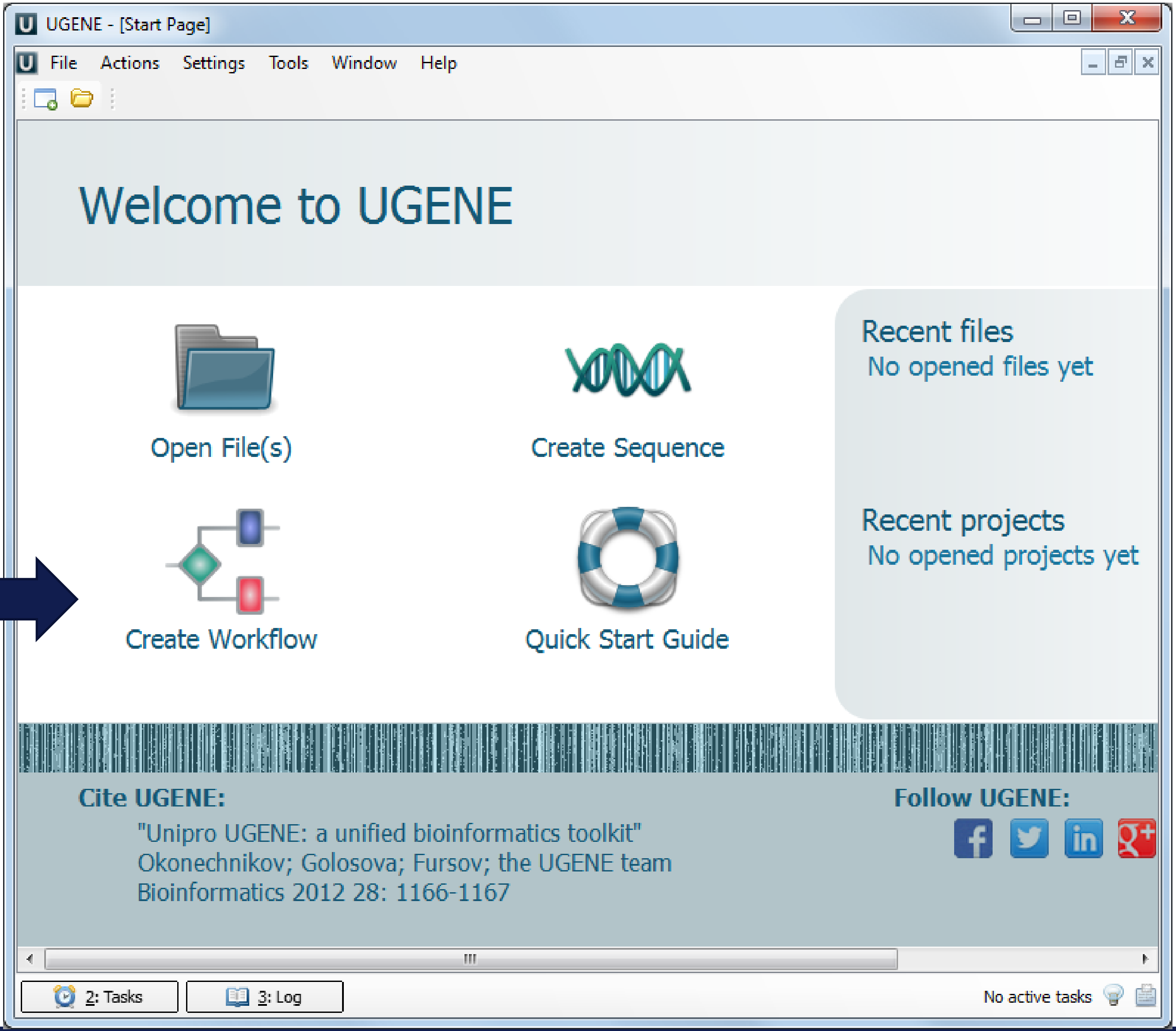
UGENE

- alignments



Ugene-Workflows

Workflows (scripts) can be generated to facilitate repeated actions



Welcome to UGENE

Recent files

No opened files yet

Recent projects

No opened projects yet

Cite UGENE:

"Unipro UGENE: a unified bioinformatics toolkit"
Okonechnikov; Golosova; Fursov; the UGENE team
Bioinformatics 2012 28: 1166-1167

Follow UGENE:

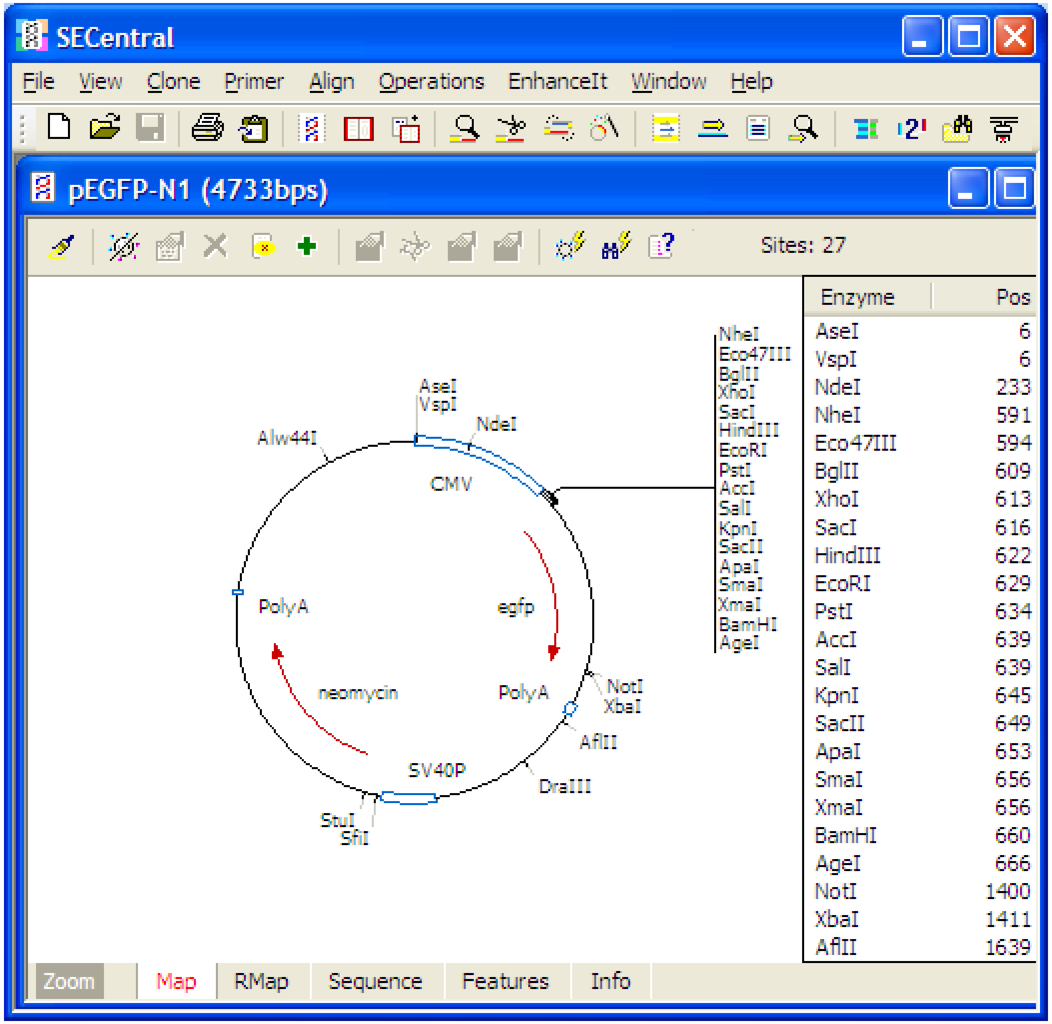
NGS
(Next generation sequencing) data is supported

Some key UGENE features

- Alignments: ClustalW, ClustalO, MUSCLE, Kalign, MAFFT, T-Coffee, optimized Smith-Waterman algorithm
- PCR *in silico*; Integrated Primer3 package for PCR primer design
- Search through online databases: NCBI, PDB, UniProtKB/Swiss-Prot, UniProtKB/TrEMBL, DAS servers
- Local and NCBI Genbank BLAST search
- Restriction enzyme finder with integrated REBASE restriction enzymes list; Open reading frames finder
- Plasmid construction and annotation; Cloning *in silico* by designing of cloning vectors
- Genome mapping short reads with Bowtie, BWA and UGENE Genome Aligner
- Raw NGS data processing
- Visualization of next generation sequencing data (BAM files) using UGENE Assembly Browser
- RNA-seq data analysis with Tuxedo pipeline (TopHat, Cufflinks, etc.)
- ChIP-seq data analysis with Cistrome pipeline (MACS, CEAS, etc.)
- HMMER2 and HMMER3 packages integration
- Chromatogram viewer
- Search for transcription factor binding sites (TFBS) with weight matrix and SITECON algorithms
- Search for direct, inverted and tandem repeats in DNA sequences
- Building (using integrated PHYLIP Neighbor Joining, MrBayes or PhyML Maximum Likelyhood) and editing phylogenetic trees
- Combining various algorithms into custom workflows with UGENE Workflow Designer
- Contigs assembly with CAP3
- 3D Structure viewer for files in PDB and MMDB formats, anaglyph view support
- Protein secondary structure prediction with GOR IV and PSIPRED algorithms
- Constructing dotplots for nucleic acid sequences
- Creating and using a shared storage (e.g. for a lab)
- Search for complex signals with ExpertDiscovery
- Search for a pattern of various algorithms' results in a nucleic acid sequence with UGENE Query Designer

CloneManager

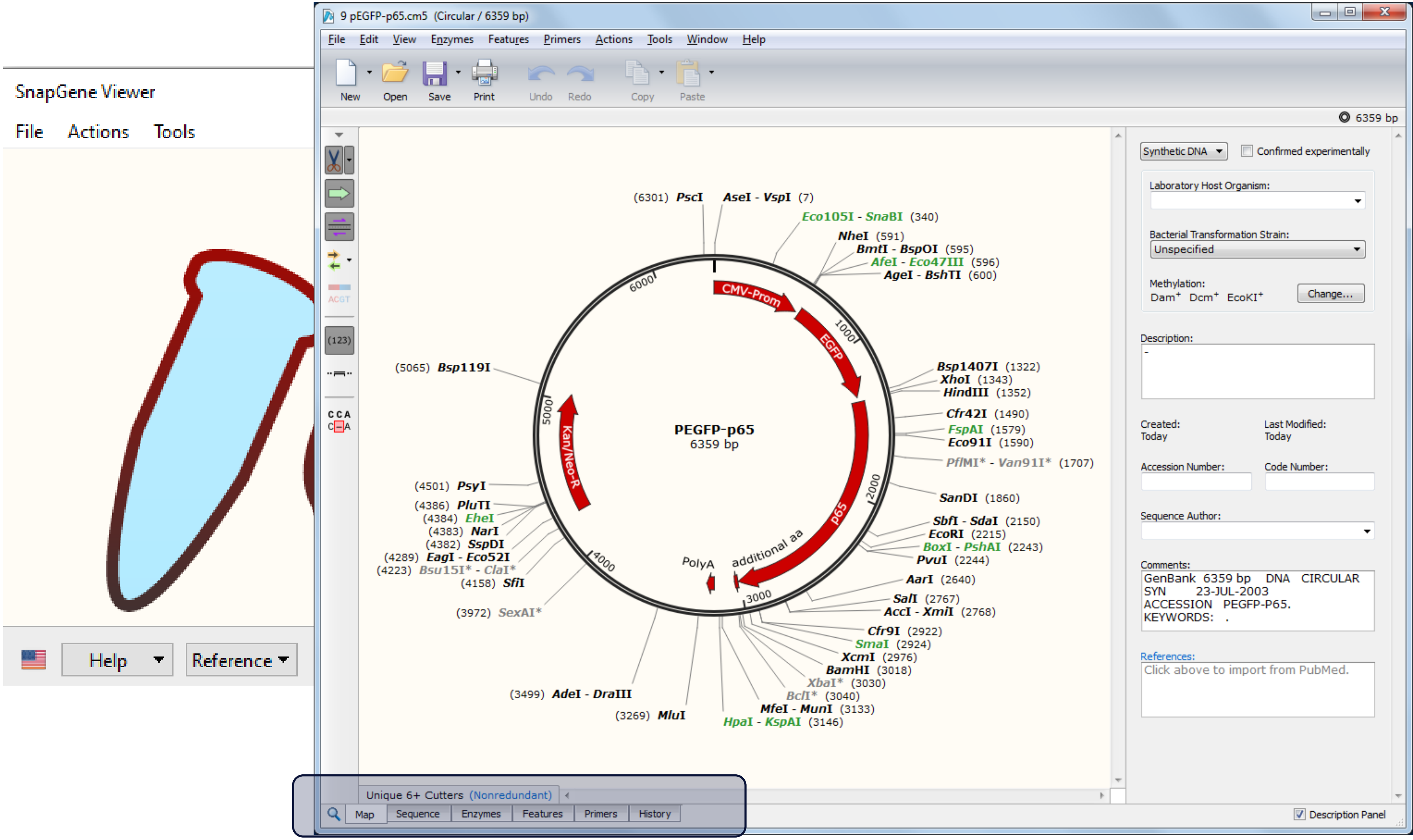
- commercial software from Scientfic Education: http://www.scied.com
- very well suited for „in silico cloning“ and handling of DNA constructs, primer design, alignments….
- Supports Genbank format
- Import from Entrez, NCBI
- basic license: 575$
- professional license: 1.100 $



Sites: 27

Enzyme	Pos
AseI	6
VspI	6
NdeI	233
NheI	591
Eco47III	594
BglII	609
XhoI	613
SacI	616
HindIII	622
EcoRI	629
PstI	634
AccI	639
SalI	639
KpnI	645
SacII	649
ApaI	653
SmaI	656
XmaI	656
BamHI	660
AgeI	666
NotI	1400
XbaI	1411
AflII	1639

SNAPGene-Viewer
(freeware: with restrictions)



Synthetic DNA ☐ Confirmed experimentally

Laboratory Host Organism:

Bacterial Transformation Strain: Unspecified

Methylation: Dam$^+$ Dcm$^+$ EcoKI$^+$

Description: -

Created: Today

Last Modified: Today

Accession Number:

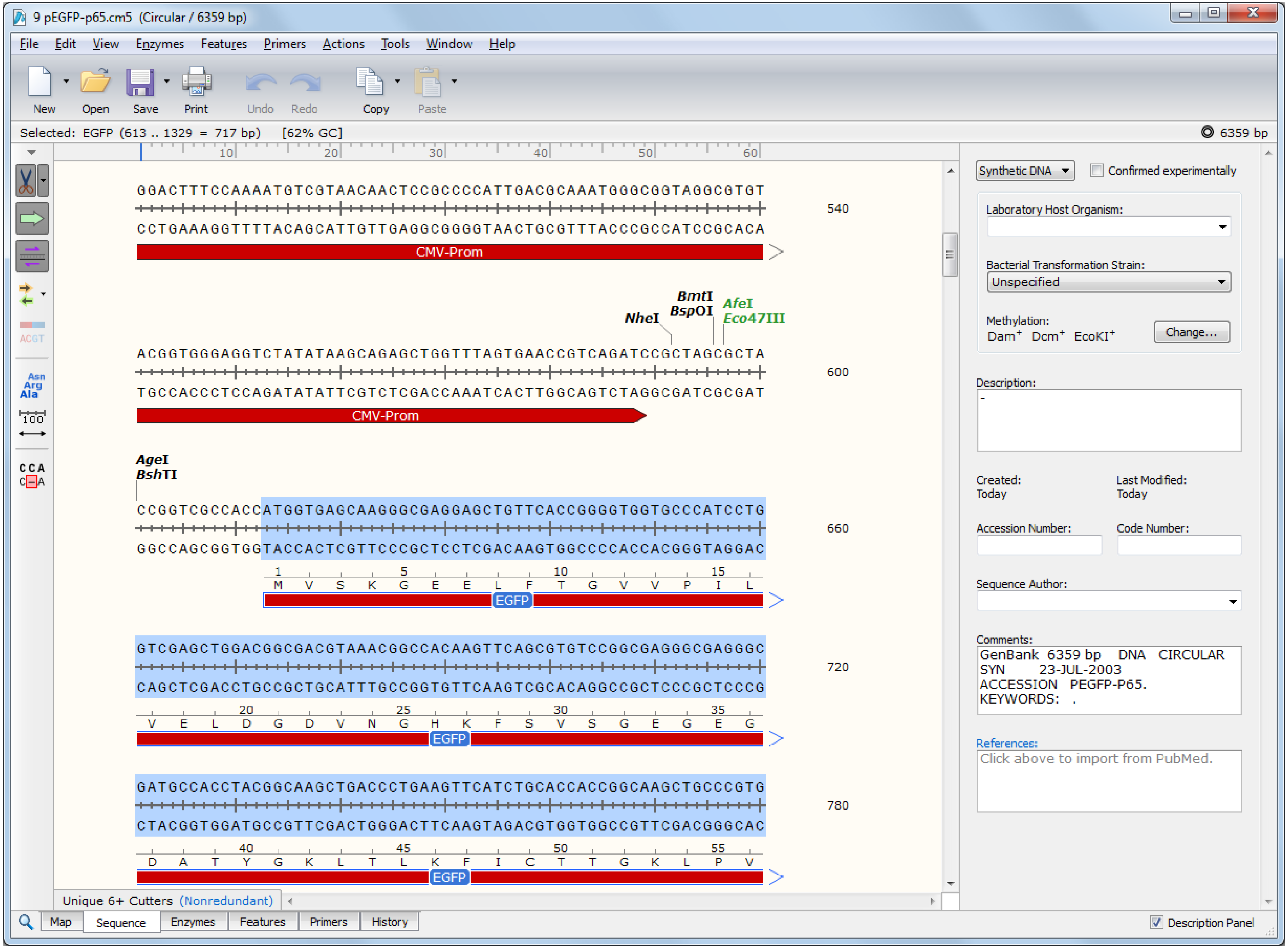
Code Number:

Sequence Author:

Comments:
GenBank 6359 bp DNA CIRCULAR
SYN 23-JUL-2003
ACCESSION PEGFP-P65.
KEYWORDS: .

References:
Click above to import from PubMed.

☑ Description Panel



Selected: EGFP (613 .. 1329 = 717 bp) [62% GC]

6359 bp

```
GGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGT    540
CCTGAAAGGTTTTACAGCATTGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACA
CMV-Prom

                                              BmtI
                                      NheI    BspOI  AfeI
                                                     Eco47III
ACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA    600
TGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
CMV-Prom

AgeI
BshTI
CCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTG    660
GGCCAGCGGTGGTACCACTCGTTCCCGCTCCTCGACAAGTGGCCCCACCACGGGTAGGAC
            1           5              10             15
            M  V  S  K  G  E  E  L  F  T  G  V  V  P  I  L
EGFP

GTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC    720
CAGCTCGACCTGCCGCTGCATTTGCCGGTGTTCAAGTCGCACAGGCCGCTCCCGCTCCCG
         20             25             30             35
V  E  L  D  G  D  V  N  G  H  K  F  S  V  S  G  E  G  E  G
EGFP

GATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTG    780
CTACGGTGGATGCCGTTCGACTGGGACTTCAAGTAGACGTGGTGGCCGTTCGACGGGCAC
         40             45             50             55
D  A  T  Y  G  K  L  T  L  K  F  I  C  T  T  G  K  L  P  V
EGFP
```

Synthetic DNA

☐ Confirmed experimentally

Laboratory Host Organism:

Bacterial Transformation Strain: Unspecified

Methylation: Dam$^+$ Dcm$^+$ EcoKI$^+$ Change...

Description: -

Created: Today

Last Modified: Today

Accession Number:

Code Number:

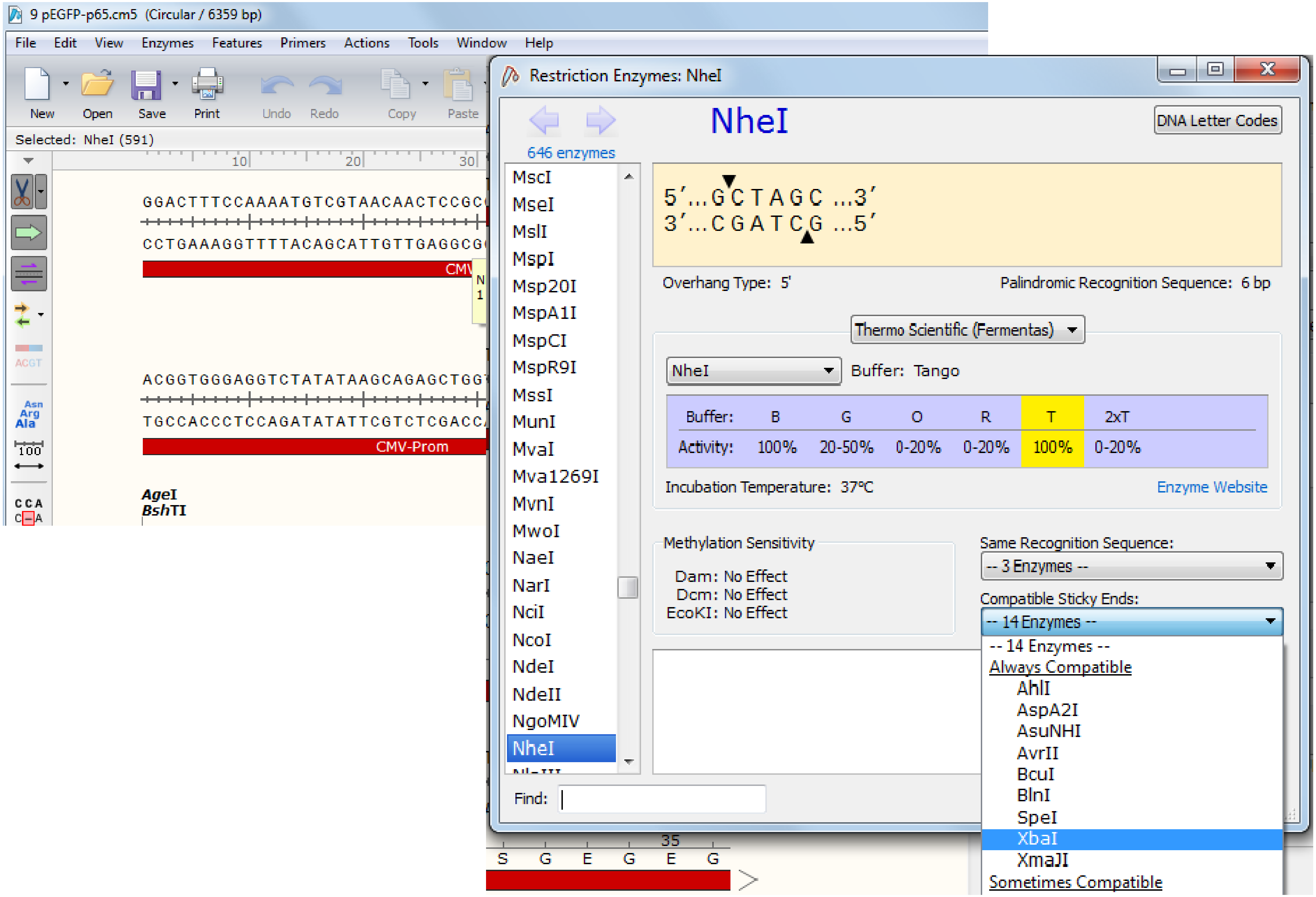
Sequence Author:

Comments:

GenBank 6359 bp DNA CIRCULAR
SYN 23-JUL-2003
ACCESSION PEGFP-P65.
KEYWORDS: .

References:

Click above to import from PubMed.



Selected: NheI (591)

NheI

5′...G CTAGC ...3′
3′...CGATC G ...5′

Overhang Type: 5′

Palindromic Recognition Sequence: 6 bp

Thermo Scientific (Fermentas)

NheI

Buffer: Tango

Buffer:	B	G	O	R	T	2xT
Activity:	100%	20-50%	0-20%	0-20%	100%	0-20%

Incubation Temperature: 37°C

Enzyme Website

Methylation Sensitivity

Dam: No Effect
Dcm: No Effect
EcoKI: No Effect

Same Recognition Sequence: -- 3 Enzymes --

Compatible Sticky Ends: -- 14 Enzymes --

-- 14 Enzymes --

Always Compatible
- AhlI
- AspA2I
- AsuNHI
- AvrII
- BcuI
- BlnI
- SpeI
- XbaI
- XmaJI

Sometimes Compatible

LinRegPCR Software for realtime PCR

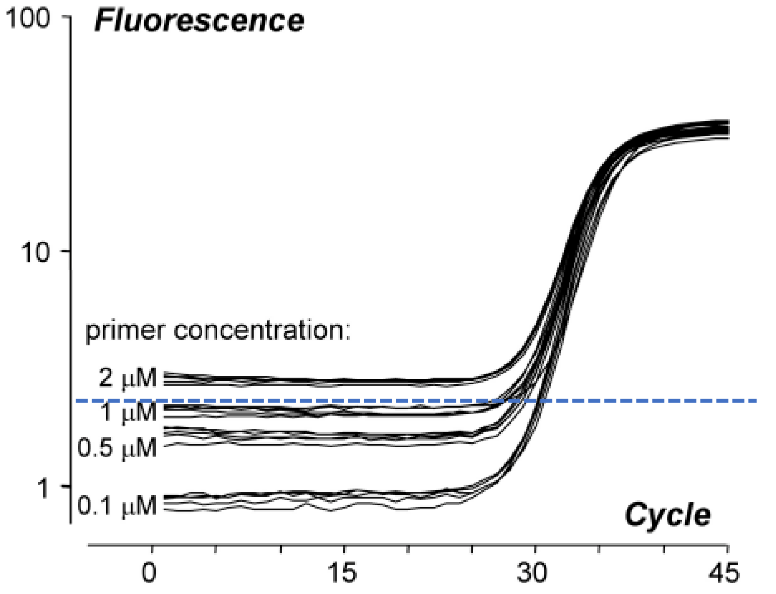
http://www.hartfaalcentrum.nl/index.php?main=files&sub=LinRegPCR

Nucleic Acids Research Advance Access published February 22, 2009

Nucleic Acids Research, 2009, ***1–12***
doi:10.1093/nar/gkp045

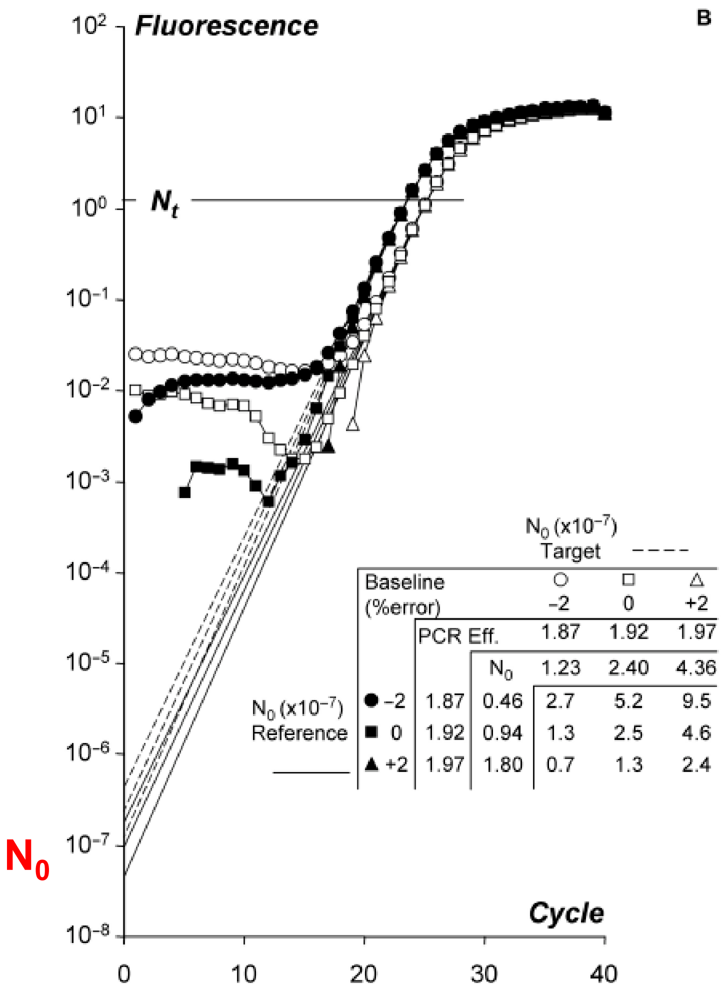
Amplification efficiency: linking baseline and bias in the analysis of quantitative PCR data

J. M. Ruijter[1,*], C. Ramakers[2], W. M. H. Hoogaars[1], Y. Karlen[3], O. Bakker[4], M. J. B. van den Hoff[1] and A. F. M. Moorman[1]



classical methods (like the ΔΔCt-method) require correct baseline settings for correct quantification

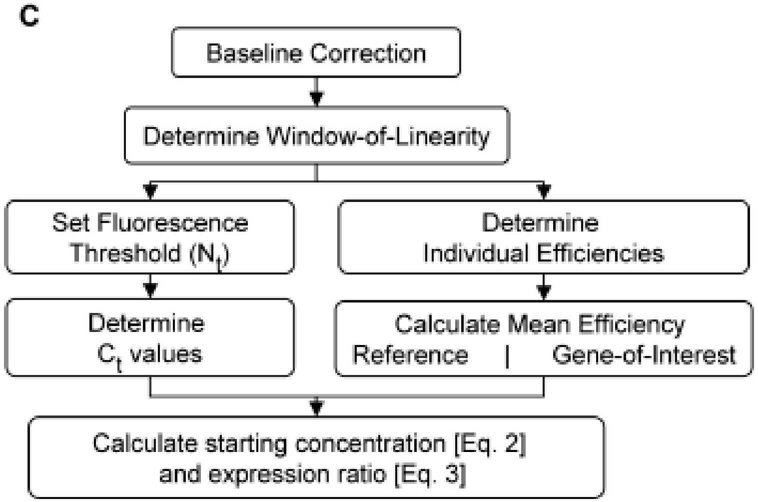
LinRegPCR uses the logarithmic part of the amplification curve to calculate a starting point N_0



N_0 (x10^{-7}) Target - - - -

N_0 (x10^{-7}) Reference ——

			Baseline (%error)	○ −2	□ 0	△ +2
			PCR Eff.	1.87	1.92	1.97
			N_0	1.23	2.40	4.36
●	−2	1.87	0.46	2.7	5.2	9.5
■	0	1.92	0.94	1.3	2.5	4.6
▲	+2	1.97	1.80	0.7	1.3	2.4



Baseline Correction

Determine Window-of-Linearity

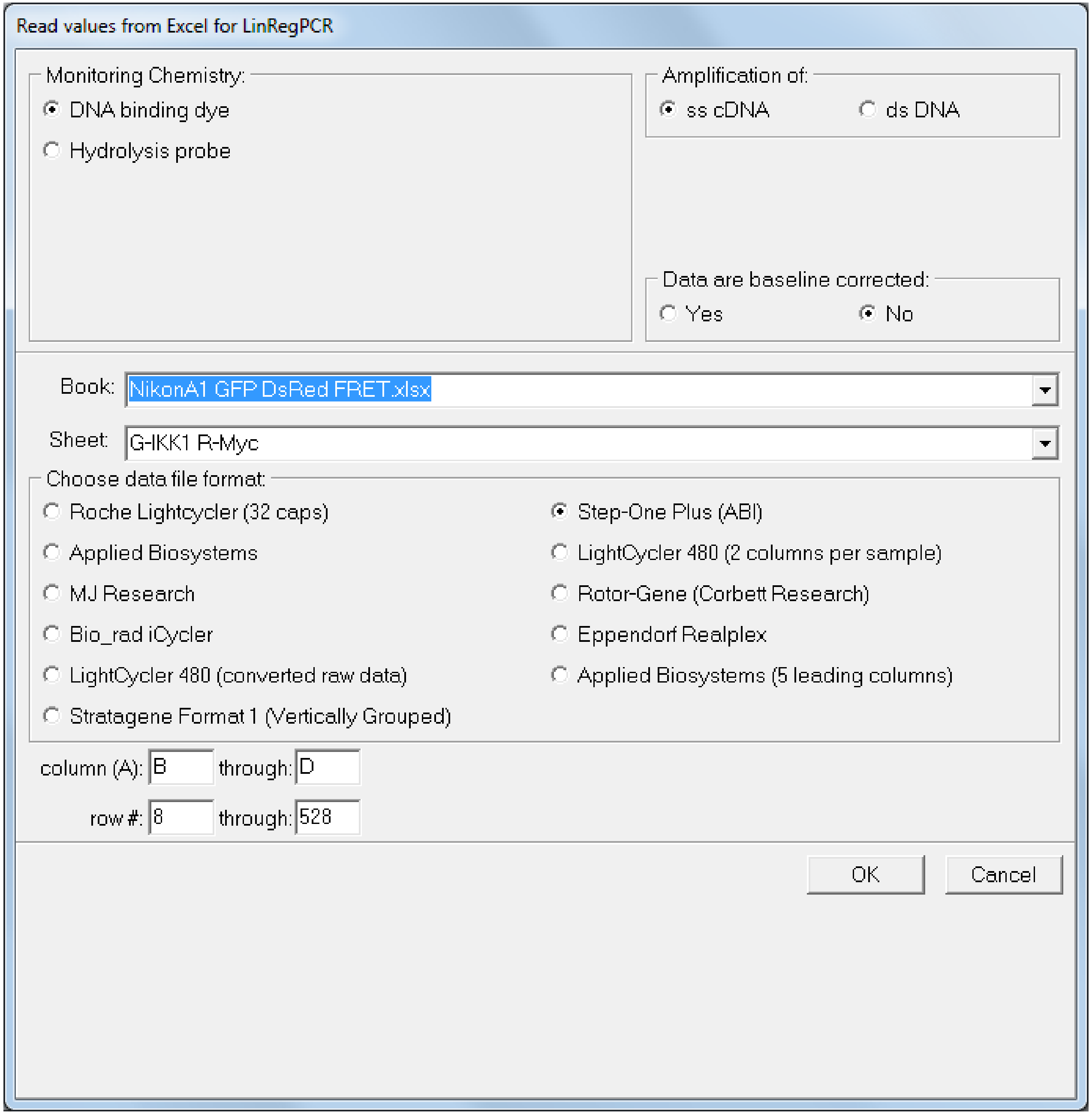
Set Fluorescence Threshold (N_t)

Determine Individual Efficiencies

Determine C_t values

Calculate Mean Efficiency Reference | Gene-of-Interest

Calculate starting concentration [Eq. 2] and expression ratio [Eq. 3]



Read values from Excel for LinRegPCR

Monitoring Chemistry:
- ● DNA binding dye
- ○ Hydrolysis probe

Amplification of:
- ● ss cDNA
- ○ ds DNA

Data are baseline corrected:
- ○ Yes
- ● No

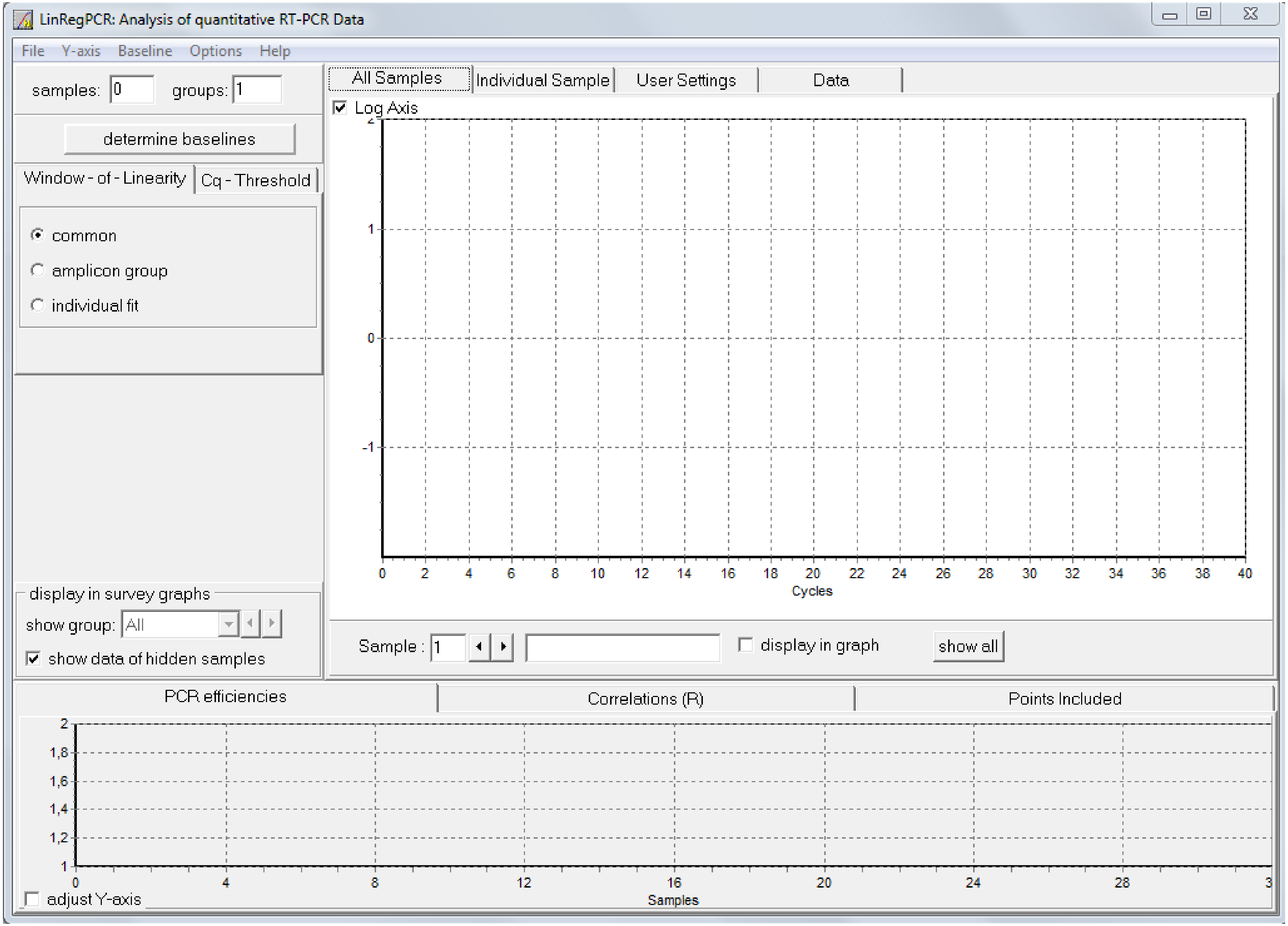
Book: NikonA1 GFP DsRed FRET.xlsx

Sheet: G-IKK1 R-Myc

Choose data file format:
- ○ Roche Lightcycler (32 caps)
- ○ Applied Biosystems
- ○ MJ Research
- ○ Bio_rad iCycler
- ○ LightCycler 480 (converted raw data)
- ○ Stratagene Format 1 (Vertically Grouped)
- ● Step-One Plus (ABI)
- ○ LightCycler 480 (2 columns per sample)
- ○ Rotor-Gene (Corbett Research)
- ○ Eppendorf Realplex
- ○ Applied Biosystems (5 leading columns)

column (A): B through: D

row #: 8 through: 528



samples: 0 groups: 1

☑ Log Axis

● common
○ amplicon group
○ individual fit

show group: All

☑ show data of hidden samples

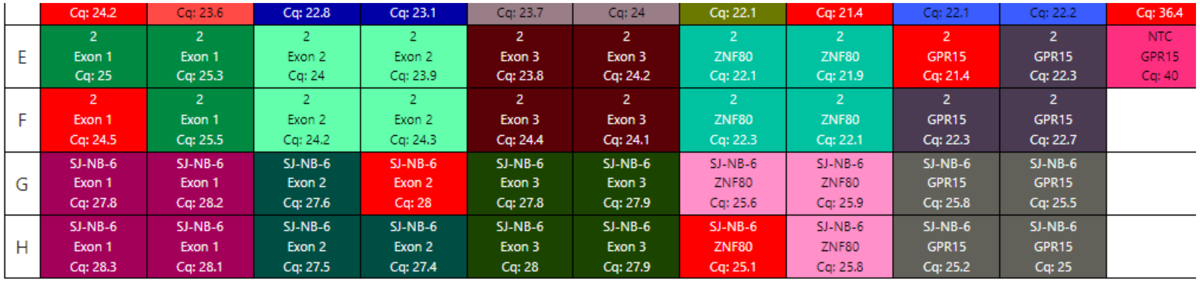
Sample : 1

☐ display in graph

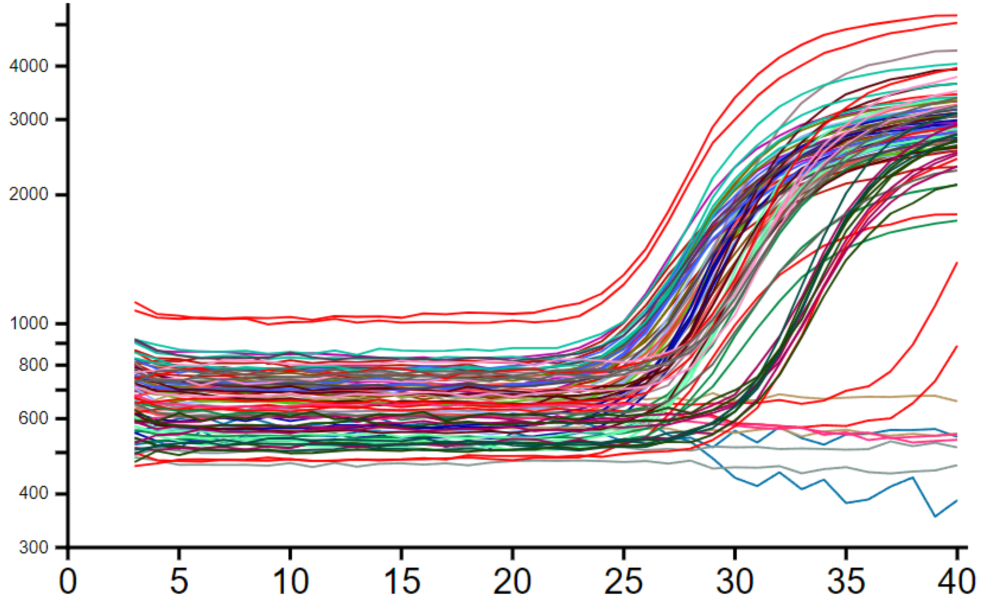
☐ adjust Y-axis

New Web-based LinRegPCR tools

- https://www.gear-genomics.com/rdml-tools/

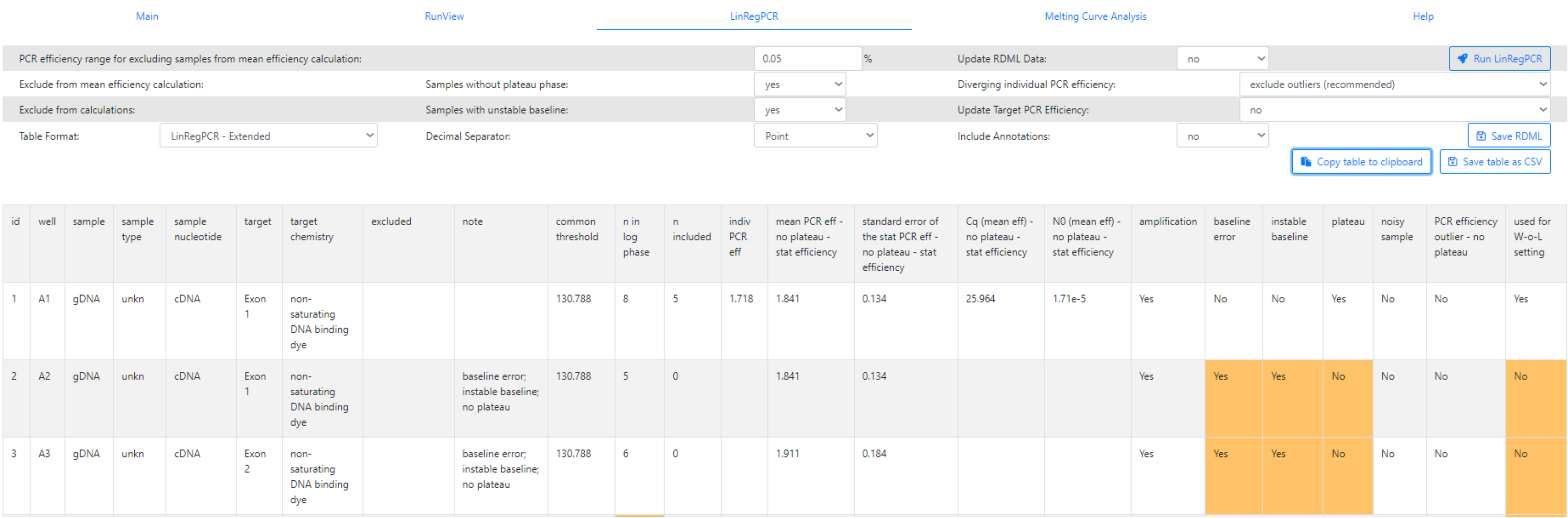


	Cq: 24.2	Cq: 23.6	Cq: 22.8	Cq: 23.1	Cq: 23.7	Cq: 24	Cq: 22.1	Cq: 21.4	Cq: 22.1	Cq: 22.2	Cq: 36.4
E	2 Exon 1 Cq: 25	2 Exon 1 Cq: 25.3	2 Exon 2 Cq: 24	2 Exon 2 Cq: 23.9	2 Exon 3 Cq: 23.8	2 Exon 3 Cq: 24.2	2 ZNF80 Cq: 22.1	2 ZNF80 Cq: 21.9	2 GPR15 Cq: 21.4	2 GPR15 Cq: 22.3	NTC GPR15 Cq: 40
F	2 Exon 1 Cq: 24.5	2 Exon 1 Cq: 25.5	2 Exon 2 Cq: 24.2	2 Exon 2 Cq: 24.3	2 Exon 3 Cq: 24.4	2 Exon 3 Cq: 24.1	2 ZNF80 Cq: 22.3	2 ZNF80 Cq: 22.1	2 GPR15 Cq: 22.3	2 GPR15 Cq: 22.7	
G	SJ-NB-6 Exon 1 Cq: 27.8	SJ-NB-6 Exon 1 Cq: 28.2	SJ-NB-6 Exon 2 Cq: 27.6	SJ-NB-6 Exon 2 Cq: 28	SJ-NB-6 Exon 3 Cq: 27.8	SJ-NB-6 Exon 3 Cq: 27.9	SJ-NB-6 ZNF80 Cq: 25.6	SJ-NB-6 ZNF80 Cq: 25.9	SJ-NB-6 GPR15 Cq: 25.8	SJ-NB-6 GPR15 Cq: 25.5	
H	SJ-NB-6 Exon 1 Cq: 28.3	SJ-NB-6 Exon 1 Cq: 28.1	SJ-NB-6 Exon 2 Cq: 27.5	SJ-NB-6 Exon 2 Cq: 27.4	SJ-NB-6 Exon 3 Cq: 28	SJ-NB-6 Exon 3 Cq: 27.9	SJ-NB-6 ZNF80 Cq: 25.1	SJ-NB-6 ZNF80 Cq: 25.8	SJ-NB-6 GPR15 Cq: 25.2	SJ-NB-6 GPR15 Cq: 25	



New Web-based LinRegPCR tools

- https://www.gear-genomics.com/rdml-tools/



PCR efficiency range for excluding samples from mean efficiency calculation: 0.05 %

Update RDML Data: no

Exclude from mean efficiency calculation: Samples without plateau phase: yes

Diverging individual PCR efficiency: exclude outliers (recommended)

Exclude from calculations: Samples with unstable baseline: yes

Update Target PCR Efficiency: no

Table Format: LinRegPCR - Extended

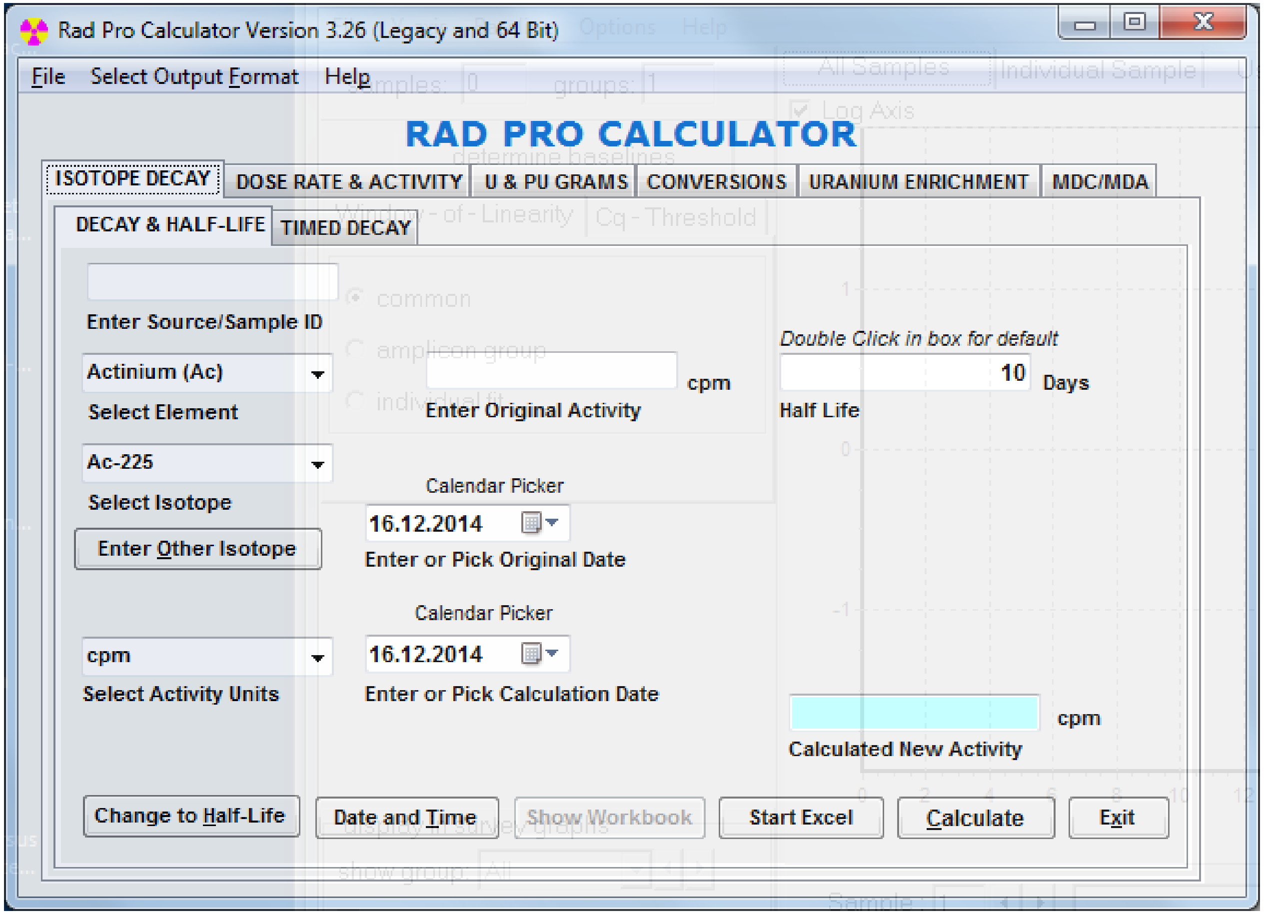
Decimal Separator: Point

Include Annotations: no

id	well	sample	sample type	sample nucleotide	target	target chemistry	excluded	note	common threshold	n in log phase	n included	indiv PCR eff	mean PCR eff - no plateau - stat efficiency	standard error of the stat PCR eff - no plateau - stat efficiency	Cq (mean eff) - no plateau - stat efficiency	N0 (mean eff) - no plateau - stat efficiency	amplification	baseline error	instable baseline	plateau	noisy sample	PCR efficiency outlier - no plateau	used for W-o-L setting
1	A1	gDNA	unkn	cDNA	Exon 1	non-saturating DNA binding dye			130.788	8	5	1.718	1.841	0.134	25.964	1.71e-5	Yes	No	No	Yes	No	No	Yes
2	A2	gDNA	unkn	cDNA	Exon 1	non-saturating DNA binding dye		baseline error; instable baseline; no plateau	130.788	5	0		1.841	0.134			Yes	Yes	Yes	No	No	No	No
3	A3	gDNA	unkn	cDNA	Exon 2	non-saturating DNA binding dye		baseline error; instable baseline; no plateau	130.788	6	0		1.911	0.184			Yes	Yes	Yes	No	No	No	No

Radioactivity software: RadPro Calculator

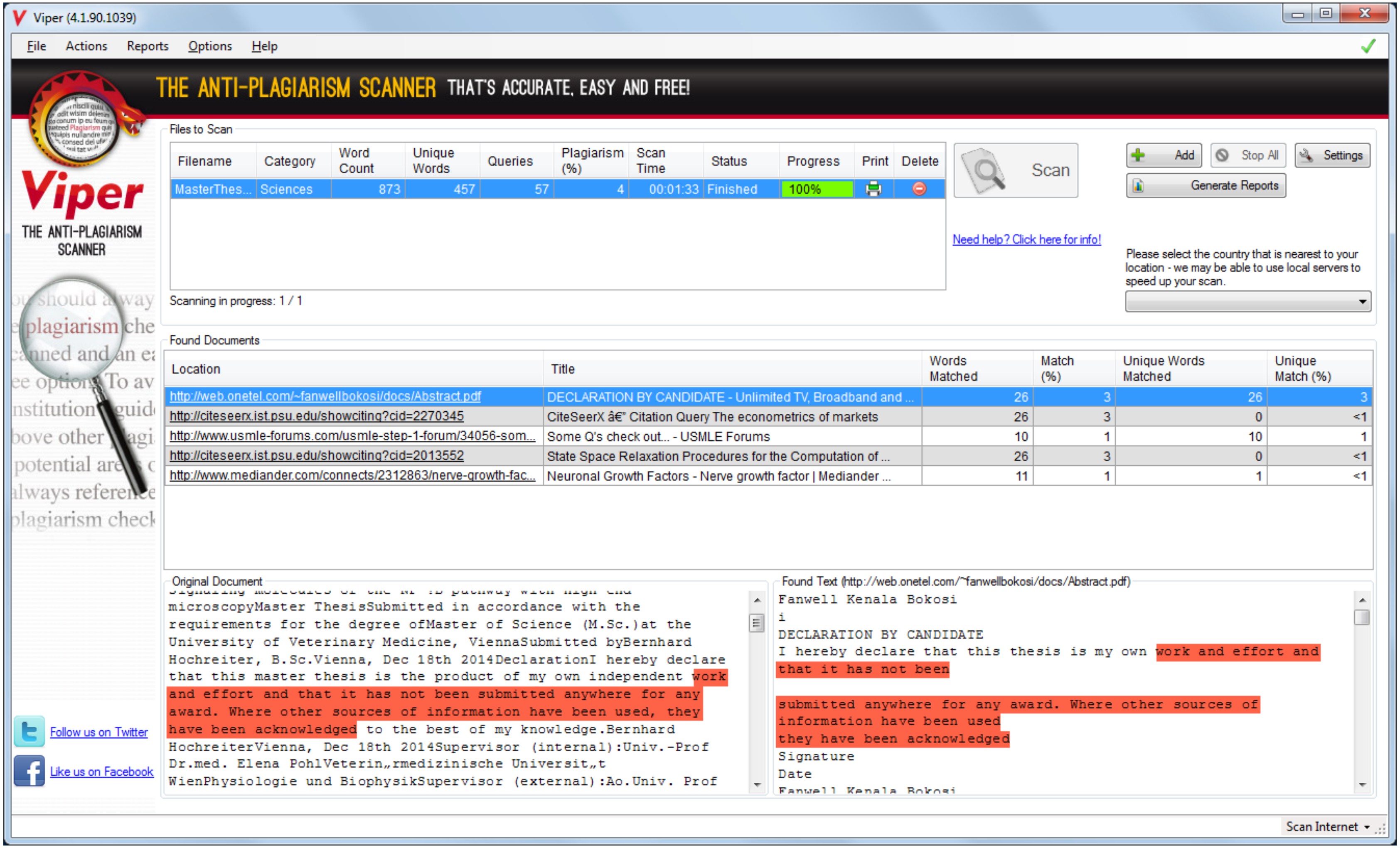
Online: http://www.radprocalculator.com/
Download link: http://www.radprocalculator.com/RadProDownloads.aspx



Actinium (Ac)
Ac-225
cpm
16.12.2014
16.12.2014
10 Days
cpm

VIPER – anti-plagiarism software

http://scanmyessay.com/



Files to Scan

Filename	Category	Word Count	Unique Words	Queries	Plagiarism (%)	Scan Time	Status	Progress	Print	Delete
MasterThes...	Sciences	873	457	57	4	00:01:33	Finished	100%		

Scanning in progress: 1 / 1

Please select the country that is nearest to your location - we may be able to use local servers to speed up your scan.

Found Documents

Location	Title	Words Matched	Match (%)	Unique Words Matched	Unique Match (%)
http://web.onetel.com/~fanwellbokosi/docs/Abstract.pdf	DECLARATION BY CANDIDATE - Unlimited TV, Broadband and ...	26	3	26	3
http://citeseerx.ist.psu.edu/showciting?cid=2270345	CiteSeerX â€" Citation Query The econometrics of markets	26	3	0	<1
http://www.usmle-forums.com/usmle-step-1-forum/34056-som...	Some Q's check out... - USMLE Forums	10	1	10	1
http://citeseerx.ist.psu.edu/showciting?cid=2013552	State Space Relaxation Procedures for the Computation of ...	26	3	0	<1
http://www.mediander.com/connects/2312863/nerve-growth-fac...	Neuronal Growth Factors - Nerve growth factor | Mediander ...	11	1	1	<1

Original Document

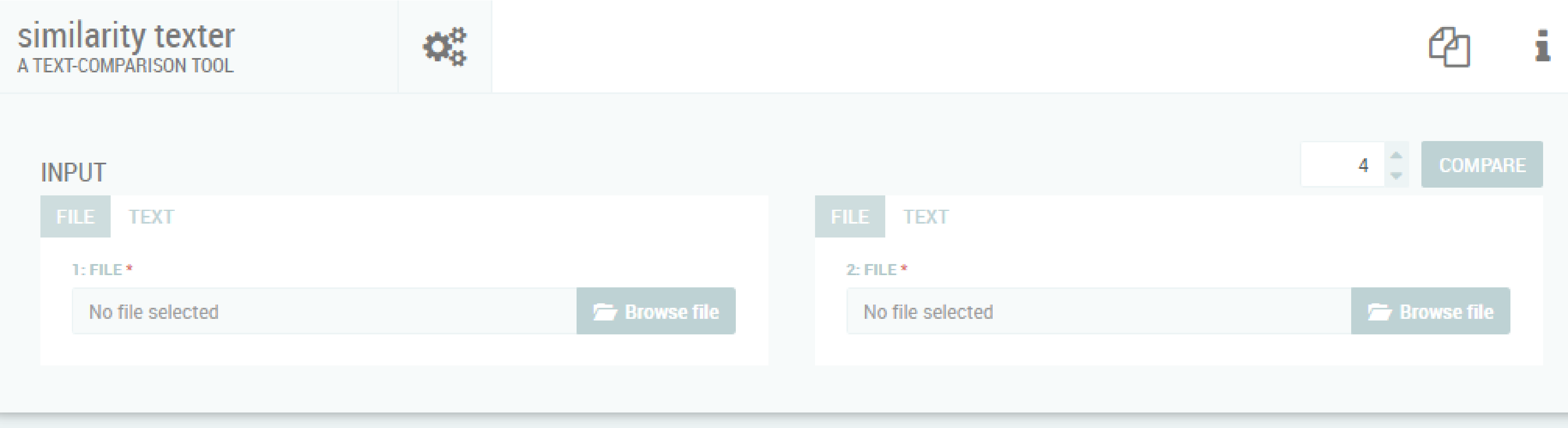
```
microscopyMaster ThesisSubmitted in accordance with the
requirements for the degree ofMaster of Science (M.Sc.)at the
University of Veterinary Medicine, ViennaSubmitted byBernhard
Hochreiter, B.Sc.Vienna, Dec 18th 2014DeclarationI hereby declare
that this master thesis is the product of my own independent work
and effort and that it has not been submitted anywhere for any
award. Where other sources of information have been used, they
have been acknowledged to the best of my knowledge.Bernhard
HochreiterVienna, Dec 18th 2014Supervisor (internal):Univ.-Prof
Dr.med. Elena PohlVeterin„rmedizinische Universit„t
WienPhysiologie und BiophysikSupervisor (external):Ao.Univ. Prof
```

Found Text (http://web.onetel.com/~fanwellbokosi/docs/Abstract.pdf)

```
Fanwell Kenala Bokosi
i
DECLARATION BY CANDIDATE
I hereby declare that this thesis is my own work and effort and
that it has not been

submitted anywhere for any award. Where other sources of
information have been used
they have been acknowledged
Signature
Date
Fanwell Kenala Bokosi
```

Plagiarism check by SimTexter

https://people.f4.htw-berlin.de/~weberwu/simtexter/app.html



Plagiarism check by using Google Scholar for table values or similar text.

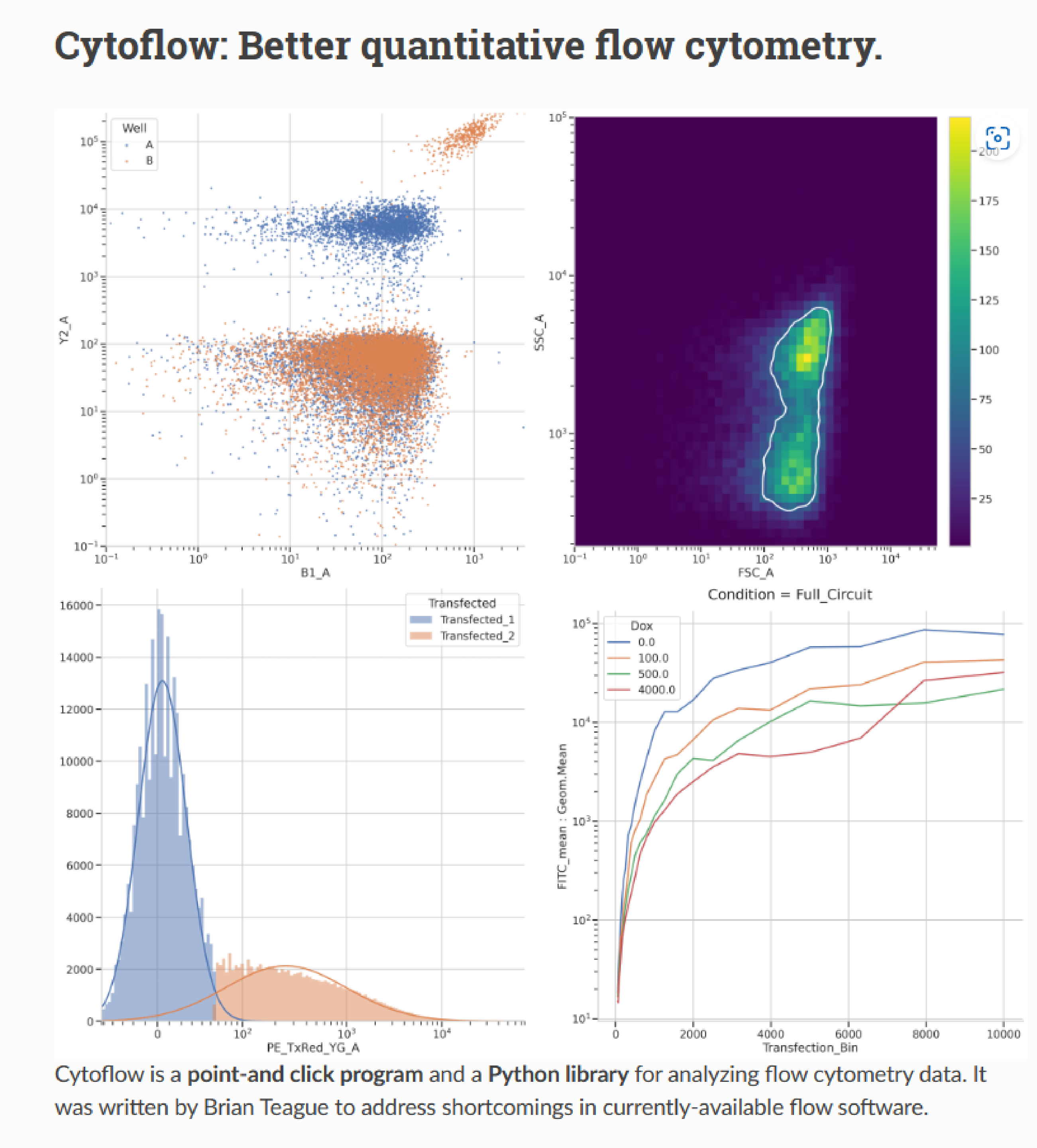
Example: Detection of an „octapaper“ (the same figures or data sets published in 8(!) different articles, with different authors and institutions in China:
https://scienceintegritydigest.com/2020/06/03/the-octopaper/

(apparently sold as service for students, who need a paper for promotion)

It took a Google Scholar search for table values to
detect that all eight papers are connected.

Cytoflow

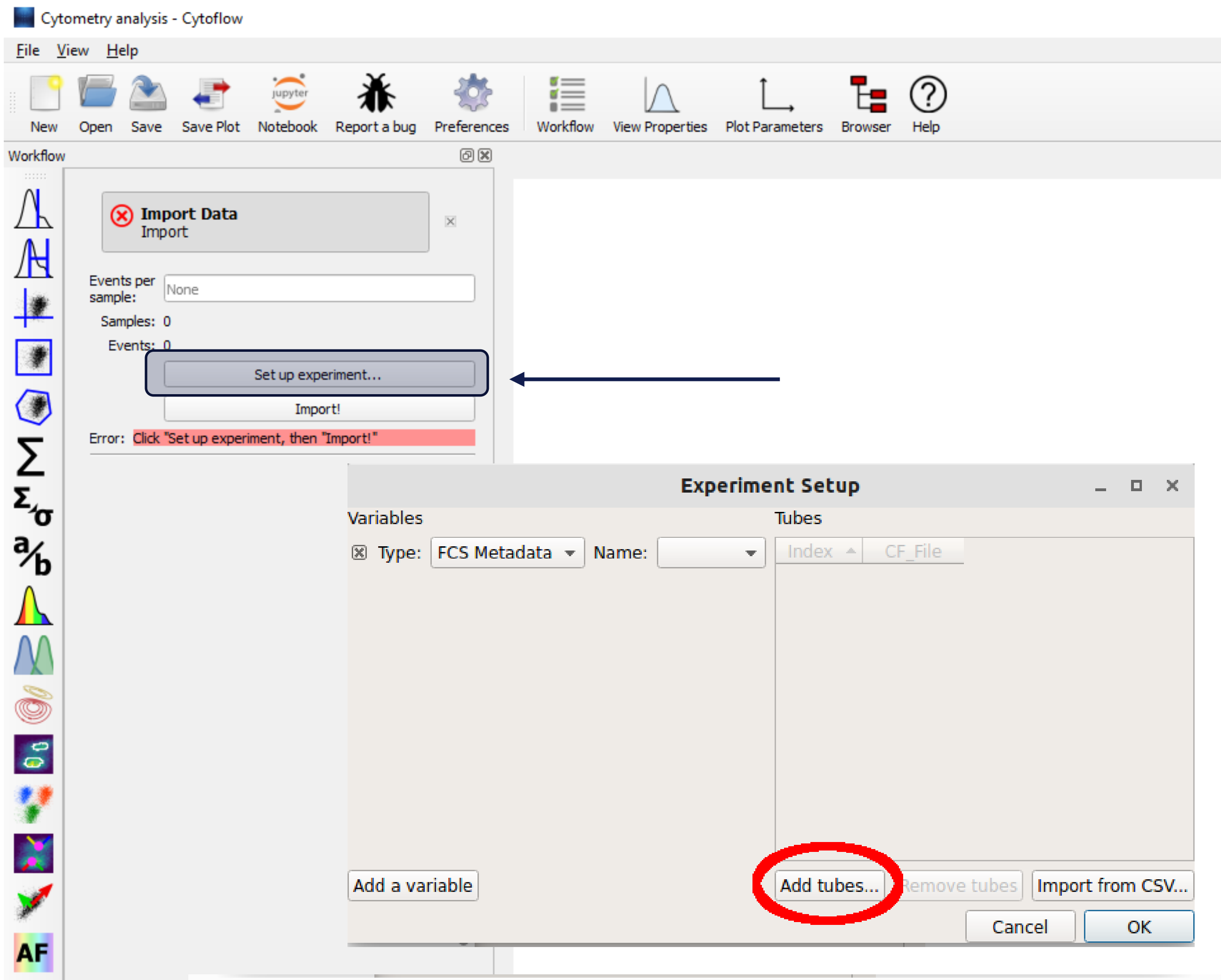
https://cytoflow.github.io



Cytoflow: Better quantitative flow cytometry.

Cytoflow is a **point-and click program** and a **Python library** for analyzing flow cytometry data. It was written by Brian Teague to address shortcomings in currently-available flow software.

Cytoflow



Events per sample: None

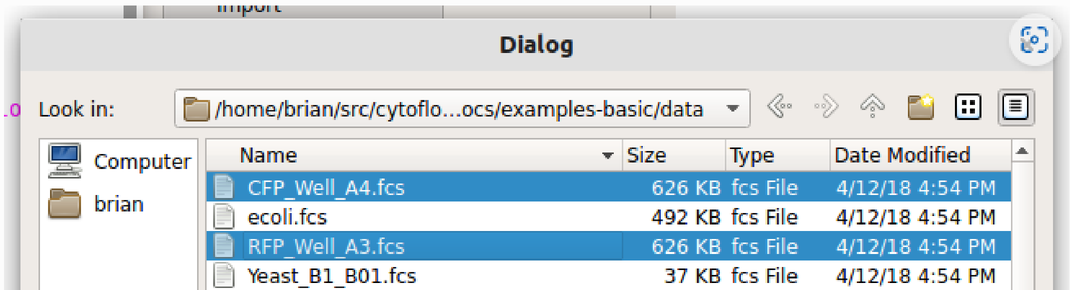
Samples: 0

Events: 0

Error: Click "Set up experiment, then "Import!"

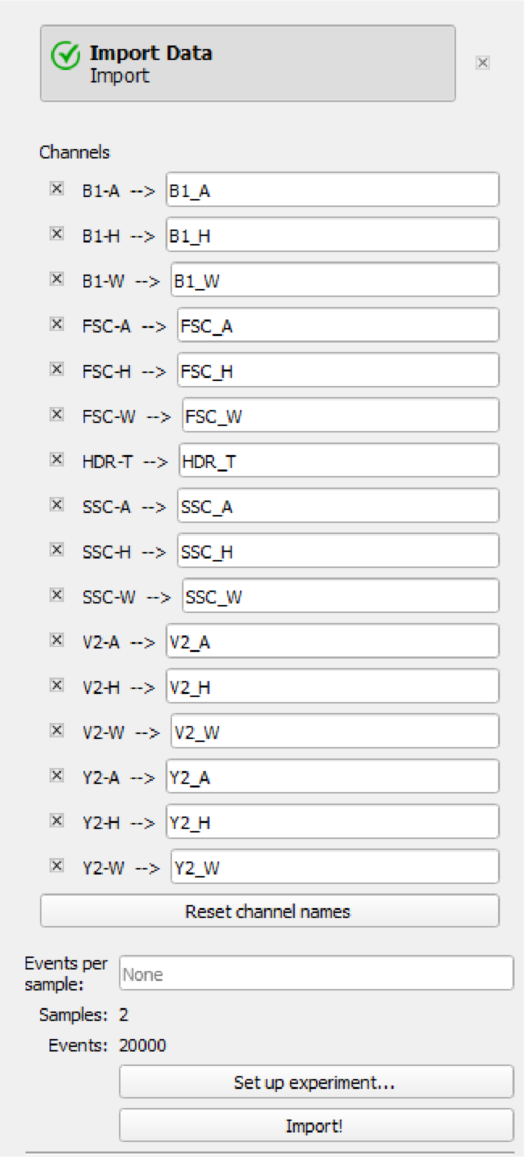
☒ Type: FCS Metadata Name:

Choose *CFP_Well_A4.fcs* and *RFP_Well_A3.fcs*. You can select multiple files by holding down th *Control* key (Windows or Linux) or the *Command* key (Mac) while clicking on the files.



Look in: /home/brian/src/cytoflo...ocs/examples-basic/data

Name	Size	Type	Date Modified
CFP_Well_A4.fcs	626 KB	fcs File	4/12/18 4:54 PM
ecoli.fcs	492 KB	fcs File	4/12/18 4:54 PM
RFP_Well_A3.fcs	626 KB	fcs File	4/12/18 4:54 PM
Yeast_B1_B01.fcs	37 KB	fcs File	4/12/18 4:54 PM


Import Data
Import

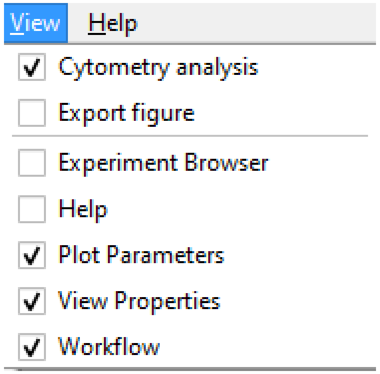
Channels

☒ B1-A --> B1_A
☒ B1-H --> B1_H
☒ B1-W --> B1_W
☒ FSC-A --> FSC_A
☒ FSC-H --> FSC_H
☒ FSC-W --> FSC_W
☒ HDR-T --> HDR_T
☒ SSC-A --> SSC_A
☒ SSC-H --> SSC_H
☒ SSC-W --> SSC_W
☒ V2-A --> V2_A
☒ V2-H --> V2_H
☒ V2-W --> V2_W
☒ Y2-A --> Y2_A
☒ Y2-H --> Y2_H
☒ Y2-W --> Y2_W

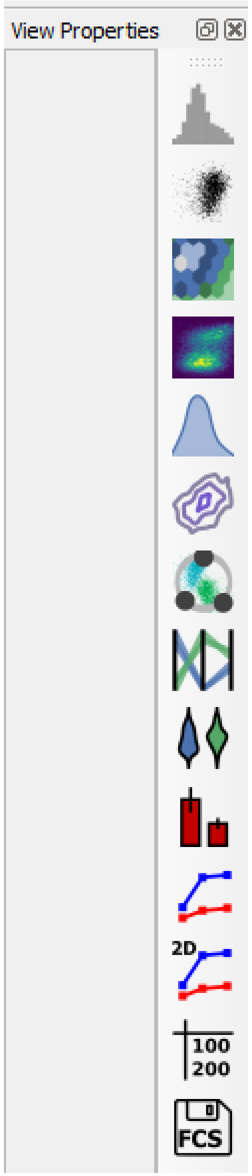
Events per sample: None

Samples: 2

Events: 20000



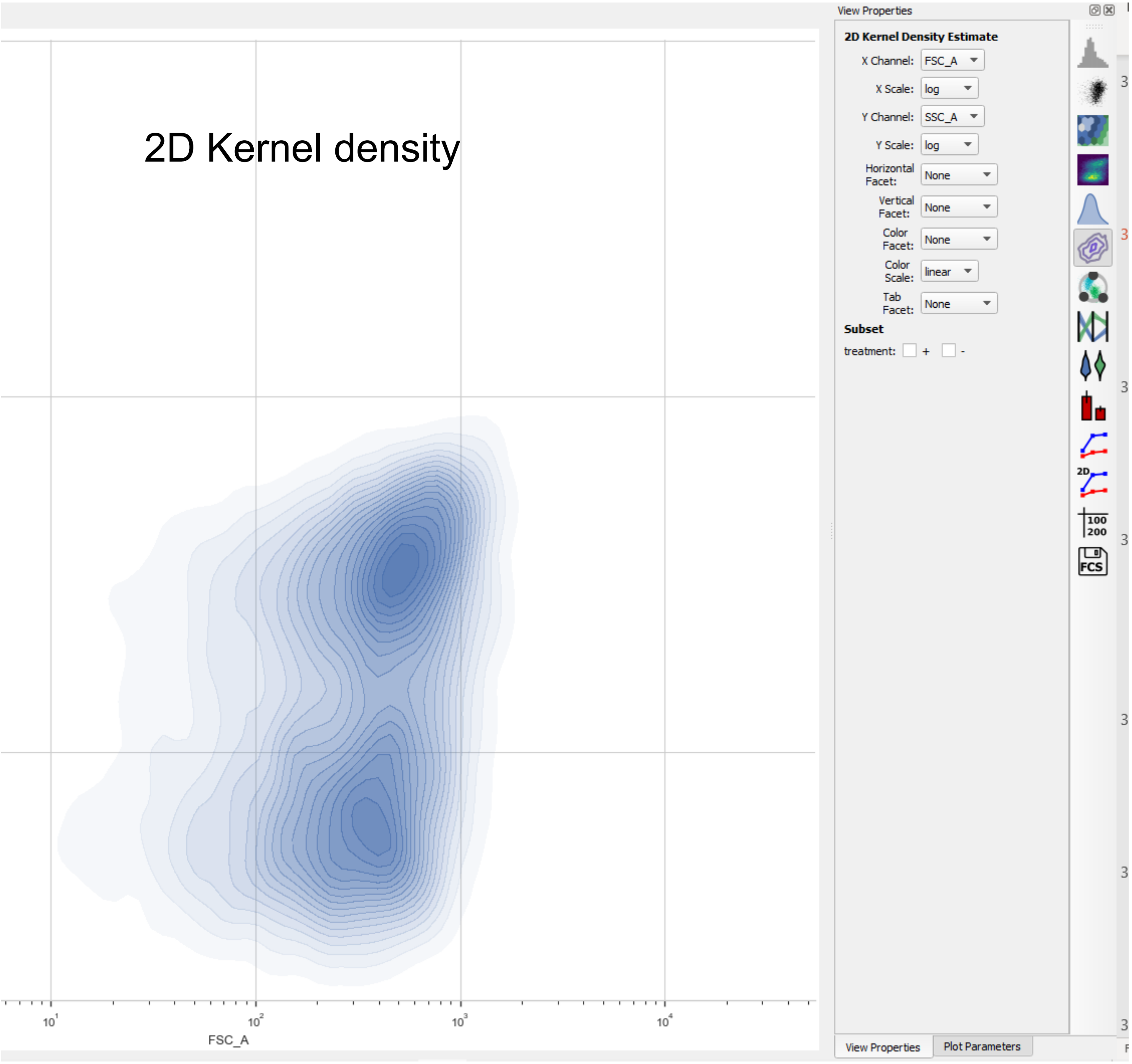
☑ Cytometry analysis
☐ Export figure
☐ Experiment Browser
☐ Help
☑ Plot Parameters
☑ View Properties
☑ Workflow



User manual link:

https://cytoflow.readthedocs.io/en/stable/user_manual/user_manual.html

2D Kernel density



View Properties

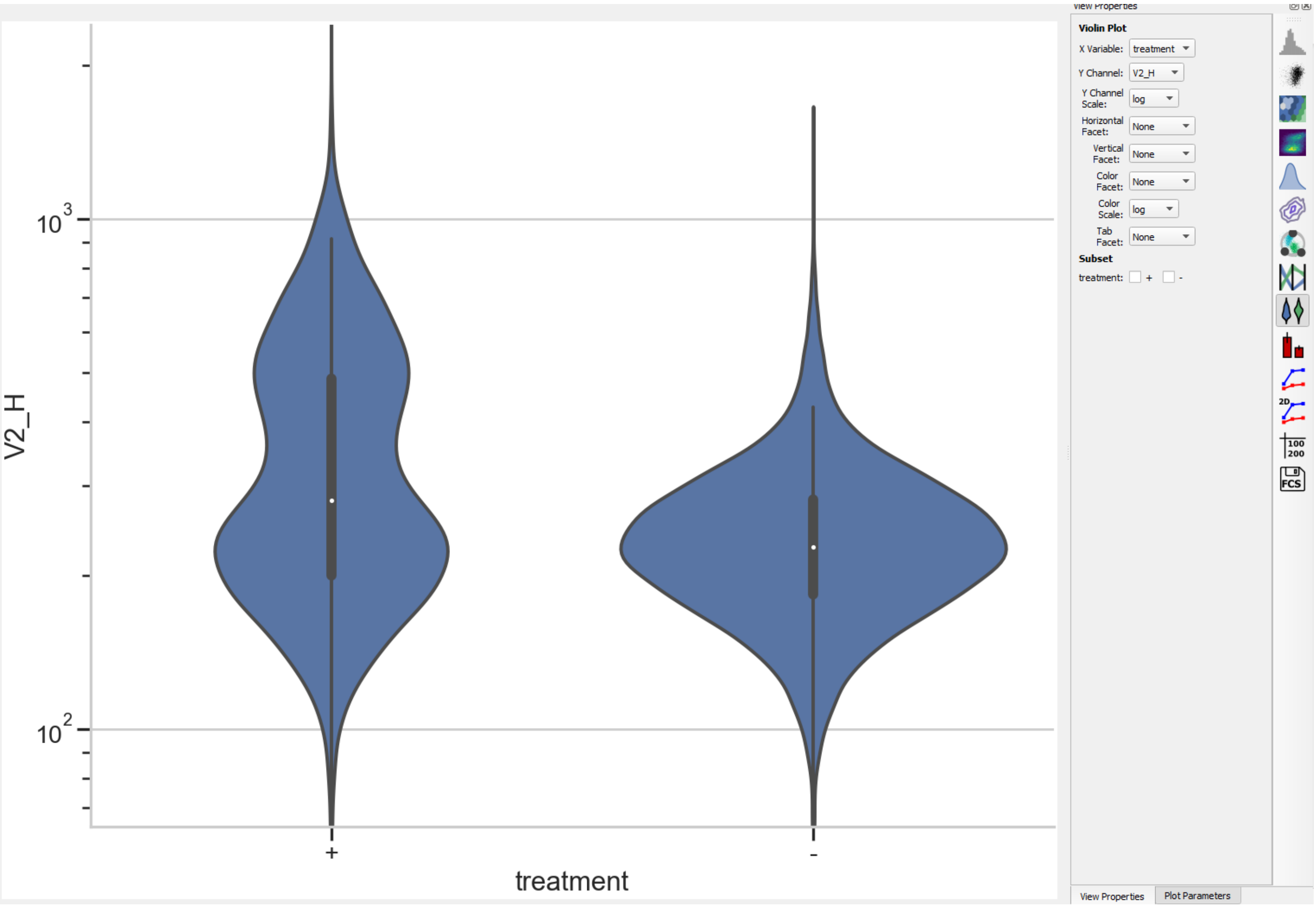
2D Kernel Density Estimate

X Channel: FSC_A
X Scale: log
Y Channel: SSC_A
Y Scale: log
Horizontal Facet: None
Vertical Facet: None
Color Facet: None
Color Scale: linear
Tab Facet: None

Subset

treatment: ☐ + ☐ -

Violin Plots



View Properties

Violin Plot

X Variable: treatment

Y Channel: V2_H

Y Channel Scale: log

Horizontal Facet: None

Vertical Facet: None

Color Facet: None

Color Scale: log

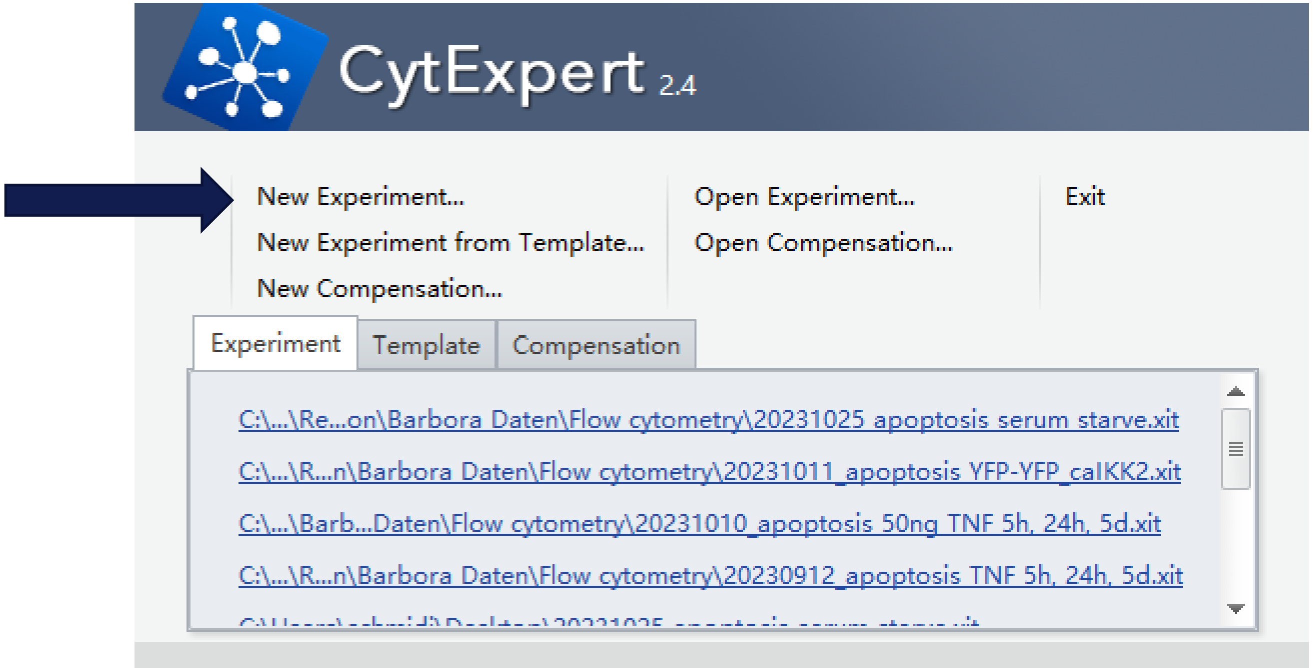
Tab Facet: None

Subset

treatment: ☐ + ☐ -

CytExpert (for Cytoflex Beckman Coulter)

https://www.beckman.com/flow-cytometry/research-flow-cytometers/cytoflex/software

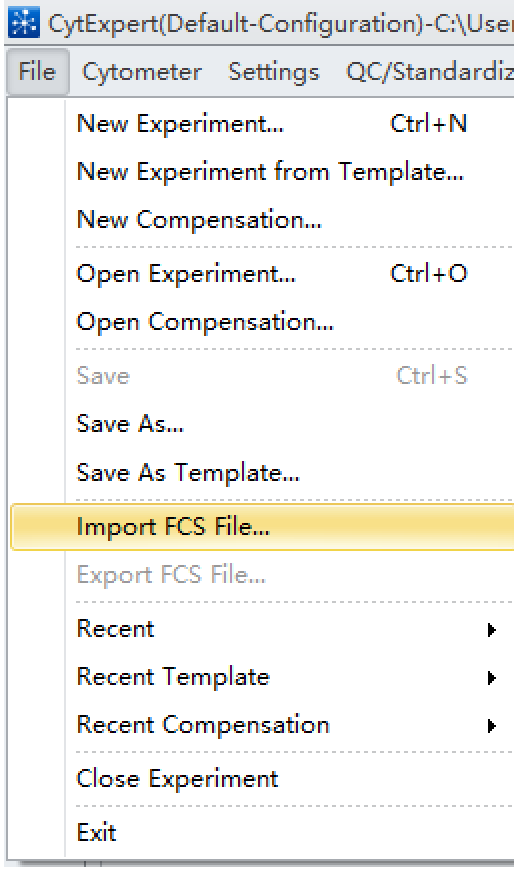


C:\...\Re...on\Barbora Daten\Flow cytometry\20231025 apoptosis serum starve.xit

C:\...\R...n\Barbora Daten\Flow cytometry\20231011_apoptosis YFP-YFP_caIKK2.xit

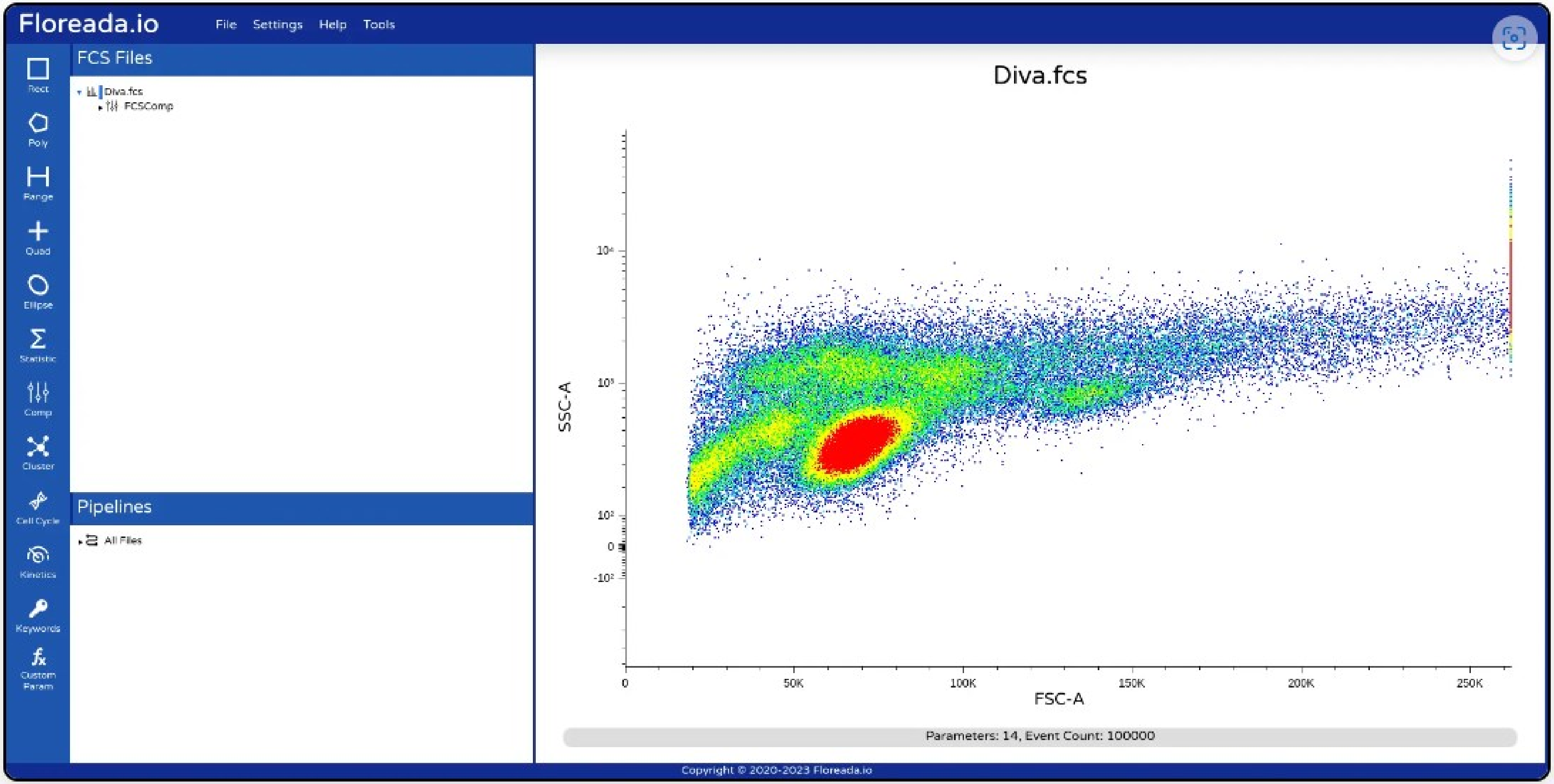
C:\...\Barb...Daten\Flow cytometry\20231010_apoptosis 50ng TNF 5h, 24h, 5d.xit

C:\...\R...n\Barbora Daten\Flow cytometry\20230912_apoptosis TNF 5h, 24h, 5d.xit



Floreada – web-based flow cytometry analysis

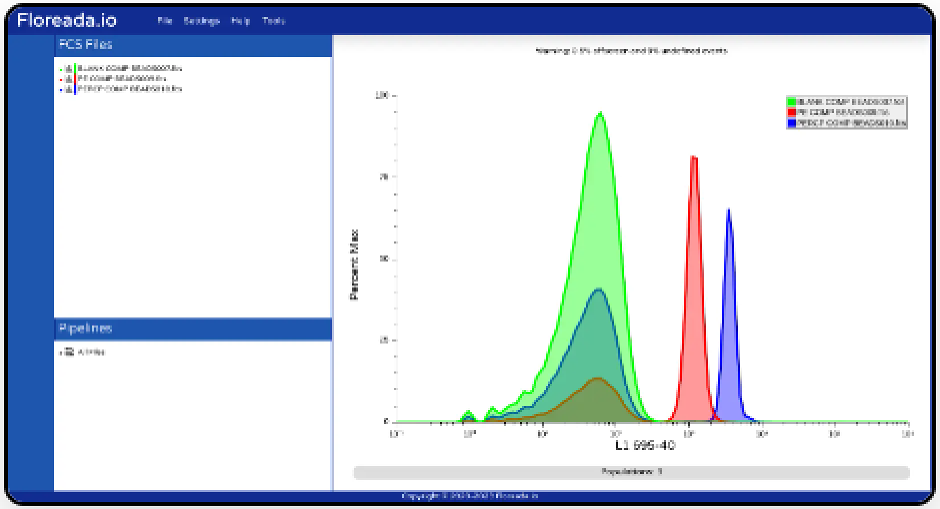
https://floreada.io/

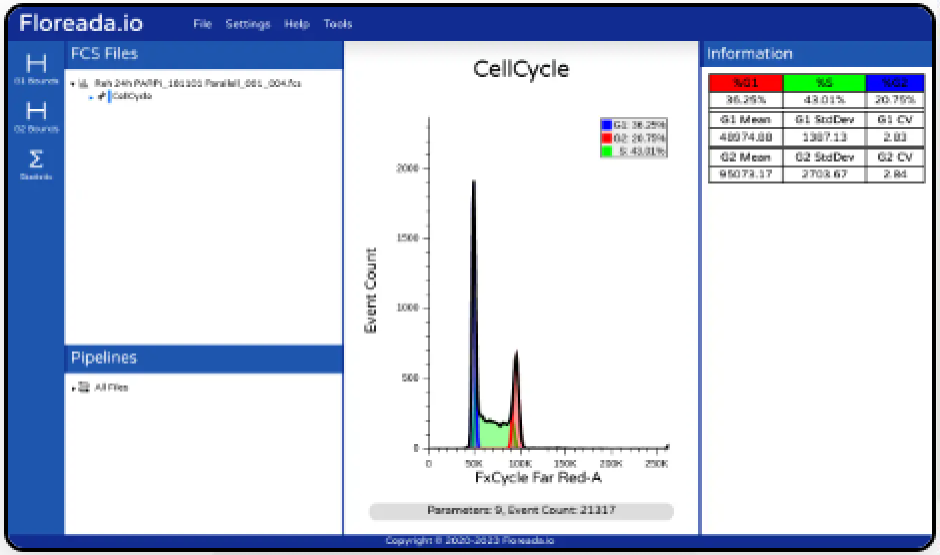


Parameters: 14, Event Count: 100000

Floreada features

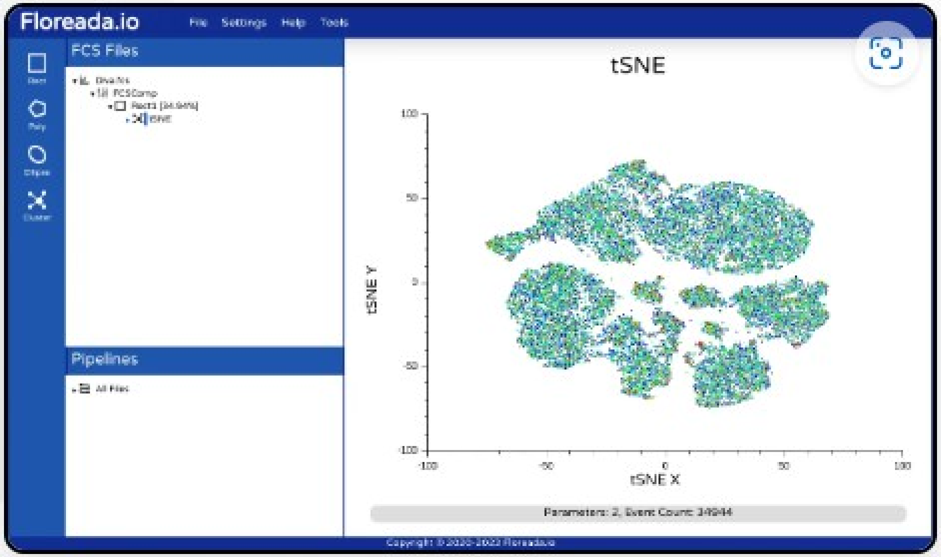
- Histogram overlays
- Compensation matrices
- Exporting of images
- Gating
- Saving analyses on workspaces
- Cell cycle analysis
- t-SNE plots





Parameters: 9, Event Count: 21317

%G1	%S	%G2
36.25%	43.01%	20.75%
G1 Mean	G1 StdDev	G1 CV
48974.88	1387.13	2.83
G2 Mean	G2 StdDev	G2 CV
95073.17	2703.67	2.84

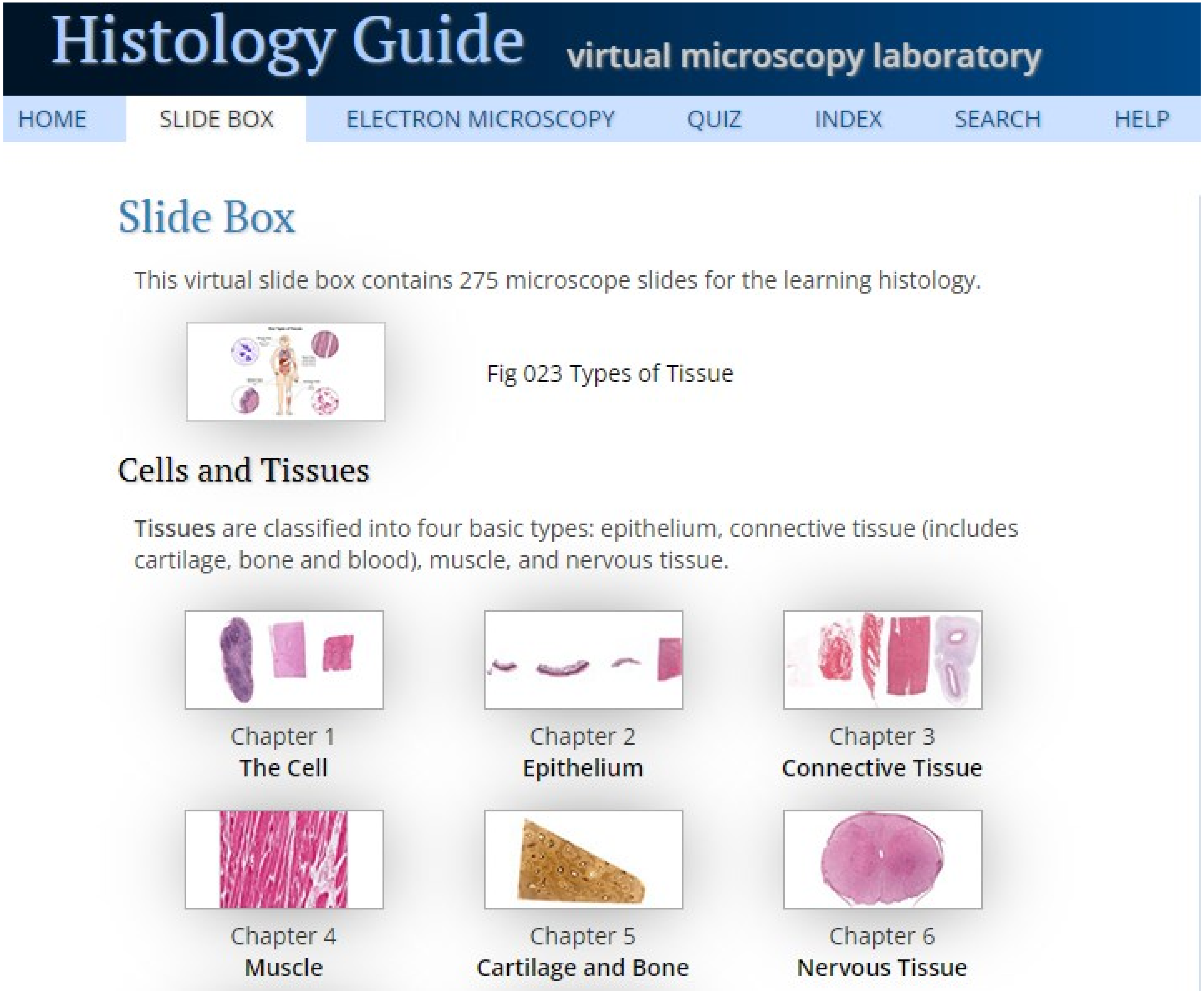


Parameters: 2, Event Count: 34944

Databases

Image databases

- https://imagescience.org/images/
- https://histologyguide.com
- mouse histology:
  https://www.emouseatlas.org/emap/home.html



Slide Box

This virtual slide box contains 275 microscope slides for the learning histology.

Fig 023 Types of Tissue

Cells and Tissues

Tissues are classified into four basic types: epithelium, connective tissue (includes cartilage, bone and blood), muscle, and nervous tissue.

Chapter 1
The Cell

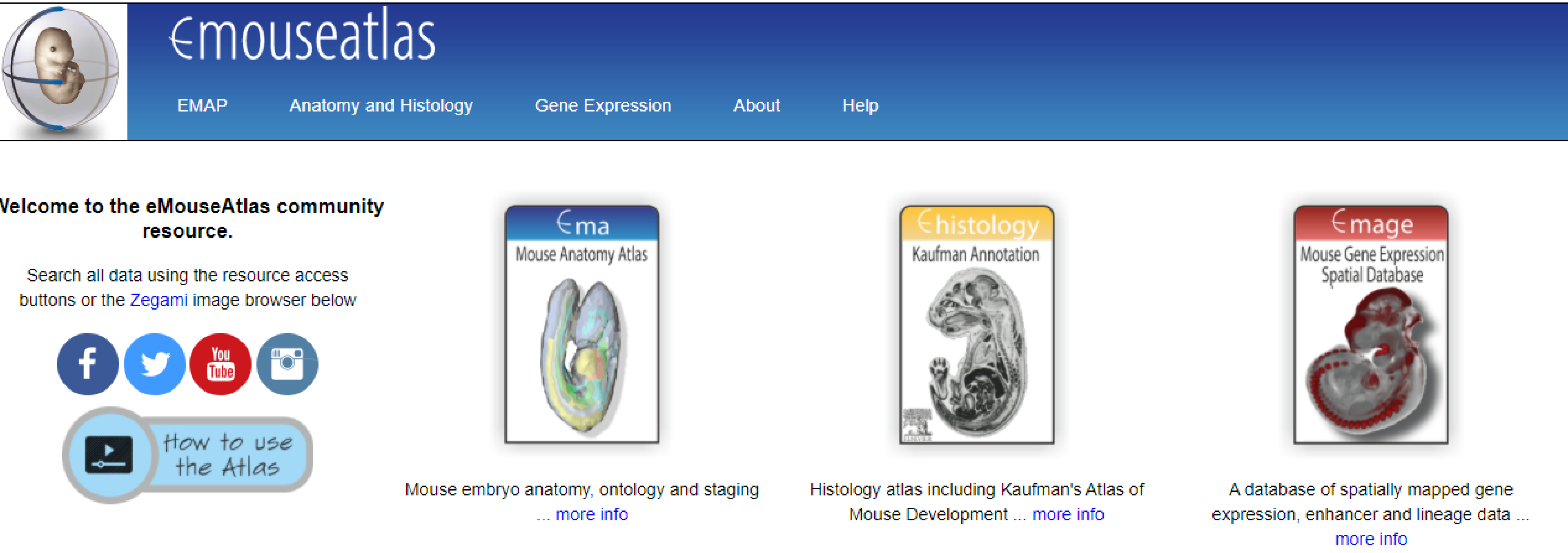
Chapter 2
Epithelium

Chapter 3
Connective Tissue

Chapter 4
Muscle

Chapter 5
Cartilage and Bone

Chapter 6
Nervous Tissue



elcome to the eMouseAtlas community resource.

Search all data using the resource access buttons or the Zegami image browser below

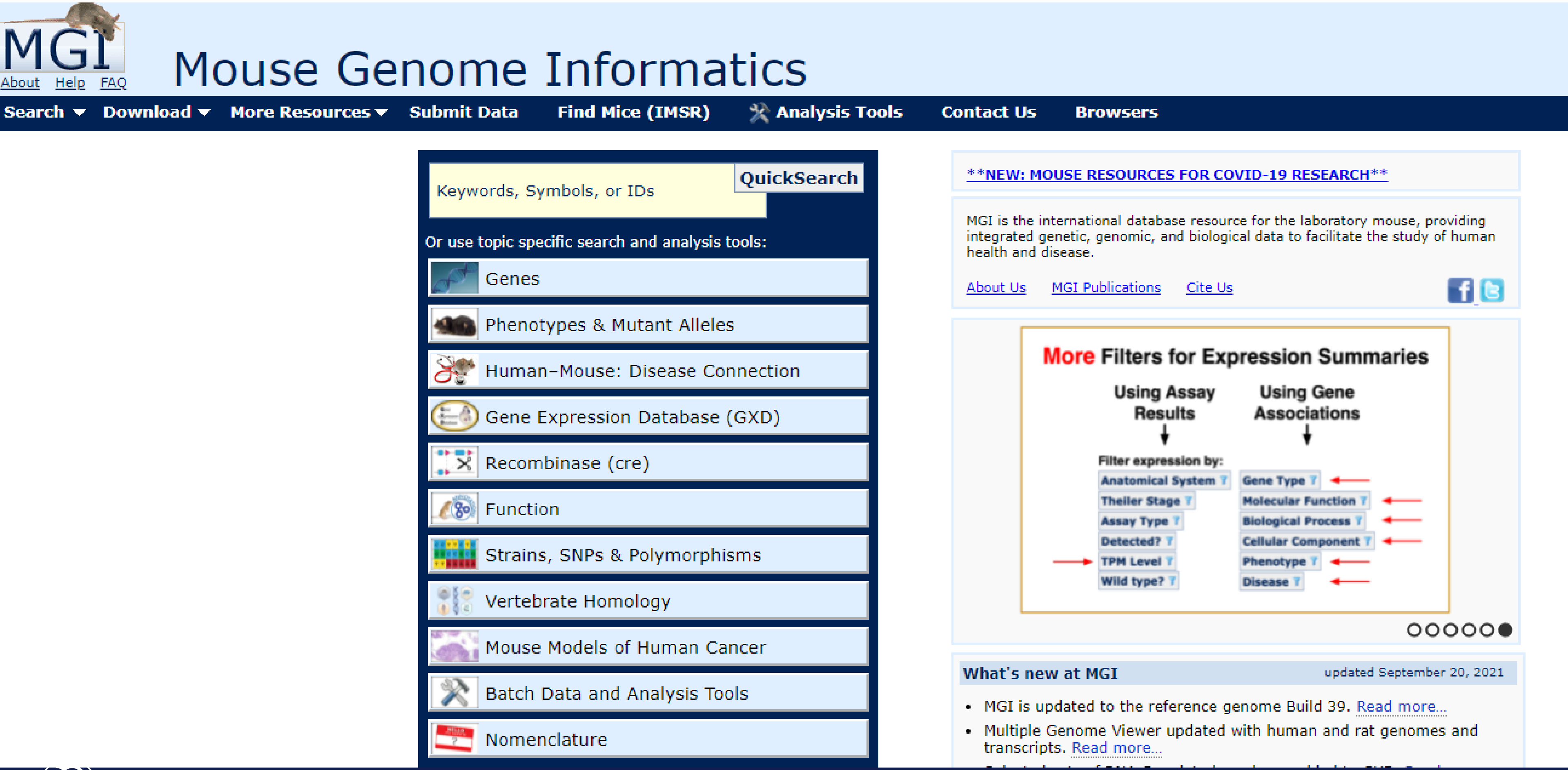
Mouse embryo anatomy, ontology and staging ... more info

Histology atlas including Kaufman's Atlas of Mouse Development ... more info

A database of spatially mapped gene expression, enhancer and lineage data ... more info

Mouse Databases

- Jackson Mouse database: http://www.informatics.jax.org
- https://www.mousephenotype.org
- Mouse repository MMHC https://frederick.cancer.gov/resources/repositories/nci-mouse-repository



Or use topic specific search and analysis tools:

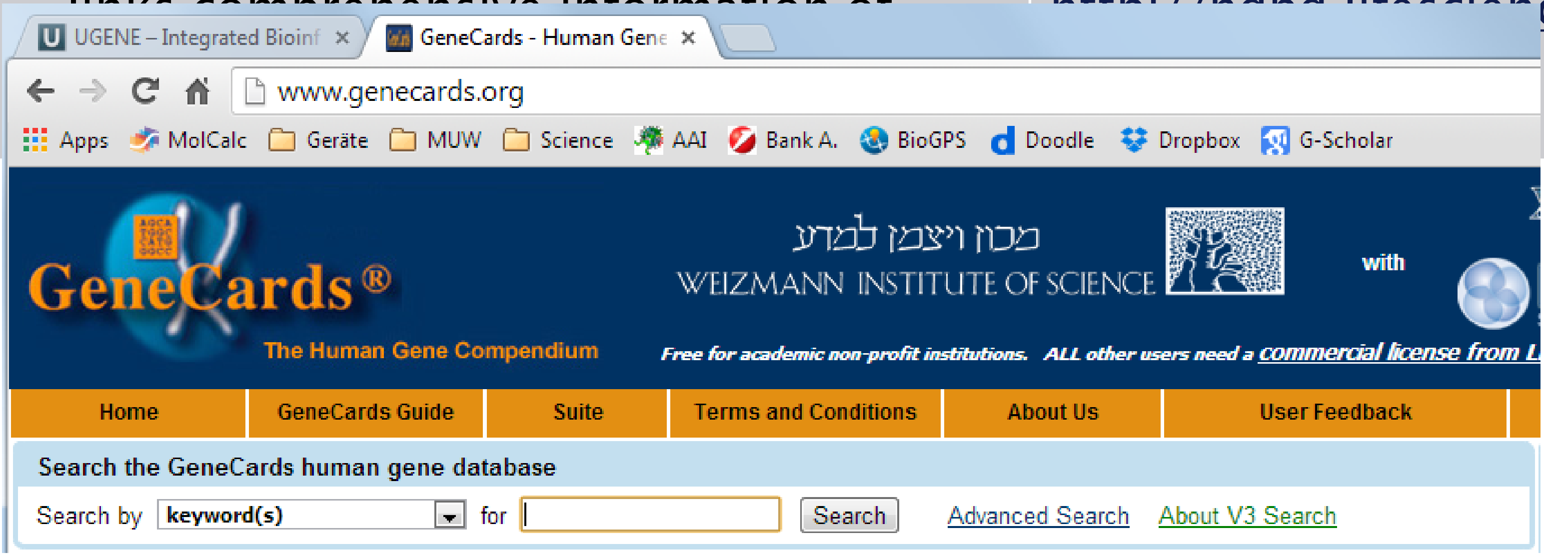
MGI is the international database resource for the laboratory mouse, providing integrated genetic, genomic, and biological data to facilitate the study of human health and disease.

What's new at MGI updated September 20, 2021

- MGI is updated to the reference genome Build 39. Read more...
- Multiple Genome Viewer updated with human and rat genomes and transcripts. Read more...

Nucleotide Databases

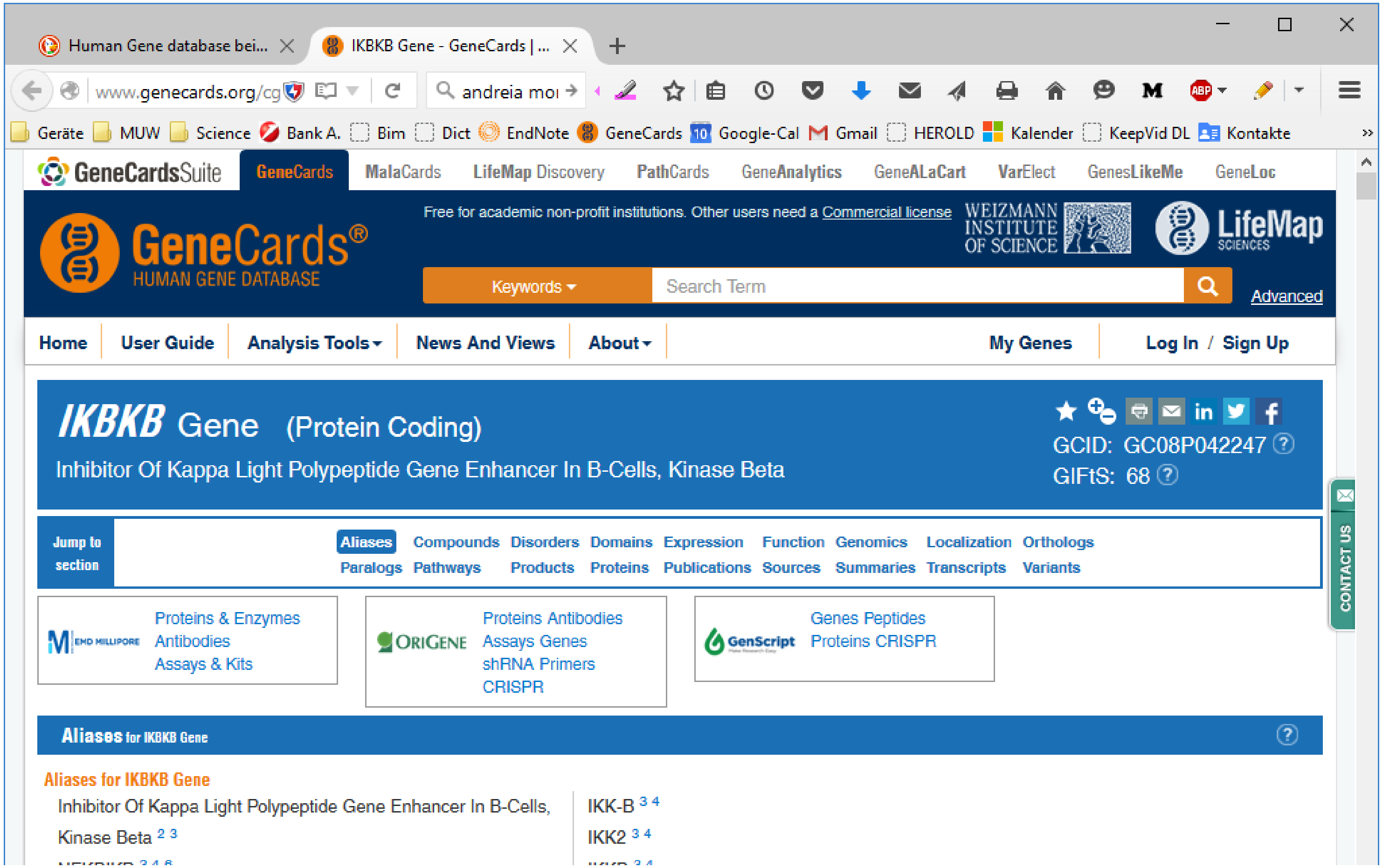
• Addgene Plasmid Repository **plasmid collection:** very comprehensive non-profit collection (appr. 65$/plasmid)	www.addgene.org
• Ensembl Genome Browser	www.ensembl.org
• Gene Expression Omnibus GEO **microarray data**	www.ncbi.nlm.nih.gov/geo
• GeneCards: **gene overview** with many links comprehensive information of	www.genecards.org
	http://hgpd.lifesciencedb.jp/



Free for academic non-profit institutions. ALL other users need a commercial license from L

Search the GeneCards human gene database

GeneCards Screenshot



Free for academic non-profit institutions. Other users need a Commercial license

IKBKB **Gene** (Protein Coding)

Inhibitor Of Kappa Light Polypeptide Gene Enhancer In B-Cells, Kinase Beta

GCID: GC08P042247

GIFtS: 68

Proteins & Enzymes
Antibodies
Assays & Kits

Proteins Antibodies
Assays Genes
shRNA Primers
CRISPR

Genes Peptides
Proteins CRISPR

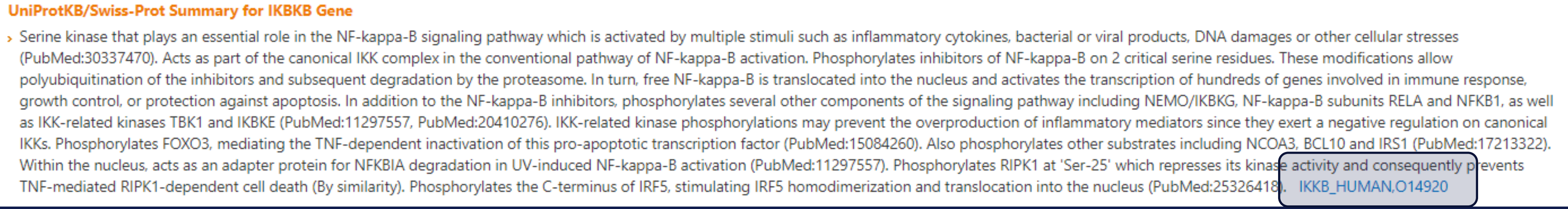
Aliases for IKBKB Gene

Aliases for IKBKB Gene

Inhibitor Of Kappa Light Polypeptide Gene Enhancer In B-Cells, Kinase Beta [2 3]

IKK-B [3 4]

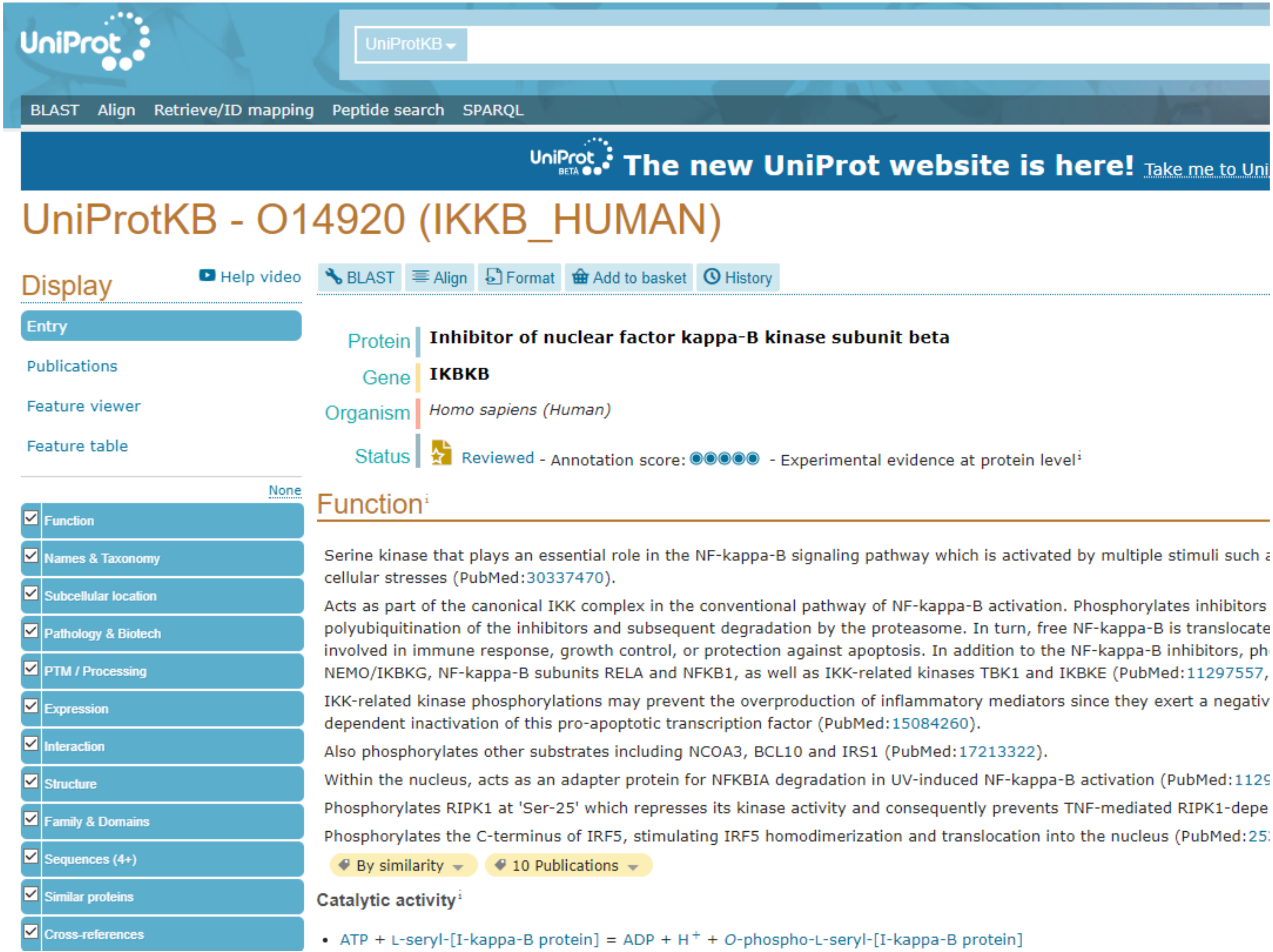
IKK2 [3 4]



UniProtKB/Swiss-Prot Summary for IKBKB Gene

› Serine kinase that plays an essential role in the NF-kappa-B signaling pathway which is activated by multiple stimuli such as inflammatory cytokines, bacterial or viral products, DNA damages or other cellular stresses (PubMed:30337470). Acts as part of the canonical IKK complex in the conventional pathway of NF-kappa-B activation. Phosphorylates inhibitors of NF-kappa-B on 2 critical serine residues. These modifications allow polyubiquitination of the inhibitors and subsequent degradation by the proteasome. In turn, free NF-kappa-B is translocated into the nucleus and activates the transcription of hundreds of genes involved in immune response, growth control, or protection against apoptosis. In addition to the NF-kappa-B inhibitors, phosphorylates several other components of the signaling pathway including NEMO/IKBKG, NF-kappa-B subunits RELA and NFKB1, as well as IKK-related kinases TBK1 and IKBKE (PubMed:11297557, PubMed:20410276). IKK-related kinase phosphorylations may prevent the overproduction of inflammatory mediators since they exert a negative regulation on canonical IKKs. Phosphorylates FOXO3, mediating the TNF-dependent inactivation of this pro-apoptotic transcription factor (PubMed:15084260). Also phosphorylates other substrates including NCOA3, BCL10 and IRS1 (PubMed:17213322). Within the nucleus, acts as an adapter protein for NFKBIA degradation in UV-induced NF-kappa-B activation (PubMed:11297557). Phosphorylates RIPK1 at 'Ser-25' which represses its kinase activity and consequently prevents TNF-mediated RIPK1-dependent cell death (By similarity). Phosphorylates the C-terminus of IRF5, stimulating IRF5 homodimerization and translocation into the nucleus (PubMed:25326418). IKKB_HUMAN,O14920

Uniprot database



UniProtKB - O14920 (IKKB_HUMAN)

Protein | **Inhibitor of nuclear factor kappa-B kinase subunit beta**

Gene | **IKBKB**

Organism | *Homo sapiens (Human)*

Status | Reviewed - Annotation score: ●●●●● - Experimental evidence at protein level[i]

Function[i]

Serine kinase that plays an essential role in the NF-kappa-B signaling pathway which is activated by multiple stimuli such a cellular stresses (PubMed:30337470).

Acts as part of the canonical IKK complex in the conventional pathway of NF-kappa-B activation. Phosphorylates inhibitors polyubiquitination of the inhibitors and subsequent degradation by the proteasome. In turn, free NF-kappa-B is translocate involved in immune response, growth control, or protection against apoptosis. In addition to the NF-kappa-B inhibitors, ph NEMO/IKBKG, NF-kappa-B subunits RELA and NFKB1, as well as IKK-related kinases TBK1 and IKBKE (PubMed:11297557,

IKK-related kinase phosphorylations may prevent the overproduction of inflammatory mediators since they exert a negativ dependent inactivation of this pro-apoptotic transcription factor (PubMed:15084260).

Also phosphorylates other substrates including NCOA3, BCL10 and IRS1 (PubMed:17213322).

Within the nucleus, acts as an adapter protein for NFKBIA degradation in UV-induced NF-kappa-B activation (PubMed:112

Phosphorylates RIPK1 at 'Ser-25' which represses its kinase activity and consequently prevents TNF-mediated RIPK1-depe

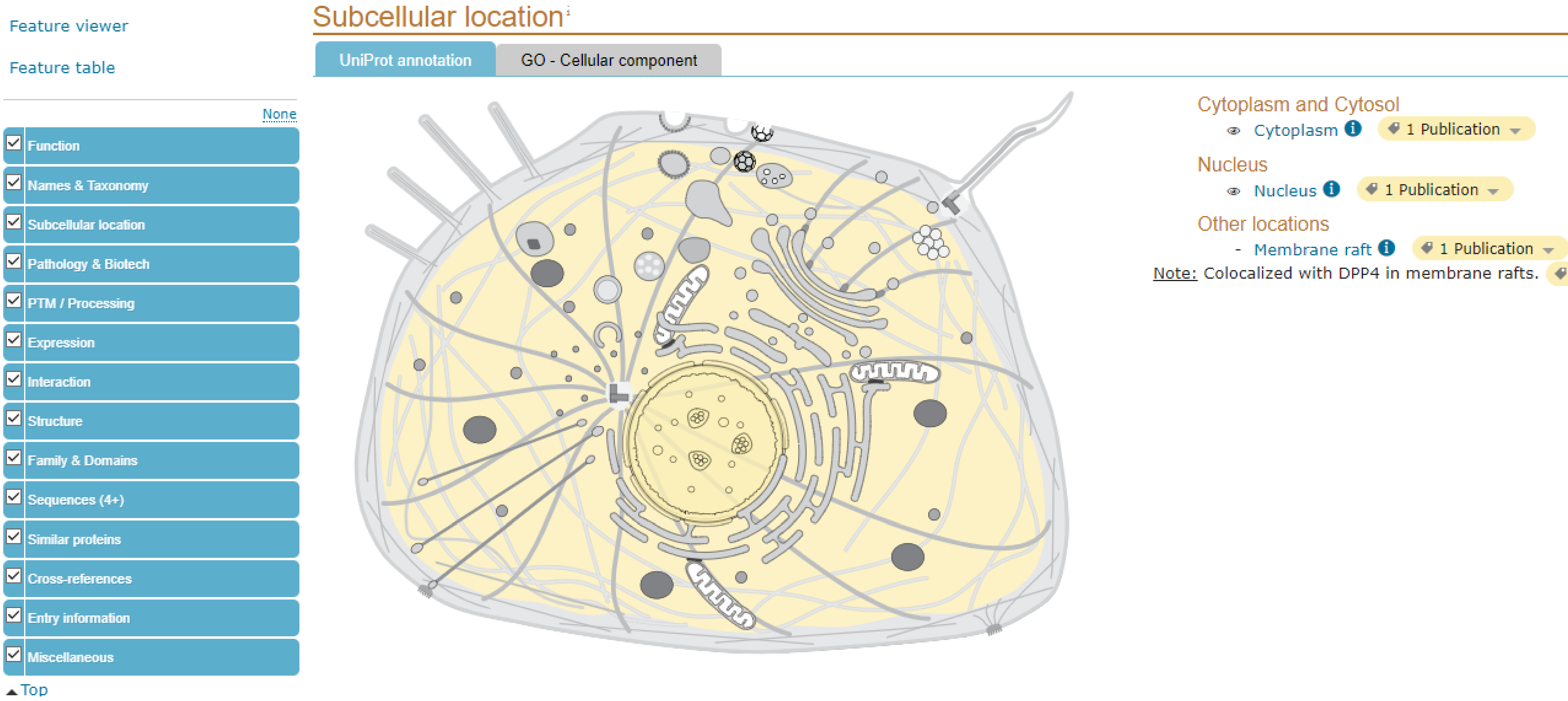
Phosphorylates the C-terminus of IRF5, stimulating IRF5 homodimerization and translocation into the nucleus (PubMed:25

By similarity ▾ 10 Publications ▾

Catalytic activity[i]

- ATP + L-seryl-[I-kappa-B protein] = ADP + H^+ + *O*-phospho-L-seryl-[I-kappa-B protein]

Uniprot database



Subcellular location

Cytoplasm and Cytosol

- Cytoplasm 1 Publication

Nucleus

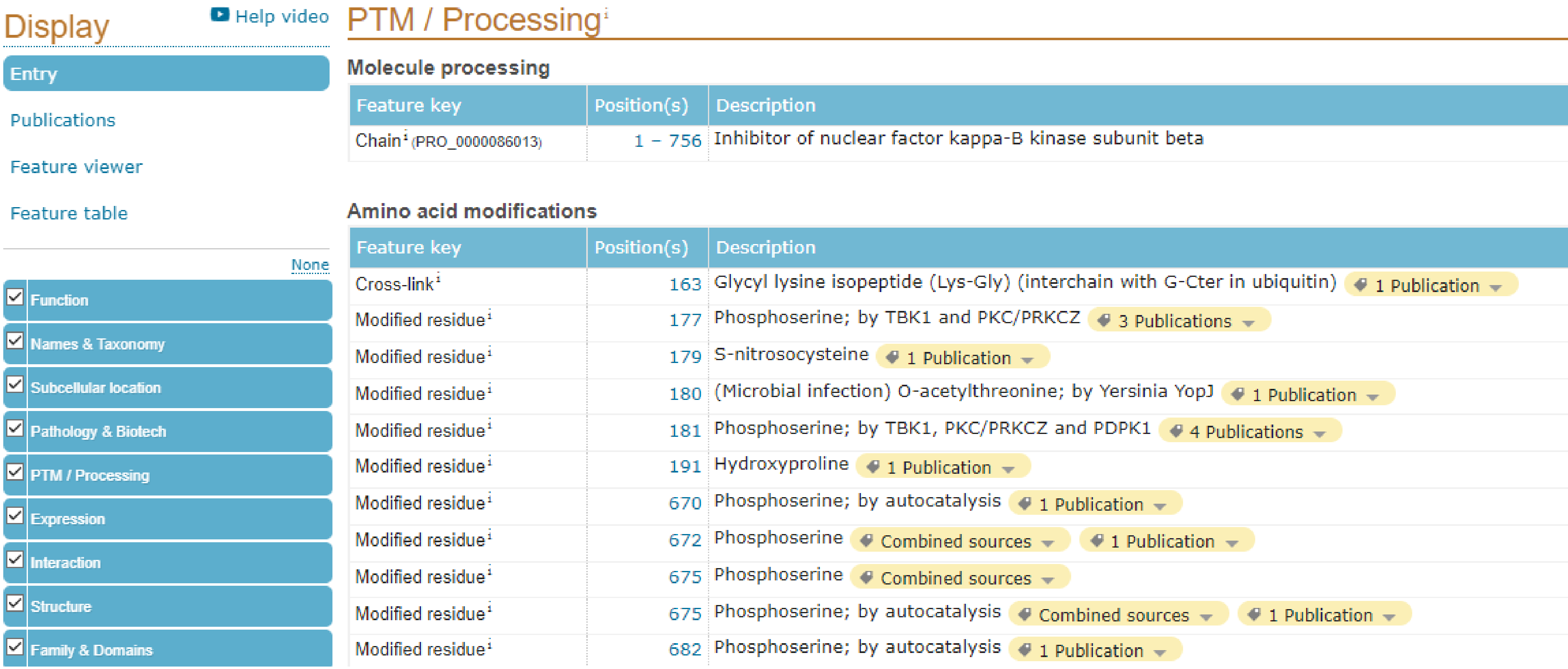
- Nucleus 1 Publication

Other locations

- Membrane raft 1 Publication

Note: Colocalized with DPP4 in membrane rafts.

Uniprot database



Display

- Entry
- Publications
- Feature viewer
- Feature table

- ☑ Function
- ☑ Names & Taxonomy
- ☑ Subcellular location
- ☑ Pathology & Biotech
- ☑ PTM / Processing
- ☑ Expression
- ☑ Interaction
- ☑ Structure
- ☑ Family & Domains

PTM / Processing

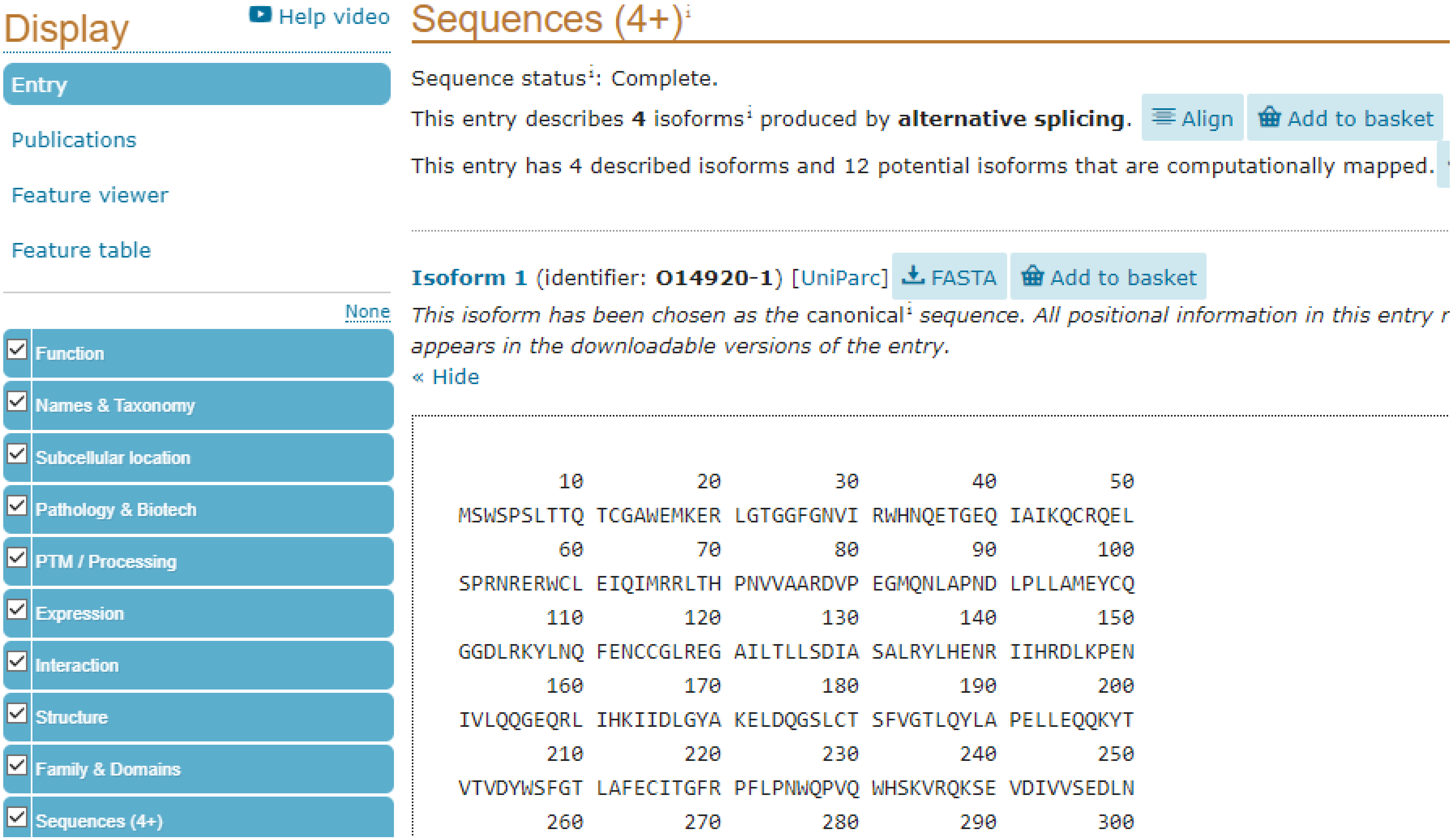
Molecule processing

Feature key	Position(s)	Description
Chain (PRO_0000086013)	1 – 756	Inhibitor of nuclear factor kappa-B kinase subunit beta

Amino acid modifications

Feature key	Position(s)	Description
Cross-link	163	Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin) 1 Publication
Modified residue	177	Phosphoserine; by TBK1 and PKC/PRKCZ 3 Publications
Modified residue	179	S-nitrosocysteine 1 Publication
Modified residue	180	(Microbial infection) O-acetylthreonine; by Yersinia YopJ 1 Publication
Modified residue	181	Phosphoserine; by TBK1, PKC/PRKCZ and PDPK1 4 Publications
Modified residue	191	Hydroxyproline 1 Publication
Modified residue	670	Phosphoserine; by autocatalysis 1 Publication
Modified residue	672	Phosphoserine Combined sources 1 Publication
Modified residue	675	Phosphoserine Combined sources
Modified residue	675	Phosphoserine; by autocatalysis Combined sources 1 Publication
Modified residue	682	Phosphoserine; by autocatalysis 1 Publication

Uniprot database



Sequences (4+)

Sequence status: Complete.

This entry describes **4** isoforms produced by **alternative splicing**.

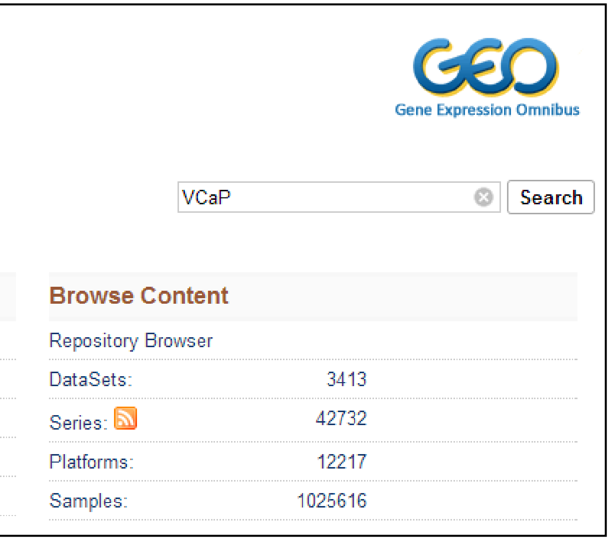
This entry has 4 described isoforms and 12 potential isoforms that are computationally mapped.

Isoform 1 (identifier: **O14920-1**) [UniParc]

This isoform has been chosen as the canonical sequence. All positional information in this entry r
appears in the downloadable versions of the entry.

```
        10         20         30         40         50
MSWSPSLTTQ TCGAWEMKER LGTGGFGNVI RWHNQETGEQ IAIKQCRQEL
        60         70         80         90        100
SPRNRERWCL EIQIMRRLTH PNVVAARDVP EGMQNLAPND LPLLAMEYCQ
       110        120        130        140        150
GGDLRKYLNQ FENCCGLREG AILTLLSDIA SALRYLHENR IIHRDLKPEN
       160        170        180        190        200
IVLQQGEQRL IHKIIDLGYA KELDQGSLCT SFVGTLQYLA PELLEQQKYT
       210        220        230        240        250
VTVDYWSFGT LAFECITGFR PFLPNWQPVQ WHSKVRQKSE VDIVVSEDLN
       260        270        280        290        300
```

GEO microarray analysis

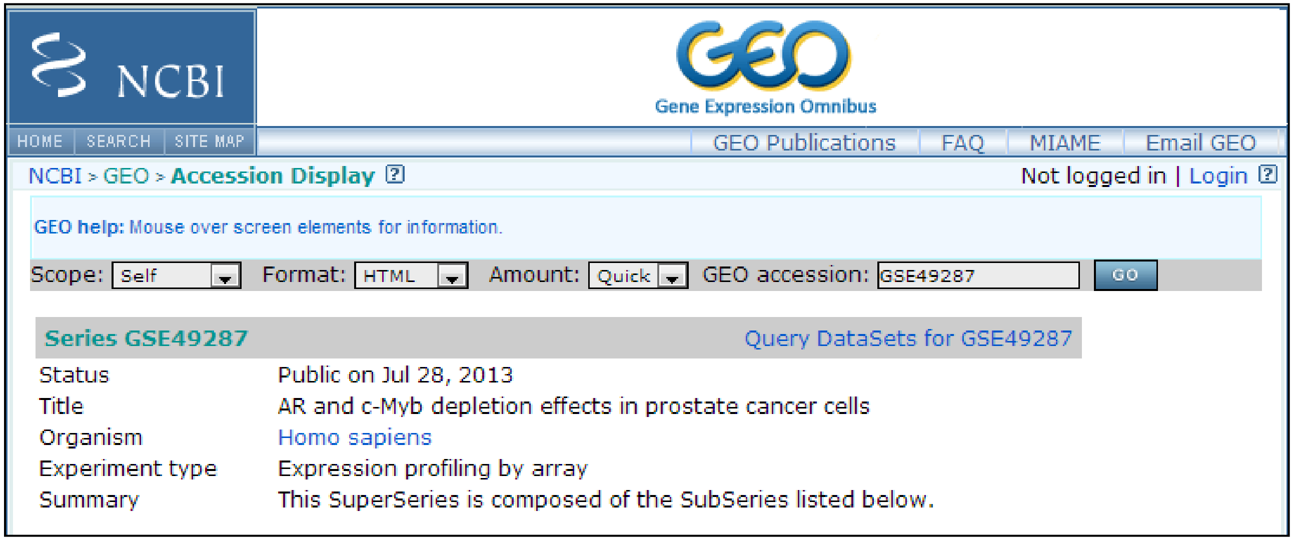


VCaP

Browse Content

Repository Browser

DataSets:	3413
Series:	42732
Platforms:	12217
Samples:	1025616



NCBI > GEO > **Accession Display**

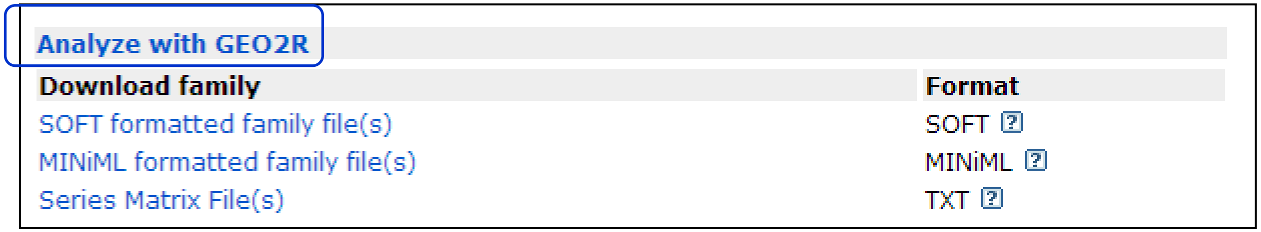
Not logged in | Login

GEO help: Mouse over screen elements for information.

Scope: Self   Format: HTML   Amount: Quick   GEO accession: GSE49287

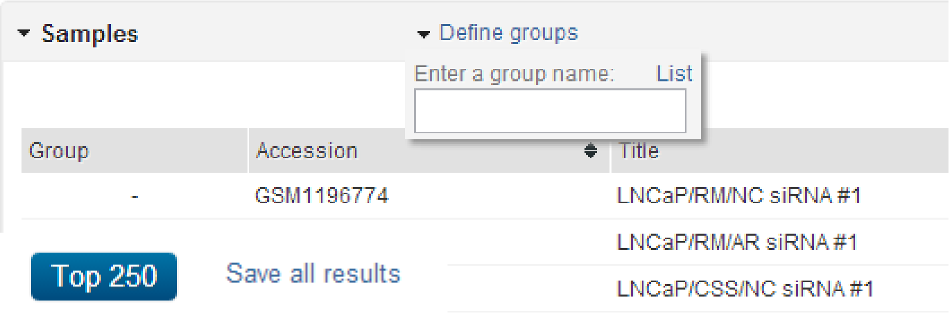
Series GSE49287   Query DataSets for GSE49287

Status	Public on Jul 28, 2013
Title	AR and c-Myb depletion effects in prostate cancer cells
Organism	Homo sapiens
Experiment type	Expression profiling by array
Summary	This SuperSeries is composed of the SubSeries listed below.



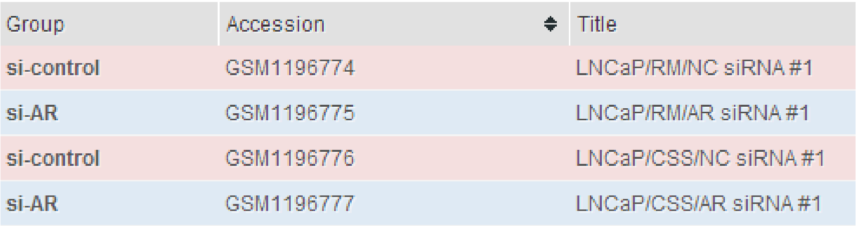
Analyze with GEO2R

Download family	**Format**
SOFT formatted family file(s)	SOFT
MINiML formatted family file(s)	MINiML
Series Matrix File(s)	TXT

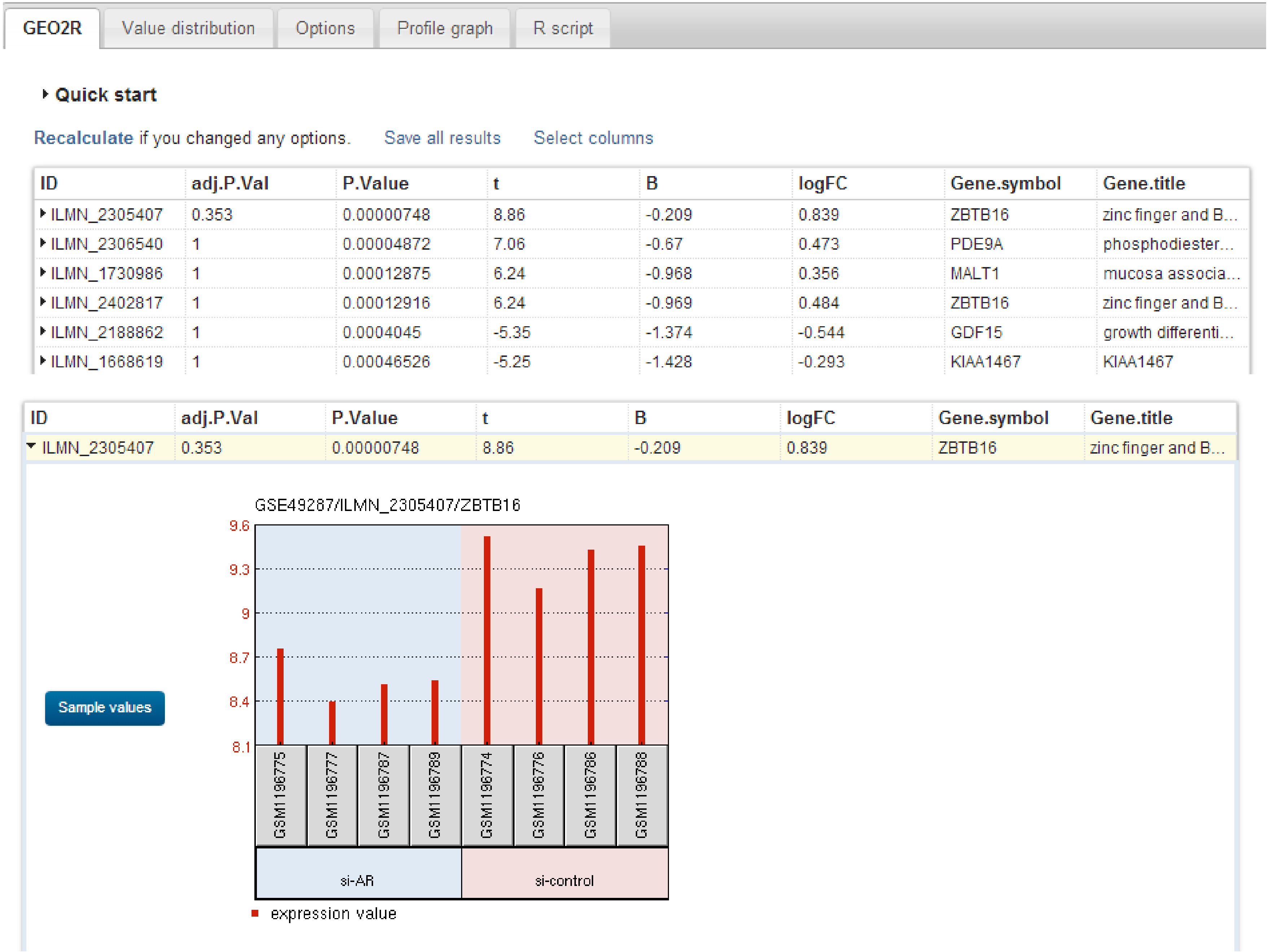


Enter a group name: List

Group	Accession	Title
-	GSM1196774	LNCaP/RM/NC siRNA #1
		LNCaP/RM/AR siRNA #1
		LNCaP/CSS/NC siRNA #1



Group	Accession	Title
si-control	GSM1196774	LNCaP/RM/NC siRNA #1
si-AR	GSM1196775	LNCaP/RM/AR siRNA #1
si-control	GSM1196776	LNCaP/CSS/NC siRNA #1
si-AR	GSM1196777	LNCaP/CSS/AR siRNA #1

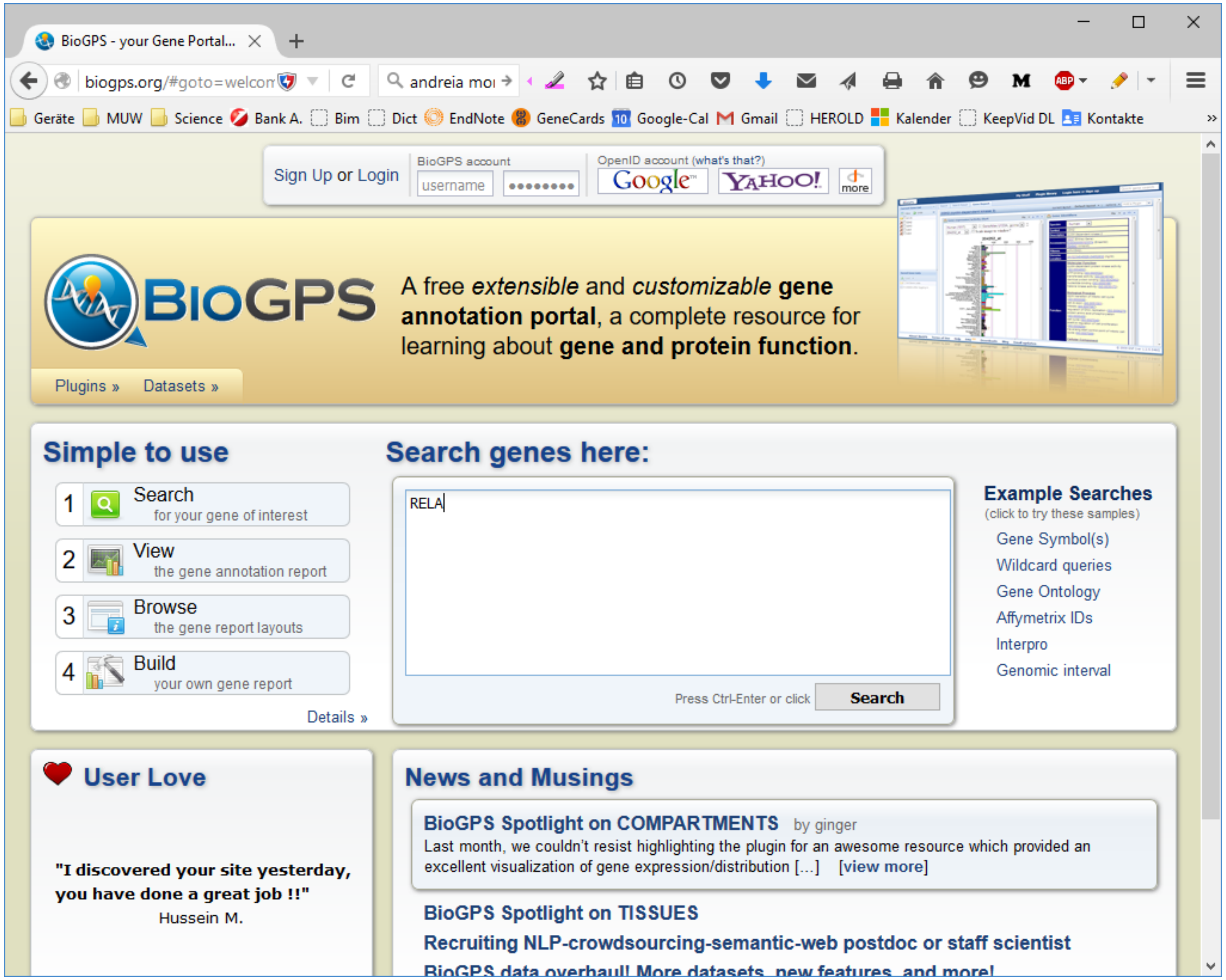


ID	adj.P.Val	P.Value	t	B	logFC	Gene.symbol	Gene.title
ILMN_2305407	0.353	0.00000748	8.86	-0.209	0.839	ZBTB16	zinc finger and B...
ILMN_2306540	1	0.00004872	7.06	-0.67	0.473	PDE9A	phosphodiester...
ILMN_1730986	1	0.00012875	6.24	-0.968	0.356	MALT1	mucosa associa...
ILMN_2402817	1	0.00012916	6.24	-0.969	0.484	ZBTB16	zinc finger and B...
ILMN_2188862	1	0.0004045	-5.35	-1.374	-0.544	GDF15	growth differenti...
ILMN_1668619	1	0.00046526	-5.25	-1.428	-0.293	KIAA1467	KIAA1467

ID	adj.P.Val	P.Value	t	B	logFC	Gene.symbol	Gene.title
ILMN_2305407	0.353	0.00000748	8.86	-0.209	0.839	ZBTB16	zinc finger and B...

BioGPS: Customizable collection of websites:

http://biogps.org
One search entry looks for results in many different databases



A free *extensible* and *customizable* **gene annotation portal**, a complete resource for learning about **gene and protein function**.

Simple to use

1 Search for your gene of interest
2 View the gene annotation report
3 Browse the gene report layouts
4 Build your own gene report

Details »

Search genes here:

RELA

Press Ctrl-Enter or click Search

Example Searches
(click to try these samples)

- Gene Symbol(s)
- Wildcard queries
- Gene Ontology
- Affymetrix IDs
- Interpro
- Genomic interval

User Love

"I discovered your site yesterday, you have done a great job !!"
Hussein M.

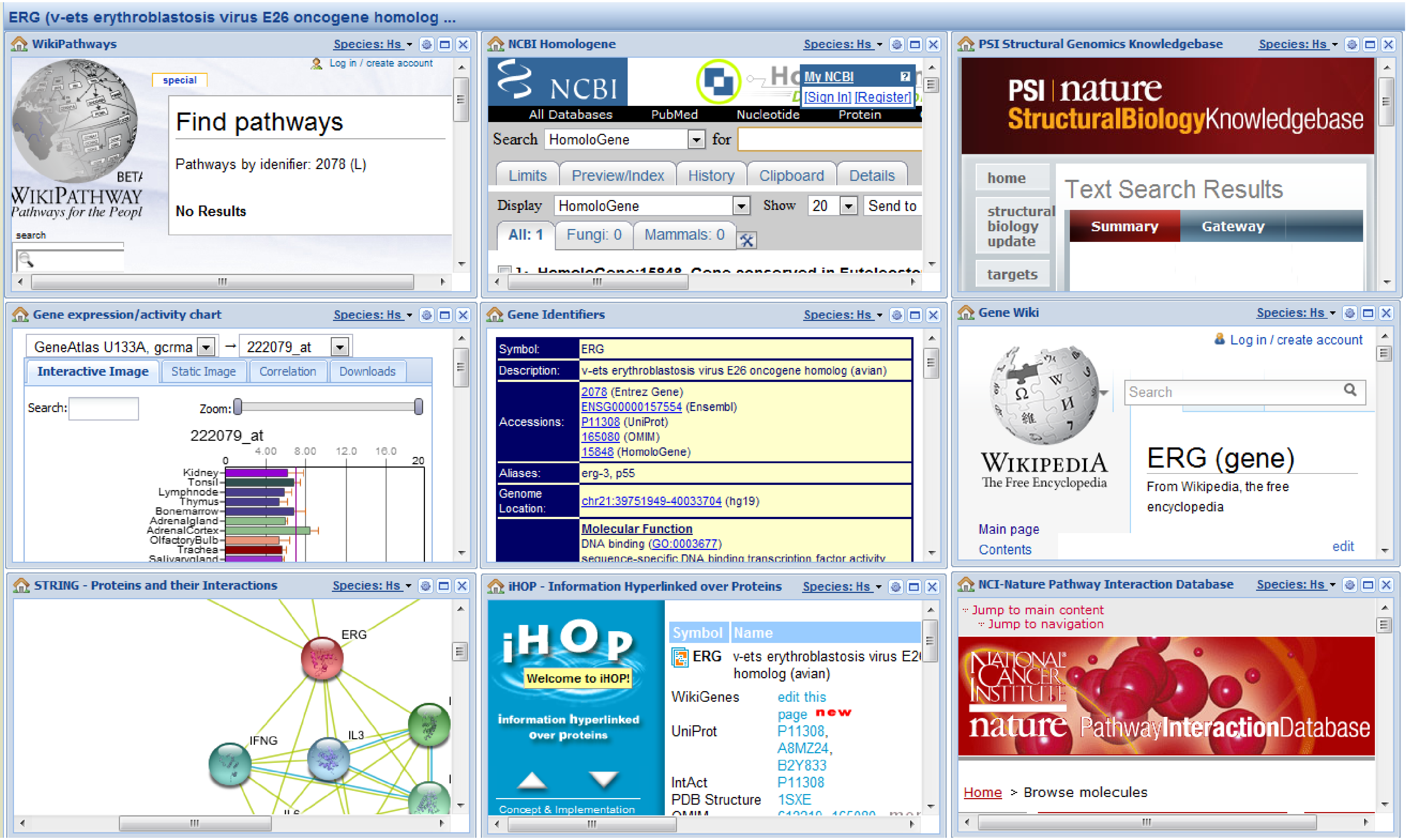
News and Musings

BioGPS Spotlight on COMPARTMENTS by ginger
Last month, we couldn't resist highlighting the plugin for an awesome resource which provided an excellent visualization of gene expression/distribution [...] [view more]

BioGPS Spotlight on TISSUES

Recruiting NLP-crowdsourcing-semantic-web postdoc or staff scientist

BioGPS data overhaul! More datasets, new features, and more!



Find pathways

Pathways by idenifier: 2078 (L)

No Results

Text Search Results

1. HomoloGene:15848. Gene conserved in Euteleosto...

Symbol:	ERG
Description:	v-ets erythroblastosis virus E26 oncogene homolog (avian)
Accessions:	2078 (Entrez Gene) ENSG00000157554 (Ensembl) P11308 (UniProt) 165080 (OMIM) 15848 (HomoloGene)
Aliases:	erg-3, p55
Genome Location:	chr21:39751949-40033704 (hg19)
	Molecular Function DNA binding (GO:0003677) sequence-specific DNA binding transcription factor activity

ERG (gene)

From Wikipedia, the free encyclopedia

Symbol	Name
ERG	v-ets erythroblastosis virus E2… homolog (avian)

WikiGenes edit this page new

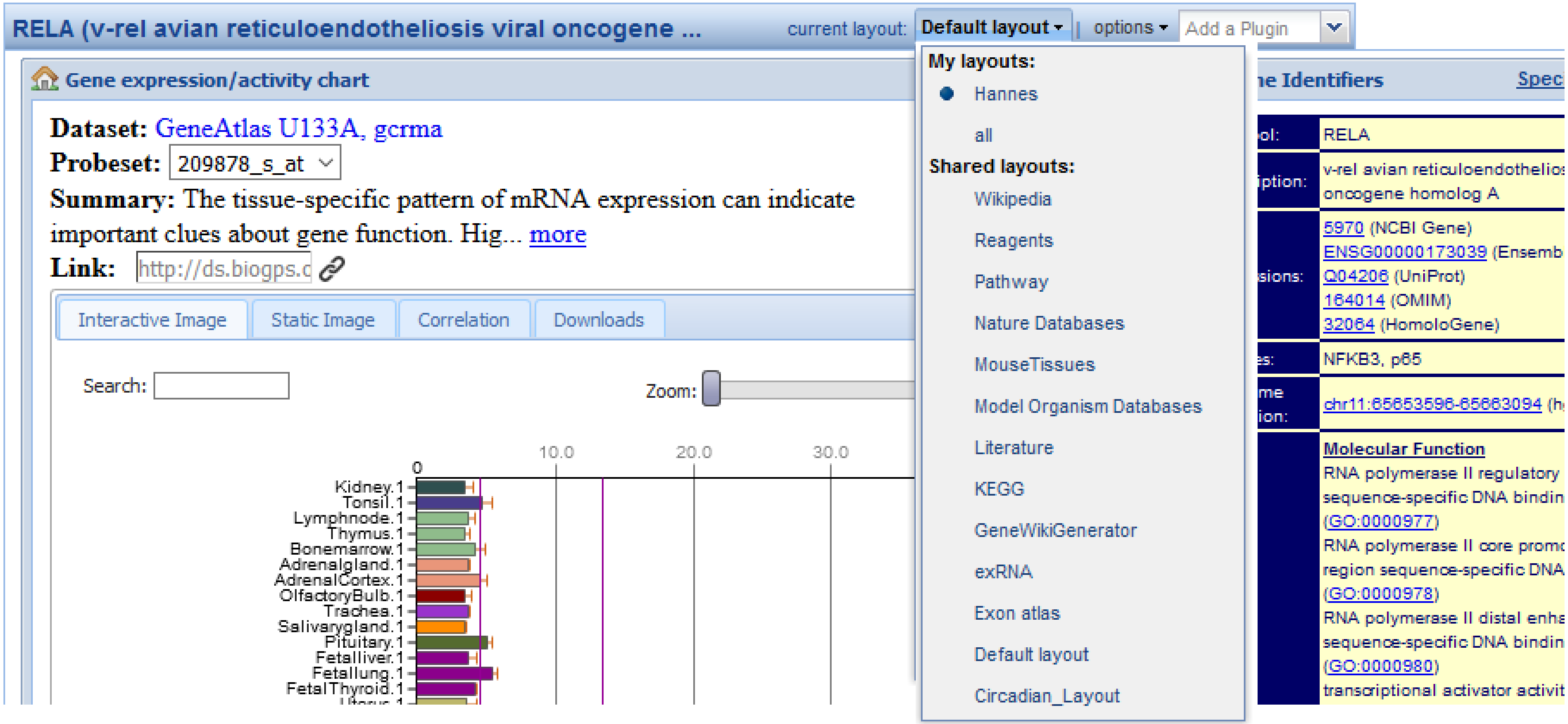
UniProt P11308, A8MZ24, B2Y833

IntAct P11308

PDB Structure 1SXE

Home > Browse molecules

The subsites can be extended to full window



RELA (v-rel avian reticuloendotheliosis viral oncogene ...

current layout: **Default layout**

Gene expression/activity chart

Dataset: GeneAtlas U133A, gcrma

Probeset: 209878_s_at

Summary: The tissue-specific pattern of mRNA expression can indicate important clues about gene function. Hig... more

Link: http://ds.biogps.c

ne Identifiers

ol:	RELA
iption:	v-rel avian reticuloendothelios oncogene homolog A
sions:	5970 (NCBI Gene) ENSG00000173039 (Ensemb Q04206 (UniProt) 164014 (OMIM) 32064 (HomoloGene)
s:	NFKB3, p65
me ion:	chr11:65653596-65663094 (h
	Molecular Function RNA polymerase II regulatory sequence-specific DNA bindin (GO:0000977) RNA polymerase II core promo region sequence-specific DNA (GO:0000978) RNA polymerase II distal enha sequence-specific DNA bindin (GO:0000980) transcriptional activator activit

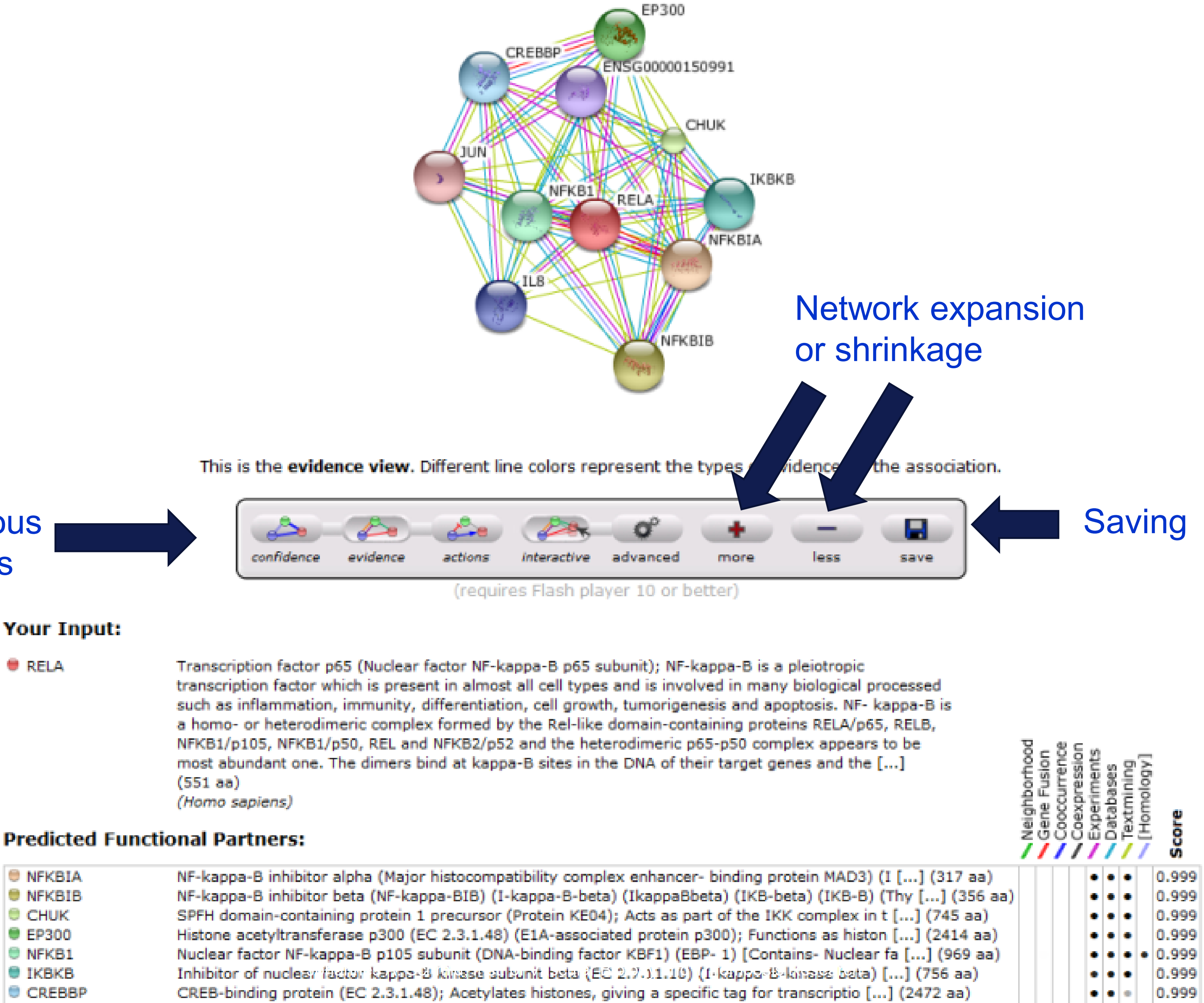
The subsites, which are opened can be customized to different layouts or an own collection layout can be saved (after free registration)

Pathway databases

Biocarta	http://www.biocarta.com/
Nature Signaling Gateway	http://www.signaling-gateway.org/
Pathway Interaction database	http://pid.nci.nih.gov/
Pathways - Biolegend	http://www.biolegend.com/index.php?page=pathways
Reactome	http://www.reactome.org/

STRING database for functional interactions and signaling networks:

http://string-db.org



This is the **evidence view**. Different line colors represent the types of evidence for the association.

(requires Flash player 10 or better)

Network expansion or shrinkage

Various views

Saving

Your Input:

RELA	Transcription factor p65 (Nuclear factor NF-kappa-B p65 subunit); NF-kappa-B is a pleiotropic transcription factor which is present in almost all cell types and is involved in many biological processed such as inflammation, immunity, differentiation, cell growth, tumorigenesis and apoptosis. NF- kappa-B is a homo- or heterodimeric complex formed by the Rel-like domain-containing proteins RELA/p65, RELB, NFKB1/p105, NFKB1/p50, REL and NFKB2/p52 and the heterodimeric p65-p50 complex appears to be most abundant one. The dimers bind at kappa-B sites in the DNA of their target genes and the [...] (551 aa) *(Homo sapiens)*

Predicted Functional Partners:

		Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
NFKBIA	NF-kappa-B inhibitor alpha (Major histocompatibility complex enhancer- binding protein MAD3) (I [...] (317 aa)					●	●	●		0.999
NFKBIB	NF-kappa-B inhibitor beta (NF-kappa-BIB) (I-kappa-B-beta) (IkappaBbeta) (IKB-beta) (IKB-B) (Thy [...] (356 aa)					●	●	●		0.999
CHUK	SPFH domain-containing protein 1 precursor (Protein KE04); Acts as part of the IKK complex in t [...] (745 aa)					●	●	●		0.999
EP300	Histone acetyltransferase p300 (EC 2.3.1.48) (E1A-associated protein p300); Functions as histon [...] (2414 aa)					●	●	●		0.999
NFKB1	Nuclear factor NF-kappa-B p105 subunit (DNA-binding factor KBF1) (EBP- 1) [Contains- Nuclear fa [...] (969 aa)					●	●	●	●	0.999
IKBKB	Inhibitor of nuclear factor kappa-B kinase subunit beta (EC 2.7.11.10) (I-kappa-B-kinase beta) [...] (756 aa)					●	●	●		0.999
CREBBP	CREB-binding protein (EC 2.3.1.48); Acetylates histones, giving a specific tag for transcriptio [...] (2472 aa)					●	●	●		0.999

Protein Databases and other tools

Human Protein references	http://www.hprd.org/
Lipidomics	http://www.lipidmaps.org/
Macromol. Movements	http://www.molmovdb.org/
Phosphorylation sites	http://www.phosida.com/
Protein Database	https://www.rcsb.org
ScanProsite	https://www.expasy.org/resources/scanprosite
Transcription factor database	https://jaspar.genereg.net
Uniport Protein database	https://www.uniprot.org/

Centrifugation DNA /protein calculator Fermentas Double digest Molarity Calculator Molarity Calculator Primer3 primer design	http://www.sciencegateway.org/tools/rotor.htm https://at.promega.com/resources/tools/biomath/ http://www.fermentas.com/en/tools/doubledigest http://www.graphpad.com/quickcalcs/Molarityform.cfm http://www.meduniwien.ac.at/user/johannes.schmid/MolarityJava.htm http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi

Other webtools

- Medical images: https://en.wikiversity.org/wiki/WikiJournal_of_Medicine/Medical_gallery_of_Blausen_Medical_2014
- Biodigital images: https://human.biodigital.com/login?returnUrl=/explore
- Interactive presentations: https://www.mentimeter.com
- Protocols, methods: https://experiments.springernature.com
- biological drawing (svg-files): https://bioicons.com
- Signaling pathways: https://apps.pathwaycommons.org
- Interactive fluorescent protein database: https://www.fpbase.org/chart/
- Gene set enrichment analysis: https://www.gsea-msigdb.org/gsea/msigdb/
- Medical biochemistry: https://themedicalbiochemistrypage.org
- NF-κB target genes: https://www.bu.edu/nf-kb/gene-resources/target-genes/
- Microvesicle database: http://microvesicles.org/index.html
- Austrian data portal: https://www.data.gv.at

Other webtools

- Open Cell – protein localization/images: https://opencell.czbiohub.org
- Cancer guidelines: https://www.onkopedia-guidelines.info/en/onkopedia/guidelines
- Online curve fitting: https://www.mycurvefit.com
- Cell line collection: https://www.dsmz.de/collection/
- Cell lines: https://www.cellosaurus.org
- Primer database: https://pga.mgh.harvard.edu/primerbank/
- Transcriptional start sites: https://dbtss.hgc.jp
- European Bioinformatics Institute: https://www.ebi.ac.uk
- Addgene plasmid repository: https://www.addgene.org

Updated Links

- **Nucleotide databases**
- Ensembl Genome Browser
- Gene Expression Omnibus (GEO)
- FuncAssociate 2.0: The Gene Set Functionator
- ENCODE Project at UCSC
- EPD The Eukaryotic Promoter Database
- **Pathways**
- BioGRID | Database of Protein and Genetic Interactions
- KEGG PATHWAY Database
- Reactome pathways

Updated Links

- STRING: functional protein association networks
- PhosphoSitePlus: a resource for protein phosphorylation and other post-translational modifications
- neXtProt - exploring the universe of human proteins

Updated Links – Tools and Methods

- Primer3Plus
- Addgene: CRISPR/Cas Plasmids for Genome Editing
- Animal Experimentation Design Assistant: https://eda.nc3rs.org.uk
- ArrayExpress < EMBL-EBI
- BCCM/LMBP plasmids catalogue: https://bccm.belspo.be
- Broad-Novartis Cancer Cell Line Encyclopedia
- cBioPortal for Cancer Genomics
- Clinical Trials Register

Updated Links – Tools and Methods

- Complex Portal < EMBL-EBI
- COXPRES co-regulated gene database
- CRISPR design
- CRISPR Design 2
- CRISPR DESKGEN
- Datasearch Elsevier
- EBI
- eClinPath | A Resource for Veterinary Clinical Pathology
- EMBL-EBI Train online |
- ENCODE at UCSC
- Enrichr
- European Data Portal
- Expression Atlas < EMBL-EBI
- Fluorescence SpectraViewer | Life Technologies
- fluorophores.org
- Garland Science - Instructor Resource Center
- GeneCopoiea cDNA and shRNA Clones
- GeneInfinity
- GENEVESTIGATOR
- Genevisible
- ImageJ
- InterPro protein sequence analysis & classification < InterPro < EMBL-EBI

Updated Links – Tools and Methods

- IPA Ingenuity Pathway Analysis
- IPA Login
- iPathwayGuide
- iPathwayGuide
- MIRUMIR miRNA survival data
- Molecular Movies - Home
- Mouse Phenotyping Consortium
- Mouse Strain Resource
- nebiocalculator.neb.com/#!/
- NEBuilder
- Open Microscopy Environment — OME
- Platelet Web - Systems Biology
- PolyGene Customized Transgenic Mouse and Rat Models |
- PRIMEGENS isoform specific PCR
- Primer - Plasmids - Enzymes | Tools for Genomics Scientists
- Prostate Cancer Cell Lines Database
- Proteins and Proteomics Opening Page
- Proteomics PRIDE Archive
- Rad Pro Calculator: Online Nuclear Calculations and Free Health Physics Software
- real-time PCR primer and probe database

Updated Links – Tools and Methods

- RNAi library Screeninc .
- RNAseq Exiqon XploreRNA
- ScanProsite
- Science Events: Scientific conferences, courses, meetings and more at Natureevents Directory
- SignalPeptide 4.1 Predictor
- TargetScanHuman 5.1
- The Medical Biochemistry Page
- transcriptomics ExAtlas
- Tronolab Lentiviral Systems
- Tsien lab Website

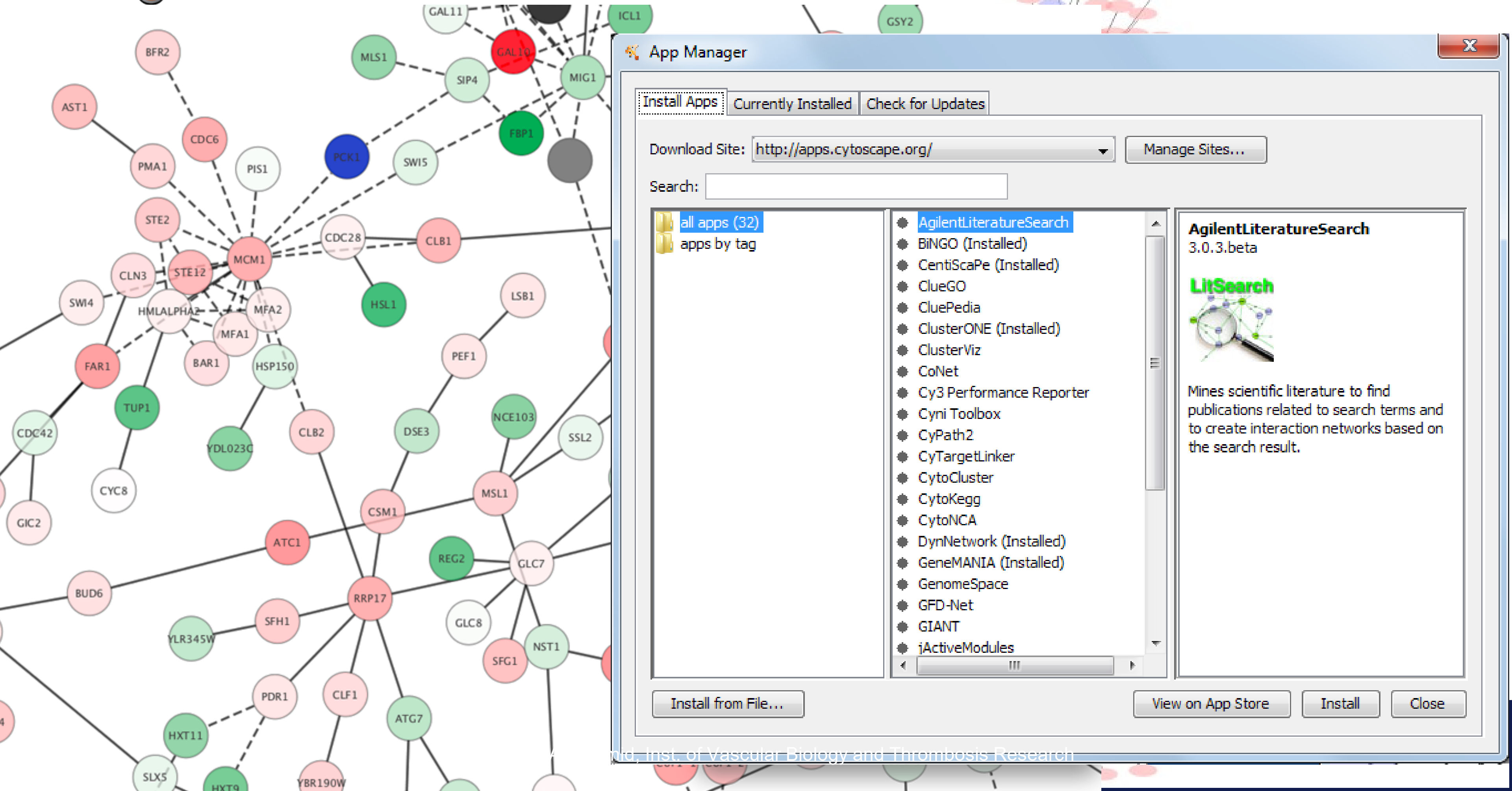
- WikiPathways
- super-enhancers in mouse and human genome dbSUPER
- GUILDify: Web server for phenotypic characterization of genes
- Phosphatome - phosphatase database
- Fluorescent protein properties
- BBMRI.at - Biobanks
- Human Cell Atlas
- miRNA expression atlas
- CIBERSORT Immune cell profiling
- Phospho.ELM

Cytoscape

www.cytoscape.org: an open source platform for network visualization and analysis

Cytoscape

http://apps.cytoscape.org



App Manager

Install Apps | Currently Installed | Check for Updates

Download Site: http://apps.cytoscape.org/

Manage Sites...

Search:

- all apps (32)
- apps by tag

- AgilentLiteratureSearch
- BiNGO (Installed)
- CentiScaPe (Installed)
- ClueGO
- CluePedia
- ClusterONE (Installed)
- ClusterViz
- CoNet
- Cy3 Performance Reporter
- Cyni Toolbox
- CyPath2
- CyTargetLinker
- CytoCluster
- CytoKegg
- CytoNCA
- DynNetwork (Installed)
- GeneMANIA (Installed)
- GenomeSpace
- GFD-Net
- GIANT
- jActiveModules

AgilentLiteratureSearch
3.0.3.beta

LitSearch

Mines scientific literature to find publications related to search terms and to create interaction networks based on the search result.

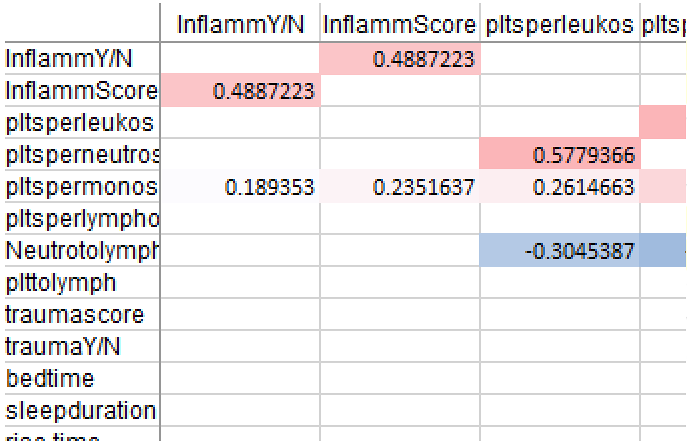
Install from File... | View on App Store | Install | Close

Cytoscape for any network data

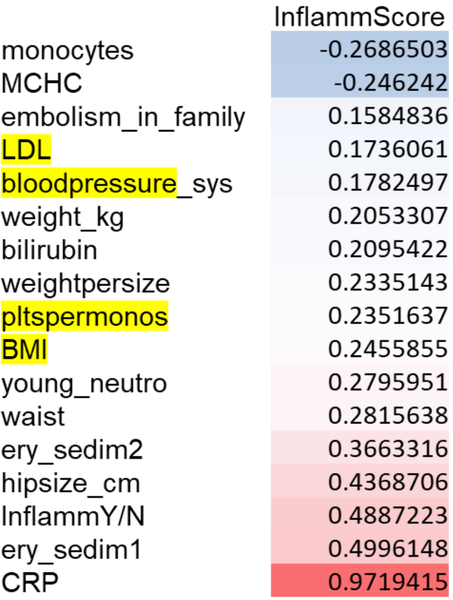
Example:

- Correlation between clinical data from a routine health check and lifestyle factors, as well as psychic traumas in childhood

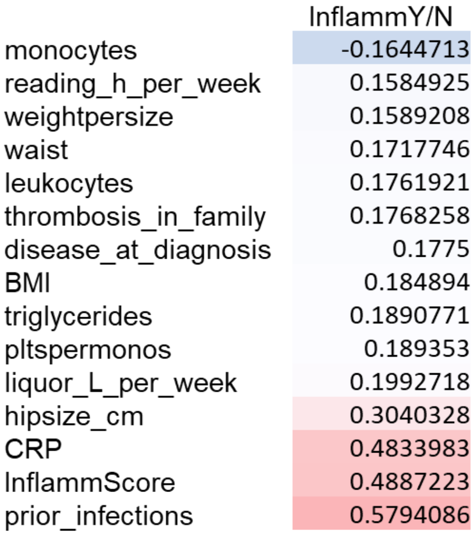
Correlation matrix



	InflammY/N	InflammScore	pltsperleukos	plts
InflammY/N		0.4887223		
InflammScore	0.4887223			
pltsperleukos				
pltsperneutros			0.5779366	
pltspermonos	0.189353	0.2351637	0.2614663	
pltsperlympho				
Neutrotolymph			-0.3045387	
plttolymph				
traumascore				
traumaY/N				
bedtime				
sleepduration				



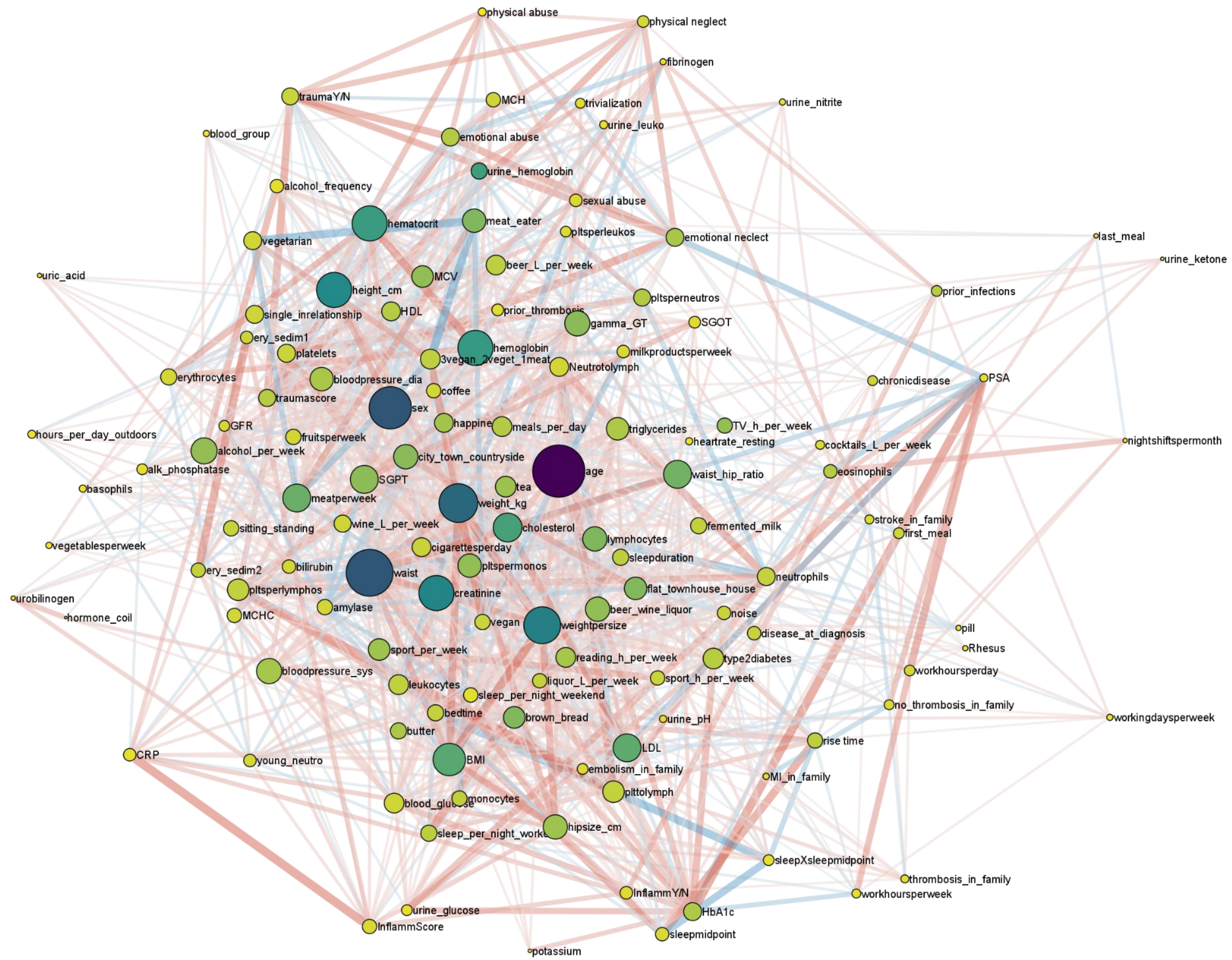
	InflammScore
monocytes	-0.2686503
MCHC	-0.246242
embolism_in_family	0.1584836
LDL	0.1736061
bloodpressure_sys	0.1782497
weight_kg	0.2053307
bilirubin	0.2095422
weightpersize	0.2335143
pltspermonos	0.2351637
BMI	0.2455855
young_neutro	0.2795951
waist	0.2815638
ery_sedim2	0.3663316
hipsize_cm	0.4368706
InflammY/N	0.4887223
ery_sedim1	0.4996148
CRP	0.9719415



	InflammY/N
monocytes	-0.1644713
reading_h_per_week	0.1584925
weightpersize	0.1589208
waist	0.1717746
leukocytes	0.1761921
thrombosis_in_family	0.1768258
disease_at_diagnosis	0.1775
BMI	0.184894
triglycerides	0.1890771
pltspermonos	0.189353
liquor_L_per_week	0.1992718
hipsize_cm	0.3040328
CRP	0.4833983
InflammScore	0.4887223
prior_infections	0.5794086

correlation matrix can be imported into Cytoscape with the **App: aMatReader**

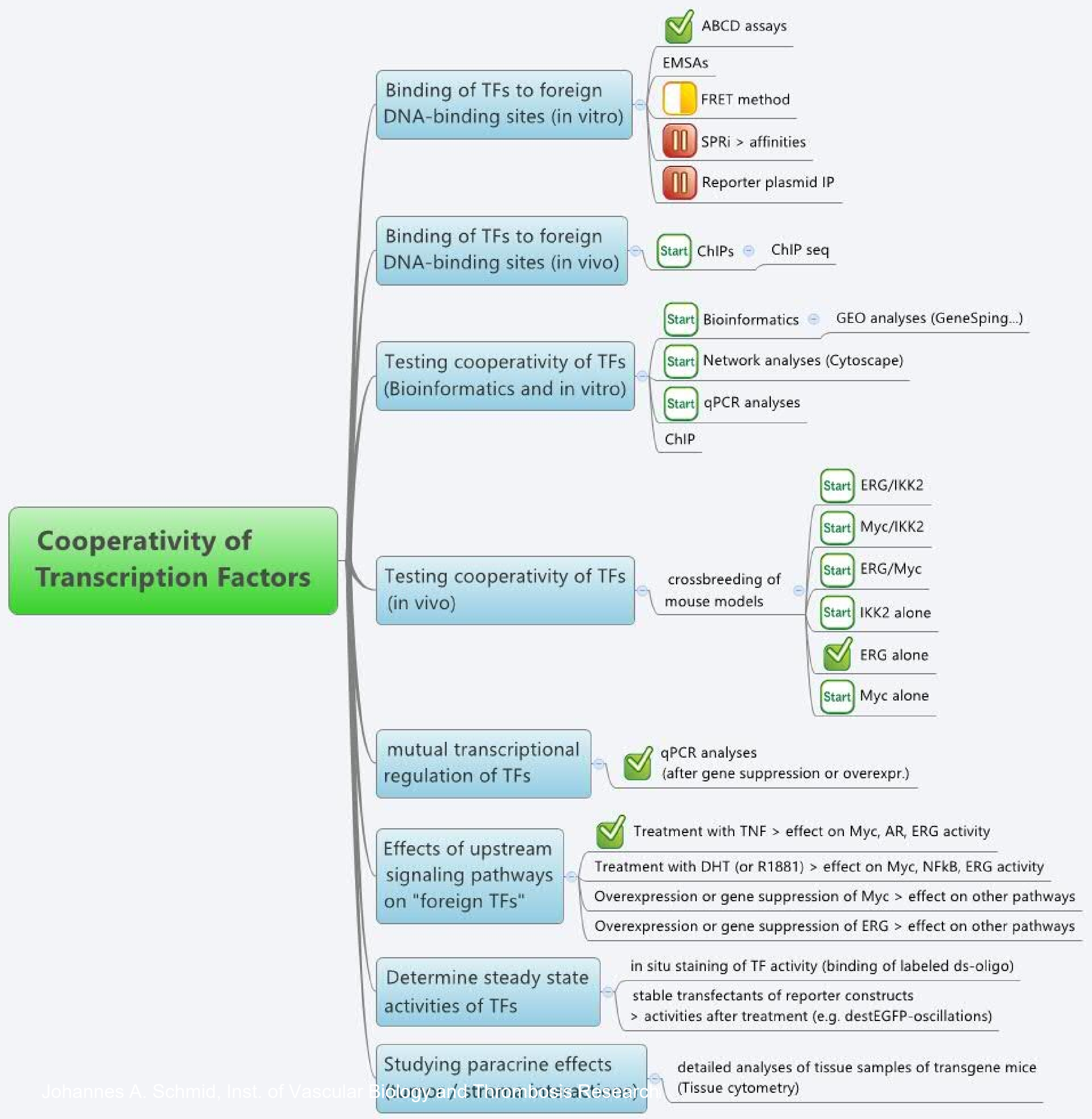
(take care to use "." and not "," for the decimal point!)


physical abuse
physical neglect
fibrinogen
traumaY/N
MCH
trivialization
urine_nitrite
urine_leuko
blood_group
emotional abuse
urine_hemoglobin
alcohol_frequency
sexual abuse
hematocrit
meat_eater
pltsperleukos
last_meal
vegetarian
emotional neclect
urine_ketone
beer_L_per_week
uric_acid
MCV
height_cm
prior_infections
pltsperneutros
HDL
prior_thrombosis
single_inrelationship
gamma_GT
SGOT
ery_sedim1
hemoglobin
platelets
milkproductsperweek
3vegan_2veget_1meat
erythrocytes
Neutrotolymph
bloodpressure_dia
chronicdisease
PSA
coffee
traumascore
sex
GFR
happine
meals_per_day
triglycerides
TV_h_per_week
hours_per_day_outdoors
fruitsperweek
heartrate_resting
cocktails_L_per_week
nightshiftspermonth
alcohol_per_week
city_town_countryside
alk_phosphatase
age
waist_hip_ratio
eosinophils
SGPT
basophils
tea
meatperweek
weight_kg
cholesterol
stroke_in_family
fermented_milk
sitting_standing
wine_L_per_week
first_meal
lymphocytes
vegetablesperweek
cigarettesperday
sleepduration
ery_sedim2
bilirubin
pltspermonos
waist
neutrophils
pltsperlymphos
creatinine
flat_townhouse_house
urobilinogen
MCHC
amylase
beer_wine_liquor
noise
hormone_coil
vegan
weightpersize
disease_at_diagnosis
pill
Rhesus
sport_per_week
reading_h_per_week
type2diabetes
bloodpressure_sys
workhoursperday
liquor_L_per_week
sport_h_per_week
leukocytes
sleep_per_night_weekend
no_thrombosis_in_family
workingdaysperweek
bedtime
brown_bread
urine_pH
butter
rise time
CRP
LDL
young_neutro
BMI
embolism_in_family
MI_in_family
plttolymph
monocytes
blood_glucose
sleep_per_night_work
hipsize_cm
sleepXsleepmidpoint
thrombosis_in_family
InflammY/N
workhoursperweek
urine_glucose
HbA1c
InflammScore
sleepmidpoint
potassium

Mind-Mapping software:

- XMind →
-

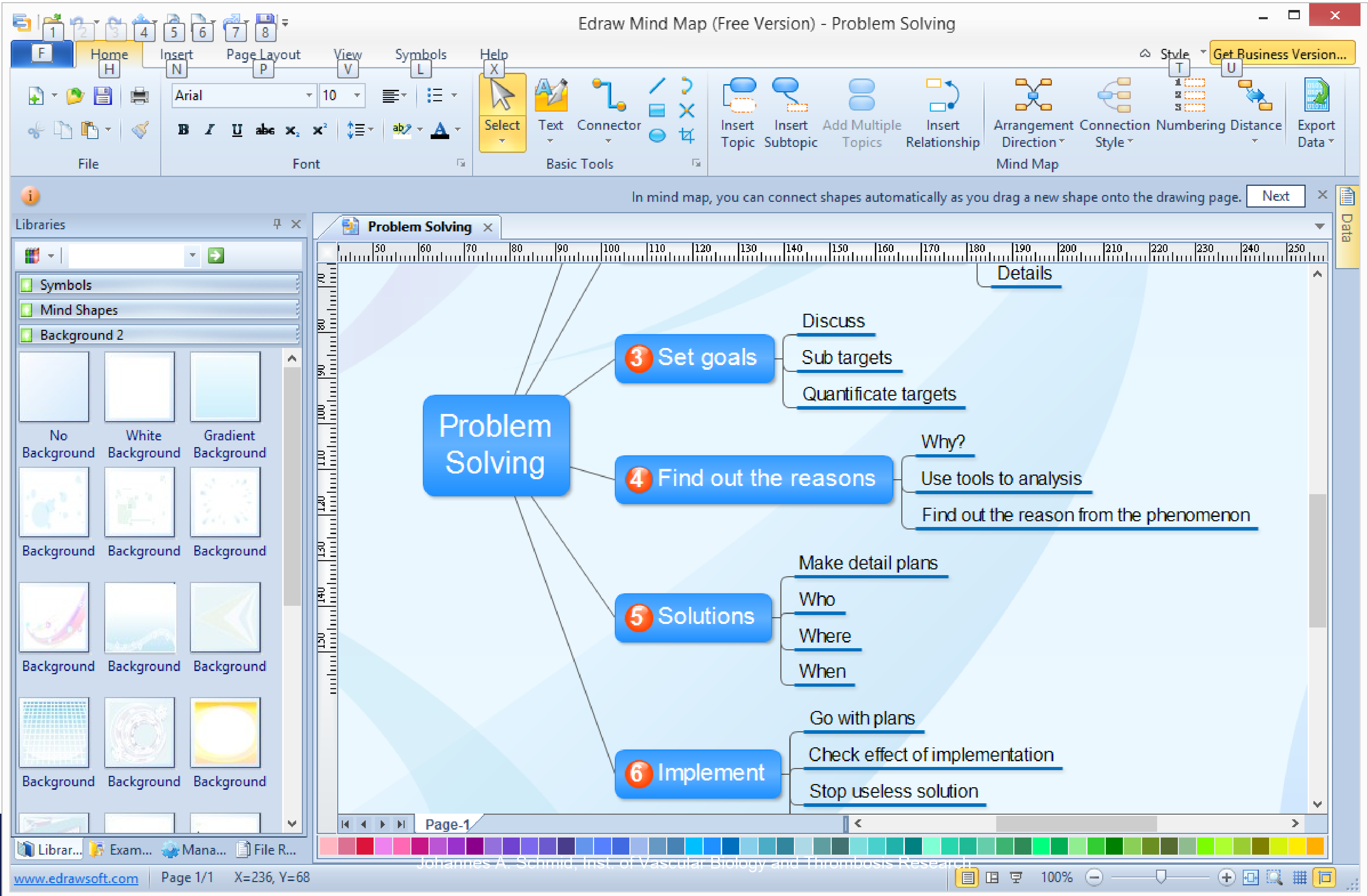
  Edraw MindMap
- Freemind
- Mindmanager
- CMapTools



Cooperativity of Transcription Factors

- Binding of TFs to foreign DNA-binding sites (in vitro)
  - ✓ ABCD assays
  - EMSAs
  - ◐ FRET method
  - ⏸ SPRi > affinities
  - ⏸ Reporter plasmid IP
- Binding of TFs to foreign DNA-binding sites (in vivo)
  - Start ChIPs
    - ChIP seq
- Testing cooperativity of TFs (Bioinformatics and in vitro)
  - Start Bioinformatics
    - GEO analyses (GeneSping...)
  - Start Network analyses (Cytoscape)
  - Start qPCR analyses
  - ChIP
- Testing cooperativity of TFs (in vivo)
  - crossbreeding of mouse models
    - Start ERG/IKK2
    - Start Myc/IKK2
    - Start ERG/Myc
    - Start IKK2 alone
    - ✓ ERG alone
    - Start Myc alone
- mutual transcriptional regulation of TFs
  - ✓ qPCR analyses (after gene suppression or overexpr.)
- Effects of upstream signaling pathways on "foreign TFs"
  - ✓ Treatment with TNF > effect on Myc, AR, ERG activity
  - Treatment with DHT (or R1881) > effect on Myc, NFkB, ERG activity
  - Overexpression or gene suppression of Myc > effect on other pathways
  - Overexpression or gene suppression of ERG > effect on other pathways
- Determine steady state activities of TFs
  - in situ staining of TF activity (binding of labeled ds-oligo)
  - stable transfectants of reporter constructs > activities after treatment (e.g. destEGFP-oscillations)
- Studying paracrine effects (Ligands and Receptors)
  - detailed analyses of tissue samples of transgene mice (Tissue cytometry)

Edraw Mind Map

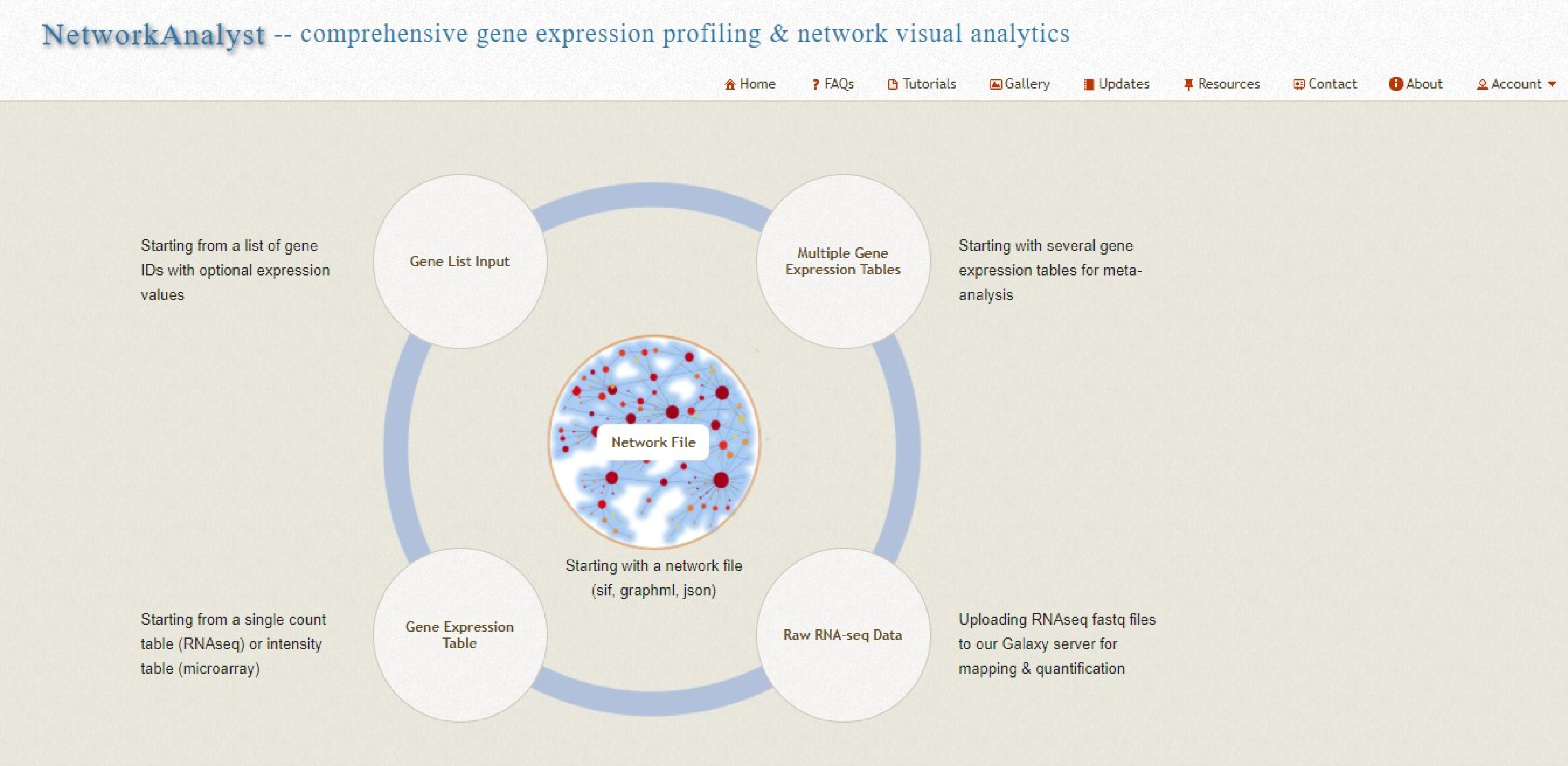


Edraw Mind Map (Free Version) - Problem Solving

In mind map, you can connect shapes automatically as you drag a new shape onto the drawing page.

Network analyst: www.networkanalyst.ca

- Tutorials: http://www.networkanalyst.ca/faces/docs/Tutorial.xhtml
- Nature Protocols article: https://www.nature.com/articles/nprot.2015.052



NetworkAnalyst -- comprehensive gene expression profiling & network visual analytics

Starting from a list of gene IDs with optional expression values

Starting with several gene expression tables for meta-analysis

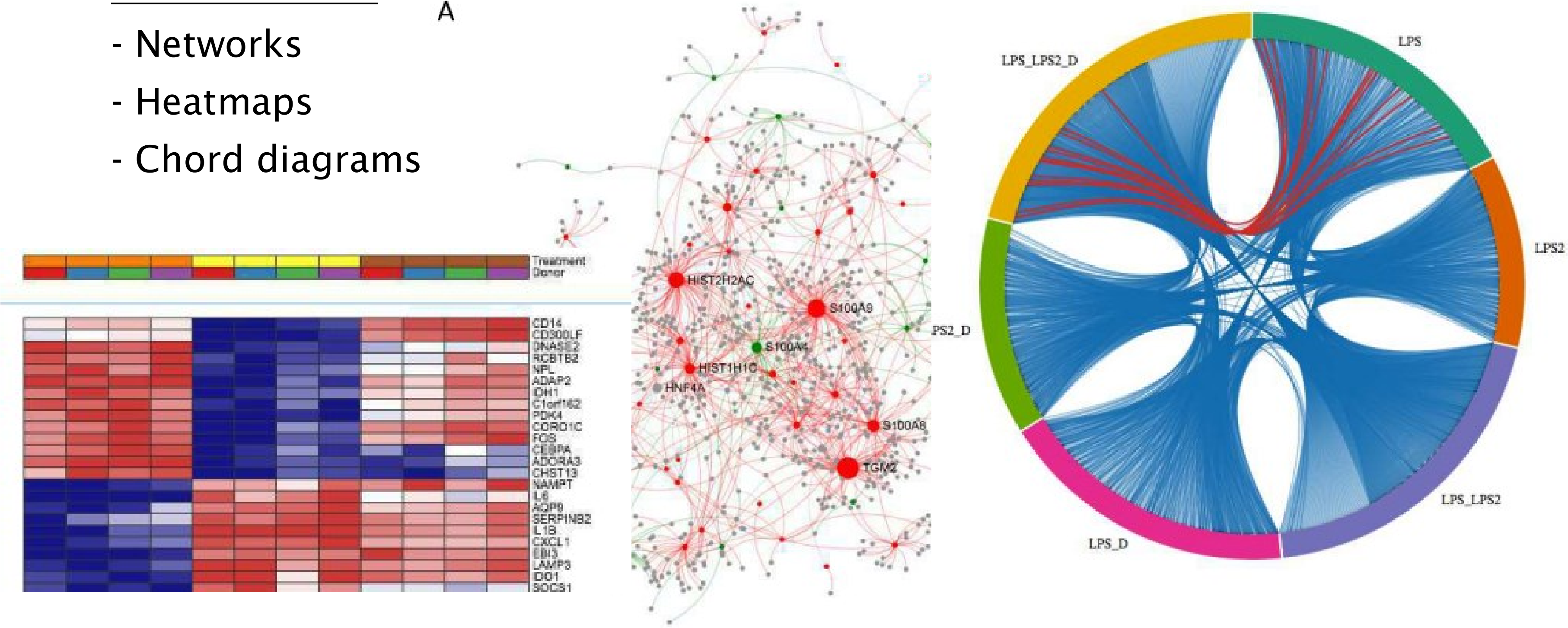
Starting with a network file (sif, graphml, json)

Starting from a single count table (RNAseq) or intensity table (microarray)

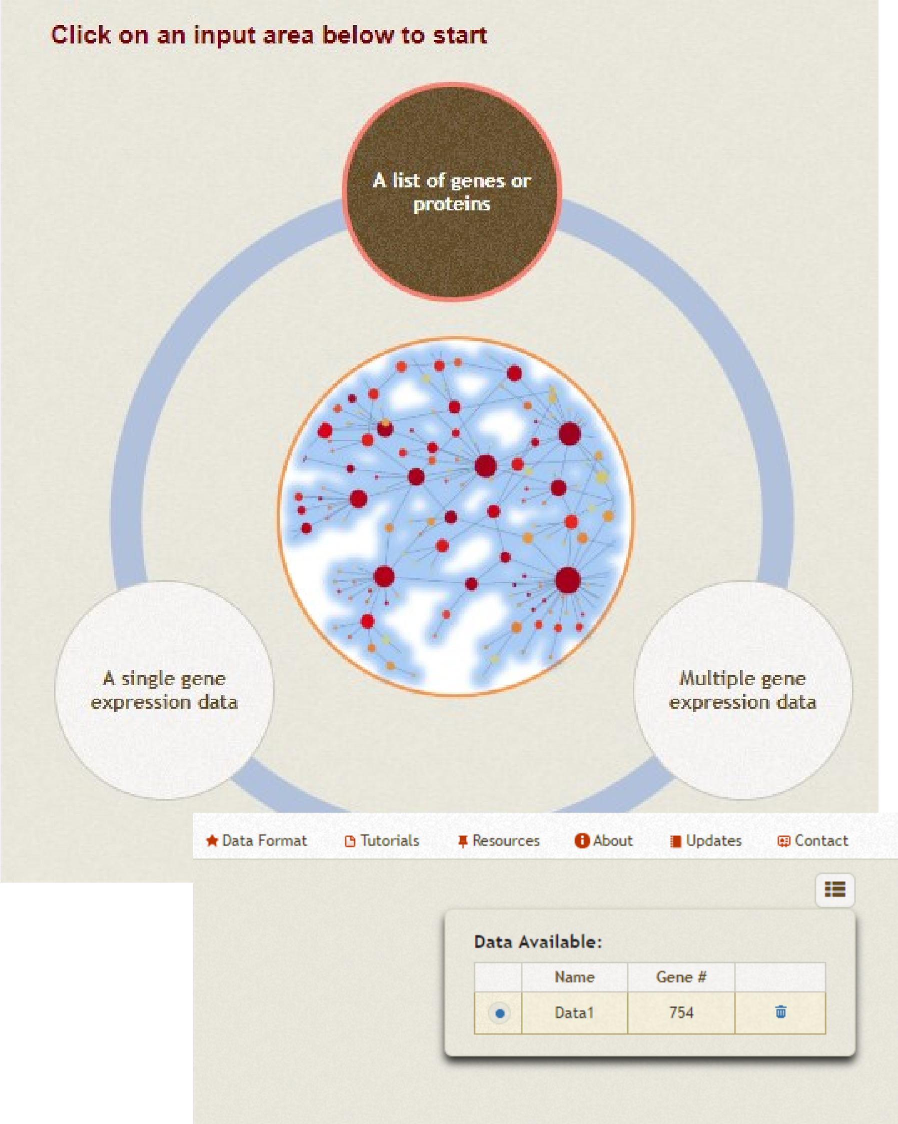
Uploading RNAseq fastq files to our Galaxy server for mapping & quantification

Features of Network Analyst

- Web application for meta-analysis and visualization of genes and proteins
- **Statistics**: summary-level data from multiple datasets; differential analysis: nested comparisons, time series, pair-wise comparisons… 2-factor analysis (e.g. donor/gender effects when comparing different treatments)
- **Visualizations**
  - Networks
  - Heatmaps
  - Chord diagrams



Data input I: List of predefined differentially expressed genes

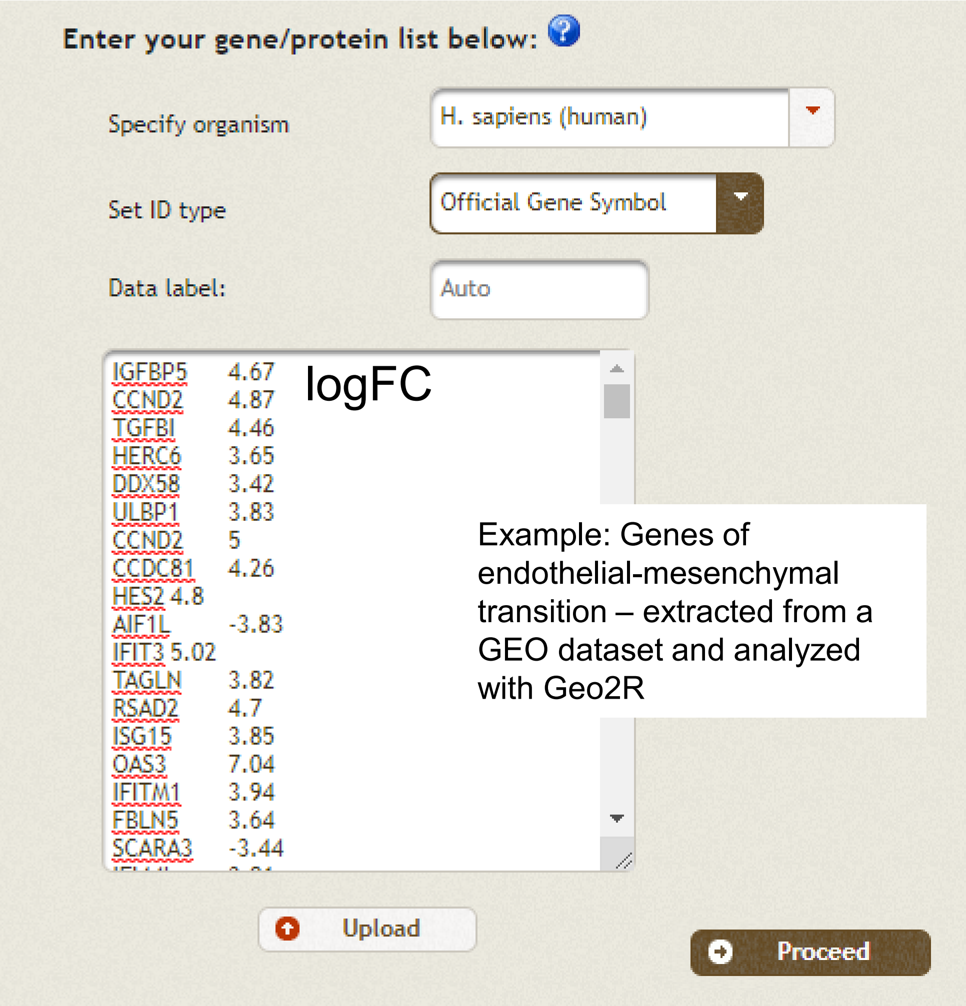


Click on an input area below to start

Data Available:

	Name	Gene #	
●	Data1	754	🗑

(choosing human might sometimes provide a richer network, even in case the experiment was done in mice!)



Enter your gene/protein list below:

Specify organism: H. sapiens (human)

Set ID type: Official Gene Symbol

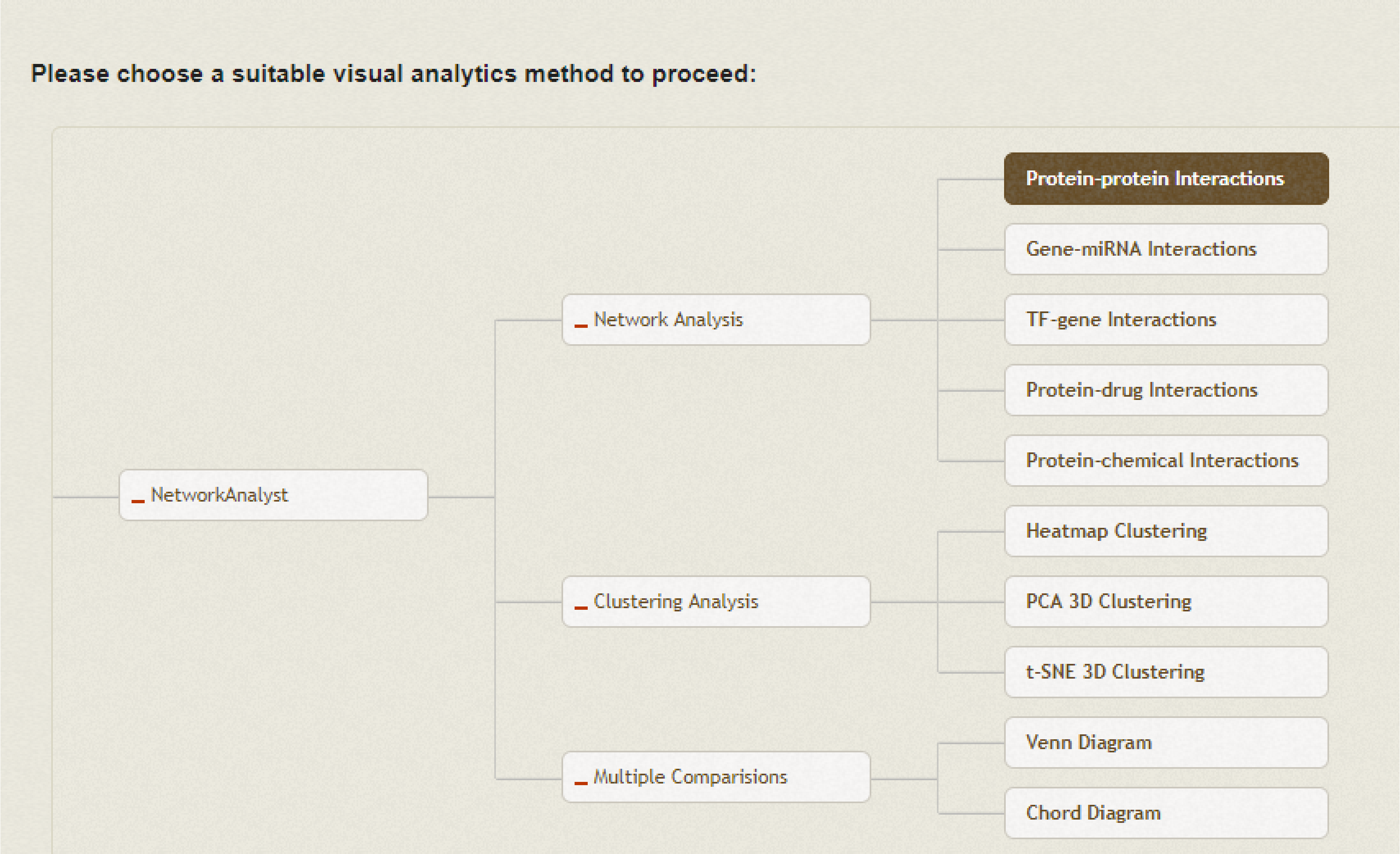
Data label: Auto

```
IGFBP5	4.67
CCND2	4.87
TGFBI	4.46
HERC6	3.65
DDX58	3.42
ULBP1	3.83
CCND2	5
CCDC81	4.26
HES2 4.8
AIF1L		-3.83
IFIT3 5.02
TAGLN	3.82
RSAD2	4.7
ISG15	3.85
OAS3	7.04
IFITM1	3.94
FBLN5	3.64
SCARA3	-3.44
```

logFC

Example: Genes of endothelial-mesenchymal transition – extracted from a GEO dataset and analyzed with Geo2R

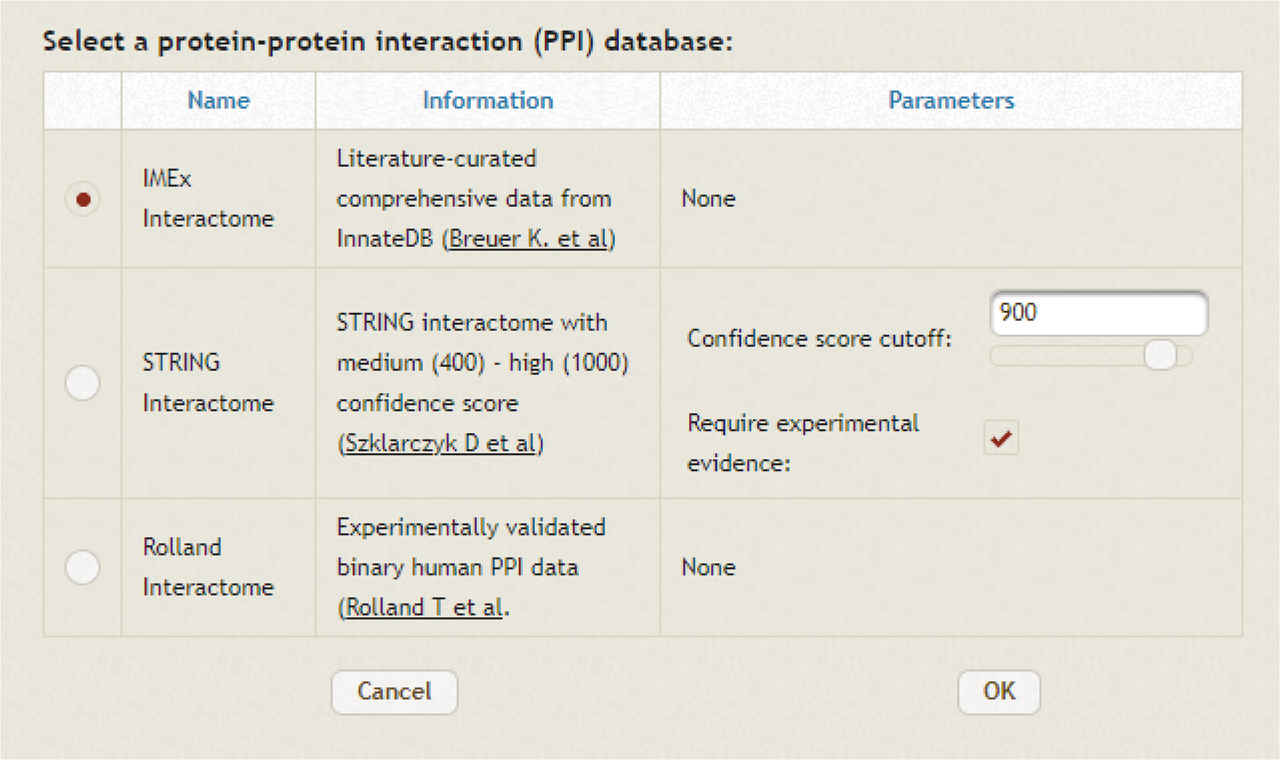
Visual analytics options



Please choose a suitable visual analytics method to proceed:

- NetworkAnalyst
  - Network Analysis
    - Protein-protein Interactions
    - Gene-miRNA Interactions
    - TF-gene Interactions
    - Protein-drug Interactions
    - Protein-chemical Interactions
  - Clustering Analysis
    - Heatmap Clustering
    - PCA 3D Clustering
    - t-SNE 3D Clustering
  - Multiple Comparisions
    - Venn Diagram
    - Chord Diagram

Chose a protein interactome database

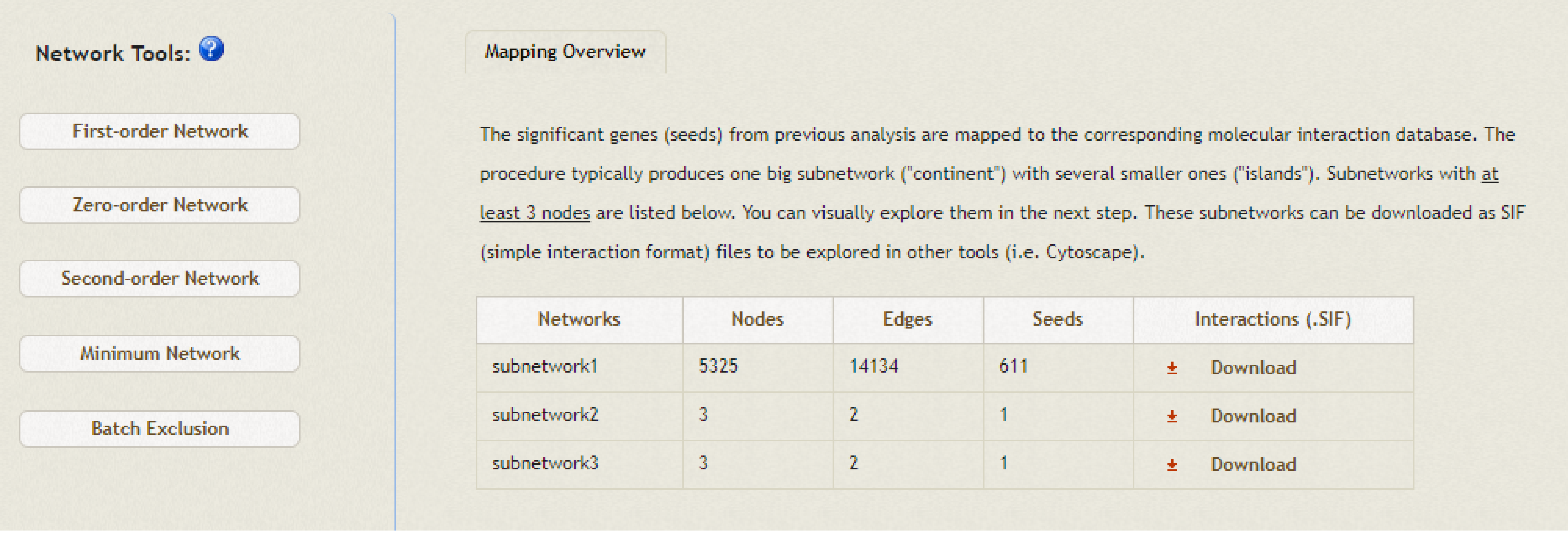


Select a protein-protein interaction (PPI) database:

	Name	Information	Parameters
●	IMEx Interactome	Literature-curated comprehensive data from InnateDB (Breuer K. et al)	None
○	STRING Interactome	STRING interactome with medium (400) - high (1000) confidence score (Szklarczyk D et al)	Confidence score cutoff: 900 Require experimental evidence: ✓
○	Rolland Interactome	Experimentally validated binary human PPI data (Rolland T et al.	None

Chose a network

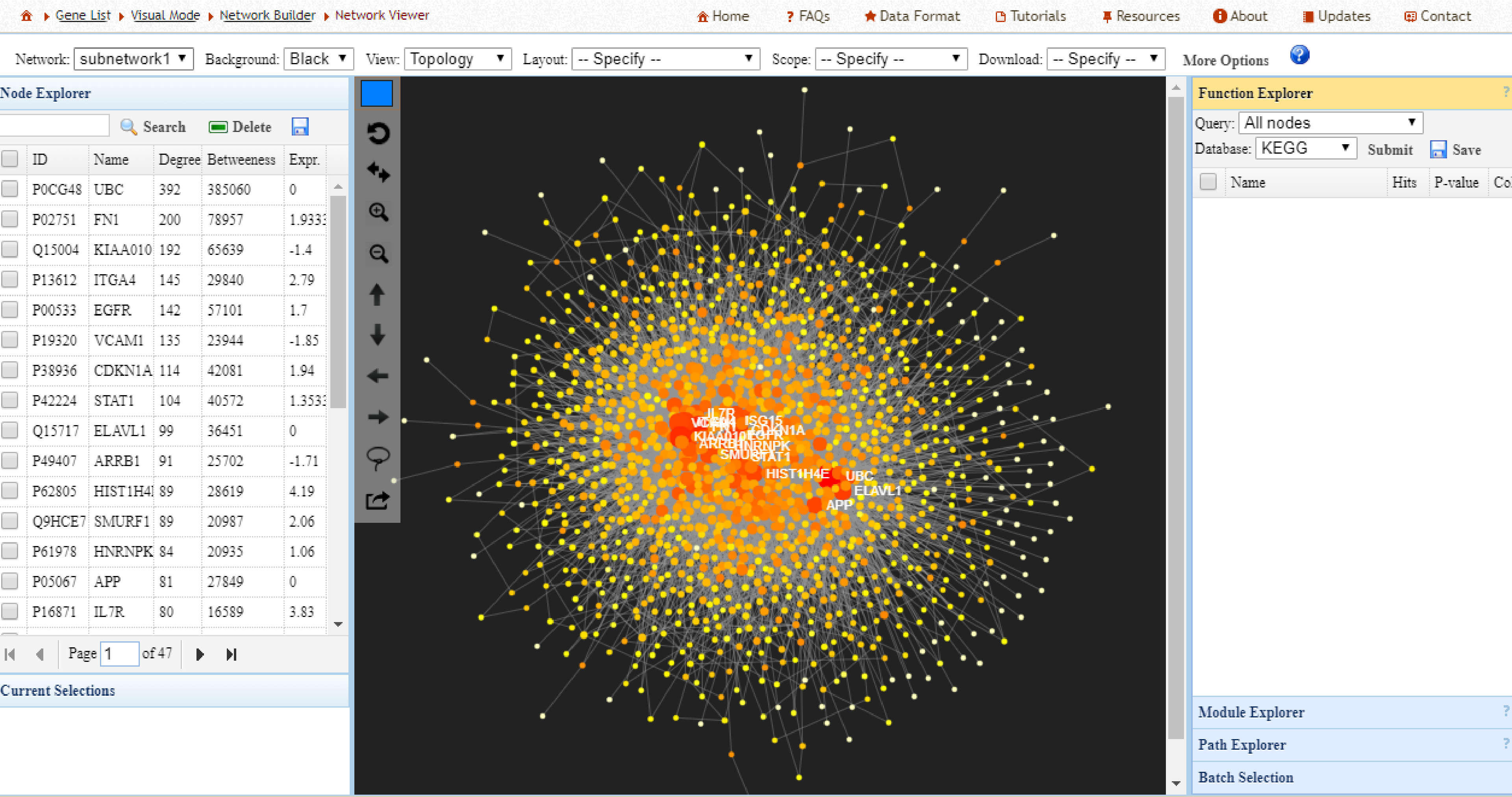
By default the 1st oder network is calculated, if this is too dense (>2000 nodes), it is advisable to switch to zero-order network or to minimum network (the lowest number of nodes required to link all the seeds of the differentially expressed genes).
If it is too sparse, you may switch to 2nd order network)



The significant genes (seeds) from previous analysis are mapped to the corresponding molecular interaction database. The procedure typically produces one big subnetwork ("continent") with several smaller ones ("islands"). Subnetworks with at least 3 nodes are listed below. You can visually explore them in the next step. These subnetworks can be downloaded as SIF (simple interaction format) files to be explored in other tools (i.e. Cytoscape).

Networks	Nodes	Edges	Seeds	Interactions (.SIF)
subnetwork1	5325	14134	611	Download
subnetwork2	3	2	1	Download
subnetwork3	3	2	1	Download

Adjustable network view



Network: subnetwork1
Background: Black
View: Topology
Layout: -- Specify --
Scope: -- Specify --
Download: -- Specify --

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	P0CG48	UBC	392	385060	0
☐	P02751	FN1	200	78957	1.933
☐	Q15004	KIAA010	192	65639	-1.4
☐	P13612	ITGA4	145	29840	2.79
☐	P00533	EGFR	142	57101	1.7
☐	P19320	VCAM1	135	23944	-1.85
☐	P38936	CDKN1A	114	42081	1.94
☐	P42224	STAT1	104	40572	1.353
☐	Q15717	ELAVL1	99	36451	0
☐	P49407	ARRB1	91	25702	-1.71
☐	P62805	HIST1H4	89	28619	4.19
☐	Q9HCE7	SMURF1	89	20987	2.06
☐	P61978	HNRNPK	84	20935	1.06
☐	P05067	APP	81	27849	0
☐	P16871	IL7R	80	16589	3.83

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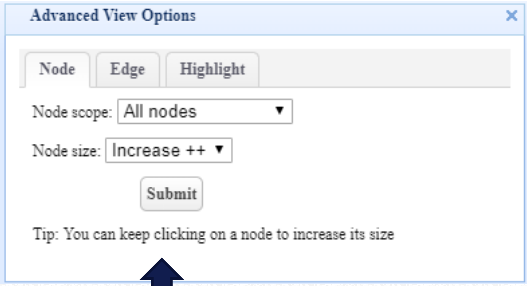
Current Selections

Function Explorer

Query: All nodes
Database: KEGG

☐	Name	Hits	P-value	Co

Adjustable network view



Advanced View Options

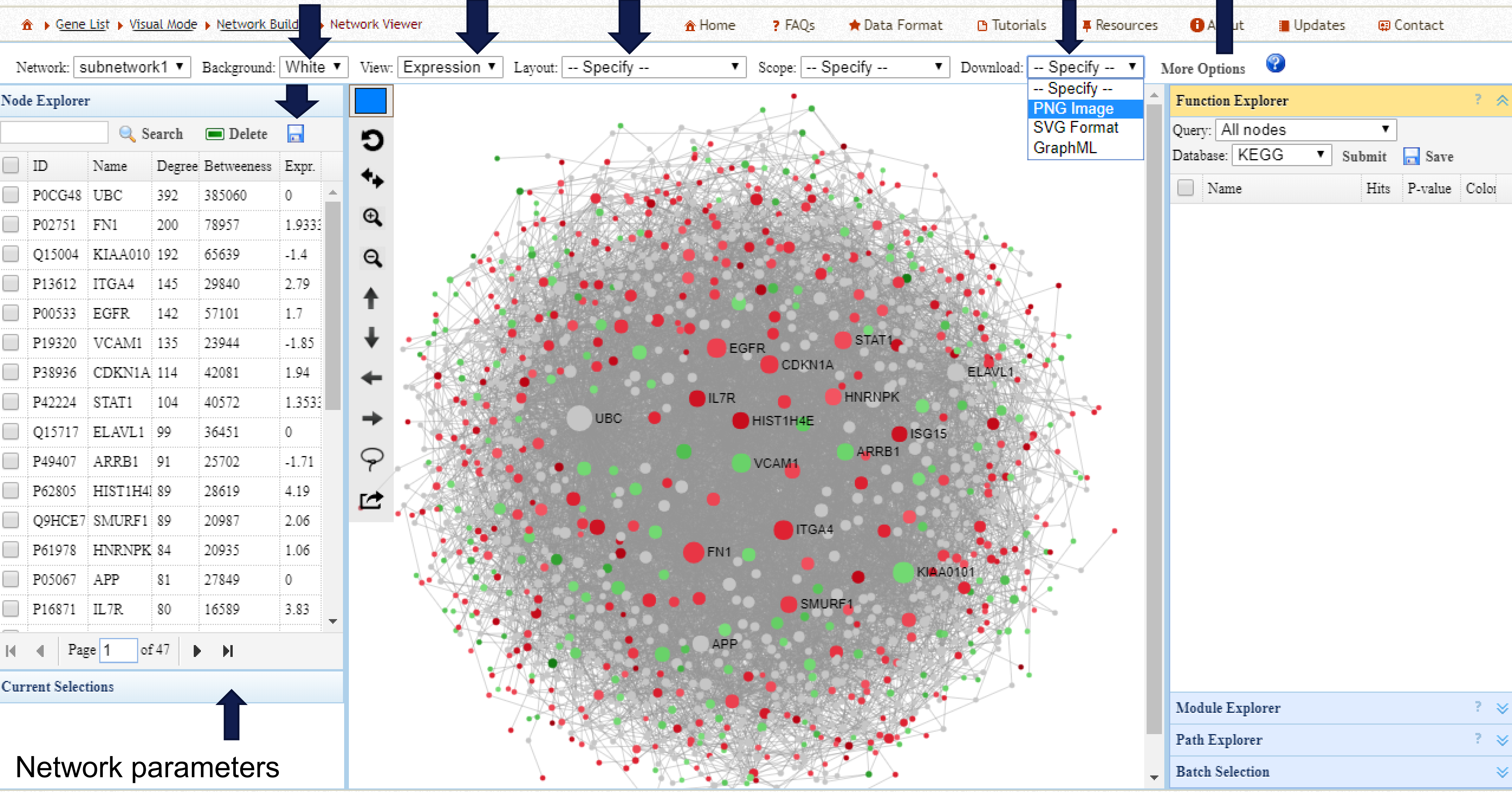
Node scope: All nodes

Node size: Increase ++

Tip: You can keep clicking on a node to increase its size

Expression up (red) or down (green) regulated

Download o



Network: subnetwork1 Background: White View: Expression Layout: -- Specify -- Scope: -- Specify -- Download: -- Specify --

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	P0CG48	UBC	392	385060	0
☐	P02751	FN1	200	78957	1.933
☐	Q15004	KIAA010	192	65639	-1.4
☐	P13612	ITGA4	145	29840	2.79
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☐	Q15717	ELAVL1	99	36451	0
☐	P49407	ARRB1	91	25702	-1.71
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☐	P05067	APP	81	27849	0
☐	P16871	IL7R	80	16589	3.83

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Current Selections

Function Explorer

Query: All nodes

Database: KEGG

☐	Name	Hits	P-value	Color

Module Explorer

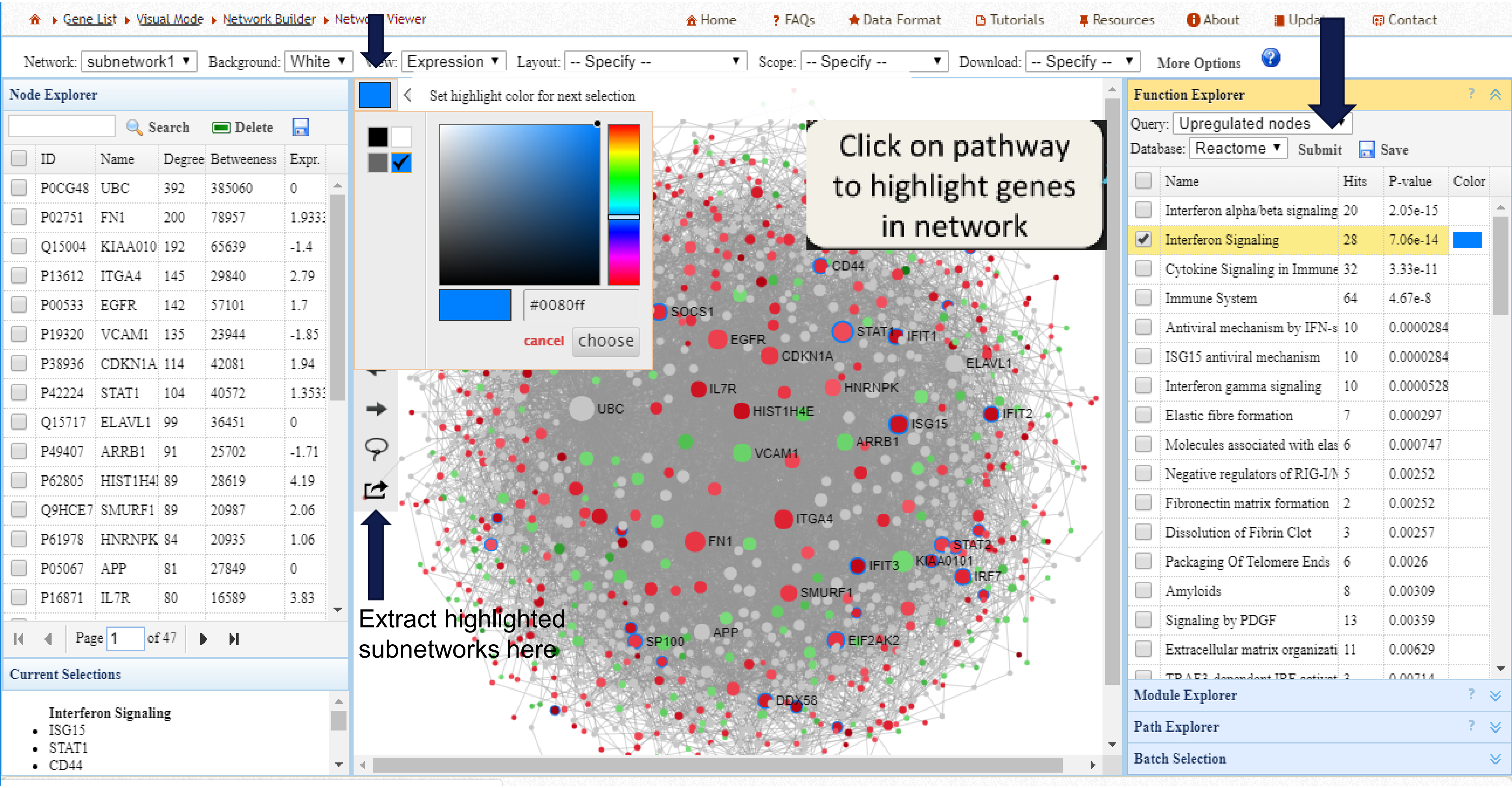
Path Explorer

Batch Selection

Network parameters

Calculation of significantly altered functions (functional enrichment analysis > Function Explorer)

Choose color here



Click on pathway to highlight genes in network

Extract highlighted subnetworks here

Node Explorer

Search Delete

☐	ID	Name	Degree	Betweeness	Expr.
☐	P0CG48	UBC	392	385060	0
☐	P02751	FN1	200	78957	1.933
☐	Q15004	KIAA010	192	65639	-1.4
☐	P13612	ITGA4	145	29840	2.79
☐	P00533	EGFR	142	57101	1.7
☐	P19320	VCAM1	135	23944	-1.85
☐	P38936	CDKN1A	114	42081	1.94
☐	P42224	STAT1	104	40572	1.353
☐	Q15717	ELAVL1	99	36451	0
☐	P49407	ARRB1	91	25702	-1.71
☐	P62805	HIST1H4	89	28619	4.19
☐	Q9HCE7	SMURF1	89	20987	2.06
☐	P61978	HNRNPK	84	20935	1.06
☐	P05067	APP	81	27849	0
☐	P16871	IL7R	80	16589	3.83

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Current Selections

Interferon Signaling
- ISG15
- STAT1
- CD44

Function Explorer

Query: Upregulated nodes

Database: Reactome Submit Save

☐	Name	Hits	P-value	Color
☐	Interferon alpha/beta signaling	20	2.05e-15	
☑	Interferon Signaling	28	7.06e-14	🟦
☐	Cytokine Signaling in Immune	32	3.33e-11	
☐	Immune System	64	4.67e-8	
☐	Antiviral mechanism by IFN-s	10	0.0000284	
☐	ISG15 antiviral mechanism	10	0.0000284	
☐	Interferon gamma signaling	10	0.0000528	
☐	Elastic fibre formation	7	0.000297	
☐	Molecules associated with elas	6	0.000747	
☐	Negative regulators of RIG-I/M	5	0.00252	
☐	Fibronectin matrix formation	2	0.00252	
☐	Dissolution of Fibrin Clot	3	0.00257	
☐	Packaging Of Telomere Ends	6	0.0026	
☐	Amyloids	8	0.00309	
☐	Signaling by PDGF	13	0.00359	
☐	Extracellular matrix organizati	11	0.00629	

Module Explorer

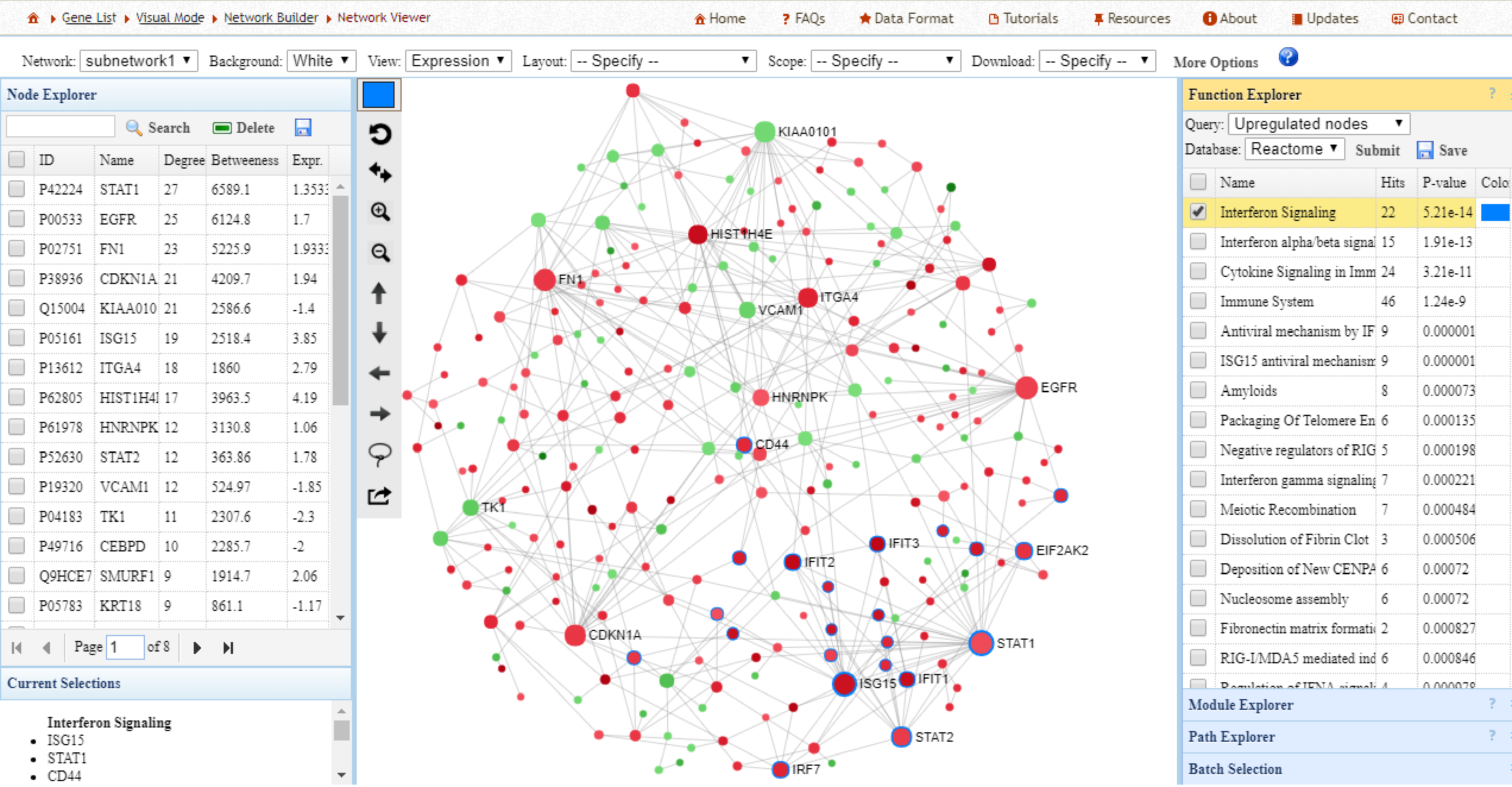
Path Explorer

Batch Selection

Zero order network of the same data set

235 nodes (instead of 5325), 409 edges, 238 seeds (from 988 diff. regulated genes)

Mostly the same pathways are enriched



Network: subnetwork1 ▾ Background: White ▾ View: Expression ▾ Layout: -- Specify -- ▾ Scope: -- Specify -- ▾ Download: -- Specify -- ▾

Node Explorer

Search Delete

☐	ID	Name	Degree	Betweeness	Expr.
☐	P42224	STAT1	27	6589.1	1.353
☐	P00533	EGFR	25	6124.8	1.7
☐	P02751	FN1	23	5225.9	1.933
☐	P38936	CDKN1A	21	4209.7	1.94
☐	Q15004	KIAA010	21	2586.6	-1.4
☐	P05161	ISG15	19	2518.4	3.85
☐	P13612	ITGA4	18	1860	2.79
☐	P62805	HIST1H4	17	3963.5	4.19
☐	P61978	HNRNPK	12	3130.8	1.06
☐	P52630	STAT2	12	363.86	1.78
☐	P19320	VCAM1	12	524.97	-1.85
☐	P04183	TK1	11	2307.6	-2.3
☐	P49716	CEBPD	10	2285.7	-2
☐	Q9HCE7	SMURF1	9	1914.7	2.06
☐	P05783	KRT18	9	861.1	-1.17

Page 1 of 8

Current Selections

Interferon Signaling
- ISG15
- STAT1
- CD44

Function Explorer

Query: Upregulated nodes ▾
Database: Reactome ▾ Submit Save

☐	Name	Hits	P-value	Colo
☑	Interferon Signaling	22	5.21e-14	🟦
☐	Interferon alpha/beta signal	15	1.91e-13	
☐	Cytokine Signaling in Imm	24	3.21e-11	
☐	Immune System	46	1.24e-9	
☐	Antiviral mechanism by IF	9	0.000001	
☐	ISG15 antiviral mechanism	9	0.000001	
☐	Amyloids	8	0.000073	
☐	Packaging Of Telomere En	6	0.000135	
☐	Negative regulators of RIG	5	0.000198	
☐	Interferon gamma signaling	7	0.000221	
☐	Meiotic Recombination	7	0.000484	
☐	Dissolution of Fibrin Clot	3	0.000506	
☐	Deposition of New CENPA	6	0.00072	
☐	Nucleosome assembly	6	0.00072	
☐	Fibronectin matrix formati	2	0.000827	
☐	RIG-I/MDA5 mediated ind	6	0.000846	

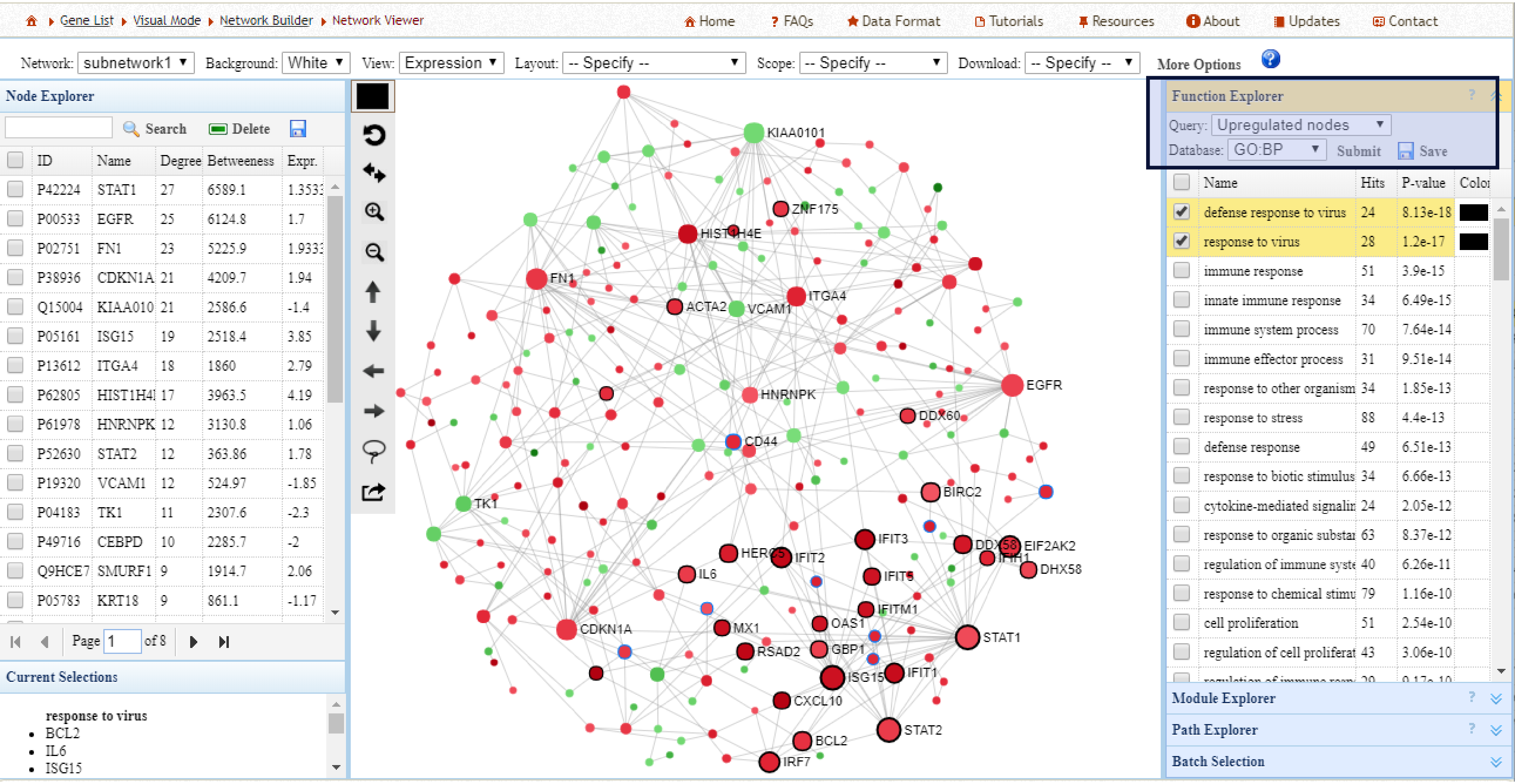
Module Explorer

Path Explorer

Batch Selection

Different databases can be searched for the network

KEGG, **Reactome**, **Gene Ontologies**:
GO:BP (biological process), GO:MF (molecular function), GO:CC (cell. compartments),
motif (transcription factor binding motifs)



Network: subnetwork1 | Background: White | View: Expression | Layout: -- Specify -- | Scope: -- Specify -- | Download: -- Specify --

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	P42224	STAT1	27	6589.1	1.3533
☐	P00533	EGFR	25	6124.8	1.7
☐	P02751	FN1	23	5225.9	1.9333
☐	P38936	CDKN1A	21	4209.7	1.94
☐	Q15004	KIAA010	21	2586.6	-1.4
☐	P05161	ISG15	19	2518.4	3.85
☐	P13612	ITGA4	18	1860	2.79
☐	P62805	HIST1H4I	17	3963.5	4.19
☐	P61978	HNRNPK	12	3130.8	1.06
☐	P52630	STAT2	12	363.86	1.78
☐	P19320	VCAM1	12	524.97	-1.85
☐	P04183	TK1	11	2307.6	-2.3
☐	P49716	CEBPD	10	2285.7	-2
☐	Q9HCE7	SMURF1	9	1914.7	2.06
☐	P05783	KRT18	9	861.1	-1.17

Page 1 of 8

Current Selections

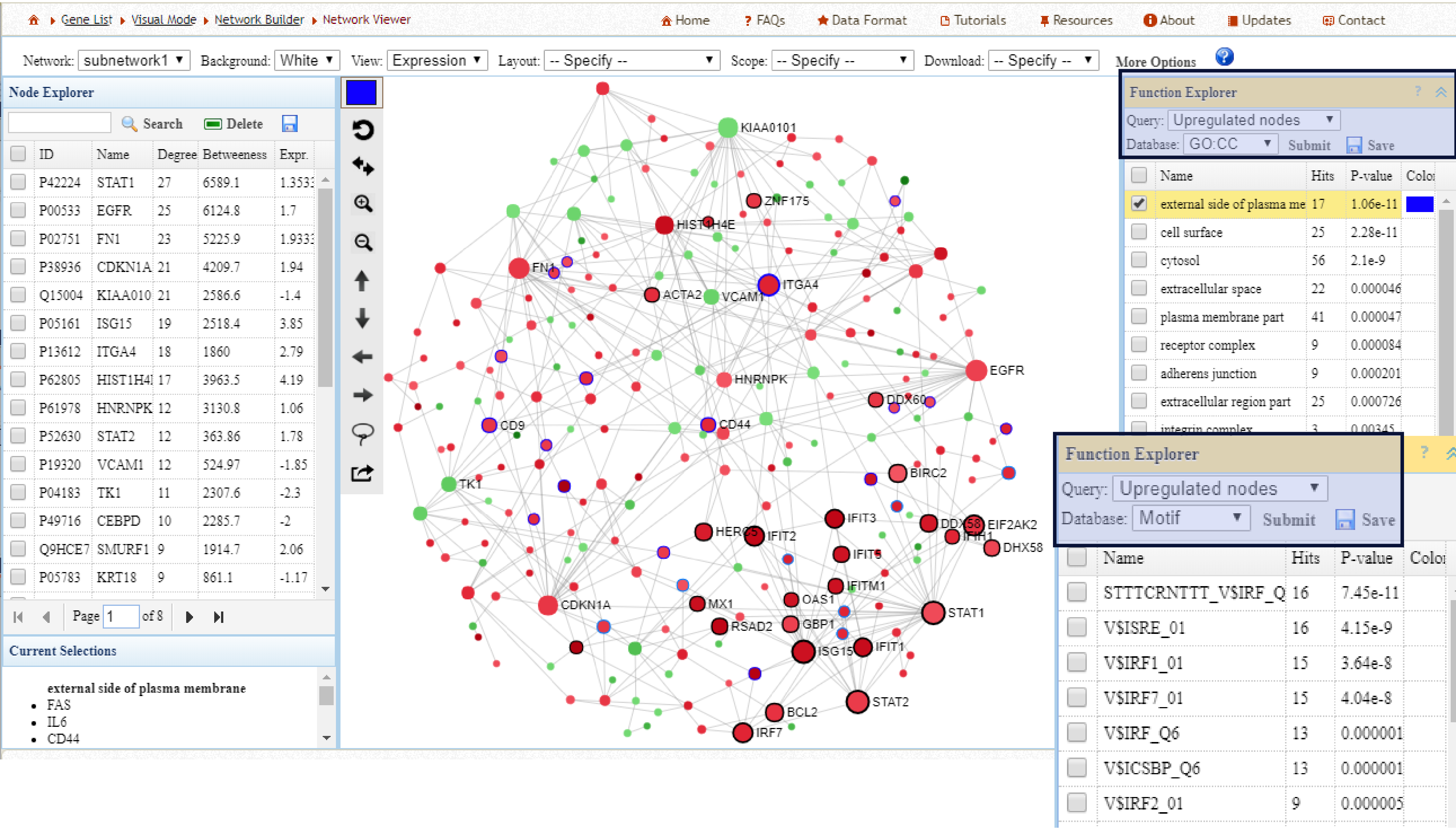
response to virus
- BCL2
- IL6
- ISG15

Function Explorer

Query: Upregulated nodes
Database: GO:BP

☐	Name	Hits	P-value	Color
☑	defense response to virus	24	8.13e-18	■
☑	response to virus	28	1.2e-17	■
☐	immune response	51	3.9e-15	
☐	innate immune response	34	6.49e-15	
☐	immune system process	70	7.64e-14	
☐	immune effector process	31	9.51e-14	
☐	response to other organism	34	1.85e-13	
☐	response to stress	88	4.4e-13	
☐	defense response	49	6.51e-13	
☐	response to biotic stimulus	34	6.66e-13	
☐	cytokine-mediated signalin	24	2.05e-12	
☐	response to organic substar	63	8.37e-12	
☐	regulation of immune syste	40	6.26e-11	
☐	response to chemical stimu	79	1.16e-10	
☐	cell proliferation	51	2.54e-10	
☐	regulation of cell proliferat	43	3.06e-10	

Different databases can be searched for the network



Network: subnetwork1 ▾ Background: White ▾ View: Expression ▾ Layout: -- Specify -- ▾ Scope: -- Specify -- ▾ Download: -- Specify -- ▾

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	P42224	STAT1	27	6589.1	1.353
☐	P00533	EGFR	25	6124.8	1.7
☐	P02751	FN1	23	5225.9	1.933
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☐	P62805	HIST1H4I	17	3963.5	4.19
☐	P61978	HNRNPK	12	3130.8	1.06
☐	P52630	STAT2	12	363.86	1.78
☐	P19320	VCAM1	12	524.97	-1.85
☐	P04183	TK1	11	2307.6	-2.3
☐	P49716	CEBPD	10	2285.7	-2
☐	Q9HCE7	SMURF1	9	1914.7	2.06
☐	P05783	KRT18	9	861.1	-1.17

Page 1 of 8

Current Selections

external side of plasma membrane

- FAS
- IL6
- CD44

Function Explorer

Query: Upregulated nodes ▾
Database: GO:CC ▾ Submit Save

☐	Name	Hits	P-value	Color
☑	external side of plasma me	17	1.06e-11	🟦
☐	cell surface	25	2.28e-11	
☐	cytosol	56	2.1e-9	
☐	extracellular space	22	0.000046	
☐	plasma membrane part	41	0.000047	
☐	receptor complex	9	0.000084	
☐	adherens junction	9	0.000201	
☐	extracellular region part	25	0.000726	
☐	integrin complex	3	0.00345	

Function Explorer

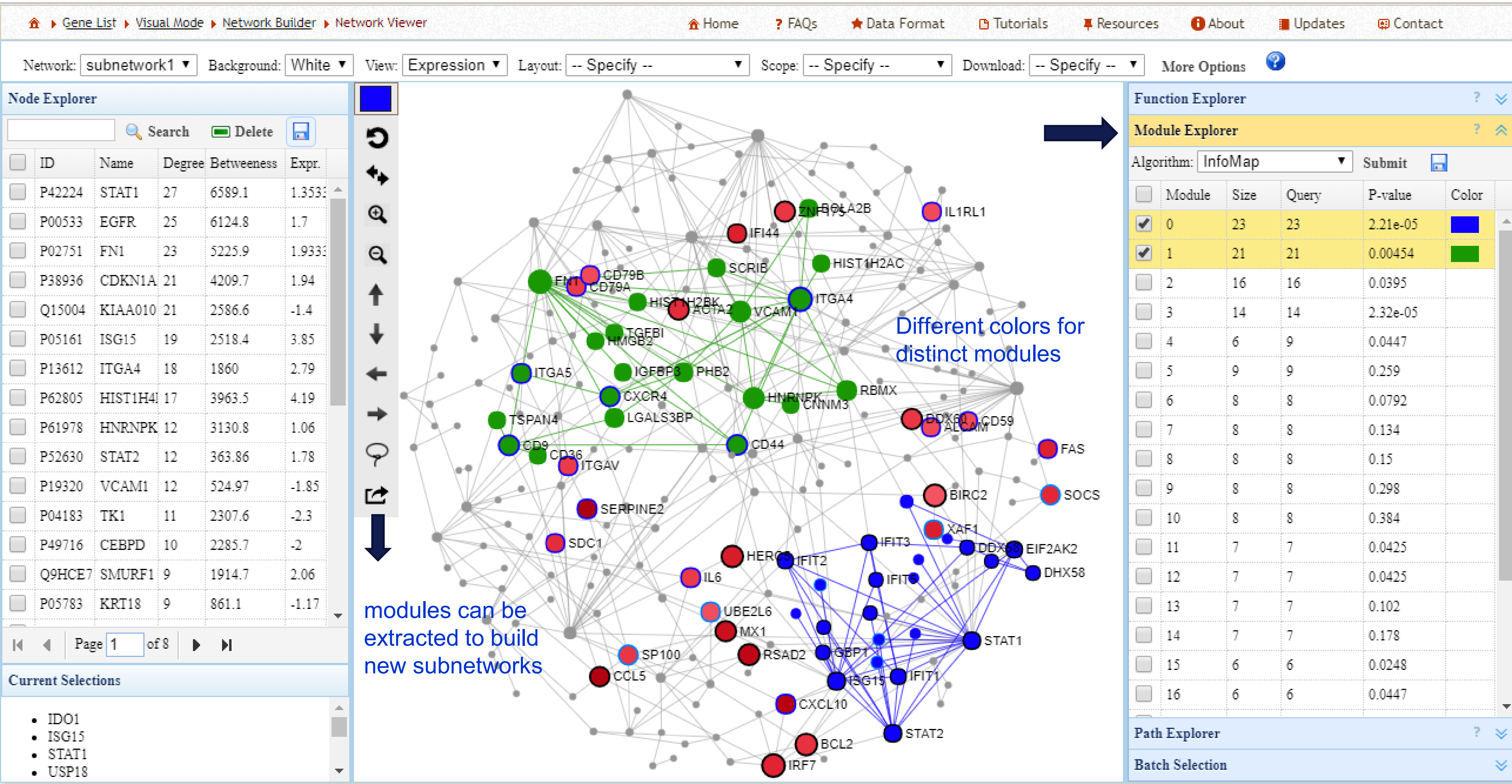
Query: Upregulated nodes ▾
Database: Motif ▾ Submit Save

☐	Name	Hits	P-value	Color
☐	STTTCRNTTT_V$IRF_Q	16	7.45e-11	
☐	V$ISRE_01	16	4.15e-9	
☐	V$IRF1_01	15	3.64e-8	
☐	V$IRF7_01	15	4.04e-8	
☐	V$IRF_Q6	13	0.000001	
☐	V$ICSBP_Q6	13	0.000001	
☐	V$IRF2_01	9	0.000005	

Module explorer

Modules are tightly clustered subnetworks with more internal connections than expected randomly in the network (module members are likely to cooperate in biological functions)

You can make all module node names visible by using „More Options“ > highlighted nodes > increase



Network: subnetwork1 | Background: White | View: Expression | Layout: -- Specify -- | Scope: -- Specify -- | Download: -- Specify --

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	P42224	STAT1	27	6589.1	1.353
☐	P00533	EGFR	25	6124.8	1.7
☐	P02751	FN1	23	5225.9	1.933
☐	P38936	CDKN1A	21	4209.7	1.94
☐	Q15004	KIAA010	21	2586.6	-1.4
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☐	P13612	ITGA4	18	1860	2.79
☐	P62805	HIST1H4	17	3963.5	4.19
☐	P61978	HNRNPK	12	3130.8	1.06
☐	P52630	STAT2	12	363.86	1.78
☐	P19320	VCAM1	12	524.97	-1.85
☐	P04183	TK1	11	2307.6	-2.3
☐	P49716	CEBPD	10	2285.7	-2
☐	Q9HCE7	SMURF1	9	1914.7	2.06
☐	P05783	KRT18	9	861.1	-1.17

Page 1 of 8

Current Selections

- IDO1
- ISG15
- STAT1
- USP18

Function Explorer

Module Explorer

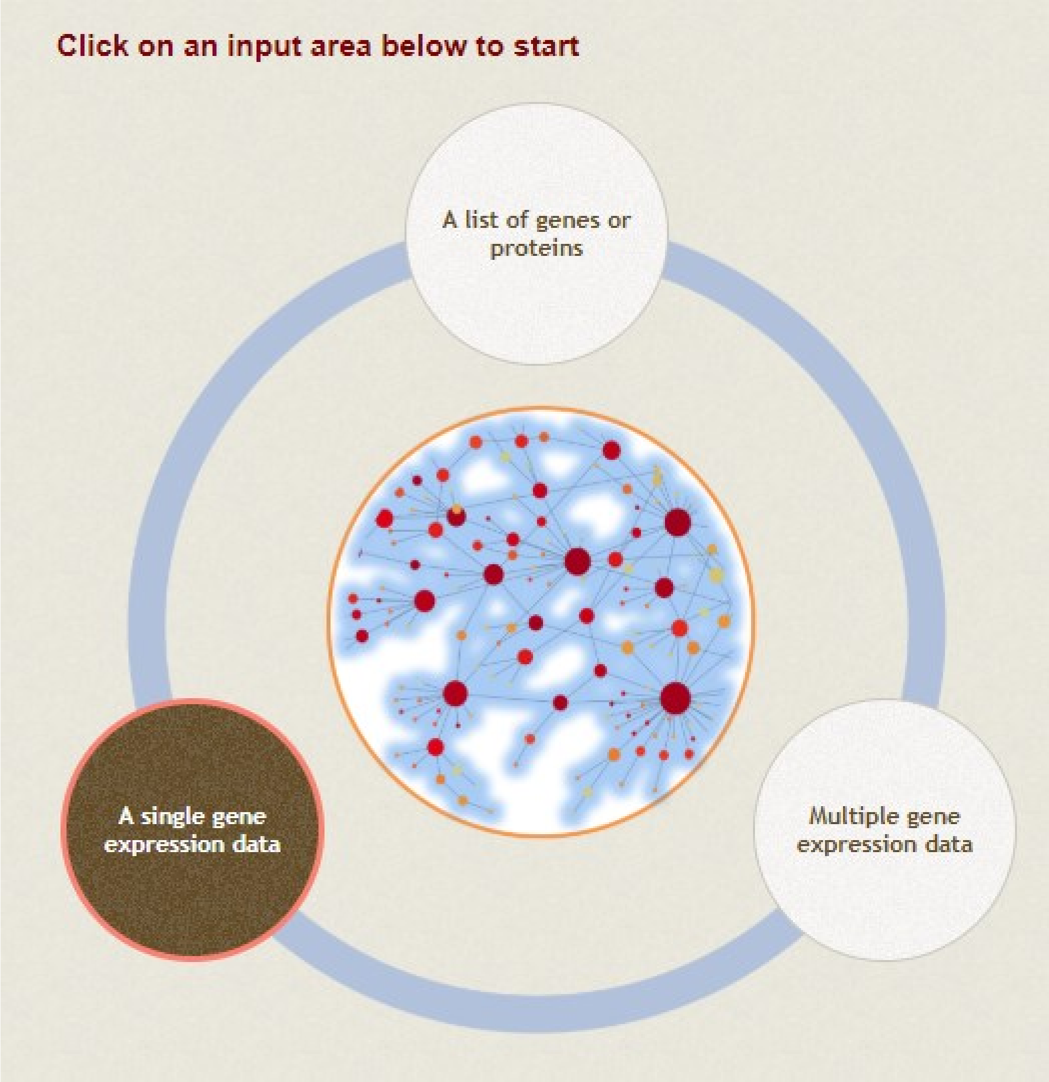
Algorithm: InfoMap

☐	Module	Size	Query	P-value	Color
☑	0	23	23	2.21e-05	🟦
☑	1	21	21	0.00454	🟩
☐	2	16	16	0.0395	
☐	3	14	14	2.32e-05	
☐	4	6	9	0.0447	
☐	5	9	9	0.259	
☐	6	8	8	0.0792	
☐	7	8	8	0.134	
☐	8	8	8	0.15	
☐	9	8	8	0.298	
☐	10	8	8	0.384	
☐	11	7	7	0.0425	
☐	12	7	7	0.0425	
☐	13	7	7	0.102	
☐	14	7	7	0.178	
☐	15	6	6	0.0248	
☐	16	6	6	0.0447	

Different colors for distinct modules

modules can be extracted to build new subnetworks

Data input II: A single gene expression data (raw data)



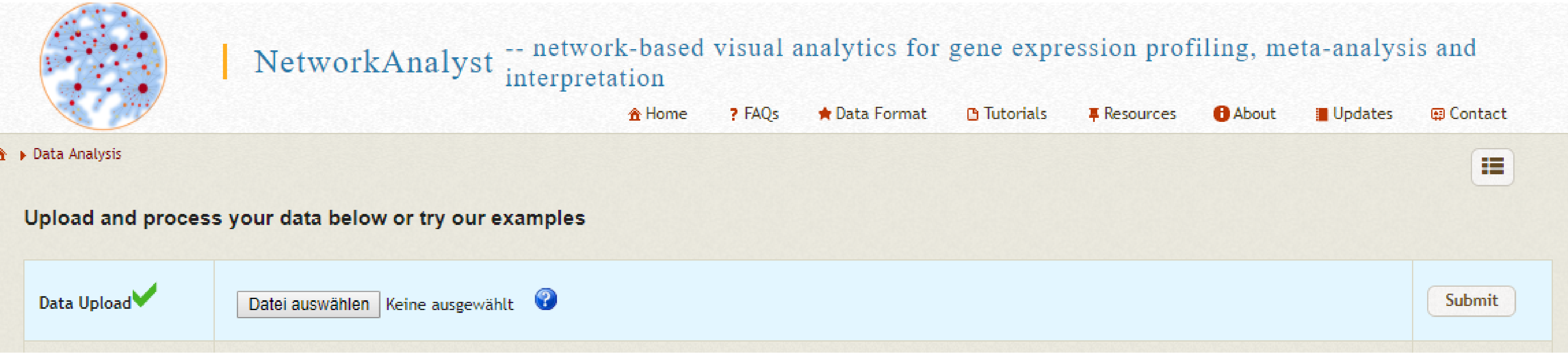
Click on an input area below to start

Input II: A single gene expression data (raw data)

The data has to be in the following format (adding: #NAME and #CLASS):

#NAME	Column2	Column3	Column4	Column5	Column6
#CLASS:EXP	C4-4BO	D4-4IL	E4-4PD	F4-4CON	C6-3BO
#CLASS:TREATMENT	IL-1a_PDGF	IL-1a	PDGF	control	IL-1a_PDGF
DDX11L1	0.424898092812381	0.700476587867491	0.314804949796422	0.964096737476719	0.395740854386969
CICP27	0.48738310646126	0.794771513157345	0.839479866123791	0.471569056374482	0.949778050528727
RP4-669L17.10	5.06128610555924	4.66086345004138	4.00064623699619	6.26662879359867	5.87015600674005
MTND1P23	78.6061471702905	74.1427526850513	52.9396990574316	74.4974315948043	271.623331089403
MTND2P28	643.233227504296	423.451568069511	365.016339288951	494.110057269182	229.358207840875
hsa-mir-6723	986.863311564944	869.466564690523	852.268817209271	1014.82708863025	1062.90716943615

Example data: Transition of smooth muscle cells from a contractile to a synthetic phenotype by IL-1 and PDGF



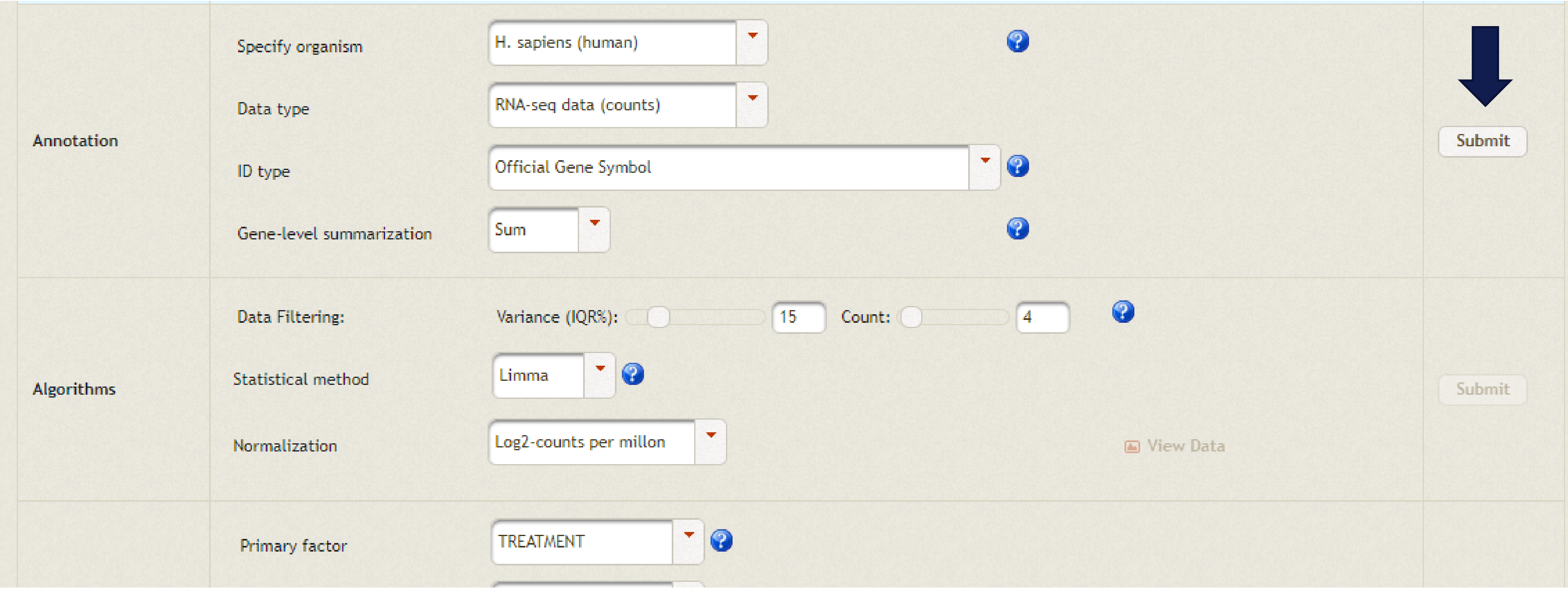
NetworkAnalyst -- network-based visual analytics for gene expression profiling, meta-analysis and interpretation

Upload and process your data below or try our examples

Data Upload ✓

Input of all the relevant parameter

Clicking on question marks provides very good support for chosing the correct options



Annotation

Specify organism: H. sapiens (human)

Data type: RNA-seq data (counts)

ID type: Official Gene Symbol

Gene-level summarization: Sum

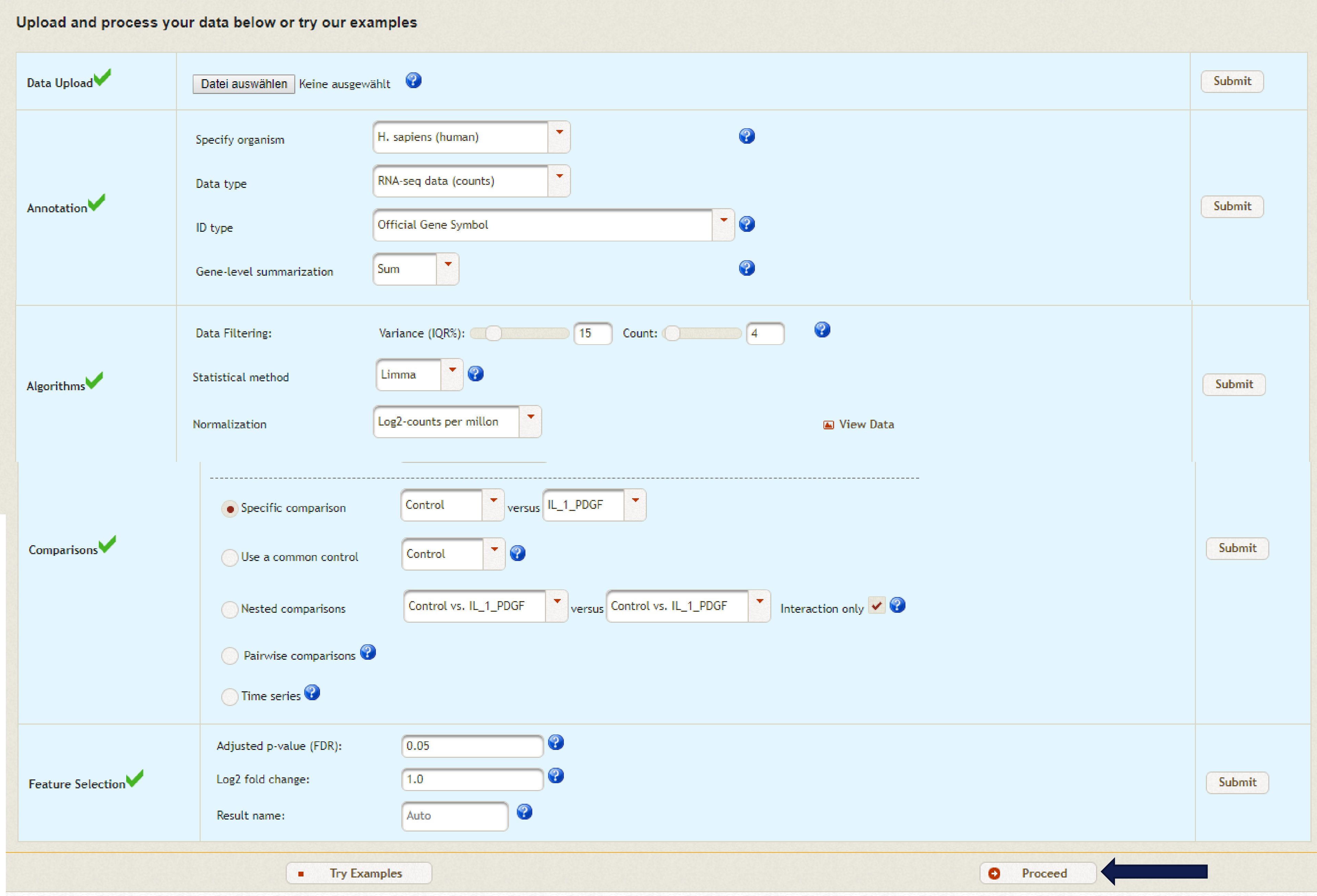
Algorithms

Data Filtering: Variance (IQR%): 15 Count: 4

Statistical method: Limma

Normalization: Log2-counts per millon

Primary factor: TREATMENT



Upload and process your data below or try our examples

Data Upload ✓

Datei auswählen Keine ausgewählt

Annotation ✓

Specify organism: H. sapiens (human)

Data type: RNA-seq data (counts)

ID type: Official Gene Symbol

Gene-level summarization: Sum

Algorithms ✓

Data Filtering: Variance (IQR%): 15 Count: 4

Statistical method: Limma

Normalization: Log2-counts per millon

Comparisons ✓

- ● Specific comparison: Control versus IL_1_PDGF
- ○ Use a common control: Control
- ○ Nested comparisons: Control vs. IL_1_PDGF versus Control vs. IL_1_PDGF Interaction only ☑
- ○ Pairwise comparisons
- ○ Time series

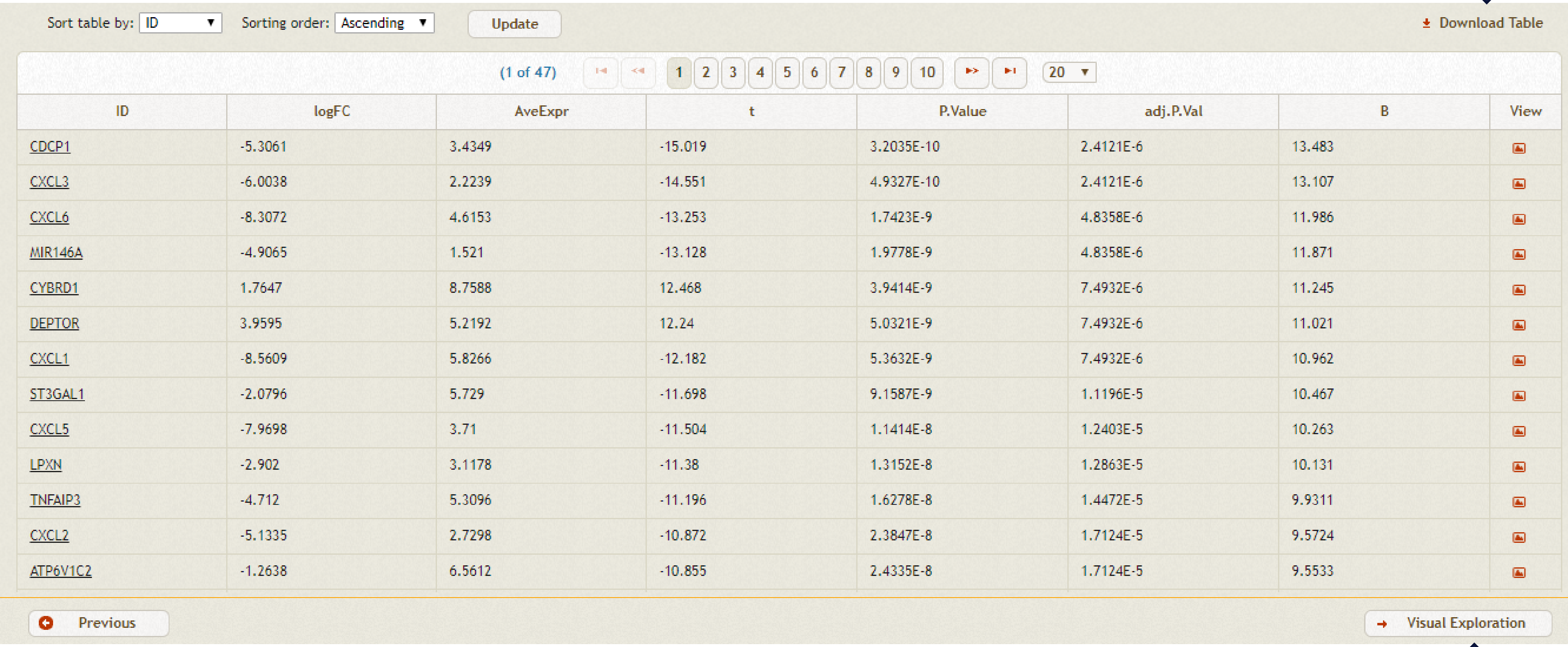
Feature Selection ✓

Adjusted p-value (FDR): 0.05

Log2 fold change: 1.0

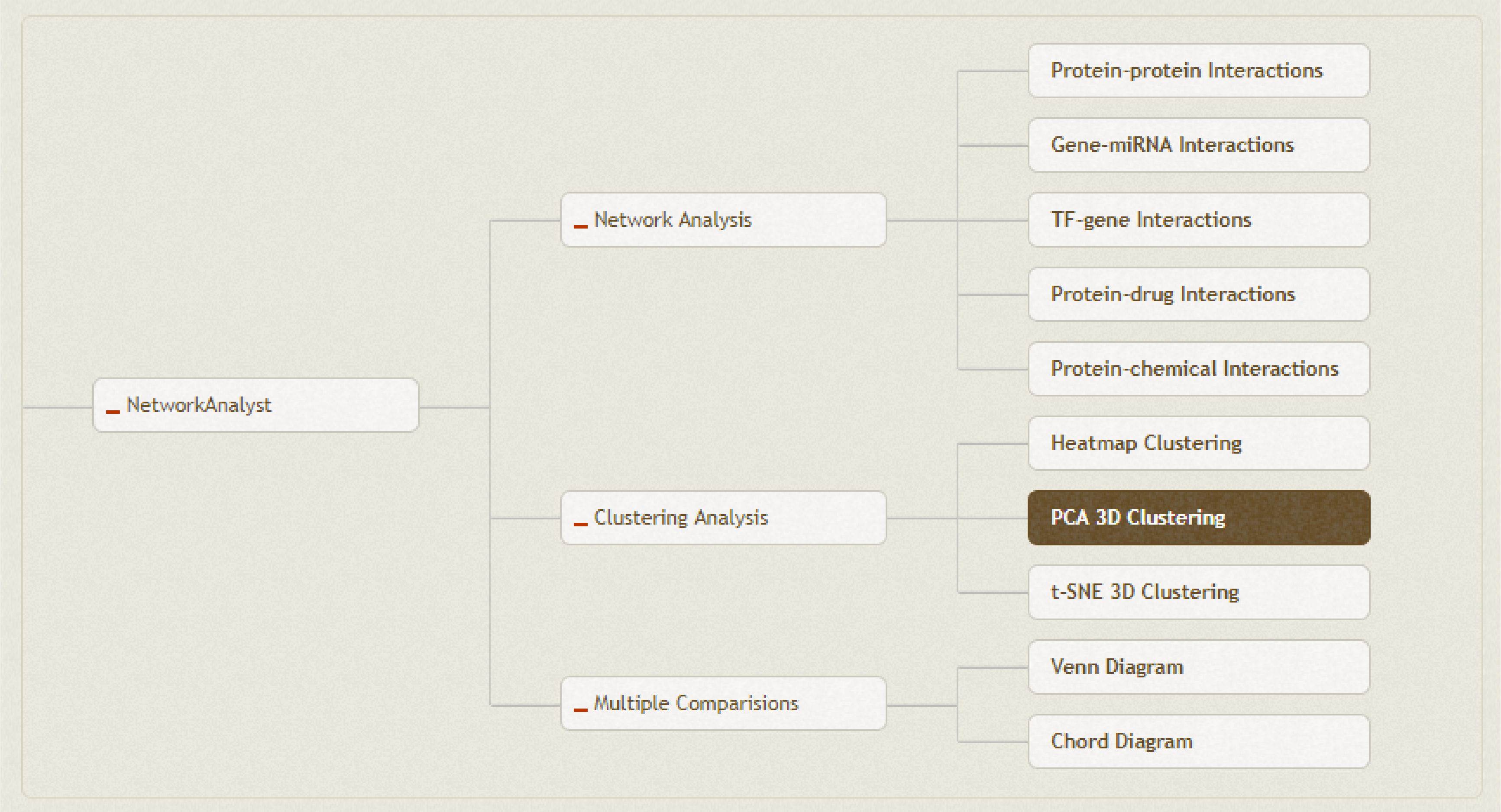
Result name: Auto

Results of differential gene expression analysis



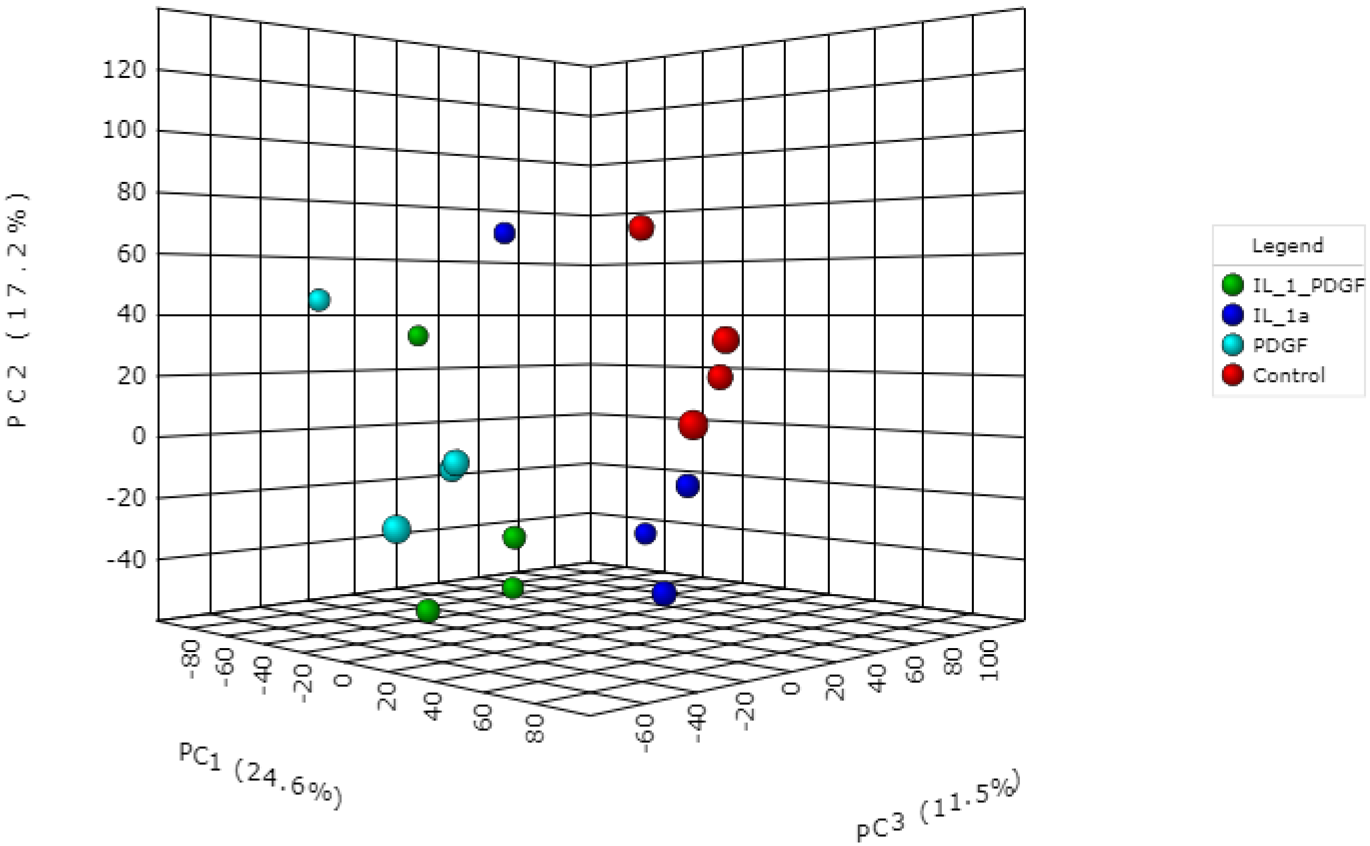
ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	View
CDCP1	-5.3061	3.4349	-15.019	3.2035E-10	2.4121E-6	13.483	🖼
CXCL3	-6.0038	2.2239	-14.551	4.9327E-10	2.4121E-6	13.107	🖼
CXCL6	-8.3072	4.6153	-13.253	1.7423E-9	4.8358E-6	11.986	🖼
MIR146A	-4.9065	1.521	-13.128	1.9778E-9	4.8358E-6	11.871	🖼
CYBRD1	1.7647	8.7588	12.468	3.9414E-9	7.4932E-6	11.245	🖼
DEPTOR	3.9595	5.2192	12.24	5.0321E-9	7.4932E-6	11.021	🖼
CXCL1	-8.5609	5.8266	-12.182	5.3632E-9	7.4932E-6	10.962	🖼
ST3GAL1	-2.0796	5.729	-11.698	9.1587E-9	1.1196E-5	10.467	🖼
CXCL5	-7.9698	3.71	-11.504	1.1414E-8	1.2403E-5	10.263	🖼
LPXN	-2.902	3.1178	-11.38	1.3152E-8	1.2863E-5	10.131	🖼
TNFAIP3	-4.712	5.3096	-11.196	1.6278E-8	1.4472E-5	9.9311	🖼
CXCL2	-5.1335	2.7298	-10.872	2.3847E-8	1.7124E-5	9.5724	🖼
ATP6V1C2	-1.2638	6.5612	-10.855	2.4335E-8	1.7124E-5	9.5533	🖼

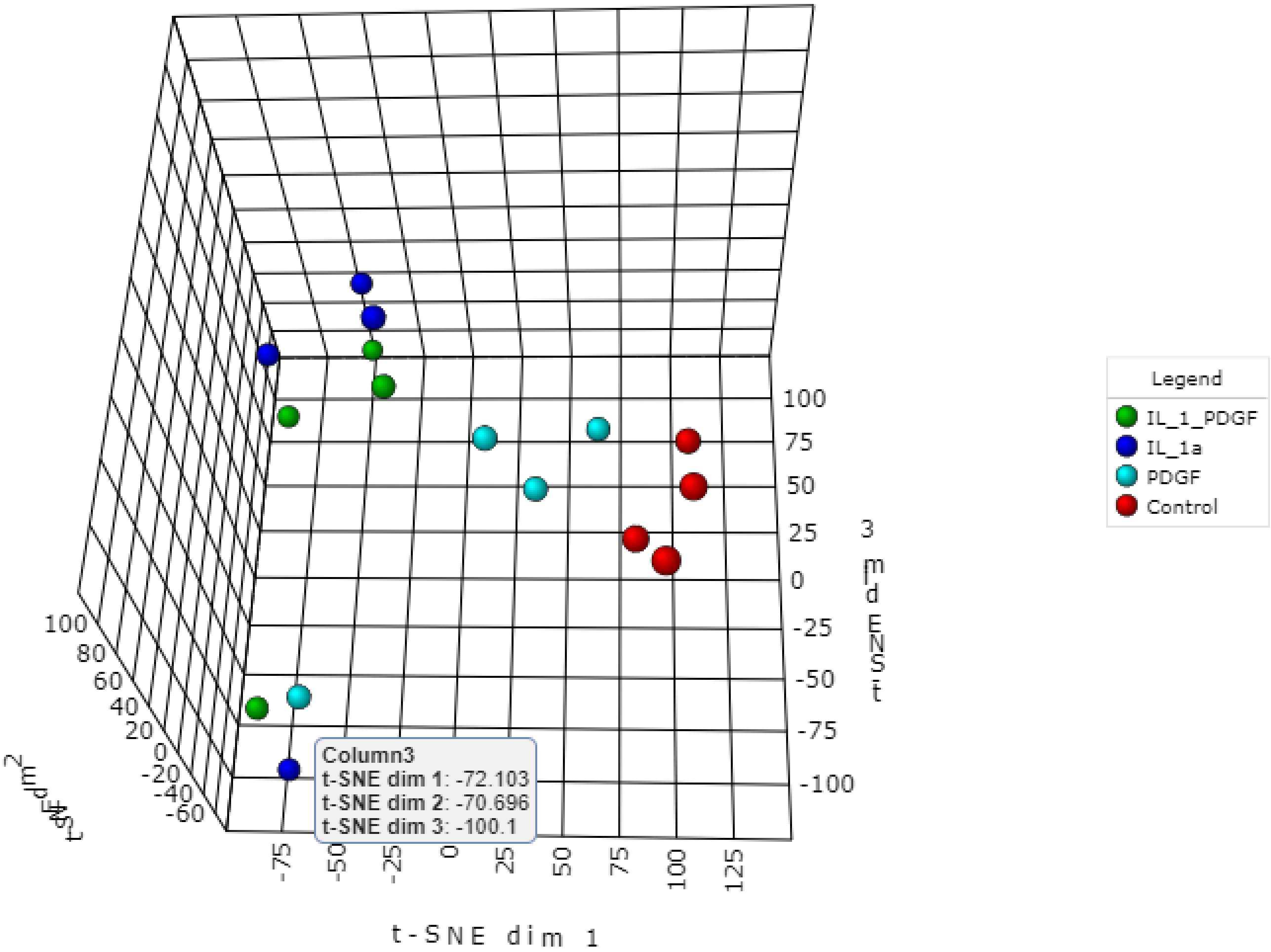
Diagnostics of the analysis



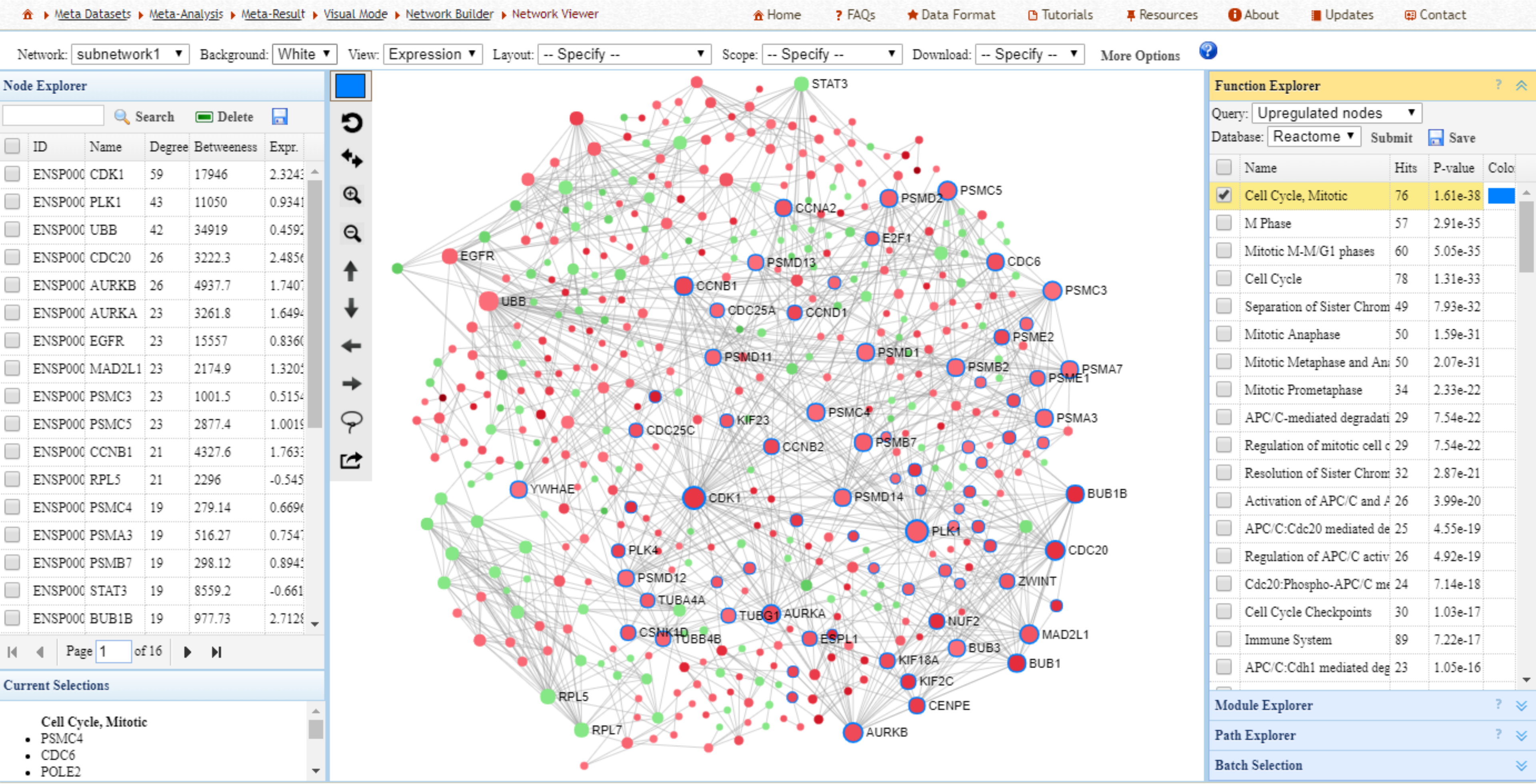
- NetworkAnalyst
  - Network Analysis
    - Protein-protein Interactions
    - Gene-miRNA Interactions
    - TF-gene Interactions
    - Protein-drug Interactions
    - Protein-chemical Interactions
  - Clustering Analysis
    - Heatmap Clustering
    - **PCA 3D Clustering**
    - t-SNE 3D Clustering
  - Multiple Comparisions
    - Venn Diagram
    - Chord Diagram

Principal component analysis (PCA)




Legend
IL_1_PDGF
IL_1a
PDGF
Control
Column3
t-SNE dim 1: -72.103
t-SNE dim 2: -70.696
t-SNE dim 3: -100.1
t-SNE dim 1
t-SNE dim 2
t-SNE dim 3
-75
-50
-25
0
25
50
75
100
125
100
80
60
40
20
0
-20
-40
-60
100
75
50
25
0
-25
-50
-75
-100

Protein interaction network



Network: subnetwork1 ▾ Background: White ▾ View: Expression ▾ Layout: -- Specify -- ▾ Scope: -- Specify -- ▾ Download: -- Specify -- ▾

Node Explorer

Search Delete

☐	ID	Name	Degree	Betweeness	Expr.
☐	ENSP000	CDK1	59	17946	2.324
☐	ENSP000	PLK1	43	11050	0.9341
☐	ENSP000	UBB	42	34919	0.459
☐	ENSP000	CDC20	26	3222.3	2.485
☐	ENSP000	AURKB	26	4937.7	1.740
☐	ENSP000	AURKA	23	3261.8	1.649
☐	ENSP000	EGFR	23	15557	0.836
☐	ENSP000	MAD2L1	23	2174.9	1.320
☐	ENSP000	PSMC3	23	1001.5	0.515
☐	ENSP000	PSMC5	23	2877.4	1.001
☐	ENSP000	CCNB1	21	4327.6	1.763
☐	ENSP000	RPL5	21	2296	-0.545
☐	ENSP000	PSMC4	19	279.14	0.669
☐	ENSP000	PSMA3	19	516.27	0.754
☐	ENSP000	PSMB7	19	298.12	0.894
☐	ENSP000	STAT3	19	8559.2	-0.661
☐	ENSP000	BUB1B	19	977.73	2.712

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Current Selections

Cell Cycle, Mitotic

- PSMC4
- CDC6
- POLE2

Function Explorer

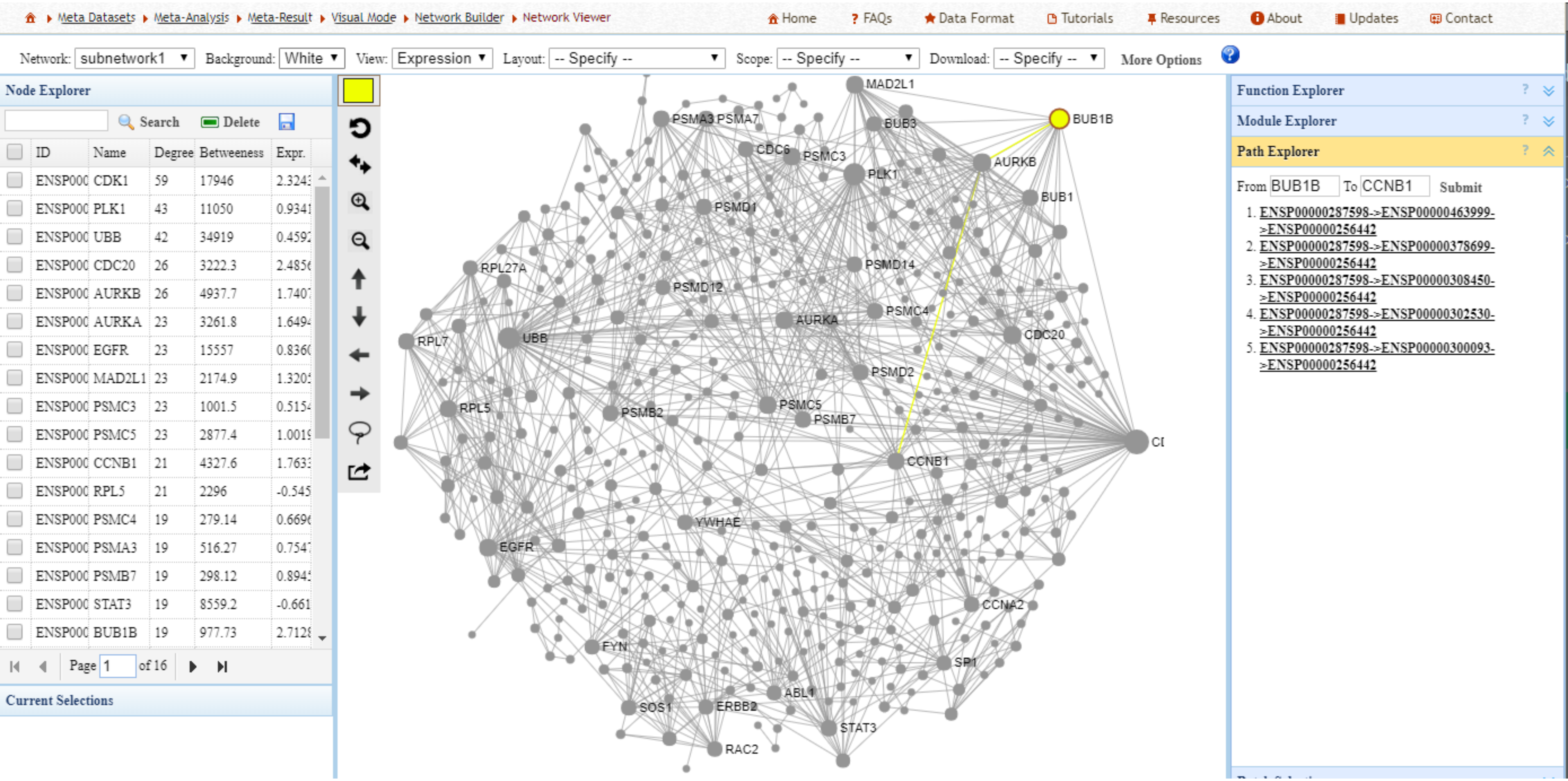
Query: Upregulated nodes ▾

Database: Reactome ▾ Submit Save

☐	Name	Hits	P-value	Colo
☑	Cell Cycle, Mitotic	76	1.61e-38	🟦
☐	M Phase	57	2.91e-35	
☐	Mitotic M-M/G1 phases	60	5.05e-35	
☐	Cell Cycle	78	1.31e-33	
☐	Separation of Sister Chrom	49	7.93e-32	
☐	Mitotic Anaphase	50	1.59e-31	
☐	Mitotic Metaphase and An	50	2.07e-31	
☐	Mitotic Prometaphase	34	2.33e-22	
☐	APC/C-mediated degradati	29	7.54e-22	
☐	Regulation of mitotic cell c	29	7.54e-22	
☐	Resolution of Sister Chrom	32	2.87e-21	
☐	Activation of APC/C and	26	3.99e-20	
☐	APC/C:Cdc20 mediated de	25	4.55e-19	
☐	Regulation of APC/C activ	26	4.92e-19	
☐	Cdc20:Phospho-APC/C me	24	7.14e-18	
☐	Cell Cycle Checkpoints	30	1.03e-17	
☐	Immune System	89	7.22e-17	
☐	APC/C:Cdh1 mediated deg	23	1.05e-16	

Path Explorer

…defines the shortest path between two nodes



Network: subnetwork1 ▾ Background: White ▾ View: Expression ▾ Layout: -- Specify -- ▾ Scope: -- Specify -- ▾ Download: -- Specify -- ▾

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	ENSP000	CDK1	59	17946	2.324
☐	ENSP000	PLK1	43	11050	0.9341
☐	ENSP000	UBB	42	34919	0.459
☐	ENSP000	CDC20	26	3222.3	2.485
☐	ENSP000	AURKB	26	4937.7	1.740
☐	ENSP000	AURKA	23	3261.8	1.649
☐	ENSP000	EGFR	23	15557	0.836
☐	ENSP000	MAD2L1	23	2174.9	1.320
☐	ENSP000	PSMC3	23	1001.5	0.515
☐	ENSP000	PSMC5	23	2877.4	1.001
☐	ENSP000	CCNB1	21	4327.6	1.763
☐	ENSP000	RPL5	21	2296	-0.545
☐	ENSP000	PSMC4	19	279.14	0.669
☐	ENSP000	PSMA3	19	516.27	0.754
☐	ENSP000	PSMB7	19	298.12	0.894
☐	ENSP000	STAT3	19	8559.2	-0.661
☐	ENSP000	BUB1B	19	977.73	2.712

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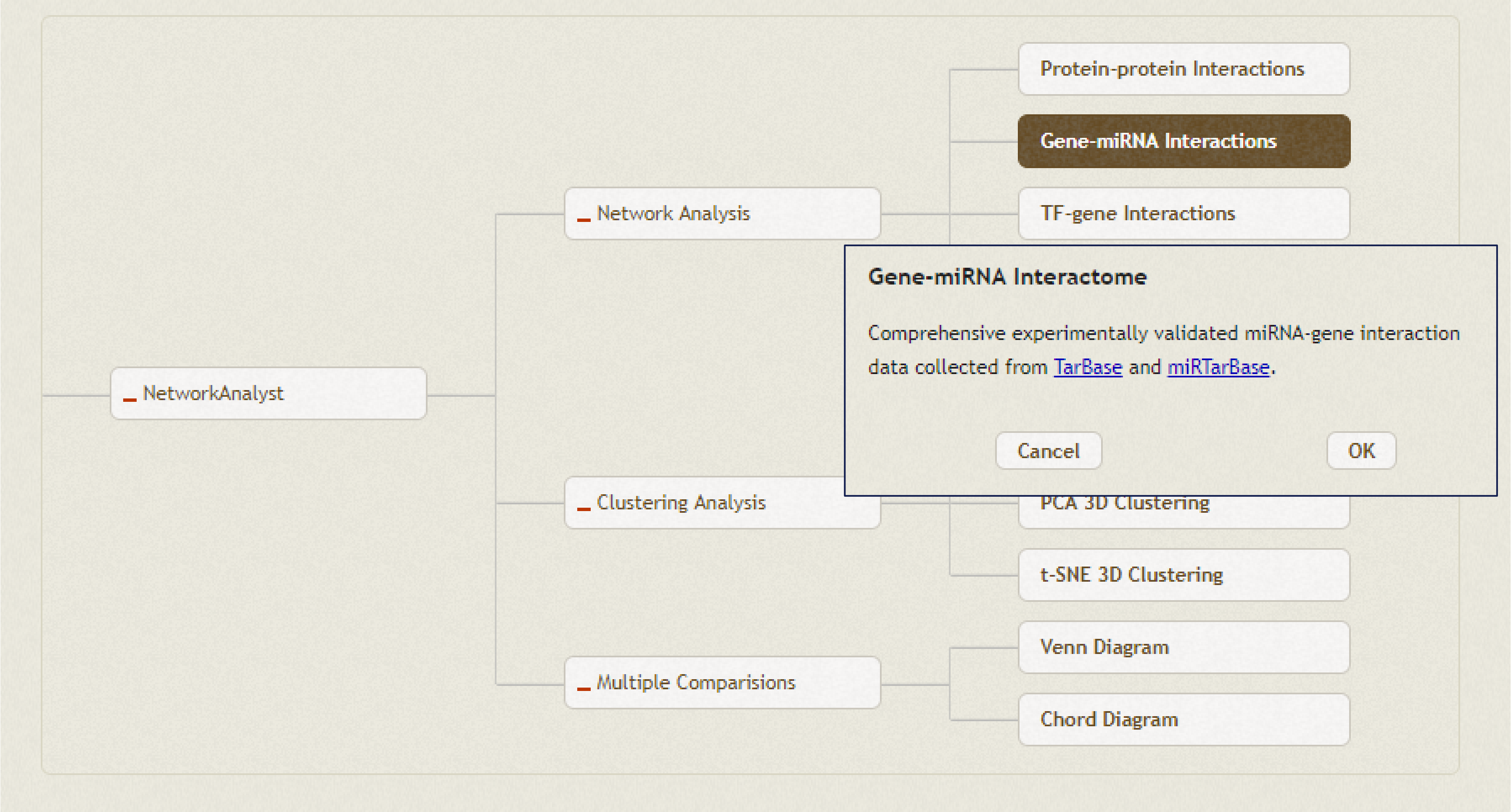
Current Selections

Path Explorer

From BUB1B To CCNB1 Submit

1. ENSP00000287598->ENSP00000463999->ENSP00000256442
2. ENSP00000287598->ENSP00000378699->ENSP00000256442
3. ENSP00000287598->ENSP00000308450->ENSP00000256442
4. ENSP00000287598->ENSP00000302530->ENSP00000256442
5. ENSP00000287598->ENSP00000300093->ENSP00000256442

New visual mode:

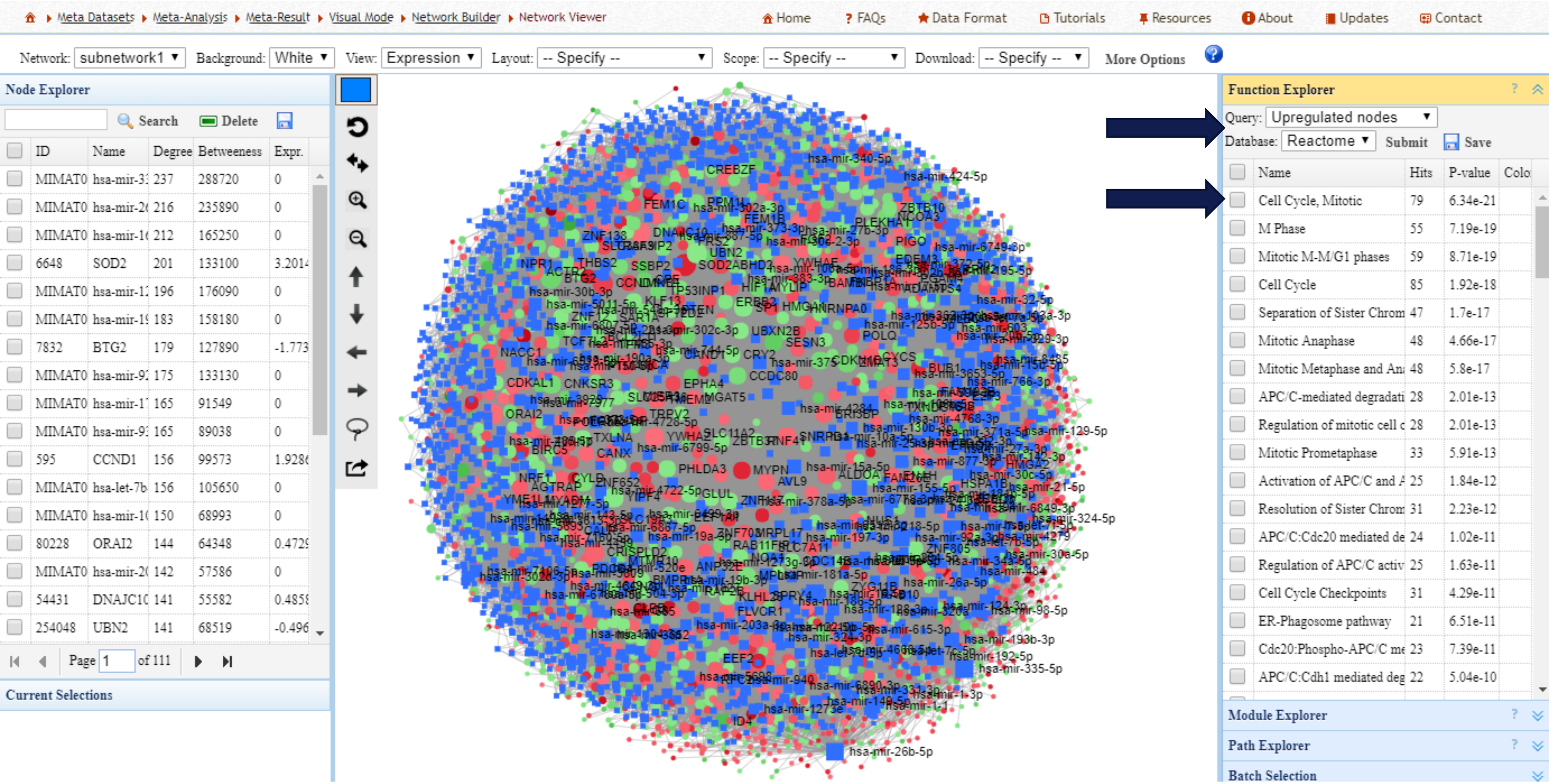


Gene-miRNA Interactome

Comprehensive experimentally validated miRNA-gene interaction data collected from TarBase and miRTarBase.

Gene-miRNA network

Function explorer often leads to very similar results as the protein interaction network analysis



Network: subnetwork1 ▼ Background: White ▼ View: Expression ▼ Layout: -- Specify -- ▼ Scope: -- Specify -- ▼ Download: -- Specify -- ▼

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	MIMAT0	hsa-mir-3:	237	288720	0
☐	MIMAT0	hsa-mir-2(	216	235890	0
☐	MIMAT0	hsa-mir-1(	212	165250	0
☐	6648	SOD2	201	133100	3.2014
☐	MIMAT0	hsa-mir-1:	196	176090	0
☐	MIMAT0	hsa-mir-1!	183	158180	0
☐	7832	BTG2	179	127890	-1.773
☐	MIMAT0	hsa-mir-9:	175	133130	0
☐	MIMAT0	hsa-mir-1'	165	91549	0
☐	MIMAT0	hsa-mir-9:	165	89038	0
☐	595	CCND1	156	99573	1.9286
☐	MIMAT0	hsa-let-7b	156	105650	0
☐	MIMAT0	hsa-mir-1(	150	68993	0
☐	80228	ORAI2	144	64348	0.4729
☐	MIMAT0	hsa-mir-2(	142	57586	0
☐	54431	DNAJC1(	141	55582	0.4858
☐	254048	UBN2	141	68519	-0.496

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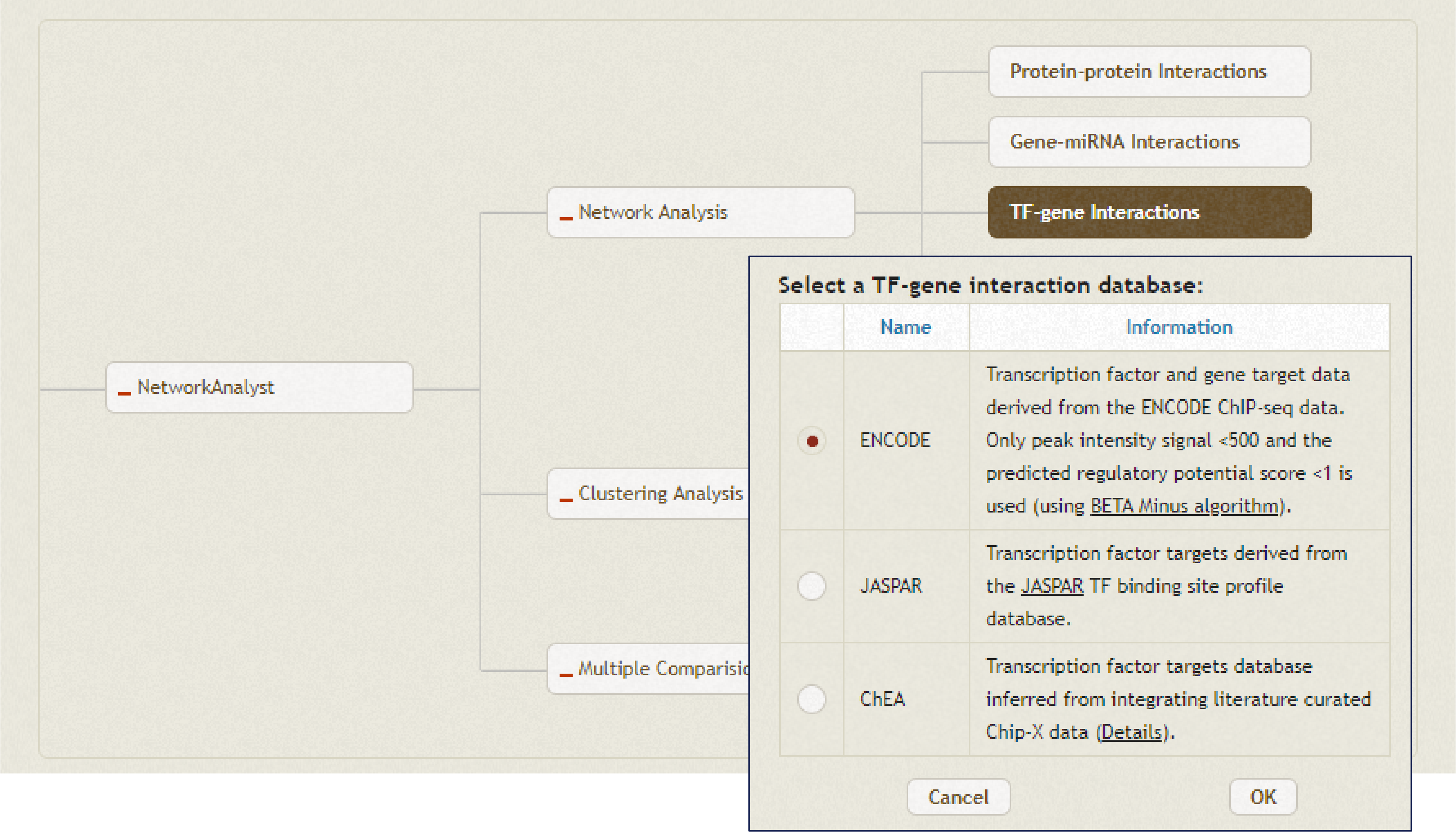
Function Explorer

Query: Upregulated nodes ▼
Database: Reactome ▼

☐	Name	Hits	P-value	Colo
☐	Cell Cycle, Mitotic	79	6.34e-21	
☐	M Phase	55	7.19e-19	
☐	Mitotic M-M/G1 phases	59	8.71e-19	
☐	Cell Cycle	85	1.92e-18	
☐	Separation of Sister Chrom	47	1.7e-17	
☐	Mitotic Anaphase	48	4.66e-17	
☐	Mitotic Metaphase and An:	48	5.8e-17	
☐	APC/C-mediated degradati	28	2.01e-13	
☐	Regulation of mitotic cell c	28	2.01e-13	
☐	Mitotic Prometaphase	33	5.91e-13	
☐	Activation of APC/C and A	25	1.84e-12	
☐	Resolution of Sister Chrom	31	2.23e-12	
☐	APC/C:Cdc20 mediated de	24	1.02e-11	
☐	Regulation of APC/C activ	25	1.63e-11	
☐	Cell Cycle Checkpoints	31	4.29e-11	
☐	ER-Phagosome pathway	21	6.51e-11	
☐	Cdc20:Phospho-APC/C me	23	7.39e-11	
☐	APC/C:Cdh1 mediated deg	22	5.04e-10	

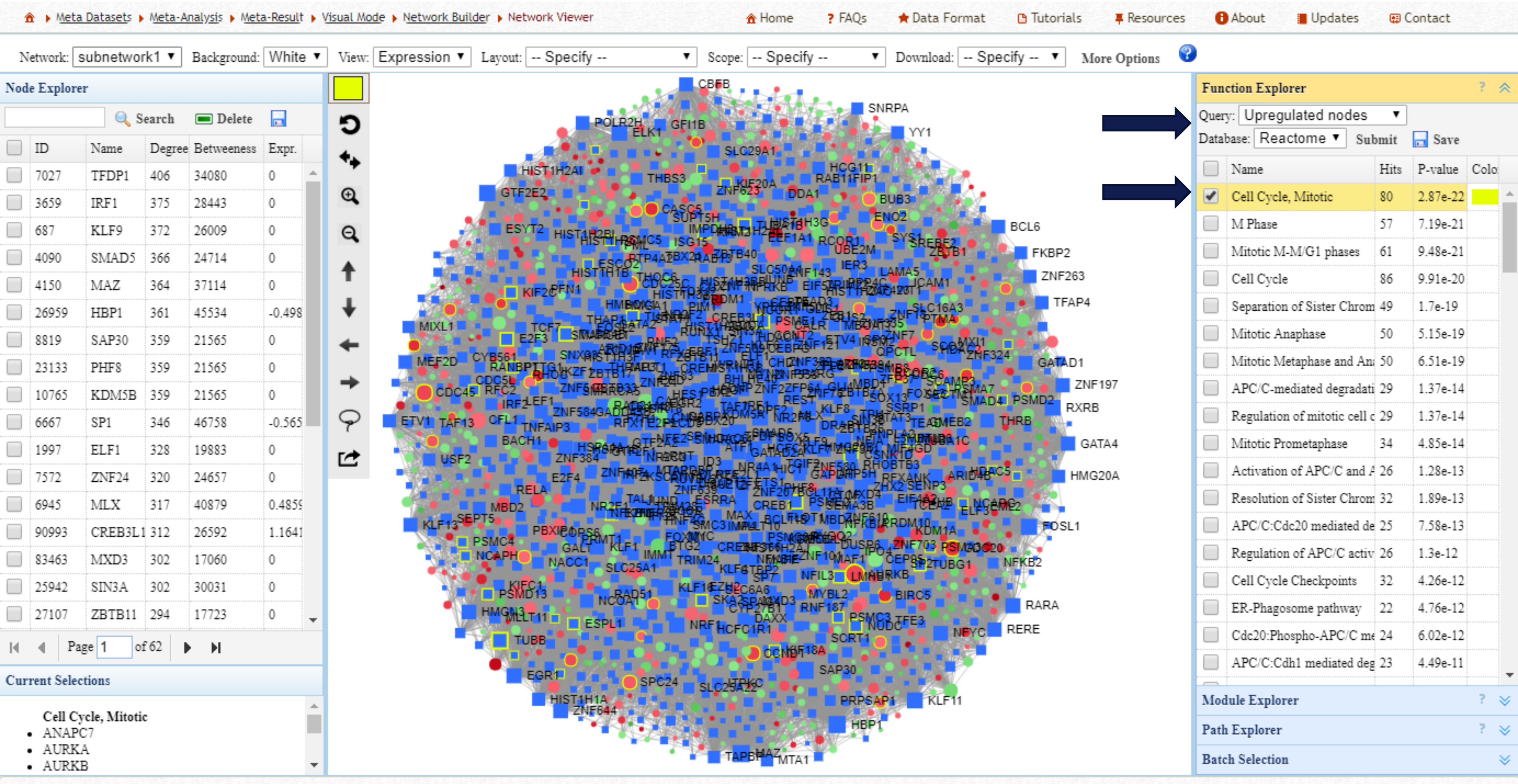
Transcription factor – gene interaction network



Select a TF-gene interaction database:

	Name	Information
●	ENCODE	Transcription factor and gene target data derived from the ENCODE ChIP-seq data. Only peak intensity signal <500 and the predicted regulatory potential score <1 is used (using BETA Minus algorithm).
○	JASPAR	Transcription factor targets derived from the JASPAR TF binding site profile database.
○	ChEA	Transcription factor targets database inferred from integrating literature curated Chip-X data (Details).

Transcription factor – gene interaction network



Meta Datasets ▸ Meta-Analysis ▸ Meta-Result ▸ Visual Mode ▸ Network Builder ▸ Network Viewer

Home | ? FAQs | Data Format | Tutorials | Resources | About | Updates | Contact

Network: subnetwork1 ▾ Background: White ▾ View: Expression ▾ Layout: -- Specify -- ▾ Scope: -- Specify -- ▾ Download: -- Specify -- ▾ More Options

Node Explorer

Search | Delete

☐	ID	Name	Degree	Betweeness	Expr.
☐	7027	TFDP1	406	34080	0
☐	3659	IRF1	375	28443	0
☐	687	KLF9	372	26009	0
☐	4090	SMAD5	366	24714	0
☐	4150	MAZ	364	37114	0
☐	26959	HBP1	361	45534	-0.498
☐	8819	SAP30	359	21565	0
☐	23133	PHF8	359	21565	0
☐	10765	KDM5B	359	21565	0
☐	6667	SP1	346	46758	-0.565
☐	1997	ELF1	328	19883	0
☐	7572	ZNF24	320	24657	0
☐	6945	MLX	317	40879	0.4859
☐	90993	CREB3L1	312	26592	1.1641
☐	83463	MXD3	302	17060	0
☐	25942	SIN3A	302	30031	0
☐	27107	ZBTB11	294	17723	0

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Current Selections

Cell Cycle, Mitotic
- ANAPC7
- AURKA
- AURKB

Function Explorer

Query: Upregulated nodes ▾

Database: Reactome ▾ Submit Save

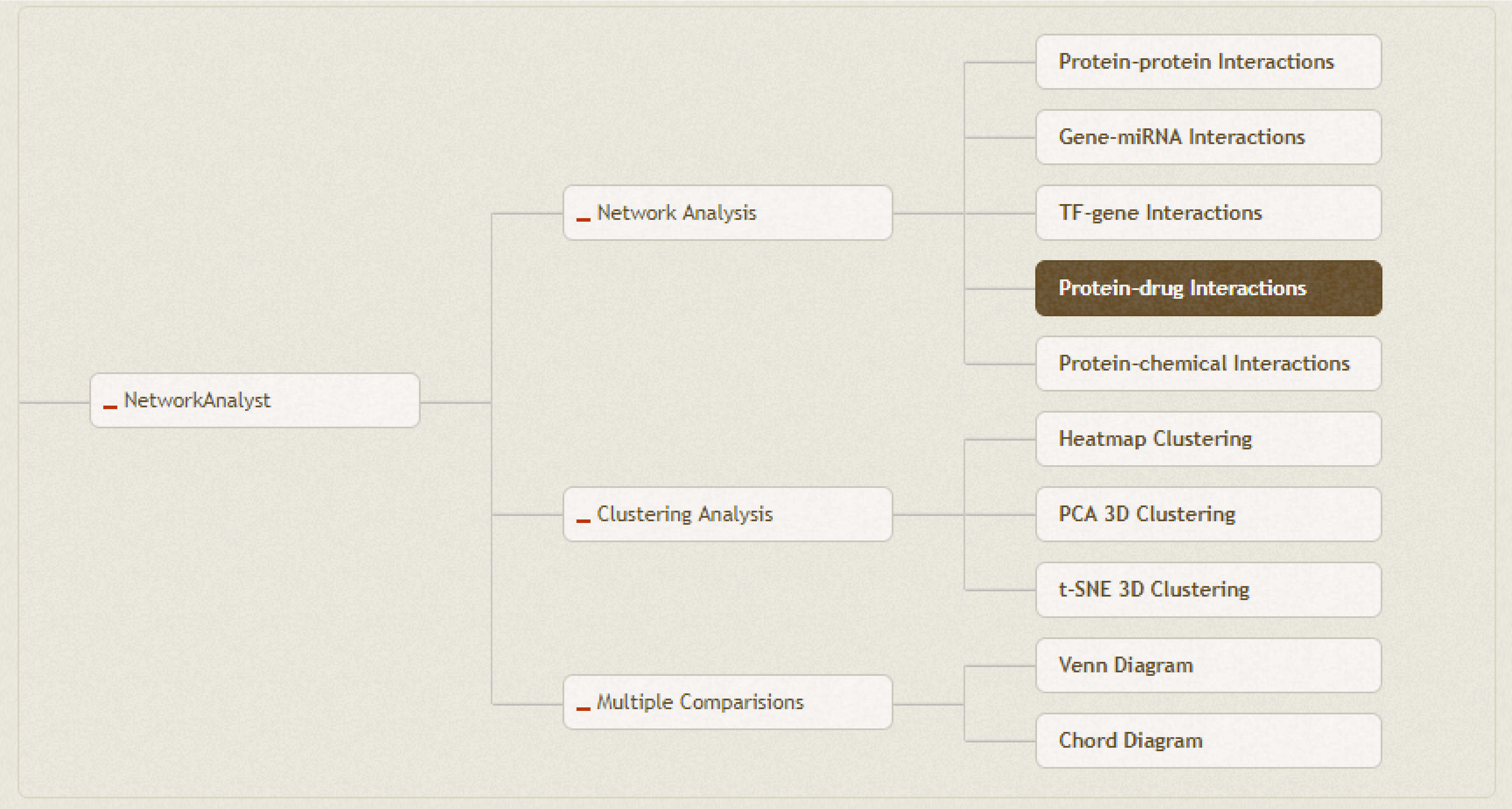
☐	Name	Hits	P-value	Colo
☑	Cell Cycle, Mitotic	80	2.87e-22	🟨
☐	M Phase	57	7.19e-21	
☐	Mitotic M-M/G1 phases	61	9.48e-21	
☐	Cell Cycle	86	9.91e-20	
☐	Separation of Sister Chrom	49	1.7e-19	
☐	Mitotic Anaphase	50	5.15e-19	
☐	Mitotic Metaphase and Ana	50	6.51e-19	
☐	APC/C-mediated degradati	29	1.37e-14	
☐	Regulation of mitotic cell c	29	1.37e-14	
☐	Mitotic Prometaphase	34	4.85e-14	
☐	Activation of APC/C and A	26	1.28e-13	
☐	Resolution of Sister Chrom	32	1.89e-13	
☐	APC/C:Cdc20 mediated de	25	7.58e-13	
☐	Regulation of APC/C activ	26	1.3e-12	
☐	Cell Cycle Checkpoints	32	4.26e-12	
☐	ER-Phagosome pathway	22	4.76e-12	
☐	Cdc20:Phospho-APC/C me	24	6.02e-12	
☐	APC/C:Cdh1 mediated deg	23	4.49e-11	

Module Explorer

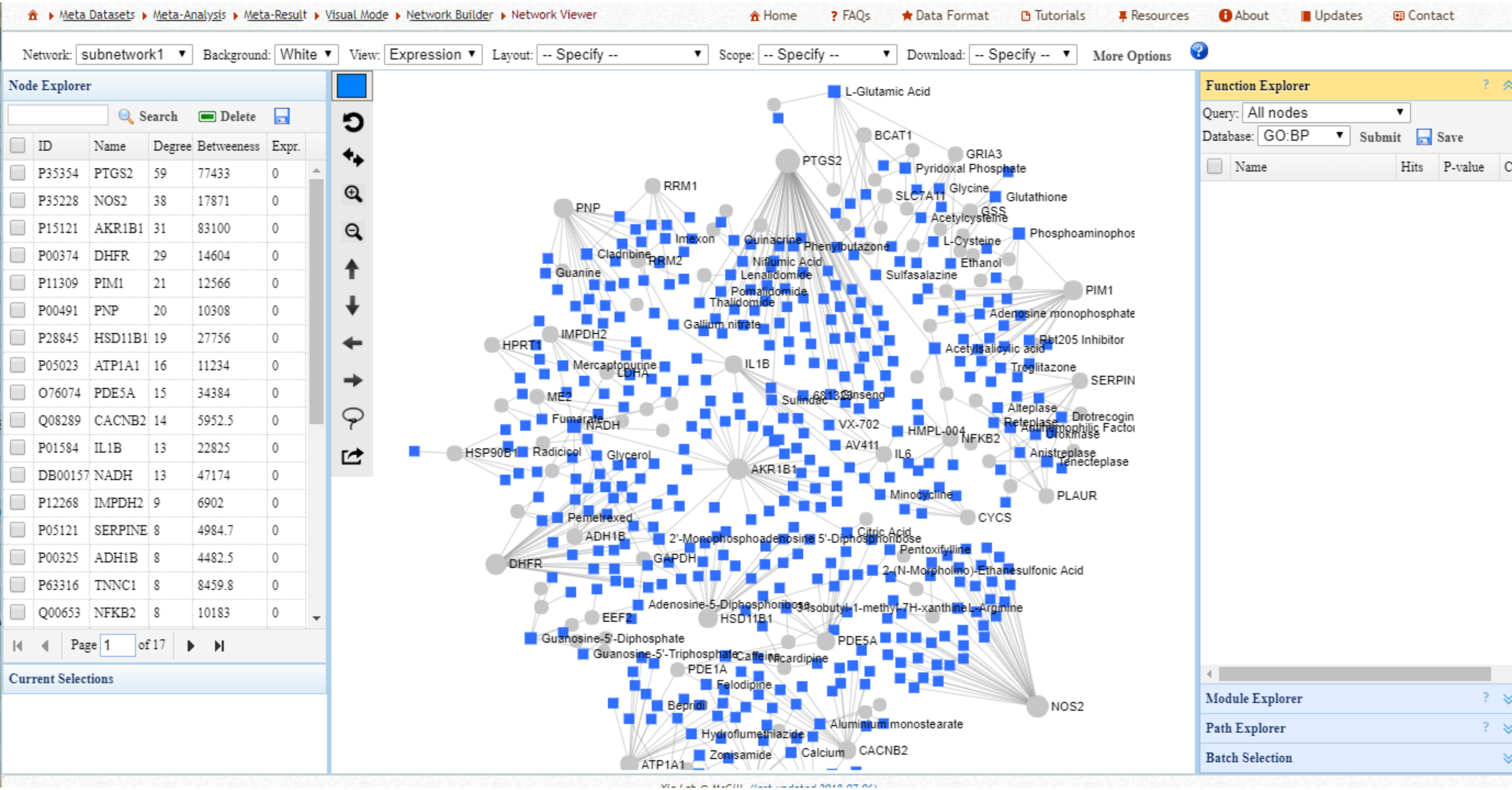
Path Explorer

Batch Selection

Protein – drug interaction network



Protein – drug interaction network



Network: subnetwork1 ▾ Background: White ▾ View: Expression ▾ Layout: -- Specify -- ▾ Scope: -- Specify -- ▾ Download: -- Specify -- ▾

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	P35354	PTGS2	59	77433	0
☐	P35228	NOS2	38	17871	0
☐	P15121	AKR1B1	31	83100	0
☐	P00374	DHFR	29	14604	0
☐	P11309	PIM1	21	12566	0
☐	P00491	PNP	20	10308	0
☐	P28845	HSD11B1	19	27756	0
☐	P05023	ATP1A1	16	11234	0
☐	O76074	PDE5A	15	34384	0
☐	Q08289	CACNB2	14	5952.5	0
☐	P01584	IL1B	13	22825	0
☐	DB00157	NADH	13	47174	0
☐	P12268	IMPDH2	9	6902	0
☐	P05121	SERPINE	8	4984.7	0
☐	P00325	ADH1B	8	4482.5	0
☐	P63316	TNNC1	8	8459.8	0
☐	Q00653	NFKB2	8	10183	0

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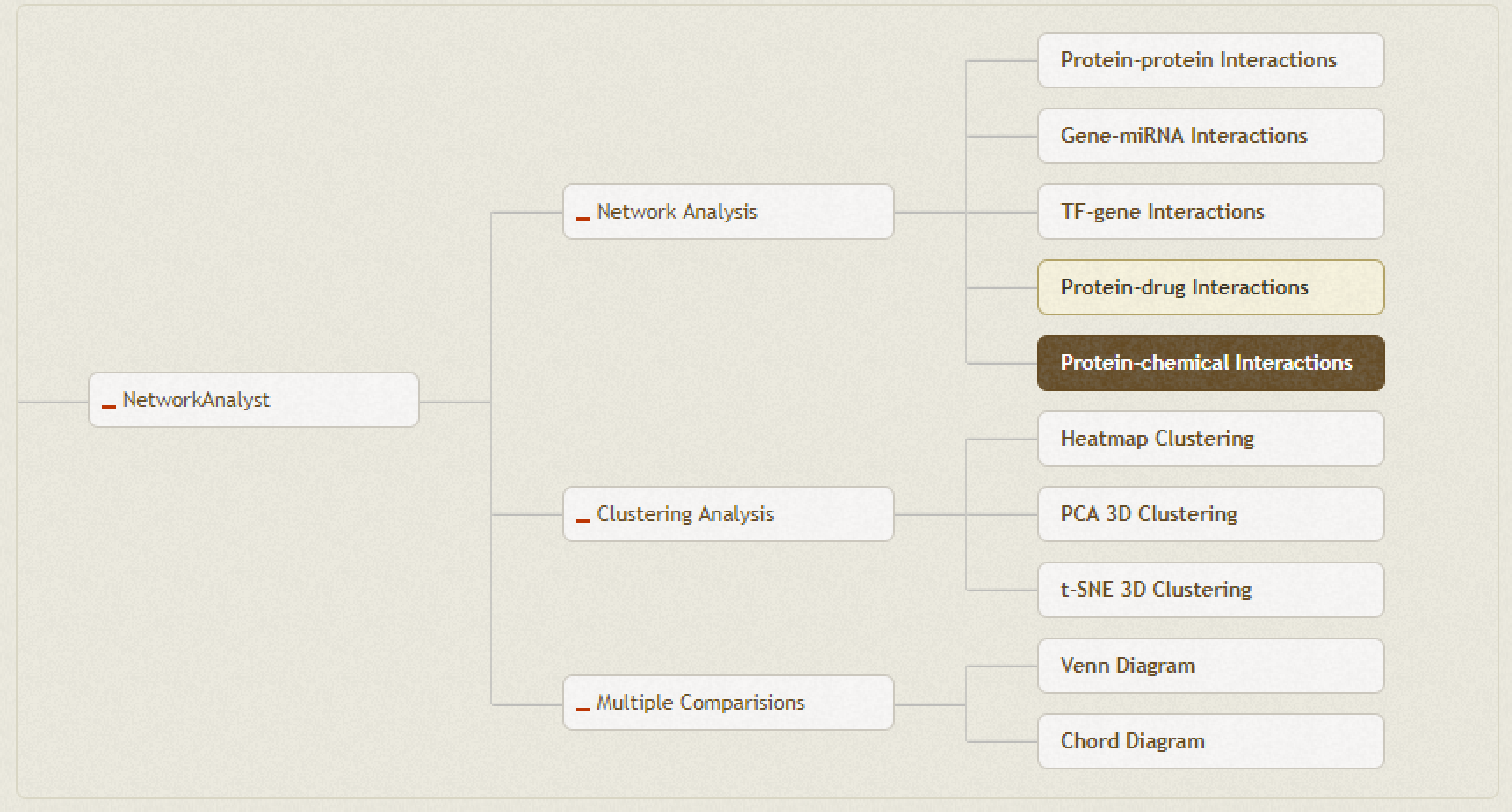
Current Selections

Function Explorer

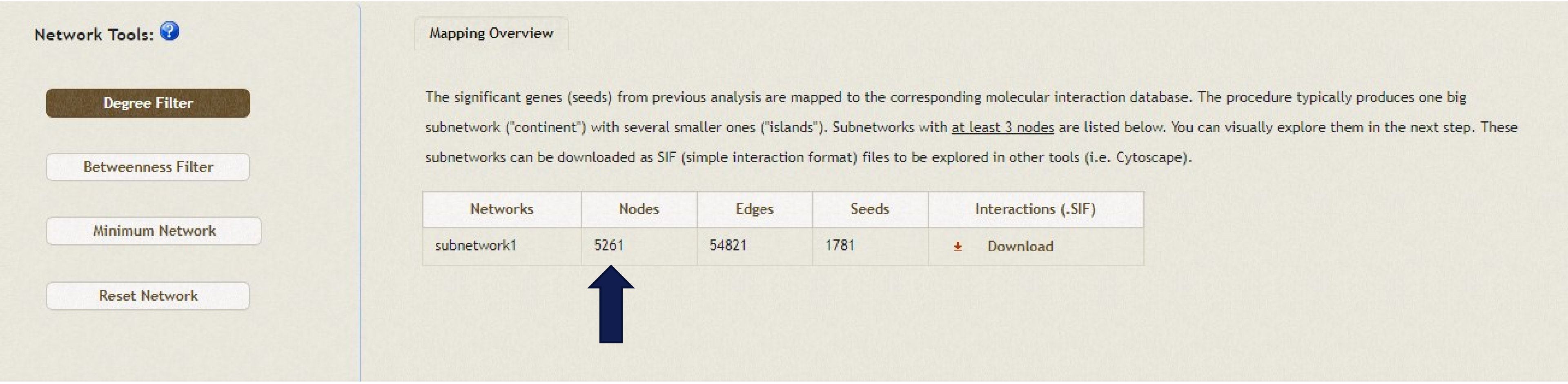
Query: All nodes ▾
Database: GO:BP ▾

☐	Name	Hits	P-value

Protein – chemical interaction network

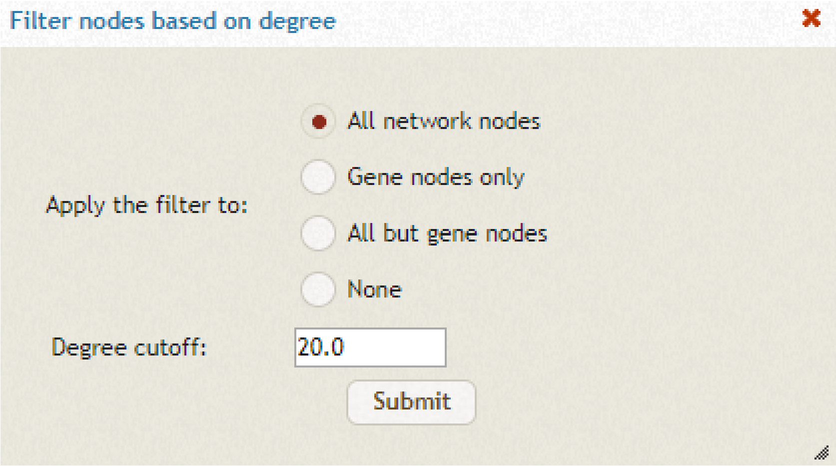


Reduction of complexity by using filters



The significant genes (seeds) from previous analysis are mapped to the corresponding molecular interaction database. The procedure typically produces one big subnetwork ("continent") with several smaller ones ("islands"). Subnetworks with at least 3 nodes are listed below. You can visually explore them in the next step. These subnetworks can be downloaded as SIF (simple interaction format) files to be explored in other tools (i.e. Cytoscape).

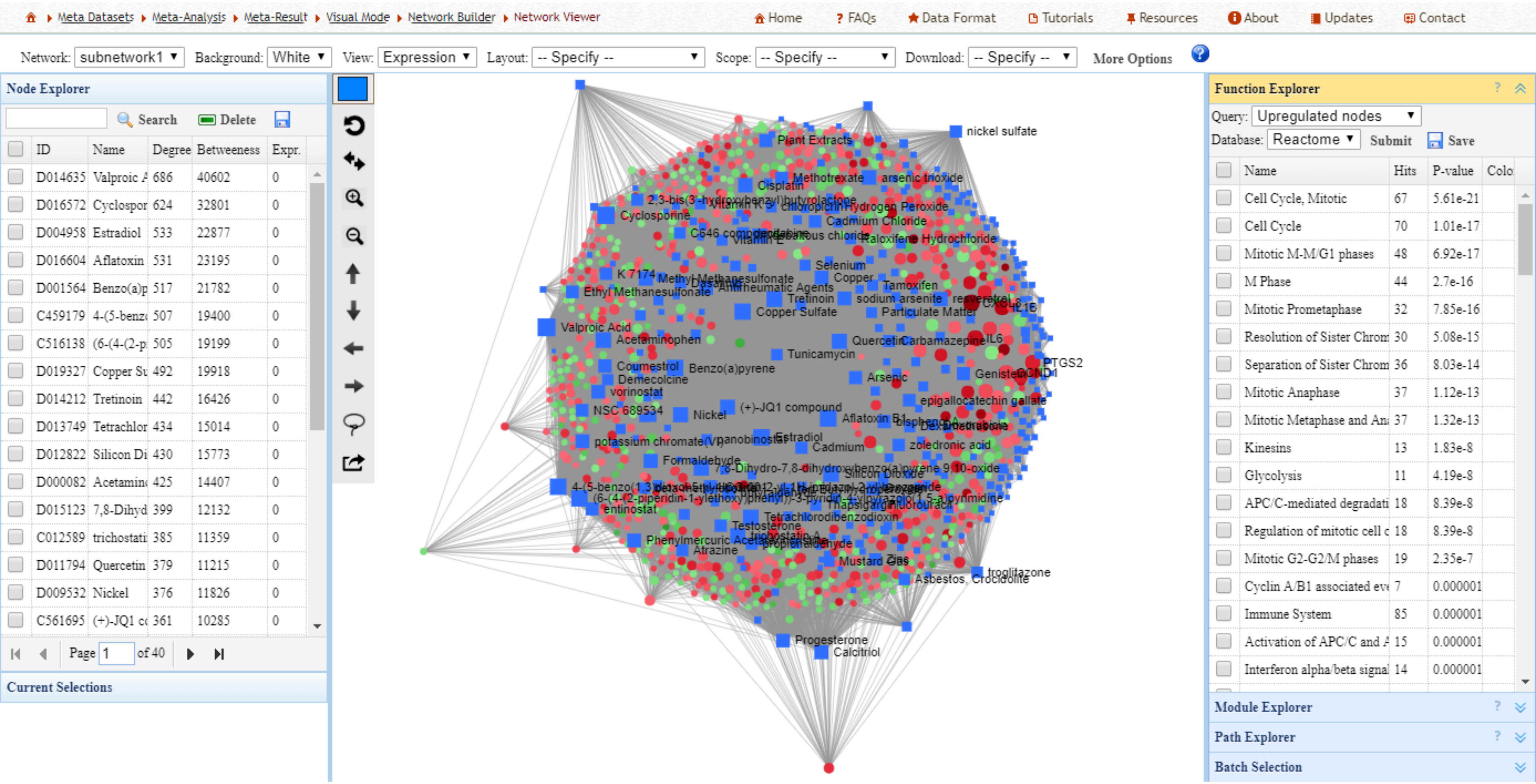
Networks	Nodes	Edges	Seeds	Interactions (.SIF)
subnetwork1	5261	54821	1781	Download



Apply the filter to:
● All network nodes
○ Gene nodes only
○ All but gene nodes
○ None

Degree cutoff: 20.0

Protein – chemical interaction network



Meta Datasets ▸ Meta-Analysis ▸ Meta-Result ▸ Visual Mode ▸ Network Builder ▸ Network Viewer

Network: subnetwork1 ▾ Background: White ▾ View: Expression ▾ Layout: -- Specify -- ▾ Scope: -- Specify -- ▾ Download: -- Specify -- ▾ More Options

Node Explorer

☐	ID	Name	Degree	Betweeness	Expr.
☐	D014635	Valproic A	686	40602	0
☐	D016572	Cyclospor	624	32801	0
☐	D004958	Estradiol	533	22877	0
☐	D016604	Aflatoxin	531	23195	0
☐	D001564	Benzo(a)p	517	21782	0
☐	C459179	4-(5-benz	507	19400	0
☐	C516138	(6-(4-(2-p	505	19199	0
☐	D019327	Copper Su	492	19918	0
☐	D014212	Tretinoin	442	16426	0
☐	D013749	Tetrachlor	434	15014	0
☐	D012822	Silicon Di	430	15773	0
☐	D000082	Acetamin	425	14407	0
☐	D015123	7,8-Dihyd	399	12132	0
☐	C012589	trichostati	385	11359	0
☐	D011794	Quercetin	379	11215	0
☐	D009532	Nickel	376	11826	0
☐	C561695	(+)-JQ1 cc	361	10285	0

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Current Selections

Function Explorer

Query: Upregulated nodes ▾

Database: Reactome ▾ Submit Save

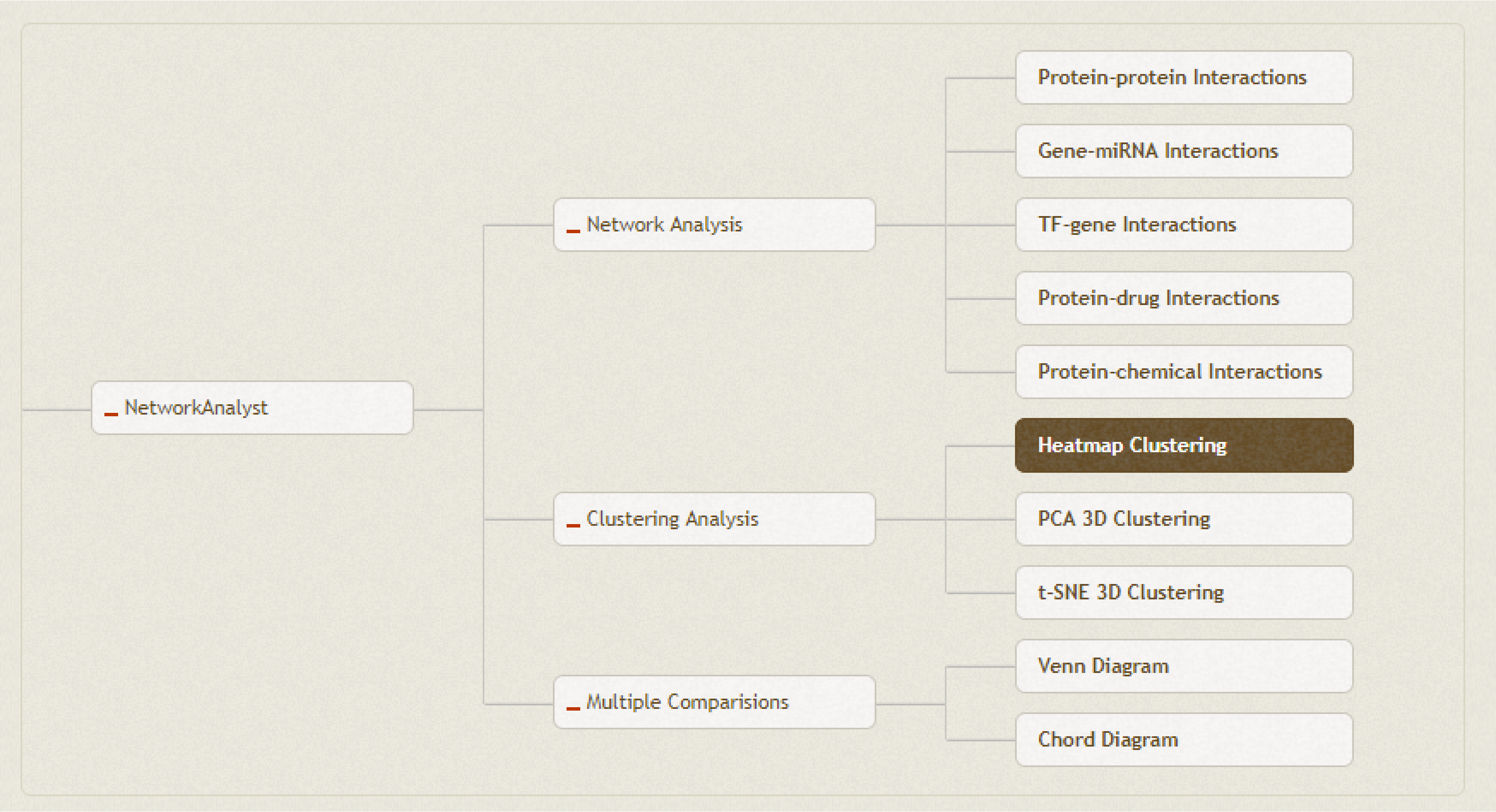
☐	Name	Hits	P-value	Colo
☐	Cell Cycle, Mitotic	67	5.61e-21	
☐	Cell Cycle	70	1.01e-17	
☐	Mitotic M-M/G1 phases	48	6.92e-17	
☐	M Phase	44	2.7e-16	
☐	Mitotic Prometaphase	32	7.85e-16	
☐	Resolution of Sister Chrom	30	5.08e-15	
☐	Separation of Sister Chrom	36	8.03e-14	
☐	Mitotic Anaphase	37	1.12e-13	
☐	Mitotic Metaphase and An	37	1.32e-13	
☐	Kinesins	13	1.83e-8	
☐	Glycolysis	11	4.19e-8	
☐	APC/C-mediated degradati	18	8.39e-8	
☐	Regulation of mitotic cell c	18	8.39e-8	
☐	Mitotic G2-G2/M phases	19	2.35e-7	
☐	Cyclin A/B1 associated eve	7	0.000001	
☐	Immune System	85	0.000001	
☐	Activation of APC/C and A	15	0.000001	
☐	Interferon alpha/beta signal	14	0.000001	

Module Explorer

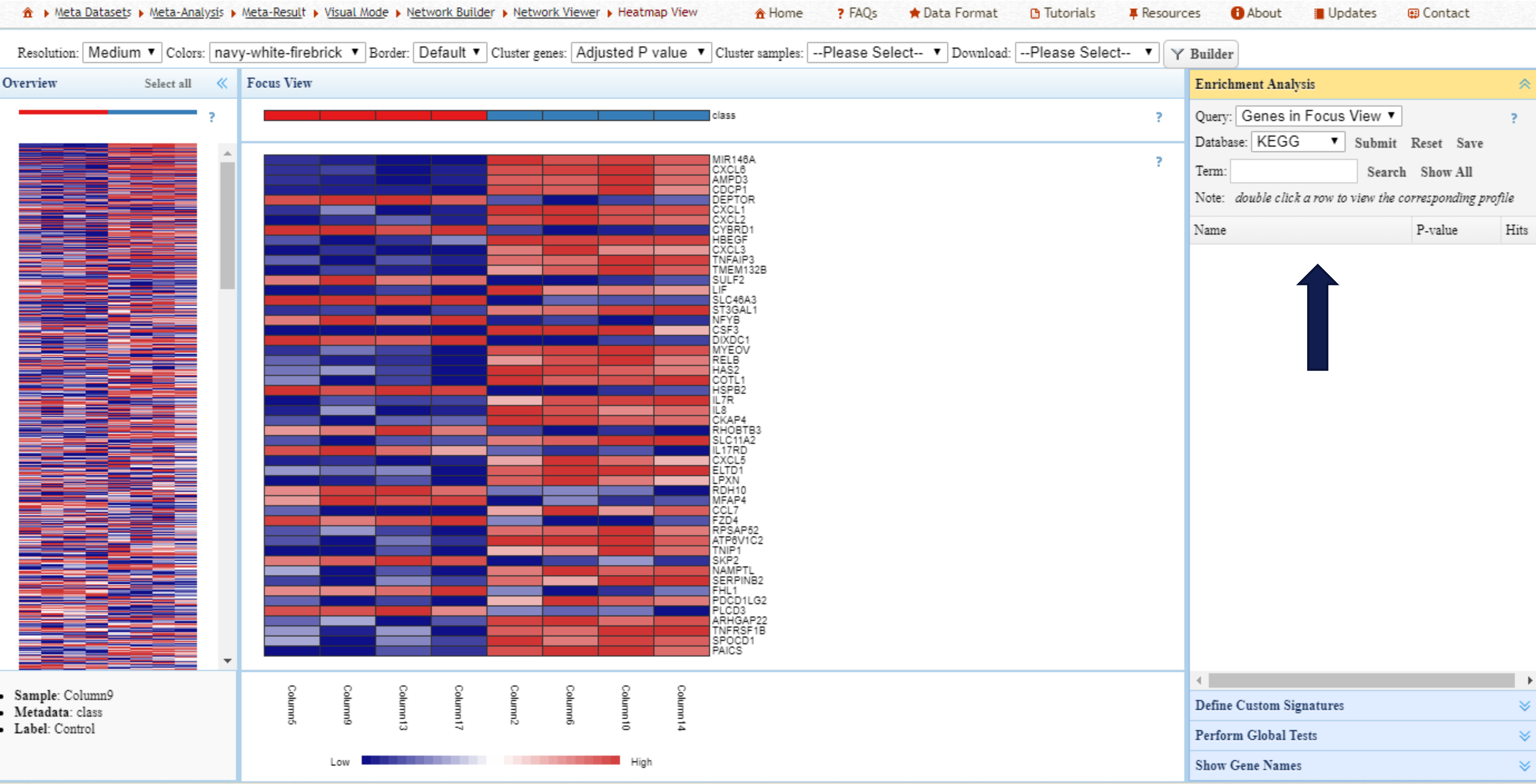
Path Explorer

Batch Selection

Heatmap clustering



Heatmaps

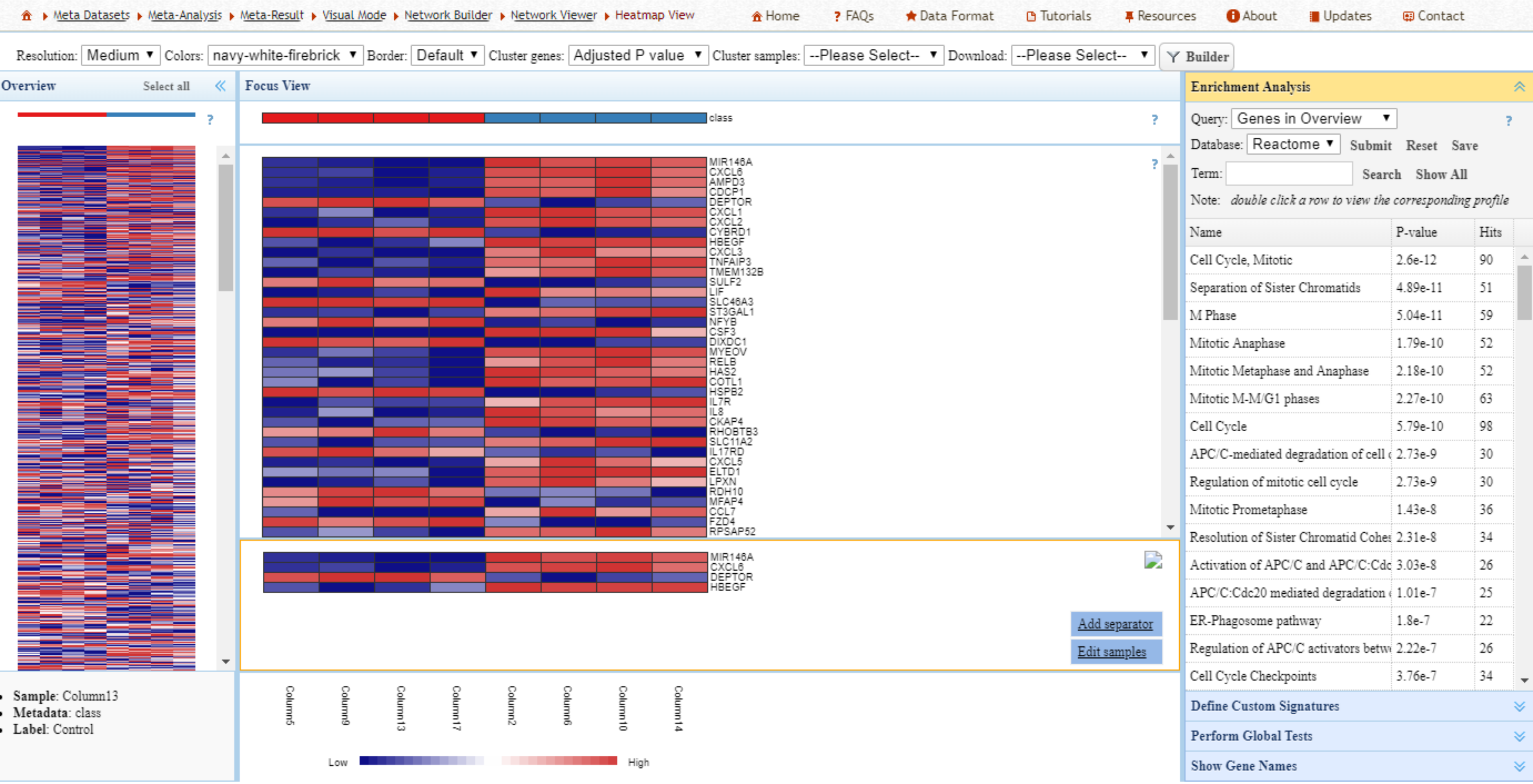


Resolution: Medium
Colors: navy-white-firebrick
Border: Default
Cluster genes: Adjusted P value
Cluster samples: --Please Select--
Download: --Please Select--

Query: Genes in Focus View
Database: KEGG
Term:
Note: *double click a row to view the corresponding profile*

- **Sample**: Column9
- **Metadata**: class
- **Label**: Control

Overview > selection of region > Focus View



Resolution: Medium Colors: navy-white-firebrick Border: Default Cluster genes: Adjusted P value Cluster samples: --Please Select-- Download: --Please Select--

- **Sample**: Column13
- **Metadata**: class
- **Label**: Control

Enrichment Analysis

Query: Genes in Overview

Database: Reactome

Term:

Note: *double click a row to view the corresponding profile*

Name	P-value	Hits
Cell Cycle, Mitotic	2.6e-12	90
Separation of Sister Chromatids	4.89e-11	51
M Phase	5.04e-11	59
Mitotic Anaphase	1.79e-10	52
Mitotic Metaphase and Anaphase	2.18e-10	52
Mitotic M-M/G1 phases	2.27e-10	63
Cell Cycle	5.79e-10	98
APC/C-mediated degradation of cell	2.73e-9	30
Regulation of mitotic cell cycle	2.73e-9	30
Mitotic Prometaphase	1.43e-8	36
Resolution of Sister Chromatid Cohes	2.31e-8	34
Activation of APC/C and APC/C:Cdc	3.03e-8	26
APC/C:Cdc20 mediated degradation	1.01e-7	25
ER-Phagosome pathway	1.8e-7	22
Regulation of APC/C activators betw	2.22e-7	26
Cell Cycle Checkpoints	3.76e-7	34