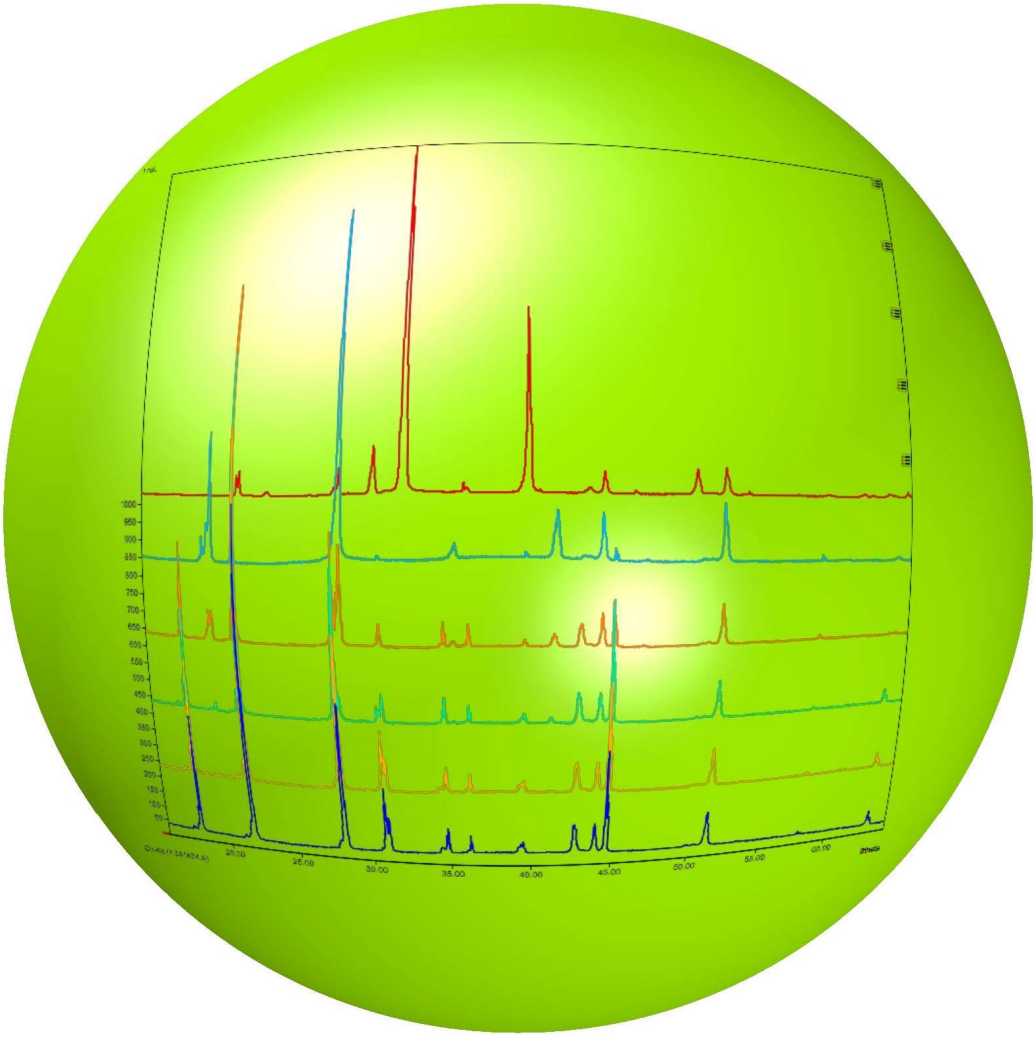
MATCH!

Phase Analysis using Powder Diffraction



Progress in Phase Analysis from Powder

CRYSTAL IMPACT

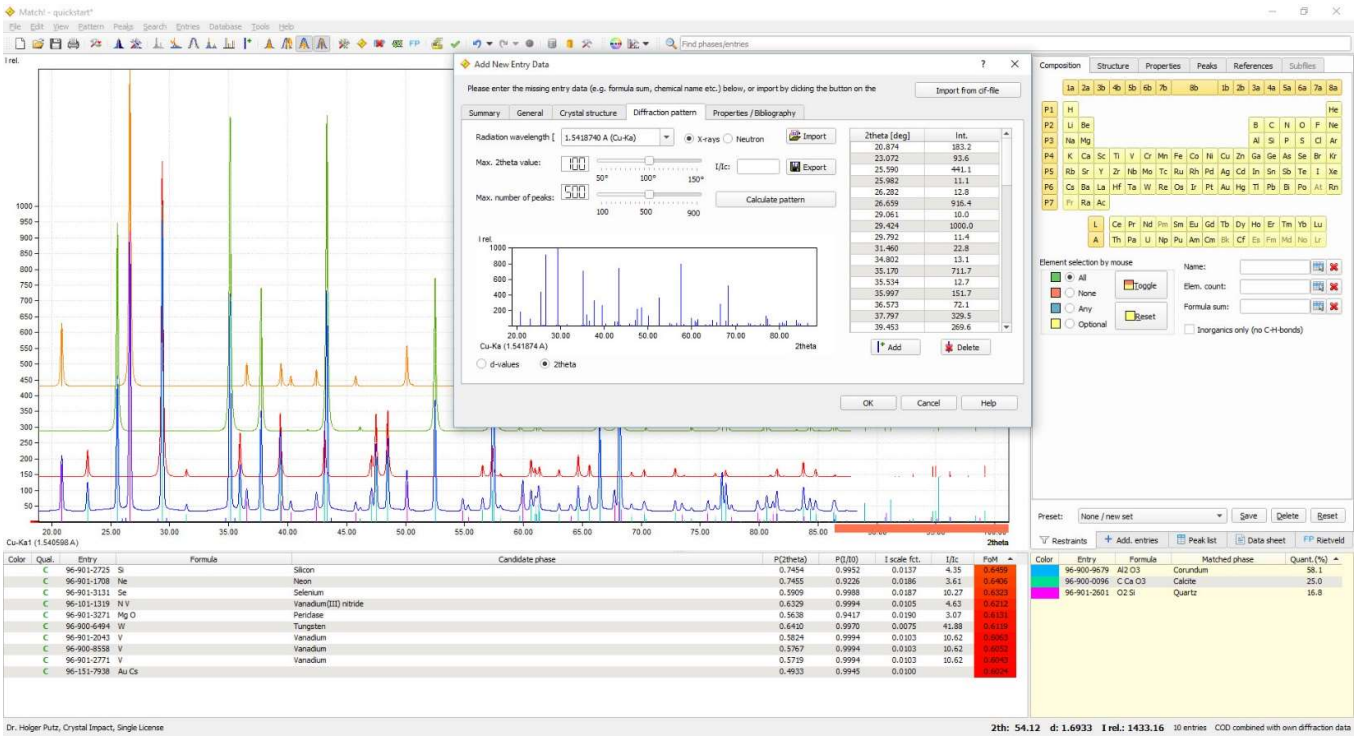
Match! is an easy-to-use software for phase analysis from powder diffraction data. It compares the diffraction pattern of your sample to a database containing reference patterns, in order to identify the phases that are present. Additional knowledge about the sample (like known phases, elements or density) can be applied easily. In addition to this **qualitative analysis**, a **quantitative analysis** can be performed as well, using Toraya's "Direct Derivation", RIR, Rietveld, DOC or internal standard method.

As reference database, you can apply the included **free-of-charge COD database** and/or any **ICDD PDF** product and/or **your own diffraction patterns** or crystal structure data.

You can quickly setup and run **Rietveld refinements** from within Match!, with the actual calculations being performed automatically, using the well-known program **FullProf** (by J. Rodriguez-Carvajal) in the background. Match! provides a **gentle introduction into Rietveld refinement**, from fully automatic operation (user-configurable) to the "Expert" mode.

More information and free-of-charge test version:

https://www.crystalimpact.de/match



Features

- Fast multiple phase identification from powder diffraction data
- Runs on Windows, macOS and Linux
- Use free-of-charge reference patterns calculated from the COD (incl. I/I_c), any ICDD PDF database, and/or your own diffraction or crystal structure data in phase identification
- Quantitative analysis using Toraya's "Direct Derivation", reference intensity ratio (RIR), Rietveld, degree-of-crystallinity (DOC) and/or internal standard method
- Indexing (using Treor or Dicvol)
- Crystal structure solution (using Endeavour)
- Rietveld refinement calculations (e.g. for quantitative analysis) using the well-known FullProf in the background
- Instant usage of additional information (known phases, elements, density, colour etc.) using perpetual restraining
- Automatic raw data processing
- Comfortable background definition/modification using the mouse
- Convenient editing of peaks (add/shift/delete/fit) using the mouse
- Improved zooming and tracking using mouse or dialog
- Display several piled experimental patterns e.g. for comparison
- Crystallite size estimation based on Scherrer approach

System requirements

- **Windows** XP, Vista, Windows 7, 8/8.1 or 10; **macOS** 10.12 "Sierra" or higher; **Linux** (Intel 64-bit)
- 2 GB of RAM
- 2.5 GB of free disc space
- **Supported diffraction data file formats (automatic recognition)**: Bruker/Siemens, DBWS, DRON-3, G670, Inel, GNR (formerly Ital Structures), Jade/MDI/SCINTAG, JEOL Export, PANalytical/Philips, Rigaku, SCINTAG, Seifert, Shimadzu, various text files (profile or peak list data), Siemens, Sietronics, Stoe, TXRD export, XPowder, XRDML

Prices for new licenses*

	non-profit org.	profit org.
Single licence	599 €	1,198 €
Site licence**	1,198 €	2,396 €
Campus licence***	2,396 €	4,792 €

* Prices include a 3-year permission for updates; they do not include taxes that may be due.
** Unlimited number of installations within one institute/dept.
*** Unlimited number of installations within one university/company.

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