

— PSDI Autrans, 29-31.10.2007

---

# ELIAS, the Electronic Laboratory Information and Archiving System

Tatjana Köhler (information systems department)

Stefan Hörer

Dirk Reinert

## What ELIAS is:

---

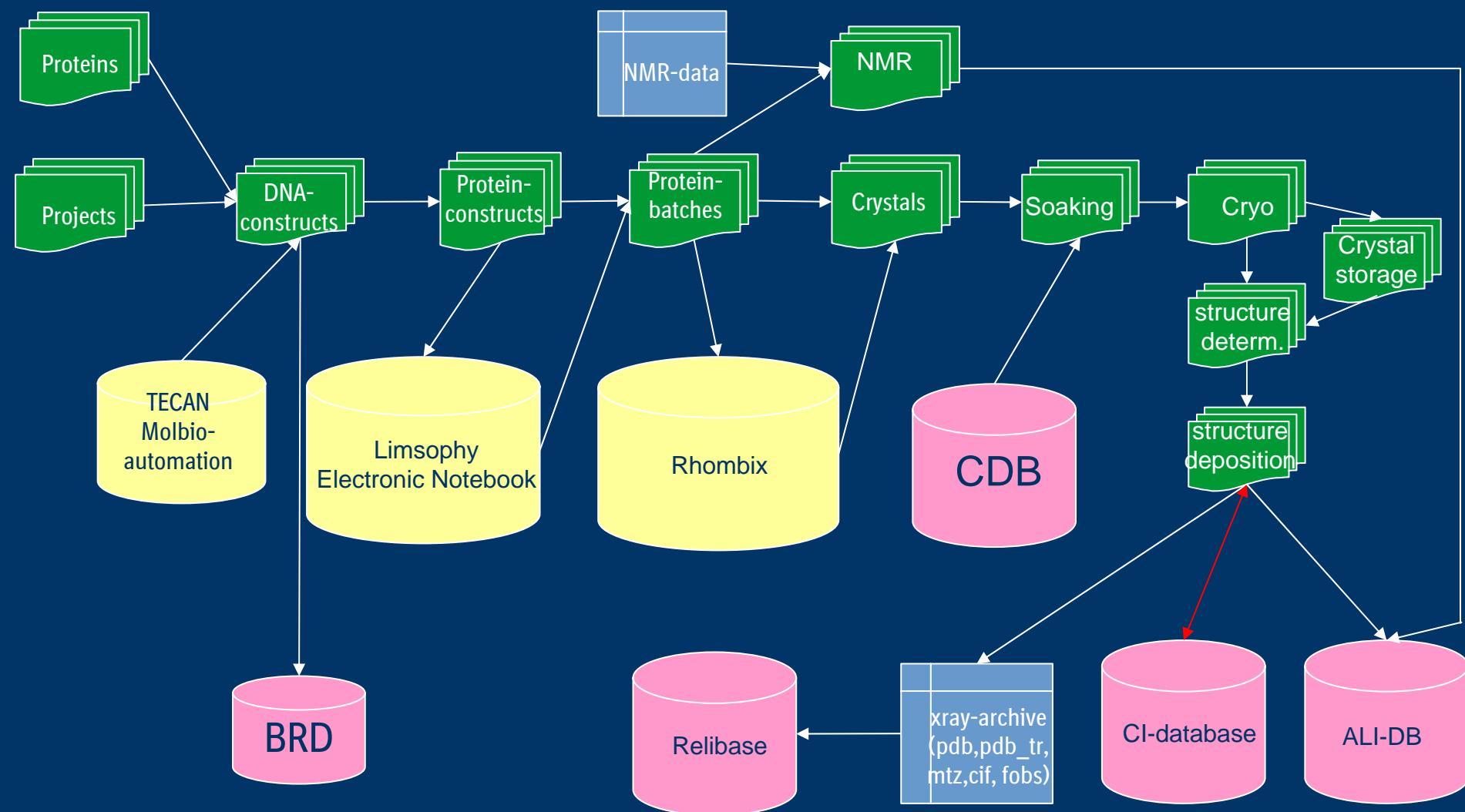
- ELIAS is a workflow software which was developed to represent the processes within the Biberach structural research group.
- The emphasis is on the exchange of information between all automation systems and the electronic laboratory notebook system.

The aim of the project is to

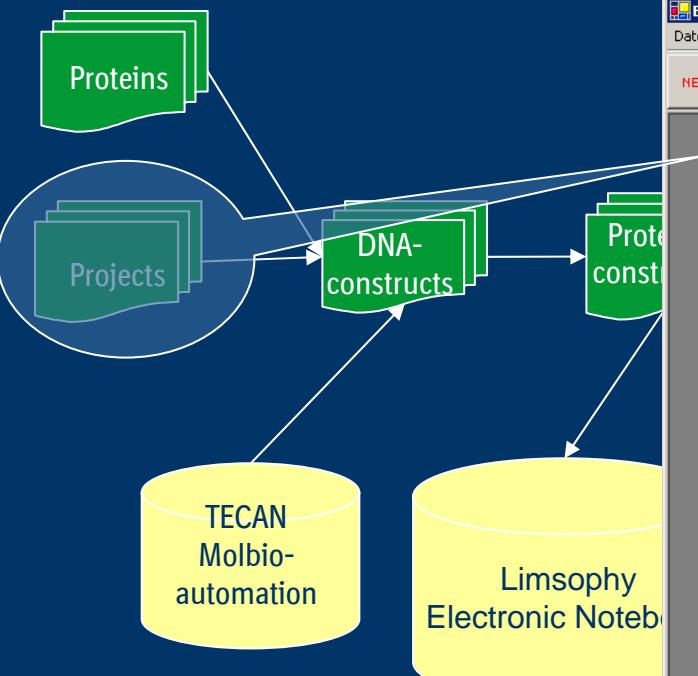
- enable every member of the group to track all information on a certain sample.
- Simplify “high throughput crystallography”

# System overview

ELIAS  
SR-databases  
other databases



# ELIAS workflow (1) Projects



ELIAS

Projekte

ID	Name	Therapiegebiet	Projektle...	Beschreibung	ProjektStart	ProjektEnde	Status	Benutzer
1	...		N. Red...		02.04.2001		LO	Dr. Hörer
2	...		N. Red...		01.11.2004	nach H...	Dr. Hörer	
4			N. Red...		01.11.2004		Präprojekt	Dr. Bauer
5			C. Dorn...		27.07.2004		LO	Dr. Bauer
10			P. Nick...		07.11.2003		LO	Dr. Schna...
11			Dr. Heik...		06.01.2004		vor HTS	Dr. Bauer
13			Dr. Strei...		01.01.2002		LO	Dr. Pautsch
14			Dr. Silk...		01.04.2005		vor HTS	Dr. Bauer
16			Dr. Udo...		01.04.2005		LO	Dr. Pautsch
17			Dr. Stef...		26.10.2004		vor HTS	Dr. Pautsch
19			Dr. Ralp...		19.09.2005		nach H...	Dr. Bauer
20			Dr. Arndt		01.07.2005		Präprojekt	Dr. Schna...
21			Dr. Krei...		03.01.2005		nach H...	Dr. Nar
22			Dr. Brad...				nach H...	Dr. Bauer
23			C. Dorn...		10.10.2005		vor HTS	Dr. Schna...

ID:

Name:

Therapiegebiet:

Projektleiter:

Beschreibung:

ProjektStart:  Start Datum

ProjektEnde:  Ende Datum  Datum löschen

Status:

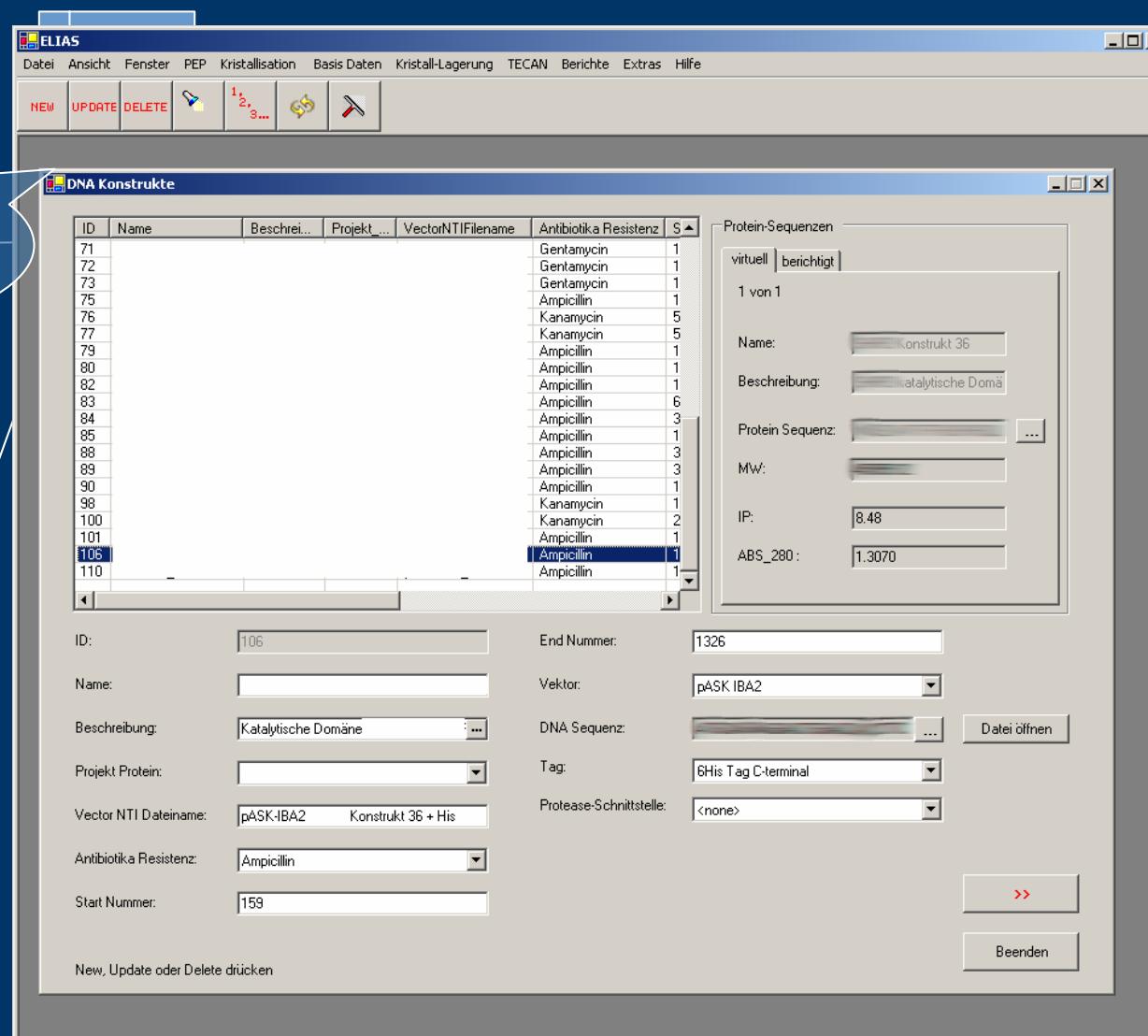
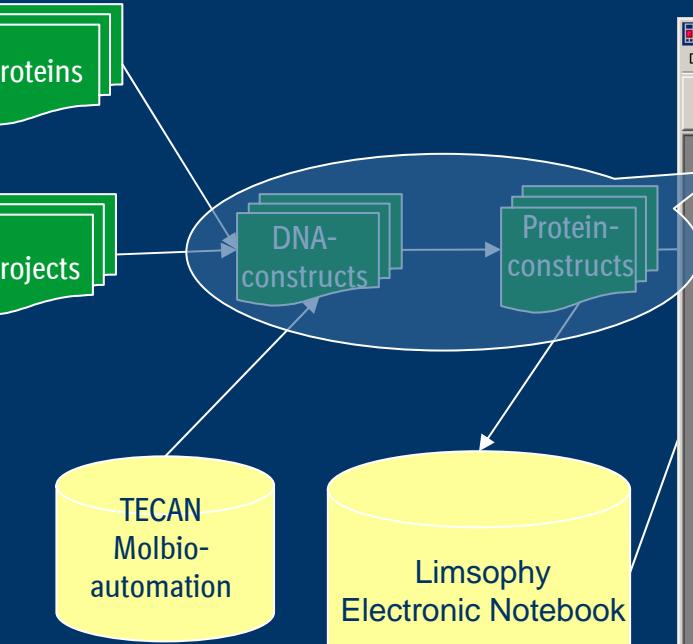
New, Update oder Delete drücken

>>

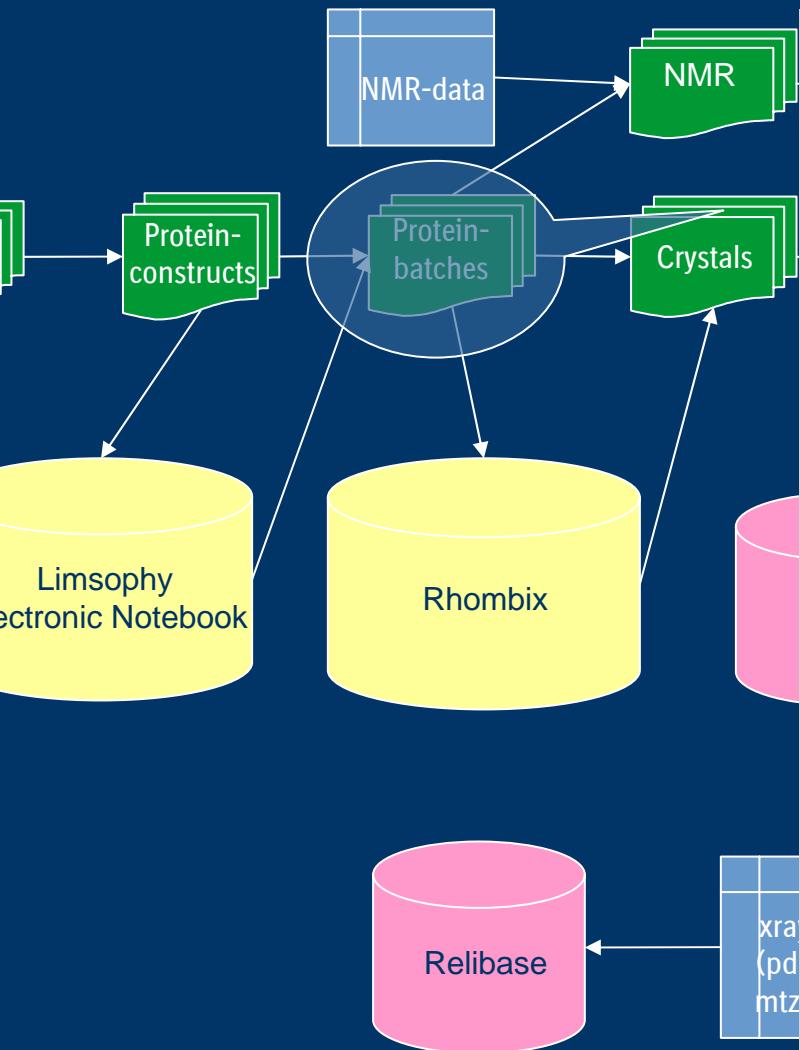
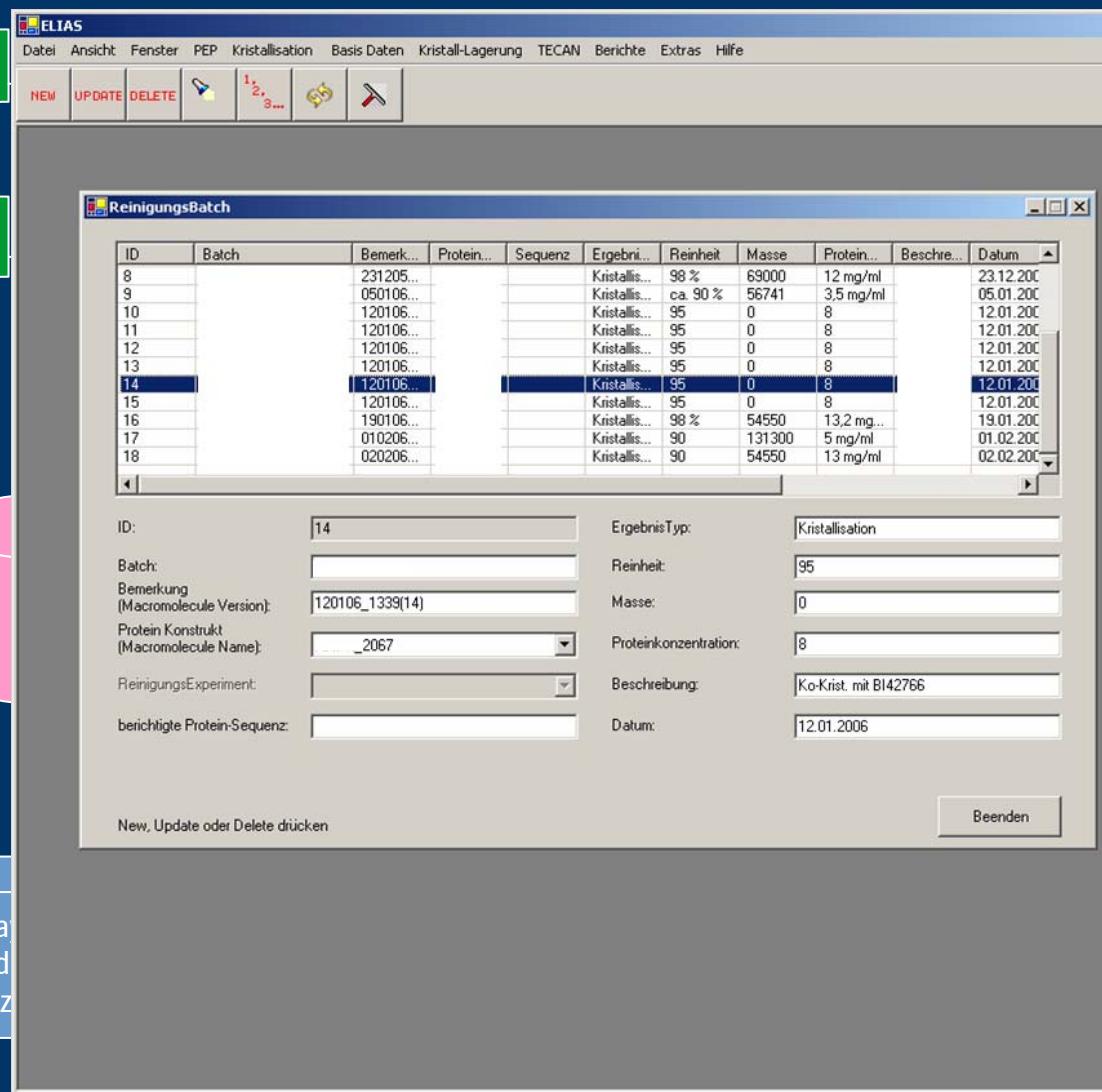
Beenden

# ELIAS workflow (2)

## DNA and protein constructs



# ELIAS workflow (3) protein batches

**ELIAS** Software Interface Screenshot:

**ReinigungsBatch**

ID	Batch	Bemerk...	Protein...	Sequenz	Ergebnis...	Reinheit	Masse	Proteinkon...	Beschre...	Datum
8	231205...				Kristallis...	98 %	69000	12 mg/ml		23.12.200...
9	050106...				Kristallis...	ca. 90 %	56741	3.5 mg/ml		05.01.200...
10	120106...				Kristallis...	95	0	8		12.01.200...
11	120106...				Kristallis...	95	0	8		12.01.200...
12	120106...				Kristallis...	95	0	8		12.01.200...
13	120106...				Kristallis...	95	0	8		12.01.200...
<b>14</b>	<b>120106...</b>				<b>Kristallis...</b>	<b>95</b>	<b>0</b>	<b>8</b>		<b>12.01.200...</b>
15	120106...				Kristallis...	95	0	8		12.01.200...
16	190106...				Kristallis...	98 %	54550	13,2 mg...		19.01.200...
17	010206...				Kristallis...	90	131300	5 mg/ml		01.02.200...
18	020206...				Kristallis...	90	54550	13 mg/ml		02.02.200...

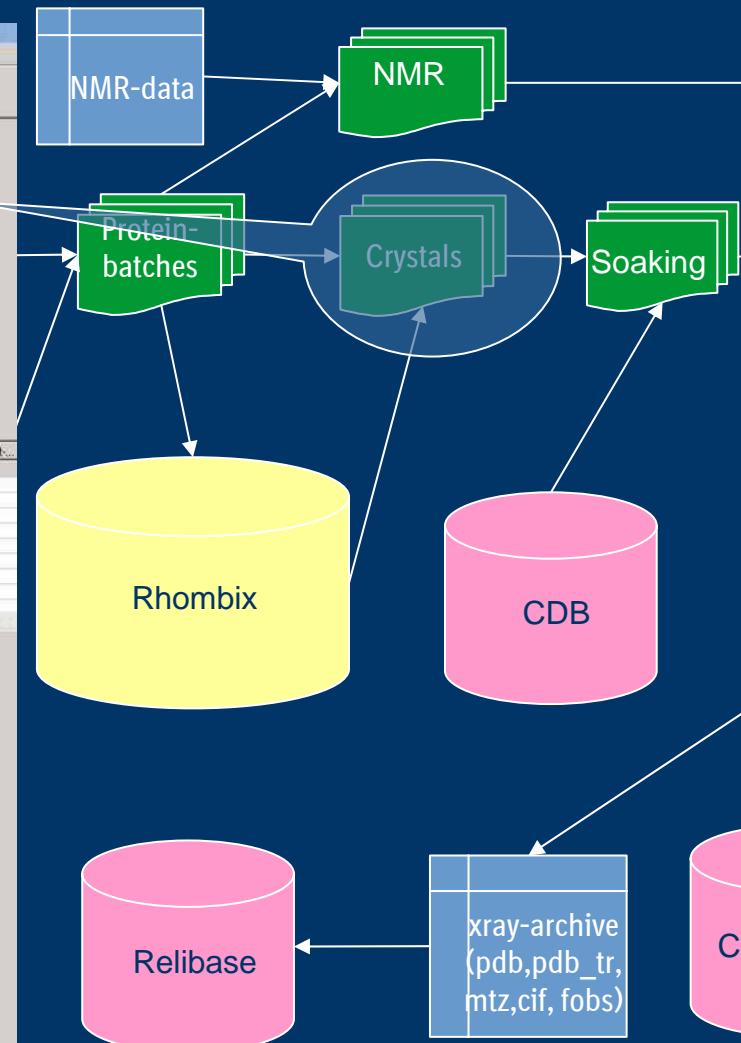
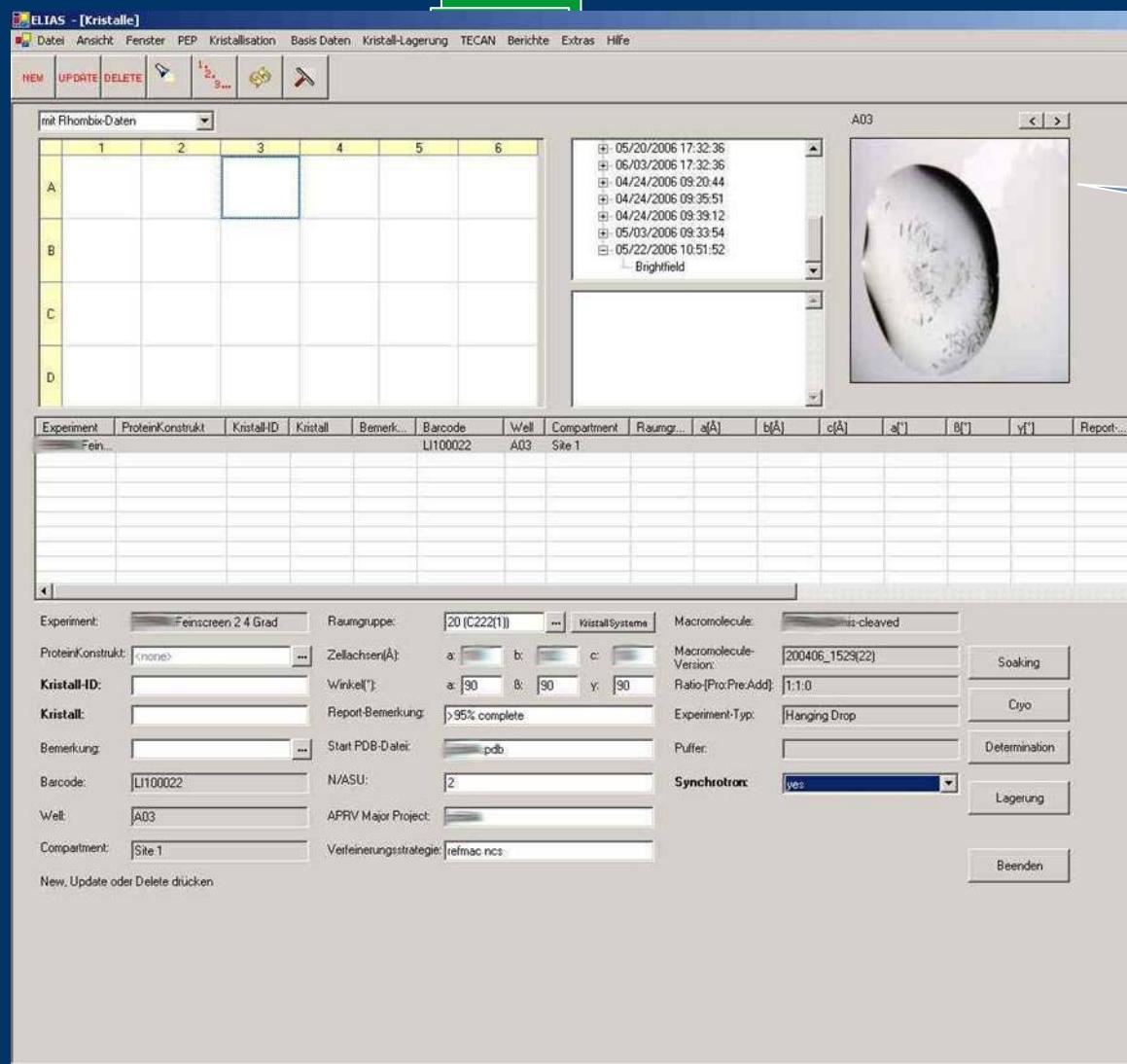
**Details for Row 14:**

ID:	14	ErgebnisTyp:	Kristallisation
Batch:		Reinheit:	95
Bemerkung (Macromolecule Version):	120106_1339(14)	Masse:	0
Protein Konstrukt (Macromolecule Name):	_2067	Proteinkonzentration:	8
ReinigungsExperiment:		Beschreibung:	Ko-Krist. mit BI42766
berichtigte Protein-Sequenz:		Datum:	12.01.2006

New, Update oder Delete drücken      Beenden

# ELIAS workflow (4)

## Crystals



# Soaking, Cryo, Storage

---

## Soaking:

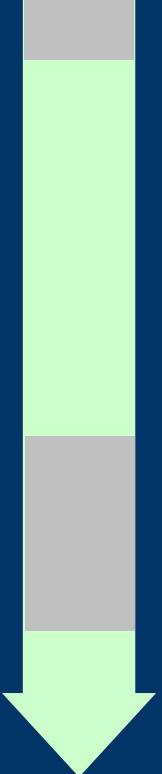
- Biological assay data is loaded from the CDB
- a detailed soaking protocol can be stored as a method

## Cryo:

- Cryo-conditions can be tracked when optimizing a cryo-protocol

## Storage:

- A storage position can be assigned to a crystal  
⇒ Reports for synchrotron trips

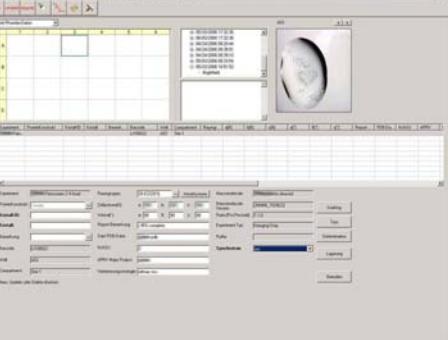
- 
- data collection
  - setup of data processing and refinement (information retrieved from ELIAS)
  - data processing
  - initial refinement
  - setup of ligand and ligand libraries (information retrieved from ELIAS and CDB)
  - ligand fitting, water picking and refinement
  - manual inspection, rebuilding of protein and / or ligand
  - further refinement
  - validation
  - deposition to ELIAS and RELIBASE

automatic process

manual process

# HTX Automation

## current workflow

- data collection on Friday
  - setup of data
  - data processing
  - initial refinement
  - setup of ligand
  - ligand fitting
  - manual inspection, rebuilding of protein and / or ligand on Monday
  - further refinement
  - validation
  - deposition to ELIAS and RELIBASE

automate

manually

automatic process

## manual process

# Structure Deposition

---

1. Selection of the files to deposit (pdb,mtz,cif,mol)
2. Generation of the pdb-file header  
Header is assembled from data stored for the specified crystal
3. Shell scripts generate the final pdb-file
4. Files are deposited to a network-drive
5. ELIAS stores the final files
6. Cronjob stores them to Relibase

# Data exchange with other databases

Relibase (CCDC):

Is the tool within BI to exchange structures between sites.

CDB (compound database):

ELIAS retrieves assay data available for compounds.

BRD (biological reagents database):

Stores all bioreagents available BI worldwide.

ELIAS reports DNA-constructs.

ALI-DB (alternative lead identification):

Global initiative to enable fragment based screening for all sites.

ELIAS reports NMR and X-ray experiments.

CI-DB (chemoinformatics):

Has read access and can retrieve information on crystal structures.

# Acknowledgement



Stefan Höller, ALF/SR