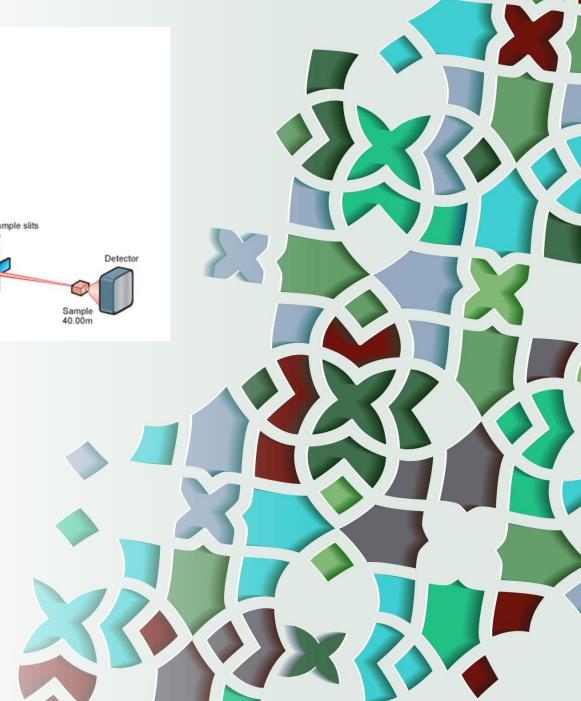


104 beamline

A versatile & high-throughput instrument that delivers high quality diffraction data

Ralf Flaig David Aragão Pierpaolo Romano Marco Mazzorana



Main reasons to use 104

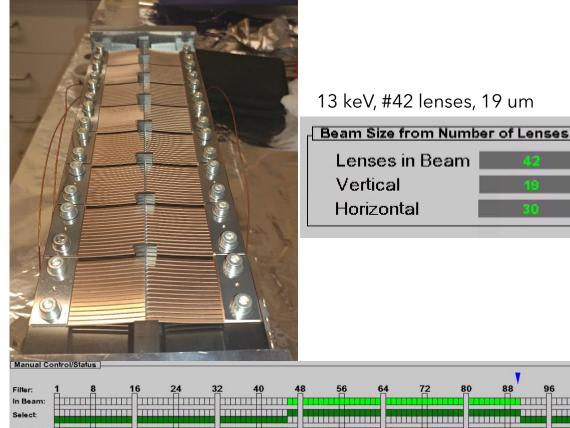


- Λ Variable focus & microfocus beam
- Variable energy
 - High flux/flux density
 - Extremely stable beam & hardware
- \mathcal{D} Multi-axis goniometry
 - Dose aware data collection
- Automation and high reliability ч <u>-</u>

• Interactive locally and remote data collections as well as UDC

Variable focus & microfocus beam

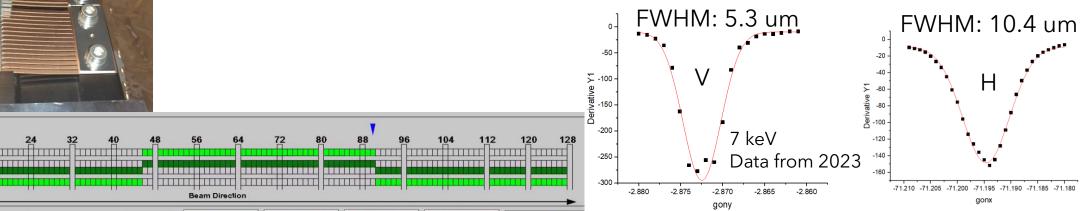
CRL/lenses base mechanism to focus the beam

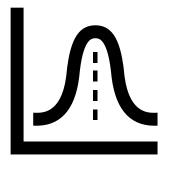


- Fast & easy change from a list of discrete beam sizes
 - Varies with energy but normally (5, 10, 15, 20, 30, 50, 75, 100 μm)

Operate from

- microfocus level (e.g. 5 µm vertical)
- large beam level (E.g. 100 μm vertical)

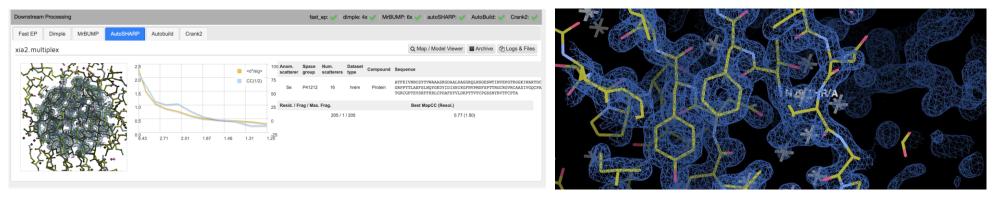






Variable energy (6000-18000 eV / 0.69 -1.55 Å)

• Phasing, edge scans, Fluorescence spectra



Good insulin crystals solve by S-SAD at 13 keV

Reaches most common edges: Cu, Fe, Mn, Se, Ni, Br, Os, etc

 Can get diffraction up to 0.94 Å resolution (edge of detector) by going to maximum energy

Beam and Det	ector	
Maximum resolution	0.9377	Â
Detector distance	170.0	mm
Wavelength	0.68880	Â
Energy	18000.0	eV

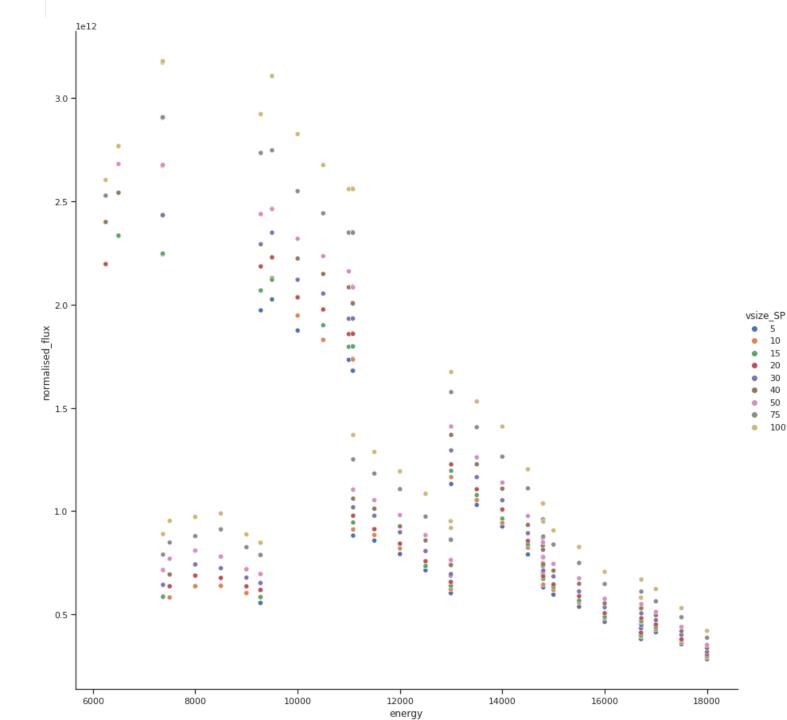
Edge				
Atom	Fe		on	•
Edge	К	•		
Pre-ed	ge regio	n		
Start e	energy	7012.00	eV	

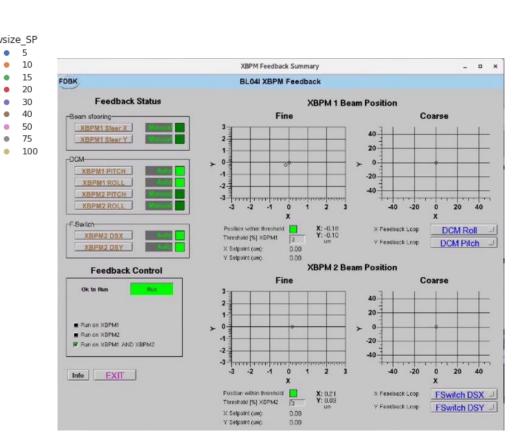
Edge	Edge	
Atom Mn 👻 Manganese	Atom Se 👻 Selenium 👻	
Edge K 👻	Edge K 👻	
Pre-edge region	Pre-edge region	
Start energy 6439.00 e	Start energy 12558.00 eV	

High flux/flux density



- Flux profile with energy & beam sizes
- Eiger has a flux density limit
 - For well diffracting samples the Eiger count rate limit is reached

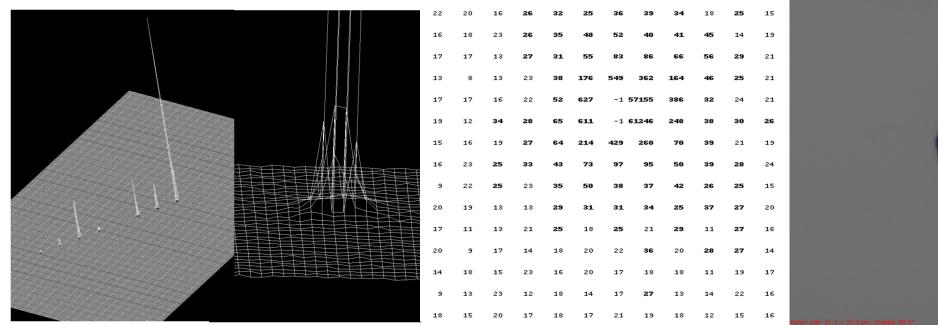


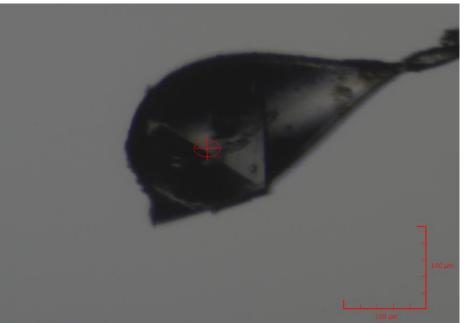




High flux/flux density

- Eiger has a flux density limit (see https://www.dectris.com/features/features-eiger-r/outstanding-count-rate-performance/)
 - For well diffracting samples (e.g thicker) the Eiger count rate limit is exceeded







360° / 7.2 s / 500 Hz

Ω Osc: 0.10°

No. Images: 3600

Extremely stable beam & hardware

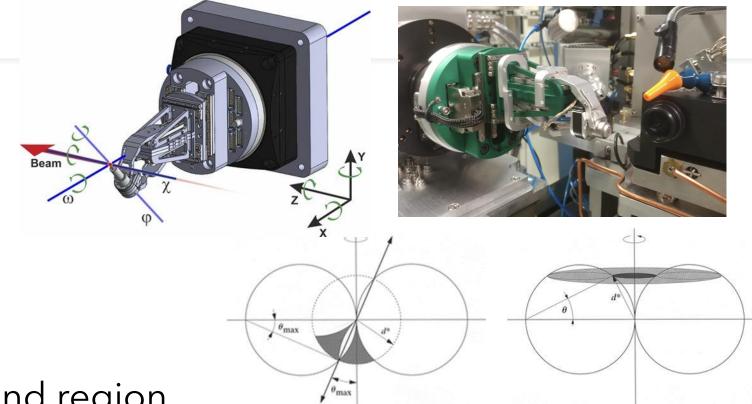
Feb 2023 • Data quality in general very high at fastest speed

Shell	Observations	Unique	Resolution	Rmeas	l/sig(l)	CC Half	Completeness	Multiplicity		Wavelength: 0.9537Å
outerShell	44923	1841	1.35 - 1.39	0.755	4.2	0.9	97.0	24.4	ISa	Dose: 1.50MGy
innerShell	8126	364	6.05 - 28.03	0.023	134.0	1.0	99.1	22.3	41.92	Dose. 1.00May
overall	682225	26292	1.35 - 28.03	0.051	37.6	1.0	99.8	25.9		Beamsize: 32x20µm

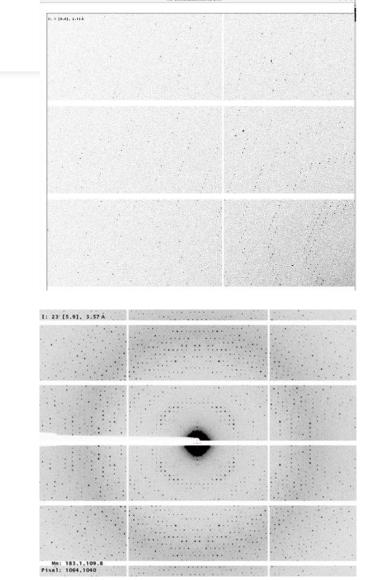
• Data quality even higher when lower speed and slightly larger beam size

Dose (Mgy)	1.5	1.5	1.5	1.5	1.33	0.72	0.46	0.37
Beam size (um HxV)	32x20	43x30	54x40	63x50	32x20	43x30	54x40	63x50
Speed (Hz)	500	500	500	370	500	500	500	500
ISa	33.8	38.8	43.6	44.4	41.6	45.0	46.7	45.9

Multi-axis goniometry



- Blind region
- Use of corners for completeness (e.g. higher res)
- High symmetry cell axis aligned



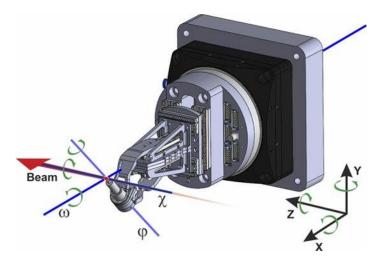


Multi-axis goniometry

- Lower systematic errors & redundancy
 - Spread of the dose is something that makes sense with modern detectors. Using multi-axis makes sense too because only adds and does not remove
- Complicated experiments (e.g. custom phasing recipe)

Omega start (°)	Omega Oscillation (°)	Omega oscillation per frame (°)	Chi (°)	Phi (°)	Or St (°)
0	2x180 (360)	0.1	0	0	0.
0	2x180 (360)	0.1	30	0	0. 0.

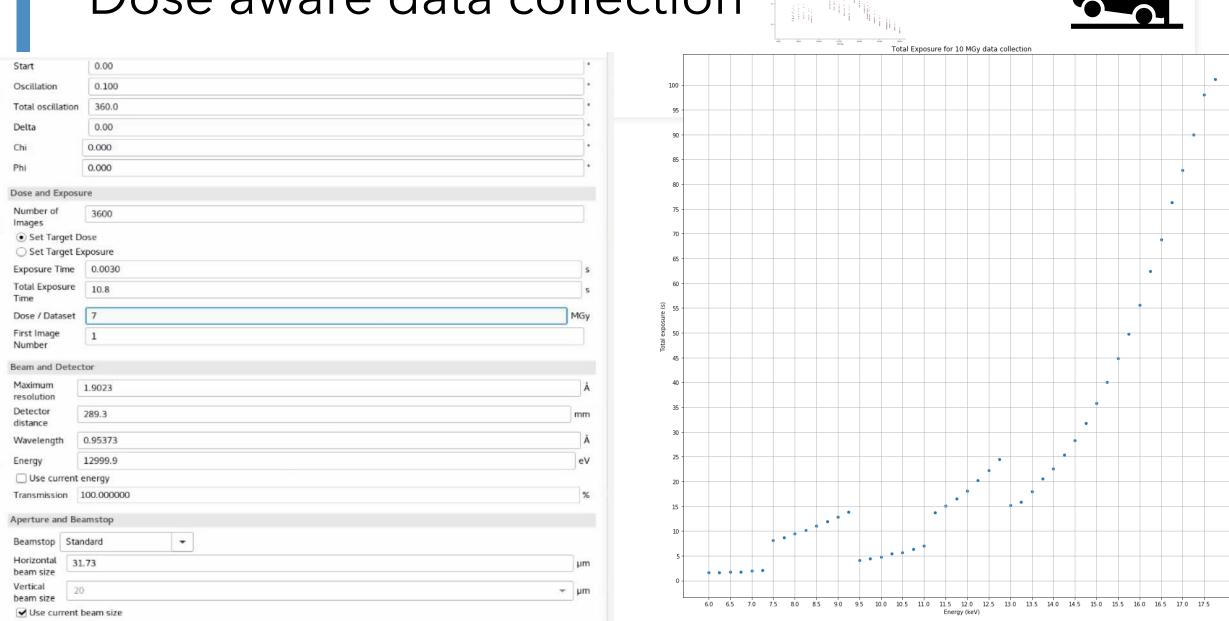
Omega Start (°)	Omega Oscillatio (°)	Omega Delta (°)	Chi (°)	Phi (°)
0.00	0.100	0.00	44.467	148.321
0.00	0.100	0.00	0.000	0.000
0.00	0.100	0.00	45.000	0.000
0.00	0.100	0.00	45.000	120.000
0.00	0.100	0.00	45.000	240.000





Dose aware data collection

- Dose as an extra information
- Dose has a tool to drive the experiment
- Dose is critical to setup an experiment with different beam size, energy or when flux is different from usual



Dose aware data collection



Total dose for native recipe



Data Collection Settings

illes Visit directory /dls/i04/data/2021/cm28182-1 Folder <u>Configure Defaults</u> \${date}/\${proteinacronym}/\${samplename}/ 20210308/TestThermolysin/Themolysin2 Prefix <u>Configure Defaults</u> \${samplename} Themolysin2 ✓ Automatic run number Run number 0 Comment Comme	L	
Visit directory /dls/i04/data/2021/cm28182-1 Folder <u>Configure Defaults</u> \${date}/\${proteinacronym}/\${samplename}/ 20210308/TestThermolysin/Themolysin2 Prefix <u>Configure Defaults</u> \${samplename} Themolysin2 Intermolysin2 Int	Position 2	
//dls/i04/data/2021/cm28182-1 Folder Configure Defaults \${date}/\${proteinacronym}/\${samplename}/ 20210308/TestThermolysin/Themolysin2 Prefix Configure Defaults \${samplename} Themolysin2 Image: Automatic run number Run number 0 Comment 3.237e+11 Predicted Flux 3.237e+11 Average Absorption 0.185775	iles	
Folder Configure Defaults \${date}/\${proteinacronym}/\${samplename}/ 20210308/TestThermolysin/Themolysin2 Prefix Configure Defaults \${samplename} Themolysin2 ✓ Automatic run number Run number 0 Comment 0 Fully and Dose {beta version} Predicted Flux 3.237e+11 Average Absorption Coefficient 0.185775	Visit directory	
\${date}/\${proteinacronym}/\${samplename}/ 20210308/TestThermolysin/Themolysin2 Prefix Configure Defaults \${samplename} Themolysin2 ✓ Automatic run number Run number 0 Comment Flux and Dose (beta version) Predicted Flux 3.237e+11 Predicted Flux 0.185775 0.185775	/dls/i04/data/2021/c	m28182-1
20210308/TestThermolysin/Themolysin2 Prefix Configure Defaults \${samplename} Themolysin2 Automatic run number Run number 0 Comment Uux and Dose (beta version) Predicted Flux Average Absorption Coefficient 0.185775 0.185775	Folder	Configure Defaults
Prefix <u>Configure Defaults</u> \${samplename} Themolysin2 Automatic run number Run number 0 Comment Uux and Dose (beta version) Predicted Flux 3.237e+11 Average Absorption Coefficient	\${date}/\${proteinac	ronym}/\${samplename}/
\${samplename} Themolysin2 Automatic run number Run number 0 Comment Sux and Dose (beta version) Predicted Flux 3.237e+11 Predicted Flux 0.185775	20210308/TestTher	molysin/Themolysin2
Themolysin2 Automatic run number Run number Comment C	Prefix	Configure Defaults
Automatic run number Run number 0 Comment Comment Predicted Flux 3.237e+11 Predicted Flux 0.185775 Coefficient	\${samplename}	
Run number 0 Comment	Themolysin2	
Comment Predicted Flux Average Absorption Coefficient	Automatic run nur	mber
Predicted Flux 3.237e+11 pho- Average Absorption Coefficient	Run number	0
Predicted Flux 3.237e+11 photometry Average Absorption 0.185775 Coefficient	Comment	
Predicted Flux 3.237e+11 photometry Average Absorption 0.185775 Coefficient		
Average Absorption 0.185775	lux and Dose (beta v	version)
Coefficient	Predicted Flux	3.237e+11 ph
Calculated 22.8239 MG	Average Absorption Coefficient	0.185775
Dose / Dataset	Calculated Dose / Dataset	22.8239 N

Image	
Number of images	3600
Exposure tim	ne 0.0100 s
Total exposu time	se 36.0 s
First image number	1
Beam and De	etector
Maximum resolution	1.3369 Å
Detector distance	170.0 mm
Wavelength	0.97949 Å
Energy	12658.0 eV
Use curr	ent energy
Transmissior	100.000000 %
Aperture and	l Beamstop
Beamstop	Standard 🗸
Horizontal beam size	18.8 µm
Vertical beam size	10 • µm
✓ Use curr	ent beam size



	Position 2			Image	
	Files			Number of images	3600
	Visit directory			Exposure time	0.0100
	/dls/i04/data/2021/c	m28182-1		Total exposure time	36.0
	Folder	Configure Defaults		First image	1
	\${date}/\${proteinac	ronym}/\${samplename}/		number	-
	20210308/TestTher	molysin/Themolysin2		Beam and Detec	tor
	Prefix \${samplename}	Configure Defaults		Maximum resolution	1.3369
	Themolysin2			Detector distance	170.0
	Automatic run nur	nber		Wavelength	0.97949
	Run number	0		Energy	12658.0
	Comment			Use current	energy
				Transmission	100.000000
	Flux and Dose (beta v	ersion)		Aperture and Be	amstop
	Predicted Flux	3.237e+11	ph s⁻¹	Beamstop Sta	ndard
	Average Absorption Coefficient	0.185775		Horizontat 3: beam size	L.7
	Calculated Dose / Dataset	6.7680	MGY	Vertical 2 beam size	0
Diamond	Sample Exitinnce			Use current	beam size

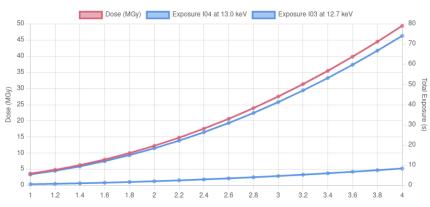


Image	
Number of images	3600
Exposure tim	e 0.0100 s
Total exposu time	re 36.0 s
First image number	1
Beam and De	tector
Maximum resolution	1.3369 Å
Detector distance	170.0 mm
Wavelength	0.97949 Å
Energy	12658.0 eV
Use curre	ent energy
Transmission	100.000000 %
Aperture and	Beamstop
-1 Beamstop	Standard 👻
Horizontat beam size	31.7 µm
Vertical beam size	20 🗸 🗸 🗸

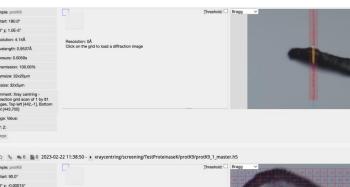


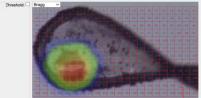
Automation and high reliability

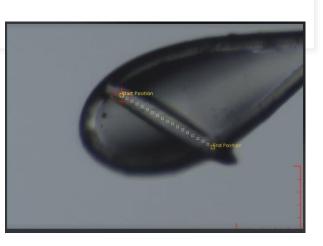
- Xray centering
- Line scans
- Data collection queue

• UDC

Omega Start (°)	Omega Oscillatio (°)	Omega Delta (°)	Chi (°)	Phi (°)
0.00	0.100	0.00	44.467	148.321
0.00	0.100	0.00	0.000	0.000
0.00	0.100	0.00	45.000	0.000
0.00	0.100	0.00	45.000	120.000
0.00	0.100	0.00	45.000	240.000







/is	isit Folder	/dls/i04/data/2023/cm33903-1				Default Folder	\${date}/\${proteinacronym}/\${samplename}					Default Prefix	\${samplename}		Developeration Queue All		Queue Selected		
1	Omega Start (°)	Omega Oscillatior (°)	Omega Delta (°)	Chi (°)	Phi (°)) Centring Mode	Number of Images	Time per Image (s)	Target Dose (MGy)	Maximum Resolution (Å)	Distance (mm)	Wavelength (Å)	Energy (eV)	Transmission (%)	Beamstop position	Horz. Beam Size (µm)	Vert. Beam Size (µm)	Run Number	F
	0.00	0.100	0.00	0.000	0.000	Auto X-ray	3600	0.0020	2.00	1.2985	170.0	0.95372	13000.0	43.000000	Standard	31.73	20.00	0	1
	0.00	0.100	0.00	44.467	148.32	l None	3600	0.0020	2.00	1.2985	170.0	0.95372	13000.0	83.500000	Standard	43.12	30.00	0	1
	0.00	0.100	0.00	45.000	0.000	None	3600	0.0020	2.00	1.2985	170.0	0.95372	13000.0	83.500000	Standard	43.12	30.00	0	1
	0.00	0.100	0.00	45.000	120.000) None	3600	0.0020	2.00	1.2985	170.0	0.95372	13000.0	83.500000	Standard	43.12	30.00	0	1
	0.00	0.100	0.00	45.000	240.000) None	3600	0.0020	2.00	1.2985	170.0	0.95372	13000.0	43.100000	Standard	31.73	20.00	0	

At our fastest speed (7.2 seconds exposure per dataset) we do 2 pucks (32 pins) per hour (single 360° wedge). This equates to 750 samples loaded and a data set collected in a day.

Interactive locally and remote data collections as well as UDC



- We train local users (*)
- We help remote users if requested (e.g via zoom) (*)
- * We operate all currently available UDC recipes

(*) Please remember to note that, at scheduling time, so that a suitable time and local contact is allocated