DEPFETs for Photon Factory Status Update and Plans

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Christian Pulvermacher

Collaborators

High Energy Accelerator Research Organization (KEK)

Institute of Materials Structure Science Soichi Wakatsuki*, Naohiro Matsugaki, Nobutaka Shimizu

Institute of Particle and Nuclear Science Yutaka Ushiroda, Shuji Tanaka, Takeo Higuchi**, Hideki Miyake, Koji Hara, Christian Pulvermacher, Tomoyuki Konno

Asuka Shiino(Mechanics), Hiroyuki luchi(DAQ)



Need for fast & high spatial resolution 2D detector for micro/ nano beam

DEPFET (<u>DE</u>pleted <u>P</u>-channel <u>FET</u>)



Sensor chip development by Max Plank Institute, Munchen

Decision at FY2014: DEPFET detector optimized for low energy photons (< 4keV)

Focusing on the biological applications which low energy X-ray benefits

- Using dead-copy of Belle-II PXD sensor (thickness: 75 μm, not an efficient detector at higher energy photons (> 8 keV))
- Better positional resolution expected
- Tiled flat detector with 16 or 12 sensors instead of original cylindrical-shape design
- Number of Pixels: 2~3M (originally 8M)





Identifying calcium atoms in the molecule



Anomalous difference Fourier map for above and below absorption edge of calcium



Niwa et.al, Structure of the LH1–RC complex from Thermochromatium tepidum at 3.0 Å, Nature (2014)

- Identifying biologically important light atoms in protein molecules by using anomalous scattering.
- The experiment was performed at KEK-PF BL-1A using X-ray beam energy of around 4 keV.
- Need accurate measurement to detect the weak anomalous signal

Characterization studies

Preliminary experiments to characterize DEPFET sensors for structural biology applications

DEPFET - prototype sensor

- Pixel size: 20 μm x 20 μm
- Sensor thickness: 450 μm
- Sensor size : 5120 x 1280 μm (256 x 64 pixels)
- Slow readout (~100Hz)



Confirm the response to the X-ray

- ✓ Quality of image of diffracted X-ray from Protein
 - X-ray image for the protein crystal
 - X-ray image for the solution scattering
- ✓ Position resolution

X-ray Diffraction Image from Protein Crystal



Photon Factory BL-5A station X-ray energy: 12.4 keV





Diffraction image from a Hen-egg lysozyme crystal

Concatenated image from a small DEPFET sensor

Detector mechanics



Schematic view of the complete detector with 16 DEPFET sensors mounted

Principle of the mechanics



Unit module(4 types)



Overlapped tiling



Non-overlapped tiling

Kapton cable support structure



Water-cooled base

The common water-cooled base plate allows:

- both overlapped and non-overlapped tiling
- Each module can be mounted and unmounted (for reconfiguration, repair, etc.)

DAQ development

Aurora2PCIe system



Status of DAQ development

- ✓ Production of 18 aurora2PCle boards has been finished.
- ✓ FPGA firmware design was completed.
- ✓ The board functional check was started in a state where attached to the PCI-Express.
- ✓ The board functional test should be completed in middle of June 2016 for the beam test at the Photon Factory.

Board functions check environment



Aurora interface (optical cable)



Training Session at MPI (2 – 10 May)



- Upcoming beam tests use system quite different from that of previous study
- Learning how to use current state of hardware, as well as slow control and DAQ software
- Successful setup and readout of matrix attached to EMCM

Plan in FY2016

The last year of the project

- Beam test in 6 8th of June at KEK-PF BL-5A and BL-6A for protein crystallography and solution scattering experiment, respectively. An EMCM or a DEPFET prototype sensor will be used.
- Sensor production. 16 sensors must be delivered in the end of 2016.
- Additional beam test will be scheduled in the autumn run (Oct. – Dec.) to further understand the DEPFET system. Data processing software should be developed in parallel.
- The final beam test in Jan Mar 2017. Protein crystallography and solution scattering experiment will be performed using the complete detector with the 16 sensors.

Summary

- Higher positional resolution and frame rate is required for Xray detector in structural biology. DEPFET is one of very promising candidates.
- Basic properties has been successfully tested using a small prototype DEPFET sensor for ILC
 - Clear signal image of diffracted X-ray
 - Good position resolution for single photon
- 16 dead copy of Belle II PXD are used for the detector optimized for low energy applications in structural biology.
- DAQ systems and the detector mechanics are under development aiming for the beam test in this June and for the final experiment in early 2017.

Bonus Slides

Applications to challenging targets

signalosomes

I Solution studies of domain association-

dissociation dynamics and kinetics of

I Structural analysis and dynamics of membrane protein complexes & large complexes



Aurora2PCIe FPGA blockdiagram



Experimental apparatus









Scanned with XY-stage to make the image on the detection plane

Front view



De-novo Crystal structure determination using anomalous signals from light atoms

- Most biological macromolecules naturally contain sulfurs or phosphors
- Demonstrated first in 1980 for a small protein
- Experimental difficulty is in the week anomalous signals at the conventional energy at around 10 keV
- Need low energy photons to enhance the anomalous signals

Energy dependence of anomalous signals from biologically important light atoms



Constructing a detector: Work Packages

Nr.	Work Package	Prod. Group				
1	DEPFET Modules		ר			
1.1	Sensor production	HLL				
1.2	Sensor testing	MPI @ HLL				
2	ASICs (incl. Test)					
2.1	Switcher	HEI		_	-	
2.2	Current Digitizer (DCD)	HEI		Se	Sensor	Sensor and r
2.3	Data Handling Processor (DHP)	BON				
	ASIC test by KEK		L	_ pr	_ produc	_ production, A
3	Module Production			· .		
3.1	Flip Chipping	HLL		te	tests	tests
3.2	passives & test	MPI @ HLL				
3.3	Kapton Flex + Patch Panel prod.	KEK				
3.4	Kapton attachment	HLL				
3.5	sanity testing, calibration	HLL by KEK pers.				
4	Power					
4.1	Power Supplies	LMU				
4.2	Cables	LMU				
5	DAQ					
5.1	Data Handling Hybrid (DHH)	TUM				
5.2	Signal cables	KEK				
5.3	DAQ System and Software	KEK		M	Mechar	Mechanics &
6	Mechanics					
6.1	Sensor Support & Cooling (H2O)	KEK				
7	System Integration					
7.1	Assembly	KEK				
7.2	Commissioning	KEK				

Structure determination using anomalous signals from sulfur atoms

X-ray beam of 3.7 keV was used to enhance the anomalous signal

Heavy atom search

	000	Distance			A H
1	1.41	0.126	MET369		
2	1.46	0.082	MET306		
3	1.43	0.072	MET222		
4	1.34	0.194	MET83		- TV
5	1.48	0.101	CYS305	S. WAR TABBALISAN SA INTA	
6	1.19	0.167	MET379		
7	1.41	0.07	MET87		
8	0.86	0.337	MET157		R
9	1.01				
10	0.57				· ····································
11	0.56				
12	0.33				
13	0.67	0.328	CL		
14	0.39				222
15	0.20			Electron density of 40kDa glucose isomeras	e. 322 out of
16	0.75			residues are automatically built in 18	fragments
17	0.73	0.23	CA	(R=0.3, Rfree=0.37)	
18	0.65	0.401	MG	(N=0:3, Nii ce 0:37)	SS 1 ABM

2G4J (C.MUELLER-DIECKMANN)

Detector: Pilatus 2M