

# Geant4 Low Energy Electromagnetic Physics

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on behalf of both Geant4 Electromagnetic WG

2015 Geant4 Collaboration Meeting  
Fermilab  
Sept. 28 – Oct. 2

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1. Low energy limit treatment of **gamma** models
2. Monash **gamma** models
  - Compton model **G4LowEPComptonModel**
  - Compton model **G4LowEPPolarizedComptonModel** including polarization
3. Update of **atomic de-excitation**
  - **UI** commands
  - New set of **fluorescence line data** by Bearden et al.
  - **Auger cascade** simulation
  - Issue with Penelope and atomic deexcitation
4. **ICRU'73** ion models
5. Further **verification & validation** activities
  - Gamma models
  - Bremsstrahlung
6. **Geant4-DNA** updates

# What is included in **LowE EM** Physics ?

## **Low Energy Electromagnetic Processes**

### **Livermore processes for gamma and electrons**

Information on **Livermore processes** is available from this [page](#).

### **Penelope processes for gamma, electrons and positrons**

Information on **Penelope processes** is available from this [page](#).

### **Ion processes**

Information on the **ICRU'73 ion parameterized model** is available from this [page](#).

### **Geant4-DNA processes**

Information on **Geant4-DNA processes** is available from this [page](#).

### **MicroElec processes**

Information on **MicroElec processes** for microdosimetry in Silicon from this [page](#).

### **Monash University processes**

Information on **Monash University processes** for gammas from this [page](#).

### **How to simulate atomic deexcitation?**

Follow this [page](#).

Twiki page

<https://twiki.cern.ch/twiki/bin/view/Geant4/LowEnergyElectromagneticPhysicsWorkingGroup><sup>3</sup>

# 1) Handling of low energy limits

Apply uniform handling of low energy limits of models for gammas, after infinite loops where reported by CMS for very low energy gammas

## – Compton scattering

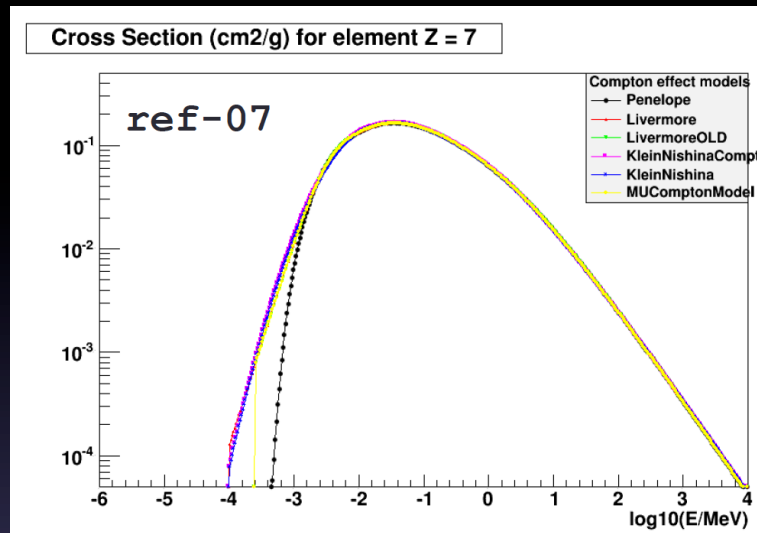
- Cross section is set to zero below  $E_{\min}$ , where  $E_{\min}$  is the first data point of tabulated value: if  $E < E_{\min}$ ,  $\sigma(E) = 0$

## – Photoelectric effect

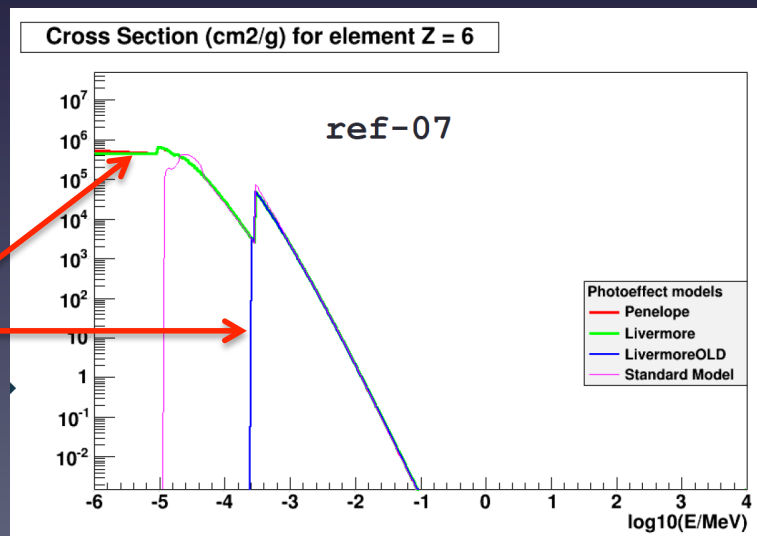
- Non-zero cross section below  $E_{\min}$ : if  $E < E_{\min}$ ,  $\sigma(E) = \sigma(E_{\min})$

# Handling of low energy limits

Compton scattering



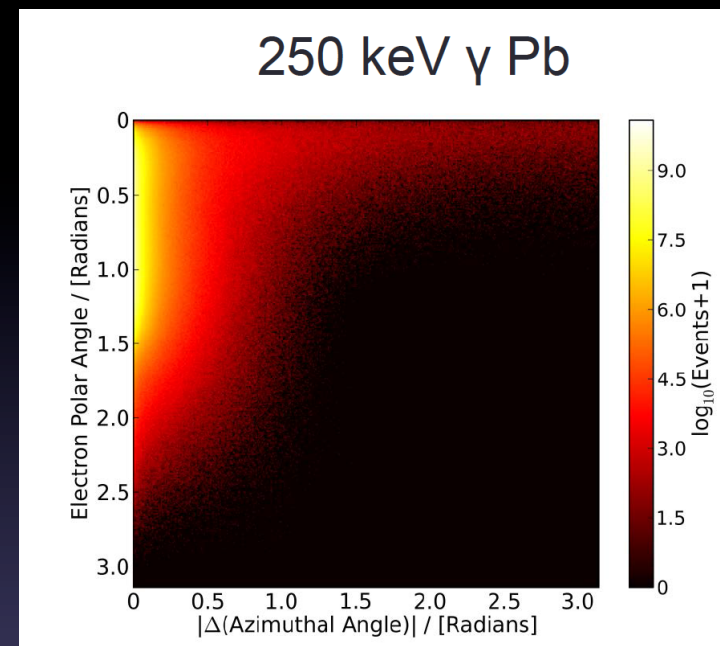
Photoelectric effect



Livermore  
(current & old)

## 2) Monash Compton model


- **G4LowEPComptonModel**
  - Developed by J. M. C. Brown @ Monash U.
  - Two-body relativistic **3D framework**
  - Relativistic impulse approximation
  - **Electron distribution** is not uniform in  $\phi$  wrt **photon** scattering plane
  - Bound atomic electrons
- CPU penalty of 10% compared to Penelope
- In **G4EmStandardPhysics\_option4** below 20 MeV




<http://dx.doi.org/10.1016/j.nimb.2014.07.042>


Nuclear Instruments and Methods in Physics Research B 338 (2014) 77–88

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 Nuclear Instruments and Methods in Physics Research B

journal homepage: [www.elsevier.com/locate/nimb](http://www.elsevier.com/locate/nimb)



A low energy bound atomic electron Compton scattering model for Geant4 

J.M.C. Brown <sup>a,\*</sup>, M.R. Dimmock <sup>b</sup>, J.E. Gillam <sup>c,d</sup>, D.M. Paganin <sup>a</sup>

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<sup>c</sup>IFIC CSIC Universitat de Valencia, Valencia E-46071, Spain  
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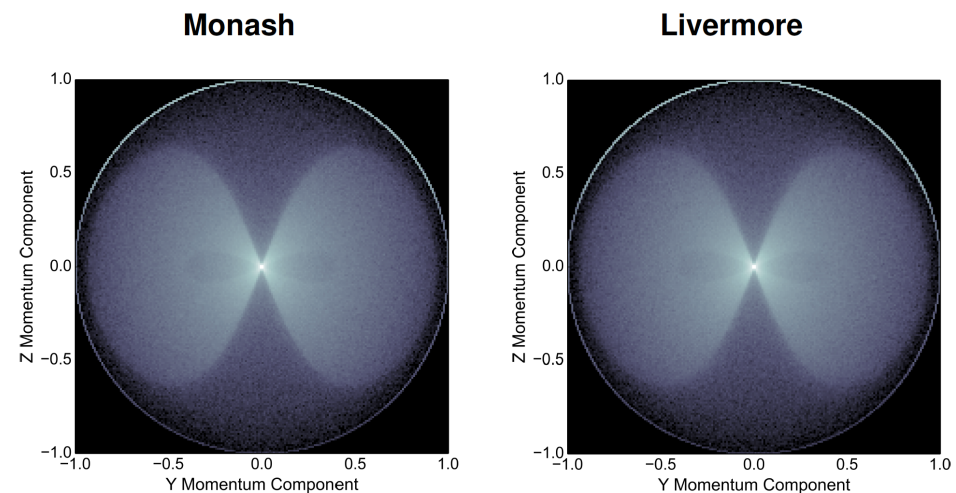
# Monash pol. Compton model

- New model model `G4LowEPPolarizedComptonModel` for polarized Compton scattering by [J. M. C. Brown @ Monash U.](#)
- Adapted from **new MT version** of `G4LowEPComptonModel`
- Polarisation algorithms implemented from `G4LivermorePolarizedComptonModel`
- Both scatter **momentum distributions and polarisation distributions match** with respect to `G4LivermorePolarizedComptonModel`
- Fixed **additional FPE issue** in Livermore that reset photon polarisation plane after scattering

Implementation

Momentum Distributions

## Scattered Photon Distributions: Si 250 keV (Log Intensity Scale)



Courtesy of J.M.C. Brown

# 3) Atomic deexcitation: UI commands

- Initialisation of fluorescence

```
/run/initialize  
/process/em/deexcitation region true true true  
/process/em/fluo true  
/process/em/auger true  
/process/em/pixe true
```

- Production cuts for cuts < 990 eV

```
/cuts/setLowEdge 250 eV
```

- Selection of shell ionisation cross section models for protons and electrons

```
/process/em/pixeXSmodel value (value is ECPSSR_Analytical or ECPSSR_FormFactor or Empirical)  
/process/em/pixeElecXSmodel value (value is Livermore or Penelope)
```

- New flag to disable the use of production thresholds

```
/process/em/deexcitationIgnoreCut true
```



# Atomic deexcitation: new set of fluorescence lines

- Transition energies are taken from the [Evaluated Atomic Data Library \(EADL\)](#)
- This library contains **calculated** data for **isolated neutral atoms**
- It is known that the simplifications used in this library for the calculation of transition probabilities and transition energies can lead to **visible inconsistencies**, as explained in the interesting review by [Salvat and Fernandez-Varea \(2009\)](#) :  
they suggest to correct transition energies during the simulation

- Energy shifts can be observed when simulating lines with Geant4, compared to expected values

- The set of **measured** transition lines by [Bearden et al. \(1967\)](#) is used worldwide for material analysis ([X-Ray Data Booklet](#))
- A new alternative set has been provided by [S. Paltani \(U. of Geneva\)](#)

Default: `$G4LEDATA/fluor`

New set: `$G4LEDATA/fluor_Bearden`

- To use this set, add in your Physics list:

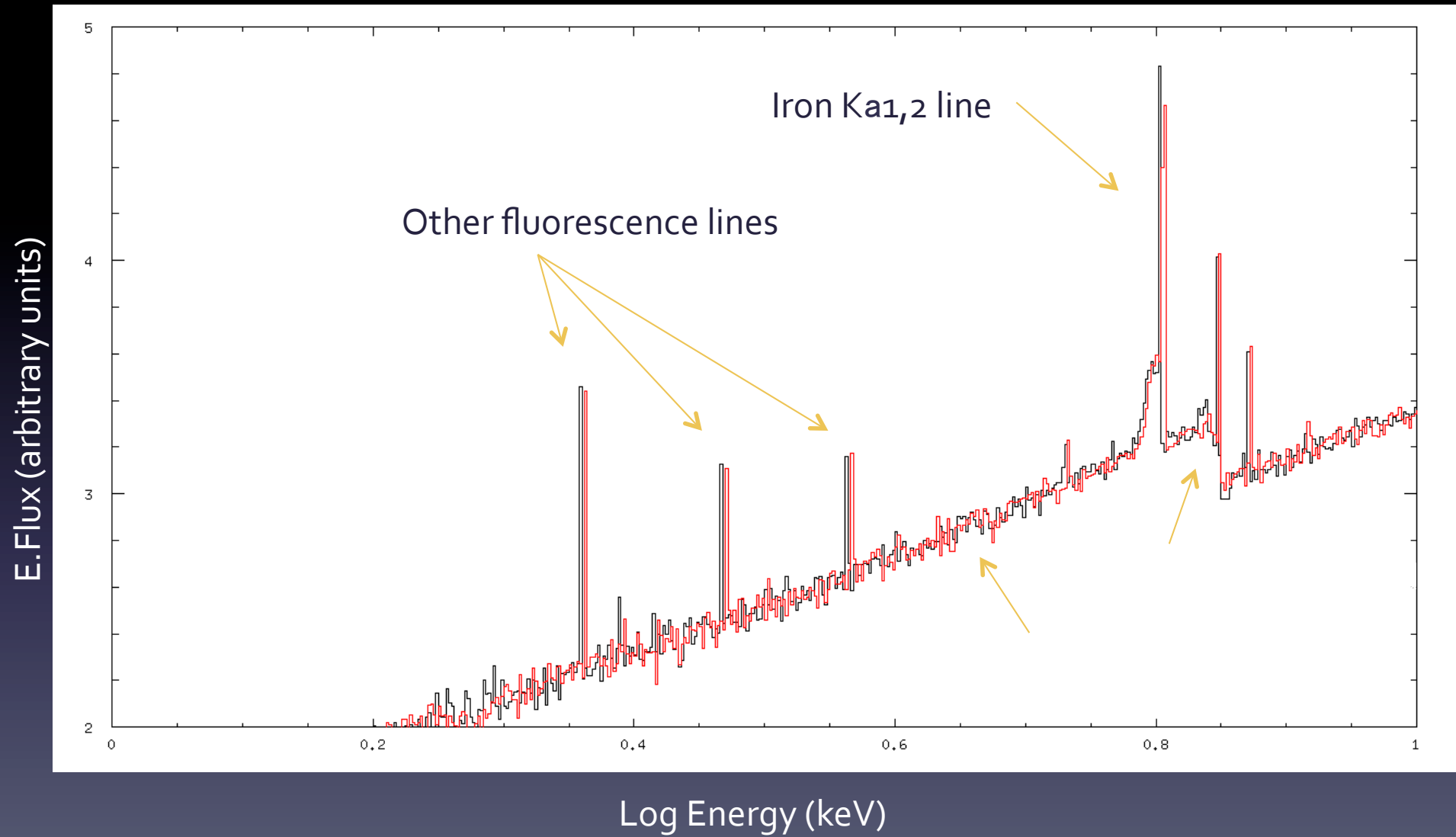
```
G4AtomicTransitionManager::Instance()->SetFluoDirectory("fluor_Bearden");
```

or dedicated UI command

```
/process/em/fluoBearden true
```

- **Principle** of change
  - Replacement of fluorescence lines available in Bearden (1967) directly into Geant4 files
  - Lines **not** in Bearden (1967) left as they are (most of them are absent)
  - Some lines resolved in Geant4 are not resolved in Bearden (1967)
  - Astrophysical impact of lines not in Bearden (1967) (or unresolved) negligible

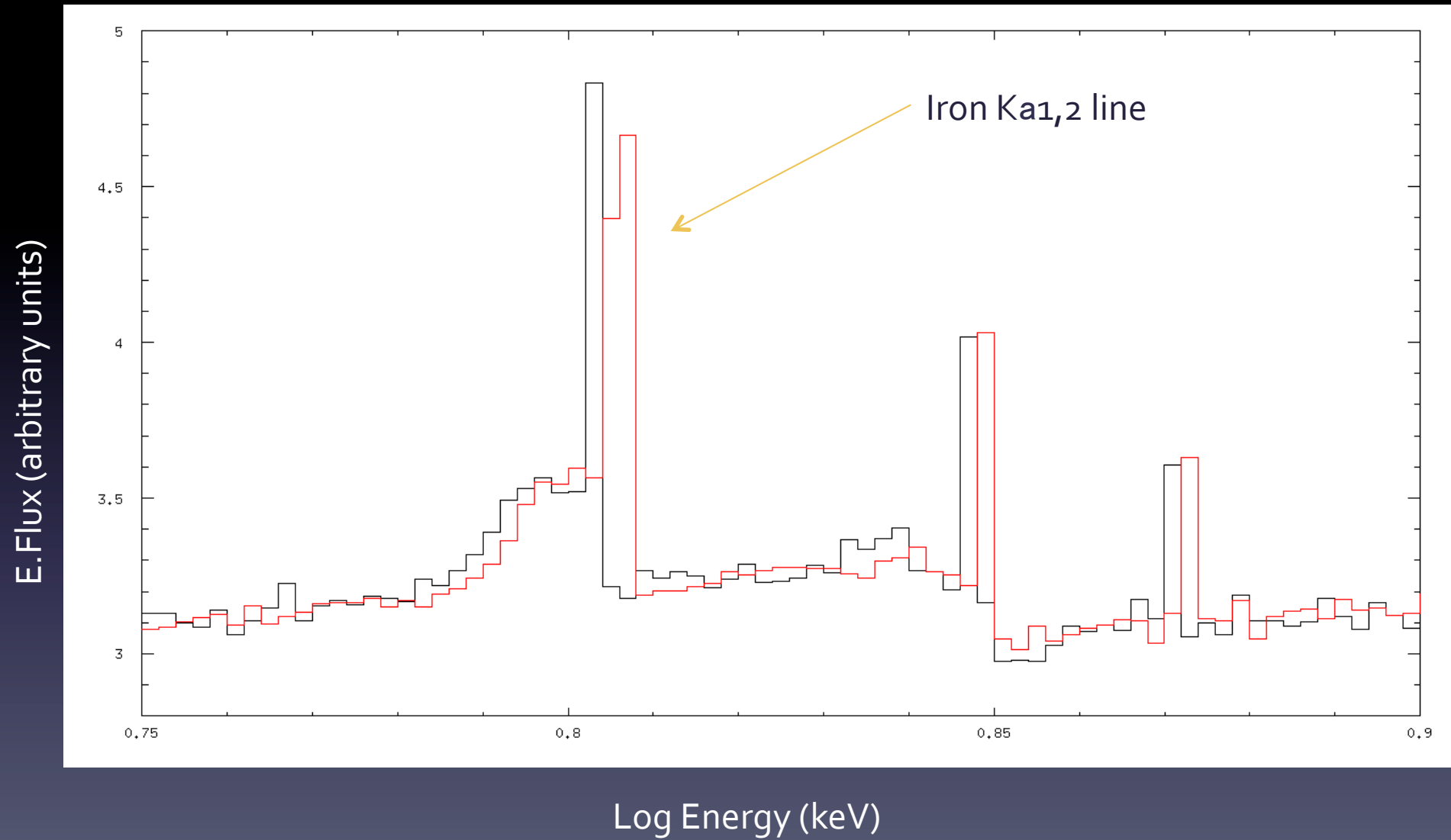
# X-ray reflection on a disk



— Geant4  
— Bearden (1967)

Courtesy of S. Paltani, Geneva U.

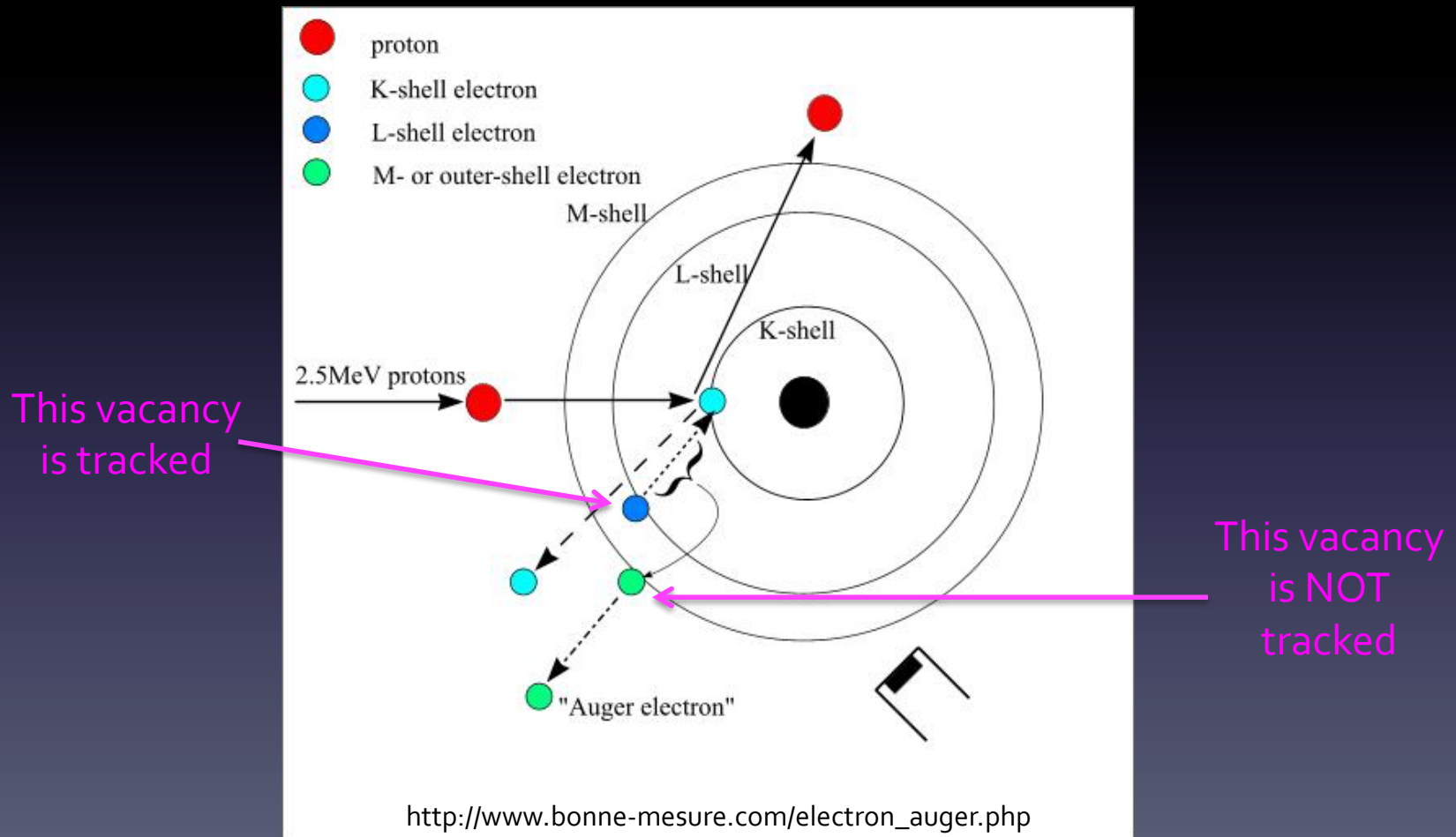
# X-ray reflection on a disk



— Geant4  
— Bearden (1967)

Courtesy of S. Paltani, Geneva U.

# Atomic deexcitation: Auger cascade simulation

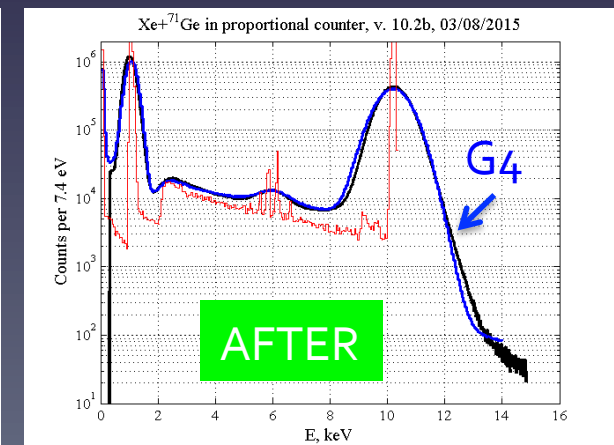
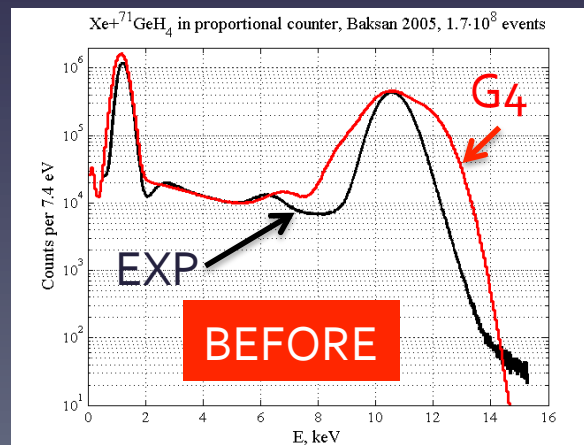


# Atomic deexcitation: Auger cascade simulation

- Added the possibility to **simulate Auger cascades** and the series of occurring vacancies, leading to multiple emission of Auger electrons
  - Bugzilla report #1727 by B. Suerfu
  - Provided a prototype extension
  - Confirmed by Y. Malyskin
- We added specific UI command to explicitly simulate (or not) the Auger cascade (active only when Auger production is active)
  - `/process/em/augerCascade true` or `false`
  - `/process/em/deexcitationIgnoreCut true`
  - To be put just after `/run/initialize`

Note: combination with  
RadioactiveDecay will be  
ready for 10.2  
G4ECDecay & G4ICDecay

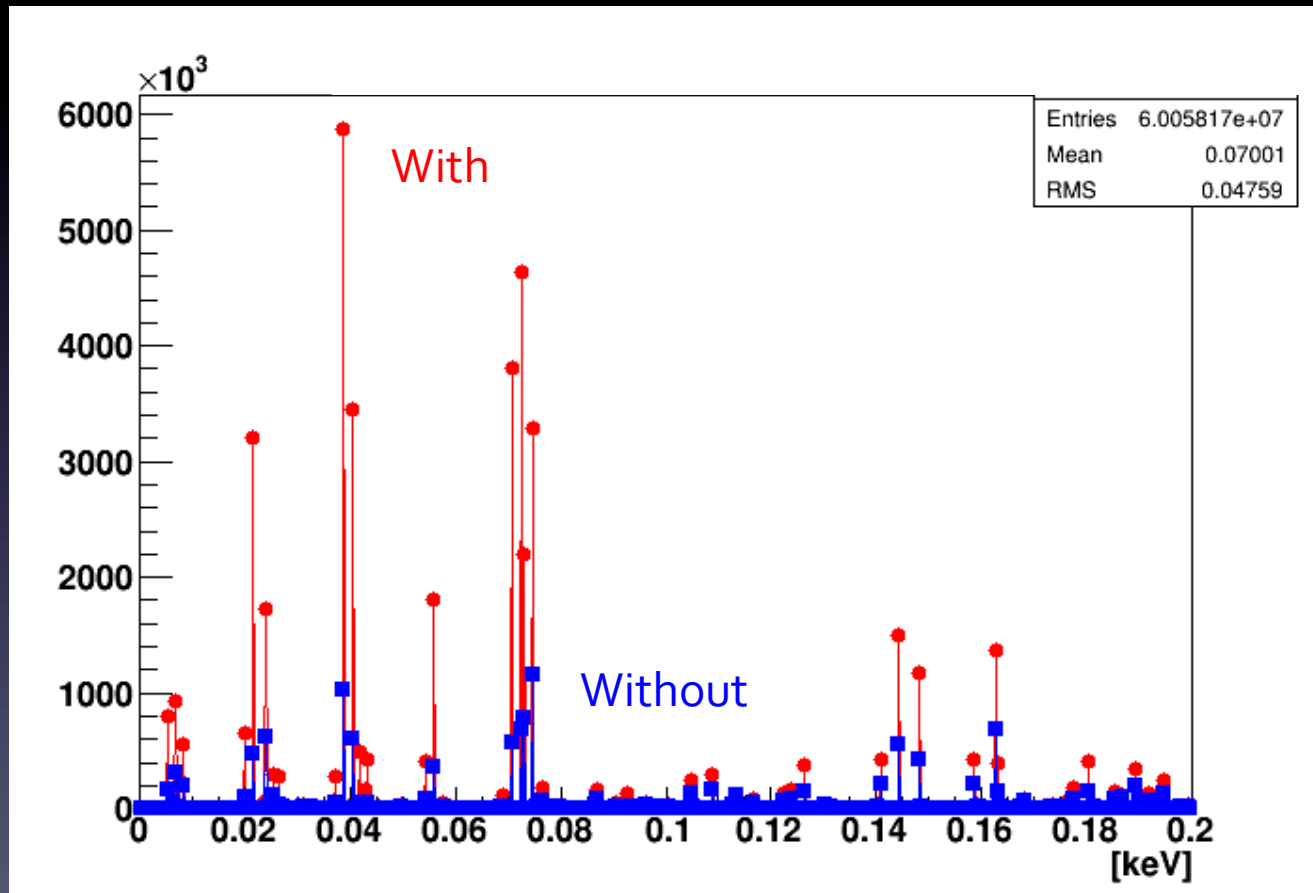
Ge 71 decay in Xe prop. counter  
- Simulation smeared with Gaussian  
- Measurements



# Atomic deexcitation: Auger cascade simulation

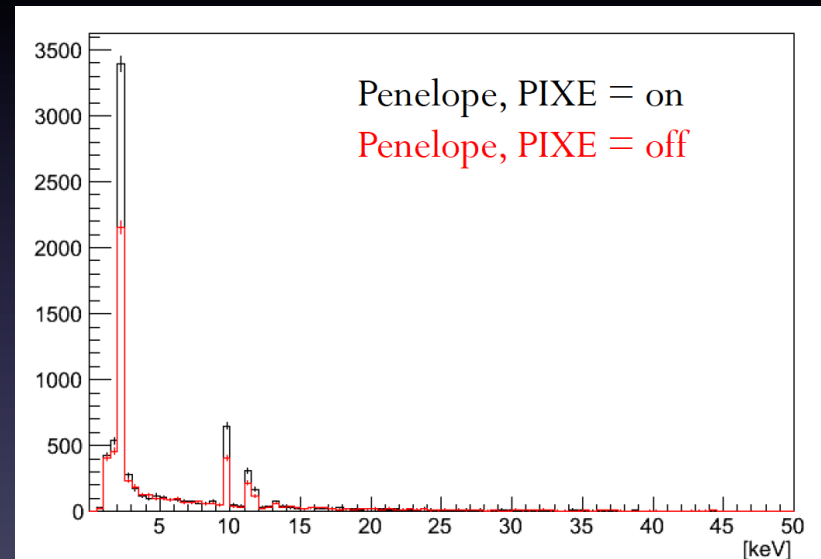
## Example

- Release 10.2 BETA
- TestEm5
- pixe.mac
- $10^7$  gammas
- 100 keV
- 50  $\mu\text{m}$ -thick Au target



# Atomic Deexcitation: fixing of Penelope deexcitation

- Bugzilla #1761 by M. Maire
- The Penelope Ionisation model has a built-in management of the atomic de-excitation
- If the PIXE flag is TRUE, the Penelope model produces de-excitation cascade twice
  - Once via the internal mechanism and once via the PIXE universal interface
  - The net result is an over-production of x-rays
- Fix: the Penelope ionisation model will
  - use its own internal mechanism for atomic de-excitation when PIXE is FALSE
  - use the G<sub>4</sub> EM unified atomic deexcitation interface when PIXE is TRUE



50 keV electrons in Au

## 4) ICRU'73 files for ions

- Updated **ICRU'73 files** for the computation of ions stopping powers
  - Reminder
    - $Z > 2$
    - 25 atomic elements
    - 31 simple compounds (a few revised compounds by [P. Sigmund](#))
  - This year, substituted 2016 files (new files for atomic elements and old files for compounds) by new PASS computations provided by [A. Schinner](#) in collaboration with [P. Truscott](#) ( $\geq$ G4EMLOW6.44).
  - Located in `$G4LEDATA/ion_stopping_data`



## 5) Verification and validation: gamma models

- Verification of **gamma attenuation coefficients** in a variety of element and materials
  - **18 elements** from  $Z=4$  to 92
  - **3 compounds**: water, PMMA, BGO (+other plastic phantoms)
- Performed by **S. Guatelli**, Wollongong U., as in IEEE TNS 52 (2005) 910 by Amako et al.
- Comparison with XCOM/NIST
- **5 EM Physics constructors**  
opto, op3, opt4, Livermore, Penelope
- **Attenuation coefficients** to test
  - Total, Rayleigh, Compton, photoelec, conversion

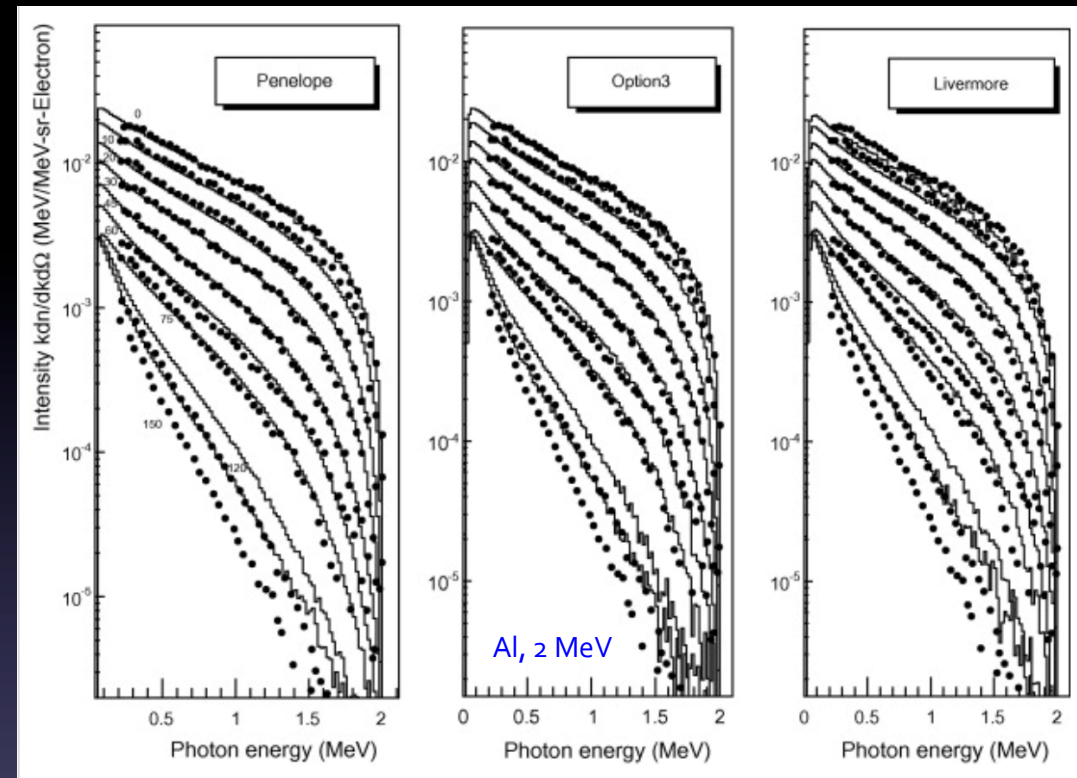
# Results: discussion

- ▶ In the last year, added:
  - New materials
  - Rayleigh scattering
  - Regression test
  - Standard\_option0
- ▶ Regression test: Geant4 10.1 agrees with Geant4 10.0 within statistical error bars.

- ▶ In general good agreement with NIST (within 5%, which is the NIST uncertainty).
- ▶ Penelope approach, Standard Option 0 and 3 Compton scattering report differences below  $\sim 20$  keV, where this process is negligible

# Verification and validation: bremsstrahlung

- Validation activity of **Geant4 bremsstrahlung** for thick targets, **< 3 MeV**, by L. Pandola et al.
- **Too much** energy/photon irradiated in the backward direction
- Good quantitative agreement for the forward direction



« The **Penelope model** shows the **best agreement with measurements** for incident electrons energies in the **MeV range**, but the choice is much less evident at lower energy (below 100 keV) ».

<http://dx.doi.org/10.1016/j.nimb.2015.03.033>

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Validation of the GEANT4 simulation of bremsstrahlung from thick targets below 3 MeV

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CrossMark

# 6) Status of Geant4-DNA

## Main objective

Extend the general purpose **Geant4** Monte Carlo toolkit for the simulation of interactions of radiation with biological systems at the cellular and DNA level in order to predict **early DNA damage** in the context of manned space exploration missions (« bottom-up » approach).

Designed to be developed and delivered in a **FREE software spirit** under Geant4 license, easy to **upgrade and improve**.

**2001**

Initiated at the European Space Agency/ESTEC by Petteri Nieminen

**2007**

First prototypes of **physics models** for liquid water added to Geant4 **9.1**

**2008**

Development coordinated by CNRS/IN2P3 (physics, chemistry, geometries)

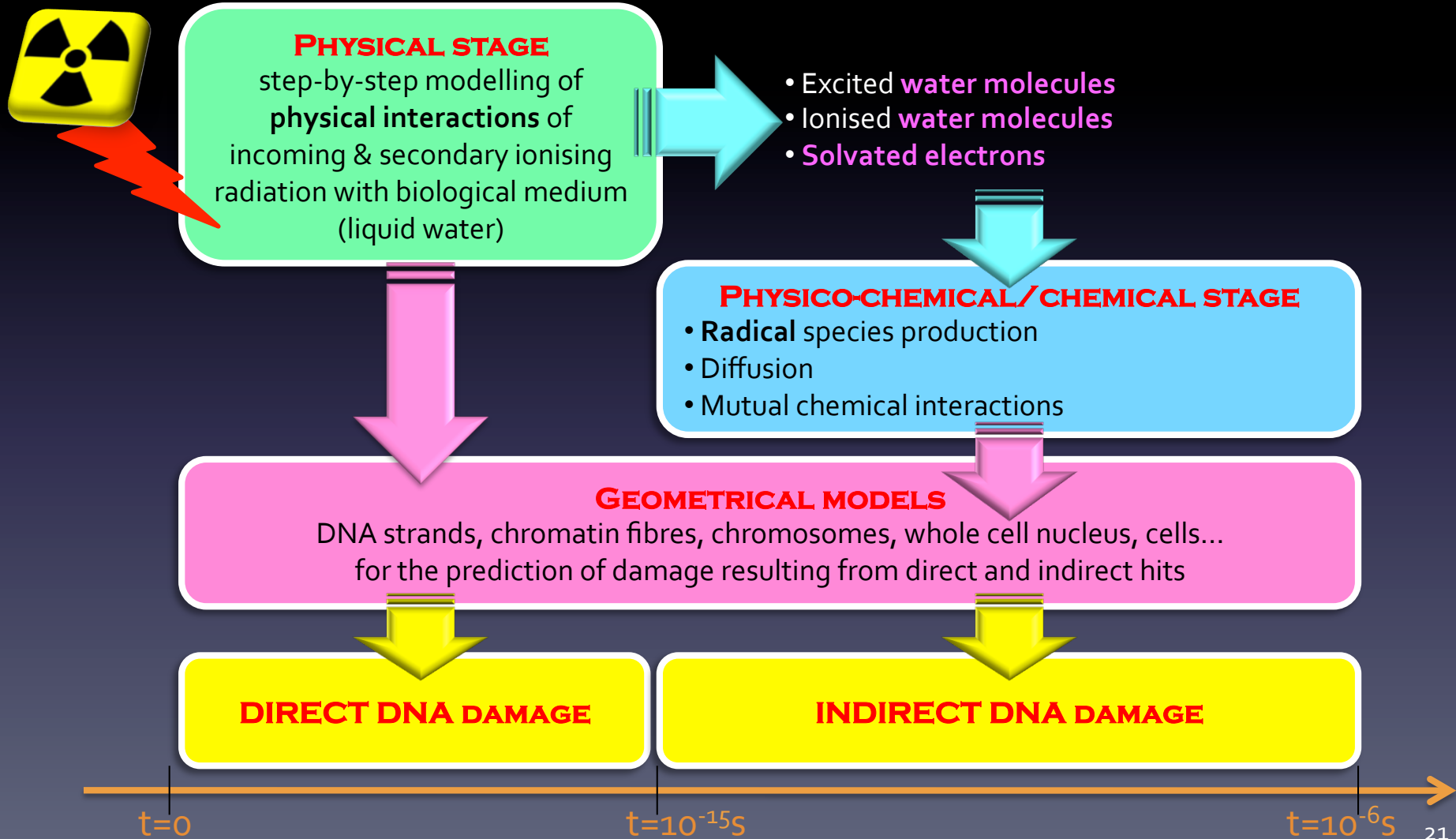
**2014**

**Chemistry stage** extension ready for end users in Geant4 **10.1**



W. Friedland  
D. Emfietzoglou  
M. Dingfelder

# How can Geant4-DNA model early DNA damage ?



# Overview of physics models for liquid water

## Electrons

### Elastic scattering

- Screened [Rutherford](#) and [Brenner-Zaider](#) below 200 eV
- Updated alternative version by [Uehara](#) from 10.2B
- Partial wave framework model by [C. Champion et al.](#), 3 contributions to the interaction potential

### Ionisation

- 5 levels for H<sub>2</sub>O
- Dielectric formalism & FBA using [H. Heller](#) optical data up to 1 MeV, and low energy corrections, derived from the work of [D. Emfietzoglou et al.](#)
- Improved alternative version by [D. Emfietzoglou and I. Kyriakou](#) from 10.2B

### Excitation (\*)

- 5 levels for H<sub>2</sub>O
- Dielectric formalism & FBA using [H. Heller](#) optical data and semi-empirical low energy corrections, derived from the work of [D. Emfietzoglou et al.](#)
- Improved alternative version by [D. Emfietzoglou and I. Kyriakou](#) from 10.2B

### Vibrational excitation (\*)

- [M. Michaud et al.](#) xs measurements in amorphous ice
- Factor 2 to account for phase effect

### Dissociative attachment (\*)

- [C. Melton](#) xs measurements

## G4LowECapture process for capture

See [Med. Phys. 37 \(2010\) 4692-4708 \(link\)](#)  
[Appl. Radiat. Isot. 69 \(2011\) 220-226 \(link\)](#)  
[Med. Phys. 42 \(2015\) 3870 \(link\)](#)

(\*) only available in Geant4-DNA

## Protons & H

### Excitation (\*)

- Miller & Green speed scaling of e<sup>-</sup> excitation at low energies and Born and Bethe theories above 500 keV, from [M. Dingfelder et al.](#)

### Ionisation

- Rudd semi-empirical approach by [M. Dingfelder et al.](#) and Born and Bethe theories & dielectric formalism above 500 keV (relativistic + Fermi density)

### Charge change (\*)

- Analytical parametrizations by [M. Dingfelder et al.](#)

### Nuclear scattering

- Classical approach by [Everhart et al.](#)

## He<sup>0</sup>, He<sup>+</sup>, He<sup>2+</sup>

### Excitation (\*) and ionisation

- Speed and effective charge scaling from protons by [M. Dingfelder et al.](#)

### Charge change (\*)

- Semi-empirical models from [M. Dingfelder et al.](#)

### Nuclear scattering

- Classical approach by [Everhart et al.](#)

## Li, Be, B, C, N, O, Si, Fe

### Ionisation

- Speed scaling and global effective charge by [Booth and Grant](#)




## Photons

- from EM « standard » and « low energy »

- Default: « Livermore » ([EPDLg](#))

# Geant4-DNA Physics constructors

6 constructors are available (4 new as BETA)

Constructor name	Content
<b>G4EmDNAPhysics</b>	Default models
G4EmDNAPhysics_option1 (beta)	Same as G4EmDNAPhysics but uses New multiple scattering model G4LowEWentzelVIModel
G4EmDNAPhysics_option2	Same as G4EmDNAPhysics but faster (usage of CDCS for ionisation processes)
 G4EmDNAPhysics_option3 (beta)	Same as G4EmDNAPhysics but includes nuclear scattering for protons and alphas
 G4EmDNAPhysics_option4 (beta)	New electron ionisation and excitation models by loannina team
 G4EmDNAPhysics_option5 (beta)	Same but usage of CDCS

All are located in

`$G4INSTALL/source/physics_lists/constructors/electromagnetic`

# New DRF models for electrons

- Some **deficiencies** in Geant4-DNA physics have been reported by collaboration members and users, for incident electrons
  - **Too low electronic excitation cross section** compared to experimental data or other MC codes (see for eg. *Med. Phys.* 37 (2010) 4692)
  - **Too low average energy transferred per ion pair  $W$**  (see for eg. *Phys. Med. Biol* 57 (2012) 3657)
  - Dose Point Kernels simulated with the **current Screened Rutherford elastic model** are not reliable (see for eg. *Appl. Radiat. Isot.* 83 (2014) 137)
- Thanks to **I. Kyriakou et al. at Univ of Ioannina**, Greece, these electron models have been improved
  - **Inelastic models** (based on the DRF theory by D. Emfietzoglou et al.)
    - inclusion of a truncation algorithm which accounts for broadened ionization thresholds; the truncated part is re-partitioned leading to higher excitation yield
    - Refinement of exchange and Coulomb corrections
  - **Elastic**: screening factor proposed by Uehara from vapor experimental data, instead of Grosswendt-Waibel

<http://dx.doi.org/10.1118/1.4921613>

## Technical Note: Improvements in GEANT4 energy-loss model and the effect on low-energy electron transport in liquid water

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*Centre d'Etudes Nucléaires de Bordeaux-Gradignan, CENBG, Chemin du Solarium, Université de Bordeaux, Gradignan 33175, France and Centre d'Etudes Nucléaires de Bordeaux-Gradignan, CENBG, Chemin du Solarium, CNRS/IN2P3, Gradignan 33175, France*

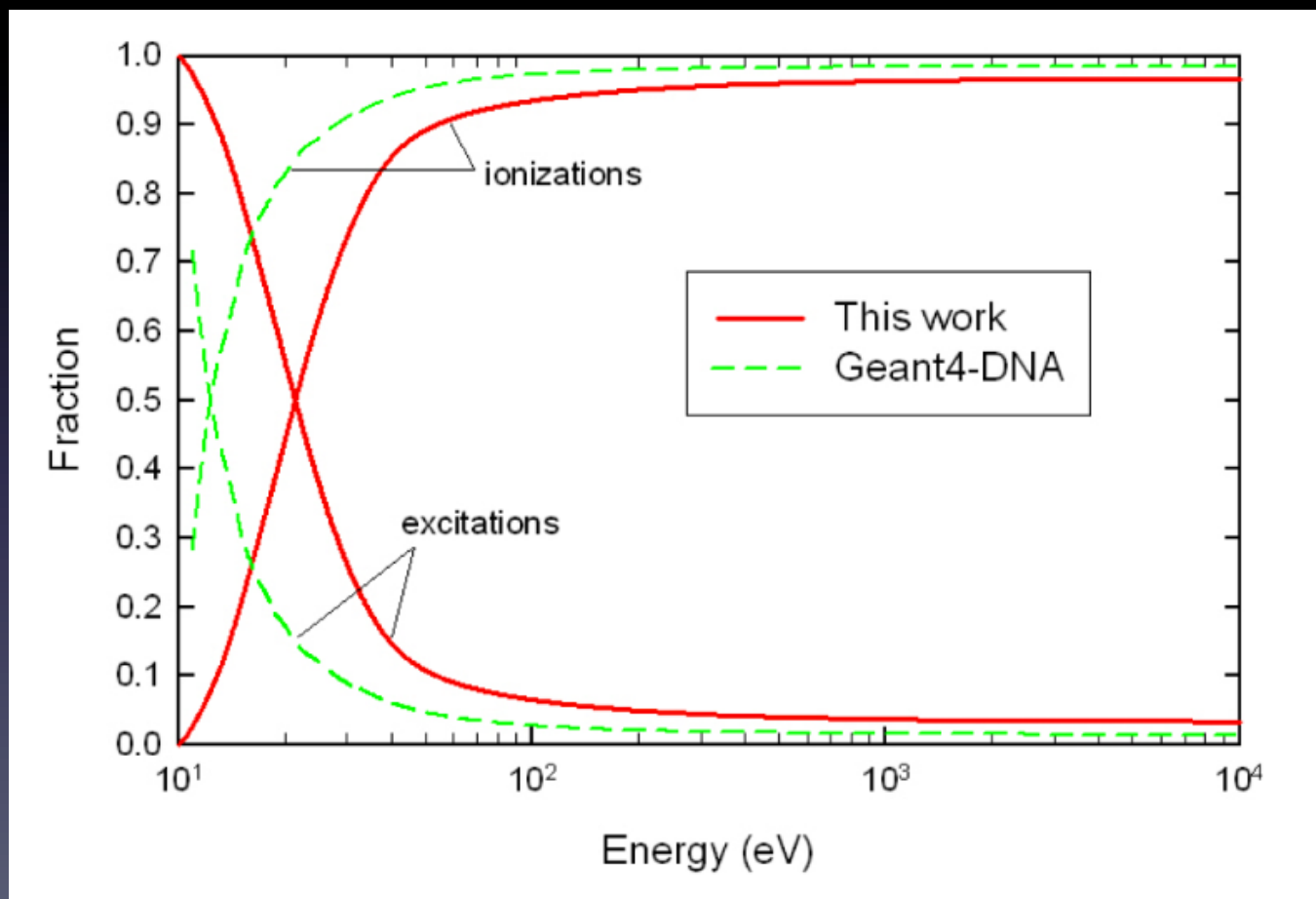
Z. Francis

*Department of Physics, Faculty of Sciences, Saint Joseph University, Mkalles, Beirut, Lebanon*



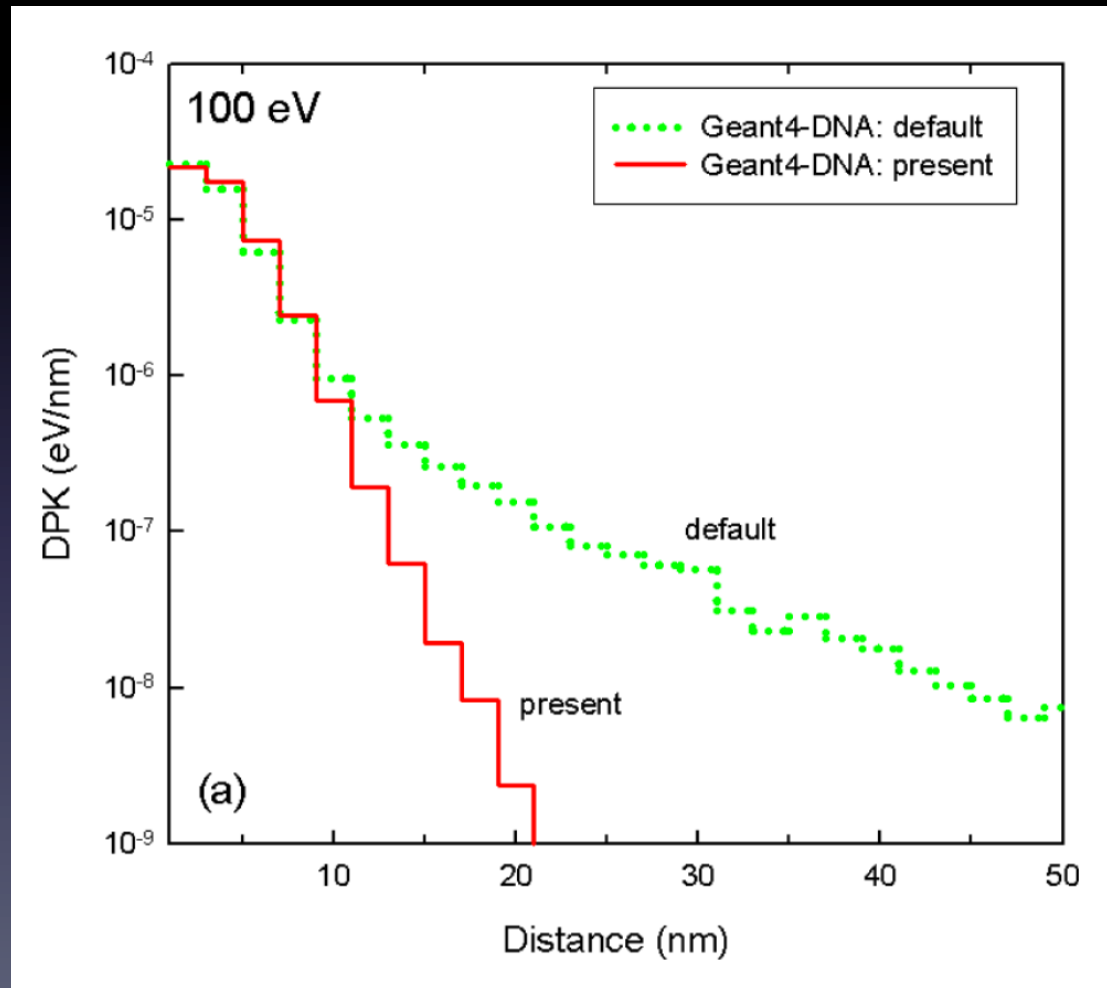
# Illustration of new DRF models

Contributions of ionisation & excitation



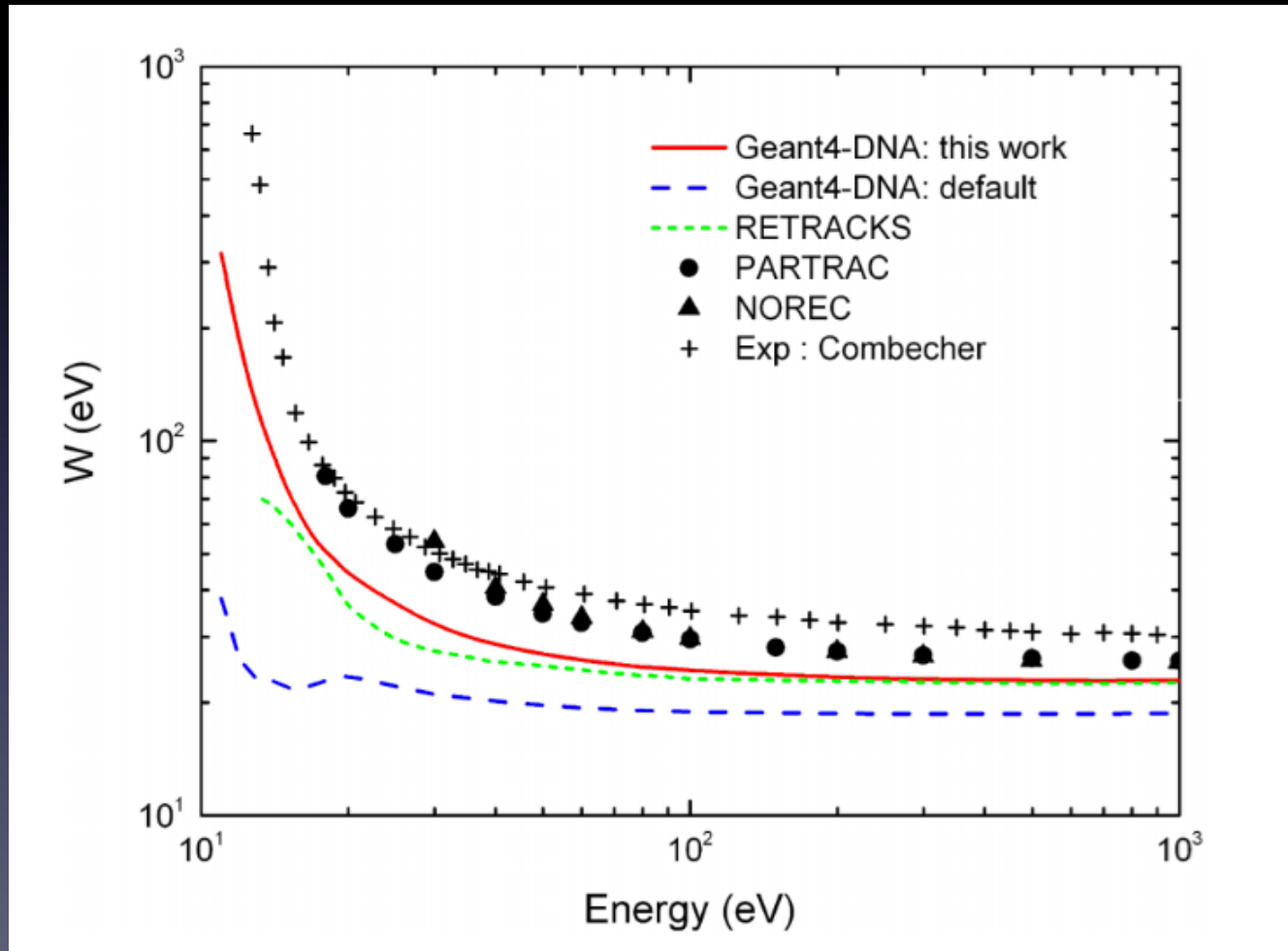
# Illustration of new DRF models

DPK



# Illustration of new DRF models

W-value



# Elastic scattering for protons and alphas

Classical mechanics approach: scattering angle may be numerically calculated and expressed in the CM frame (Everhart *et al.*, 1955)

$$\theta = \pi - 2(p / r_s) \int_0^{z_0} \frac{1}{\sqrt{1 - \frac{p^2}{r_s^2} z^2 - \frac{b}{r_s} z F_s(1/z)}} dz$$

The screening function used for proton projectiles is that reported from ICRU49

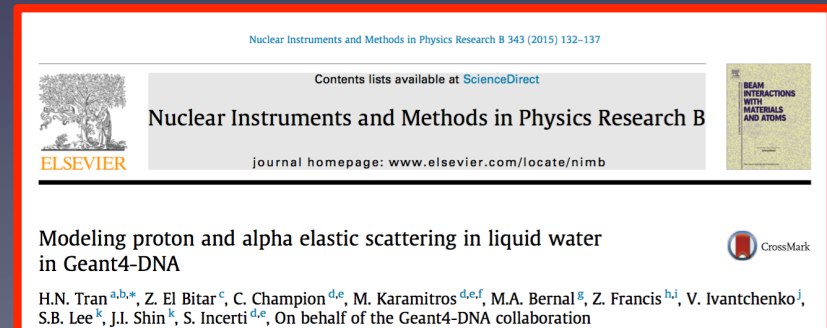
$$F_s(r / r_s) = 0.10e^{-6r/r_s} + 0.55e^{-1.2r/r_s} + 0.35e^{-0.3r/r_s}$$

The integral elastic scattering cross section is obtained from

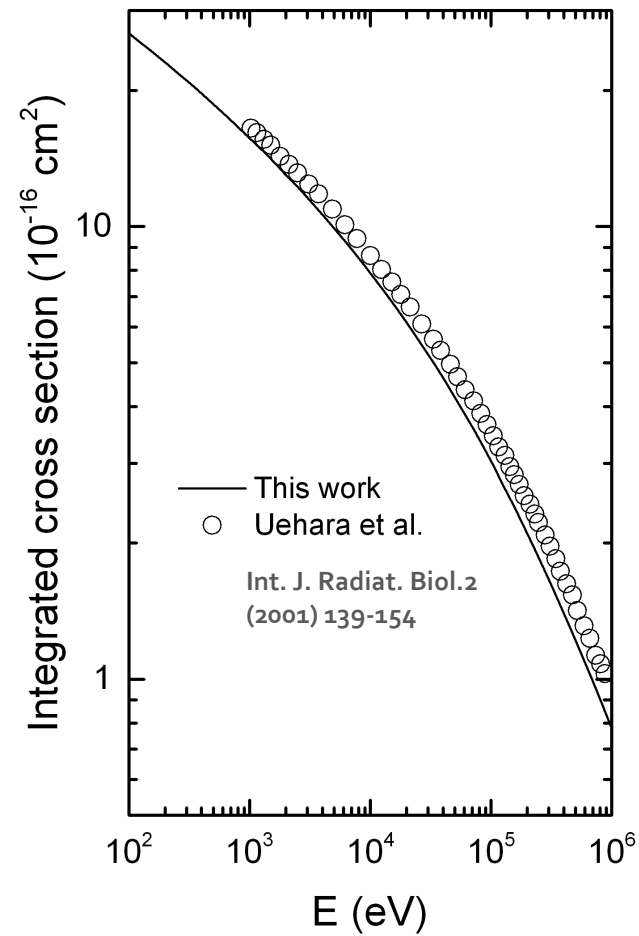
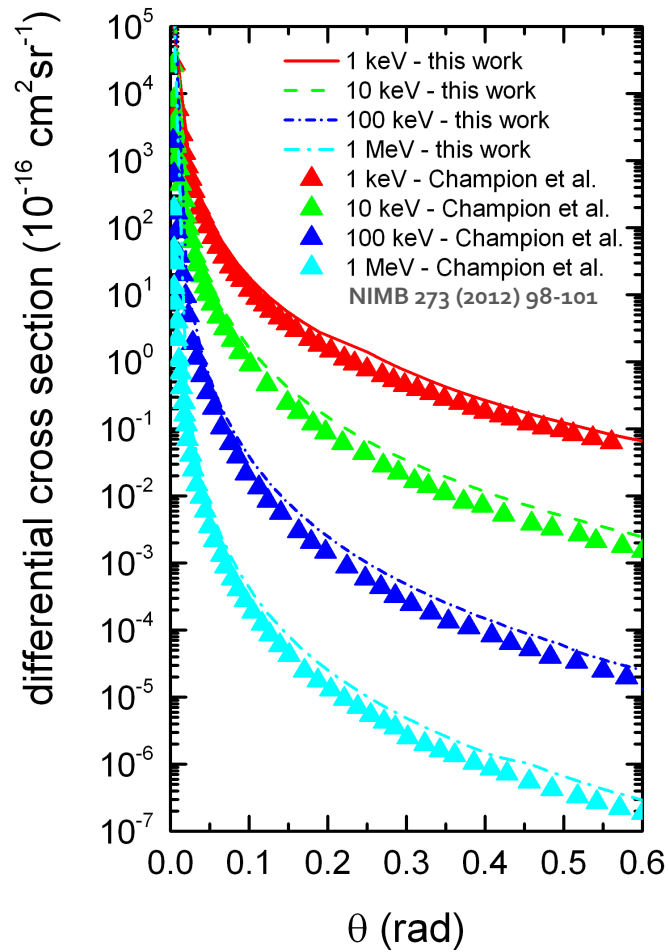
$$\frac{d\sigma_{el}}{d\Omega} = -\frac{p}{\sin\theta} \frac{dp}{d\theta}$$

$$\sigma_{el}(T) = 2\pi \int_{\theta_{cut}}^{\pi} \frac{d\sigma_{el}}{d\Omega} \sin\theta d\theta$$

<http://dx.doi.org/10.1016/j.nimb.2014.10.016>

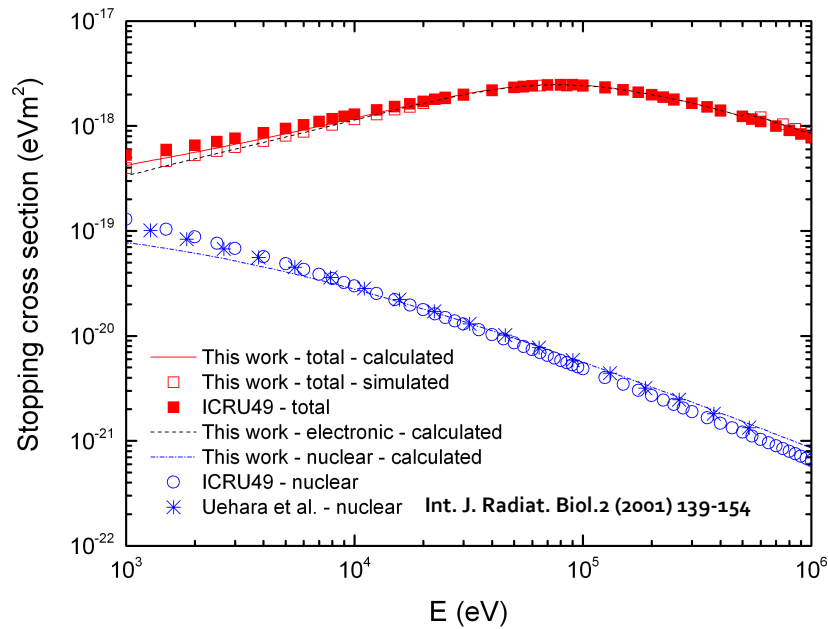


# Differential cross section and Integral cross section for protons

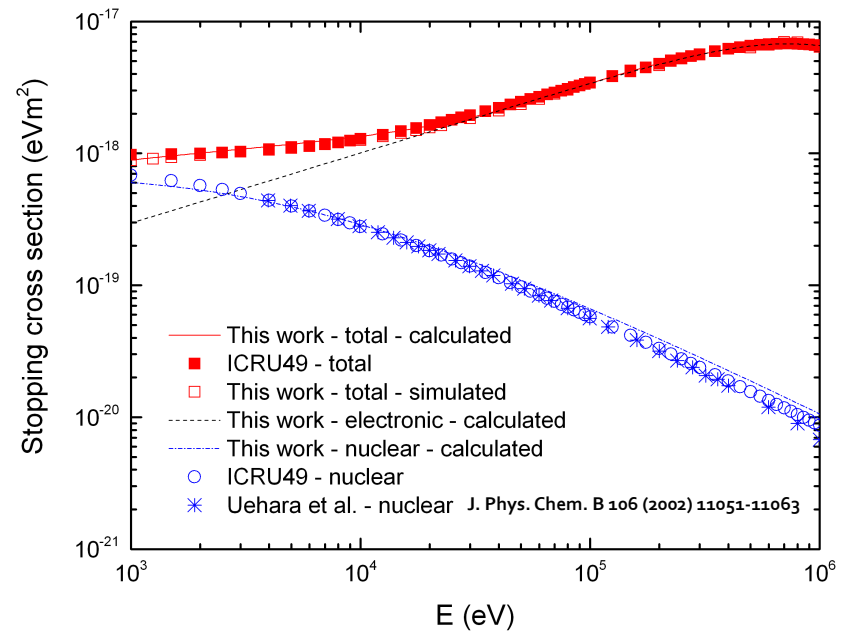


# Stopping cross section

Protons



Alphas



Total, electronic and nuclear stopping cross sections

- calculated from Geant4-DNA cross sections
- simulated with Geant4-DNA

compared to ICRU49 and Uehara et al. Monte Carlo simulations

# Other changes in models

- Handling of **G4IonTable**
  - Li, Be, B, C, N, O, Si, Fe
- Possibility to switch to a **stationary regime** in all energy loss models directly from PhysicsList
- **While loops** performance has been verified
  - For **Geant4-DNA physics**
  - For **Penelope physics**
  - Dedicated Twiki page

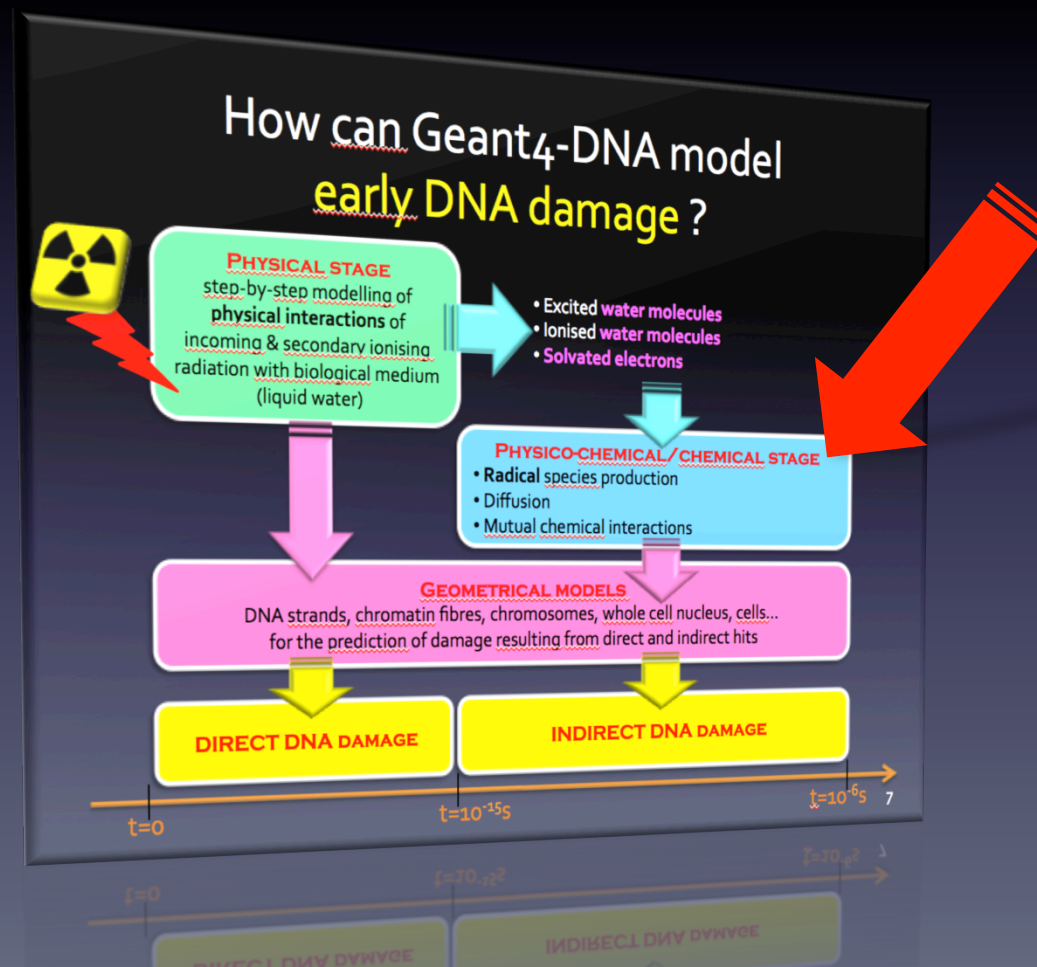
<https://twiki.cern.ch/twiki/bin/view/Geant4/LoweSystemTesting>

## While loops

Verification of the performance of "while loops" is on-going. The following classes have been checked:

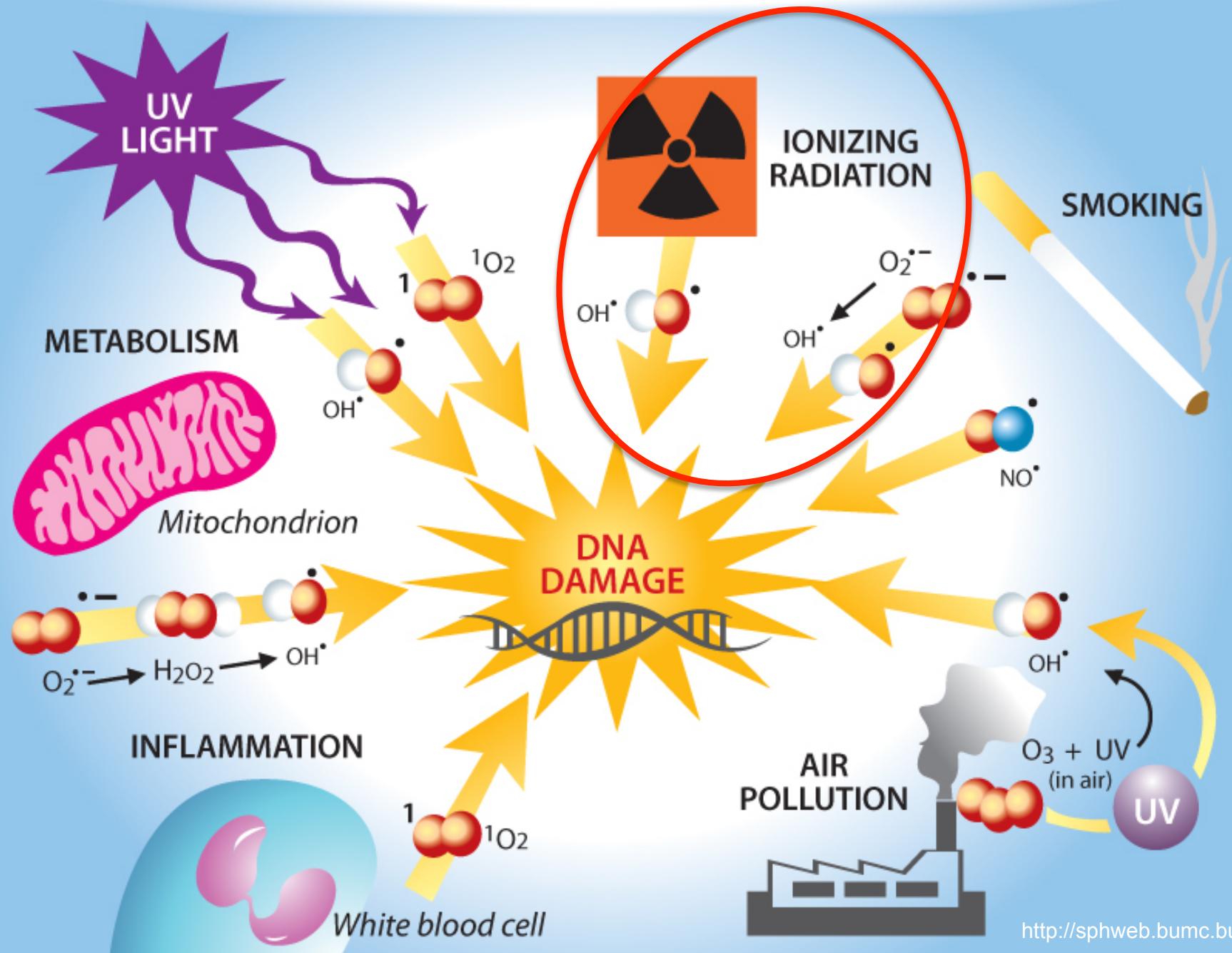
Directory	Class name	G4 version	line numbers of loop	Fix by tag ?	Verifier name
dna/models/src	G4DNABornExcitationModel1.cc	Geant4 10.2Beta	238, 248	no	SI
dna/models/src	G4DNABornExcitationModel2.cc	Geant4 10.2Beta	303	not used	SI
dna/models/src	G4DNAEmfietzoglouExcitationModel.cc	Geant4 10.2Beta	284, 295	no	SI
dna/models/src	G4DNABornIonisationModel1.cc	Geant4 10.2Beta	180, 244, 448, 590, 608 (longest for e- when fasterCode is false), 638, 937, 948	no	SI
dna/models/src	G4DNABornIonisationModel2.cc	Geant4 10.2Beta	194, 331, 473, 491 (longest for e- when fasterCode is false), 521, 765, 776	no	SI
dna/models/src	G4DNAEmfietzoglouIonisationModel.cc	Geant4 10.2Beta	175, 481, 494, 731, 742	no	SI
dna/models/src	G4DNACHampionElasticModel.cc	Geant4 10.2Beta	168	no	SI

# Geant4-DNA: PHYSICO-CHEMICAL & CHEMICAL STAGE





# FORMATION OF FREE RADICALS

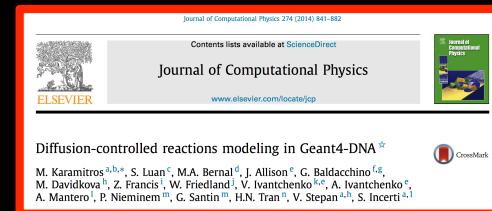


$t=10^{-15}s$

$t=10^{-12}s$

# Physico-chemical stage

- During this stage, water molecules
  - Dissociate if ionized
  - Relax or dissociate if excited



<http://dx.doi.org/10.1016/j.jcp.2014.06.011>

Electronic state	Dissociation channels	Fraction (%)
All <b>single ionization</b> states	$H_3O^+ + \bullet OH$	100
<b>Excitation</b> state A <sub>1</sub> B <sub>1</sub> : (1b <sub>1</sub> ) → (4a <sub>1</sub> /3s)	$\bullet OH + H\bullet$ $H_2O + DE$	65 35
<b>Excitation</b> state B <sub>1</sub> A <sub>1</sub> : (3a <sub>1</sub> ) → (4a <sub>1</sub> /3s)	$H_3O^+ + \bullet OH + e^-_{aq} (AI)$ $\bullet OH + \bullet OH + H_2$ $H_2O + DE$	55 15 30
<b>Excitation</b> state: Rydberg, diffusion bands	$H_3O^+ + \bullet OH + e^-_{aq} (AI)$ $H_2O + DE$	50 50
Dissociative attachment	$\bullet OH + OH^- + H_2$	100

- Products thermalize down to their energy of diffusion at equilibrium

$t=10^{-15}s$

$t=10^{-12}s$

$t=10^{-6}s$

# Chemical stage

Species	Diffusion coefficient D ( $10^{-9} m^2 s^{-1}$ )
$H_3O^+$	9.0
$H^\bullet$	7.0
$OH^-$	5.0
$e^-_{aq}$	4.9
$H_2$	4.8
$\bullet OH$	2.8
$H_2O_2$	2.3

In ConstructMolecules()

Reaction	Reaction rate ( $10^{10} M^{-1} s^{-1}$ )
$H_3O^+ + OH^- \rightarrow 2 H_2O$	14.3
$\bullet OH + e^-_{aq} \rightarrow OH^-$	2.95
$H^\bullet + e^-_{aq} + H_2O \rightarrow OH^- + H_2$	2.65
$H_3O^+ + e^-_{aq} \rightarrow H^\bullet + H_2O$	2.11
$H^\bullet + \bullet OH \rightarrow H_2O$	1.44
$H_2O_2 + e^-_{aq} \rightarrow OH^- + \bullet OH$	1.41
$H^\bullet + H^\bullet \rightarrow H_2$	1.20
$e^-_{aq} + e^-_{aq} + 2 H_2O \rightarrow 2 OH^- + H_2$	0.50
$\bullet OH + \bullet OH \rightarrow H_2O_2$	0.44

In ConstructReactionTable()

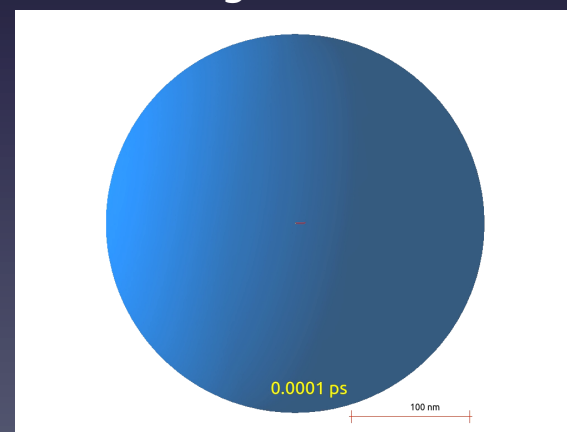
We followed the set of parameters published by the authors of the **PARTRAC** software (Kreipl et al., REB 2009). However, **these parameters can be modified by the user.**

# How to use Geant4-DNA for radiation chemistry ?

- Three examples have been released publicly in Geant4 10.1 in the « extended examples/medical/dna » category of Geant4 examples
  - CHEM1: activating chemistry
    - Display of chemical reactions at initialization
    - Illustration of usage of radiolysis macro commands « /scheduler/... »:
      - Verbosity
      - Stop of simulation after a certain time duration
      - Or after a maximum number of steps in time
  - CHEM2: altering chemistry run
    - How to access information at the time step level
    - How to set user minimum time step limits using a G4UserTimeStepAction user action class (TimeStepAction)
    - How to retrieve information from a given time step
      - Molecule names, reaction products...
  - CHEM3: user interactivity and visualization
    - How to handle user interactivity
      - SteppingAction, TrackingAction, visualization
    - Enables drawing of cumulative trajectory of species

Work in MT  
+  
G4\_WATER

Chem3 for 1 keV e-



<http://dx.doi.org/10.6084/mg.figshare.978887>

# Chemistry is activated using 3 instructions **only**...

## PhysicsList

- Register the `G4EmDNAChemistry` « physics-chemistry list »  
`RegisterConstructor( "G4EmDNAChemistry" );`

## Action Initialization

- In `Build()` method, creation of a `StackingAction`

The chemistry module is triggered when all physical tracks have been processed

## StackingAction

- Start **handling of chemistry tracks** at new stage  
`G4DNAChemistryManager::Instance()->Run();`

# Validation: radiochemical yields VS time

- We compared **measured G values of OH radicals** in liquid water to Monte Carlo simulations
- **Experiment**
  - **30 MeV proton beam** at NPI in Prague
  - Target is coumarin-3-carboxylic acid scavenger (**C<sub>3</sub>CA**), 3 concentrations (2, 20, 200 mM). C<sub>3</sub>CA forms fluorescent product with OH, 7-hydroxycoumarin-3-carboxylic acid (**7-OH-C<sub>3</sub>CA**)
  - The inverse of the reaction rate  $k$  [C<sub>3</sub>CA] corresponds to the **time scale of the reaction**.
- **Simulations**
  - **Geant4-DNA physics + RADAMOL** for radiolysis (15 & 30 MeV) developed at NPI (M. Davidkova et al.)
  - **Geant4-DNA physics + radiolysis** (20 MeV)
  - Same geometry as in previous setup : we selected three energies in order to cover the energy decrease of protons in the sample

## CONTRIBUTION OF INDIRECT EFFECTS TO CLUSTERED DAMAGE IN DNA IRRADIATED WITH PROTONS

K. Pachnerová Brabcová<sup>1,2</sup>, V. Štěpán<sup>3,2</sup>, M. Karamitros<sup>3</sup>, M. Karabin<sup>4</sup>, P. Dostálek<sup>4</sup>, S. Incerti<sup>3</sup>, M. Davidková<sup>2,\*</sup> and L. Sihver<sup>1,5</sup>

<sup>1</sup>Department of Applied Physics, Chalmers University of Technology, Fysikgränd 3, Göteborg SE-412 96, Sweden

<sup>2</sup>Department of Radiation Dosimetry, Nuclear Physics Institute of the CAS, Na Truhlářce 39/64, Prague 180 00, Czech Republic

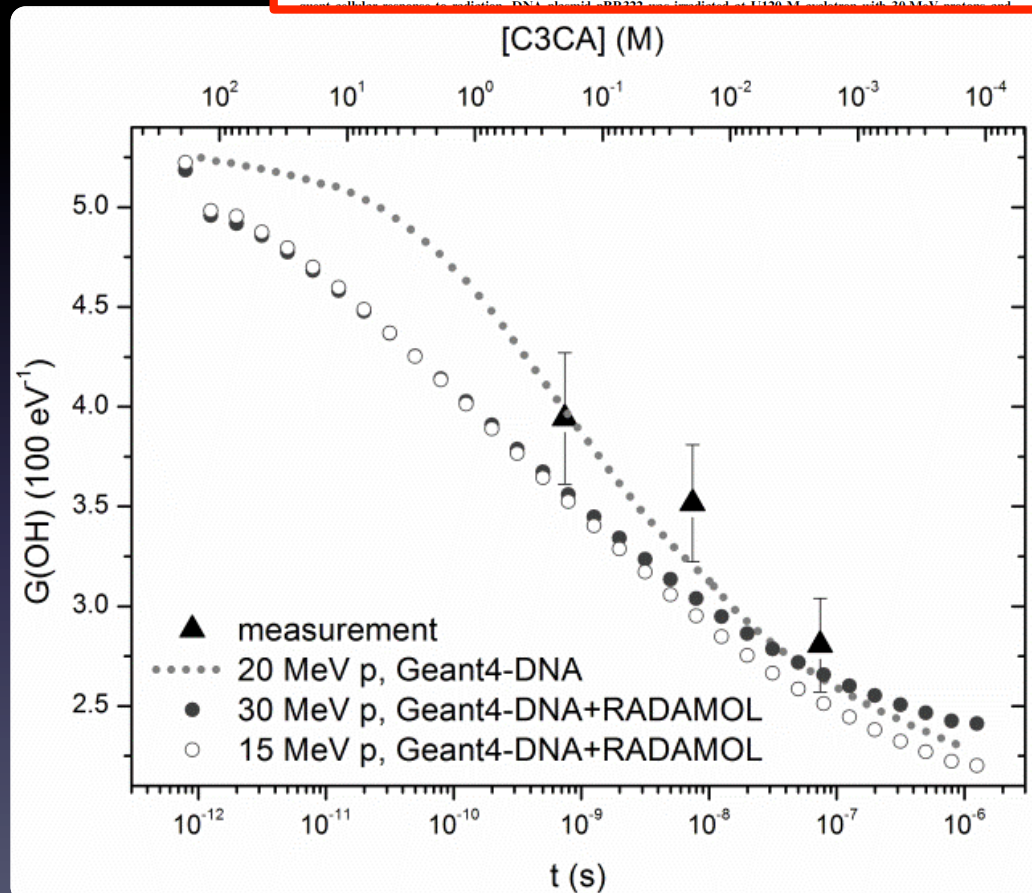
<sup>3</sup>Université de Bordeaux, CNRS/IN2P3, Centre d'Etudes Nucléaires de Bordeaux-Gradignan, CENBG, Chemin du Solarium, BP 120, 33175 Gradignan, France

<sup>4</sup>Department of Biotechnology, Institute of Chemical Technology Prague, Technická 5, Prague 166 28, Czech Republic

<sup>5</sup>Atominstytut, TU Wien, Stadionallee 2, 1020 Vienna, Austria

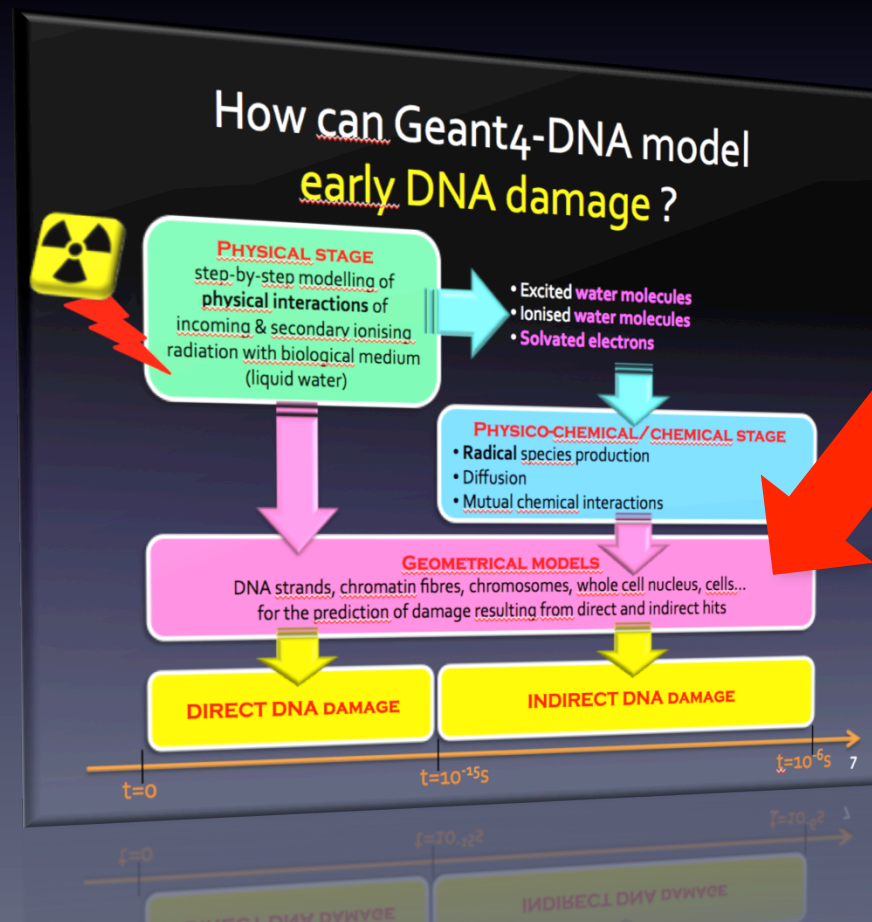
\*Corresponding author: davidkova@ujf.cas.cz

Protons are the dominant particles both in galactic cosmic rays and in solar particle events and, furthermore, proton irradiation becomes increasingly used in tumour treatment. It is believed that complex DNA damage is the determining factor for the consequences of the irradiation. DNA damage induced by protons is simulated by Geant4-Monte Carlo with 30 MeV proton



Calculated OH radical yields in time are in acceptable agreement with the experimental data, notably when utilising Geant4-DNA chemistry simulation capabilities

# Geant4-DNA: GEOMETRICAL MODELS



# A new interface to describe geometries in Geant4-DNA

- PDB : Protein Data Bank

<http://www.rcsb.org/pdb/>

- 3D structure of molecules
- Proteins
- Nucleic acids

- Description of DNA molecules

– **1FZX.pdb**

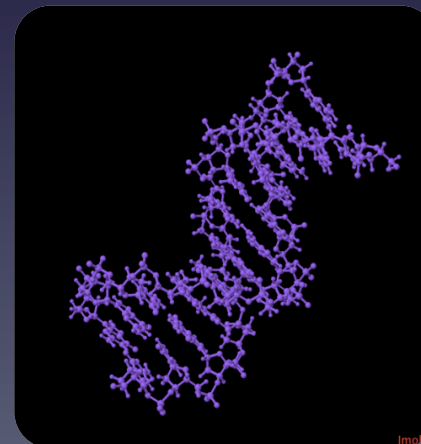
- Dodecamer
- 12 DNA base pairs
- $(2,8 \times 2,3 \times 4,01 \text{ nm}^3)$

– **1ZBB.pdb**

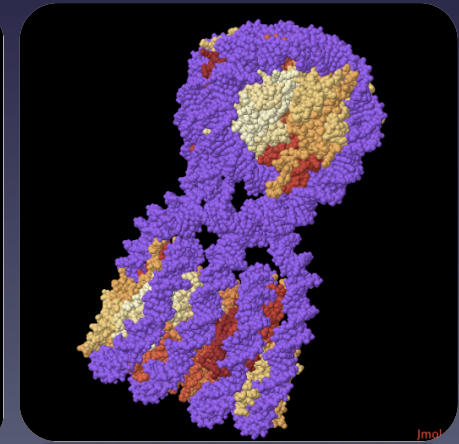
- Tetranucleosome
- 2 nucleosomes : 347 pairs of bases
- $(9,5 \times 15,0 \times 25,1 \text{ nm}^3)$

```

HEADER  STRUCTURAL PROTEIN/DNA          08-APR-05  1ZBB
TITLE   STRUCTURE OF THE 4_601_167 TETRANUCLEOSOME
...
ATOM    1  O5' DA I  1    70.094  16.969 123.433  0.50238.00  O
ATOM    2  C5' DA I  1    70.682  18.216 123.054  0.50238.00  C
ATOM    3  C4' DA I  1    69.655  19.289 122.776  0.50238.00  C
...
TER     14223    DT J 347
...
HELIX   1  1 GLY A  44  SER A  57  1              14
HELIX   2  2 ARG A  63  ASP A  77  1              15
...
SHEET   1  A 2 ARG A  83  PHE A  84  0
SHEET   2  A 2 THR B  80  VAL B  81  1  O VAL B  81  N ARG A  83
    
```



**1FZX.pdb**

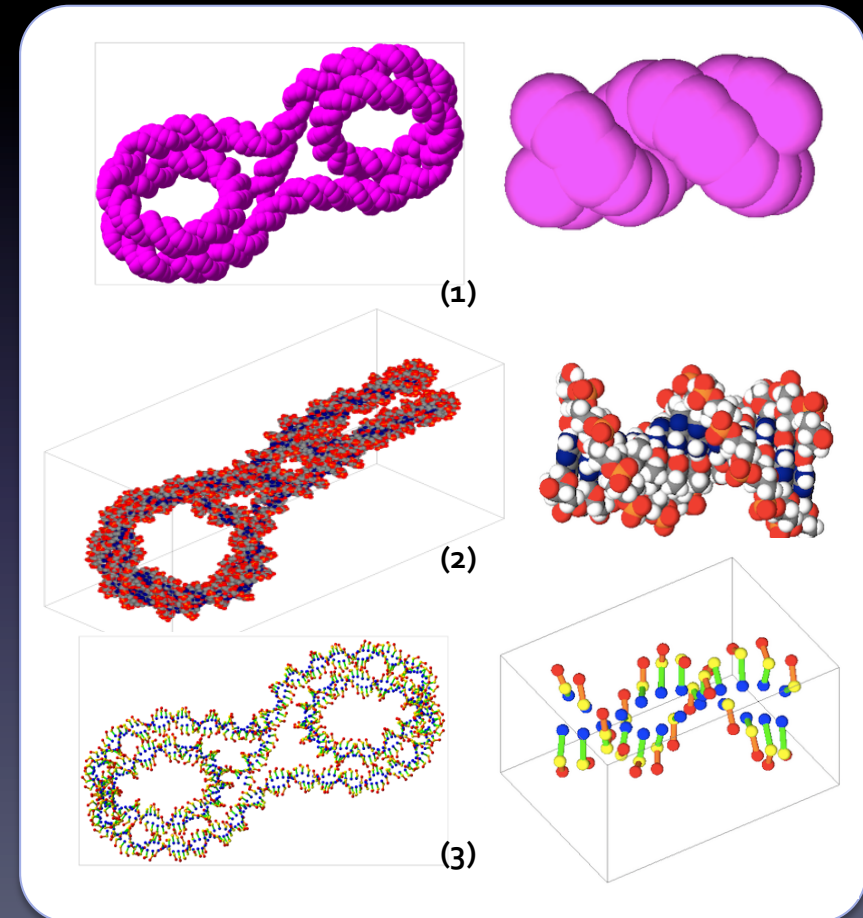


**1ZBB.pdb**



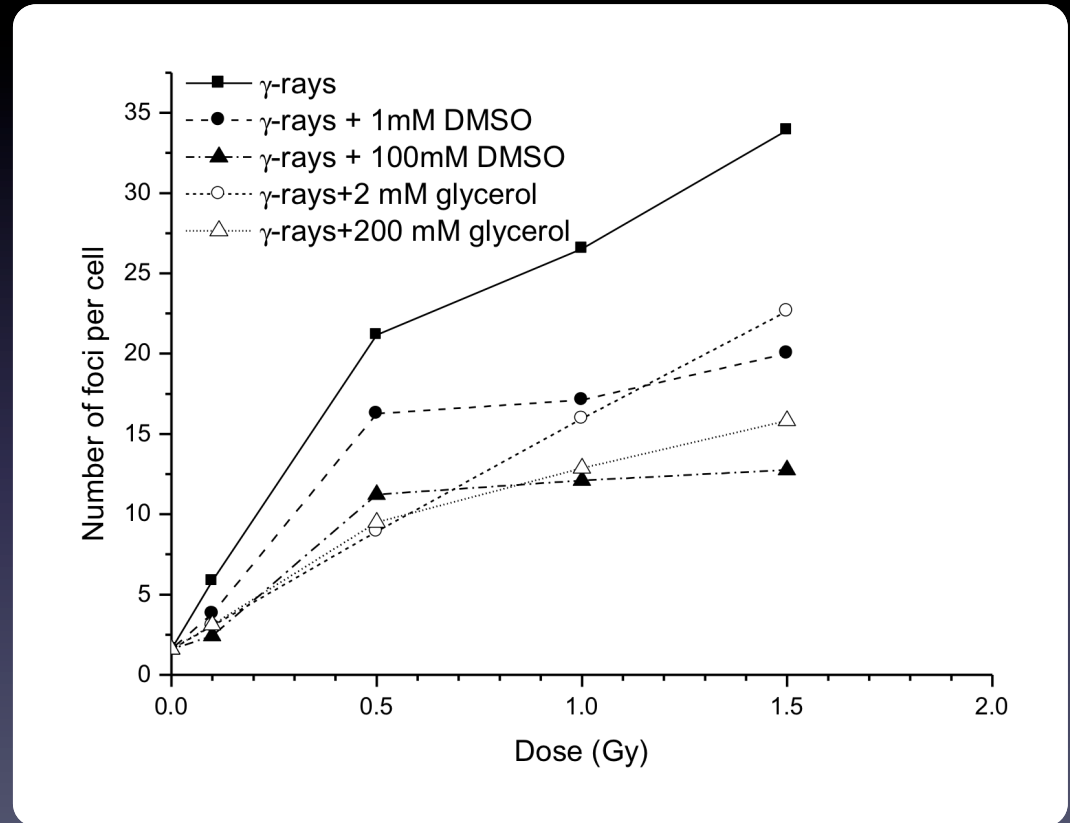
# « PDB4DNA » suite

- 1) A C++ library
  - Reading of PDB files
  - Build bounding boxes from atom coordinates
  - Search for closest atom from a given point
  - Geometry and visualization : 3 granularities
    - (1) Barycenter of nucleotides
    - (2) Atomistic
    - (3) Barycenter of nucleotide components
- 2) A Geant4-DNA example
  - Water box surrounding the molecule
  - The output results consists in a ROOT file, containing for each event:
    - energy deposit in bounding boxes
    - number of single strand breaks (SSB)
    - number of double strand breaks (DSB)
- Available on-line under Geant4 license



# Biological damage: **validation** on-going

- On-going validation activity for the prediction of **direct** damage under **gamma and proton** irradiation of **biological cells**
- Two  $^{\circ}\text{OH}$  **scavengers @ increasing concentration**
  - DMSO
  - Glycerol
- Several **cancer cell lines**
  - Eg. MCF-7 (breast)
- **University of Belgrade :**  
A. Ristic-Fira and I. Petrovic



# Geant4-DNA **examples included** in Geant4

10

Example code name	Purpose	Location
dnphysics	<ul style="list-style-type: none"> <li>• Usage of Geant4-DNA Physics processes</li> <li>• variable density</li> </ul>	\$G4INSTALL/examples/extended/medical/dna
microdosimetry	Combination of Standard EM or Low Energy EM processes with Geant4-DNA Physics processes	\$G4INSTALL/examples/extended/medical/dna
range	Usage of Geant4-DNA Physics processes for range simulation	\$G4INSTALL/examples/extended/medical/dna
svalue	Usage of Geant4-DNA Physics processes in spheres for S-value calculation	\$G4INSTALL/examples/extended/medical/dna
wvalue	Usage of Geant4-DNA Physics processes for W-value calculation	\$G4INSTALL/examples/extended/medical/dna
chem1, chem2, chem3	Usage of Geant4-DNA chemistry	\$G4INSTALL/examples/extended/medical/dna
wholeNuclearDNA	Cell nucleus	\$G4INSTALL/examples/extended/medical/dna
pdb4dna	Interface to PDB database	\$G4INSTALL/examples/extended/medical/dna
(microbeam)	(3D cellular phantom)	(\$G4INSTALL/examples/advanced)

# Summary

- Low energy EM Physics
  - Low energy limit treatment of gamma models
  - New Monash models
  - Update of atomic de-excitation
  - Update of ICRU73
  - Further verification & validation activities
- Geant4-DNA
  - New electron models
  - Chemistry prototype + 3 examples
  - Geometries : pdb4dna
  - New extended/medical/dna examples

# Thanks for your attention

and specials thanks to

J.M.C. Brown, S. Guatelli, V. Ivantchenko, S. Paltani, L. Pandola, B. Suerfu, the Geant4-DNA Collaboration

P. Nieminen and G. Santin @ ESA

## The Geant4 Low Energy Electromagnetic Physics Working Group

Welcome to the [official web site](#) of the Geant4 collaboration Low Energy Electromagnetic Physics working group.

### Purpose

The Geant4 Low Energy Electromagnetic Physics Working Group develops and maintains a set of models to describe the electromagnetic interactions of photons, electrons, hadrons and ions with matter down to very low energies (eV scale), including the [Geant4-DNA project](#) ([link](#)), initiated and partly funded by the [European Space Agency](#). Applications of such models range from high energy physics experiments to space science and astrophysics to the medical and biological fields. These activities take place in full collaboration with the [Standard Electromagnetic Physics working group](#) of the Geant4 collaboration.

### What's new in Geant4 10.1 ? (December 2014)

- [Overview](#) of our most recent developments.
- Version 6.41 of the set of Low Energy electromagnetic data files is required.

### Physics

- [Processes](#) is a link to the catalog of [Geant4 low energy electromagnetic Physics processes](#) and to other useful information related to these processes.
- [Physics Lists](#) describes [recommended Physics lists](#) for applications involving low energy electromagnetic Physics processes.
- [Examples](#) recommended for the usage of Geant4 electromagnetic Physics.

# Backup

# Initialization of chemistry: List of chemical reactions & reaction rates

# chem1

## Verbose(1) Occuring reactions

Reaction	Reaction Rate [dm3/(mol*s)]
H3O <sup>+</sup> + e <sub>aq</sub> <sup>-</sup> -> H <sup>0</sup>	2.11e+10
H3O <sup>+</sup> + OH <sup>-</sup> -> No product	1.43e+11
OH <sup>0</sup> + e <sub>aq</sub> <sup>-</sup> -> OH <sup>-</sup>	2.95e+10
OH <sup>0</sup> + OH <sup>0</sup> -> H2O2 <sup>0</sup>	4.4e+09
OH <sup>0</sup> + H <sup>0</sup> -> No product	1.44e+10
e <sub>aq</sub> <sup>-</sup> + e <sub>aq</sub> <sup>-</sup> -> OH <sup>-</sup> + OH <sup>-</sup> + H <sub>2</sub> <sup>0</sup>	5e+09
e <sub>aq</sub> <sup>-</sup> + H <sup>0</sup> -> OH <sup>-</sup> + H <sub>2</sub> <sup>0</sup>	2.65e+10
e <sub>aq</sub> <sup>-</sup> + H2O2 <sup>0</sup> -> OH <sup>-</sup> + OH <sup>0</sup>	1.41e+10
H <sup>0</sup> + H <sup>0</sup> -> H <sub>2</sub> <sup>0</sup>	1.2e+10

```
G4WT0 > Physics stage ends
G4WT0 > *** G4Scheduler starts processing
G4WT0 > At time :      1 ps Reaction : OH^-1 (-69) + H3O^1 (-73) -> No product
G4WT0 > At time :      3 ps Reaction : e_aq^1 (-64) + OH^0 (-72) -> OH^-1 (-142)
G4WT0 > At time :      3 ps Reaction : H3O^1 (-71) + OH^-1 (-142) -> No product
G4WT0 > At time : 59.3971 ps Reaction : OH^0 (-94) + H^0 (-141) -> No product
G4WT0 > At time : 103.14 ps Reaction : e_aq^1 (-36) + OH^0 (-88) -> OH^-1 (-143)
G4WT0 > At time : 127.186 ps Reaction : e_aq^1 (-65) + OH^0 (-78) -> OH^-1 (-144)
G4WT0 > At time : 169.258 ps Reaction : H3O^1 (-85) + OH^-1 (-143) -> No product
G4WT0 > At time : 201.482 ps Reaction : e_aq^1 (-49) + H3O^1 (-125) -> H^0 (-145)
G4WT0 > At time : 600.47 ps Reaction : e_aq^1 (-46) + OH^0 (-104) -> OH^-1 (-146)
G4WT0 > At time : 4.96327 ns Reaction : OH^0 (-82) + OH^0 (-106) -> H2O2^0 (-147)
G4WT0 > At time : 16.0101 ns Reaction : e_aq^1 (-32) + H3O^1 (-129) -> H^0 (-148)
G4WT0 > At time : 96.4559 ns Reaction : e_aq^1 (-22) + H3O^1 (-93) -> H^0 (-149)
G4WT0 > *** G4Scheduler ends at time : 1 mus
```

## Verbose(2) Detail of time steps: reaction & duration

```
G4WT1 > Physics stage ends
G4WT1 > *** G4Scheduler starts processing
G4WT1 > *** End of step N°1      T_i= 1 ps      dt= 0 ps      T_f= 1 ps
At time :      1 ps Reaction : OH^-1 (-69) + H3O^1 (-73) -> No product
G4WT1 > *** End of step N°2      T_i= 1 ps      dt= 0 ps      T_f= 1 ps
*** End of step N°3      T_i= 1 ps      dt= 1 ps      T_f= 2 ps      eCollisi
At time :      3 ps Reaction : e_aq^1 (-64) + OH^0 (-72) -> OH^-1 (-142)
G4WT1 > *** End of step N°4      T_i= 2 ps      dt= 1 ps      T_f= 3 ps
At time :      3 ps Reaction : H3O^1 (-71) + OH^-1 (-142) -> No product
G4WT1 > *** End of step N°5      T_i= 3 ps      dt= 0 ps      T_f= 3 ps
*** End of step N°6      T_i= 3 ps      dt= 3.19769 ps      T_f= 6.19769 ps
*** End of step N°7      T_i= 6.19769 ps      dt= 4.24303 ps      T_f= 10.
*** End of step N°8      T_i= 10.4407 ps      dt= 5.1737 ps      T_f= 15.6144 ps
```

## Verbose(3) Detail of time step duration calculation

```
G4WT1 > Physics stage ends
G4WT1 > *** G4Scheduler starts processing
G4WT1 >
G4WT1 > *** Start Of Step N°1 ***
G4WT1 > Current Global time : 1 ps
G4WT1 > *** Time stepper returned : 1.54648 ps ***
G4WT1 > *** The minimum time returned by the processes is : 0 ps ***
G4WT1 > *** End of step N°1      T_i= 1 ps      dt= 0 ps      T_f= 1 ps
It has also reached the user time limit

*** Start Of Step N°2 ***
G4WT1 > Current Global time : 1 ps
G4WT1 > *** Time stepper returned : 0 ps ***
G4WT1 > *** The minimum time returned by the processes is : 4.32364 mus ***
G4WT1 > At time :      1 ps Reaction : OH^-1 (-69) + H3O^1 (-73) -> No product
G4WT1 > *** End of step N°2      T_i= 1 ps      dt= 0 ps      T_f= 1 ps
It has also reached the user time limit

*** Start Of Step N°3 ***
G4WT1 > Current Global time : 1 ps
G4WT1 > *** Time stepper returned : 1 ps ***
G4WT1 > *** The minimum time returned by the processes is : 4.32364 mus ***
G4WT1 > *** End of step N°3      T_i= 1 ps      dt= 1 ps      T_f= 2 ps
It has also reached the user time limit
```

(verbose level is selected using UI commands)

# chem1

Verbose(4)

Maximum detail:

- trackID (<o)

- Pre & post-step positions

- Volumes

- Chemical processes

```
G4WT1 > Physics stage ends
G4WT1 > *** G4Scheduler starts processing
G4WT1 >
G4WT1 > *** Start Of Step N°1 ***
G4WT1 > Current Global time : 1 ps
G4WT1 > *** Time stepper returned : 1.54648 ps ***
G4WT1 > *** The minimum time returned by the processes is : 0 ps ***
G4WT1 > *** G4Scheduler::DoIt ***
G4WT1 > #Name          trackID      Position                Pre step volume      Post step volume      Process
G4WT1 > H20^-1          -66          -0.0276062 -0.0635558 1.21083 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^-1          -66          -0.0276062 -0.0635558 1.21083 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -62          -0.0262441 -0.0657665 1.20832 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -62          -0.0262441 -0.0657665 1.20832 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -61          -0.0266101 -0.0649094 1.21005 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -61          -0.0266101 -0.0649094 1.21005 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -60          -0.0261657 -0.0652823 1.21039 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -60          -0.0261657 -0.0652823 1.21039 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -59          -0.025907  -0.0673742 1.21049 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -59          -0.025907  -0.0673742 1.21049 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -54          -0.0299001 -0.0945952 1.50938 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -54          -0.0299001 -0.0945952 1.50938 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -51          -0.027727  -0.121723  1.93883 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -51          -0.027727  -0.121723  1.93883 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -47          -0.0293585 -0.144776  2.24876 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -47          -0.0293585 -0.144776  2.24876 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -34          -0.0322278 -0.233501  3.49242 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -34          -0.0322278 -0.233501  3.49242 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -33          -0.030755  -0.233669  3.49276 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -33          -0.030755  -0.233669  3.49276 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -25          -0.00715171 -0.317087  4.55492 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -25          -0.00715171 -0.317087  4.55492 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -24          -0.00647864 -0.31762  4.55433 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -24          -0.00647864 -0.31762  4.55433 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -20          0.0140478  -0.346855  4.89029 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -20          0.0140478  -0.346855  4.89029 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -14          -0.0283664 -0.29422  4.15272 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -14          -0.0283664 -0.29422  4.15272 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -12          -0.0294111 -0.228729  3.42316 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -12          -0.0294111 -0.228729  3.42316 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -11          -0.0283104 -0.222311  3.33667 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -11          -0.0283104 -0.222311  3.33667 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -9          -0.027194  -0.209459  3.1837 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -9          -0.027194  -0.209459  3.1837 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -7          -0.0277828 -0.147386  2.28426 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -7          -0.0277828 -0.147386  2.28426 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -8          -0.051704  -0.508428  3.1833 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -8          -0.051704  -0.508428  3.1833 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -11          -0.0583704 -0.555377  3.33001 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -11          -0.0583704 -0.555377  3.33001 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -15          -0.0504777 -0.558158  3.45370 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -15          -0.0504777 -0.558158  3.45370 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -14          -0.0583004 -0.58455  4.12515 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -14          -0.0583004 -0.58455  4.12515 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -58          0.0740418  -0.240022  4.00058 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -58          0.0740418  -0.240022  4.00058 um          ---                  World                H2O_DNAMolecularDecay
G4WT1 > H20^1          -58          0.0740418  -0.240022  4.00058 um          World                ---                    H2O_DNAMolecularDecay
G4WT1 > H20^1          -58          0.0740418  -0.240022  4.00058 um          ---                  World                H2O_DNAMolecularDecay
```