

COULOMB EXCITATION OF ^{140}Sm

by

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THESIS

for the degree of

MASTER OF SCIENCE



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Abstract

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Collaboration details

ENSAR2: European Nuclear Science and Applications Research - 2 <http://www.ensarfp7.eu>, UiO, ISOLDE, other contributors to the experiment?

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Chapter 1

Introduction

+ Motivation

kinsim [1]

The experiment has been done before, with lower energy (and another target), Malin Klintefjord. <http://urn.nb.no/URN:NBN:no-56121>

Experiment conducted 8th - 14th of August 2017.

Chapter 2

Theory

Quadrupole deformation of nuclei.

Shape coexistence possible for certain regions of N and Z .

- triaxial shape / shape coexistence
- benchmark for theoretical models
- transition probabilities and quadrupole moments between several excited states are not known
- fundamental research

COULEX:

- nucleus excited by electromagnetic interaction.
- de-excitation → gamma

2.1 Oppgaveteksten

Oppgavens mål:

The ISOLDE facility at CERN has been upgraded to provide higher energies and intensities for radioactive ion beams. A new experiment to study ^{140}Sm was performed in the summer of 2017. The goal of the experiment was to measure electromagnetic transition probabilities and electric quadrupole moments for several excited states in ^{140}Sm by measuring Coulomb excitation probabilities. A large data set was obtained using silicon detectors to determine the energies and angles of scattered particles, and germanium detectors to measure gamma rays from excited states in ^{140}Sm .

The goal of the master thesis is to analyze the data from this experiment. The required tasks include development and improvement of data analysis software to determine Coulomb excitation yields. These yields will then, in a second step, be

compared to theoretical calculations and transition probabilities and quadrupole moments will be extracted using chi-square minimization procedures.

Prosjektbeskrivelse (omfang 60 studiepoeng):

The shape of an atomic nucleus is determined by a delicate interplay between macroscopic (liquid drop) properties and microscopic shell effects. Nuclei with filled proton or neutron shells (i.e. magic nuclei) are generally spherical in shape, whereas nuclei with open shells gain energy by assuming a deformed shape. Depending on the occupation of specific orbitals, the nuclear shape can change drastically by adding or removing protons or neutrons. Certain nuclei exhibit shape coexistence, i.e. the coexistence of quantum states that correspond to different shapes. Because the shape of a nucleus is so sensitive to the underlying nuclear structure and to changes of the proton and neutron numbers, the excitation energy, or the angular momentum, observables related to the nuclear shape are used as benchmarks for theoretical models.

Nuclei in the rare earth region, and in particular the chain of samarium isotopes, exhibit a variety of shape effects. The Sm isotope with closed neutron shell at $N=82$, ^{144}Sm , is spherical in shape. Adding neutrons to ^{144}Sm changes the deformation to an elongated (prolate) quadrupole shape. The transition from spherical to prolate shape, which occurs for ^{152}Sm at $N=90$, can be interpreted as a shape-phase transition. Flattened (oblate) quadrupole shapes are predicted by theory to occur below the $N=82$ shell closure. An earlier experiment studying ^{140}Sm at CERN-ISOLDE found triaxial shape for this isotope, i.e. a shape where all three principal axes of the ellipsoid have different lengths. ^{140}Sm can therefore be considered to lie at the critical point of a phase transition from spherical to deformed, and from prolate to oblate shape.

Foreløpig tittel:

Coulomb excitation of ^{140}Sm

Metoder som tenkes benyttet:

Multi-step Coulomb excitation with radioactive beam, isotope separation on-line technique, nuclear spectroscopy, particle-gamma and particle gamma-gamma coincidence analysis, advanced chi-square minimization procedures.

2.2 Information sources

- CD: <https://www.ikp.uni-koeln.de/~warr/doc/cd.pdf>
- Why CoulEx? https://iks32.fys.kuleuven.be/wiki/brix/images/5/58/10_20151123_

[Illana_BriX15_web.pdf](#)

- 2017: <https://iopscience.iop.org/article/10.1088/1361-6471/aa5c4e#jgaa5c4es2>
- 2017: <http://iopscience.iop.org/article/10.1088/1361-6471/aa990f/pdf>
- http://publications.lib.chalmers.se/records/fulltext/175494/local_175494.pdf
- https://www.euroschoolonexoticbeams.be/site/files/nlp/LNP700_contrib2.pdf
- 2004: <http://accelconf.web.cern.ch/AccelConf/e04/PAPERS/TUXCH01.PDF>
- 2003: https://ac.els-cdn.com/S0168583X02018864/1-s2.0-S0168583X02018864-main.pdf?_tid=64f42a8d-b37c-42a6-a3c5-f01dcee73366&acdnat=1545049646_8918b985af428e17c97411
- 2002: https://ac.els-cdn.com/S0168900201009548/1-s2.0-S0168900201009548-main.pdf?_tid=71a410a3-6554-4268-ac1a-1b43cae4039d&acdnat=1545056166_15ff5318affd89c7e63f81

Post-accelerated beams ISOLDE <http://iopscience.iop.org/article/10.1088/1361-6471/aa78ca>

PSB <https://home.cern/science/accelerators/proton-synchrotron-booster>

Chapter 3

Coulomb excitation experiment

3.1 ISOLDE at CERN

The acronym ISOLDE stands for Isotope Separator On Line DEvice. ISOLDE is a Radioactive Ion Beam (RIB) facility at CERN in Meyrin, Switzerland. [Figure 3.1](#) shows the CERN accelerator complex [2], where ISOLDE is located beside the Proton Synchrotron Booster (PSB).

kan gjerne forklare figuren litt mer

The facility can produce over 1000 different radionuclides to be used in a wide variety of experiments in nuclear physics, atomic physics, solid state physics, life sciences and fundamental interactions. Experiments have been performed at ISOLDE since 1967 and since 2001 experiments with post-accelerated RIBs have been conducted. The high intensity and energy upgrade (HIE-ISOLDE) have made it possible to deliver energies up to 10 MeV/u in 2018 [3–5].

Most of the around 4000 known nuclides are radioactive. In many cases it is not possible to make radioactive nuclei targets and perform an experiment because of the short half-life of the nucleus of interest. To study these radioactive nuclei, RIBs are used on stable targets. One way of obtaining a RIB is to use the Isotope Separator On Line (ISOL) method. In the ISOL method, two accelerator systems is needed. The first accelerator is used to produce the radioactive atoms at rest, and the second accelerator is used to accelerate these atoms [6].

3.1.1 Beam production

A continuous proton beam of 1.4 GeV ($\sim 10^{18}$ protons) from the PSB comes into the ISOLDE facility and collide with a thick production target of tantalum (Ta), producing the elements in the chart of nuclides up to tantalum by fragmentation reactions (basically smashing the Ta target into pieces). Tantalum is not used in all experiments, but it was in this experiment. The production target is chosen from a stable region heavier than the nucleus of interest.

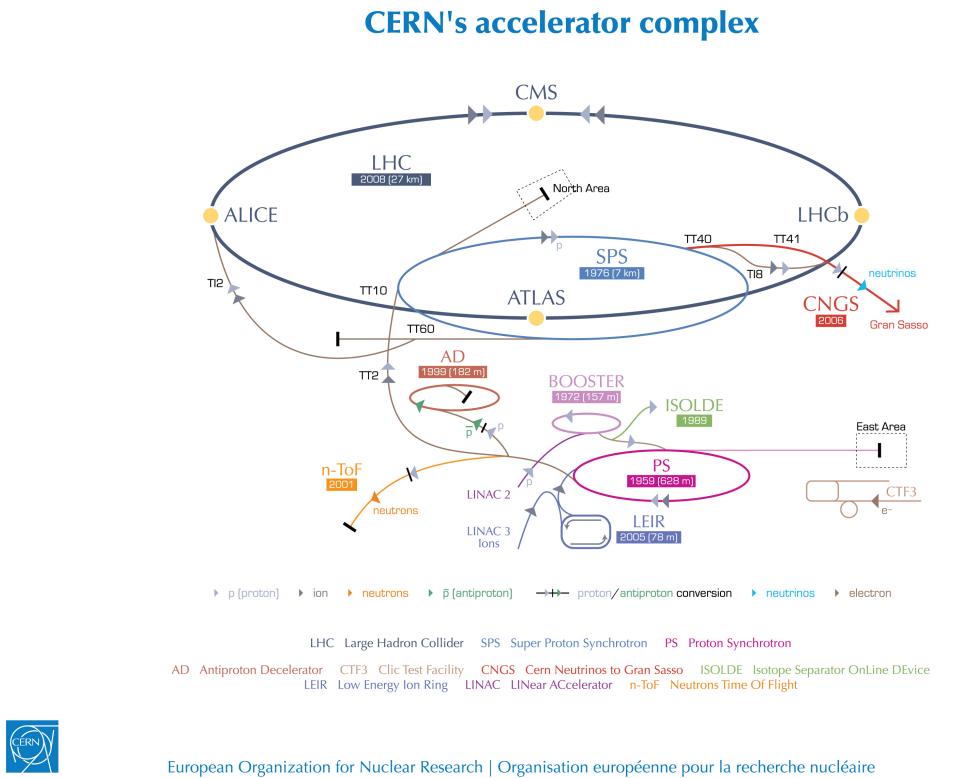


Figure 3.1: The CERN accelerator complex. ISOLDE gets accelerated protons from LINAC 2 and the PS BOOSTER.

Fra Andreas:

These bunches are accelerated by the PSB continuously, one bunch every 1.2 s. ISOLDE typically takes 50% of all proton bunches from the PSB, the rest goes to the LHC (and other experiments).

Production target:

*bruker laser on/off for å se hva annet som kommer ut av beamen

RILIS:

The resonance ionization laser ion source (RILIS) is based on the method of step-wise excitation and ionization of the atom. It is an element-selective process which is used to produce ion beams of the correct element [7]. In this experiment RILIS was used to select samarium with atomic number $Z = 62$.

* 2-3 step ionization * also other elements come through

Other refs: <http://rilis.web.cern.ch> and https://www.research.manchester.ac.uk/portal/files/60831252/FULL_TEXT.PDF and <https://www.sciencedirect.com/science/article/pii/S0168583X13008914?via%3Dihub>

GPS:

The beam can collide in one of two target stations, either the general purpose separator (GPS) or the high resolution separator (HRS). The GPS has one bend-

ing magnet and can deliver beams of different masses simultaneously into three beam lines, while the HRS has two bending magnets with high mass resolving power which delivers the beam into the main beam line [8]. In this experiment the GPS was used to select the isotope of samarium with mass number $A = 140$.

Other refs: <http://isolde.web.cern.ch/targets-and-separators> and Klintefjord's PhD

REXTRAP:

REXTRAP is a penning trap which has the tasks of accumulation, bunching and cooling of the RIB. [3] The ions are released in bunches and transferred to the REXEBIS.

Other refs: <https://www.sciencedirect.com/science/article/pii/S0168900204020169> and <https://www.sciencedirect.com/science/article/abs/pii/S0375947401016426>

REXEgis:

REXEgis is a charge breeder where the RIB is bred to a high charge state [9], with a mass-to-charge (A/q) ratio typically between 2.5 and 4.5 [10]. REXEBIS releases the beam with a certain energy through a mass separator and into the HIE-ISOLDE LINAC (LINear ACcelerator) [3].

excites the nucleus in three steps ionizing the atom, which leaves the nucleus in a high charge state. ?

Other refs: <http://cds.cern.ch/record/478399/files/> and <http://rex-isolde.web.cern.ch>

HIE-ISOLDE LINAC:

The HIE-ISOLDE LINAC accelerates the beam through the beam line and magnets bend the beam into MINIBALL.

* one of the first Miniball experiments with the new accelerator

HIE-ISOLDE (Superconducting LINAC Upgrade): Linear accelerator, HIE-LINAC

HIE-ISOLDE <http://hie-isolde-project.web.cern.ch>, technical design <http://cds.cern.ch/record/2635892?ln=en>, direct to doc: http://cds.cern.ch/record/2635892/files/HIE-ISOLDE_TDR.pdf

MINIBALL:

Cite: https://ac.els-cdn.com/0168583X92959079/1-s2.0-0168583X92959079-main.pdf?_tid=0ccb0647-5870-48f9-ac38-df8c0077981c&acdnat=1545216224_d359ddcc40ea1f94369c85a141 and https://cds.cern.ch/record/2025701/files/epjconf_inpc2013_11005.pdf and <http://isolde.web.cern.ch/targets-and-separators>

Magnets....

ISOLDE actually uses the most protons at CERN [ref?].

ISOLDE <http://iopscience.iop.org/article/10.1088/1361-6471/aa5f03/pdf>

Very pure beam (did we have statistics of this?) - resultat til avhandling. sjekk etter doppler-korrigering. Nd-contaminasjon? i så fall veldig lite, 1-2 prosent?

MINIBALL <http://isolde.web.cern.ch/experiments/miniball> and https://www.miniball.york.ac.uk/wiki/Main_Page

ENSAR2 <http://www.ensarfp7.eu>

Beam production http://tuprints.ulb.tu-darmstadt.de/4599/1/TUDthesis_Christoph%20Seiffert.pdf

Test [2], copyright: <https://copyright.web.cern.ch>

CERN Document Server <https://cds.cern.ch>

3.1.2 Target

* Kan skrive om dette i motivasjonen

^{208}Pb was chosen as a target. Want high Z so that the probability of excitation is high.

Doubly magic, very hard to excite. No quadrupole deformation/excitation.
Need quadrupole for first state (see nndc)

ja og nei: Not enough beam energy to excite ^{208}Pb .

Highest Z for maximum excitation probability.

Contamination... finger print [picture]

3.2 Miniball

Pictures <https://cds.cern.ch/record/844871?ln=en>

3.2.1 Particle detector, DSSSD (CD)

DSSSD: Double sided silicon strip detector

16 rings, 12 strips effectively (24 strips, 12 pairs with two strips making a pair)

Rings = annular strips, strips = radial strips or sector strips

CD distance: 26.98 mm, Inner angle (min): 9 mm, Outer angle (max): 40.9 mm

Table 3.1: CD angles in laboratory frame. Adjacent (CD distance): 26.98 mm.

Ring	Opposite (mid ring)	Angle
0	40	56.0°
1	38	54.6°
2	36	53.1°
3	34	51.6°
4	32	49.9°
5	30	48.0°
6	28	46.1°
7	26	43.9°
8	24	41.7°
9	22	39.2°
10	20	36.5°
11	18	33.7°
12	16	30.7°
13	14	27.4°
14	12	24.0°
15	10	20.3°

Angle coverage: [18.4°, 56.6°]

See [Table 3.1](#)

Vis en figur av trekanten?

$$\theta = \tan^{-1} \left(\frac{\text{opposite}}{\text{adjacent}} \right)$$

3.2.2 γ detectors, HPGe

24 six-fold segmented. 8 clusters of 3 crystals each. Each crystal segmented in 6 parts (144 segments in total).

Cryo-modules

3.3 Experimental setup

^{140}Sm Coulomb excitation experiment.

Experiment code: IS558

Ta: tantalum ($Z = 73$)

Sm: samarium ($Z = 62$)

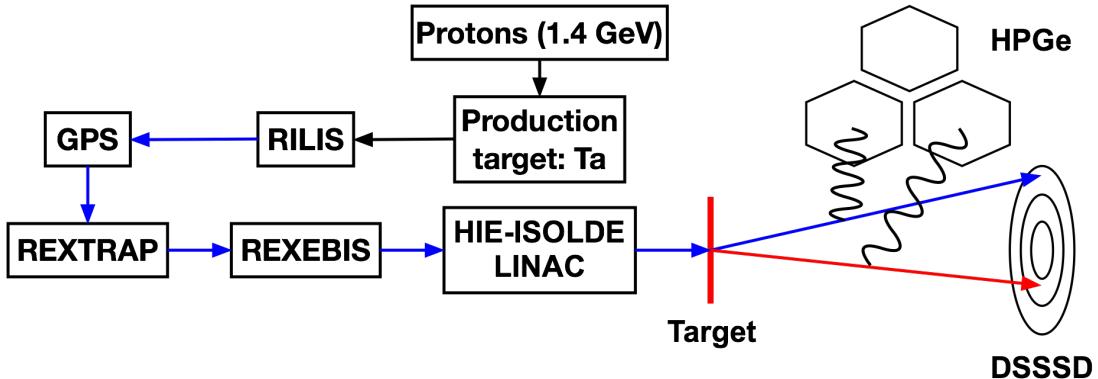


Figure 3.2: The Coulomb excitation setup at ISOLDE. Adapted from Malin Klintefjord's PhD thesis [11].

Pb: lead ($Z = 82$)

Beam: ^{140}Sm ($T_{1/2} = 14.82$ min, $4.65 \text{ MeV}/u$, total 651 MeV), excellent purity

Target: ^{208}Pb (Thickness: 1.4 mg/cm^2)

Small angle: Forward scattering: Larger distance, weaker EM-field, less excitation probability.

Large angle: Backward scattering: Closer distance, stronger EM-field, higher excitation probability.

Expect to measure transition probabilities $B(E2)$ and quadrupole moment (nuclear deformation).

Chapter 4

Data analysis

ROOT: analysere data

kinsim3 <https://github.com/lpgaff/kinsim> + SRIM <http://www.srim.org>

Table 4.1: Computer used for data analysis

Model	MacBook Air (13-inch, 2017)
Processor	1.8 GHz (Intel Core i5)
Memory	8 GB (1600 MHz DDR3)

Run time for sorting data:

TreeBuilder (online calibration): \sim 40-45 min

AQ4Sort (online calibration): \sim 120 min

Table 4.2: Run time for sorting data.

Executable	Run time [min]
TreeBuilder	\sim 45
AQ4Sort	\sim 120

The run time of the bash script was done with the built in script time

```
$ time ./AQ4S.sh Sm online TB
...
real 45m19.265s
user 42m49.653s
sys 0m39.665s
```

```
$ time ./AQ4S.sh Sm online Q4
...
real 121m40.830s
```

```
user 116m18.361s
sys 1m17.809s
```

```
$ time ./AQ4S.sh Sm user TB
...
real 41m11.282s
user 39m45.592s
sys 0m27.777s
```

```
$ time ./AQ4S.sh Sm user Q4
...
real 143m47.600s
user 128m6.174s
sys 1m50.921s
```

particle-gamma and particle-gamma-gamma coincidence
 sjekk opp om energi fra online kalibrering passer med simuleringen.

4.1 Data and sorting

The analysis code for Miniball data is named MiniballCoulexSort and is available on GitHub at <https://github.com/Miniball/MiniballCoulexSort>. The main steps of how to download, install and use it is outlined in the README.md file in the GitHub repository.

Data from Miniball comes in the form of .med-files (Miniball Event Data). In order to analyze this data in ROOT¹ the first part of the sorting is just to convert the .med-files into .root-files with the script MedToRoot.

To get useful information out of the converted .root-files, the Treebuilder script is used. The .root-file(s) and a calibration file is given to the Treebuilder so it can make event trees that can be used for analyzing the Coulomb excitation events.

One script that is mentioned in the Miniball GitHub repository, but not showed how to use, is the AQ4Sort. It is used in the same way as the TreeBuilder script, but it sorts the histograms in another way. This script is used before and during the calibration of the detectors, because it gives information about every single ring and every single back strip. The one thing to note here, is that the numbering of the detector rings and strips are different from the ones used in Treebuilder.

The histograms sorted by Treebuilder starts counting from 0 and the AQ4Sort starts counting from 1.

¹ROOT is a data analysis framework made at CERN.

The ADC spectras from the file sorted by Treebuilder have a naming convention of `adc_q_s`, where q corresponds to the quadrant and s corresponds to the channel. The front energy is saved in `adc_[0-3]_[0-15]` and the back energy from strips 1-12 from all 16 rings (the whole quadrant) is saved in `adc_[0-3]_[16-27]`.

`adc_0_0` in the file sorted by Treebuilder is the same as `fE_Q1_f1` sorted by AQ4Sort. All the front detectors can be found in the Treebuilder-sorted file, but when it comes to the back detector, the single pixels from the strips are not shown. These are available through the AQ4Sort sorted file. For the front detectors the histograms `adc_[0-3]_[0-15]` and `fE_Q[1-4].f[1-16]` are the same. For the back detectors, we have that `adc_[0-3]_[16-27]` and `bE_Q[1-4].b[1-12]` are the same. In addition in AQ4Sort we can see the different pixels. The histograms `fE_Q[1-4].f[1-16].b[1-12]` shows the front energy of quadrant 1-4 gated on ring 1-16 and back strip 1-12, while the `bE_Q[1-4].f[1-16].b[1-12]` shows the same, only for the back energy.

In the naming convention of `adc_q_s` or `fE_Qu_fv`, where $q \in [0, 1, 2, 3], s \in [0, 1, \dots, 27]$ and $u \in [1, 2, 3, 4], v \in [1, 2, \dots, 16]$, the $s = 0$ and $v = 1$ is the outermost ring, while $s = 15$ and $v = 16$ is the innermost ring. In our case, the innermost ring was so destroyed that we have to remove it from the data analysis.

`adc_q_s`, where $q \in [0, 1, 2, 3], s \in [0, 1, \dots, 27]$.

`pE_Qq_fr_bs`, where $\in [b, f], q \in [1, 2, 3, 4], r \in [1, 2, \dots, 16]$ and $s \in [1, 2, \dots, 12]$.

The `adc_[0-3]_[16-27]` or `bE_Q[1-4].b[1-12]` are a combination of all the 16 rings of `bE_Q[1-4].f[1, 2, \dots, 16].b[1-12]`.

Don't blame me for the naming convention, I did not write the code. I just tried to make sense of it.

4.2 Helping scripts

All of my scripts are available in the GitHub repository <https://github.com/wiggoen/MasterThesis>.

In order to not copy and paste the sorting command in the terminal for every data file, I made two bash scripts to do this. The script **M2R.sh** is using MedToRoot to take in as many files as you want, and sort it in one go. The other script is **AQ4S.sh**, which is using either AQ4Sort or Treebuilder to sort a lot of files in one go.

I also made other helping scripts to get histograms, do fitting, comparison and calibration.

My scripts: MultiFit.cpp, MultiPlot.cpp, ++ (python, bash,..)

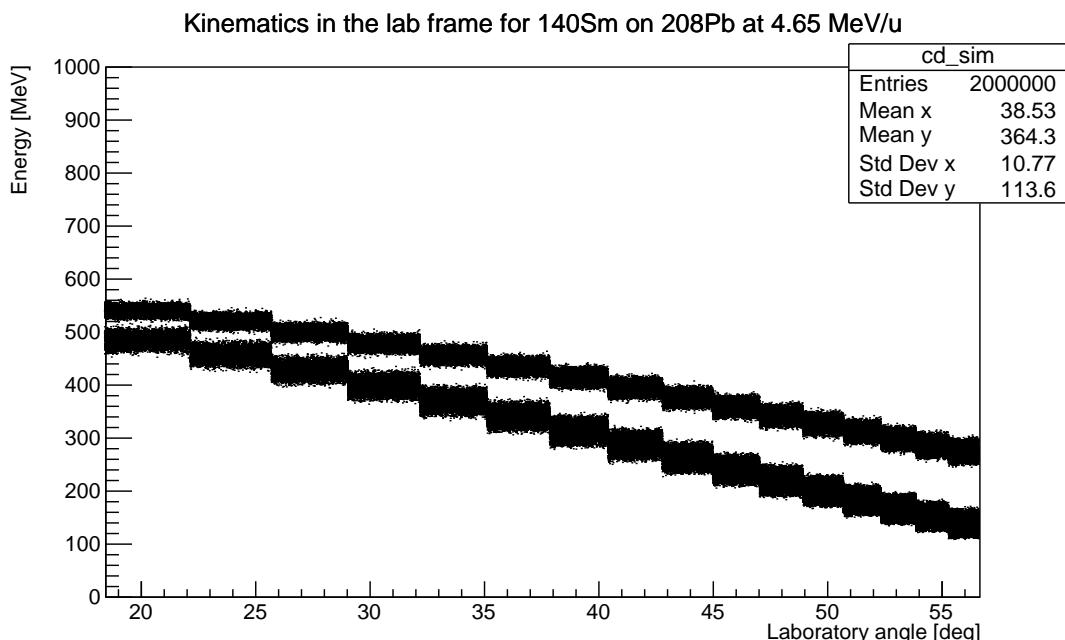
4.3 Simulation

To calibrate the data, we need to know the expected energy of the centroids of the peaks. This was done by simulating the experiment in a program called kinsim3. The program is written by Liam Gaffney² and the purpose of the program is to simulate the kinematics of the experiment. It takes into account the Silicon dead layer.

kinsim3 generates pdf-files of the stopping powers automatically. The rest of the plots are available inside the root-file. To get the energy simulation for each ring, the function `cd_sim_plots()` from the script `MultiPlot.cpp` was used.

CD to target distance: 26.98 mm.

Simulation done by kinsim3



— Mail from Liam started —

”the source has a thickness of 1.23 mm, which needs to be factored in so that the CD to target distance is the CD to source distance PLUS the source thickness, i.e. $25.78 \text{ mm} + 1.23 \text{ mm} = 27.01 \text{ mm}$. This is very close to the 26.98 mm you got from us in August. I think that the source data was reanalysed since the original blog entry, giving the 0.03 mm difference!”

— Mail from Liam ended —

Terminal: Simulation: 140Sm on 208Pb:

²Liam Gaffney is a fellow at ISOLDE, affiliated with MINIBALL.

```
$ cd GitHub/Miniball/kinsim
$ root
root [0] .L kinsim3.cc+
root [1] kinsim3(62, 82, 140, 208, 1.4, 4.65, 0.02, 1.0, 0.6,
26.98, false, 1e6, "../SRIM")
```

kinsim3 function:

```
void kinsim3( int Zb, int Zt, double Ab, double At, double
    thick /* mg/cm^2 */, double Eb /* MeV/u */,
    double dEb = 0.1 /* MeV/u */, double Ex = 1.0 /* MeV */,
    double res = 0.6 /* % */,
    double cd_dist = 28.0 /* mm */, bool flat = false /* angular
        distribution? */,
    long Nevts = 1E6, string srim_dir = "../srin" )
```

Say something about SRIM files.

4.4 Calibration

My goal of the calibration was to make a program that could automatically fit the plots I needed, but it became more and more manual labor. Because of the shape of the data peaks, it demands very much individual care. This I could not do with an automatic program. The downfall of the automatic centroid collector came when trying it on the back detectors.

The total amount particle front detectors to calibrate is 4 quadrants * 16 rings = 64 front detectors

back detectors: 4 quadrants * 12 strips = 48 back detectors

but to do this, one needs all the centroids of the peaks from both sides:

front: 64 detectors * 2 peaks/ring = 128 centroids

back: 48 detectors * 2 peaks/ring * 16 rings = 1536 centroids

total centroids to collect: 1664 centroids (this I did not want to do manually)

Full calibration with 16 rings and 12 back strips. We had to remove the innermost ring.

MOVE THE BELOW TO APPENDIX?

For each file converted with MedToRoot, the program makes four files; OffBeam, OnBeam, OnBeamBackground and Scaler. The file we are interested in for analysis is the OnBeam file.

First all of the interesting files are converted with the M2R.sh script.

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/sorting
```

```
$ ./M2R.sh Sm
```

Then the OnBeam files from M2R.sh is run through using Treebuilder in the AQ4S.sh script.

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/sorting
$ ./AQ4S.sh Sm user TB
$ mv Sm_user-TreeBuilder-2019-04-10.root ../../Sorted_data/
```

After the sorting, I moved the file to a folder of sorted data, and gave the relative path in the setup_Sm.txt file in Scripts/plotting/ used as input in the MultiPlot.cpp script. Using the MultiPlot.cpp script, the ADC time offsets can be extracted by the following commands

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/plotting
$ root
root [0] .L MultiPlot.cpp++
root [1] check_ADC_time_offsets("setup_Sm.txt")
```

or they can be manually reached by

```
$ cd /Users/trondwj/GitHub/MasterThesis/Sorted_data
$ root Sm_user-TreeBuilder-2019-04-10.root
root [1] new TBrowser()
```

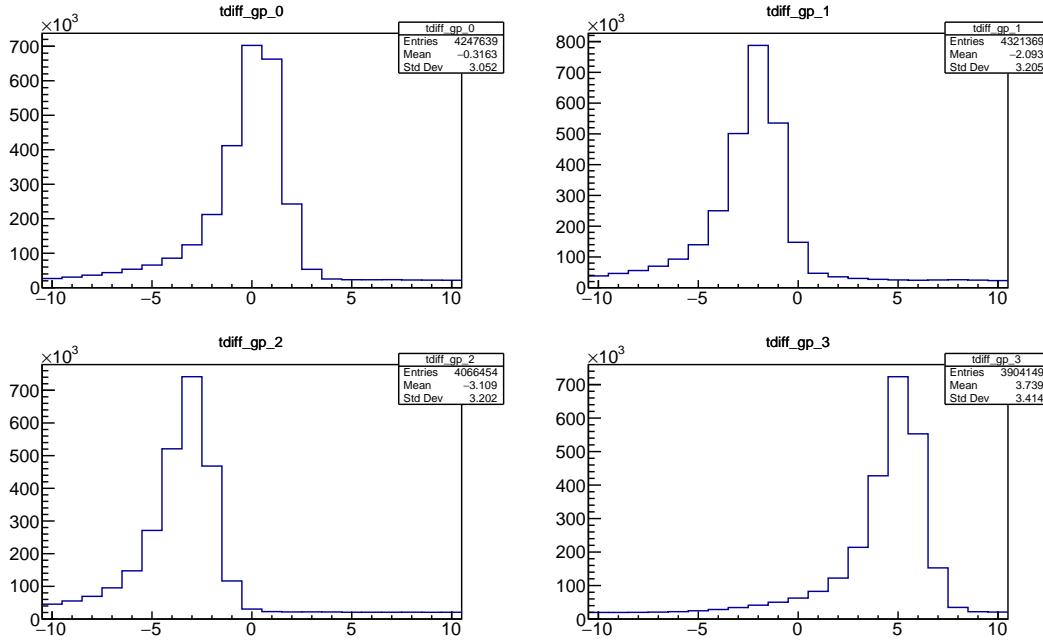
and in the browser, the histograms named tdiff_gp_ *i* (where *i* is a number between 0 and 3) will lie under all the folders. The peaks of these plots have the interesting x-value. Zooming into the peaks, it is very clear what value it is. These values are provided in the calibration file under ADC time offsets (ticks). These values can change depending on the amount of data sorted, so it is wise to double check them.

After the peak values have been collected, they should be written into the calibration file

```
# ADC time offsets (ticks)
adc_0.TimeOffset: 0
adc_1.TimeOffset: -2
adc_2.TimeOffset: -3
adc_3.TimeOffset: 5
```

HUSK: Si noe om ADC time offsets + Threshold. Og at man må se på det tidlig, så resortere.

M2R.sh → AQ4S.sh → check time offset → threshold → AQ4.fit() → particle-calibration.py → ADC-generator.py → copy the calibration from the terminal and paste into calibration file

**Figure 4.1:** ADC time offsets.

Simulation fit → AQ4_fit() → particle-calibration.py → ADC_generator.py
→ copy the calibration from the terminal and paste into calibration file

Visualize plots using ROOT and the scripts.

Skriv om scriptene som er lagd, og at det var litt vanskelig å automatisere kalibreringen. Hvis det skulle vært gjort måtte vi funnet en funksjon med ”negatively skewed distribution” or ”negative skewness” (right modal), en ”left skewed function” (most data is more than the mean).

I log-skala ser dette mer Gaussisk ut, men det er ikke det i non-log skala.

Back detector calibration: There are just too much individual differences to calibrate the back detectors with a simple script given a range for all 12 back strips. I found out this way to late. There isn’t any range to rule them all, at least since the fitting function can behave very strange given a too small or too big range.

— Mail from Liam begins —

”You might have to investigate the threshold a little bit. The continuum of events at low energy comes from charge sharing between the strips. For these very heavy ions, the total amount of charge deposited gets split between neighbouring strips of the CD. The code does performs some tricks to try and recover the correct energy and position, but that depends on counting the number of strips that fire. Therefore, if the threshold is too low you will include ”pedestal” events and it will get things wrong. If the threshold is too high, you will miss some events that have charge sharing and get the wrong energy for your particle.

The key spectra to look at are "part" and "cd_debug". The latter counts how many particles have X strips fired on the front side and Y strips fired on the back side.

If you have too many cd_debug events = 3, then your thresholds are too low. If you have a large continuum/background in the "part" spectrum, your thresholds are too high. Best thing to do is play about with different values.

Bin 20 is when no particle can be found, because there is no energy registered in either the front or the back strips. This can only happen when the front energy is below the software threshold that you set and the back energy is either in a broken strip or is also below the software threshold. Likely it is some noise events or charge sharing that comes below the threshold.

The major problem with the online calibration is that a number of the back strips have the wrong gains, but it otherwise looks quite good. Have you identified which strips these are, by comparing the gains between the 'online' and 'user' calibrations? You could maybe correct those strips as an intermediate step and see how things look.

the source has a thickness of 1.23 mm, which needs to be factored in so that the CD to target **distance is the CD** to source distance PLUS the source thickness, i.e. $25.78 \text{ mm} + 1.23 \text{ mm} = 27.01 \text{ mm}$. This is very close to the 26.98 mm you got from us in August. I think that the source data was reanalyzed since the original blog entry, giving the 0.03 mm difference!"

— Mail from Liam ended —

Pedestal

The pedestal is like a massive statue in front of the interesting data.

We use a threshold to cut away the pedestal.

Threshold

* Threshold (forskjellig i log/ikke-log skala)

Using a logarithmic y-axis, the threshold value will decrease very much. So don't use that.

Threshold: The code has a default threshold of 100, but in some cases this is too much and some cases this is not enough. So for each adc channel, the threshold can be set. We don't want to include the "pedestal". Charge sharing. Won't cut too much or too little..

CD debug:

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/plotting
$ root
root [0] .L MultiPlot.cpp++
root [1] check_cd_debug("setup_Sm.txt")
```

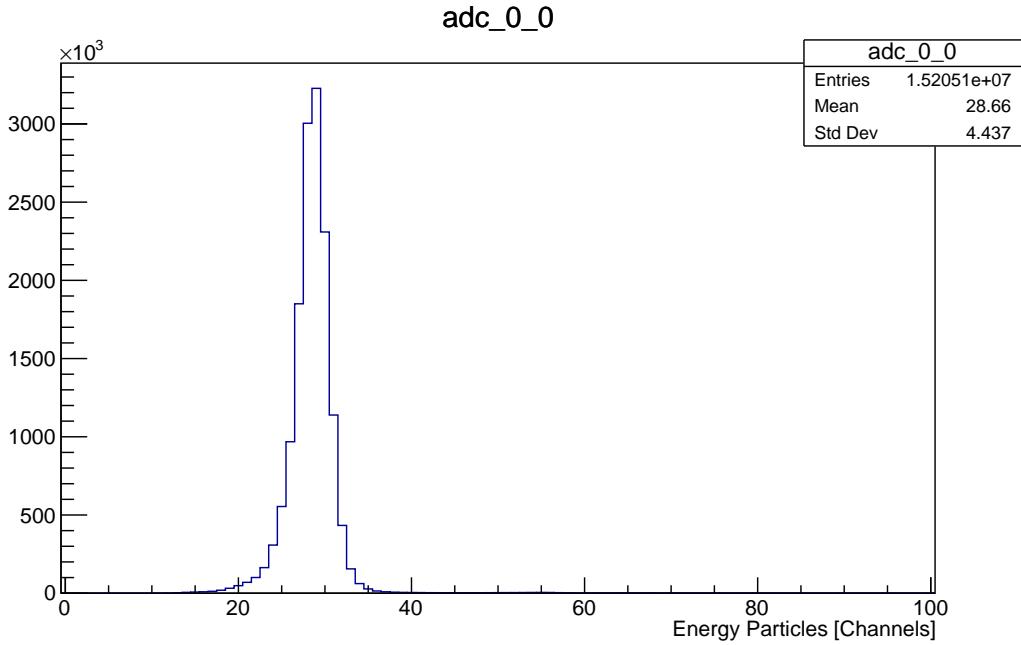


Figure 4.2: Pedestal Q1, f6.

4.4.1 Particle detector

User calibration

ADC: Analog to digital converter (Mesytec)

TDC: Time to digital converter

DSSSD: Double-Sided Silicon Strip Detector \Rightarrow CD

must remove the inner ring from data analysis because of damage

$$\text{gain} = \frac{E_{\text{Sm}} - E_{\text{Pb}}}{Ch_{\text{Sm}} - Ch_{\text{Pb}}}$$

$$\text{offset} = E_{\text{Sm}} - \text{gain} \cdot Ch_{\text{Sm}}$$

in keV.

Hvis man har flere sentroider bruker man bare lineær regresjon. Gjelder spesielt for baksiden!

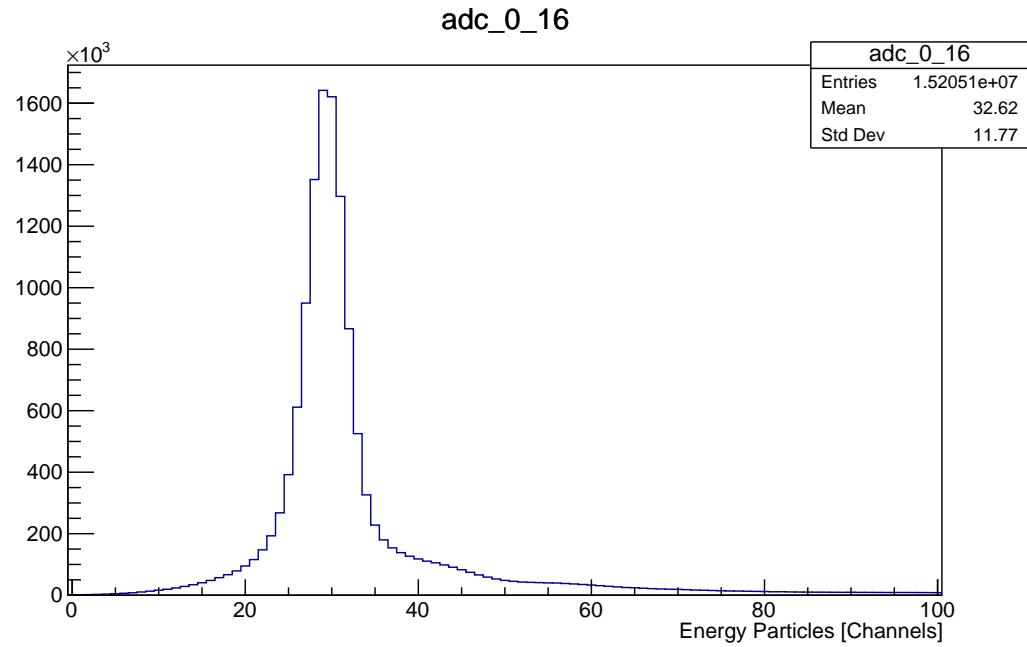


Figure 4.3: Pedestal Q1, f6.

Online calibration

4.4.2 Gamma detectors

DGF: Digital γ finder
addback, singles, ...

4.5 Doppler correction

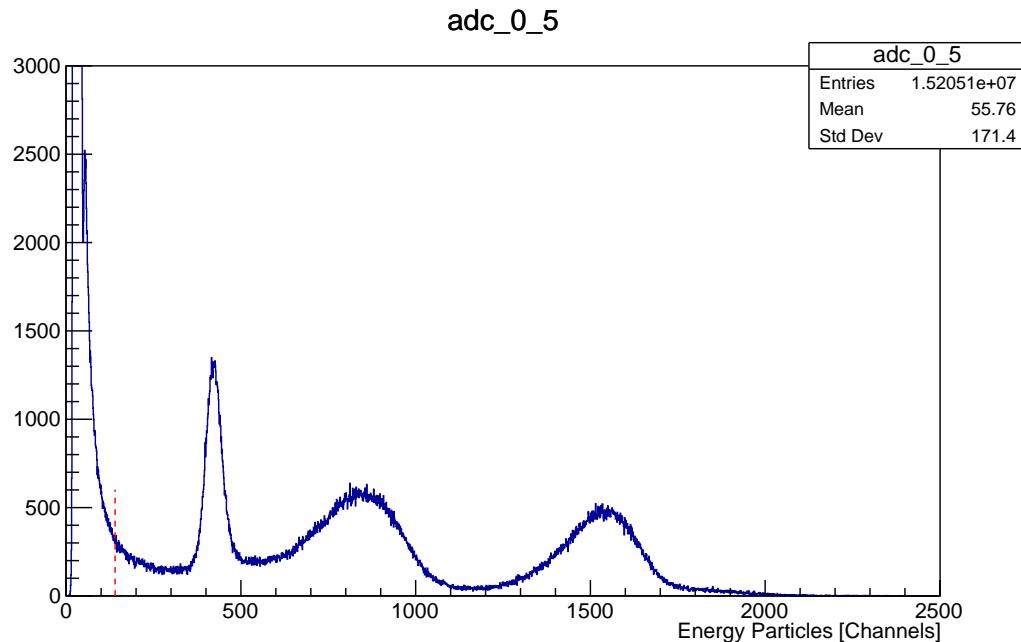


Figure 4.4: Threshold Q1, f6.

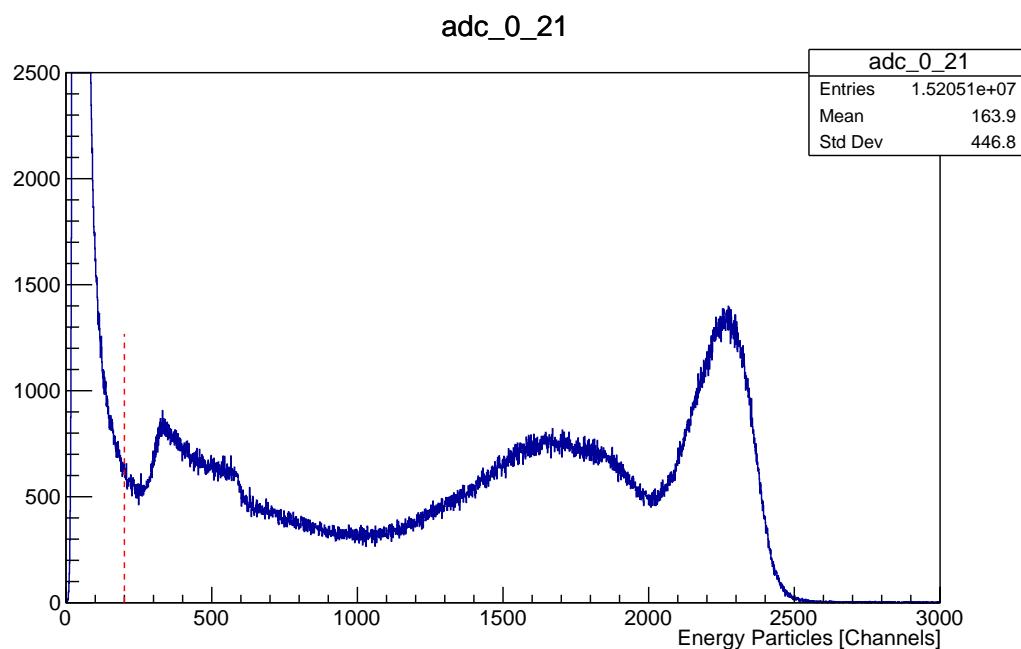
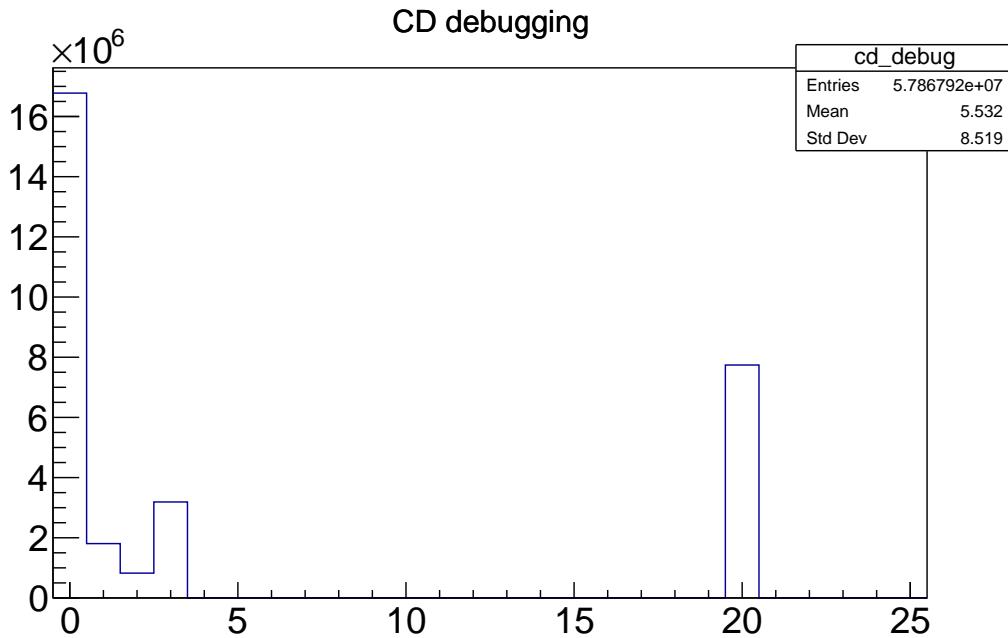
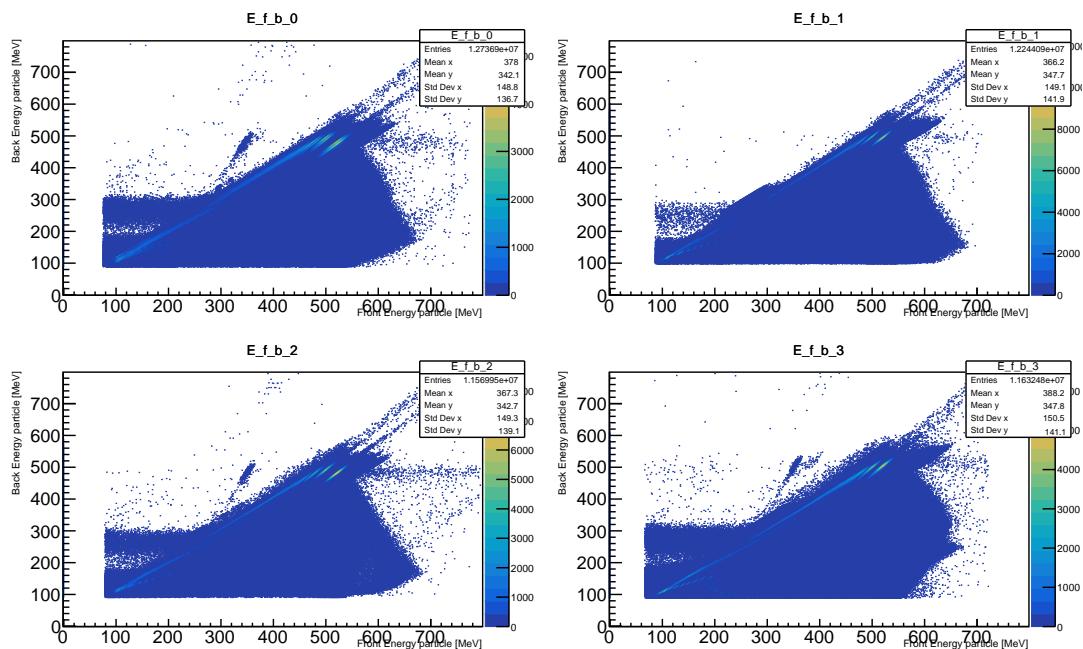
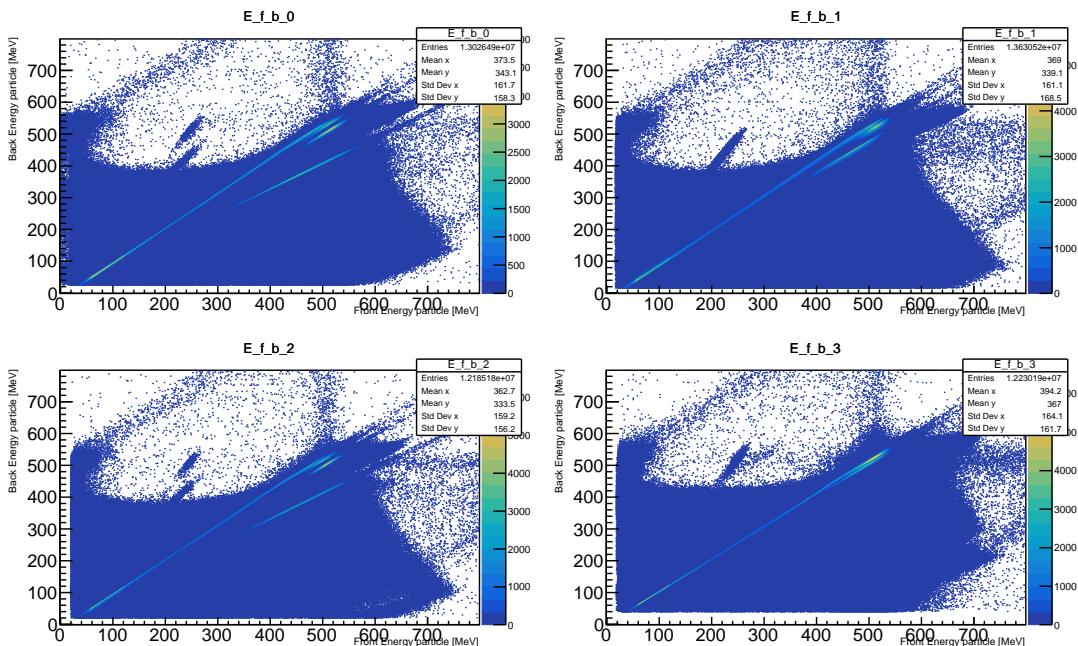


Figure 4.5: Threshold Q1, b6.

Table 4.3: ADC

ADC	Quadrant	Channel	Front [F] or Back [B]
0 - 3	1 - 4	0	F
0 - 3	1 - 4	1	F
0 - 3	1 - 4	2	F
0 - 3	1 - 4	3	F
0 - 3	1 - 4	4	F
0 - 3	1 - 4	5	F
0 - 3	1 - 4	6	F
0 - 3	1 - 4	7	F
0 - 3	1 - 4	8	F
0 - 3	1 - 4	9	F
0 - 3	1 - 4	10	F
0 - 3	1 - 4	11	F
0 - 3	1 - 4	12	F
0 - 3	1 - 4	13	F
0 - 3	1 - 4	14	F
0 - 3	1 - 4	15	F
0 - 3	1 - 4	16	B
0 - 3	1 - 4	17	B
0 - 3	1 - 4	18	B
0 - 3	1 - 4	19	B
0 - 3	1 - 4	20	B
0 - 3	1 - 4	21	B
0 - 3	1 - 4	22	B
0 - 3	1 - 4	23	B
0 - 3	1 - 4	24	B
0 - 3	1 - 4	25	B
0 - 3	1 - 4	26	B
0 - 3	1 - 4	27	B
0 - 3		28	Empty
0 - 3		29	Empty
0 - 3		30	Empty
0 - 3	1 - 4	31	PAD
4		0	Ionization Chamber
4		1	Ionization Chamber

**Figure 4.6:** CD debugging.**Figure 4.7:** User calibration.

**Figure 4.8:** Online calibration.

Chapter 5

Experimental results

Chapter 6

Discussion

Level scheme (from Klintefjord?)

Chapter 7

Summary and outlook

GOSIA and GOSIA2 analysis?

https://www.pas.rochester.edu/~cline/Gosia/Gosia_Manual_20110609.pdf

Appendices

Appendix A

Symbol list

Table A.1: Table of symbols with explanations.

$T_{1/2}$	Half-life
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Appendix B

Acronyms and abbreviations

Table B.1: Table of acronyms and abbreviations.

ADC	Analog to Digital Converter
CERN	European Council for Nuclear Research (in French Conseil Européen pour la Recherche Nucléaire)
Coulex	Coulomb excitation
EBIS	Electron Beam Ion Source
GPS	General Purpose Separator
HIE-ISOLDE	High Intensity and Energy upgrade of ISOLDE
HRS	High Resolution Separator
ISOL	Isotope Separator On Line
ISOLDE	ISOL DEvice
LINAC	LINear ACcelerator
PSB	Proton Synchrotron Booster
REXEBIS	Radioactive beam EXperiment EBIS
REX-ISOLDE	Radioactive beam EXperiment at ISOLDE
RIB	Radioactive Ion Beam
RILIS	Resonance Ionization Laser Ion Source
TDC	Time to Digital Converter (or time digitizer)

Appendix C

Source code

The sorting and analysis code used in this thesis has been developed at CERN-ISOLDE and can be found at <https://github.com/Miniball/MiniballCoulexSort>

The code for theoretical predictions of energy used in the calibration was developed by Liam Gaffney who is working at ISOLDE and has to do with analysis of data from Miniball and ISS. kinsim can be found here <https://github.com/lpgaff/kinsim>

Some calibration code is based on the codes of Ville Virtanen and Liam Gaffney.

Other code/scripts have been written by the author. C++ / Python.

Table C.1: Table of source code.

Name/Link	Description
MiniballCoulexSort	Sorting and analysis code
	Kinematic simulation

Appendix D

Connecting MiniballCoulexSort with ROOT

To connect MiniballCoulexSort with ROOT you need them to share their libraries with each other. This is done with a dynamic loader. You can find out more here: <https://root.cern.ch/root/html/doc/guides/users-guide/ROOTUsersGuide.html#file-system.rootrc>.

You have to make a `.rootrc` file in your home folder on your computer. In the `.rootrc` file you want to write something like this

```
Unix .*. Root .DynamicPath:    .:/Users/trondwj/GitHub(ROOT-
framework/build/lib >:/Users/trondwj/GitHub/Miniball/
MiniballCoulexSort/lib :
```

This should all be in one line. The first part is to tell the system to use the dynamic loader of ROOT to connect the given paths that follow. In my case the lib folder of the ROOT install was at

```
/Users/trondwj/GitHub(ROOT-framework/build/lib
```

and the lib folder of the MiniballCoulexSort was at

```
/Users/trondwj/GitHub/Miniball/MiniballCoulexSort/lib
```

These paths is totally individual, and you will probably not have it in the same place. Therefore these paths must be changed to fit your system.

After making the file you either have restart the terminal or you can source the file by writing this in the terminal

```
$ source ~/.rootrc
```


Appendix E

Running ROOT and MiniballCoulexSort from anywhere in the terminal

To run ROOT or the different scripts of MiniballCoulexSort anywhere in the terminal, you have to edit your `.bash_profile` file [.bash_profile on MacOS, .bashrc on Linux]. In my `.bash_profile` I used this

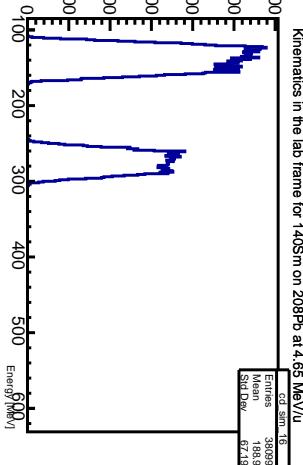
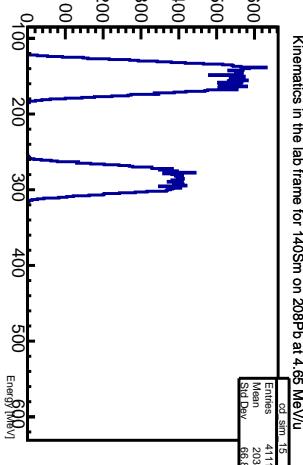
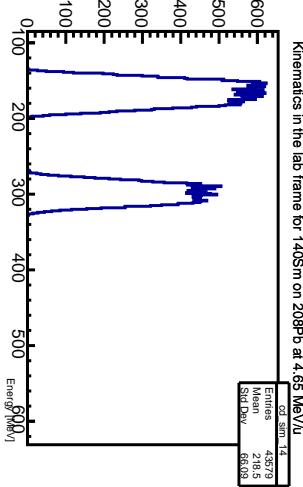
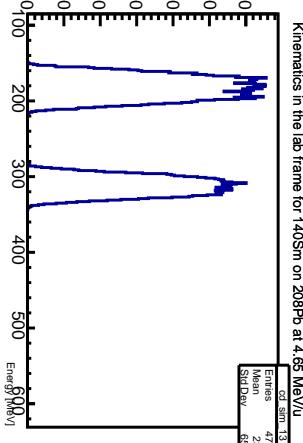
```
# Run ROOT from anywhere
export ROOTSYS=$HOME/GitHub(ROOT-framework/build
export PATH=$ROOTSYS/lib:$PATH
export PATH=$ROOTSYS/bin:$PATH
export DYLD_LIBRARY_PATH=$ROOTSYS/lib:$DYLD_LIBRARY_PATH

# Run MiniballCoulexSort from anywhere
export DYLD_LIBRARY_PATH=$HOME/GitHub/Miniball/
    MiniballCoulexSort/lib:$DYLD_LIBRARY_PATH
export PATH=$HOME/GitHub/Miniball/MiniballCoulexSort/lib:$PATH
export PATH=$HOME/GitHub/Miniball/MiniballCoulexSort/bin:$PATH
```

The DYLD_LIBRARY_PATH is used on Mac only. On other systems, use LD_LIBRARY_PATH. You need to locate the lib and bin folders for both ROOT and MiniballCoulexSort and change them to fit your system, and in addition you need the build folder of your ROOT install.

Appendix F

Other appendices

Kinematics in the lab frame for ^{140}Sm on ^{208}Po at 4.65 MeV/uKinematics in the lab frame for ^{140}Sm on ^{208}Po at 4.65 MeV/uKinematics in the lab frame for ^{140}Sm on ^{208}Po at 4.65 MeV/uKinematics in the lab frame for ^{140}Sm on ^{208}Po at 4.65 MeV/u

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