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A gas analyzer for the internal polarized target of the HERMES experiment

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Abstract

A gas analyzer has been developed for the internal polarized target of the HERMES experiment at DESY in order to determine the relative amount of atomic and molecular hydrogen or deuterium in a gas sample. The precise quantitative knowledge of this ratio is crucial because the nucleons in atoms and molecules contribute differently to the average nuclear polarization of the target gas. A new calibration technique used to derive the relative sensitivity to atoms and molecules is presented. As an example, it is shown how the gas analyzer is used within the HERMES environment to divide the molecules in the gas sample into an unpolarized and a potentially polarized fraction.

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1. Introduction

The HERMES experiment at DESY makes use of a polarized atomic hydrogen or deuterium gas

target internal to the HERA electron storage ring to study the spin structure of the nucleons via deep inelastic lepton–nucleon scattering [1,2]. Within the target setup (Fig. 1) an atomic beam source (ABS) [3] injects a spin polarized beam of hydrogen (deuterium) atoms with approximately 6.4×10^{16} atoms/s (5.0×10^{16} atoms/s) into the

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center of a thin walled storage cell via a side tube (*injection tube*). By using a storage cell technique the areal nucleon density of up to 1.4×10^{14} nucleons/cm² obtained in the interaction area with the HERA beam is more than 300 times larger than that obtained with a free jet target. The temperature of the Drifilm coated storage cell walls can be varied between 35 and 300 K in order to optimize the conditions of the storage cell such that the areal nucleon density is highest and the recombination and depolarization of the injected atoms is minimized. The target vacuum chamber (*cell chamber*) containing the storage cell is surrounded by the target magnet which provides a holding field of up to 350 mT in order to define a quantization axis for the nuclear spins and to decouple the nuclear and electron spins.

For the determination of the average nuclear polarization of the target gas a small fraction is sampled at the center of the storage cell via a second side tube (*sample tube* elongated by the *extension tube*). This gas sample is then analyzed for its atomic polarization using a Breit–Rabi polarimeter (BRP) [4] and for its atomic fraction using a target gas analyzer (TGA). The differentiation between molecules and atoms is necessary as their nuclear polarization is different. Both atoms and molecules may or may not carry nuclear polarization depending on their origin. Under the conditions in the HERMES experiment the atomic flux ϕ_a into the TGA originates exclusively from the ABS.

Experiments showed that atomic flux originating from dissociative ionization can be neglected. A measurement of the TGA beam rates with molecular gas injected into the storage cell by an unpolarized gas feed system (UGFS) showed that only 1% of the molecular beam rate needs to be subtracted from the atomic beam rate in order to correct the atomic beam rate for dissociative ionization of hydrogen/deuterium molecules. Under usual operating conditions, the effect of dissociative ionization on the measured atomic fraction $\alpha^{\text{TGA}} \approx 0.96$ is of the order of 10^{-4} and roughly a factor of 20 lower than the statistical uncertainty. The contribution from dissociative ionization of water can be expected to be zero at cell temperatures of 100 K or less, because the water freezes on the cell surface so that no significant water beam could be detected. Thus all atoms of the atomic flux ϕ_a into the TGA carry nuclear polarization.

The molecular flux ϕ_m however may have three different sources: (i) Molecules, which are produced by recombination of two polarized atoms on the inner surface of the storage cell. Recombined molecules can be polarized [5,6] and constitute the flux ϕ_r into the target gas analyzer. (ii) Molecules, which are injected into the cell by the ABS. Roughly 20% of the gas molecules pass the dissociator of the ABS undissociated [3]. A fraction of these molecules enters the storage cell by means of ballistic flow, causing the flux ϕ_{ball} into the TGA. These molecules are unpolarized.

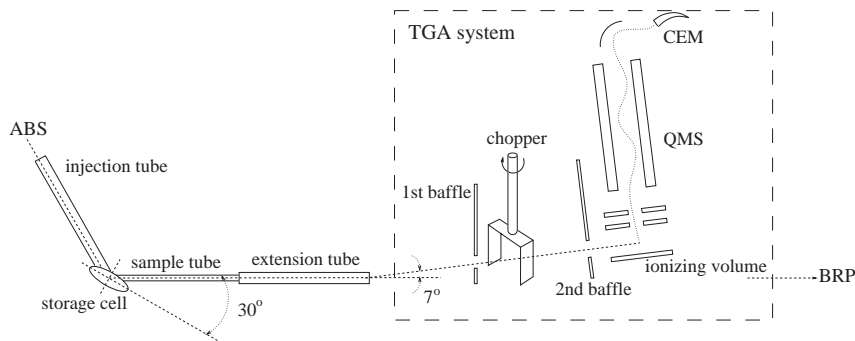


Fig. 1. Schematic diagram showing the TGA within the target setup of the HERMES experiment. The beam leaving the extension tube is chopped and filtered in a QMS before being detected by a CEM. The first baffle rejects any gas flow from sources other than the sample beam while the second baffle collimates the beam so that no atom from the beam may recombine on the wall of the ionizing volume.

(iii) Molecules from the residual background gas of the cell chamber entering the storage cell. These molecules are also unpolarized as they have left the holding field of the target magnet and experienced a high number of collisions with the stainless steel wall of the cell chamber. Residual gas molecules result in the flux ϕ_{rg} into the target gas analyzer.

In this paper the experimental setup of the TGA is described and the analysis of the measured signals and the calibration of the apparatus are presented. Additionally, the usage of the TGA within the HERMES environment to distinguish between polarized and unpolarized particles is explained.

2. Experimental setup of the TGA

The purpose of the TGA is to measure the fraction of atoms and molecules of the gas sample such that the number of nucleons in atoms relative to the total number of nucleons seen by the HERA positron/electron beam can be determined.

The TGA is located between the cell chamber and the BRP with which it shares the vacuum system, mainly consisting of titanium sublimation pumps and cryo pumps, with a total nominal pumping speed of about 7000 l/s. During operation the pressure in the chamber is typically about 3.5×10^{-9} mbar. The TGA setup shown in Fig. 1 consists of two baffles, a chopper and a 90° off-axis quadrupole mass spectrometer (QMS) (Balzers QMA 430) with a cross-beam ionizer.

A channel electron multiplier (CEM) (DeTech 401A) is used to detect the ionized atoms and molecules. The system of baffles ensures that atoms entering the ionizer volume of the QMS cannot recombine on the inner walls of the ionizer causing an artificial molecular beam signal. For this purpose one baffle is mounted at a short distance from the extension tube and the other baffle is mounted directly in front of the cross-beam ionizer. The axis of the cross-beam ionizer is tilted by 7° with respect to the beam axis of the sample and extension tube, so as not to block the beam path into the BRP. A chopper rotating at 5.5 Hz between the two baffles is used in order to distinguish between particles from the sample beam and those from residual gas.

Particles entering the ionizing volume are ionized by 70 eV electrons emitted from a filament and extracted. Measurements of the ionization cross-sections $\sigma_{\text{mass}}^{\text{ion}}$ for different masses exist and can be found in Refs. [7,8]. After being mass filtered by the QMS the remaining ions are detected by a CEM after being deflected through an angle of 90° with respect to the quadrupole axis of the QMS in order to reject neutral particles. The mass dependent detection probability ϵ_{mass} includes the transmission probability of the ions through the QMS. The detected ions are then converted into an electronically measurable pulse and counted by a multichannel time resolving counter (TRC) with 2048 bins. A time-resolved count rate spectrum is shown in Fig. 2. The bin length is adjustable and typically set to 175 μs .

A trigger signal from the chopper electronics is used to synchronize the chopper status and the correlated counting rate. The beam rates are calculated by the difference of the counts per time in the periods with open and closed chopper. The counts of 16–32 chopper periods are summed up for a beam intensity measurement.

3. Analysis of the measured TGA signals

The measured atomic (molecular) signal S_a (S_m) of the TGA is proportional to the corresponding particle flux Φ_a (Φ_m) into the TGA, the ionization cross-section σ_a^{ion} (σ_m^{ion}), the detection probability

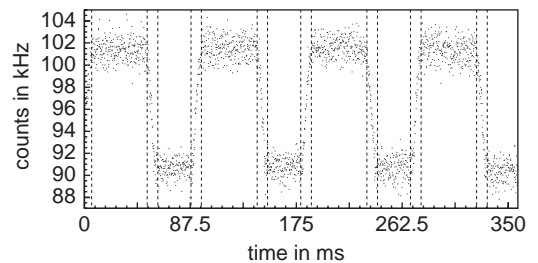


Fig. 2. Time spectrum of atomic count rates in the TGA. The vertical lines indicate the bin numbers corresponding to the limits between the chopper positions open, undefined and closed.

ε_a (ε_m) and the mean inverse velocity of the particles $\langle 1/v_a \rangle$ ($\langle 1/v_m \rangle$).

Additionally, the fringe fields of nearby strong magnets, i.e. the target magnet and the HERMES spectrometer magnet, may influence the trajectories of the ions inside the cross-beam ionizer and the mass spectrometer. Therefore, the magnetic field values are kept constant during all measurements. The dependence on the emission current I_{emis} from the electron gun of the cross-beam ionizer has been measured. Taking all parameters into account one finds

$$S_{a,m} \propto f(B, I_{\text{emis}}) \sigma_{a,m}^{\text{ion}} \varepsilon_{a,m} \left\langle \frac{1}{v_{a,m}} \right\rangle \Phi_{a,m} \quad (1)$$

where $f(B, I_{\text{emis}})$ is a proportionality constant depending on the magnetic field setting B and the emission current I_{emis} . The total effective flux of atoms into the TGA $\tilde{\Phi}^{\text{TGA}}$ is given by the sum of atomic flux and twice the molecular flux, since a hydrogen molecule contains two atoms.

$$\tilde{\Phi}^{\text{TGA}} = \Phi_a + 2\Phi_m. \quad (2)$$

For thermalized atoms and molecules one finds

$$\left\langle \frac{1}{v_m} \right\rangle = \sqrt{2} \left\langle \frac{1}{v_a} \right\rangle. \quad (3)$$

Using Eqs. (1)–(3) it can be shown that the partial beam rates $S_{a,m}$ can be interpreted as parts of the total rate $S_{\text{tot}} \propto \tilde{\Phi}^{\text{TGA}}$

$$S_{\text{tot}} = S_a + \sqrt{2}\kappa S_m \quad (4)$$

where κ is the calibration constant of the TGA giving the relative sensitivity of the TGA for atomic and molecular beams:

$$\kappa = \frac{\sigma_a^{\text{ion}} \varepsilon_a}{\sigma_m^{\text{ion}} \varepsilon_m}. \quad (5)$$

The velocity of a particle depends on the temperature of the surface where it thermalizes. The TGA acceptance is tilted by 7° with respect to the extension tube axis. Thus it only detects particles that had their last wall collisions in the extension tube. Simulations of the molecular flow showed, that any particle experiences on average more than 100 collisions [9,10] with the wall of the extension tube before it is detected by the TGA. Hence, the flowrate into the TGA depends on the temperature of the

extension tube T_{ext} because the particles entering the TGA have thermalized within the extension tube.

Comparable, normalized nucleon flow rates $\phi_{a,m}$, which are independent of temperature and emission current, can be defined using the dependence of velocity on temperature $\langle v_{a,m} \rangle = g^{-1}(T_{\text{ext}}) = \sqrt{T_{\text{ext}}}$ and the measured function $f(B, I_{\text{emis}})$.

$$\phi_a = \frac{S_a}{g(T_{\text{ext}})f(B, I_{\text{emis}})} \quad (6)$$

$$\phi_m = \frac{\sqrt{2}\kappa S_m}{g(T_{\text{ext}})f(B, I_{\text{emis}})}. \quad (7)$$

The fraction of nucleons in atoms relative to all nucleons of the particles entering the TGA can then be defined by

$$\alpha^{\text{TGA}} = \frac{\phi_a}{\phi_a + \phi_m} = \frac{S_a}{S_a + \sqrt{2}\kappa S_m}. \quad (8)$$

4. Calibration of the TGA

Besides the measured partial beam rates $S_{a,m}$ Eq. (8) contains the unknown relative sensitivity κ which is determined by a calibration of the TGA. This calibration can be determined by variation of the relative number of atoms and molecules at constant injected flux of the ABS and thus at constant total flux into the TGA $\tilde{\Phi}^{\text{TGA}}$ as defined by Eq. (2). The detected total rate S_{tot} is then also constant. Rewriting Eq. (4) using the normalized nucleon flow rates from Eqs. (6) and (7) leads to

$$\phi_a + \phi_m = \phi_{\text{tot}} = \text{const}. \quad (9)$$

The calibration constant κ can now be determined by a linear fit of ϕ_m versus ϕ_a as

$$\frac{\partial \phi_m}{\partial \phi_a} = -1 \quad (10)$$

and thus

$$\frac{\partial \left(\frac{S_m}{g(T_{\text{ext}})f(B, I_{\text{emis}})} \right)}{\partial \left(\frac{S_a}{g(T_{\text{ext}})f(B, I_{\text{emis}})} \right)} = -\frac{1}{\sqrt{2}\kappa}. \quad (11)$$

To obtain a low systematical uncertainty of the derived κ -value it is necessary to vary the atomic fraction α^{TGA} over a wide range. A fit to the corrected partial molecular beam rates as a function

of the corrected partial atomic beam rates for varying α^{TGA} results in a straight line with a slope of $-1/\sqrt{2}\kappa$ as shown in Fig. 3.

As the strength of recombination processes is temperature dependent, α^{TGA} varies with the temperature of the storage cell. A detailed description of the processes and conditions leading to recombination in the HERMES target environment is presented in Ref. [11]. Thus performing a so-called temperature scan is one possibility to calibrate the TGA. This requires the application of the temperature correction function $g(T_{\text{ext}})$.

An additional but unintended way to calibrate the TGA is to employ the strong variation of α^{TGA} at constant cell temperature after an accidental beam loss of the HERA electron/positron beam near the HERMES target region. This beam loss calibration does not require any knowledge about the temperature correction function $g(T_{\text{ext}})$.

4.1. Method 1: Temperature scans

In order to vary the temperature of the storage cell the helium flow through its cooling rails is changed. After the temperature becomes stable the

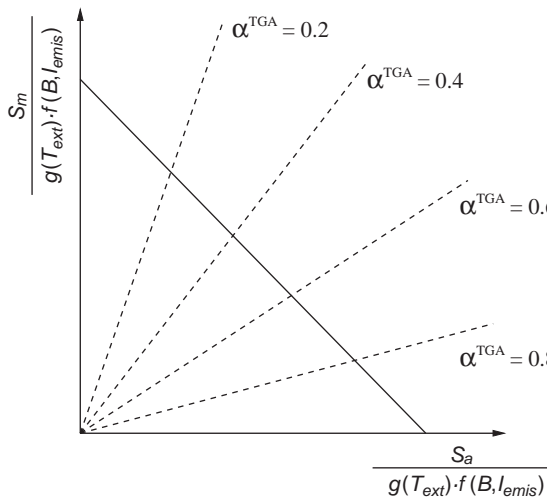


Fig. 3. The corrected partial molecular beam rate as a function of the corrected partial atomic beam rate of the TGA at a constant intensity of the ABS ϕ^{ABS} . The slope of the solid line equals the right-hand side of Eq. (11). The dashed lines correspond to constant α^{TGA} at different ϕ^{ABS} .

partial beam rates are measured for about an hour at constant cell temperature and constant output intensity of the ABS. This is repeated for many temperature values. A complete temperature scan typically takes 5–10 h.

The data of one polarized temperature scan, corrected by the two correction functions $g(T_{\text{ext}})$ and $f(B, I_{\text{emis}})$ are displayed in Fig. 4 for the determination of κ from a fit to the data. A cross check of the calibration is the plot of Eq. (9) versus the cell temperature to show the constancy of ϕ_{tot} and thus the validity of the calibration.

Seven reliable temperature scan calibrations of the TGA have been made in the deuterium running period of the HERMES experiment between August 1998 and September 2000 resulting in an average κ of

$$\kappa = 0.861 \pm 0.024. \quad (12)$$

4.2. Method 2: HERA beam losses

As the cell temperature is not influenced by an accidental loss of the HERA electron beam near the HERMES target region, one can apply the observed partial beam rates $S_{a,m}$ without corrections to a plot of Eq. (9).

A beam loss causes a sudden and sharp drop of α^{TGA} . After the beam loss α^{TGA} typically recovers slowly within a couple of hours. For the deuterium running period from August 1998 to September 2000 in total three reliable and consistent beam loss calibrations give an averaged κ of

$$\kappa = 0.859 \pm 0.007 \quad (13)$$

which is in perfect agreement with the result for κ from temperature scans in that period as given in Eq. (12).

5. Sources of molecular contributions to α^{TGA}

The molecular flux is sum of three separate contributions, from recombined polarized atoms, from ballistic flow from the ABS, and from residual gas in the target chamber. Thus ϕ_m can

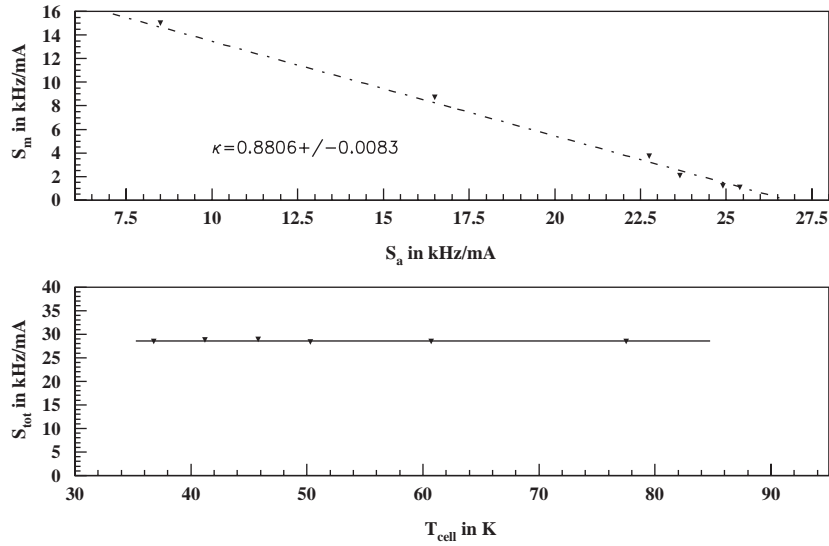


Fig. 4. Analysis of the data from a temperature scan. The upper plot shows the derivation of κ as seen in Fig. 3. The data points are averaged for constant temperatures and the measured beam rates are corrected for temperature and emission current. The lower plot shows S_{tot} (Eq. (4)) versus the cell temperature proving the validity of the calibration.

be written as

$$\phi_m = \phi_r + \phi_{ball} + \phi_{rg}. \quad (14)$$

To separate potentially polarized and unpolarized molecules one can split α^{TGA} into two parts, one defining the fraction α_r^{TGA} of atoms surviving recombination in the storage cell, and one defining the atomic fraction in the absence of recombination α_0^{TGA} as measured by the TGA by

$$\alpha^{TGA} = \frac{\phi_a}{\phi_a + \phi_m} = \alpha_0^{TGA} \alpha_r^{TGA}. \quad (15)$$

Using Eq. (14) gives:

$$\alpha_r^{TGA} = \frac{\phi_a}{\phi_a + \phi_r} \quad (16)$$

and

$$\alpha_0^{TGA} = \frac{\phi_a + \phi_r}{\phi_a + \phi_r + \phi_{ball} + \phi_{rg}}. \quad (17)$$

The flow rate ϕ_{rg} caused by residual gas from the cell chamber is proportional to the cell chamber pressure p_{TC} :

$$\phi_{rg} = c_{rg} p_{TC}. \quad (18)$$

The proportionality factor c_{rg} can be determined by changing the cell chamber pressure and measuring the molecular flow into the TGA. The fitted slope of ϕ_m versus p_{TC} then yields the residual gas calibration constant c_{rg} . For this purpose, molecular hydrogen or deuterium gas is injected into the cell chamber by the UGFS. This allows a variation of the background pressure with the corresponding gas type. Due to instabilities in the pressure gauge readings this type of residual gas calibration is repeated periodically.

In order to derive the contribution from molecules which are ballistically injected by the ABS, one has to separate them from other classes of molecules. The ABS is able to change the atomic flux into the storage cell while the molecular flux from the ABS ϕ_{ball} stays constant. This is accomplished using a combination of sextupole magnets, deflecting hyperfine states with $m_S = -\frac{1}{2}$, and radio-frequency transitions, interchanging the population of certain hyperfine states. Thus the atomic flux into the cell is varied while the trajectories of molecules stay unaffected by the magnetic field. The ABS can inject 1 or 2 (1,2 or 3) hyperfine states in case of hydrogen

(deuterium) with a constant ϕ_{ball} for all of them. Details about the ABS and its setup and properties can be found in Ref. [3]. Denoting different injection modes of the ABS by the index (i), Eq. (14) may be written as

$$\phi_{\text{m}}^{(i)} = \phi_{\text{r}}^{(i)} + \phi_{\text{ball}} + \phi_{\text{rg}}^{(i)} \quad (19)$$

with $\phi_{\text{ball}} = \text{const.}$ Rewriting Eq. (16) as

$$\phi_{\text{r}}^{(i)} = \left(\frac{1}{\alpha_{\text{TGA}}^{(i)}} - 1 \right) \phi_{\text{a}}^{(i)} \quad (20)$$

then leads to

$$\phi_{\text{m}}^{(i)} - \phi_{\text{rg}}^{(i)} - \phi_{\text{ball}} = \left(\frac{1}{\alpha_{\text{TGA}}^{(i)}} - 1 \right) \phi_{\text{a}}^{(i)}. \quad (21)$$

For the determination of ϕ_{ball} two different injection modes of the ABS are chosen with $\phi_{\text{a}}^{(1)} < \phi_{\text{a}}^{(2)}$. The corresponding values for $\phi_{\text{m}}^{(i)}$ and $\phi_{\text{rg}}^{(i)}$ are measured with the TGA. $\phi_{\text{rg}}^{(i)}$ is calculated from the measured pressure in the cell chamber p_{TC} using Eq. (18). By dividing the two Eqs. (21) one obtains

$$\phi_{\text{ball}} = \frac{(\phi_{\text{m}}^{(1)} - \phi_{\text{rg}}^{(1)})\phi_{\text{a}}^{(2)} - (\phi_{\text{m}}^{(2)} - \phi_{\text{rg}}^{(2)})\phi_{\text{a}}^{(1)}}{\phi_{\text{a}}^{(2)} - \phi_{\text{a}}^{(1)}}. \quad (22)$$

For the running period in 2000 with two deuterium hyperfine states injected by the ABS the averaged values of the normalized nucleon flow rates are

$$\begin{aligned} \phi_{\text{a}} &= 39.92 \pm 3.50 \text{ kHz/mA} \\ \phi_{\text{rg}} &= 0.63 \pm 0.09 \text{ kHz/mA} \\ \phi_{\text{m}} &= 1.72 \pm 0.66 \text{ kHz/mA} \\ \phi_{\text{ball}} &= 0.31 \pm 0.08 \text{ kHz/mA} \end{aligned} \quad (23)$$

which leads to $\alpha_{\text{r}}^{\text{TGA}} = 0.997 \pm 0.003$ and $\alpha_0^{\text{TGA}} = 0.961 \pm 0.009$.

6. Conclusions

It has been shown that the gas analyzer is able to measure the atomic fraction of a thermal beam effusing out of a storage cell. With the presented method based on the temperature variation of the cell, the calibration constant κ describing the relative sensitivity of the gas analyzer to atoms and molecules has been extracted with a relative error $\Delta\kappa/\kappa$ below 3%. These results have been shown to be comparable within errors to an alternative calibration method after an accidental HERA beam loss. In the HERMES experiment, under normal running conditions, the value of the measured atomic fraction α^{TGA} is typically about 0.96.

The results of the α^{TGA} measurements obtained in the data taking period of 2000 with deuterium gas are shown in Fig. 5. With low molecular content of the sample beam, the effect of the $\Delta\kappa/\kappa$ on the uncertainty in α^{TGA} becomes negligible, i.e. $\Delta\alpha/\alpha \approx 0.15\%$ with the value of α^{TGA} as given above.

Furthermore the gas analyzer has proven to be a reliable instrument in identifying the contributions from potentially polarized and unpolarized molecules. However, all measured quantities of the effusing beam in case of the HERMES target are not identical to the effective quantities as seen by the HERA electron/positron beam. In order to

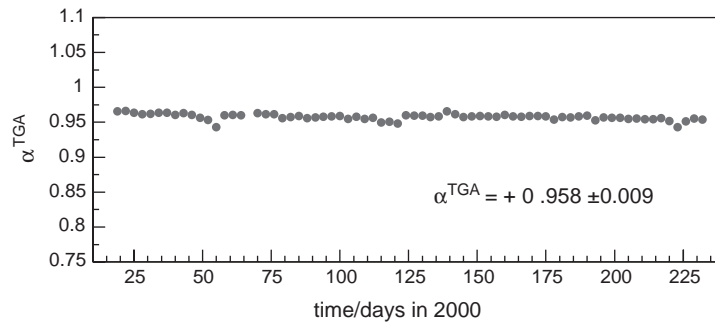


Fig. 5. Behaviour of the measured atomic fraction by the TGA during the HERA running period in 2000. The average value is also given. The data have been binned in bins of 60 h each.

derive these effective values a sampling correction has to be applied. This correction takes into account the difference in the number of wall collisions of the atoms within the sample beam and the storage cell and of the possibility of a non-uniform surface in the cell and sample tube with respect to the recombination probabilities per wall collision [8,12,13].

The gas analyzer has been continuously in operation (except for the HERA shutdown periods) at the HERMES target since 1996, the first 2 years with hydrogen, from 1998 to 2000 with deuterium and since 2001 again with hydrogen. It is found to be a very reliable instrument.

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