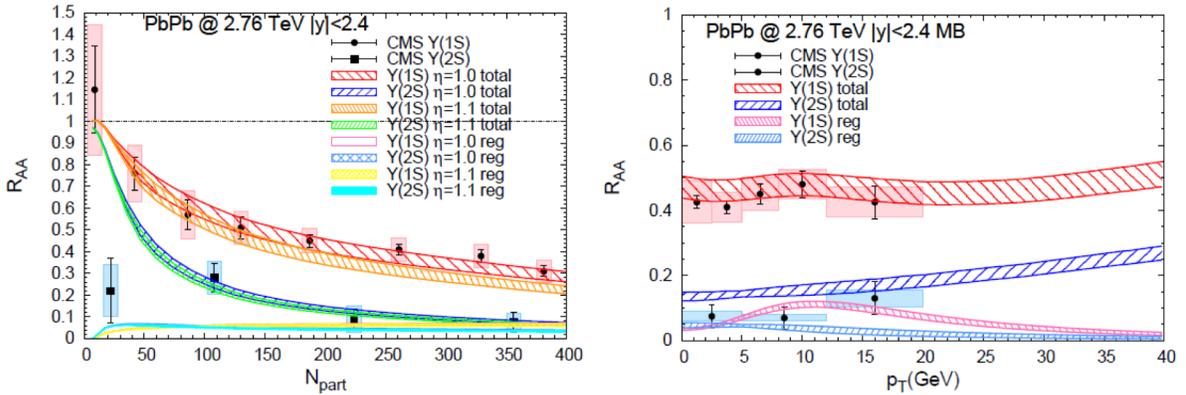


## Color screening and regeneration of bottomonia at RHIC and the LHC

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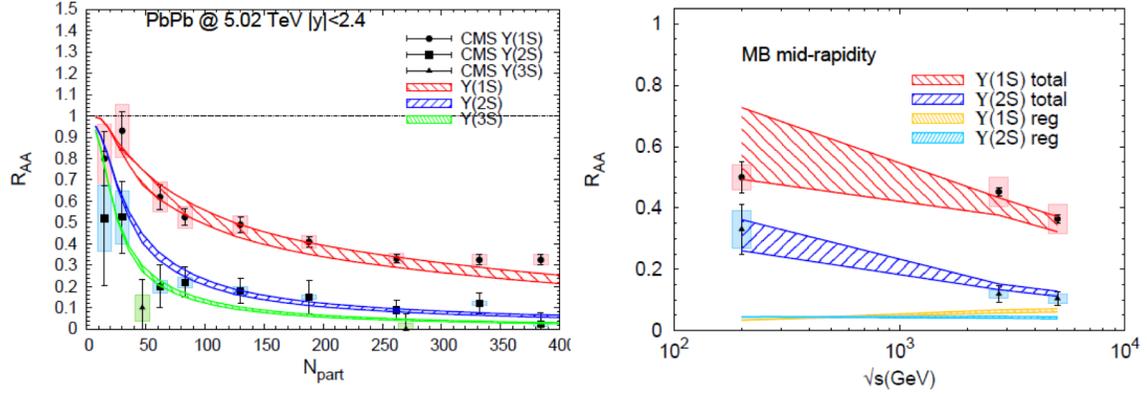
Heavy quarkonia are key probes of the medium effects on the fundamental QCD force in strongly interacting matter. Large experimental and theoretical efforts are devoted to measure charmonium and bottomonium observables in heavy-ion collisions (HICs) [1] and to interpret the results. Kinetic-rate equation approaches have proven a successful tool to unravel the interplay of suppression and regeneration mechanisms for charmonia [2]. For bottomonia, regeneration processes are expected to be less important, providing a more direct window on their dissolution mechanisms.

In this work [3], we investigate  $Y(nS)$  production in HICs at RHIC and LHC energies using a rate equation approach [4]. Improving on previous work [5], we implement in-medium binding energies from T-matrix calculations [6] to compute inelastic reaction rates, B-meson resonances in calculating  $Y$  equilibrium limits near  $T_c$ , a lattice-QCD equation of state in the fireball evolution, and realistic b-quark spectra from Langevin simulations [7] to compute transverse-momentum ( $p_T$ ) spectra from coalescence processes [8]. The resulting centrality and  $p_T$ -dependent production yields are generally in good agreement with experiments at RHIC ( $\sqrt{s}=0.2\text{TeV}$ ) and the LHC ( $\sqrt{s}=2.76$  and  $5.02$  TeV).



**FIG. 1.** Nuclear modification factor of  $Y(1S)$  and  $Y(2S)$  in 2.76TeV Pb-Pb collisions as a function of centrality (left) and  $p_T$  (right). Calculations with the baseline TBS ( $\eta=1.0$ ) are compared to CMS data [9]; the orange band for the  $Y(1S)$  in the left panel includes a 10% stronger reduction of the TBS binding energies ( $\eta=1.1$ , encoded in the reaction rates).

In Fig. 1 we show the comparison to CMS data in Pb-Pb(2.76TeV) collisions. The  $Y(1S)$  nuclear modification factor ( $R_{AA}$ ) shows a promising sensitivity to the in-medium binding energy, with the baseline T-matrix binding scenario (TBS) providing good agreement with data. Regeneration contributions are generally small, mostly limited by the strongly suppressed  $R_{AA}$  of the  $Y(2S)$ . However, the  $p_T$  dependence of the  $Y(1S)$   $R_{AA}$  shows a slight maximum structure due to regeneration which is not inconsistent with data. An assumption of thermalized b-quark spectra leads to discrepancies with the measured  $R_{AA}(p_T)$ 's for both  $Y(1S)$  and  $Y(2S)$  (not shown). The model predictions for 5.02 TeV Pb-Pb collisions are also in fair agreement with recent CMS data [10], cf. the left panel of Fig. 2.



**FIG. 2.** Left: centrality-dependent  $R_{AA}$  for  $\Upsilon(1S)$ ,  $\Upsilon(2S)$  and  $\Upsilon(3S)$  in 5.02 TeV Pb-Pb collisions in the baseline TBS, compared to CMS data [10]. Right: excitation function of  $\Upsilon(1S)$  and  $\Upsilon(2S)$   $R_{AA}$  in MB AA collisions, compared to RHIC [11] and LHC [9,10] data.

The calculation of excitation functions of the  $R_{AA}$  for  $\Upsilon(1S)$  and  $\Upsilon(2S)$  are compared to minimum-bias (MB) data in the right panel of Fig. 2. From the suppression pattern of the  $\Upsilon(2S)$  we conclude that the confining force, which is the main agent for  $\Upsilon(2S)$  binding in vacuum, is screened at RHIC and fully suppressed at the LHC. On the other hand, the  $\Upsilon(1S)$ , which is mostly bound by the color-Coulomb force, survives up to temperatures of 500-600 MeV, indicating that color screening penetrates down to 0.1-0.2 fm at the LHC. Regeneration contributions are generally small, but possibly play a role in the flattening of  $\Upsilon(2S)$   $R_{AA}(\sqrt{s})$  from 2.76 to 5.02 TeV.

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