

# Optimising top-quark pair-production threshold scan at future e+e- colliders

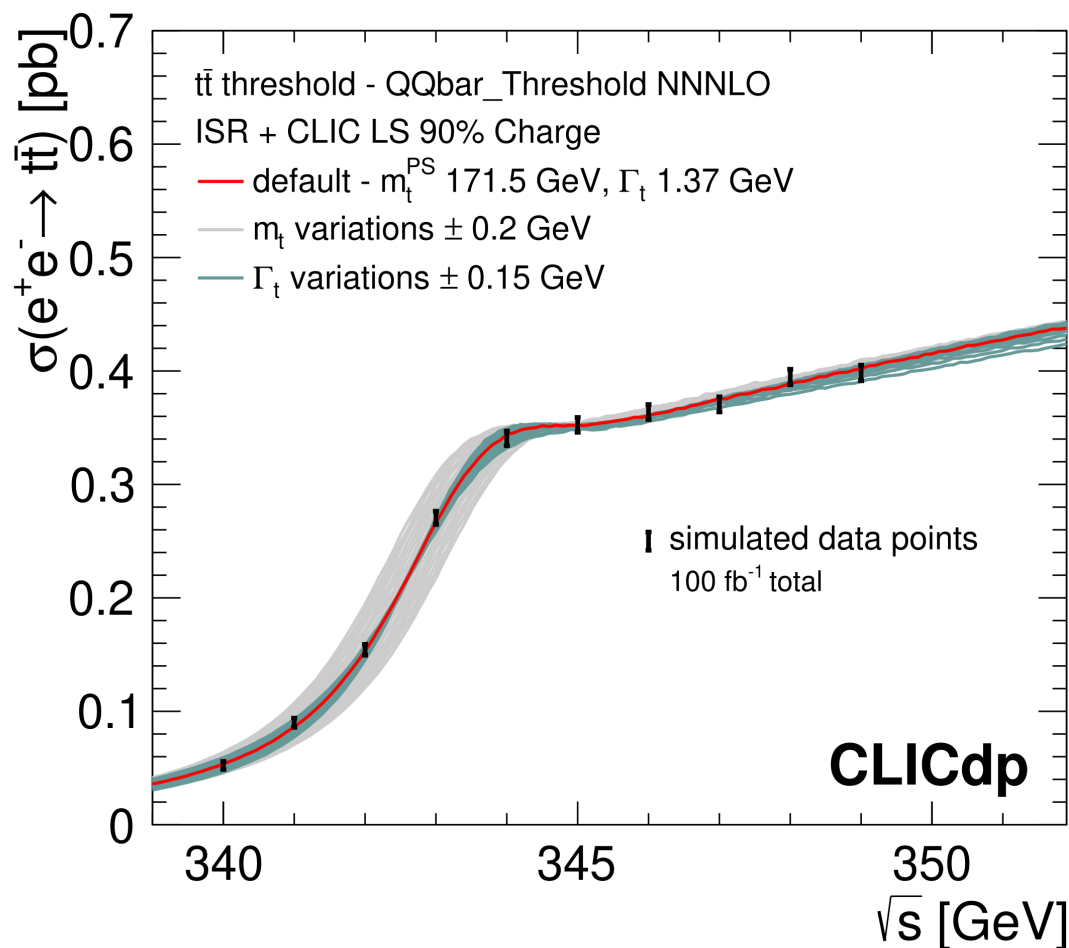


DIS 2021

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**FACULTY OF PHYSICS UW**

# Motivation

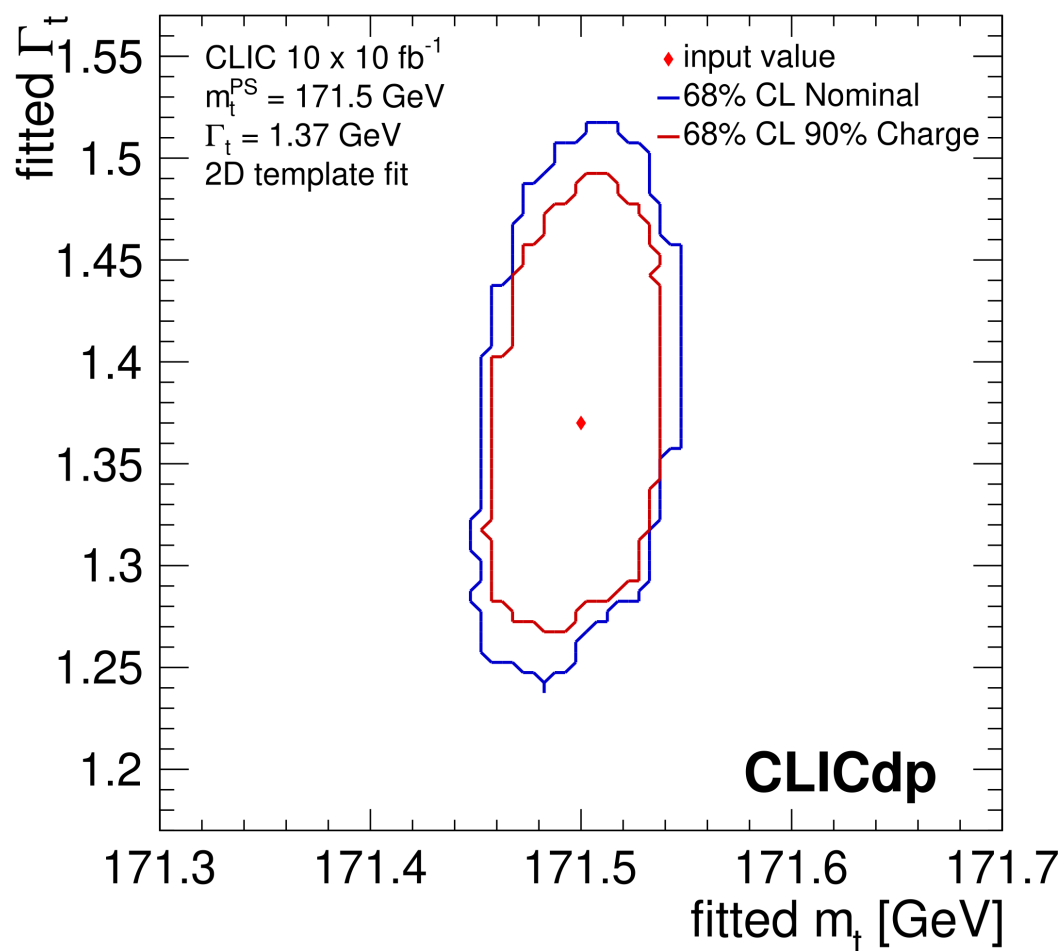


Threshold scan is assumed to be the most precise method to determine the top quark mass.

Baseline scenario assumes 10 scan points with 10 fb<sup>-1</sup> each

H.Abramowicz et al. (CLICdp Collaboration), *Top-Quark Physics at the CLIC Electron-Positron Linear Collider*, **JHEP 11 (2019) 003**, [arXiv:1807.02441](https://arxiv.org/abs/1807.02441),

# Motivation

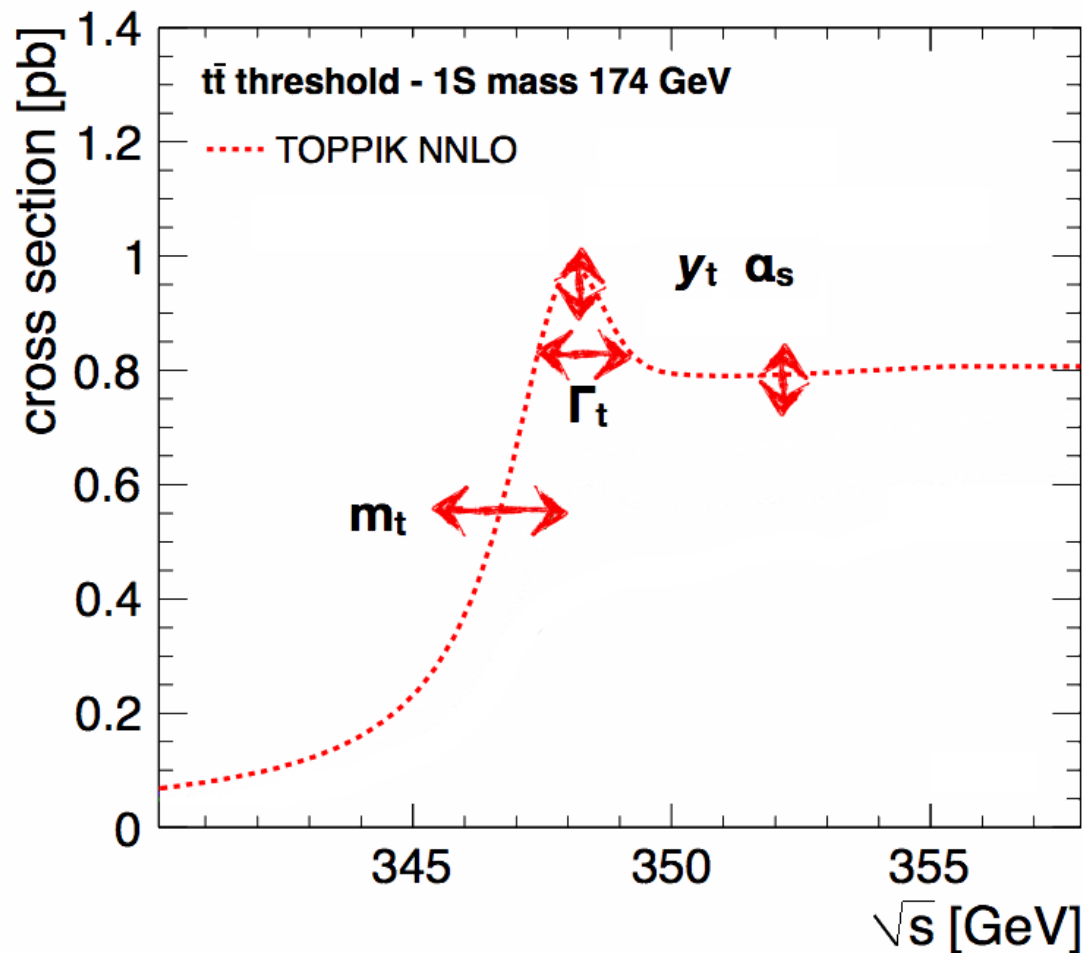


Dedicated study for CLIC indicates that the statistical precision of the measurement is around 20 MeV

However, this is based on a 2-D mass-width fit...

H.Abramowicz et al. (CLICdp Collaboration), *Top-Quark Physics at the CLIC Electron-Positron Linear Collider*, **JHEP 11 (2019) 003**, [arXiv:1807.02441](https://arxiv.org/abs/1807.02441),

# Motivation

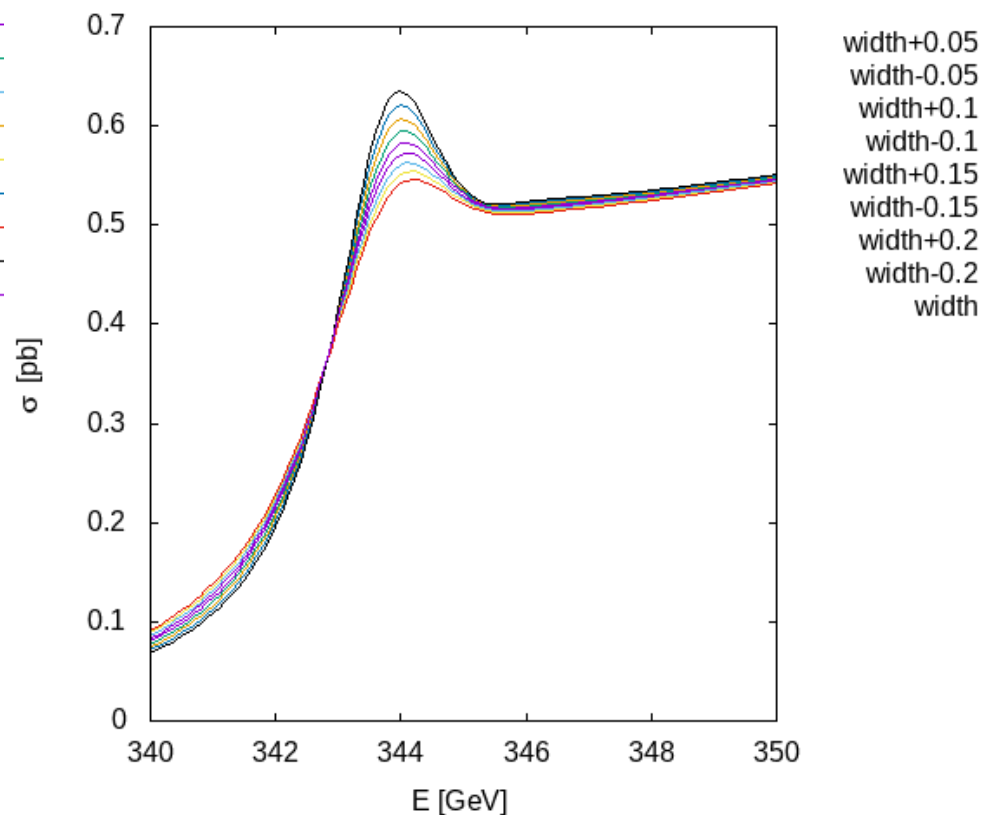
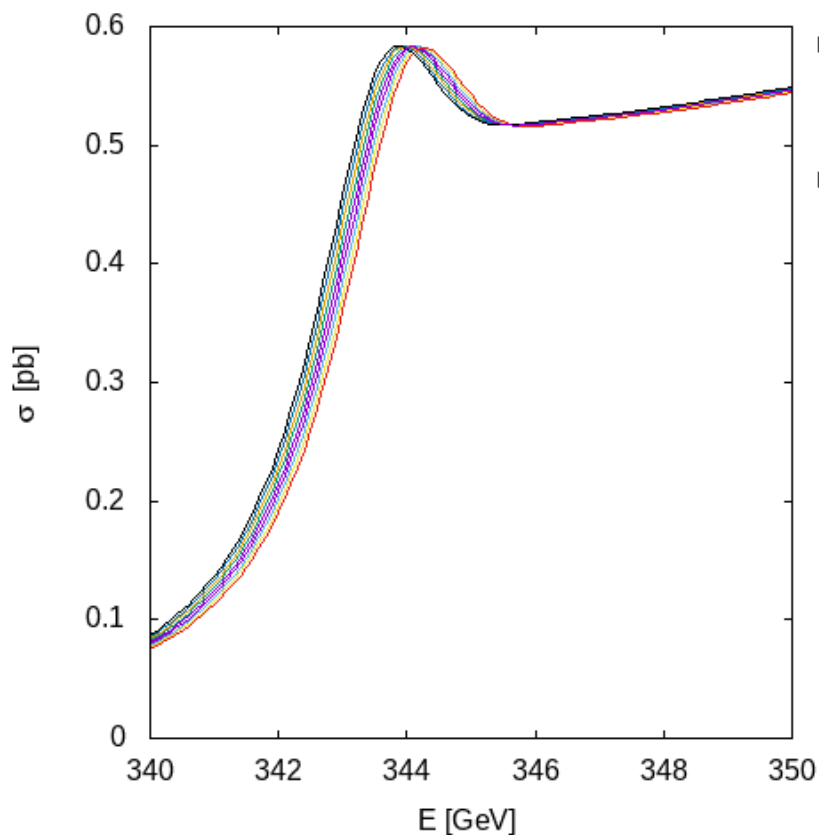


Threshold cross section depends on other model parameters as well...

Does it influence  $m_t$  determination precision?

Can the scan procedure be optimized?

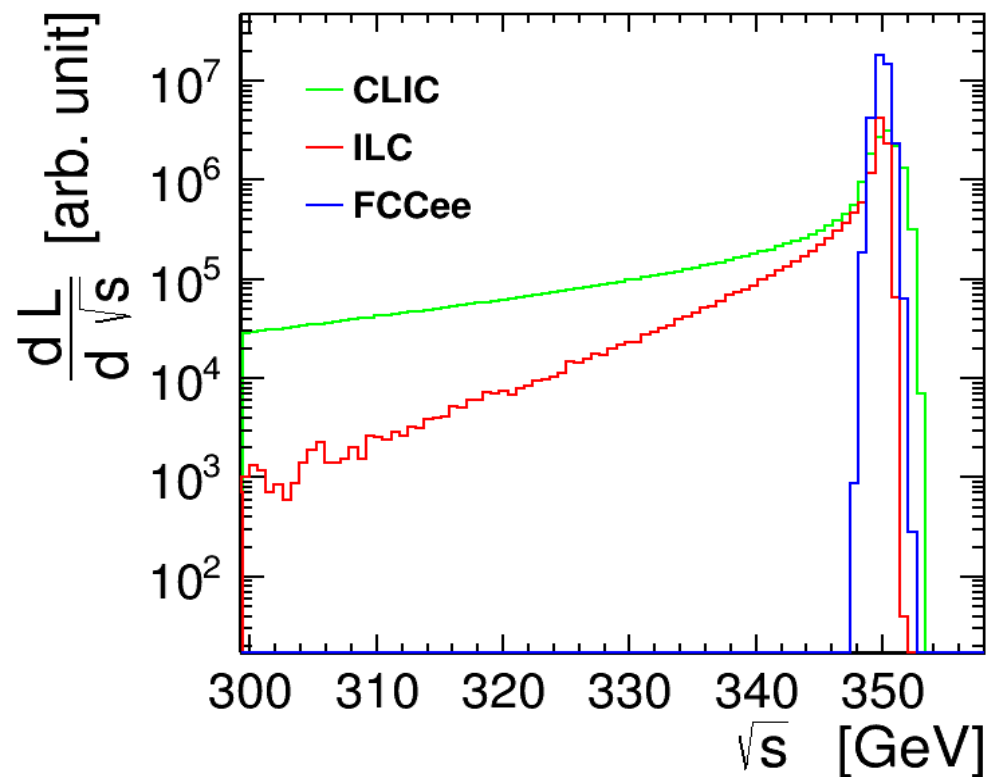
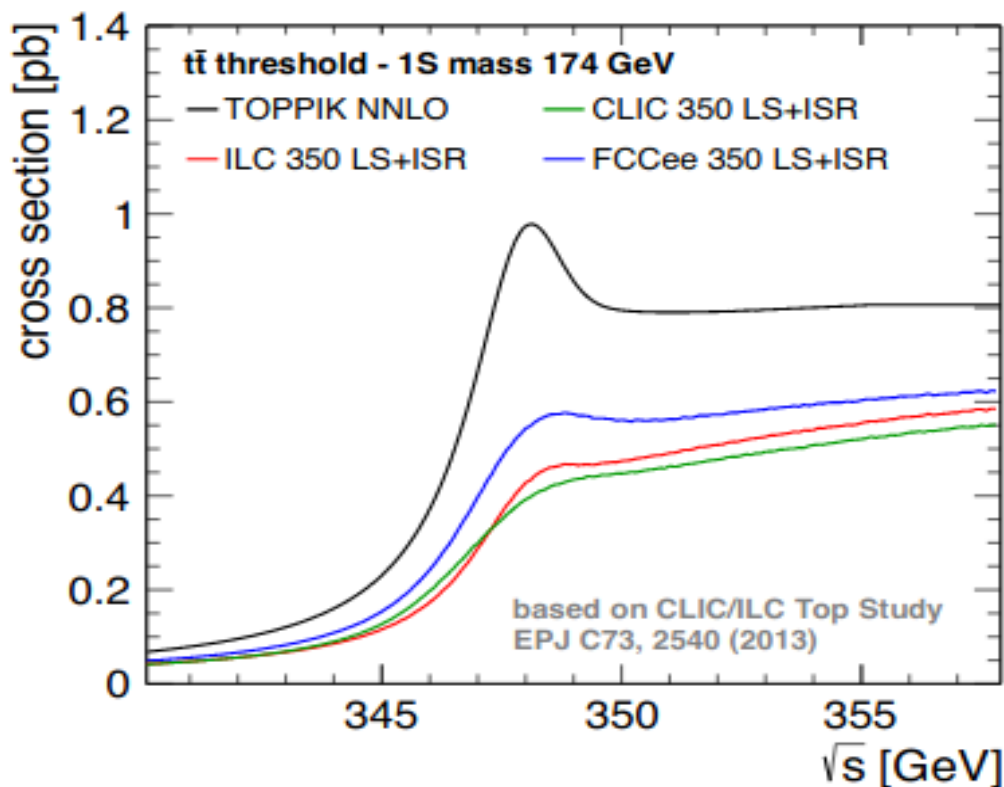
# Cross-section templates



Templates generated with **Qqbar\_threshold**

Beneke, M. et al. "Near-threshold production of heavy quarks with QQbar\_threshold," Comput. Phys. Commun. 209, 96–115 (2016).

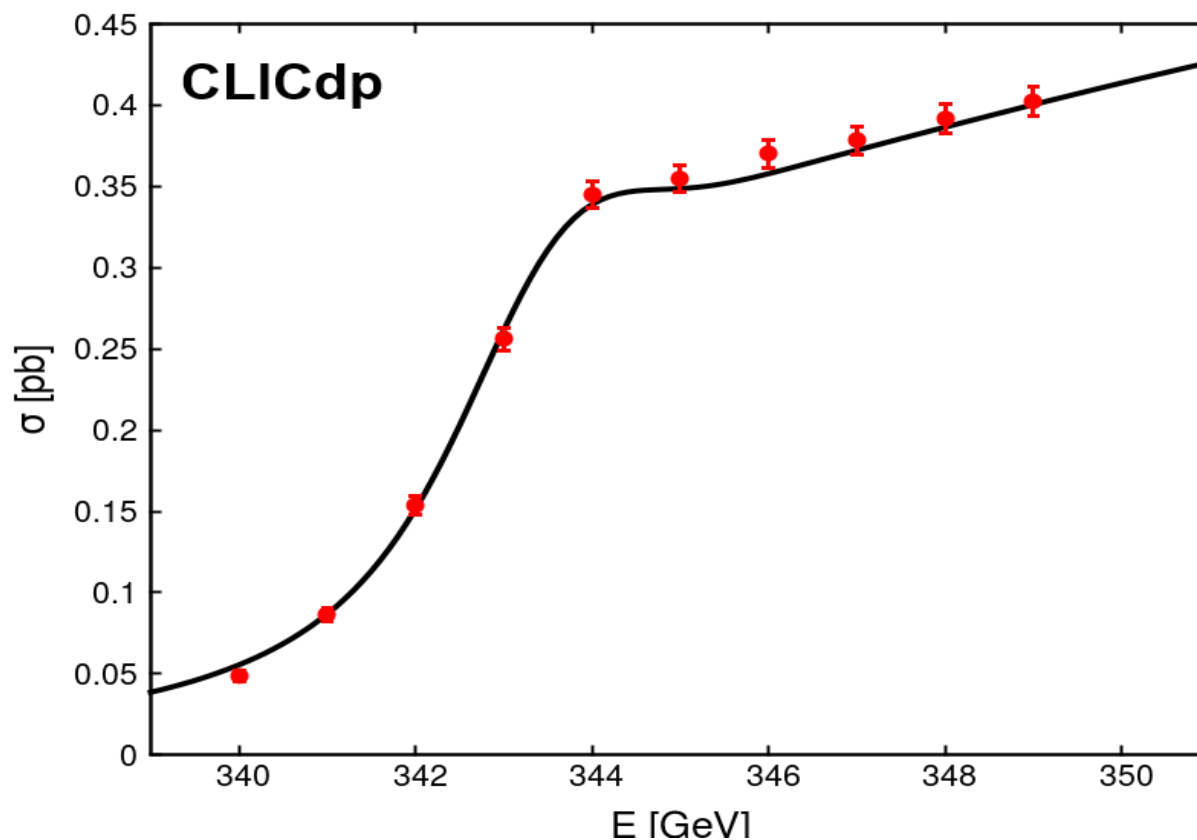
# Luminosity spectra



For CLIC we use luminosity spectra with 90% bunch charge

# Benchmark scenario

Assume 10 measurements at the threshold, with 1 GeV step in energy, with  $10 \text{ fb}^{-1}$  taken at each energy point ( $100 \text{ fb}^{-1}$  total).



Generate statistical fluctuation assuming 70.2% event reconstruction efficiency and background level (remaining after cuts) corresponding to the 73 fb

[K. Seidel et al., Eur. Phys. J. C 73 \(2013\) 2530 \[arXiv:1303.3758\]](#)

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# Fit procedure

For each generated data set (pseudo-experiment)  $\chi^2$  value is calculated for different parameter values (different templates)

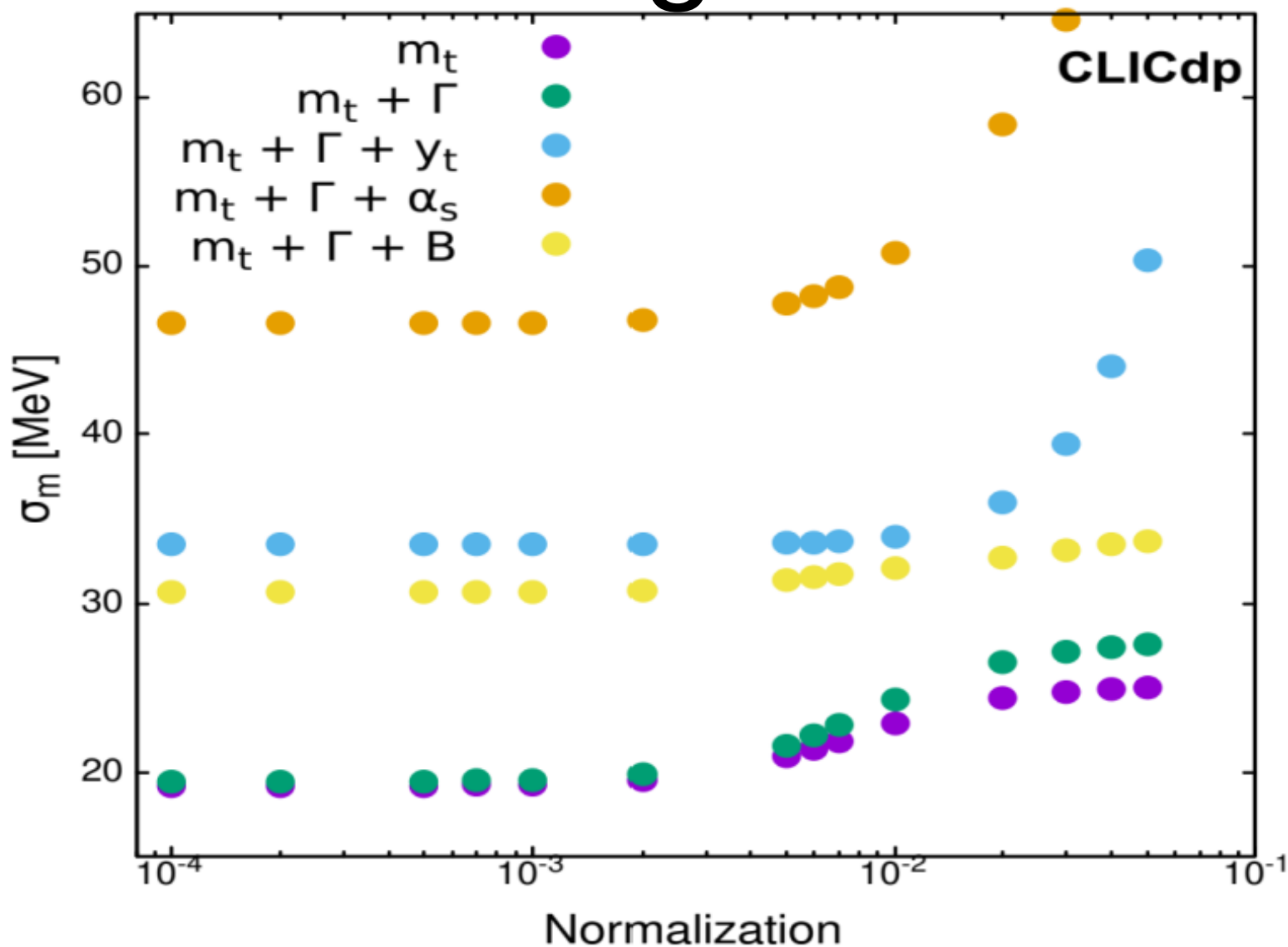
Quadratic dependence of the  $\chi^2$  value on the model parameters is fitted to find the best fit parameter values and the estimated uncertainty (corresponding to  $\Delta\chi=1$ )

Fits resulting in the parameter values outside the range used to generate templates are ignored.

More details on the fit method: [arXiv:2103.00522](https://arxiv.org/abs/2103.00522)



# Fit configuration

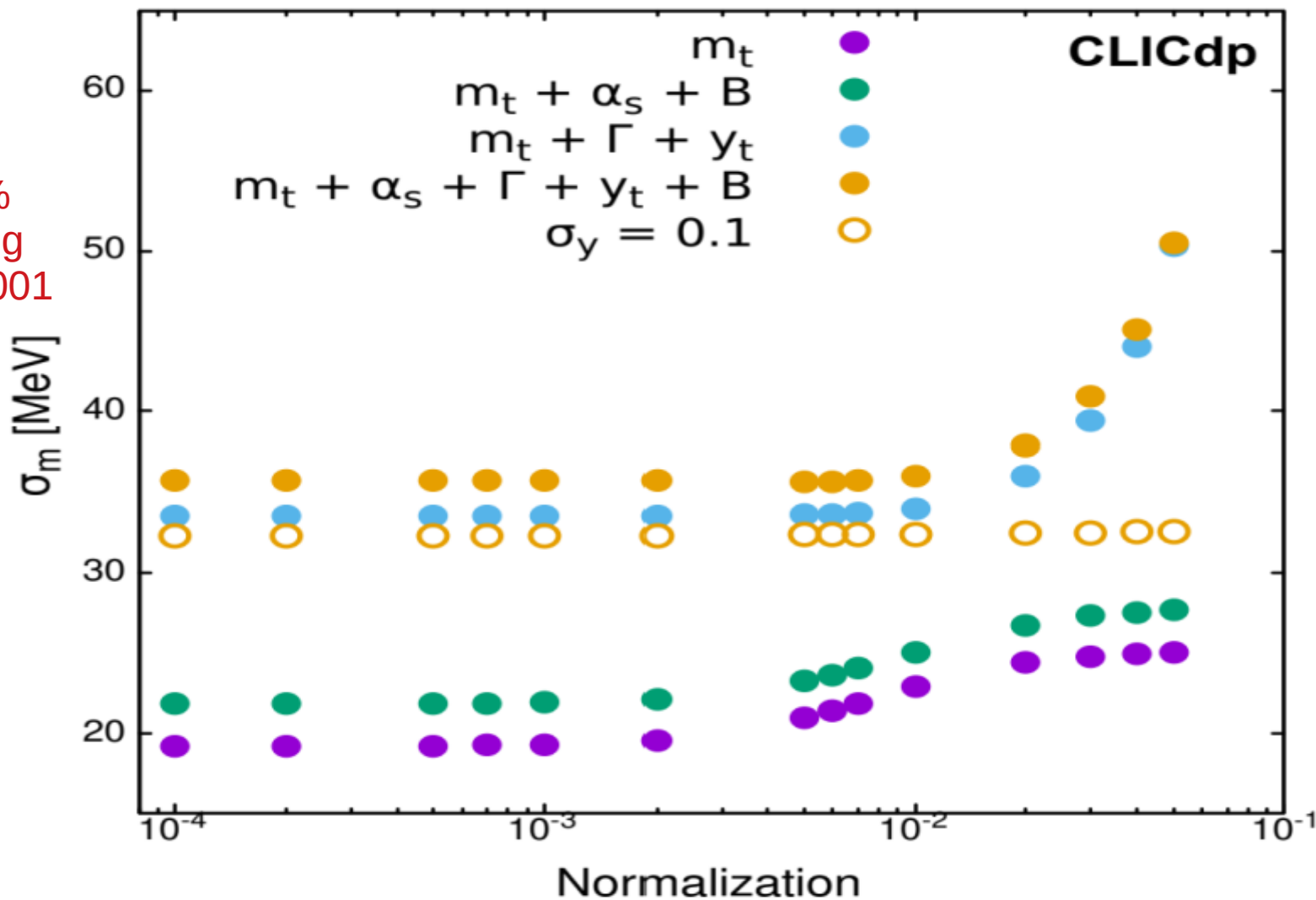


Expected top quark mass uncertainty for different choices of free fit parameters

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# Systematic uncertainties

Assuming  
Background  
uncertainty 2%  
Strong coupling  
uncertainty 0.001

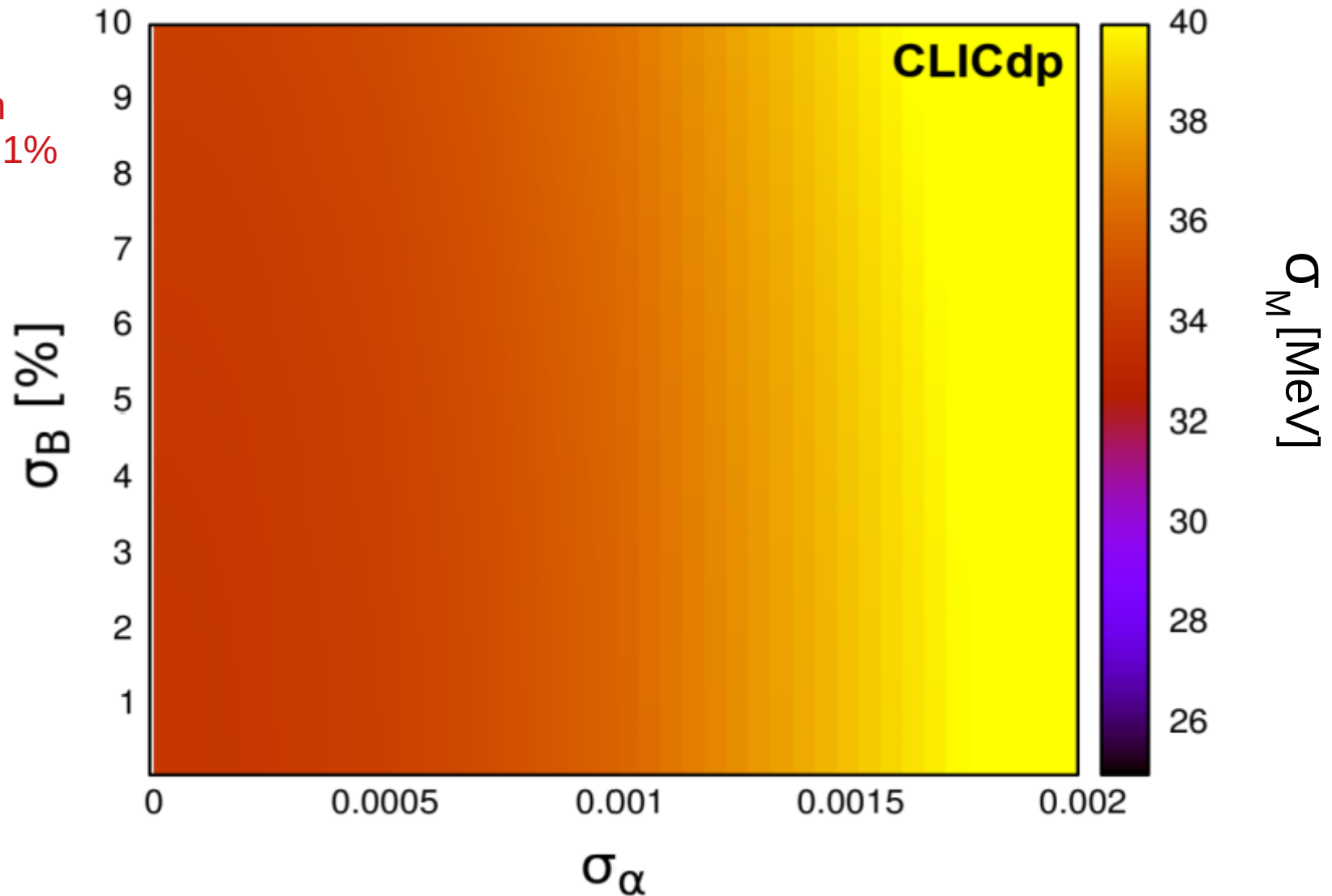


Systematic effects described by constrained fit parameters

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# Baseline fit results

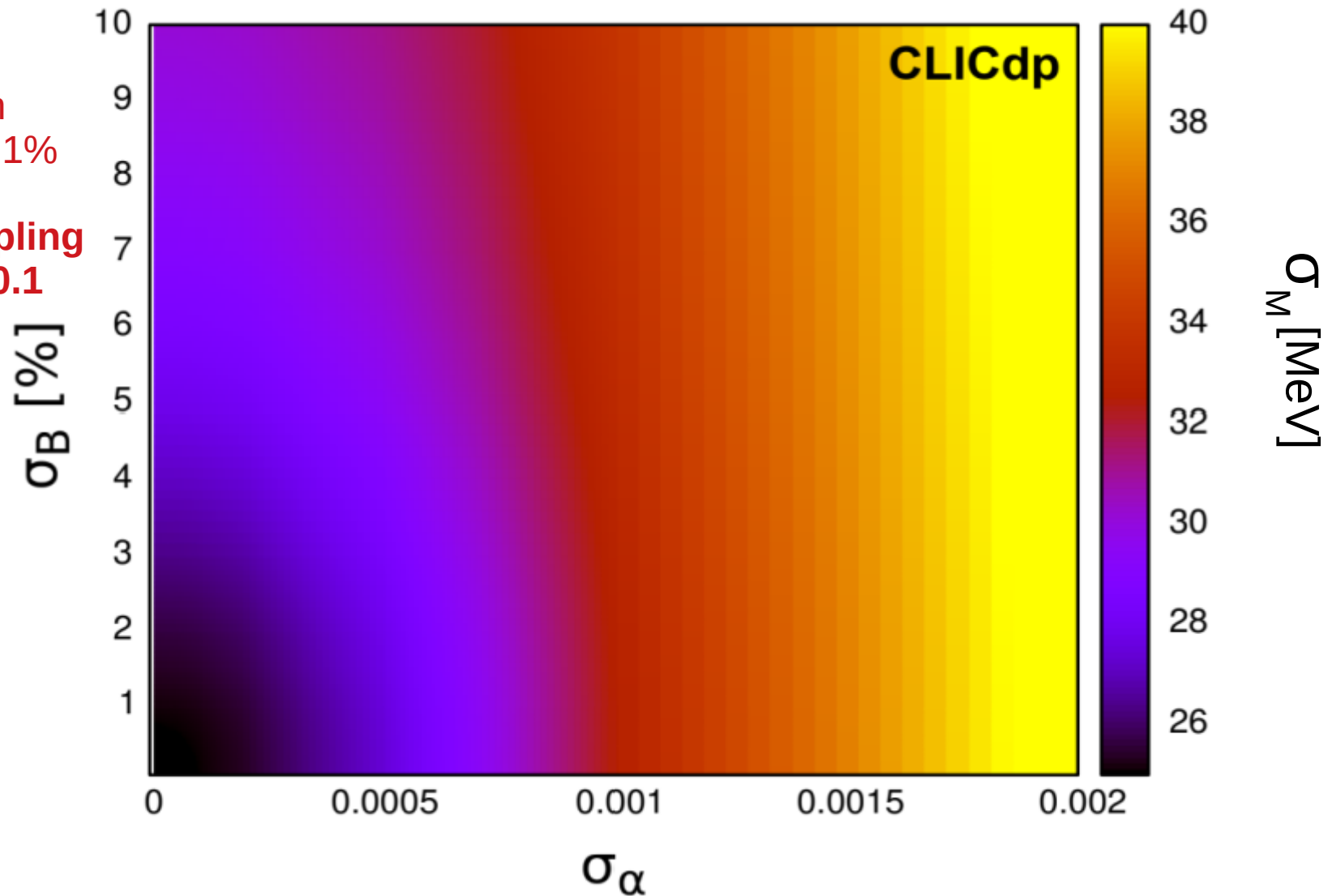
Assuming  
Normalization  
uncertainty 0.1%



# Baseline fit results

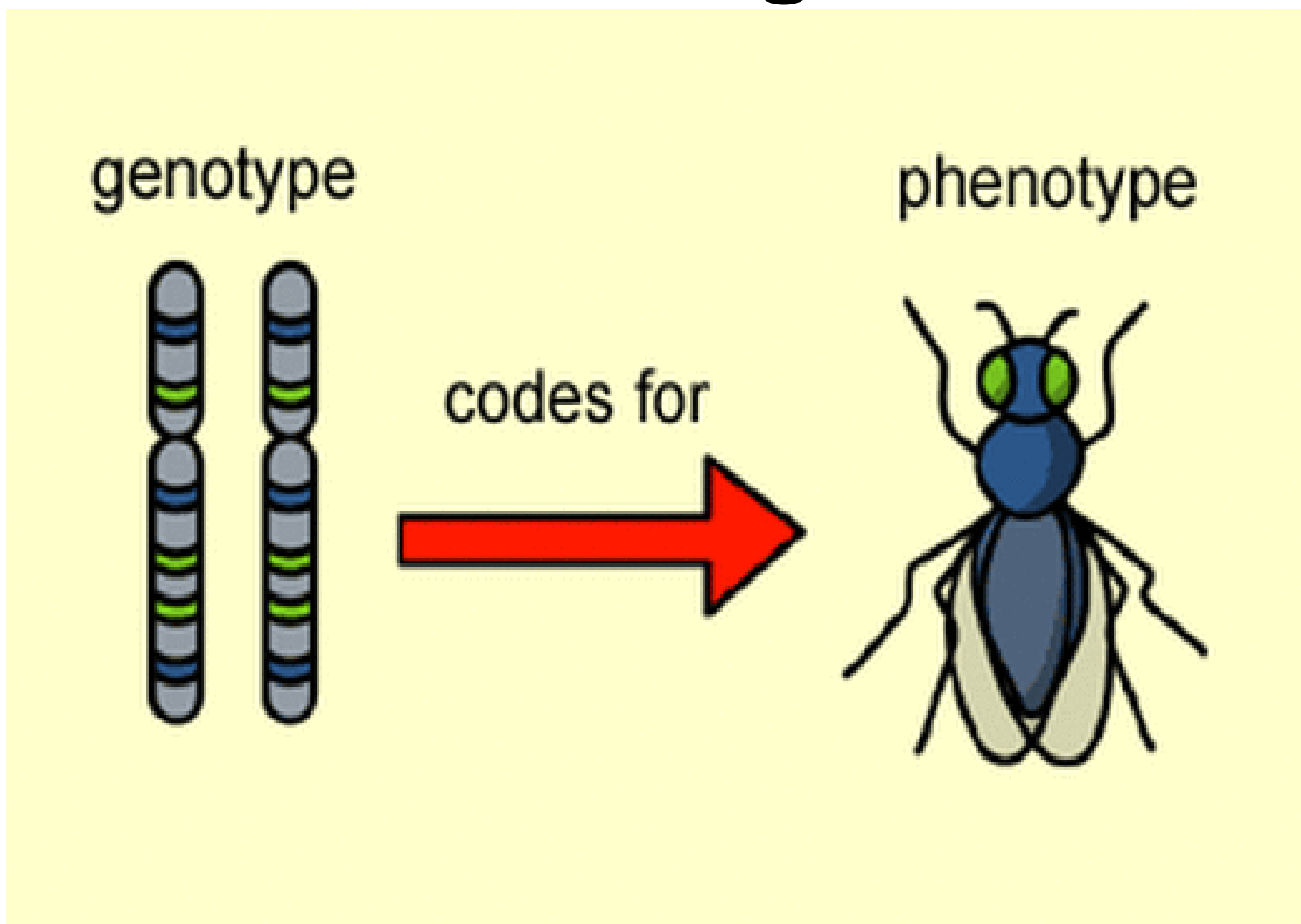
Assuming  
Normalization  
uncertainty 0.1%

Yukawa coupling  
uncertainty 0.1



# Scan optimization

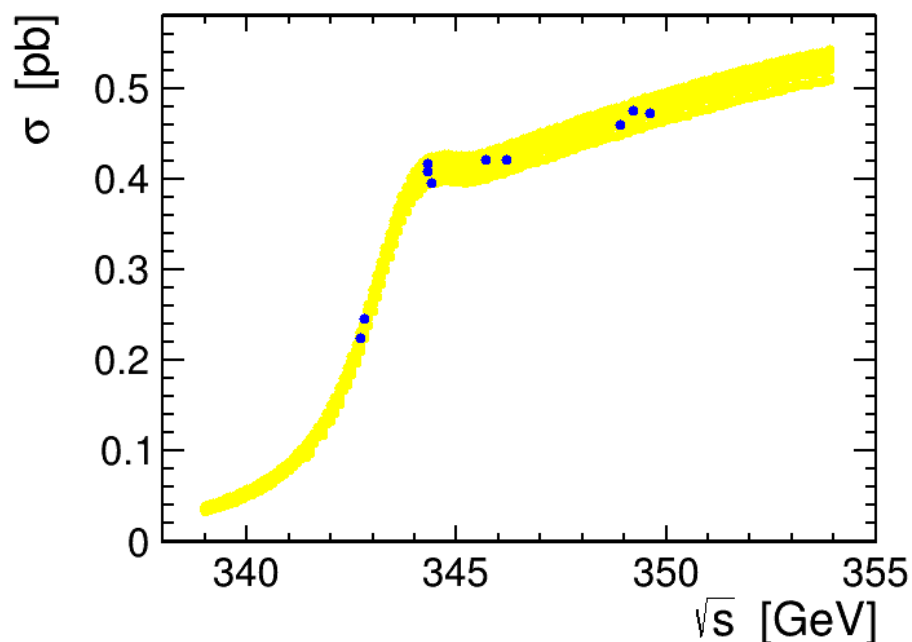
# Genetic algorithm



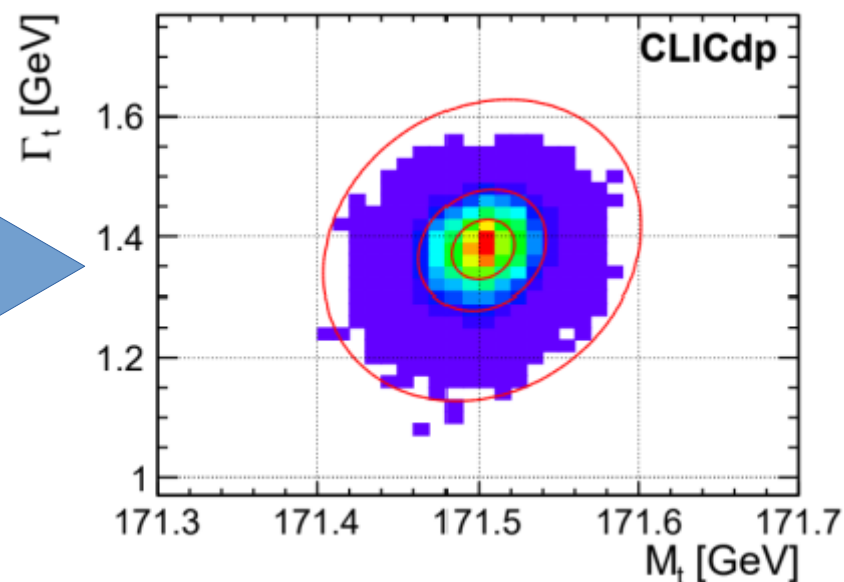
# Genetic algorithm

Each measurement point makes a chromosome.  
We assume total luminosity is always  $100 \text{ fb}^{-1}$  and is equally distributed.

Genotype



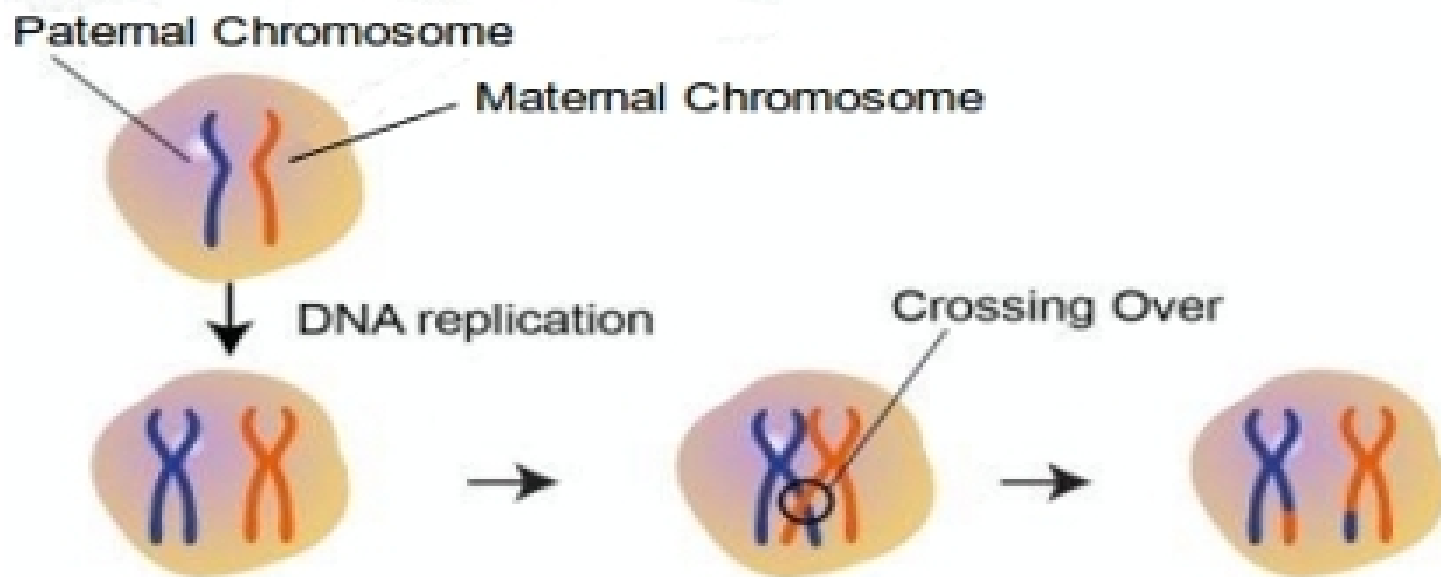
Phenotype



Fits resulting in the parameter values outside the range used to generate templates are ignored.

# Creating new individuals

Randomly choosing parts of parents genotype and  
add random mutation  $\pm 0.5$  GeV

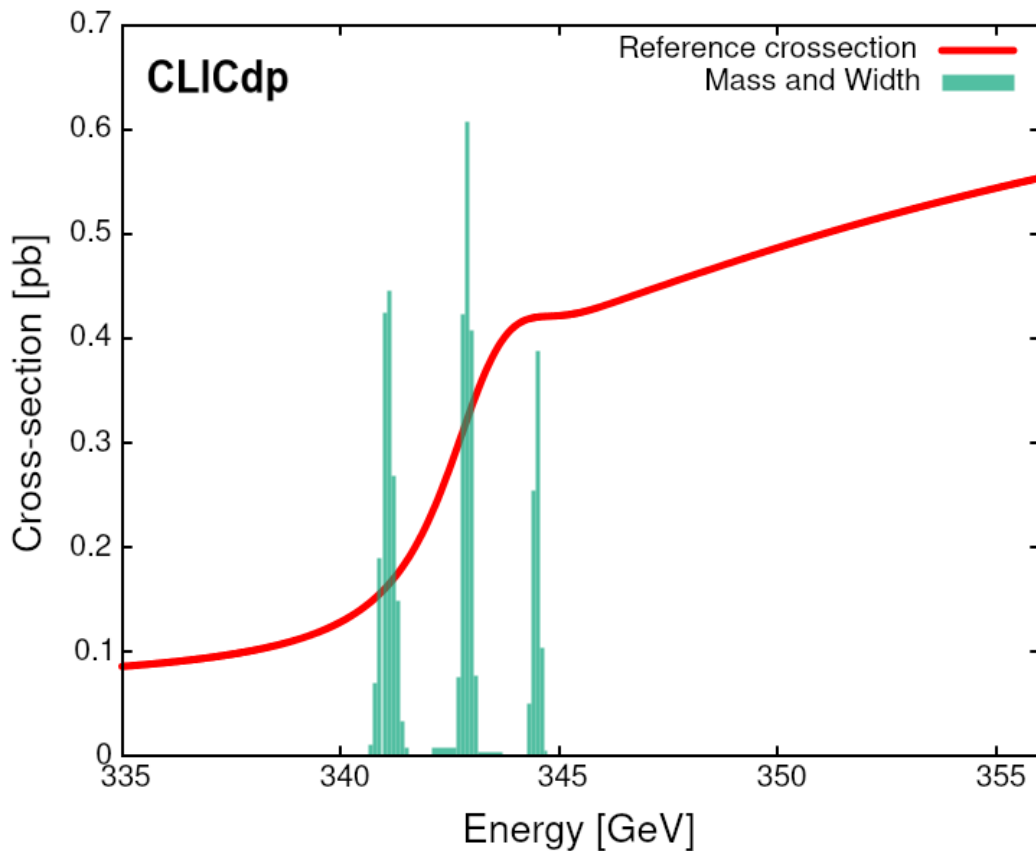
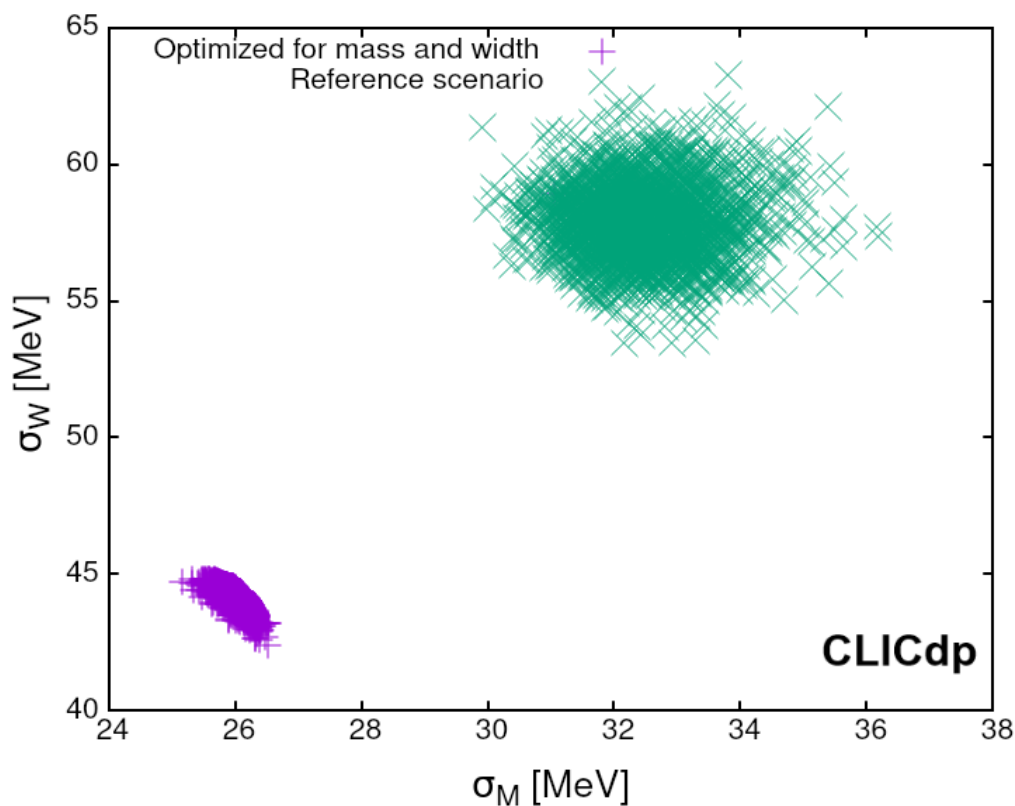


Recombination between 2 homologous chromosomes

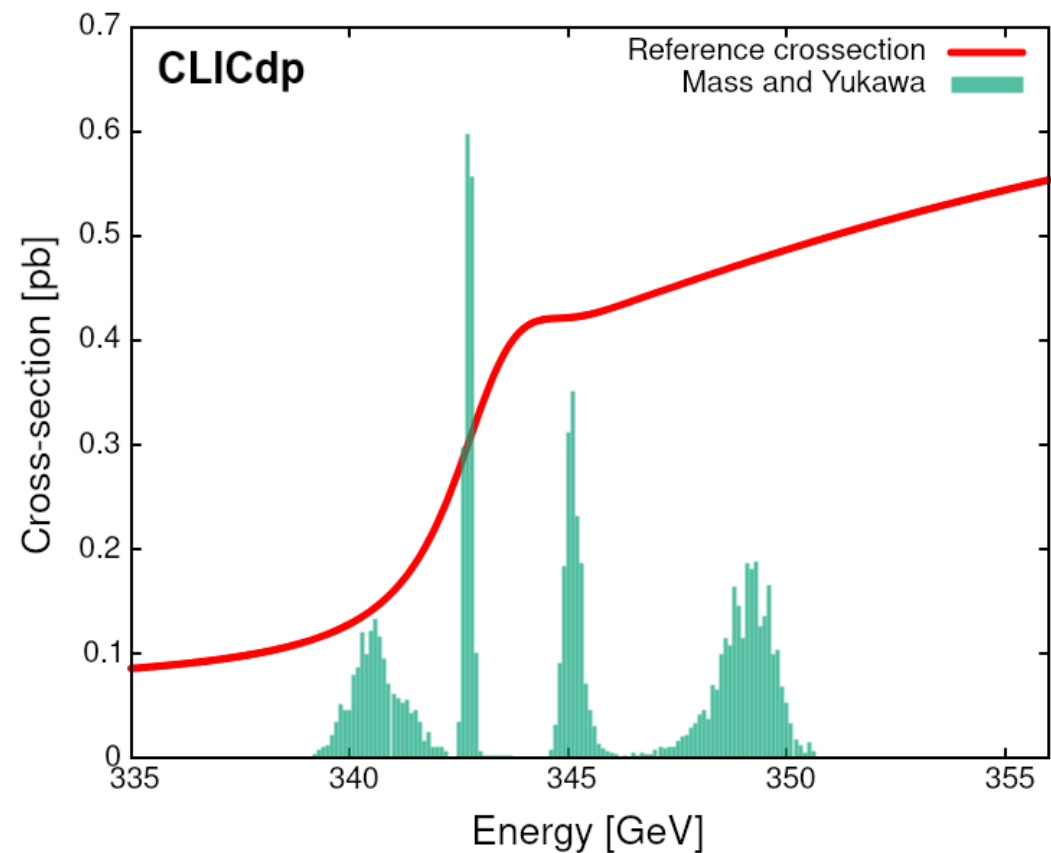
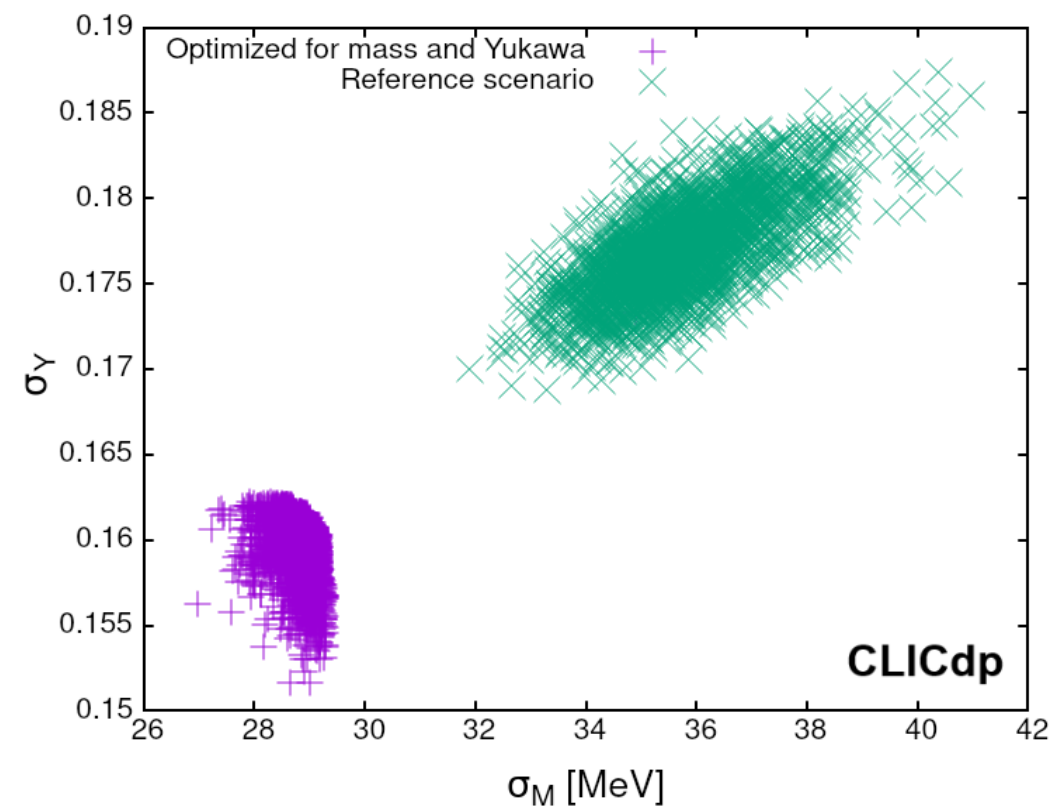
We add 5% chance to drop any of measurement points.



# Mass and Width optimization

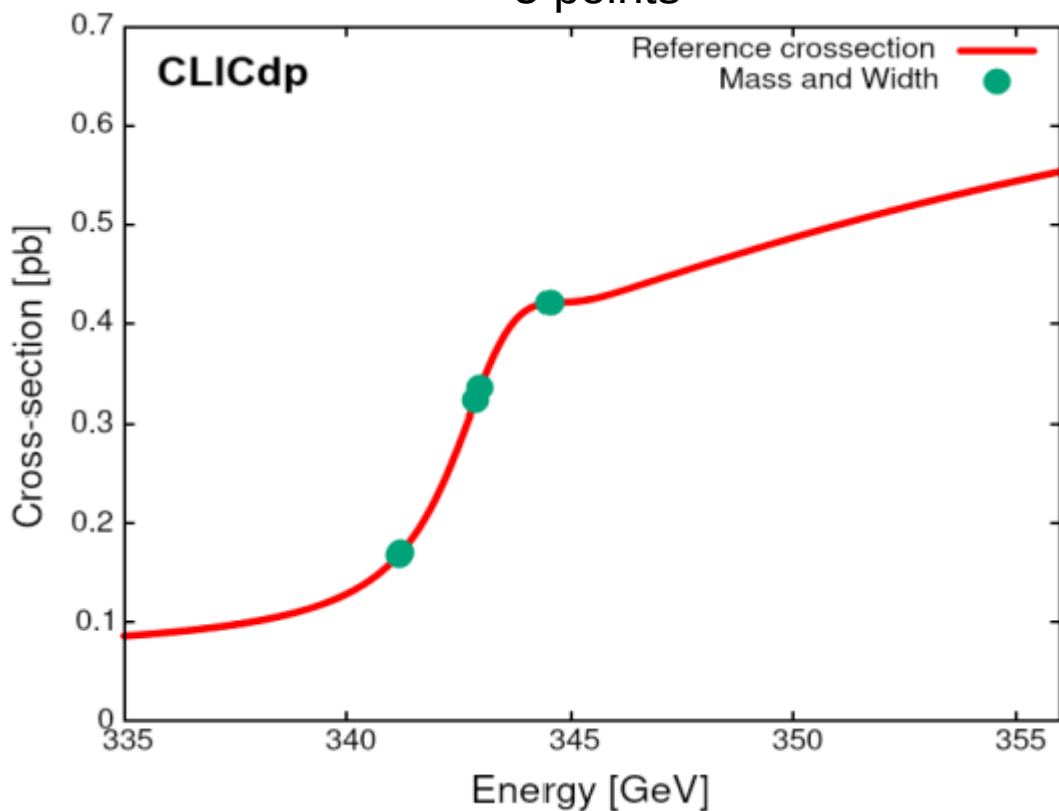


# Mass and Yukawa optimization

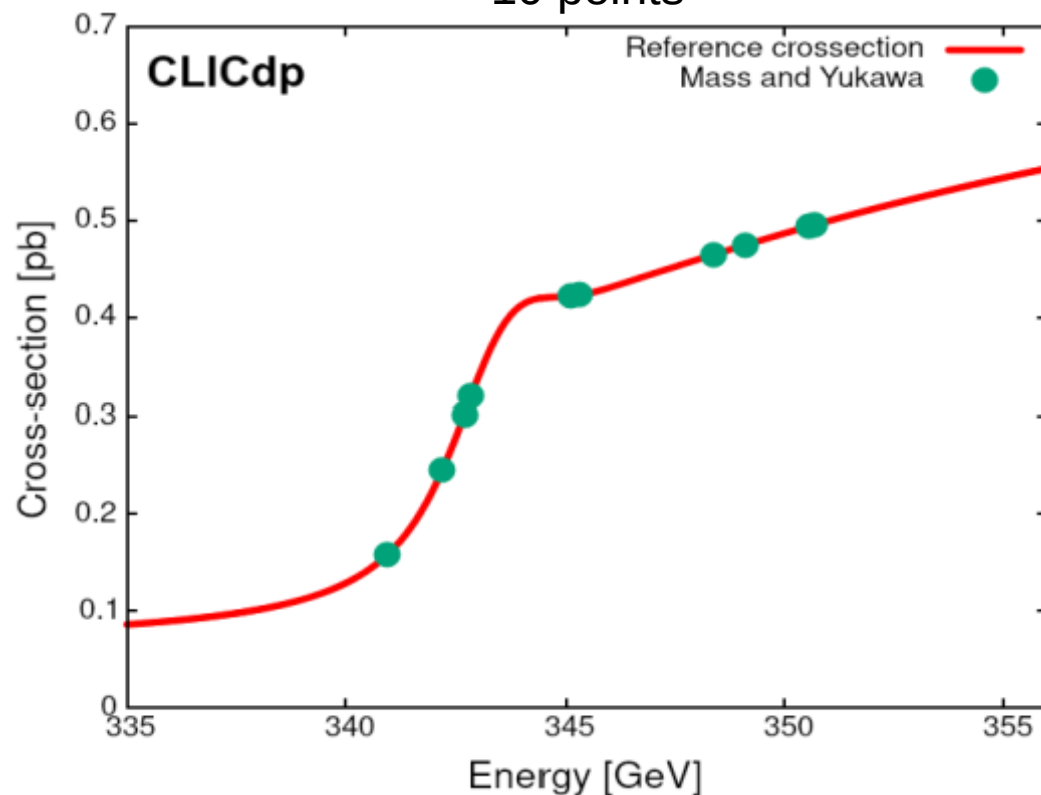


# Optimized scenarios

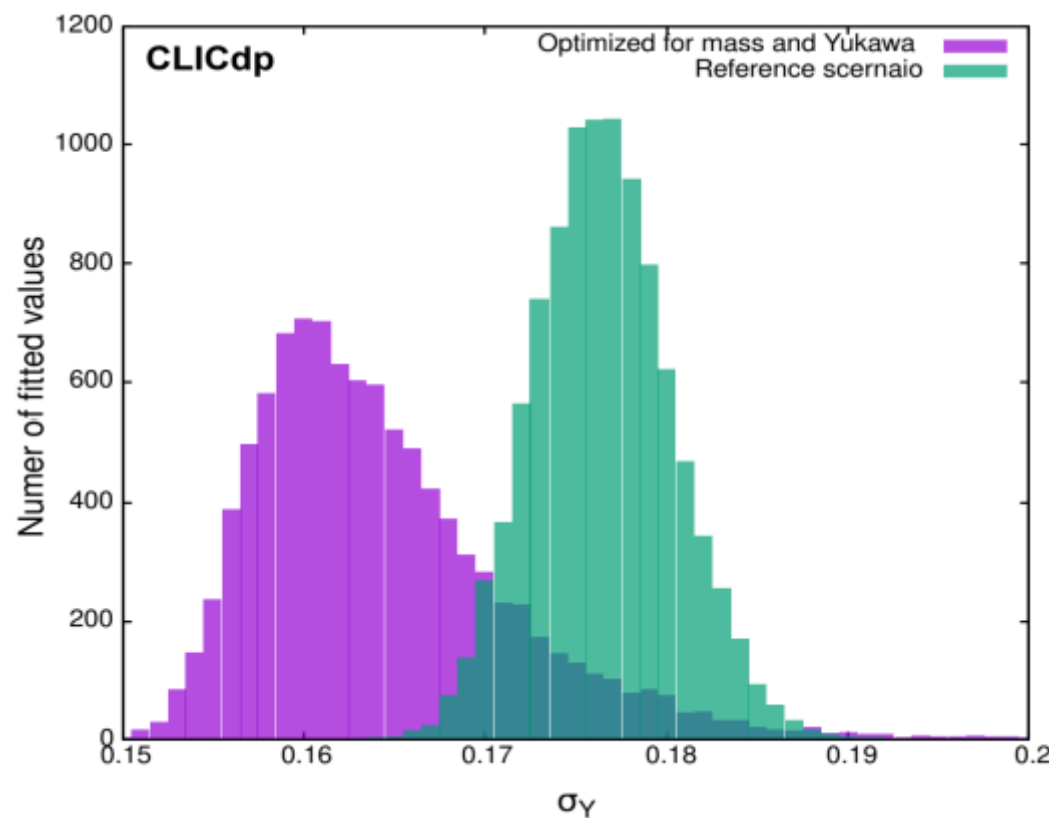
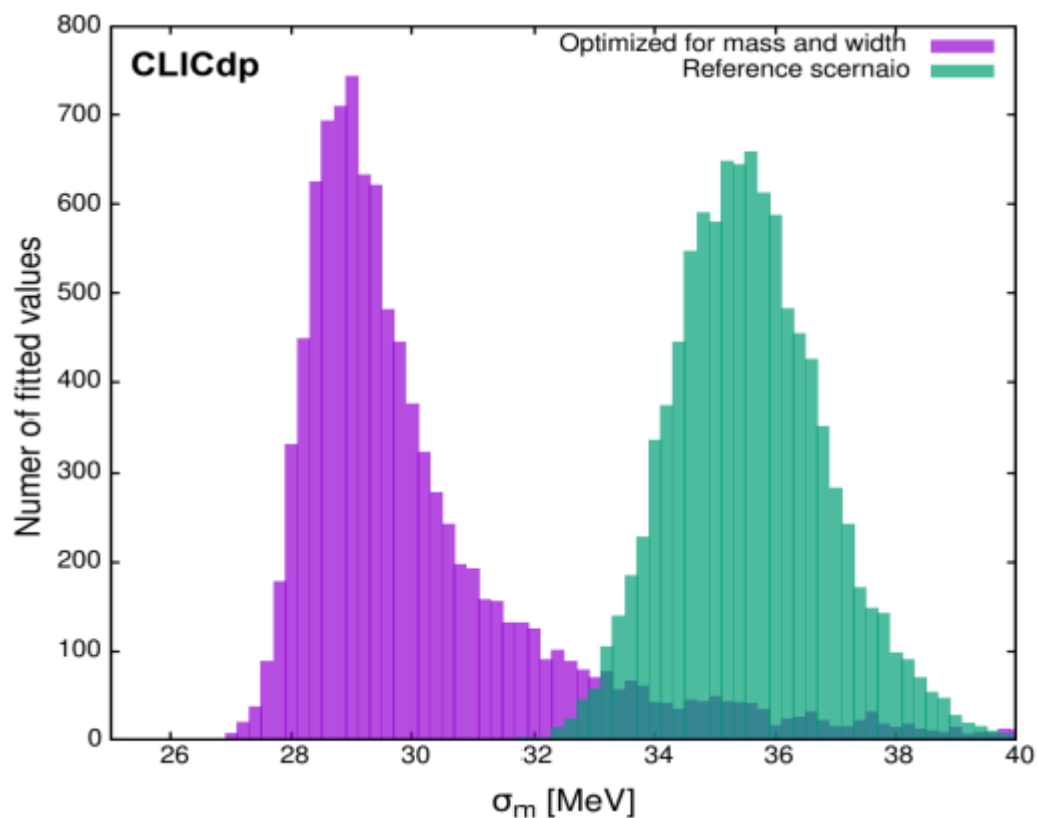
Mass and Width  
5 points



Mass and Yukawa  
10 points

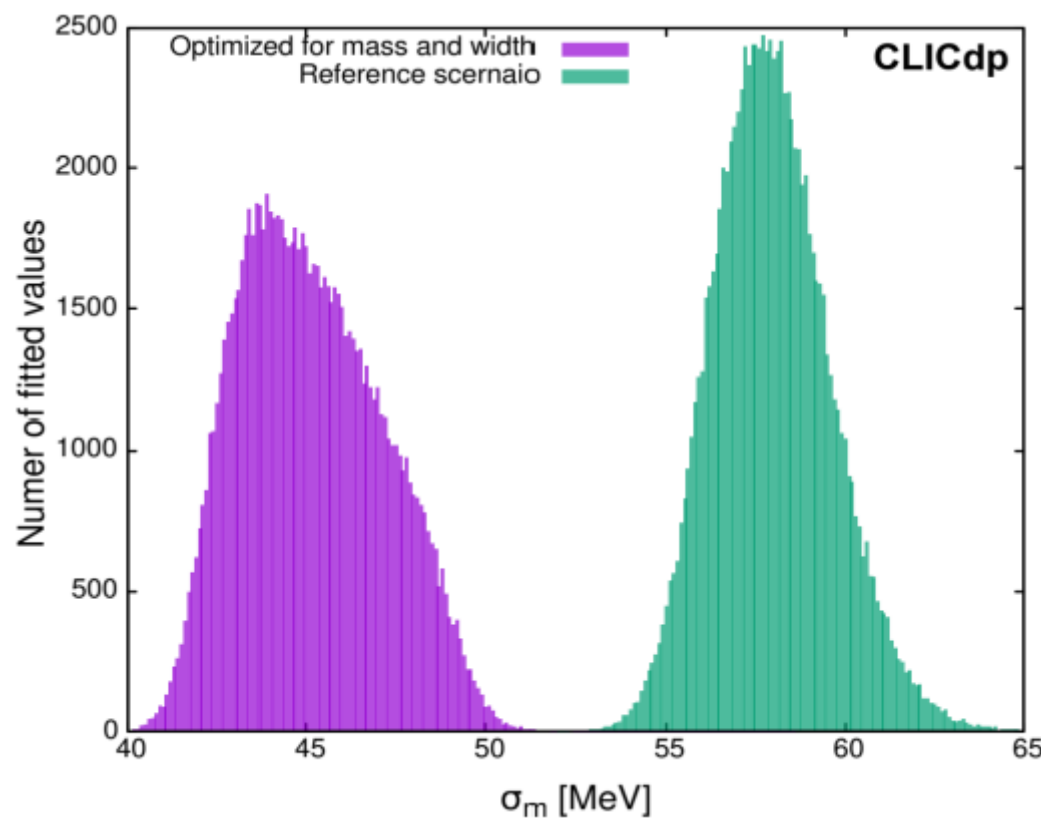
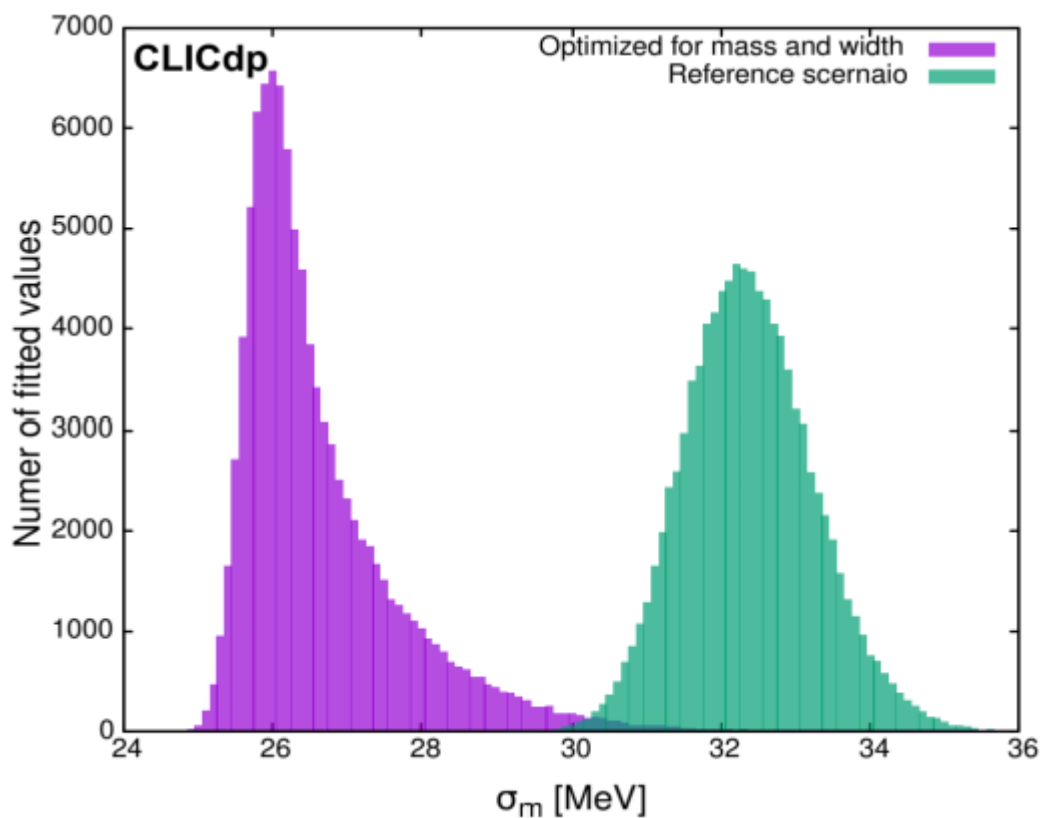


# Mass and Yukawa scenario



Normalization uncertainty 1%  
 Strong coupling uncertainty 0.001  
 Background uncertainty 2%

# Mass and width scenario

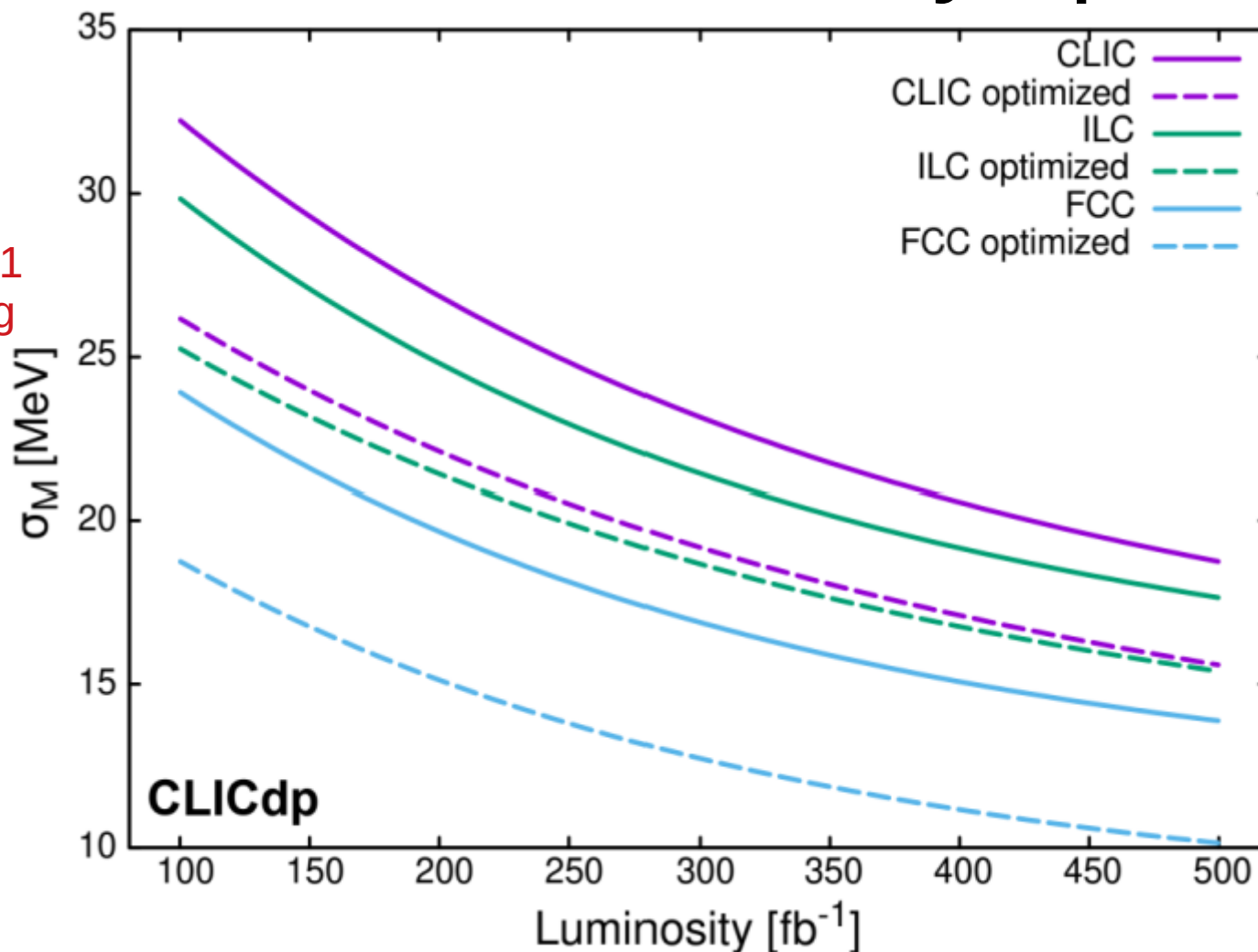


Normalization uncertainty 1%  
Strong coupling uncertainty 0.001  
Yukawa coupling uncertainty 0.1  
Background uncertainty 2%

# Influence of luminosity spectra

Normalization  
uncertainty 1%  
Strong coupling  
uncertainty 0.001  
Yukawa coupling  
uncertainty 0.1

Optimized for  
mass and width  
determination  
precision

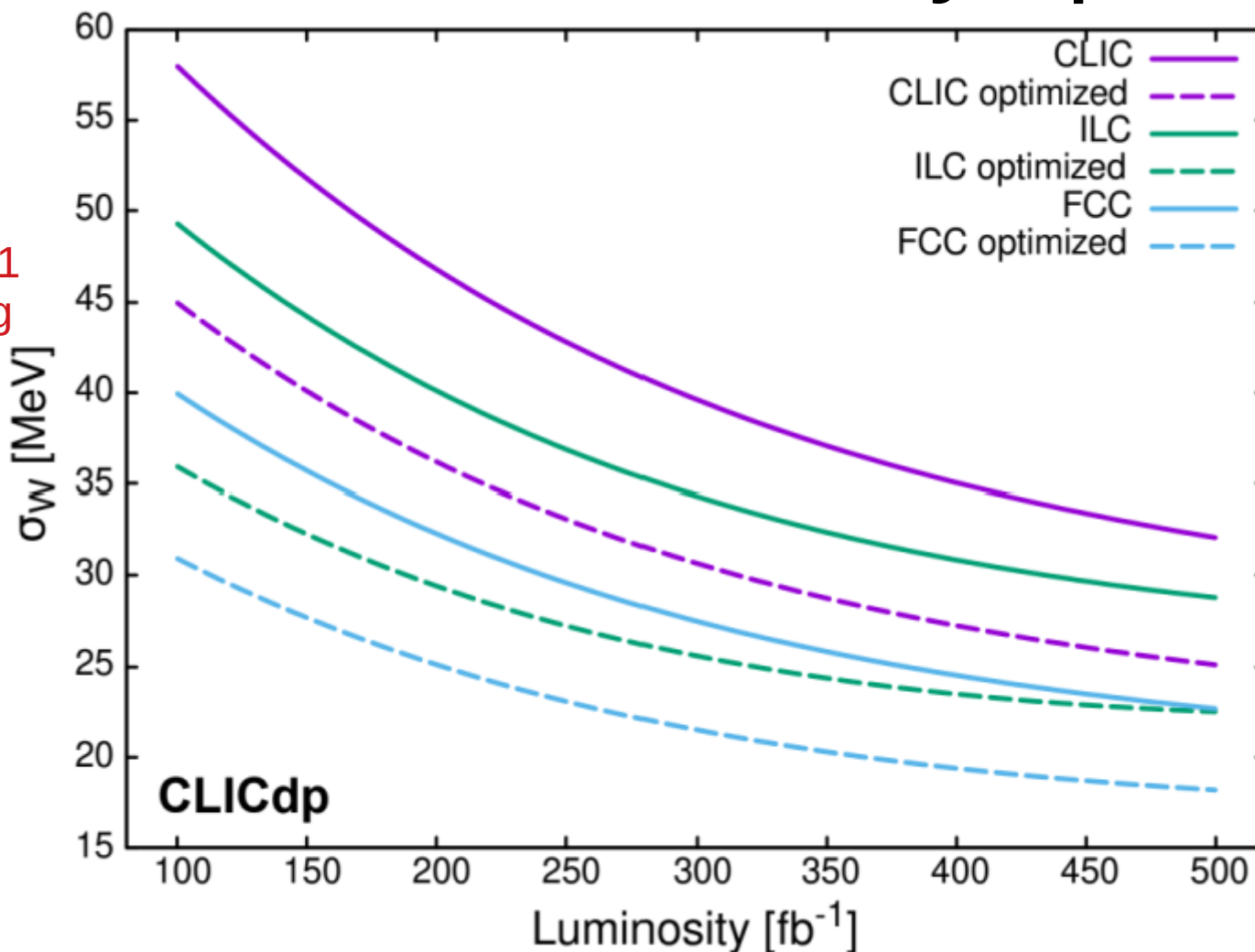


Assuming **same background and efficiency, no polarisation**

# Influence of luminosity spectra

Normalization  
uncertainty 1%  
Strong coupling  
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Optimized for  
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Assuming **same background and efficiency, no polarisation**

# Conclusions

## Top-quark mass

can be extracted with  $\sim 25$  MeV statistical uncertainty even in the most general approach, when expected parameter constraints are taken into account.

## Scan optimization

Statistical uncertainty of the extracted top-quark mass can be reduced by  $\sim 25\%$ , without losing precision in width or Yukawa determination

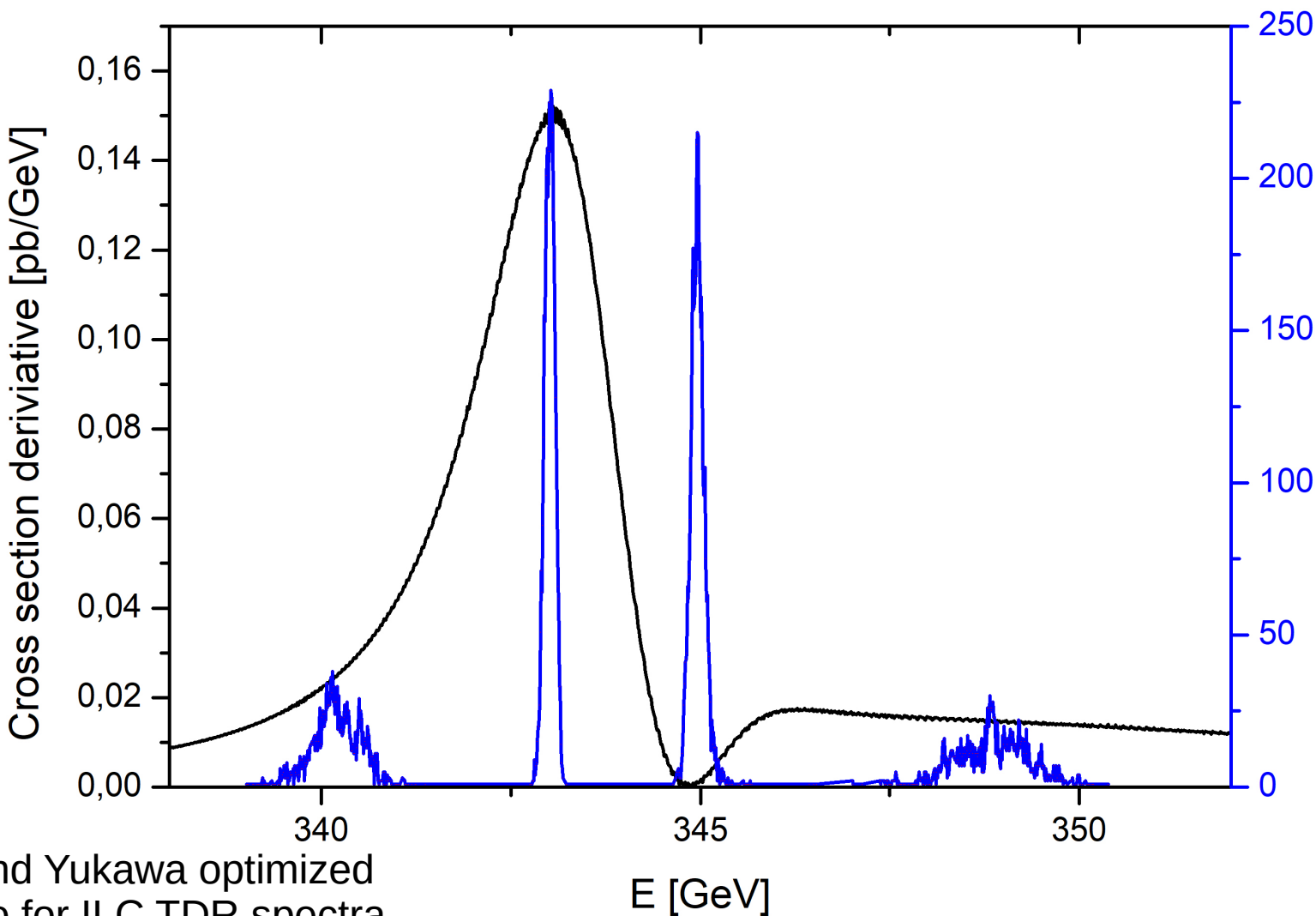
For more results see [arXiv:2103.00522](https://arxiv.org/abs/2103.00522)



# Backup slides



# What is the algorithm looking for?



Mass and Yukawa optimized  
scenario for ILC TDR spectra