



sample name, x-fold  
dilution, sample volume ( $\mu$ l)



edit file and  
upload to app



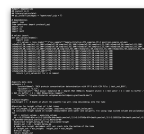
download  
template file from  
app



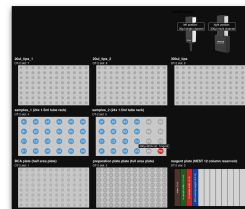
analysis meta file



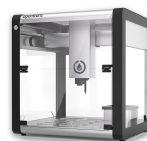
HTML how-to file



python protocol



follow the instructions  
in the html file and  
perform assay on OT-2



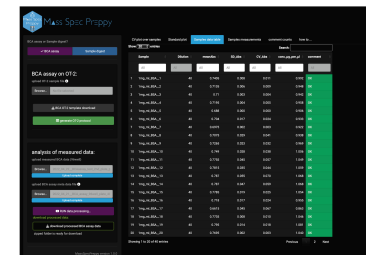
incubate in  
the dark at  
60°C



read-out  
on plate  
reader



upload files to  
app and analyse



BCA assay modul

sample digest modul

sample name, protein concentration  
( $\mu$ g/ $\mu$ l), sample volume ( $\mu$ l)

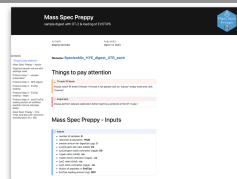


edit file and  
upload to app



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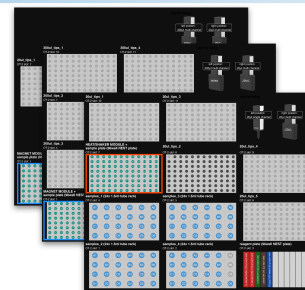
parameter	options
sample amount to digest	1-10 $\mu$ g
enzyme: sequential or mix digest	mix or sequential
enzyme to protein ratio	25, 50, 100
reduction & alkylation	yes or no
elution in MS vials or Evotips	Evotips or MS vials
Evotip loading (if Evotip is selected)	100 - 2000 ng



HTML how-to file



python protocols



follow the instructions in the  
html file and perform assay  
on OT-2

