**Instructions for general good practice updated according to Nature publishing guidelines.**

**1. Check instructions to authors and follow**

Eg subheading rules, manuscript length (some journals eg nature family don’t apply length constraints pre-review so you can send out longer versions, but be prepared to have to shorten it.

Eg

*Title  
Author list  
Affiliations  
Abstract  
Main text  
Methods  
Data Availability  
Code Availability (if relevant)  
Acknowledgements  
Author Contributions Statement  
Competing Interests Statement  
Tables  
Figure Legends/Captions (for main text figures)  
References*

**2. Please supply Source Data files** for all data presented in graphs within the Figures and Extended Data. (Note need to have all source files ready. This should be easy for your own data but if you’re the study lead, you need to get all of the data from collaborators, in our lab and beyond, in a good format that you understand, ideally done while everyone remembers what the data are.

Notes on Source Data format:  
- Numerical source data files may be supplied in .xls(x), .csv, .txt or .zip format  
- Image source data files may be supplied in .tif, .jpg, .pdf or .zip format.   
- Separate files should be supplied for each Figure.   
- Source Data files must be listed in the Inventory of Supplementary Information  
- Source Data files may be provided for Figures and Extended Data only. For Supplementary Information items, please supply source data as Supplementary Data files (or for image data such as uncropped, unprocessed scans of blots and gels, at the end of the Supplementary Information file).

**3. Immunoblots**

Please ensure that uncropped scans of all blots and gels in Figures and Extended Data are supplied

as Source Data files. Those presented in Supplementary Figures should be supplied at the end of the Supplementary Information file. Scan the whole gel where possible (sometimes you can’t if you’re also detecting a second protein. So far this is OK to detect >1 protein per gel.)

Please ensure that all blots and gels are accompanied by the locations of molecular weight/size markers. Where it is necessary to crop blots, please ensure that at least one marker position is present.   
  
Please supply uncropped scans of blots and gels in Figures and Extended Data as Source Data files. Those presented in Supplementary Figures should be supplied at the end of the Supplementary Information file. Please pay close attention to our image integrity guidelines when preparing figures containing blots and gels:  
  
https://www.nature.com/nature-research/editorial-policies/image-integrity.  
  
Quantitative comparisons between samples on different gels/blots are discouraged; if this is unavoidable, the figure legend must state that the samples derive from the same experiment and that gels/blots were processed in parallel.

Vertically sliced images that juxtapose lanes that were non-adjacent in the gel must have a clear separation or a black line delineating the boundary between the gels. Loading controls (e.g. GAPDH, actin) must be run on the same blot.  
  
Sample processing controls run on different gels must be identified as such in the figure legends, and distinctly from loading controls.

**We should not compare samples on different gels. Rerun the gel where necessary**

**4. Avoid “data not shown”.**

We do not allow statements based on data that are not present in the manuscript or unpublished. Please include all the data that are not shown or remove the statements referring to these data.

**5. All data should now be plotted visibly**

Don’t cut axes and don’t use data as labels rather than plotting

Please ensure that data presented in a plot, chart or other visual representation format shows data distribution clearly (e.g. dot plots, box-and-whisker plots, violin plots). When using bar charts, please overlay the corresponding data points (as dot plots) whenever possible and always for n ≤ 10. All box-plot elements (center line, limits, whiskers, points) should be defined in the legends accompanied by precise n numbers.

**6. Use your statistical tests appropriately**

Wherever statistics have been derived (e.g. error bars, box plots, statistical significance) the legend needs to provide and define the n number (i.e. the sample size used to derive statistics) as a precise value (not a range), using the wording “n=X biologically independent samples/animals/cells/independent experiments/n= X cells examined over Y independent experiments” etc. as applicable.  
  
We strongly discourage deriving statistics from technical replicates, unless there is a clear scientific justification for why providing this information is important. Conflating technical and biological variability, e.g., by pooling technically replicates samples across independent experiments is strongly discouraged.

**All error bars need to be defined in the legends** (e.g. SD, SEM) together with a measure of centre (e.g. mean, median). For example, the legends should state something along the lines of “Data are presented as mean values +/- SEM” as appropriate. All box plots need to be defined in the legends in terms of minima, maxima, centre, bounds of box and whiskers and percentile.

The figure legends must indicate the statistical test used. Where appropriate, please indicate in the figure legends whether the statistical tests were one-sided or two-sided and whether adjustments were made for multiple comparisons. For null hypothesis testing, please indicate the test statistic (e.g. F, t, r) with confidence intervals, effect sizes, degrees of freedom and P values noted. Please provide the test results (e.g. P values) as exact values whenever possible and with confidence intervals noted.

**7. Methods**

Methods sections tend to have word limits (loosely 3000 words for nature).

Sufficient details of the experiments must be provided in the Methods section such that they could be reproduced without reference to published papers. Use of the term "as described previously" is not encouraged.

**8. Contributions**

Please supply an "Author Contributions" section after the "Acknowledgements" section that refers to all authors. For more information on the Author Contributions statement, please refer to our authorship policy(https://www.nature.com/nature-research/editorial-policies/authorship), and to the following Nature Editorial: <https://www.nature.com/articles/4581078a>.

**9. Acknowledgements**

Cite all grant numbers and remember to thank everyone who’s chipped in by eg reading the manuscript.

**10. Additional info required**

**Antibodies**

As well as all the data the journals now want a more detailed description of your reagents.

Antibodies are particularly important. You now need to cite, the antibody antigen, the species, the clone number of catalogue number, the supplier, the concentration used at and the justification of using it for the specific purpose. This can come from the company website, which you must then cite.

Eg Goat anti- tubulin Ab (Abcam, #ab6046) (1:20,000 dilution). Abcam datasheet provides evidence for use of anti-tubulin Ab by WB and cites 955 examples of published use

<file:///Users/newuser/Downloads/datasheet_6046.pdf>

**Software**

All software used must be cited **including the version number used**

**Cell lines**

The source of cell lines should be cited and cells that have a history of being mixed up should be avoided. We can deal with this on a case by case basis but we should know where the lines we’re using came from. Establish origin, make stocks, use your own stocks and don’t pass the cells around endlessly leading you to lose track of what they are and where they came from.

Cells should be periodically tested for mycoplasma. Signs of mycoplasma infection include, poor recovery after freezing, dapi positive spots in the cytoplasm, high levels of innate immune activation prior to stimulation, cells dying unexpectedly or not behaving like they used to. Note that a change in serum (often realised when you thaw old stocks) can also lead to change in behaviour. This change can take weeks.