***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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No explicit power analysis was used to estimate sample size because the number of replicates to test for statistical significance with the pre-defined significance and confidence criteria have been previously established, as reported in papers cited within the respective sections of the manuscript.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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* Statistical analysis methods should be described and justified
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* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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The above information is not applicable to our study, which did not feature separately weighted experimental groups. Where different conditions were tested, equally-sized groups were used.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

In relation to the computational results shown in Figure 4, we have deposited the software listed below at: [https://github.com/Fraternalilab/ALLOHUBMAT](https://emea01.safelinks.protection.outlook.com/?url=https%3A%2F%2Fgithub.com%2FFraternalilab%2FALLOHUBMAT&data=01%7C01%7Cfranca.fraternali%40kcl.ac.uk%7C6e285dd0d0804788cf2508d685d61956%7C8370cf1416f34c16b83c724071654356%7C0&sdata=tdy6gWLZ%2Ftpr5hLPE99N96%2BpL81zV578lTh5CitXyus%3D&reserved=0)

- sa\_encode.R : Encode trajectory into stacked alignment of structural alphabet strings

- kabsch.R : Kabsch superpositioning routine

- MI.R : Mutual Information and other entropy metrics between two character vectors, here intended for two alignment columns