***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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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* 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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This is a theoretical paper. All of the data generated during this study are theoretical calculations from the given simple equations included in the manuscript. All the parameters placed in those equations are clearly stated in the manuscript throughout.

(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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**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
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* Avoid stating that data files are “available upon request”

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

Figure 3a is generated by plotting the equations 1 and 2 from a simple MatLab code:

bohr=9.274\*10^(-24);

boltz=1.381\*10^(-23);

B=0:0.001:2;

t=310;

N=4500;

n=1;

x=N\*5\*bohr.\*B;

y=(n\*boltz\*t).^(-1);

z=y\*x;

r=(z).^(-1);

moment=N\*5\*bohr\*(coth(z)-r);

plot(B,moment)

Figure 3b is generated by plotting the energy equation on page 7 of the manuscript from a simple MatLab code:

bohr=9.274\*10^(-24);

boltz=1.381\*10^(-23);

B=0:0.001:2;

T=310;

N=4500;

n=15;

x=N\*5\*bohr.\*B;

y=(n\*boltz\*T).^(-1);

z=y\*x;

r=(z).^(-1);

energy=N\*5\*bohr\*(coth(z)-r).\*B;

figure

semilogy(B,energy)

Figure 6 is generated by plotting the equation 6 from a simple MatLab code:

bohr=9.274\*10^(-24);

boltz=1.381\*10^(-23);

n=1:1:4500;

B=0.25;

T=310;

x=boltz\*T.\*n;

N=4500;

y=x.^(-1);

z=N\*5\*bohr\*B.\*y;

q=z.^(-1);

p=sinh(z).\*q;

deltaE=-T\*boltz.\*n.\*(1-z.\*coth(z)+log(p));

figure

semilogx(n,deltaE)