

**Materials Design Analysis Reporting (MDAR)  
Checklist for Authors**

The [MDAR framework](#) establishes a minimum set of requirements in transparent reporting mainly applicable to studies in the life sciences.

*eLife* asks authors to **provide detailed information within their article** to facilitate the interpretation and replication of their work. Authors can also upload supporting materials to comply with relevant reporting guidelines for health-related research (see [EQUATOR Network](#)), life science research (see the [BioSharing Information Resource](#)), or animal research (see the [ARRIVE Guidelines](#) and the [STRANGE Framework](#); for details, see *eLife's* [Journal Policies](#)). Where applicable, authors should refer to any relevant reporting standards materials in this form.

For all that apply, please note **where in the article** the information is provided. Please note that we also collect information about data availability and ethics in the submission form.

**Materials:**

<b>Newly created materials</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>
The manuscript includes a dedicated "materials availability statement" providing transparent disclosure about availability of newly created materials including details on how materials can be accessed and describing any restrictions on access.		N/A

<b>Antibodies</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>
For commercial reagents, provide supplier name, catalogue number and <a href="#">RRID</a> , if available.		N/A

<b>DNA and RNA sequences</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>
Short novel DNA or RNA including primers, probes: Sequences should be included or deposited in a public repository.	Source Data File 1	

<b>Cell materials</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>
Cell lines: Provide species information, strain. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.		N/A
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		N/A

Experimental animals	Indicate where provided: section/figure legend	N/A
Laboratory animals or Model organisms: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.		N/A
Animal observed in or captured from the field: Provide species, sex, and age where possible.		N/A

Plants and microbes	Indicate where provided: section/figure legend	N/A
Plants: provide species and strain, ecotype and cultivar where relevant, unique accession number if available, and source (including location for collected wild specimens).		N/A
Microbes: provide species and strain, unique accession number if available, and source.	Wild-type <i>E. coli</i> (DH5 $\alpha$ , Takara item # 9027). See the " <b>Molecular Cloning</b> " subsection in <b>Methods</b> .  <i><math>\Delta</math>hns</i> <i>E. coli</i> (KEIO collection, strain JW1225). See the " <b>Histone-like nucleoid-structuring protein (H-NS) represses P12-RFP and P22-GFP</b> " subsection in <b>Results</b> .	

Human research participants	Indicate where provided: section/figure legend) or state if these demographics were not collected	N/A
If collected and within the bounds of privacy constraints report on age, sex, gender and ethnicity for all study participants.		N/A

**Design:**

Study protocol	Indicate where provided: section/figure legend	N/A
If the study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number OR cite DOI.		N/A

Laboratory protocol	Indicate where provided: section/figure legend	N/A

Provide DOI OR other citation details if detailed step-by-step protocols are available.	See <b>Methods</b> section for all of the protocols.	
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<b>Experimental study design (statistics details) *</b>		
<b>For in vivo studies: State whether and how the following have been done</b>	<b>Indicate where provided: section/figure legend. If it could have been done, but was not, write "not done"</b>	<b>N/A</b>
Sample size determination		N/A
Randomisation		N/A
Blinding		N/A
Inclusion/exclusion criteria		N/A

<b>Sample definition and in-laboratory replication</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>
State number of times the experiment was replicated in the laboratory.	<p>The sort-seq experiment was carried out once. See the subsection "<b>Sort-Seq</b>" in <b>Methods</b> for more information. The data was randomly partitioned into three groups for calculating the standard deviations of the mutual information.</p> <p>Experiments measuring fluorescence with the plate reader were carried out once with either 3, 10, or 12 biological replicates (individual colonies of E. coli harboring the same plasmid). See the subsection "<b>Measuring fluorescence with a plate reader</b>" in <b>Methods</b> for more information.</p>	
Define whether data describe technical or biological replicates.	See " <b>Measuring fluorescence with a plate reader</b> " and " <b>Sort-Seq</b> " in <b>Methods</b> for more information.	

<b>Ethics</b>	<b>Indicate where provided: section/submission form</b>	<b>N/A</b>

Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		N/A
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		N/A
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.	None. <i>E. coli</i> is not an animal.	

<b>Dual Use Research of Concern (DURC)</b>	<b>Indicate where provided: section/submission form</b>	<b>N/A</b>
If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval.		N/A

**Analysis:**

<b>Attrition</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>
Describe whether exclusion criteria were pre-established. Report if sample or data points were omitted from analysis. If yes, report if this was due to attrition or intentional exclusion and provide justification.	See the “ <b>Processing sequencing reads</b> ” subsection in <b>Methods</b> for information about which sequences were removed from the dataset after Illumina sequencing.	

<b>Statistics</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>
Describe statistical tests used and justify choice of tests.	See the “ <b>Analysis of motif gain and loss</b> ” and “ <b>Sigmoid curve-fitting</b> ” subsections in <b>Methods</b> , along with the figure legends for this information. Sample sizes are reported in all figure legends for each statistical test.  Briefly, this study uses two-sided Mann-Whitney U (MWU) tests to compare the fluorescence scores of sequences with and without a particular motif. We chose to use the MWU test instead of a student t-test because the distributions of fluorescence scores do not follow a normal distribution. Because we ran multiple MWU tests, we also	

	corrected for multiple-hypothesis testing by using a Benjamini-Hochberg correction. In Figure 5B we also use a student two-tailed t-test because both distributions are normal.	
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<b>Data availability</b>	<b>Indicate where provided: section/submission form</b>	<b>N/A</b>
For newly created and reused datasets, the manuscript includes a data availability statement that provides details for access (or notes restrictions on access).	See “ <b>Data availability</b> ” subsection of <b>Methods</b> :  A Jupyter notebook with all of the python scripts to recreate the analysis and figures in this study, as well as Source Data Files 1-8 are available at the Github repository: <a href="https://github.com/tfuqua95/promoter_islands">https://github.com/tfuqua95/promoter_islands</a>  Sequence reads are available at the Sequence Read Archive (SRA) with accession number: PRJNA1071572: <a href="https://www.ncbi.nlm.nih.gov/bioproject/1071572">https://www.ncbi.nlm.nih.gov/bioproject/1071572</a>	
When newly created datasets are publicly available, provide accession number in repository OR DOI and licensing details where available.	See “ <b>Data availability</b> ” subsection of <b>Methods</b> :  A Jupyter notebook with all of the python scripts to recreate the analysis and figures in this study, as well as Source Data Files 1-8 are available at the Github repository: <a href="https://github.com/tfuqua95/promoter_islands">https://github.com/tfuqua95/promoter_islands</a>  Sequence reads are available at the Sequence Read Archive (SRA) with accession number: PRJNA1071572: <a href="https://www.ncbi.nlm.nih.gov/bioproject/1071572">https://www.ncbi.nlm.nih.gov/bioproject/1071572</a>	
If reused data is publicly available provide accession number in repository OR DOI, OR URL, OR citation.		N/A

<b>Code availability</b>	<b>Indicate where provided: section/figure legend</b>	<b>N/A</b>

<p>For any computer code/software/mathematical algorithms essential for replicating the main findings of the study, whether newly generated or re-used, the manuscript includes a data availability statement that provides details for access or notes restrictions.</p>	<p>See <b>“Data availability”</b> subsection of <b>Methods</b>:</p> <p>A Jupyter notebook with all of the python scripts to recreate the analysis and figures in this study, as well as Source Data Files 1-8 are available at the Github repository: <a href="https://github.com/tfuqua95/promoter_islands">https://github.com/tfuqua95/promoter_islands</a></p> <p>Sequence reads are available at the Sequence Read Archive (SRA) with accession number: PRJNA1071572: <a href="https://www.ncbi.nlm.nih.gov/bioproject/1071572">https://www.ncbi.nlm.nih.gov/bioproject/1071572</a></p>	
<p>Where newly generated code is publicly available, provide accession number in repository, OR DOI OR URL and licensing details where available. State any restrictions on code availability or accessibility.</p>	<p>See <b>“Data availability”</b> subsection of <b>Methods</b>:</p> <p>A Jupyter notebook with all of the python scripts to recreate the analysis and figures in this study, as well as Source Data Files 1-8 are available at the Github repository: <a href="https://github.com/tfuqua95/promoter_islands">https://github.com/tfuqua95/promoter_islands</a></p> <p>Sequence reads are available at the Sequence Read Archive (SRA) with accession number: PRJNA1071572: <a href="https://www.ncbi.nlm.nih.gov/bioproject/1071572">https://www.ncbi.nlm.nih.gov/bioproject/1071572</a></p>	
<p>If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation.</p>		N/A

**Reporting:**

The MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives.

Adherence to community standards	Indicate where provided: section/figure legend	N/A
<p>State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE, STRANGE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.</p>		N/A

\* We provide the following guidance regarding transparent reporting and statistics; we also refer authors to [Ten common statistical mistakes to watch out for when writing or reviewing a manuscript](#).

### **Sample-size estimation**

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

### **Replicates**

- 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
- If you encountered any outliers, you should describe how these were handled
- 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)

### **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.

### **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