**JHEP Reports**

**CTAT methods**

Tables for a “Complete, Transparent, Accurate and Timely account” (CTAT) are now mandatory for all revised submissions. The aim is to enhance the reproducibility of methods.

* Only include the parts relevant to your study
* Refer to the CTAT in the main text as ‘Supplementary CTAT Table’
* Do not add subheadings
* Add as many rows as needed to include all information
* Only include one item per row

**If the CTAT form is not relevant to your study, please outline the reasons why:**

|  |
| --- |
| Only clinical work was performed – no animal work |

* 1. **Antibodies**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **Citation** | **Supplier** | **Cat no.** | **Clone no.** |
| Not applicable |  |  |  |  |

* 1. **Cell line**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Name** | **Citation** | **Supplier** | **Cat no.** | **Passage no.** | **Authentication test method** |
| Not applicable |  |  |  |  |  |

* 1. **Organisms**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Name** | **Citation** | **Supplier** | **Strain** | **Sex** | **Age** | **Overall n number** |
| Not applicable |  |  |  |  |  |  |

* 1. **Sequence based reagents**

|  |  |  |
| --- | --- | --- |
| **Name** | **Sequence** | **Supplier** |
| Not applicable |  |  |

* 1. **Biological samples**

|  |  |  |
| --- | --- | --- |
| **Description** | **Source** | **Identifier** |
| Not applicable |  |  |

* 1. **Deposited data**

|  |  |  |
| --- | --- | --- |
| **Name of repository** | **Identifier** | **Link** |
| Not applicable |  |  |
| All data used in this manuscript are kept on the secured server at the University of British Columbia, Canada | | |

* 1. **Software**

|  |  |  |
| --- | --- | --- |
| **Software name** | **Manufacturer** | **Version** |
| Python/Matplotlib | https://www.python.org | 3.7 |
| Stata | StataCorp, College Station, Texas | 14.0 |
| Piktochart (infographics) | https://piktochart.com |  |

* 1. **Other (*e.g*. drugs, proteins, vectors etc.)**

|  |  |  |
| --- | --- | --- |
|  |  |  |
|  |  |  |

* 1. **Please provide the details of the corresponding methods author for the** manuscript:

|  |
| --- |
| The codon aligned sequences were generated using a program adapted from from HIV (Tzou PL, Huang X, Shafer RW. NucAmino: a nucleotide to amino acid alignment optimized for virus gene sequences. BMC Bioinformatics 2017;18:138)  The HCV sequences used for genotype determination were downloaded from the International Committee on Taxonomy of Viruses. (<https://talk.ictvonline.org/ictv_wikis/flaviviridae/w/sg_flavi/56/hcv-classification>; 2017. The HCV reference sequences were resistance-associated substitution were based on the Guidance for submitting HCV resistance data draft guidance, the US Foods and Drugs Administration (02/04/2013) |

**2.0 Please confirm for randomised controlled trials all versions of the clinical protocol are included in the submission. These will be published online as supplementary information.**

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