

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:

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1.1 Antibodies

Name	Citation	Supplier	Cat no.	Clone no.
NA				

1.2 Cell lines

Name	Citation	Supplier	Cat no.	Passage no.	Authentication test method
NA					

1.3 Organisms

Name	Citation	Supplier	Strain	Sex	Age	Overall n number
NA						

1.4 Sequence based reagents

Name	Sequence	Supplier
NA		

1.5 Biological samples

Description	Source	Identifier
Serum	patients	samples were coded on collection and handled anonymously in the lab.

1.6 Deposited data

Name of repository	Identifier	Link
NA		

1.7 Software

Software name	Manufacturer	Version
SeqScape Software	Thermo Fisher Scientific	3.0
MAFFT (Multiple Alignment using Fast Fourier Transform)	Authors	
CLC Sequence Viewer 8	QIAGEN Bioinformatics	
jumping profile Hidden Markov Model	Authors	
PhyML	Authors	3.1
GTR+G4 evolutionary model	ModelFinder	
iTOL	Authors	3.0
Ion Torrent Suite Software	Thermoscience Fisher, Waltham, MA	5.0.2.
Integrated Genome Browser	Broad Institute	2.3.55
STATA	Stata Corporation, USA	13.0
MACSE	Authors	2.03
BMGE	Authors	1.0
Torrent Variant Caller	Thermoscience Fisher, Waltham, MA	5.8

1.8 Other (e.g. drugs, proteins, vectors etc.)

NA		
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1.9 Please provide the details of the corresponding methods author for the manuscript:

Dr Isabelle Chemin
 INSERM U1052, CNRS UMR5286, Centre de Recherche en Cancérologie de Lyon
 Université Claude Bernard. 151 cours Albert Thomas, Lyon, France
 Phone (Fax): 0033472681973 (71)
 Mail: isabelle.chemin@inserm.fr

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.

NA
