MIARE: Minimum Information About an RNAi Experiment

Reporting Checklist

Draft (v0.8.0)

May 2011

Minimum Information About an RNAi Experiment (MIARE)

(www.miare.org)

Checklist of Required Information*

The purpose of this check-list is to guide and help experimentalists to ensure that the data supporting their results based on RNA interference experiments can be made publicly available, in a format that enables unambiguous interpretation of the data and potential verification of the conclusions.

The following check-list only contains mandatory information, describing the information that SHALL[1] be reported for an RNAi experiment. OPTIONAL information has been omitted and can be found in the full MIARE Reporting Guideline document at www.miare.org

Checklist

A. Assay description:

A.1. Assay ID
A.2. Assay name
A.3. Assay type (primary/confirmatory/other)
A.4. Target organism (Taxonomy ID)
A.5. Number of distinct genes targeted for knock-down
A.6. Experiment publication (PubMed ID)
A.7. Primary contact information

B. Protocol:

B.1. Experimental description

B.1.1. Experiment title
B.1.2. Biological question description - (*including sample description and keywords*)

B.2. Assay

B.2.1. Assay protocol and design -(*including number and description of replicates (biological/technical*)
B.2.2. Pre- and post-treatment (protocol/type/compound)
B.2.3. Bio-material manipulations (*including growth conditions/cell culture conditions and if applicable cell separation technique*)
B.2.4. Number of cells per well
B.2.5. Compound(s) name (if applicable)
  B.2.5.1. Assay reagent name
  B.2.5.2. Assay reagent manufacturer
B.2.6. Instrument (repeat this section for each instrument used)
  B.2.6.1. Instrument name
  B.2.6.2. Instrument manufacturer
  B.2.6.3. Type of readout
  B.2.6.4. Instrument settings

B.3. Delivery

- B.3.1. Delivery type and protocol
  - B.3.1.1. Percentage of cell confluence (if applicable)
  - B.3.1.2. Complexing protocol
  - B.3.1.3. Complexing Time
- B.3.2. Delivery reagent
  - B.3.2.1. Delivery reagent type
  - B.3.2.2. Delivery reagent manufacturer
  - B.3.2.3. Delivery reagent name
  - B.3.2.4. Delivery reagent final concentration
- B.3.3. Silencing reagent final concentration

B.4. Silencing RNA reagent (Substance)

- B.4.1. Silencing RNA reagent ID
  - B.4.1.1. Probe ID (if applicable)
- B.4.2. Target gene ID or accession number (NCBI/EMBL/DDBJ)
- B.4.3. Target gene name (if available)
- B.4.4. Silencing RNA reagent sequence(s) (if available, cross-reference to GenBank ID)
- B.4.5. Silencing RNA reagent library description (provider/version number)
- B.4.6. Silencing RNA reagent type (if applicable)
- B.4.7. Unique silencing RNA molecules per reagent pool (if applicable)
- B.4.8. Modification(s) to silencing RNA reagent (if applicable)
- B.4.9. Taxonomy ID
- B.4.10. Vector/Plasmid reference (if applicable)
- B.4.11. Comments

B.5. Assay plate description

- B.5.1. Assay plate manufacturer
- B.5.2. Assay plate type

B.6. Assay plate

- B.6.1. Media changes
  - B.6.1.1. Media composition
  - B.6.1.2. Time of media change

C. Results:

C.1. Data analysis

- C.1.1. Bioactivity outcome threshold
- C.1.2. Bioactivity score assignment method
- C.1.3. Data normalisation method
- C.1.4. Artefacts
- C.1.5. Data filtering description
- C.1.6. Data transformation details
- C.1.7. Analysis program
  - C.1.7.1. Analysis script description
  - C.1.7.2. Analysis Software (name/version)
- C.1.8. Quantitative data
  - C.1.8.1. Description of quantified data
- C.1.9. Qualitative data
  - C.1.9.1. Description of qualitative data

C.2. Result Definitions

- C.2.1. Data column definitions for assay results
  - C.2.1.1. Name
  - C.2.1.2. Data type (float, integer, string or NCBI Entrez database ID)
  - C.2.1.3. Unit
  - C.2.1.4. Description
  - C.2.1.5. Constraint (min, max, range or set of values)

C.3. Data

- C.3.1. Quantitative data
  - C.3.1.1. Unprocessed quantified data (raw data, if applicable)
  - C.3.1.2. Normalised quantified data
  - C.3.1.3. Scored data
    - C.3.1.3.1. Bioactivity outcome (active/inactive/inconclusive)
- C.3.2. Qualitative data
  - C.3.2.1. Qualitative data

References

[1] S. Bradner, Key words for use in RFCs to Indicate Requirement Levels, Internet Engineering Task Force, RFC 2119. http://www.ietf.org/rfc/rfc2119.txt, March 1997.

Main Contributors:

Nigel Binns[1], Peter Ghazal[1], Amanda Birmingham[2], Steve Bryant[3], Sean Erickson[4], Graeme Grimes[5], Jon Karpilow[2], Anastasia Khvorova[2], Javier Santoyo-Lopez[6], Caroline Shamu[4], Queta Smith[2], Andrew Tolopko[4], Yanli Wang[3] and the RNAi Global Informatics Workgroup (www.rnaiglobal.org).

Additional Contributors†:

Miriam Barrios-Rodiles[7], Alfonso Bellacosa[8], Roderick L. Beijersbergen[9], Rene Bernards[9], Brian Bodemann[10], Michael Boutros[11], Kenneth H. Cowan[12], Alessandro Datti[13], James W. Dennis[7], Julian Downward[14], Daniel Durocher[7], Christophe Echeverri[15], David Egan[9], Armida W. Fabius[9], Florian Fuchs[10], Florian Hahne[16], David Hancock[14], Hiroyoshi Hattori[17], David Kelly[12], Nadine K. Kolas[7], Devin Leake[2], Robert Lewis[12], Yiling Lu[18] , Xu Luo[12], Tak Mak[19], Elena Maksimova[2], William S. Marshall[2], Alexander Mehrle[16], Gordon B. Mills[18], Thomas Moloshok[8], Stuart Moodie[20], James Pan[7], Annemarie Poustka[16], Paul Russell[17], Birte Soennichsen[15], Michael Steckel[14], Sandra Steinbrink[11], Thomas Sun[13], Charles Swanton[13], Ashok R. Venkitaraman[21], Michael A. White[10], Angelique Whitehurst[10], Stefan Wiemann[22], Jeffrey L. Wrana[7], Timothy J.Yen[8], Xian-Jin Xie[10], Jarkko Ylanko[7].

[1] Division of Pathway Medicine, University of Edinburgh Medical School, Edinburgh, EH16 4SB, UK
[2] Dharmacon, Inc., a part of Thermo Fisher Scientific, 2650 Crescent Drive, Suite 100, Lafayette, Colorado 80026, USA
[3] National Center for Biotechnology Information, National Library of Medicine, Building 38A, Bethesda, MD 20894, USA
[4] ICCB-Longwood, Harvard Medical School, 250 Longwood Avenue, Seeley Mudd Room 604, Boston MA 02115, USA
[5] MRC Human Genetics Unit, Western General Hospital, Crewe Road, Edinburgh, EH4 2XU, UK
[6] Bioinformatics & Genomics Department, Prince Felipe Research Centre (CIPF), Av. Autopista del Saler 16, 46012 Valencia, Spain
[7] Centre for Systems Biology, Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, Canada
[8] Division of Basic Science, Fox Chase Cancer Center, Philadelphia, Pennsylvania 19111, USA
[9] Division of Molecular Carcinogenesis and Center for Biomedical Genetics, The Netherlands Cancer Institute, Plesmanlaan 121, 1066 CX Amsterdam, The Netherlands
[10] Cell Biology, UT Southwestern Medical Center, Dallas, Texas, USA
[11] Functional Genomics Programme, German Cancer Research Center D-69120 Heidelberg, Germany
[12] Department of Biochemistry and Molecular Biology, College of Medicine, Omaha, NE 68198-5870, USA
[13] Sinai-McLaughlin Assay and Robotic Technologies Facility, Mount Sinai Hospital, Toronto, ON, Canada M5G 1X5

[14] Cancer Research UK London Research Institute, Signal Transduction Laboratory, London, Research Institute, 44 Lincoln's Inn Fields, London, WC2A 3PX, UK
[15] Cenix BioScience GmbH, Tatzberg 47, Dresden 01307, Germany
[16] Division of Molecular Genome Analysis, German Cancer Research Center D-69120 Heidelberg, Germany
[17] University of Cambridge, MRC Cancer Cell Unit & CRUK Department of Oncology, Hutchison/MRC Research Centre, Hills Road, Cambridge, CB2 2XZ, UK
[18] Molecular Therapeutics, The University of Texas M.D. Anderson Cancer Center, Houston, Texas 77030, USA
[19] The Advanced Medical Discovery Institute and The Campbell Family Institute for Breast Cancer Research, Toronto, Ontario, Canada
[20] School of Informatics, The University of Edinburgh, Informatics Forum, 10 Crichton Street, Edinburgh, EH8 9AB, UK
[21] Department of Oncology, Hutchison/MRC Research Centre, Cambridge, UK
[22] Division of Molecular Genome Analysis, German Cancer Research Center D-69120 Heidelberg, Germany

[†] In alphabetical order.