

<p>Deborah BOURC'HIS</p> <p>25/03/1972 Nationalité française 1 enfant (2015)</p>	<p>Directrice de Recherche Classe 1 (DR1) INSERM Chef d'équipe « <i>Epigenetic Decisions and Reproduction</i> » Inserm U934/CNRS UMR3215 Institut Curie 26 rue d'Ulm 75248 Paris Cedex 05</p>
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EDUCATION

2011	HDR, Sorbonne Université
2000	Doctorat es <i>Sciences</i> , spécialité Génétique Humaine, Université Paris Diderot
1996	Master de Biologie et Génétique Appliquées, Université Paris Diderot

PARCOURS PROFESSIONNEL

Depuis 2015	Group leader Senior - « <i>Epigenetic decisions and reproduction</i> », Institut Curie, U934/UMR3215, Paris
2009-2014	Group leader Junior - « <i>Epigenetic decisions and reproduction</i> », Institut Curie, U934/UMR3215, Paris
2005-2008	Chargée de Recherche - « <i>Genomic and functional characterization of genomic imprinting</i> », Lab. d'E. Viegas-Péquignot, Inserm U741, Paris
2000-2005	Post-doctorat - « <i>Genomic imprinting and transposon control during gametogenesis</i> », Lab. de T. Bestor, Columbia University, New York
1996-2000	Thèse de sciences - « <i>Genetic and embryonic origins of the DNA methylation defect in ICF patients</i> », Lab. d'E. Viegas-Péquignot, Inserm U383, Paris

PROMOTIONS

2018	INSERM DR1
2011	INSERM DR2
2009	INSERM CR1
2005	INSERM CR2

RESPONSABILITES INSTITUTIONNELLES

Institut Curie

2025-	Directrice adjointe de l'Unité U934/UMR 3215
2021-	Membre du SAB de l'initiative Single Cell
2020-	Membre du comité de pilotage de la Plateforme Animale
2019-	Supervision scientifique de la Plateforme de Transgénèse souris
2019-	Présidente du comité de pilotage de la Plateforme Bioinformatique
2018-	Membre du comité de gouvernance du LABEX DEEP (Université PSL)

PRIX et DISTINCTIONS

2023	ERC Advanced Grant
2021	Grand Prix de la Fondation pour la Recherche Médicale (FRM)
2018	Grand Prix Robert Debré pour la Recherche Médicale
2017	Grand Prix Liliane Bettencourt , Fondation Bettencourt Schueller
2016	Suffrage Award-Women in Science , MRC London
2014	Elue Membre EMBO

2014	ERC Consolidator Grant
2013	Académie des Sciences , Prix Jayle
2010	Prix FSER , Fondation Schlumberger Education et Recherche
2006	EURYI Award , EURopean Young Investigator (ex ERC Starting Grant)
2006	New Emerging Team (NET) , EU Epigenome Network of Excellence

FINANCEMENTS RECENTS (10 dernières années)

2023-2028	European Research Council, ERC Advanced Grant “HOTIMAGE”
2023-2026	Agence Nationale pour la Recherche (ANR) “biCHLORE” , coordinatrice
2022-2025	ANR “MomDad” , partenaire
2021-2024	Association pour la Recherche contre le Cancer (ARC) , Labellisation Equipe
2021-2024	ANR “MARMER” , coordinatrice
2020-2023	ANR “ImpacTE” , partenaire
2020-2021	ARC « Projet » , coordinatrice
2019-2022	Fondation pour la Recherche Médicale (FRM) , Labellisation Equipe
2019-2022	ANR “MATIn” , coordinatrice
2018-2021	Fondation Bettencourt Schueller , Liliane Bettencourt Prize for Life Sciences
2017-2020	ANR “SPERMethyl” , coordinatrice
2017-2018	Cancéropôle , Emergence Program
2014-2019	European Research Council, ERC Consolidator “EpiREPRO”
2013-2015	ANSES (Agence Nationale de Sécurité Sanitaire) , partenaire
2013-2014	FRM , Labellisation Equipe
2013-2014	ARC « Projet » , coordinatrice
2012-2016	ANR Investissement d’Avenir « ABS4NGS » network, partenaire
2012-2024	National LABEX Grant « DEEP network » , partenaire

ENCADREMENT

2009-2024 12 post-doctorants / 13 doctorants / 29 étudiants Master

THESES

2010	Charlotte PROUDHON - <i>Genomic and functional characterization of genomic imprinting using the Dnmt3L mutant mouse model</i>
2013	Rachel DUFFIE - <i>Epigenetic inheritance from the oocyte</i>
2015	Sophie AJJAN - <i>Atypical forms of genomic imprinting: transient, tissue-specific and strain-specific</i>
2015	Marius WALTER - <i>Transposon regulation upon dynamic loss of DNA methylation</i>
2018	Juliane GLASER - <i>Functional characterization of the imprinted Zdbf2 locus in mice: from the early embryo to adult physiology</i>
2018	Aurélie TEISSANDIER - <i>Bioinformatic analysis of transposable element regulation in mammals</i>
2021	Mathilde DURA - <i>Various critical roles of DNA methylation in male germ cell development</i>
2022	Mathieu SCHULZ - <i>Deciphering the role of DNA methylation in early cellular transitions</i>
2022	Lorraine BONNEVILLE - <i>Chromatin mark interplays in the mammalian oocyte</i>
2023	Emeline ROGER - <i>A novel chromatin pathway controlling transposable elements and genomic stability</i>
En cours	Elena de la MATA – <i>Impact of transposable element activity on genome stability and organisation during meiosis</i>
En cours	Marie LE PAGE - <i>SPIN1, a new chromatin actor in the protection of male fertility against retrotransposons</i>
En cours	Hugo SAAVEDRA – <i>Reading and interpreting chromatin dynamics in the early embryo</i>

ANCIENS MEMBRES devenus CHEFS d'EQUIPE INDEPENDANTS

- ° Juliane GLASER (ex doctorante): 2025, Max Planck Institute, Freiburg-Germany
- ° Charlotte PROUDHON (ex doctorante et CR): 2022, IRSET, Rennes-France
- ° Maxim GREENBERG (ex post-doc): 2019, Institut Jacques Monod, Paris-France
- ° Joan BARAU (ex post-doc): 2019, IMB, Mainz-Germany
- ° Raquel PEREZ-PALACIOS: 2021, Zaragoza University-Espagne

ENSEIGNEMENT ANNUEL

- Intervenante: - Master de Génétique (M1), Université Paris Cité
- Master Ecole Normale Supérieure de Paris, (M1), ENS/Sorbonne Université
- Cours Pasteur, Génétique de la Souris, Institut Pasteur
- Cours International *Developmental Biology*, Institut Curie/Sorbonne Université
- Organisatrice : - International Course *Noncoding Genome*, Institut Curie/Sorbonne Université
- Winter School *Transposon bioinformatics*, QLife programme/ Université PSL

PARTICIPATION à DES CONSEILS SCIENTIFIQUES

Membre pérenne

- 2023- ERC, LS2 Advanced Grant panel
2023- SAB - Institut de Génétique Humaine (IGH), Montpellier, France
2021-2026 Conseil Scientifique de la Fondation des Treilles
2021-2025 EMBO Council
2020-2024 SAB - Babraham Institute, Cambridge, UK
2018-2021 Comité d'expertise de la FRM, Programme Amorçage
2016-2021 CNRS- Comité national de la recherche scientifique, section 21
2019-2020 Comité d'expertise de la Research Foundation Flanders (FWO), Belgique
2014-2018 Comité d'expertise de la FRM, Financements généraux
2011-2017 Comité d'expertise de l'Agence de la Biomédecine « Recherche sur l'embryon humain et les cellules souches embryonnaires humaines»

Evaluations ad hoc

- 2024 Recrutement Group Leader – Institut de Génétique Humaine (IGH), Montpellier
2024 Evaluation de site, EMBL Monterotondo, Italy
2021 Evaluation de site, EMBL-EBI Cambridge, UK
2021 Recrutement Group Leader - EMBL-EBI Cambridge, UK
2020 HCERES- IGH, Montpellier
2020 Recrutement Group Leader - EMBL Monterotondo, Italy

ORGANISATION de CONFERENCES INTERNATIONALES

- 2027 Gordon Conference *Epigenetics*, USA
2026-2028-2030 Cold Spring Harbor Asia *Chromatin, Epigenetics & Transcription*, China
2023, 2025 EMBO Workshop *The Mobile Genome*, EMBL, Germany
2017 Les Treilles Workshop, *The Dynamic Genome*, France
2015 Jacques Monod Conference *DNA Methylation and Demethylation*, France

INVITATIONS en CONFERENCES et SEMINAIRES INSTITUTIONNELS

Depuis 2014 (10 ans), j'ai présenté les travaux de mon équipe sur invitation avec une fréquence annuelle d'environ 3 séminaires en institut et 5 conférences/an, dont :

- 2024, 2016 EMBL Conference *Chromatin & Transcription*, Heidelberg-Germany
2023 Gordon Conference *Epigenetics*, NH-USA
2022, 2018 FEBS *Danube Epigenetics Meeting*, Budapest-Hungary
2022 Conference of the *American Society of Andrology*, CA-USA
2021, 2017 EMBO Workshop *Mobile Genome*, Heidelberg-Germany
2020, 2018 CSHL *Transposable Elements Meeting*, NY-USA
2018 CSH Asia *Chromatin, Epigenetics and Transcription*, Suzhou-China

2017 Gordon Conference *Germinal Stem Cells*, Hong Kong
2015 Keystone Symposium *DNA Methylation*, CO-USA

EXEMPLES d'ENGAGEMENT VERS LE GRAND PUBLIC et LA JEUNESSE

- « En quête de bio, la science dans les écoles » organisé par la Société Française de Biologie, Ecole Élémentaire Varlin-Paris (7/3/2024)
- Interview pour le journal Le Monde « Ces virus qui ont colonisé notre génome : amis ou ennemis ? » (26/2/2024)
- Invitée Radio France Culture, Emission La Science CQFD « La banque génomique des mammifères » (30/05/2023)
- Interview pour le magazine Sciences et Avenir, Numéro Hors Serie n°206 « Les découvertes majeures de la science » (2021)
- relecture scientifique et participation à la traduction française du livre “*A crack in creation/Un coup de ciseaux dans la création*”. Auteurs: Jennifer Doudna (Co-Nobel 2020) and Samuel Sternberg. H&O Editions (2020)
- Capitaine Programme DECLICS (Dialogue Entre Chercheurs et les Lycéens pour les Intéresser à la Construction des Savoirs), Lycée Colbert-Paris (15/11/2019)
- Conférence-débat Cycle Université Ouverte « Epigénétique : comment s'expriment nos gènes? », Cergy Pontoise (21/2/2019)

PUBLICATIONS

Total number of **82** publications referenced in PubMed, with **55** peer-reviewed articles

RESEARCH ARTICLES (n= 55)

Schulz M., Teissandier A., De la Mata E., Armand M., Iranzo J., El Marjou F., Gestraud P., Walter M., Kinston S., Göttgens B., Greenberg M.V.C. and Bourc'his D. (2024). DNA methylation restricts coordinated germline and neural fates in embryonic stem cell differentiation. ***Nature Structural & Molecular Biology*** 31, 102-114. doi :10.1038/s41594-023-01162-w

Gentien D., Saberi-Ansari E., Servant N., Jolly A., de la Grange P., Némati F., Liot G., Saule S., Teissandier A., Bourc'his D., Girard E., Wong J., Masliah-Planchon J., Narmanli E., Liu Y., Torun E., Goulancourt R., Rodrigues M., Gaudé L.V., Reyes C., Bazire M., Chenegros T., Henry E., Rapinat A., Bohec M., Baulande S., M'kacher R., Jeandidier E., Nicolas A., Ciriello G., Margueron R., Decaudin D., Cassoux N., Piperno-Neumann S., Stern M.H., Gibcus J.H., Dekker J., Heard E., Roman-Roman S. and Waterfall J.J. (2023). Multi-omics comparison of malignant and normal uveal melanocytes reveals molecular features of uveal melanoma. ***Cell Rep*** 42, 113132

Ducieux B., Barberet J., Guilleman M., Pérez-Palacios R., Teissandier A., Bourc'his D. and Fauque P. (2023). Assessing the influence of distinct culture media on human pre-implantation development using single-embryo transcriptomics. ***Front Cell Dev Biol*** 11, 1155634

Dura M., Teissandier A., Armand M., Barau J., Bonneville L., Lapoujade C., Fouchet P., Schulz M., Weber M., Baudrin L.G., Lameiras S. and Bourc'his D. (2022). DNMT3A-dependent DNA methylation is required for spermatogonial stem cells to commit to spermatogenesis. ***Nature Genetics*** 54, 469-480. doi: 10.1038/s41588-022-01040-z

Glaser J., Iranzo J., Borensztein M., Marinucci M., Gualtieri A., Jouhanneau C., Teissandier A., Gaston Massuet C. and Bourc'his D. (2022). The imprinted *Zdf2* gene finely tunes control of feeding and growth in neonates. ***eLife*** 11:e65641. doi: [10.7554/eLife.65641](https://doi.org/10.7554/eLife.65641)

Dubois A., Vincenti L., Chernova A., Greenberg M.V.C., Vandormael-Pournin S., Bourc'his D., Cohen-Tannoudji M. and Navarro P. (2022). H3K9 tri-methylation at Nanog times differentiation

commitment and enables the acquisition of primitive endoderm fate. **Development** 149, dev201074. doi: 10.1242/dev.201074

Barberet J., Ducreux B., Bruno C., Guilleman M., Simonot R., Liury N., Guilloteau A., Bourc'his D. and Fauque P. (2022). Comparison of oocyte vitrification using a semi-automated or a manual closed system in human siblings: survival and transcriptomic analyses. **J Ovarian Res** 15, 128. doi: 10.1186/s13048-022-01064-3

Marion-Poll L., Roussarie J.P., Taing L., Dard-Dascot C., Servant N., Jaszczyszyn Y., Jordi E., Mulugeta E., Hervé D., Bourc'his D., Greengard P., Thermes C. and Girault J.A. (2022). DNA methylation and hydroxymethylation characterize the identity of D1 and D2 striatal projection neurons. **Commun Biol** 5, 1321. doi: 10.1038/s42003-022-04269-w

Ducreux B., Frappier J., Bruno C., Doukani A., Guilleman M., Simon E., Martinaud A., Bourc'his D., Barberet J. and Fauque P. (2021). Genome-wide analysis of DNA methylation in buccal cells of children conceived through IVF and ICSI. **Genes** 12, 1912. doi: [10.3390/genes12121912](https://doi.org/10.3390/genes12121912)

Klibi J., Joseph C., Delord M., Teissandier A., Lucas B., Chomienne C., Toubert A., Bourc'his D., Guidez F. and Benlagha K. (2021). PLZF acetylation levels regulate NKRT cell differentiation. **J Immunol** 207, 809-823. doi: [10.4049/jimmunol.2001444](https://doi.org/10.4049/jimmunol.2001444)

Chelmicki T., Roger E., Teissandier A., Dura M., Bonneville L., Rucli S., Dossin F., Fouassier C., Lameiras S. and Bourc'his D. (2021). m6A RNA methylation regulates the fate of endogenous retroviruses. **Nature** 591, 312-316. doi: 10.1038/s41586-020-03135-1

Barberet J., Biquet C., Guilleman M., Doukani A., Choux C., Bruno C., Bourredjem A., Chapusot C., Bourc'his D., Duffourd D., and Fauque P. (2021). Do assisted reproductive technologies and *in vitro* embryo culture influence the epigenetic control of imprinted genes and transposable elements in children? **Hum Reprod** 36, 479-492. doi: 10.1093/humrep/deaa310

Molaro A., Malik H.S and Bourc'his D. (2020). Dynamic evolution of *de novo* DNA methyltransferases in rodent and primate genomes. **Mol Biol Evol** 37, 1882-1892. doi: 10.1093/molbev/msaa044

Teissandier A., Servant N., Barillot E. and Bourc'his D. (2019). Tools and best practices for retrotransposon analysis using high-throughput sequencing data. **Mobile DNA** 10, 52. doi: 10.1186/s13100-019-0192-1

Hanna C.W.*, Pérez-Palacios R.*, Gahurova L., Schubert M., Krueger F., Biggins L., Andrews S., Colomé-Tatché M., Bourc'his D., Dean W. and Kelsey G. (2019). Non-canonical imprinting in extra-embryonic tissues is driven by endogenous retroviral insertions. **Genome Biology** 20, 225. doi: 10.1186/s13059-019-1833-x

Ragazzini R.*, Pérez-Palacios R.*, Baymaz I., Diop S., Ancelin K., Zielinski D., Michaud A., Givélet M., Borsos M., Aflaki S., Legoix P., Jansen P., Servant N., Torres Padilla M.E., Bourc'his D., Fouchet P. and Margueron R. (2019). EZHIP constrains Polycomb Repressive Complex 2 activity in germ cells. **Nature Comm** 10, 3858. doi: 10.1038/s41467-019-11800-x

Greenberg M.V., Teissandier A., Walter M., Noordermeer D. and Bourc'his D. (2019). Dynamic enhancer partitioning instructs activation of a growth regulator during exit from naïve pluripotency. **eLife** 8:e44057. doi: 10.7554/eLife.44057

Carmignac V., Barberet J., Iranzo J., Quéré R., Guilleman M., Bourc'his D. and Fauque P. (2019). Effects of assisted reproductive technologies on transposon regulation in the mouse preimplantation embryo. **Hum Reprod** 34, 612-622. doi: 10.1093/humrep/dez020

Choux C., Biquet C., Carmignac V., Bruno C., Chapusot C., Barberet J., Lamotte M., Sagot P., Bourc'his D. and Fauque P. (2018). The epigenetic control of transposable elements and imprinted genes in newborns is affected by the mode of conception: ART versus spontaneous conception without underlying infertility. *Hum Reprod* 33, 331-340. doi: [10.1093/humrep/dex366](https://doi.org/10.1093/humrep/dex366)

Tarabay Y., Achour M., Teletin M., Ye T., Teissandier A., Mark M., Bourc'his D. and Viville S. (2017). TEX19 paralogs are new members of the piRNA pathway. *J Cell Science* 130, 1463-1474. doi: [10.1242/jcs.188763](https://doi.org/10.1242/jcs.188763)

Greenberg M.V.*, Glaser J.*, Borsos M., El Marjou F., Walter M., Teissandier A. and Bourc'his D. (2017). Transient transcription in the early embryo sets an epigenetic state that programs post-natal growth. *Nature Genetics* 49, 110-118. doi: [10.1038/ng.3718](https://doi.org/10.1038/ng.3718)

Barau J., Teissandier A., Zamudio N., Roy S., Nalesso V., Héroult Y., Guillou F. and Bourc'his D. (2016). The DNA methyltransferase DNMT3C protects male germ cells from transposon activity. *Science* 354, 909-912. doi: [10.1126/science.aah5143](https://doi.org/10.1126/science.aah5143)

Walter M., Teissandier A., Pérez-Palacios R. and Bourc'his D. (2016). An epigenetic switch ensures transposon repression upon dynamic loss of DNA methylation in embryonic stem cells. *eLife*, January 27:5, pii: e11418. doi: [10.7554/eLife.11418](https://doi.org/10.7554/eLife.11418)

Zamudio N., Barau J., Teissandier A., Walter M., Borsos M., Servant N. and Bourc'his D. (2015). DNA methylation restrains transposons from adopting a chromatin signature permissive for meiotic recombination. *Genes & Dev* 29, 1256-1270. doi: [10.1101/gad.257840.114](https://doi.org/10.1101/gad.257840.114)

Liao H.F., Mo C.F., Cheng D.H., Yu C.Y., Chang K.W., Kao T.H., Lu C.W., Pinskaya M., Morillon A., Lin S.S., Cheng W.T., Bourc'his D., Bestor T.H., Sung L.Y. and Lin S.P. (2015). Dnmt3L-knockout donor cells improve somatic cell nuclear transfer reprogramming efficiency. *Reproduction* 150, 245-256

Bruno C., Carmignac V., Netchine I., Choux C., Duffourd Y., Faivre L., Thauvin-Robinet C., Le Bouc Y., Bourc'his D. and Fauque P. (2015). Germline correction of an epimutation related to Silver Russell syndrome. *Hum Mol Genet* 24, 3314-3321

Pastor W.A., Stroud H., Nee K., Liu W., Pezic D., Manakov S., Lee S.A., Moissiard G., Zamudio N., Bourc'his D., Aravin A.A., Clark A.T. and Jacobsen S.E. (2014). MORC1 represses transposable elements in the mouse male germline. *Nature Comm* 5, 5795

Duffié R., Ajjan S., Greenberg M.V., Zamudio N., Escamilla del Arenal M., Iranzo J., Okamoto I., Barbaux S., Fauque P. and Bourc'his D. (2014). The *Gpr1/Zdbf2* locus provides new paradigms for transient and dynamic genomic imprinting in mammals. *Genes & Dev* 28, 463-478

Tarabay Y., Kieffer E., Teletin M., Celebi C., Montfoort A.V., Zamudio N., Achour M., ElRamy R., Gazdag E., Tropel P., Mark M., Bourc'his D. and Viville S. The mammalian-specific Tex19.1 plays an essential role in pluripotency, fertility and placenta-supported development. (2013). *Human Reprod* 28, 2201-2214

Guenatri M.*, Duffié R.*, Iranzo J., Fauque P. and Bourc'his D. (2013). Plasticity in DNMT3L-dependent and -independent modes of *de novo* methylation in the developing mouse embryo. *Development* 140, 562-572

Proudhon C.*, Duffié R.*, Ajjan S., Cowley M., Iranzo J., Carbajosa G., Saadeh H., Holland M.H., Oakey R.J., Rakan V.K., Schulz R. and Bourc'his D. (2012). Protection against *de novo* methylation is instrumental in maintaining parent-of-origin methylation inherited from the gametes. *Mol Cell* 47, 909-920. doi: [10.1016/j.molcel.2012.07.010](https://doi.org/10.1016/j.molcel.2012.07.010)

Iglesias-Platas I., Martin-Trujillo A., Cirillo D., Court F., Guillaumet-Adkins A., Camprubi C., Bourc'his D., Hata K., Feil R., Tartaglia G., Arnaud P., and Monk D. (2012). Characterization of novel paternal ncRNAs at the *Plag1* locus, including *Hymai*, predicted to interact with regulators of active chromatin. ***Plos One*** 7, e38907

Monk D., Arnaud P., Frost J.M., Wood A.J., Cowley M., Martin-Trujillo A., Guillaumet-Adkins A., Iglesias Platas I., Camprubi C., Bourc'his D., Feil R., Moore G.E and Oakey R.J. (2011). Human imprinted retrogenes exhibit non-canonical imprint chromatin signatures and reside in non-imprinted host genes. ***Nucl Acids Res*** 39, 4577-4586

Schulz R.*, Proudhon C.*, Bestor T.H., Woodfine K., Lin C.-S., Lin S.-P., Prissette M., Oakey R.J. and Bourc'his D. (2010). The parental non-equivalence of imprinting control regions during mammalian development and evolution. ***Plos Genet*** 6, e1001214

Aravin A.A., Sachidanandam R., Bourc'his D., Schaefer C., Bestor T.H. and Hannon G.J. (2008). A piRNA pathway primed by individual transposons is linked to de novo DNA methylation in mice. ***Mol Cell*** 31, 785-799

Mahadevaiah S.K., Bourc'his D., De Rooij D., Bestor T.H, Turner J.M.A. and Burgoyne P.S. (2008) Extensive meiotic asynapsis in mice antagonises the meiotic silencing of unsynapsed chromatin and consequently disrupts meiotic sex chromosome inactivation. ***J Cell Biol*** 182, 263-276

Monk D., Wagschal A., Arnaud P., Muller P., Parker L., Bourc'his D., Magnuson T., Scherer S., Feil R., Stanier P. and Moore G.E. (2008). Comparative analysis of human chromosome 7q21 and mouse proximal chromosome 6 reveals a placentally imprinted gene, *Tfp12*, which requires G9a and Eed for allelic-silencing. ***Genome Res*** 18, 1270-1281

Wood A.J., Schulz R., Woodfine K., Koltowska K., Beechey C.V., Peters J., Bourc'his D. and Oakey R. (2008). Regulation of alternative polyadenylation by genomic imprinting. ***Genes & Dev*** 22, 1141-1146

Schulz R., Woodfine K., Menhenniott T.R., Bourc'his D., Bestor T.H. and Oakey R. (2008). WAMIDEX: a web atlas of murine genomic imprinting and differential expression. ***Epigenetics*** 3, 89-96

Wood A.J., Bourc'his D., Bestor T.H. and Oakey R.J. (2007). Allele-specific demethylation at an imprinted mammalian promoter. ***Nucl Acid Res*** 35, 7031-7039

La Salle S., Oakes C.C., Neaga O.R., Bourc'his D., Bestor T.H. and Trasler J.M. (2007). Loss of spermatogonia and wide-spread DNA methylation defects in newborn male mice deficient in DNMT3L. ***BMC Dev Biol*** 7, 104

Lucifero D., La Salle S., Bourc'his D., Martel J., Bestor T.H and Trasler JM. (2007). Coordinate regulation of DNA methyltransferase expression during oogenesis. ***BMC Dev Biol*** 7, 36

Carmell M.A., Girard A., van de Kant H.J.G, Bourc'his D., Bestor T.H., de Rooij D.G. and Hannon G.J. (2007). Miwi2 is essential for spermatogenesis and repression of transposons in the mouse male germ line. ***Dev Cell*** 12, 503-514

Shovlin T.C., Bourc'his D., La Salle S., O'Doherty A., Trasler J.M., Bestor T.H. and Walsh C.P. (2007). Sex-specific promoters regulate Dnmt3L expression in mouse germ cells. ***Hum Reprod*** 22, 457-467

Liu J., Chen M., Deng C., Bourc'his D., Nealon J.G., Erlichman B., Bestor T.H. and Weinstein L.S. (2005). Identification of the control region for tissue-specific imprinting of the stimulatory G protein alpha-subunit. **Proc Natl Acad Sci USA** 102, 5513-5518

Jiang Y.L., Rigolet M., Bourc'his D., Nigon F., Bokesoy I., Fryns J.P., Hultén M., Jonveaux P., Maraschio P., Mégabarné A., Moncla A. and Viegas-Péquignot. (2005). DNMT3B mutations and DNA methylation defect define two types of ICF syndrome. **Hum Mut** 25, 56-63

Bourc'his D. and Bestor T.H. (2004). Meiotic catastrophe and retrotransposon reactivation in male germ cells lacking Dnmt3L. **Nature** 431, 96-99

Bourc'his D., Xu G.-L., Lin C.S., Bollman B. and Bestor T.H. (2001). Dnmt3L and the establishment of maternal genomic imprints. **Science** 294, 2536-2539

Bourc'his D., Lebourhis D., Patin D., Niveleau A., Comizolli P., Renard J.-P. and Viegas-Péquignot E. (2001). Delayed and incomplete reprogramming of chromosome methylation patterns in early bovine cloned embryos. **Curr Biol** 11, 1542-1546

Kondo T., Bobek M.P., Kuick R., Lamb B., Zhu X., Narayan A., Bourc'his D., Viegas-Péquignot E., Ehrlich M. and Hanash S.M. (2000). Whole-genome methylation scan in ICF syndrome : hypomethylation of non-satellite DNA repeats *D4Z4* and *NBL2*. **Hum Mol Genet** 9, 597-604

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