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[YS Aulchenko, MV Struchalin...](#) - European Journal of ..., 2009 - nature.com

Abstract In the Victorian era, Sir Francis Galton showed that 'when dealing with the transmission of stature from parents to children, the average height of the two parents ... is all we need care to know about them'(1886). One hundred and twenty-two years after ...

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There has long been interest in understanding the genetic basis of human adaptation. To what extent are phenotypic differences among human populations driven by.

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[M Kayser, PM Schneider](#) - Forensic Science International: Genetics, 2009 - Elsevier

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MLA Aulchenko, Yuri S., et al. "Predicting human height by Victorian and genomic methods." *European Journal of Human Genetics* 17.8 (2009): 1070-1075.

APA Aulchenko, Y. S., Struchalin, M. V., Belonogova, N. M., Axenovich, T. I., Weedon, M. N., Hofman, A., ... & Borodin, P. M. (2009). Predicting human height by Victorian and genomic methods. *European Journal of Human Genetics*, 17(8), 1070-1075.

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The screenshot shows the Readcube web application interface. At the top, the 'readcube' logo is on the left, and an 'Import' button is circled in red. Below the logo, the 'my library' tab is selected, with 'google scholar' and 'pubmed' tabs also visible. The left sidebar contains a 'search' section, a 'FEEDS' section with 'Recommendations', and a 'library' section with 'Recently Read' and 'Favorites'. Below these are various topic-based feeds like 'melosis', 'evo-devo', 'human evoluti...', 'natural selection', 'comparative g...', 'phylogeny', 'borodin', 'chromosomes', 'sex', 'Downloads', 'XY', 'pdf', 'Inquisition', 'dog', 'fox', 'agadzanyan', 'cat', 'speciation', and 'shrew'. At the bottom of the sidebar is 'ReadCube Media'. The main content area features a large 'search my library' logo and a search bar. In the bottom right corner, there is a link to 'Watch intro video' with a hand icon. The bottom status bar includes 'Show Tips', 'Watch Video', and 'Support' buttons.

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At the bottom of the application window, there is a footer with links for 'Show Tips', 'Watch Video', and 'Support'. A handwritten note at the bottom of the main area says 'Tip: Drag and Drop PDF files or folders here' with an arrow pointing to the main content area.

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- A Second-Generation Genetic Linkage Map of the Do
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dog chromosomes.xls	30.07.2007 11:39	
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author Doggett N

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Yang F, Graphodatsky AS, O'Brien PC, Colabella A, Solanky N, Squire M, Sargan DR, Ferguson-Smith MA

Chromosome Res.

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General pattern of meiotic recombination in male dogs estimated by MLH1 and RAD51 immunolocalization.

2008

Basheva EA, Bidau CJ, Borodin PM

Chromosome Res.

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General pattern of meiotic recombination in male dogs estimated by MLH1 and RAD51 immunolocalization.

2008

Basheva EA, Bidau CJ, Borodin PM

Chromosome Res.

★

A comparative chromosome map of the Arctic fox, red fox and dog defined by chromosome painting and high res...

2000

Graphodatsky AS, Yang F, O'Brien PC, Serdukova N, Milne BS, Trifonov V, Ferguson-Smith MA

Chromosome Res.

★

A comprehensive linkage map of the dog genome.

2010

Wong AK, Ruhe AL, Dumont BL, Robertson KR, Guerrero G, Shull SM, Ziegler JS, Millon LV, Broman KW, Payseur BA, Neff M...

Genetics

★

The dog genome: survey sequencing and comparative analysis.

2003

Kirkness EF, Bafna V, Halpern AL, Levy S, Remington K, Rusch DB, Delcher AL, Pop M, Wang W, Fraser CM, Venter JC

Science

★

Mapping of the silver gene in mink and its association with the dilution gene in dog.

2007

Anistoroaei R, Christensen K

Cytogenet. Geno...

★

Phylogenomics of the dog and fox family (Canidae, Carnivora) revealed by chromosome painting.

2008

Graphodatsky AS, Perelman PL, Sokolovskaya NV, Beklemisheva VR, Serdukova NA, Dobigny G, O'Brien SJ, Ferguson-Smi...

Chromosome Res.

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Yang F, Graphodatsky AS, O'Brien PC, Colabella A, Solanky N, Squire M, Sargan DR, Ferguson-Smith MA

Chromosome Res.

★

The DAPI banded karyotype of the domestic dog (Canis familiaris) generated using chromosome-specific paint p...

1999

Breen M, Bullerdiel J, Langford CF

Chromosome Res.

★

An indication of major genes affecting hip and elbow dysplasia in four Finnish dog populations.

2004

Mäki K, Janss LL, Groen AF, Lillamo AE, Ojala M

Heredity (Edinb)

★

A complete comparative chromosome map for the dog, red fox, and human and its integration with canine genet...

1999

Yang F, O'Brien PC, Milne BS, Graphodatsky AS, Solanky N, Trifonov V, Rens W, Sargan D, Ferguson-Smith MA

Genomics

★

A cytogenetically characterized, genome-anchored 10-Mb BAC set and CGH array for the domestic dog.

2007

Thomas R, Duke SE, Bloom SK, Breen TE, Young AC, Feiste E, Seiser EL, Tsai PC, Langford CF, Ellis P, Karlsson EK, Lindblad-T...

J. Hered.

★

Three-Dimensional Positioning of B Chromosomes in Fibroblast Nuclei of the Red Fox and the Chinese Raccoon D...

2013

Kociucka B, Sosnowski J, Kubiak A, Nowak A, Pawlak P, Szczerbal I

Cytogenet. Geno...

★

Cladogenesis, coalescence and the evolution of the three domains of life.

2004

Zhaxybayeva O, Gogarten JP

Trends Genet.

★

The human zoo: endogenous retroviruses in the human genome

2002

Bromham L

Trends in ecolog...

★

A Dog Breakfast.pdf

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★

Ancient DNA evidence for Old World origin of New World dogs

2002

Leonard JA, Wayne RK, Wheeler J, Valadez R ...

Science

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Chromosome research : an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology. 2008 16(5):709-19

General pattern of meiotic recombination in male dogs estimated by MLH1 and RAD51 immunolocalization.

Basheva EA; Bidau CJ; Borodin PM

Russian Academy of Sciences, Siberian Department, Institute of Cytology and Genetics, Novosibirsk, Russia.

The aim of this study was to estimate a general pattern of meiotic recombination in the domestic dog (Canis familiaris) using immunolocalization of MLH1, a mismatch repair protein of mature recombination nodules. We prepared synaptonemal complex (SC) spreads from 124 spermatocytes of three male dogs and mapped 4959 MLH1 foci along 4712 autosomes. The mean number of MLH1 foci for all autosomes was 40.0 foci per cell. Total recombination length of the male dog autosomal genome map was estimated as 2000 cM. A global pattern of MLH1 foci distribution along the autosomal bivalents was rather similar to that found in the mammals studied: a high frequency near the telomeres and a low frequency near the centromeres. An obligate MLH1 focus in the X-Y pairing region was usually located very close to Xp-Yq telomeres. The distances between MLH1 foci at autosomal bivalents were consistent with crossover interference. A comparison of the interference estimates coming from the distribution of MLH1 interfocus distances and RAD51/MLH1 focus ratio indicated a substantial variation between species in the strength of interference.

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attack rates on light and dark p... fine mouse ne...

А мыши-то пластининовые.
А глупые вороны на них ловят.

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following (15) to
for ~2100 unlinked
and base pairs (kbp)
containing *Agouti*
regulatory elements (Fig. 2B) (16).

ever, this is not surprising given the large effective
population size we estimated for *P. maniculatus*
($N_e > 50,000$ mice) (13). Together, these data sug-
gest that there has been sufficient recombination
for fine-scale mapping color traits within *Agouti*.

tion traits that together give rise to the overall
cryptic appearance of the Sand Hills mice (Fig. 2A).
In addition to having a significantly lighter dor-
sum (one-tailed *t* test; $N = 10$ lab-reared mice; $P =$
 8.2×10^{-4}), Sand Hills mice also have a lighter
ventrum, an upward shift in the dorsal-ventral (d-v)
boundary, and a less pronounced tail stripe com-
pared with the ancestral form (one-tailed *t* tests;
 $N = 10$ mice; ventral color: $P = 3.9 \times 10^{-5}$; d-v
boundary: $P = 1.4 \times 10^{-4}$; tail stripe: $P = 5.5 \times 10^{-7}$).
Because these derived light-color traits are all as-
sociated with *Agouti* in laboratory strains, they
could be explained by either a single pleiotropic
mutation of large effect or multiple mutations of
smaller, more modular effect in this locus.

To distinguish between these alternatives, we
collected phenotypic (color and color pattern)
and genotypic data from 91 wild-caught mice
from a phenotypically diverse population located
near the edge of the Sand Hills. We measured
three color traits derived from a principal com-

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2. R. A. Fisher, The Genetical Theory of Natural Selection (Oxford Univ. Press, Oxford, 1930).

3. N. J. Nadeau, C. D. Jiggins A golden age for evolutionary genetics? Genomic studies of adaptation in natural populations. *Trends Genet.* 26, 484 (2010).

4. J. Ståhl Adaptation genomics: The next generation. *Trends Ecol. Evol.* 25, 705 (2010).

5. H. E. Hoekstra, R. J. Hirschmann, R. A. Bundry, P. A. Insel, J. P. Crossland A single amino acid mutation contributes to adaptive beach mouse color pattern. *Science* 315, 84 (2006).

6. M. Rebeiz, J. E. Pool, V. A. K. Aquadro, S. B. Carroll Stepwise modular enhancer underlies a *Drosophila* population. *Science* (2009).

7. N. Frankel Morphological evolution: many subtle-effect substitutions in regulatory DNA. *Nature* 474, 598 (2011).

8. K. V. S. K. Prasad A gain-of-function polymorphism controlling complex traits and fitness in nature. *Science* 337, 1081 (2012).

9. D. B. Loope, J. Swinehart Thinking like a dune field: Geologic history in the Nebraska Sand Hills. *Great Plains Res.* 10, 5 (2000).

10. L. R. Rice Variation of the deer-mouse (*Peromyscus maniculatus*) on the Sand Hills of Nebraska and adjacent areas. *Contrib. Lab. Vertebr. Genet. Univ. Mich.* 15, 1 (1941).

11. C. R. Linnen, E. P. Kingsley, J. D. Jensen, H. E. Hoekstra On the origin and spread of an adaptive allele in deer mice. *Science* 325, 1095 (2009).

12. S. N. Vignieri, J. G. Larson, H. E. Hoekstra The selective advantage of crypsis in mice. *Evolution* 64, 2153 (2010).

13. Materials and methods are available as supplementary materials on Science online.

14. L. R. Rice Effectiveness of selection by owls of deer-mice (*Peromyscus maniculatus*) which contrast in color with their background. *Contrib. Lab. Vertebr. Biol. Univ. Mich.* 34, 1 (1947).

15. V. S. Domingues Evidence of adaptation from ancestral variation in young populations of beach mice. *Evolution* 66, 3209 (2012).

16. E. P. Kingsley, M. Manseau, C. D. Wiley, H. E. Hoekstra Melanism in *peromyscus* is caused

D

Proportion of attacks

Cryptic Conspicuous

Fig. 1. Selective advantage of crypsis against predation. (A) Typical habitat in the Sand Hills (left) and the adjacent region (right). Insets show representative substrate from each habitat. (B) Typical mouse color phenotypes from on (left) and off (right) the Sand Hills, shown on light Sand Hills substrate. (C) Typical cryptic (left) and conspicuous (right) models, shown on Sand Hills substrate. (D) Proportion of predation events occurring over 2700 model nights in the Sand Hills habitat. Conspicuous models were attacked significantly more often than cryptic models (selection index = 0.545, $\chi^2 = 6.546$, $df = 1$, $P = 0.011$).

¹Department of Biology, University of Kentucky, 200A Thomas Hunt Morgan Building, Lexington, KY 40506, USA. ²Department of Organismic and Evolutionary Biology, the Museum of Comparative Zoology, Harvard University, 26 Oxford Street, Cambridge, MA 02138, USA. ³Department of Molecular and Cellular Biology, Harvard University, 26 Oxford Street, Cambridge, MA 02138, USA. ⁴Program in Bioinformatics and Integrative Biology, University of Massachusetts Medical School, Worcester, MA, USA. ⁵School of Life Science, Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland. ⁶Swiss Institute of Bioinformatics (SIB), Lausanne, Switzerland.

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Readcube

The screenshot displays the Readcube web application interface. At the top, the Readcube logo is visible on the left, and a search bar contains the query '20952088'. Below the search bar, there are tabs for 'Google Scholar' and 'PubMed'. The main content area shows a search result for the article 'Adaptation genomics: the next generation.' by Stapley J, Reger J, Feulner PG, Smadja C, Galindo J, Ekblom R, Bennison C, Ball AD, Beckerman AP, and Slate J, published in Trends Ecol. Evol. in 2010. The article title is highlighted in blue. To the right of the article title, there is a section titled 'info' containing the journal information and a brief abstract. Below the abstract, there is a 'NOTES' section with a 'create a note' button. At the bottom of the page, there are links for 'PubMed', 'Related Articles', 'Google Scholar', 'Related Articles', and 'Citations (112)'. A red circle highlights the 'Download Article' button, which is labeled '1 Direct Download Site'. Another red circle highlights the 'Related Articles' link. The bottom status bar shows 'Displaying 1 of 1' and various utility icons like 'Show Tips', 'Watch Video', and 'Support'.

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Adaptation genomics: the next generation. 2010
Trends Ecol. Evol...

Stapley J, Reger J, Feulner PG, Smadja C, Galindo J, Ekblom R, Bennison C, Ball AD, Beckerman AP, Slate J

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Trends in ecology & evolution. 2010 25(12):705-12

Adaptation genomics: the next generation.

Stapley, Jessica; Reger, Julia; Feulner, Philine G; Smadja, Carole; Galindo, Juan; Ekblom, Robert; Bennison, Clair; Ball, Alexander D; Beckerman, Andrew P; Slate, Jon

Department of Animal & Plant Sciences, University of Sheffield, Sheffield, S10 2TN, UK.

Understanding the genetics of how organisms adapt to changing environments is a fundamental topic in modern evolutionary ecology. The field is currently progressing rapidly because of advances in genomics technologies, especially DNA sequencing. The aim of this review is to first briefly summarise how next generation sequencing (NGS) has transformed our ability to identify the genes underpinning adaptation. We then demonstrate how the application of these genomic tools to ecological model species means that we can start addressing some of the questions that have puzzled ecological geneticists for decades such as: How many genes are involved in adaptation? What types of genetic variation are responsible for adaptation? Does adaptation utilise pre-existing genetic variation or does it require new mutations to arise following an environmental change?

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Nature

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2013
Nat. Genet.

Complex traits: Missing in action.
Muers M
2013
Nat. Rev. Genet.

The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human ge...
Montgomery SB, Goode DL, Kvistad E, Albers CA, Zhang ZD, Mu XJ, Ananda G, Howie B, Karczewski KJ, Smith KS, ...
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Genome Res.

A common mode of recognition for methylated CpG.
Liu Y, Zhang X, Blumenthal RM, Cheng X
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Pig Domestication and Human-Mediated Dispersal in Western Eurasia Revealed through Ancient DNA and ...
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Tubicolous enteropneusts from the Cambrian period.
Caron, Jean-Bernard B; Morris, Simon C; Cameron, Christopher B
Department of Natural History (Palaeobiology), Royal Ontario Museum, 100 Queen's Park, Toronto, Ontario M5S 2C6, Canada. jcaron@rom.on.ca

Hemichordates are a marine group that, apart from one monospecific pelagic larval form, are represented by the vermiform enteropneusts and minute colonial tube-dwelling pterobranchs. Together with echinoderms, they comprise the clade Ambulacraria. Despite their restricted diversity, hemichordates provide important insights into early deuterostome evolution, notably because of their pharyngeal gill slits. Hemichordate phylogeny has long remained problematic, not least because the nature of any transitional form that might serve to link the anatomically disparate enteropneusts and pterobranchs is conjectural. Hence, inter-relationships have also remained controversial. For example, pterobranchs have sometimes been compared to ancestral echinoderms. Molecular data identify enteropneusts as paraphyletic, and harrimanids as the sister group of pterobranchs. Recent molecular phylogenies suggest that enteropneusts are probably basal within hemichordates, contrary to previous views, but otherwise provide little guidance as to the nature of the primitive hemichordate. In addition, the hemichordate fossil record is almost entirely restricted to peridermal skeletons of pterobranchs, notably graptolites. Owing to their low preservational potentials, fossil enteropneusts are exceedingly rare, and throw no light on either hemichordate phylogeny or the proposed harrimanid-pterobranch transition. Here we describe an enteropneust, *Spartobranchus tenuis* (Walcott, 1911), from the Middle Cambrian-period (Series 3, Stage 5) Burgess Shale. It is remarkably similar to the extant harrimanids, but differs from all known enteropneusts in that it is associated with a fibrous tube that is sometimes branched. We suggest that this is the precursor of the pterobranch periderm, and supports the hypothesis that pterobranchs are miniaturized and derived from an enteropneust-like worm. It also shows that the periderm was acquired before size reduction and acquisition of feeding tentacles, and that coloniality emerged through aggregation of individuals, perhaps similar to the Cambrian rhabdopleurid *Fasciculitubus*. The presence of both enteropneusts and pterobranchs in Middle Cambrian strata, suggests that hemichordates originated at the onset of the Cambrian explosion.

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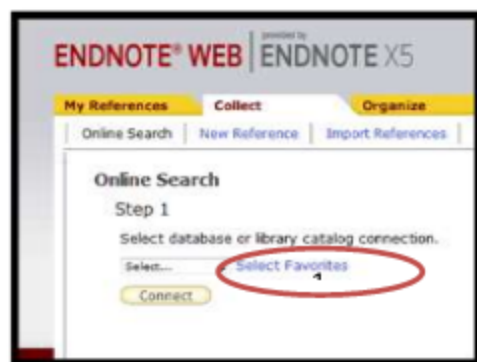
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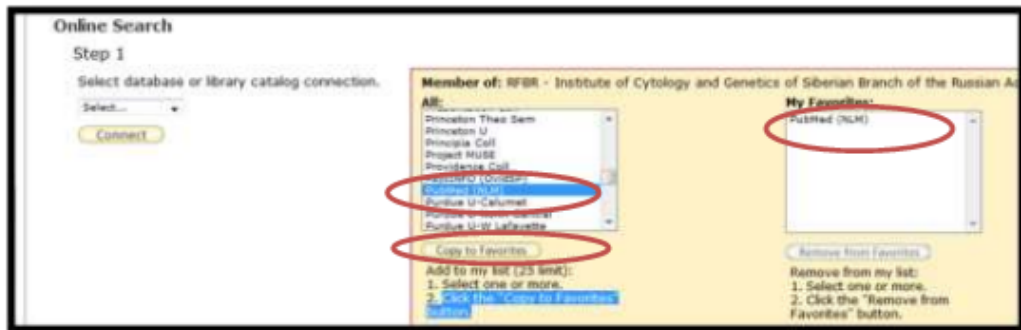


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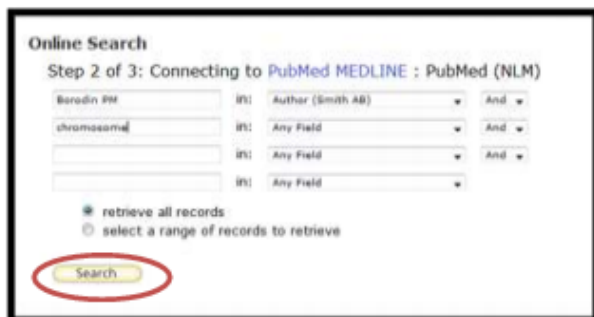
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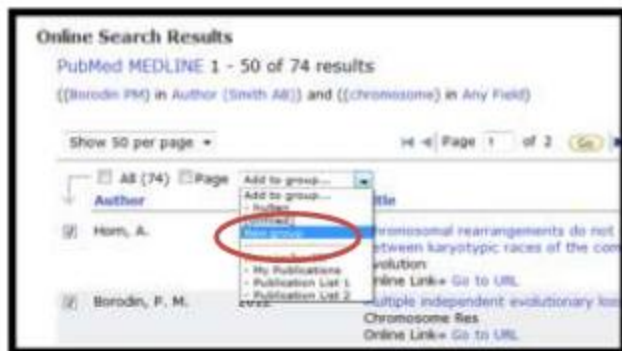


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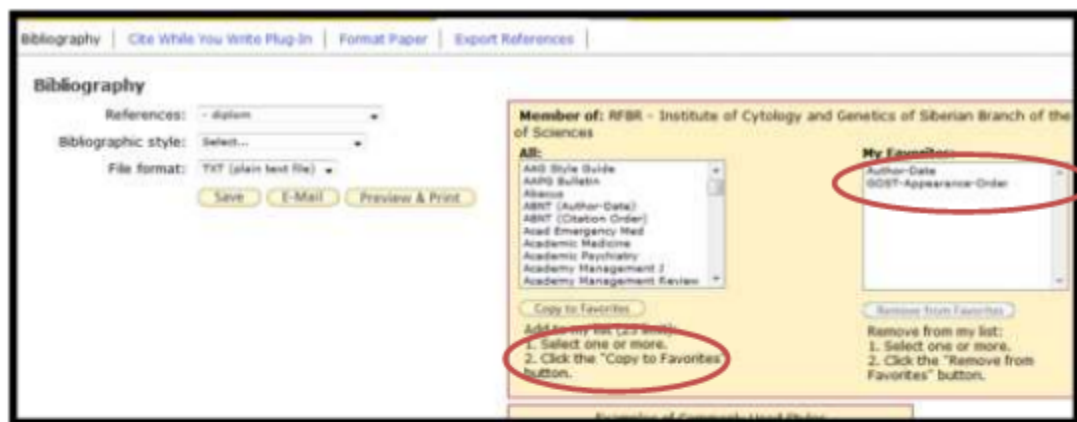


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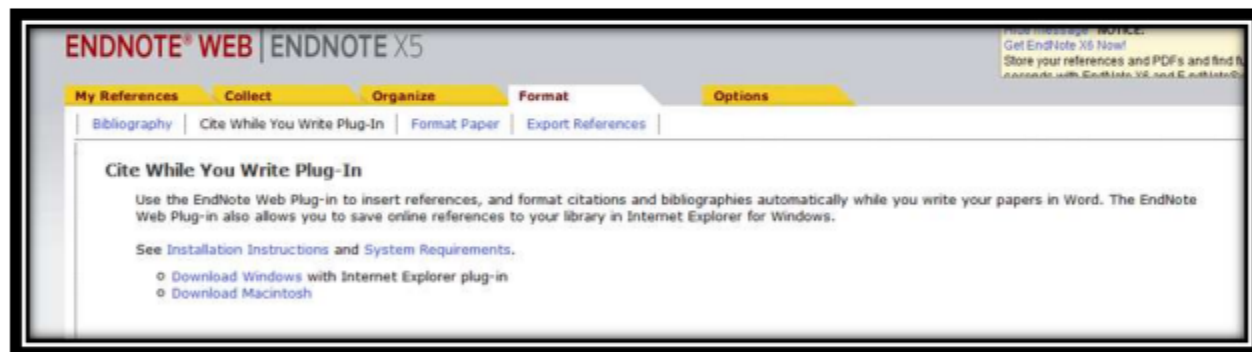


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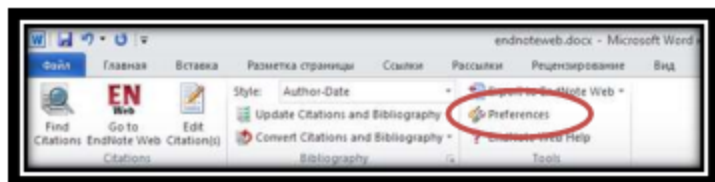
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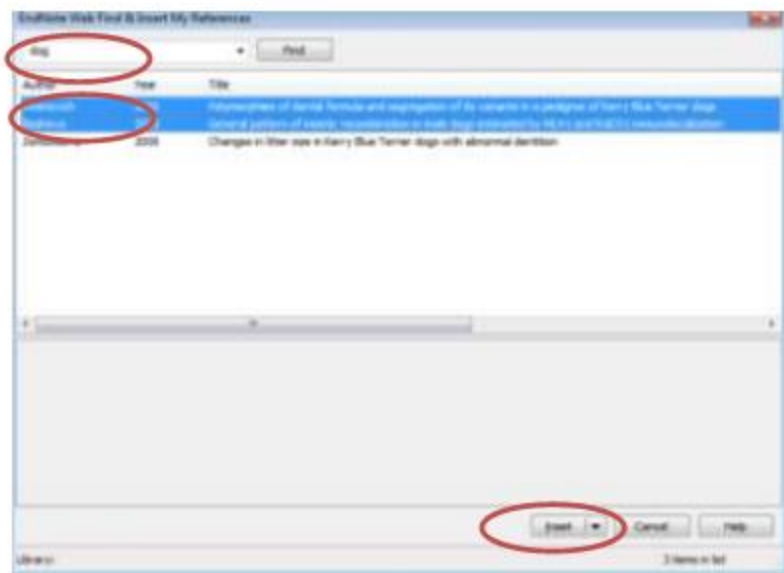


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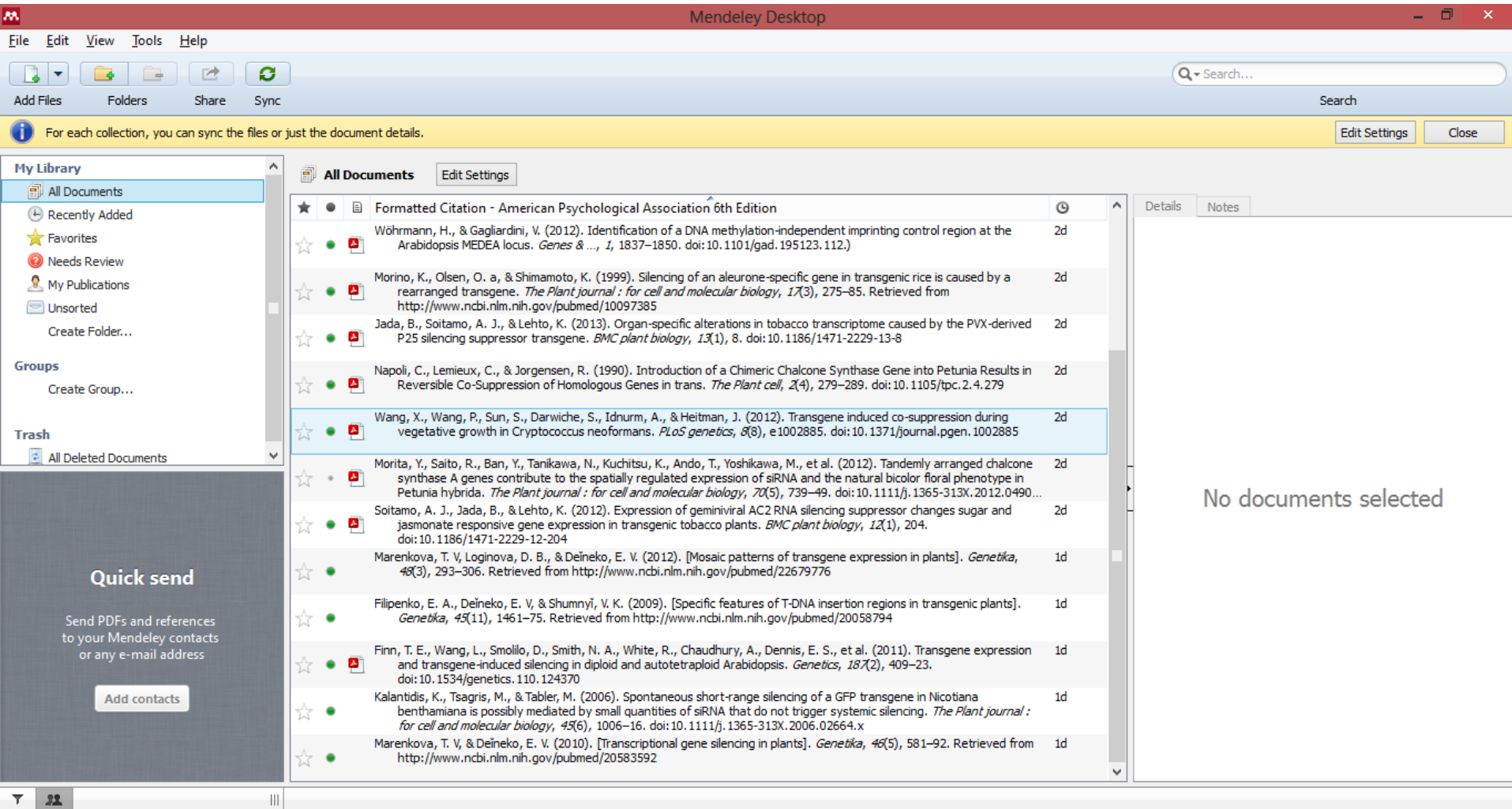
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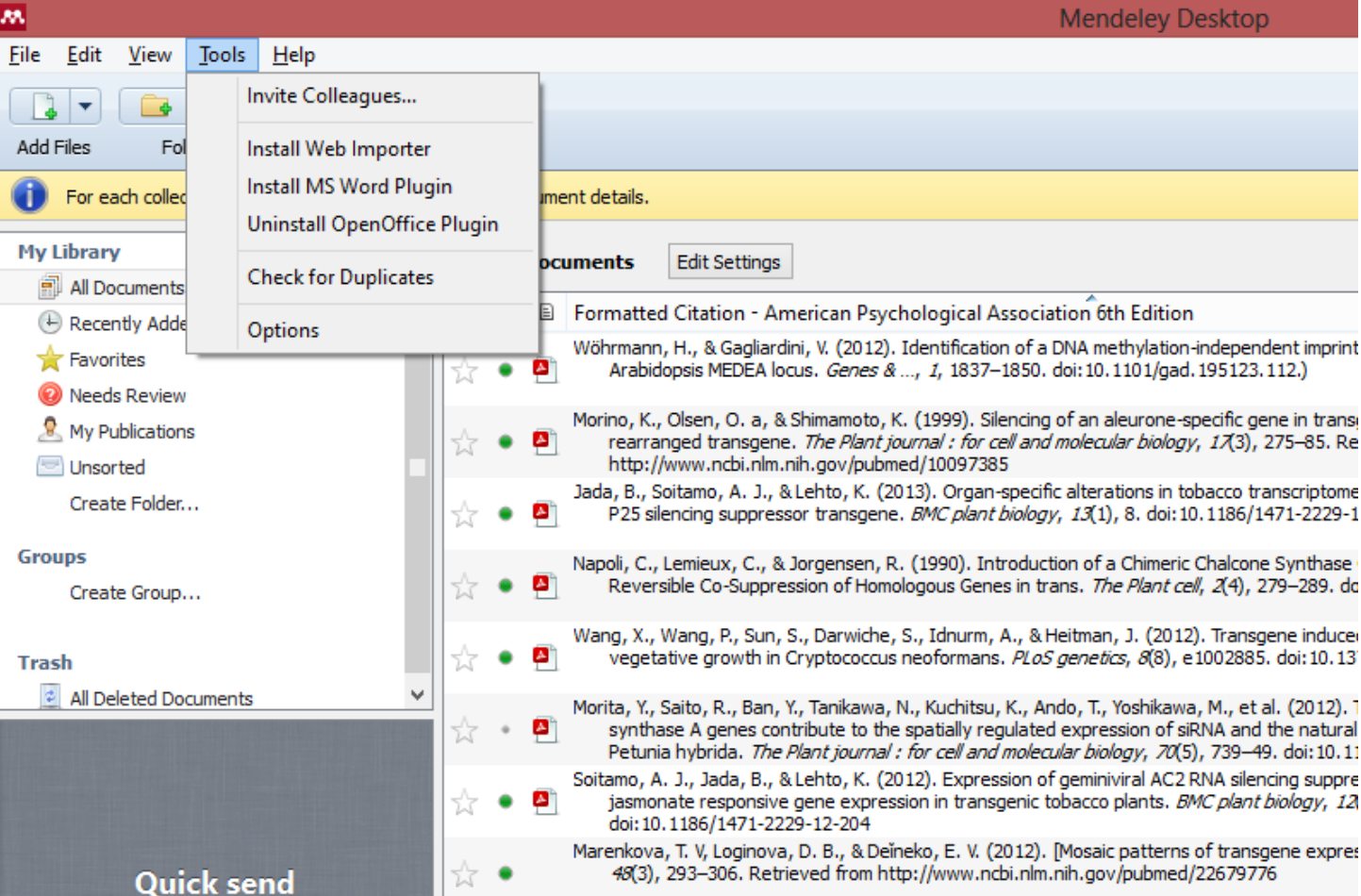
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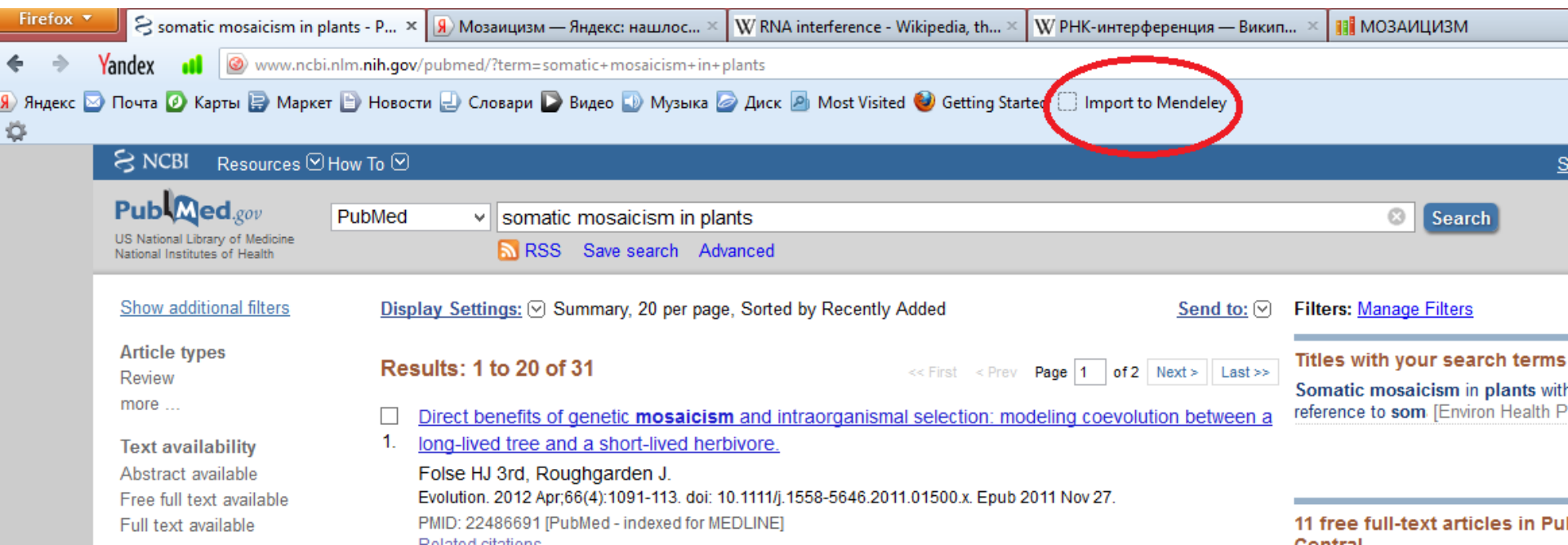
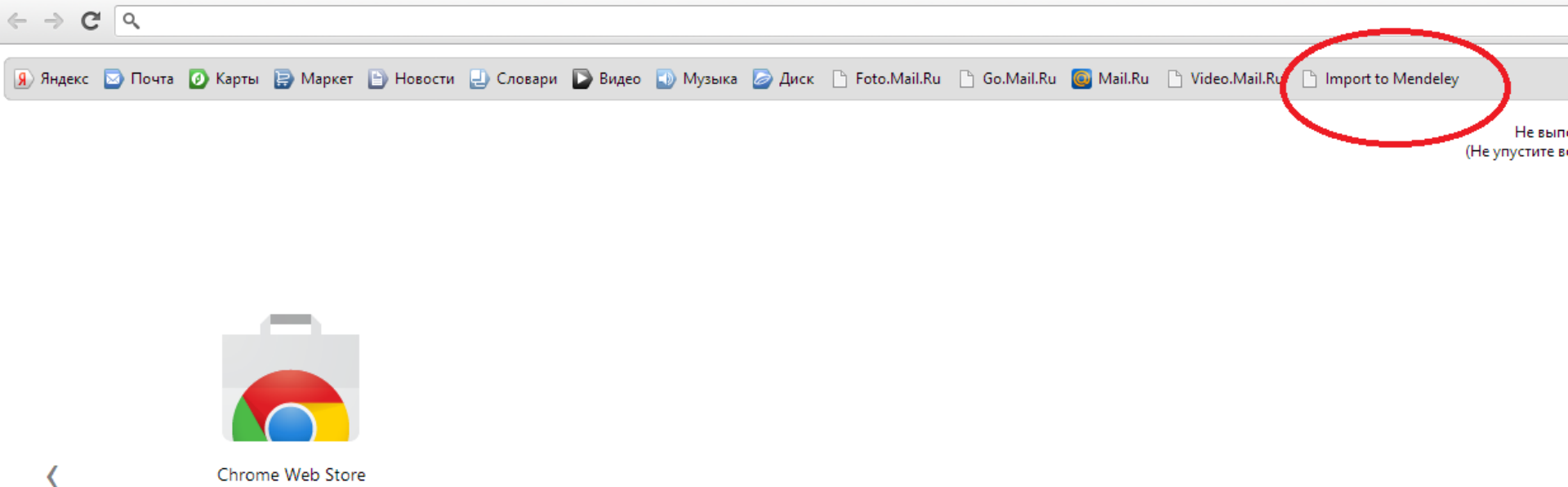


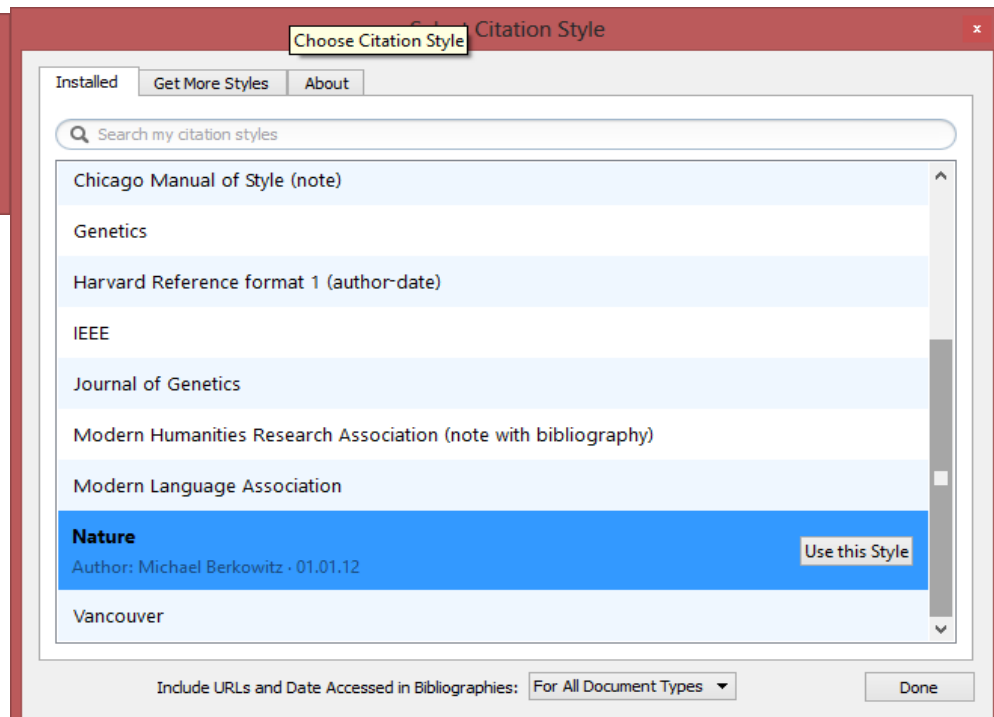
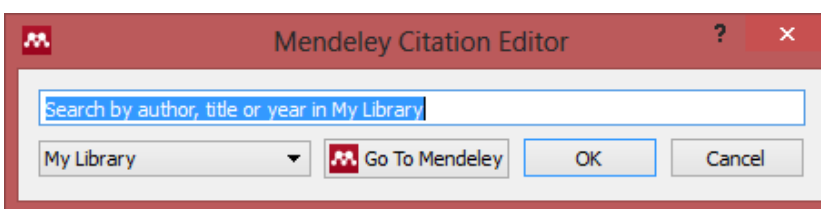
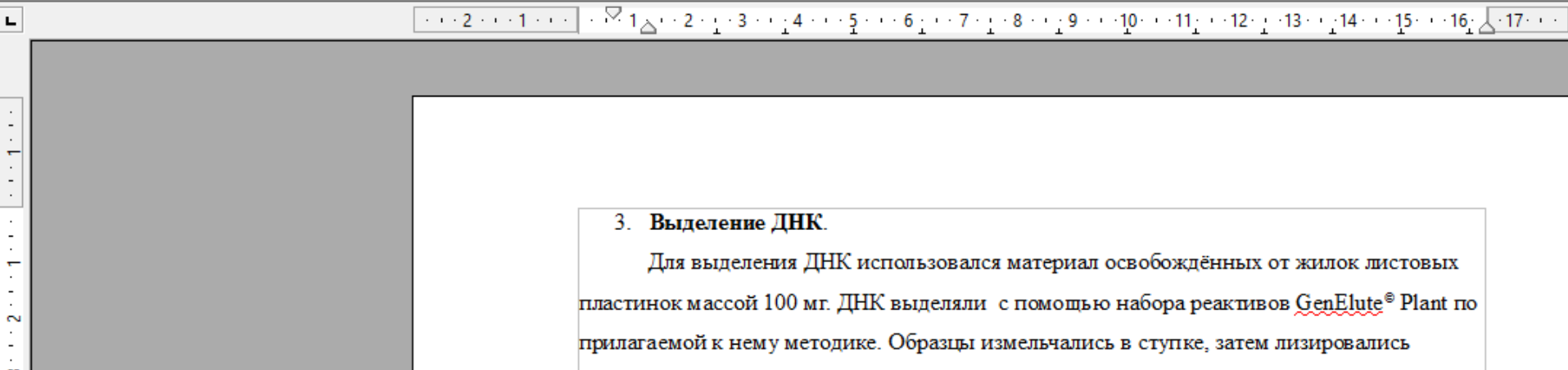
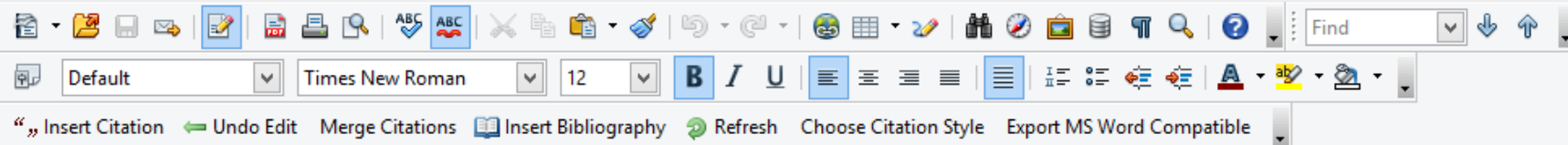
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