**Declaration:** I declare that the information given on all parts of this application form, and in any CV which accompanies it, is, to the best of my knowledge, correct. I understand that giving any false information will make my application unacceptable and, if I am appointed, lead to my dismissal. I accept that:

- if I am appointed, the information on this form may be used, in accordance with Schedule 2 of the Data Protection Act 1998, to form part of my permanent personal record
- the information in the Equal Opportunities Monitoring Form which accompanies this form, will be used in accordance with Schedule 3 of the Data Protection Act 1998 to identify and review the equality of treatment between individuals with a view to enabling such equality to be promoted and maintained

SignatureKsenia V Krasileva	Date	.July 28, 2014
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APPLICATION NO

When you submit your application document on line you will be prompted to enter

- · Your personal details,
- Names and addresses of 3 referees
- · Equal Opportunities monitoring data

## 2.1 EDUCATION

Da From	ates To	Name of School/College/University from the age of 14	Qualifications Please indicate grade and date obtained
2005	2011	University of California, Berkeley, USA	Ph.D in Microbiology with Designated Emphasis in Genomics and Computational Biology (May 2011)
2001	2005	University of California, Berkeley, USA	B.S. with double major in Genetics and Plant Biology and Microbiology. Honors. (May 2005)
2000	2001	Las Lomas High School, Walnut Creek, California, USA	High School Diploma*. Honors (June 2001)
1991	2000	Academic Classes, School N70, Saint- Petersburg, Russia	High School Diploma* (grades 5-11). Honors (June 2000)

<sup>\*</sup>In Russia, high school diploma is awarded after 11 grades (there is no grade 12), while in the United States there is a 12<sup>th</sup> grade, therefore I have two diplomas.

## 2.2 PRESENT/LAST EMPLOYMENT

Job Title: Post-doctoral fellow	Salary \$55,000		
Name and address of employer:	Starting date: 09/15/2011		
University of California, Davis			
One Shields Ave, Davis CA, 95616-8780 USA	Date appointed to present post or date promoted, if applicable:		
Post Code: 95616-8780	Period of notice required by employer: n/a		

Brief details of main duties:

In the Dubcovsky lab, I lead development of functional genomics tools for wheat. Specifically, I am focused on the tetraploid wheat species *Triticum turgidum* that provides us with pasta and couscous and serves as an important model for basic wheat research. From the very beginning of my post-doc, I focused on adopting exome-capture and next generation sequencing technologies to re-sequence EMS-mutagenized population of durum wheat and developing a publicly available resource for scientific community and wheat breeders. The prediction of the wheat proteome was the first necessary step for defining wheat exome. As such, I sequenced the transcriptome of *Triticum turgidum* and *Triticum urartu* and developed a novel strategy for assembling a tetraploid wheat transcriptome in which homeologous sequences are separated by phasing of mapped Illumina reads (Krasileva et al. Genome Biology 2013). I adapted exome capture technology and modern robotics for high-throughput sample processing and now, I resequenced 1,000 mutant wheat lines from a large durum wheat TILLING collection. Together with a bioinformatician in the Dubcovsky lab, Hans Vasquez-Gross, whom I supervise on daily basis and in collaboration with Luca Comai's group (UC Davis) and Sarah Ayling's group (TGAC), we assembled a pipeline for processing exome capture data and robust identification of mutations in each line.

This information is now used for developing a **database that catalogues discovered mutations**. I am continuing data analyses and **preparing a publication describing this resource**. This database will soon be publicly available to scientists and wheat breeders to identify and request lines with induced alleles of interest.

During 2012-2013 and 2013-2014 field seasons, I conducted a forward genetics screen by exposing our mutagenized wheat population to natural disease pressure in the field and identified mutants with either enhanced resistance or increased disease susceptibility to **wheat stripe rust**. I validated results of the study in controlled growth chamber environment and pursued genetic and molecular characterization of selected lines. Wheat exome capture technology has enabled me to rapidly identify all mutations in each line of interest. I am continuing to develop genomic tools for wheat that would allow linking the observed phenotype with its precise genomic location.

Most recently, I established collaboration with the International Atomic Energy Institute (IAEI) and the Food and Agriculture Organization (FAO) of the United Nations. I am bringing my expertise in wheat exome capture and resequencing to aid in the **Efficient Screening Techniques for Mutants with Disease Resistance** program, specifically targeted at Ug99 races of wheat rust and wheat improvement in Kenya and Ethiopia.

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# 2.3 PREVIOUS EMPLOYMENT

Please list employers in order, most recent first. Periods of unemployment should also be listed and you may include any temporary, vacation or casual work, if relevant.

Dates From To		Name and address of employer	Post held and details of main duties		
09/2005	06/2011	University of California, Berkeley Berkeley, CA 94720	Graduate Student Researcher, Graduate Student Instructor		
01/2003	06/2005	University of California, Berkeley Berkeley, CA 94720	Undergraduate Student Researcher		

# 2.4 PERSONAL STATEMENT

### UNIVERSITY OF CALIFORNIA, DAVIS

BERKELEY • DAVIS • IRVINE • LOS ANGELES • MERCED • RIVERSIDE • SAN DIEGO • SAN FRANCISCO



• SANTA BARBARA • SANTA CRUZ

Dr. Mario Caccamo, Director The Genome Analysis Center Norwich Research Park NR4 7UH, UK

July 31st, 2014

Dear Dr. Caccamo and the Search Committee,

I am writing to apply for the position of Group Leader in *Triticeae* Genomics at The Genome Analyses Center.

I completed my doctoral studies at University of California Berkeley with Prof. Brian J. Staskawicz. During my PhD I gained extensive expertise in biochemistry, cellular biology and bioinformatics earning a joined degree in Microbiology and Genomics / Computational Biology. I worked with a model organism *Arabidopsis thaliana* to elucidate the key biochemical events leading to pathogen recognition by plant innate immune receptors. My doctoral work encompasses a total of 10 publications, including 4 first/co-first author papers in such journals as *Plant Cell*, *PNAS*, *PLoS Pathogens* and *BMC Genomics*.

Currently, I am a USDA AFRI-NIFA post-doctoral fellow with Prof. Jorge Dubcovsky, a leader of wheat research at University of California Davis. I decided to work on wheat to make this important grass species highly accessible to basic science and to accelerate the efforts of breeders. I applied my bioinformatic and laboratory skills to design exome capture for wheat, a targeted enrichment that in combination with next generation sequencing enabled me to re-sequence 1,000 mutant wheat lines of tetraploid wheat. This represents a milestone in development of functional genomic tools for wheat. The first part of this research that evaluated wheat transcriptomes has been published in *Genome Biology* and I am currently preparing the publication of wheat mutant database. Throughout my postdoc I enjoyed close collaboration with John Innes Center and The Genome Analyses Center.

In the future, I will continue to advance wheat genomics and I am especially interested in leading the efforts to establish a robust physical map of wheat and adopting mapping-by-sequencing protocols. In the past year, I conducted bioinfomatic as well as forward genetic screens and identified exciting components in wheat immunity that would form foundation for my work with The Sainsbury Lab.

I am excited by the opportunity to do research at The Genome Analysis Center and The Sainsbury Laboratory. I believe that my expertise in wheat genomics and my commitment to academic excellence and innovative translational research make me a well-suited candidate for this position.

Please, find attached my complete application, including technical qualifications and a list of references. I look forward to hearing from you.

Sincerely,

## 2.5 TECHNICAL AND PROFESSIONAL QUALIFICATIONS

Please list membership of any professional bodies and give details of any other qualifications held.

### **PUBLICATIONS** 12 publications (5 as first/co-first author)

- Henry IM, Nagalakshmi U, Lieberman MC, Ngo KJ, **Krasileva KV**, Vasquez-Gross H, Alina Akunova A, Akhunov E, Dubcovsky J, Tai TH and Comai L "Efficient genome-wide detection and cataloging of EMS-induced mutations using exome capture and next-generation sequencing" *Plant Cell*, 26:1382-1397 (2014)
- **Krasileva KV**, Buffalo V, Bailey P, Pearce S, Ayling S, Tabbita F, Soria M, Wang S, Consortium I, Akhunov E, Uauy C, Dubcovsky J: "Separating homeologs by phasing in the tetraploid wheat transcriptome". *Genome Biology* 2013, 14:R66. (2013)
- Bart R, Cohn M, Kassen A, McCallum EJ, Shybut M, Petriello A, **Krasileva K**, Dahlbeck D, Medina C, Alicai T, Kumar L, Moreira LM, Neto JR, Verdier V, Santana MA, Kositcharoenkul N, Vanderschuren H, Gruissem W, Bernal A, Staskawicz BJ. "High-throughput genomic sequencing of cassava bacterial blight strains identifies conserved effectors to target for durable resistance." *Proceeding of National Academy of Sciences U S A*, 109(28):E1972-9. (2012)
- Goritschnig S, **Krasileva KV**, Dahlbeck D, Staskawicz BJ. "Computational prediction and molecular characterization of an oomycete effector and the cognate Arabidopsis resistance gene" *PLoS Genetics* 8(2):e1002502. (2012)
- Win J, **Krasileva KV**, Kamoun S, Shirasu K, Staskawicz BJ, Banfield MJ. "Sequence divergent RXLR effectors share a structural fold conserved across plant pathogenic oomycete species" *PLoS Pathogens* 8(1): e1002400. (2012)
- **Krasileva KV**, Zheng C, Leonelli L, Goritschnig S, Dahlbeck D, Staskawicz BJ. "Global analysis of *Arabidopsis I* downy mildew interactions reveals prevalence of incomplete resistance and rapid evolution of pathogen recognition" *PLoS One*, 6: e28765. (2011)
- Zhao B, Dahlbeck D, **Krasileva KV**, Fong RW, Staskawicz BJ. "Computational and Biochemical Analysis of the Xanthomonas Effector AvrBs2 and Its Role in the Modulation of Xanthomonas Type Three Effector Delivery." *PLoS Pathogens.* 12:e1002408. (2011)
- Chou S\*, **Krasileva KV**\*, Holton J, Steinbrenner A, Alber T, Staskawicz BJ. "Hyaloperonospora arabidopsidis ATR1 effector is a repeat protein with distributed recognition surfaces" *Proceeding of National Academy of Sciences U S A.* 108(32): 13323-8. (2011) \*equal contribution
- Potnis N\*, **Krasileva K**\*, Chow V, Almeida NF Jr, Patil PB, Ryan RP, Sharlach M, Behlau F, Dow JM, White FF, Preston JF, Vinatzer BA, Koebnik R, Setubal JC, Norman DJ, Staskawicz BJ, Jones JB. "Comparative Genomics Reveals Diversity among Xanthomonads Infecting Tomato and Pepper". *BMC Genomics*, 12(1): 146. (2011) \*equal contribution
- **Krasileva KV**, Dahlbeck D, Staskawicz BJ. "Activation of an *Arabidopsis* Resistance Protein Is Specified by the *in Planta* Association of Its Leucine-Rich Repeat Domain with Cognate Oomycete Effector". *Plant Cell*, 22:1-16. (2010)
- Dulla GF, **Krasileva KV**, Lindow SE. "Interference of Quorum Sensing in *Pseudomonas syringae* by Bacterial Epiphytes that Limit Iron Availability". *Environmental Microbiology*, 12(6): 1762-74. (2010)
- Win J, Morgan W, Bos J, **Krasileva KV**, Cano LM, Chaparro-Garcia A, Ammar L, Staskawicz BJ, Kamoun S. "Adaptive Evolution Has Targeted the C-terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes". *Plant Cell*, 19: 2349-69. (2007)

## **PRESENTATIONS**

- 2014 Plant and Animal Genome Conference, San Diego, CA. Invited Speaker
- 2013 Beyond the Genome Conference, San Francisco, CA. Selected Speaker
- 2012 New Phytologist Conference, Fallen Leaf Lake, CA. Poster
- 2012 Howard Hughes Medical Institute Conference, Janelia Farm, VA. Poster
- 2011 Department of Plant Pathology Seminars, Davis, CA. Invited Speaker
- 2010 Gordon Research Conference, Holderness, NH. Poster
- 2010 International Congress MPMI, Quebec, Canada. Selected Speaker
- 2008 Bay Area Microbial Pathogenesis Symposium, San Francisco, CA. Selected Speaker
- 2008 Keystone Symposium in Plant Innate Immunity, Keystone, Colorado. Poster

#### **TEACHING**

- 2014. Helping teach software carpentry workshop on R and data visualization, UC Davis.
- 2014. Panel speaker in a workshop on grant writing for post-docs, UAW UC Davis
- 2012-2014. Mentor of pre-graduate bioinformatics specialists, UC Davis
- 2007-2011. Undergraduate Research Mentor, UC Berkeley.
- 2008-2010. Guest Lecturer for "Agriculture and Society", UC Berkeley.
- 2007. Teaching Assistant for "Introduction to Programming for Bioinformatics", UC Berkeley.
- 2007. Graduate Student Instructor for "Introduction to Comparative Virology", UC Berkeley.
- 2006. Graduate Student Instructor for "Introductory Biology 1A", UC Berkeley. Outstanding Graduate Student Instructor Award
- 2006. Course Instructor, "Summer Explorations in Microbiology" 7-9th grades, UC Berkeley

#### **OUTREACH**

- 2011. Invited Speaker for Sally Ride Science Camp for girls, UC Berkeley
- 2007-2008. Panel Speaker for Biology Majors Fair, "Beyond the B.A.: Graduate and Professional Schools", UC Berkeley
- 2006. Volunteer in Community Outreach and Education: "Agriculture, Molecular Biology and Genetically Modified Organisms: GMOs in Food" Advanced training of UCCE Master Gardeners in Santa Clara County w/ Peggy Lemaux

#### **AWARDS**

- 2012-2014 Federal Principle Investigator grant "Development of Functional Genomic Tools for Wheat" through the United States Department of Agriculture AFRI-NIFA postdoctoral fellowship program.
- 2007 Outstanding Graduate Student Instructor Award, UC Berkeley.
- 2006 Honorable Mention, NSF Graduate Student Fellowship.
- 2005 Plant and Microbial Biology departmental citation, UC Berkeley.
- 2003-2005 Sponsored Projects for Undergraduate Research Fellowship, UC Berkeley.
- 2004 Summer Undergraduate Research Fellowship, UC Berkeley.

#### **SOCIETIES**

- American Association for the Advancement of Science.
- The International Society for Molecular Plant-Microbe Interactions.
- Professional twitter account @kseniakrasileva

### **EDITORIAL RESPONSIBILITIES**

- Guest associate editor of Research Topic in New Frontiers "Plant Immunity: From model systems to crops species" http://bit.ly/1pycmc9
- Reviewer, PLoS ONE

Please indicate the number of additional sheets, if any.	
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## 2.6 SKILLS

Foreign languages (please indicate degree of fluency i.e. conversation, written, technical):

Bi-lingual in English and Russian.

French.

Other, e.g. scientific, computing, word processing, (please indicate level of proficiency).

**General scientific:** Experimental design, writing and editing manuscripts, writing grants, serving as a reviewer and editor for scientific journals. Supervision of undergraduate and graduate students, and staff bioinformaticians.

**Technical (computational):** Genome assembly and annotation (both de novo and evidence-based), polymorphism discovery, evolutionary analyses, Hidden-Markov model-based searches, protein family analyses, homology-based structural modelling.

Advanced scripting in Perl and bash. Advanced command line usage and familiarity with Linux environment and R statistical package. Good knowledge of Python (reading and editing). Familiarity with MySQL.

Over seven years of experience in modern sequencing technologies and sequencing analyses.

**Technical (wet lab):** Genetics, biochemistry, plant cell biology, protein expression and purification, next-generation sequencing, exome capture. Advanced knowledge of host-microbe interactions and mechanisms in plant innate immunity.

## 2.7 TYPE OF DRIVING LICENCE HELD Please place a tick in the appropriate box.

None	Provisional	Full	PSV	HGV Group 1	HGV Group 2	HGV Group 3	Other please specify
							California DL Class C

Please add any additional information below as appropriate to your application.