

# Center for Inherited Disease Research

## Application for SNP Linkage Scans in Mice

This application should be used only for SNP Linkage Scans in Mice projects. The following items should be provided to the CIDR Access Committee in a document not to exceed 10 pages (excluding appendices). Text may be single-spaced but the type size must conform to NIH guidelines, i.e., letter height no smaller than 10 point, type density no greater than 15 characters per inch, and no more than 6 lines within a vertical inch. Applications that do not conform to these guidelines will be returned.

Extramural NIH grantees supported by a participating institute require prior approval from the institute liaison before submitting an application to CIDR. Intramural NIH investigators should contact Dr. Camilla Day before preparing an application. See CIDR web site for institute liaison contact information – [www.cidr.jhmi.edu](http://www.cidr.jhmi.edu).

Please note: Investigators who successfully use CIDR data from SNP genome scans to identify one or more linkage peaks can request SNP fine mapping without going through the usual application/review process. An expedited review of the linkage data and the plans for follow up will be carried out to determine if the project warrants SNP fine mapping at CIDR. See more details under the Project Details section of the application.

Please address the following items in the order they are listed.

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### Principal Investigator Information

Provide contact information including:

- Name
  - Institution and address
  - Telephone, fax and e-mail
  - Name and e-mail of contact person if other than PI
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### Project Analyst Information

Provide the name and affiliation of project analyst(s)

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### Co-Investigator / Collaborator Information

Provide the name and affiliation of major co-investigator(s) and collaborator(s)

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### Project Information

Provide information about the project including:

- Project title
- Whether the project has undergone previous peer review, and if so, by whom and the outcome of the review

- Whether this is a resubmission to CIDR, and if so, attach a 1-2 page cover letter addressing the criticisms from the previous review. Note: this cover letter does not count toward the page limit
  - Current and pending funding sources relevant to this project (provide NIH grant number if applicable)
  - If required, whether the project has been approved by the appropriate institute liaison
  - How genotyping costs will be paid if the project is not supported by one of the thirteen NIH supporting institutes
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## Sample Information

Provide information about the samples including:

- Approximate number of samples to be genotyped
  - Source of DNA and extraction method used. Note: approximately 4 µg of DNA is required at a concentration of 75-150 ng/ul. A higher concentration range is recommended for whole genome amplified samples
  - When samples will be available to ship to CIDR
  - Whether the project has animal care protection approval by an appropriate Institutional Animal Care and Use Committee, and if so, attach a copy of approval; if no, whether plans been made to obtain such approval. Note: samples will *not* be accepted until IACUC approval is received
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## Project Details

Provide details about the project including:

- Abstract
- Specific aims
- Description of disease/trait
  - Describe the disease/trait to be mapped, which must be a complete outline of the phenotypic evaluation of the study subjects, including, where appropriate, specific inclusion and exclusion criteria
  - Provide background information about the disease/trait to be mapped including the rationale for carrying out this particular study. Describe any unique features about the disease/trait that would single out this project for special consideration
- Strains - Provide the two strains involved in the cross. Include penetrance/expressivity information on the strains. Note: CIDR will use a standard 1,536 SNP linkage marker set or select an appropriate set of SNP markers and conduct a scan with an average inter-marker distance of 5-10 cM. The spacing will vary depending on the cross and could be as dense as 3 cM in some cases. It is incumbent on the applicant to propose a study that will have the power to map this trait using that marker density
- Evidence of genetic etiology - Provide evidence of a genetic component to the disease/trait. While this may be obvious with single gene disorders, it is not true for many complex traits
- Data management - Describe plans to manage the large number of genotypes. Provide specific information about computing resources and software, and the training and experience of personnel charged with database management
- Data analysis - Describe the analysis strategy for the resulting genotypic information. Include a discussion of the issue of power for the study, including power calculations where appropriate, and choice of analytic methods and software. If collaborations are established for analytical services with personnel at CIDR or otherwise, include letters of collaboration
- Plan for next phase - Provide the plan/strategy for the next phase of the project

**NOTE: Investigators using CIDR SNP linkage data to identify one or more linkage regions can request SNP fine mapping at CIDR immediately after analyzing their SNP linkage data. The CIDR Access Committee will conduct an expedited review to evaluate the linkage results and the plans for fine mapping and follow up studies. Applicants will be expected to provide information about the strength of the linkage signal(s), the SNP selection plan, the plans for data management and data analysis, and a detailed plan to follow up fine mapping and identify the genetic variant contributing to the phenotype, including molecular collaborators if required. More details can be provided at the time of the request**

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## Appendix

Include the following documents in the Appendix:

- Literature cited
  - CVs of key personnel in four-page, NIH format
  - Letters of support/commitment from major collaborators and/or co-investigators
  - Pedigree diagrams, if appropriate (indicate on the diagram if DNA samples are available for members of the pedigree)
  - Essential reprints or preprints
  - If required, documentation of institute liaison approval
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## Application Submission

Submit one original application and three complete copies, including appendices, to Dr. Camilla Day, Scientific Review Officer and Executive Director, CIDR Board of Governors, in the NHGRI Office of Scientific Review:

Camilla Day, Ph.D.  
Center for Inherited Disease Research (CIDR)  
Suite 4076 MSC 9306  
5635 Fishers Lane  
National Human Genome Research Institute  
National Institutes of Health  
Bethesda, MD 20892-9306  
*(Courier Services should use Rockville, MD 20852)*  
Telephone: (301) 402-8837  
FAX: (301) 435-1580  
[dayc@mail.nih.gov](mailto:dayc@mail.nih.gov)

At the time that you mail in your application, please send Dr. Day an e-mail message so that she will be looking for the application and can confirm receipt.

*Last Updated 02/04/2008*