

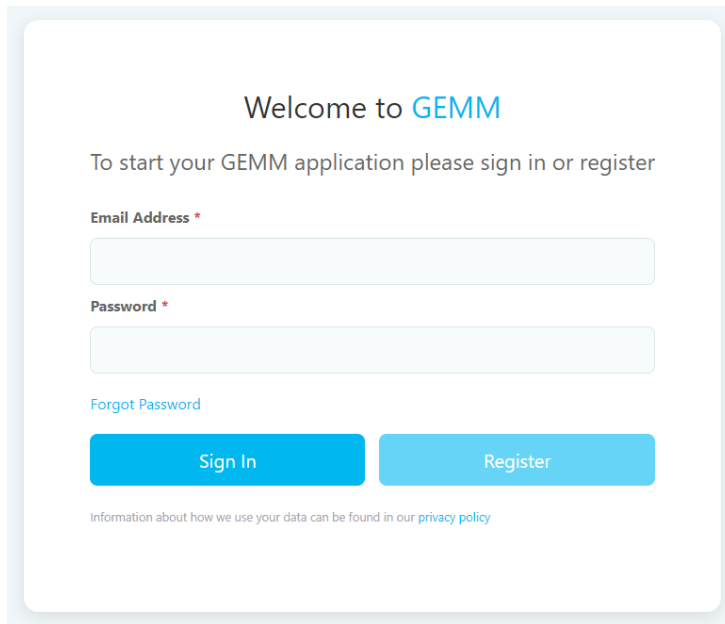
# Using the GEMM Applications System

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## Signing in

When you first access the GEMM portal, you will be presented with this login screen.

The image shows a login screen for the GEMM portal. It has a white background with a light blue border. At the top, it says "Welcome to GEMM" in black text, with "GEMM" in blue. Below that, it says "To start your GEMM application please sign in or register" in a smaller black font. There are two input fields: "Email Address \*" and "Password \*", both with red asterisks indicating they are required. Below the password field is a blue link that says "Forgot Password". At the bottom, there are two blue buttons: "Sign In" and "Register". At the very bottom, in small grey text, it says "Information about how we use your data can be found in our [privacy policy](#)".

Welcome to GEMM

To start your GEMM application please sign in or register

Email Address \*

Password \*

[Forgot Password](#)

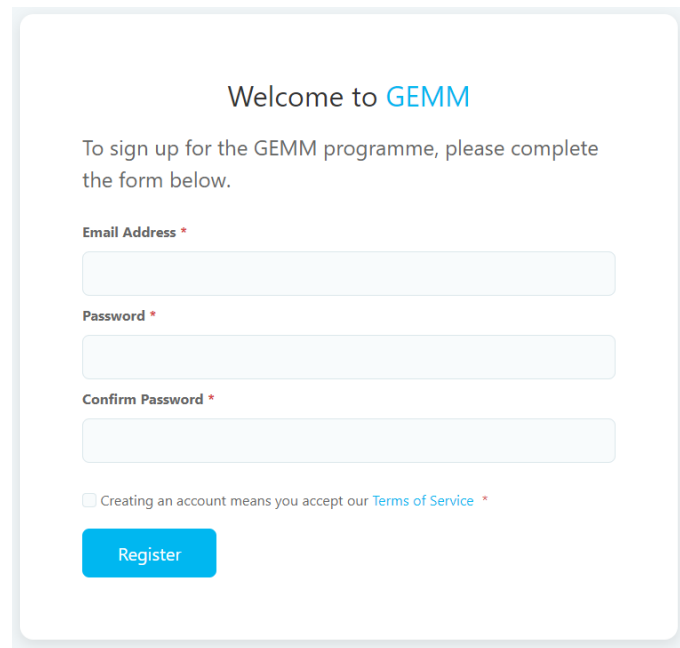
Sign In Register

Information about how we use your data can be found in our [privacy policy](#)

- If this is your first time accessing the GEMM portal, then click the registration link.
- If you already have a username and password, enter these to access your account.
  - If you've forgotten your details, click the "reset password" link.

## Registration

To register, simply fill out the form and submit it.

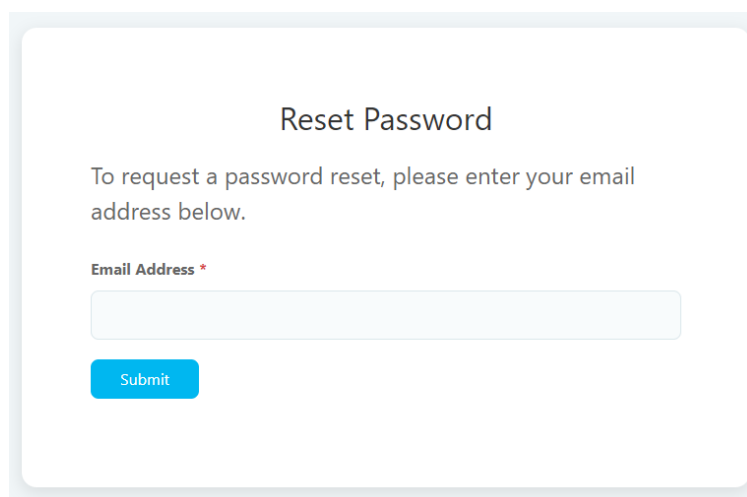


Registration form for GEMM. The form is titled "Welcome to GEMM" and instructs users to sign up for the GEMM programme by completing the form below. It includes three input fields: "Email Address \*", "Password \*", and "Confirm Password \*". Below the fields is a checkbox labeled "Creating an account means you accept our Terms of Service \*" and a blue "Register" button.

You will be returned to the login screen and should shortly receive an email containing a confirmation link. Click the link to confirm your registration.

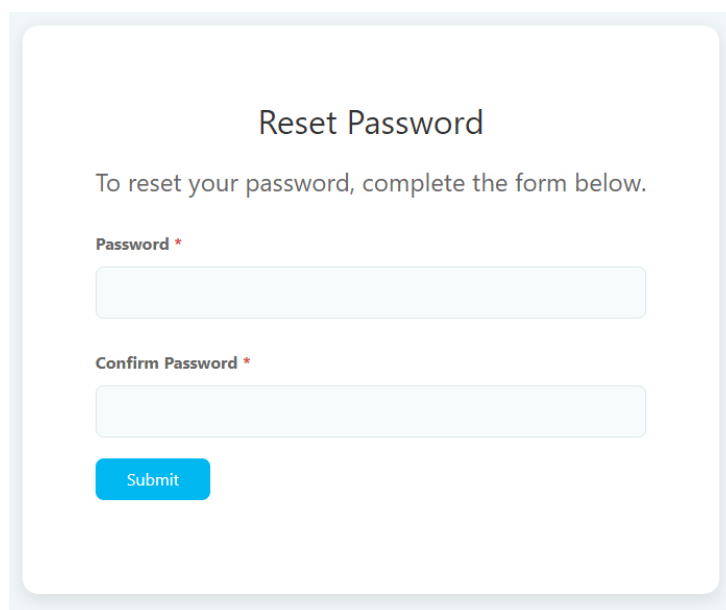
## Forgotten password

Following the 'forgotten password' link from the login page will take you to this simple form. Please enter your email address and if we have a record of it on our system, we will then email you a link.



Reset Password form. The form is titled "Reset Password" and instructs users to request a password reset by entering their email address below. It includes one input field: "Email Address \*" and a blue "Submit" button.

Click the link in the email to be taken to the below form, where you will need to enter and confirm your new password:

A screenshot of a 'Reset Password' form. The form is centered on a light blue background. It has a title 'Reset Password' at the top. Below the title is a instruction: 'To reset your password, complete the form below.' There are two input fields: the first is labeled 'Password \*' and the second is labeled 'Confirm Password \*'. Both fields are empty. Below the second field is a blue 'Submit' button.

Reset Password

To reset your password, complete the form below.

Password \*

Confirm Password \*

Submit

## Data Protection and opting-out

The information provided in this application will be shared with review panel members to enable its evaluation and subsequently with relevant members of staff to enable completion of successful projects. All data is managed in line with the General Data Protection Regulation.

Further information can be found in our privacy policy (<https://www.har.mrc.ac.uk/privacy-policy>).

However, if you wish to restrict, delete or block the cookies which are set by our website, or indeed any other website, you can do this through your browser settings. The 'Help' function within your browser should tell you how. This may however alter how the site performs. For further information or to request complete deletion of your records, please contact [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk).

## Creating a GEMM application

Once logged in, to create a new GEMM application, click the "New GEMM Call" link on the lefthand side (circled in red).

Menu

New Application

My Applications

Logout

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a.mccoy@har.mrc.ac.uk, here are your applications

Thank you for submitting your GEMM application. This table provides a view that will allow you to edit your application further as well as viewing the state of your applications.

Show 10 entries
Search:

Ref#	Date	Status	Gene Name & Type	Section					
2180	20-Oct-2020	✓ Sent	- Indel	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	...
2204	19-Nov-2020	Submit	Deletion test - Deletion	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	...
2206	19-Nov-2020	✓ Sent	Indel test - Indel	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	...
2207	19-Nov-2020	In-progress	Point Mutation test - Point Mutation	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	...
2208	19-Nov-2020	Submit	Conditional test - Conditional	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	...
2209	19-Nov-2020	Submit	Cassette test - Cassette	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	...

If completing the form in one go, there will be a 'Next section' button at the bottom of each page that will lead you through the application. Once the Nominee information has been filled in, all subsequent sections will allow you to return and edit them before submission. As such, it is possible to maintain a 'work-in-progress' application on the system. If completing the application over a series of occasions, each section will be accessed via the 'My calls' (circled in blue).

## Nominee

Enter the details of the applications' nominee. Name, address and Institution and how you heard about the GEMM call are required fields. Please attach a document detailing the nominee's CV (allowed file types are: txt, doc, docx, pdf). Files are only uploaded once the 'Next' button has been clicked. On returning to this section a green button entitled 'Remove File' will appear indicating file upload is successful. Note that uploading new files will not replace the ones that have already been uploaded.

Menu

New Application

My Applications

Logout

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1 Nominee
2 Collaborators
3 Gene Info
4 Research Outline
5 Specific Info

## Nominee

Please enter the information for the nominee of this GEMM call

Title and Full Name \*

Position \*

Please select an option

Email address \*

Phone number

Institution \*

Nominee CV

Attach files by dropping them here or [selecting one](#)

Allowed file types: txt, doc, docx, pdf

How did you hear about GEMM? \*

Please select an option

## Collaborators

Similar to the nominee screen, this is where you can enter details of additional collaborators on the application. If there are none, please press the 'Skip this Section'. In addition to the CV upload, collaborators can attach a letter of support outlining the impact of the proposed mouse line on their research (Allowed file types: txt, doc, docx, pdf, rtf). Files are only uploaded once the 'Next Section' button has been clicked. On returning to this section a green button entitled 'Remove File' will appear to the right-hand side of the file name indicating file upload is successful. Note that uploading new files will not replace the ones that have already been uploaded.

To add multiple collaborators, simply click “Add another collaborator” at the bottom of the page.

## Gene Info

Complete the fields as indicated.

The ‘Specific information’ sections to which you will be directed is dependent upon which type of mutation is selected on this page i.e. the fields for data capture are markedly different between different mutation types.

The five types of mutation/application types available are as follows:

- **Indel** interruption of coding sequence, exact outcome unspecified i.e. if wish to generate a stop codon or frameshift at an exact position then please fill in the Point Mutation form)
- **Deletion** (e.g. removal of exon or segment i.e. regulatory element)
- **Point Mutation** (specified nucleotide change, coding or otherwise)
- **Conditional** (region flanked by LoxP sites for excision upon crossing to Cre expressing line)
- **Cassette** (over-expression, tags, reporters)

Please note that once the application type has been selected (Indel, Deletion, Point mutation, Conditional, Cassette Knock-in) for an application, it cannot be changed. If you make a mistake on

this field, you will need to create a new application with the correct type specified. This can be done by using the grey 'Copy and add new Gene-Info' button to the right-hand side of the My GEMM Calls window and deleting the erroneous application.

Menu

- New Application
- My Applications
- Logout

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1 Nominee 2 Collaborators 3 Gene Info 4 Research Outline 5 Specific Info

### Gene Information - #2377

Application Type \*

Please select an option

Gene name (mouse)

Mutation or transgene name

Gene ID (MGI)

Expected Viability

Please select a Viability type

Please refer to the MGI website for the MGI id. This is a numerical value e.g. MGI:107799 and is found on the top right of the gene specific page.

Previous Next

Please visit <http://www.informatics.jax.org/> to get up to date mouse gene names (circled in red) and MGI gene ID (circled in blue). This website also has information re the viability of these genes as a note in the Mutations, Alleles and Phenotypes section of the relevant gene page.

Keywords, Symbols, or IDs Quick Search

Home Genes Phenotypes Human Disease Expression Recombinases Function Strains / SNPs Homology Pathways Tumors

Search Download More Resources Submit Data Find Mice (IMSR) Analysis Tools Contact Us

## Kcnj11 Gene Detail

Your Input Welcome

Summary

**Symbol Kcnj11**

Name potassium inwardly rectifying channel, subfamily J, member 11

Synonyms Kir6.2

Feature Type protein coding gene

IDs MGI:107501 NCBI Gene: 16514

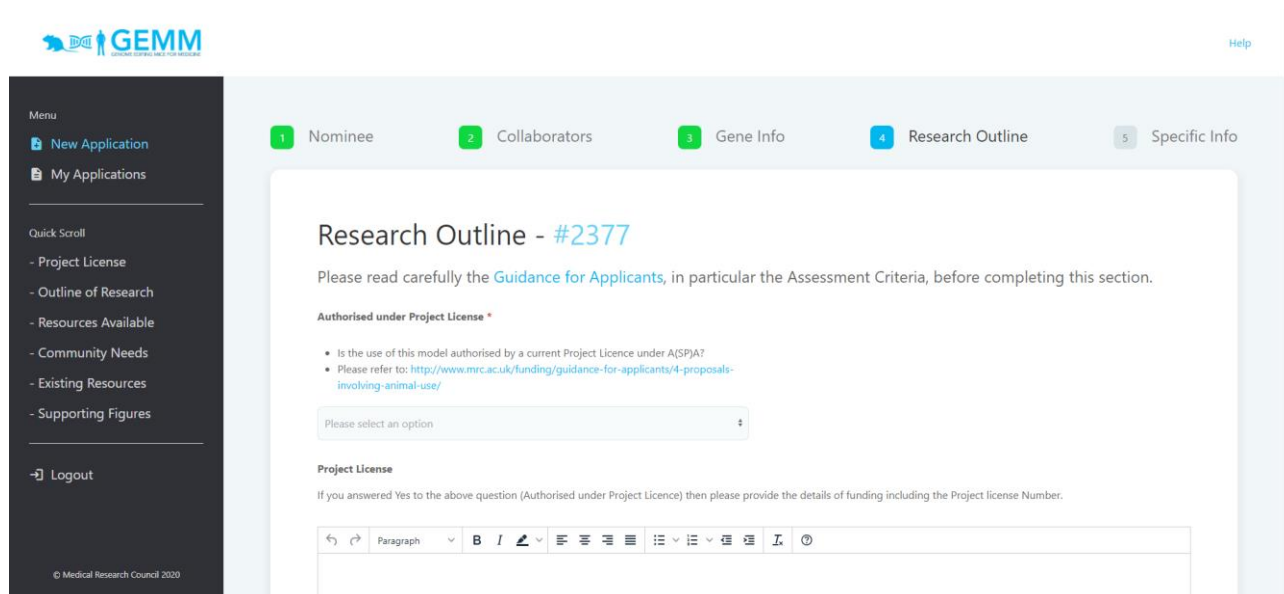
Gene Overview MyGene.info: KCNJ11

Alliance [gene page](#)



## Research Outline

This part of the application pertains to the nominee's experimental plans for the mouse line.



The screenshot displays the GEMM (Genetic Epidemiology Mouse Model) application interface. The top navigation bar includes a logo, a 'Help' link, and a progress indicator with five steps: 1. Nominee, 2. Collaborators, 3. Gene Info, 4. Research Outline (highlighted), and 5. Specific Info. A left sidebar menu contains options like 'New Application', 'My Applications', 'Quick Scroll', and 'Logout'. The main content area is titled 'Research Outline - #2377' and contains instructions to read the 'Guidance for Applicants'. It includes a section for 'Authorised under Project License' with a bulleted list of questions and a dropdown menu for selection. Below this is a 'Project License' section with a text area for details. A rich text editor toolbar is visible at the bottom of the form.

### Authorised under Project License

Required field, please answer Yes, No or N/A. Is the use of this model authorised by a current Project Licence under Animals (Scientific Procedures) Act?

Please refer to <http://www.mrc.ac.uk/funding/guidance-for-applicants/4-proposals-involving-animal-use/>

If you answered Yes to the above question (Authorised under Project Licence) then please provide the details of funding including the Project license Number. If you have any questions re this section, please email [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk).

### Outline of Research

Required field. Description of research involving proposed mouse line (including the potential to address important gaps in biomedical knowledge or/and answer important scientific questions, and why the mouse represents the best model).

For disease models, include evidence that the variant selected is robustly associated with disease/phenotype e.g. for GWAS studies include sample sizes and p values and/or evidence supporting the role of the gene selected in mediating the impact of the GWAS hit such as cis-eQTLs and/or independent coding variant associations in the same gene for example. (1000 words max)

### Resources Available

Description of the expertise, environment and resources in place to support the proposed experimental work. If existing funding is available, please provide details of the award. If it is not, please provide your plans for obtaining funding (approx. 500 words).

## Wider scientific community needs

How will this mouse line contribute to the wider scientific community needs (e.g. research or diagnostic tool, preclinical model etc) (approx. 500 words).

## Existing models/resources

Is this mouse model unique? Are there currently any mouse models which are suitable for the proposed research? (250 words max)

## Supporting Figures

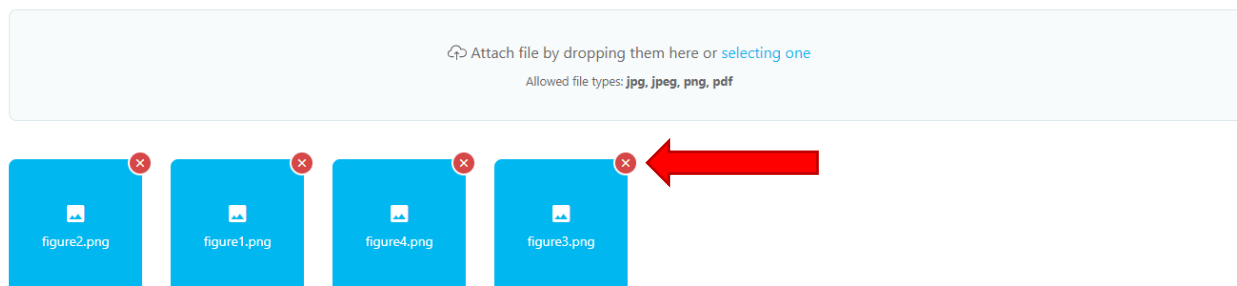
Attach image(s) to support your application. Files must be less than 10 MB.

Allowed file types: jpeg png pdf tif tiff. Please provide a description of the attached images.

You can attach multiple files here – specifics on how this is done will vary depending on the web browser you are using. Multiple files can be uploaded in a single action. To upload multiple files on a series of different occasions you must press the 'save' button to ensure the file is captured. Once the file is uploaded, a green button entitled 'Remove File' (indicated by red arrow below) will appear to the right-hand side of the file name indicating file upload is successful. If you return to this page at a later date, you will see a list of the files that you have already uploaded and will be able to remove them if necessary. Note that uploading new files will not replace the ones that have already been uploaded.

### Supporting Figures

Attach image(s) to support your application



## Specific Information

This section is to capture the details of the genetic modification you wish to introduce into the mouse genome at the sequence level. This information is used to assess feasibility of each project so please complete as fully as possible. Please direct any queries regarding this section to [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk). The options displayed in this section depends on which application type you selected on the Gene Information screen.

If you are applying to model a human allele/mutation, please provide supporting information/data on the following (or explain why these approaches might not be relevant/possible for your studies)

- Further human genetic studies (additional families etc)
- Cell-based assays

- c. Human derived tissue
- d. *In-silico* studies

The majority of inputs in these forms are free text boxes, but there is also capacity to upload schematics of the allele you wish to nominate. Example screenshots of each application type are below, but each page will also provide additional information for the five types of modification:

- **Indel** (interruption of coding sequence, exact outcome unspecified i.e. if wish to generate a stop codon at an exact position then please fill in the Point Mutation form)
- **Deletion** (e.g. removal of exon or segment i.e. regulatory element)
- **Point Mutation** (specified nucleotide change, coding or otherwise)
- **Conditional** (region flanked by LoxP sites for excision upon crossing to Cre expressing line)
- **Cassette** (over-expression, tags, reporters)

PLEASE NOTE: Different types of mutation require different data in order for the panel to make a feasibility assessment of the model to be made. As such, please take care to use the appropriate application type for your model, and please email [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk) if you require clarification as the form most appropriate for your nomination. Please see 'Creating Further Applications' section if you need to edit the Application type of an ongoing application.

The screenshot displays the GEMM web application interface. On the left is a dark sidebar with a 'Menu' section containing 'New Application', 'My Applications', and 'Logout'. The top right corner has a 'Help' link. The main area features a progress bar with five steps: 1. Nominee, 2. Collaborators, 3. Gene Info (highlighted in blue), 4. Research Outline, and 5. Specific Info. Below the progress bar is the 'Gene Information - #2377' form. The 'Application Type \*' dropdown menu is circled in red. Other form fields include 'Gene name (mouse)', 'Mutation or transgene name', 'Gene ID (MGI)', and 'Expected Viability'. A note at the bottom of the form reads: 'Please refer to the MGI website for the MGI id. This is a numerical value e.g. MGI:107799 and is found on the top right of the gene specific page.' At the bottom of the form are 'Previous' and 'Next' buttons.

## Indel Specific Information

The screenshot shows the GEMM web application interface. On the left is a dark sidebar menu with options: 'Menu', 'New Application', 'My Applications', 'Quick Scroll' (with sub-items: Genetic Background, Ensembl Version, Wildtype Sequence, Disrupted Region, Additional Notes), and 'Logout'. At the bottom of the sidebar is '© Medical Research Council 2020'. The top navigation bar has five steps: 1. Nominee, 2. Collaborators, 3. Gene Info, 4. Research Outline, and 5. Specific Info (highlighted in blue). The main content area is titled 'Specific Information - #2377'. Below the title is a paragraph: 'This section is to capture the details of the genetic modification you wish to introduce into the mouse genome at the sequence level. This information is used to assess feasibility of each project so please complete as fully as possible. Please direct any queries regarding this section to [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk)'. There are three form fields: 'Genetic Background' (a dropdown menu showing 'C57BL/6N'), 'Ensembl version' (a text input field), and 'Wildtype nucleotide sequence' (a text area with a note: '250 bp either side of region to be disrupted' and '1000 characters maximum.'). Below the text area is a rich text editor toolbar with various icons for text formatting and alignment.

Additional fields in this section include:

### Genetic Background

Required Field. Drop down box with following options:

C57BL/6N

C57BL/6J

129S9(/SvEV)

C3H.PDE

### Wildtype nucleotide sequence Required

Field.

- 250 bp either side of region to be disrupted
- 1000 characters max.

### Region to be disrupted

Required Field. This is the region in which we will search for guides which will be used to introduce a double stranded break repaired by non-homologous end joining.

- The region to search for possible guide sequences i.e. the region to target with sgRNAs.
- 1000 characters max.

### Additional Notes

Please add any additional information pertaining to the application here e.g. indel to cause frameshift after amino acid 240.

## Deletion Specific Information

The screenshot shows the GEMM web application interface. On the left is a dark sidebar menu with options: 'Menu', 'New Application', 'My Applications', 'Quick Scroll' (with sub-items: Genetic Background, Deletion Size, Wildtype Sequence, Deleted Sequence, Deleted Exons, Additional Notes), and 'Logout'. The main content area has a top navigation bar with five tabs: '1 Nominee', '2 Collaborators', '3 Gene Info', '4 Research Outline', and '5 Specific Info' (which is active). The 'Specific Information - #2308' section contains a text box with instructions: 'This section is to capture the details of the genetic modification you wish to introduce into the mouse genome at the sequence level. This information is used to assess feasibility of each project so please complete as fully as possible. Please direct any queries regarding this section to [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk)'. Below this are three form fields: 'Genetic Background' (a dropdown menu showing 'C57BL/6N'), 'Deletion size (base pairs)' (a text input field), and 'Wildtype nucleotide sequence' (a text input field with a note: 'Pre-modification nucleotide genomic sequence from relevant background, (at least 500 bp flanking either side of desired modification)'). At the bottom is a rich text editor toolbar with various icons for text formatting and alignment.

Nominations for deletions are not restricted to protein coding elements e.g. for deletions of regulatory elements, enhancer regions, silencers etc. are all permitted. Fields in this section include:

### Genetic Background

Required Field. Drop down box with following options:

C57BL/6N

C57BL/6J

129S9(/SvEV)

C3H.PDE

### Deletion size

Please specify the size of the region you wish to delete e.g. 20 bp.

### Wildtype nucleotide sequence

Required Field

Pre-modification nucleotide genomic sequence from relevant background, (at least 500 bp flanking either side of desired modification)

### Sequence to be deleted

Required Field

- Please indicate the sequence from the wild type sequence, submitted above, that should be removed.

**Exon(s) to be deleted**

If exon(s) are to be deleted, please enter a comma separated list of Ensembl IDs. Please refer to the Ensembl website for the Ensembl IDs ([http://www.ensembl.org/Mus\\_musculus/Info/Index](http://www.ensembl.org/Mus_musculus/Info/Index)).

[illegible]

## Additional Notes

Please add any additional information pertaining to the application here e.g. 'Deletions slightly larger or smaller (approx. 10 bp) than the 854 bp deletion proposed would be acceptable'.

## Point Mutation Specific Information

The screenshot shows the GEMM web application interface. On the left is a dark sidebar menu with options: 'Menu', 'New Application', 'My Applications', 'Quick Scroll' (with sub-items: Genetic Background, Pre-mod Genome, Pre-mod Protein, Post-mod Genome, Post-mod Protein, Genotyping requirement, NHEJ event, Additional Notes), and 'Logout'. The main content area is titled 'Specific Information - #2212'. It contains a paragraph explaining the purpose of the section and a list of options for modeling a human allele/mutation: 'a. Further human genetic studies (additional families etc)', 'b. Cell-based assays', 'c. Human derived tissue', and 'd. In silico studies'. Below this is a 'Genetic Background' dropdown menu with 'C57BL/6N' selected. Underneath is a text area for 'Pre-modification nucleotide genomic sequence from specified background' with a 1000-character limit. At the bottom is a rich text editor toolbar with various formatting options.

Fields in this section include:

### Genetic Background

Required Field. Drop down box with following options:

C57BL/6N

C57BL/6J

129S9(/SvEV)

C3H.PDE

### Pre-modification nucleotide genomic sequence from specified background

- Required Field
- 1000 characters max.

### Pre-modification protein sequence from relevant background

(if modification is in coding sequence, 1 letter code)

### Post-modification nucleotide genomic sequence

- Required Field
- Post-modification nucleotide genomic sequence from relevant background, (at least 250 bp flanking either side of desired modification)
- 1000 characters max.

### Post-modification protein sequence from relevant background

(if modification is in coding sequence, 1 letter code)

**Genotyping requirement**

Genotyping requirement (i.e. introduction of a restriction site) Please note, the inclusion of further modifications to facilitate genotyping is not always possible to achieve.

**NHEJ event**

The process of generating point mutations generally also yields other variants e.g. indels. Please specify if these are also of interest to you. Drop down box with following options:

- Yes, please keep the variants
- Only keep frame-shift variants
- No, I am only interested in this point mutation

**Additional Notes**

Please use this box to input details/data supporting the generation of the mouse i.e. GWAS data.



## Conditional Specific Information

The screenshot shows the GEMM web application interface. On the left is a dark sidebar menu with options: 'Menu', 'New Application', 'My Applications', 'Quick Scroll' (with sub-items: 'Ensembl Version', 'Allele Type', 'Target Sequence', 'Additional Notes'), and 'Logout'. The main content area has a top navigation bar with five tabs: '1 Nominee', '2 Collaborators', '3 Gene Info', '4 Research Outline', and '5 Specific Info' (which is active). The 'Specific Info' section is titled 'Specific Information - #2208'. It contains a text block explaining the purpose of the section and providing the email [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk). Below this are three form fields: 'Ensembl version' (a text input), 'Type of allele \*' (a dropdown menu with 'Conditional i.e. floxed' selected), and 'Target Sequence' (a text input). A small note at the bottom of the 'Target Sequence' field states: 'Target sequence to be flanked by loxP sites (at least 500 bp sequence). Please mark as unknown if support is required to select a critical region to be floxed or email [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk) for support.'

Fields in this section include:

### Ensembl version

### Type of allele

Required Field

Choose from Conditional (i.e. floxed), Tm1a, Tm1b, Tm1c, Tm1d. For detailed explanation of Tm1a-d alleles, please refer to <https://www.nature.com/articles/nature10163> )

### Target Sequence

Target sequence to be flanked by loxP sites (at least 500 bp sequence). Please mark as unknown if support is required to select a critical region to be floxed or email [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk) for support.

### Additional Notes

Please provide any additional information that pertains to the design of this nominated allele.

## Cassette Specific Information

Menu

- New Application
- My Applications

Quick Scroll

- Target Sequence
- Knock-In Cassette
- Knock-In Sequence
- Additional Notes
- Figures

Logout

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1 Nominee 2 Collaborators 3 Gene Info 4 Research Outline 5 Specific Info

### Specific Information - #2209

This section is to capture the details of the genetic modification you wish to introduce into the mouse genome at the sequence level. This information is used to assess feasibility of each project so please complete as fully as possible. Please direct any queries regarding this section to [gemm@har.mrc.ac.uk](mailto:gemm@har.mrc.ac.uk)

Ensembl version

Target Sequence \*

Target sequence (at least 500 bp sequence)

Paragraph B I Paragraph

Fields in this section include:

### Ensembl Version

### Target Sequence

Required Field.

Target sequence (at least 500 bp sequence)

### Cassette to knock in

Required Field.

Choose from Cre, Cre-ert2, Flpo, GFP or Other. If selecting Other, please specify further in the Sequence to knock in section below.

### Sequence to knock in

Please provide coding sequence or name of standard cassette.

### Additional Notes

### Figure/Vector Map

Please add a schematic of the genetic modification you would like to achieve.

Files must be less than 10 MB.

Allowed file types: jpeg png pdf tif tiff svg.

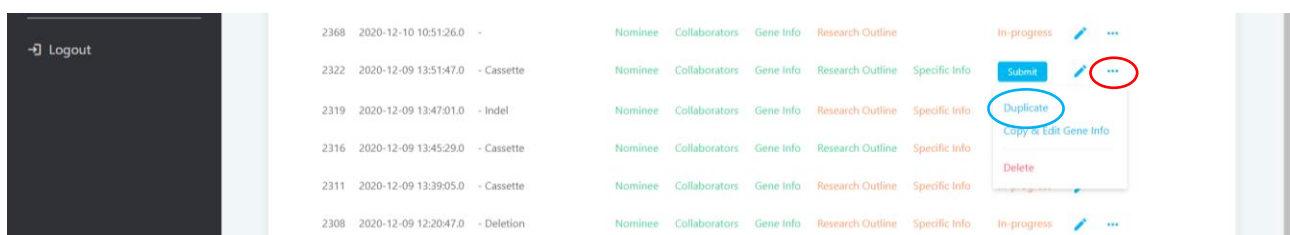
Once the file is uploaded, a green button entitled 'Remove File' (indicated by red arrow below) will appear to the right-hand side of the file name indicating file upload is successful. If you return to this page at a later date, you will see the file that you have already uploaded and will be able to

remove them if necessary. Note that uploading new files will not replace the ones that have already been uploaded.

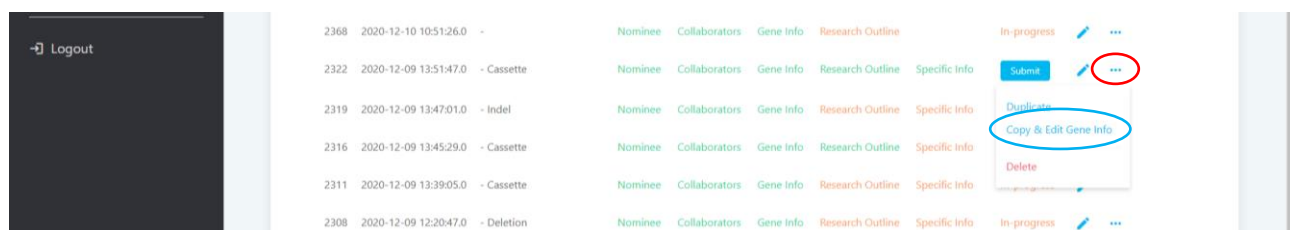
## Creating Further Applications

You can, of course, always create another application from scratch by using the New GEMM Call link on the left-hand navigation bar.

However, if you wish to submit multiple applications of the same type i.e. multiple point mutation nominations, you can use the 'Duplicate' button in the Functions column. This will create another copy of a prior application, then use the Edit buttons under the Gene Info, Research Outline and Specific-Info columns to return to those pages and make necessary edits.



If you want to submit another application of a different type, use the “Copy and add new Gene Info” button – this will allow you to change the type of the duplicated record, but as a result, the Specific Information section will not be copied.



## Deleting Applications

If, for any reason, you need to remove your application, just find the application in the “My Calls” page and click the red Delete button. Note that once you do this **IT CANNOT BE RECOVERED**, so if you delete an application in error, you will need to recreate it manually.

Logout	2368	2020-12-10 10:51:26.0	-	Nominee	Collaborators	Gene Info	Research Outline	In-progress	...
	2322	2020-12-09 13:51:47.0	- Cassette	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	Submit
	2319	2020-12-09 13:47:01.0	- Indel	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	Duplicate
	2316	2020-12-09 13:45:29.0	- Cassette	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	Copy & Edit Gene Info
	2311	2020-12-09 13:39:05.0	- Cassette	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	Delete
	2308	2020-12-09 12:20:47.0	- Deletion	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	In-progress

## Submission, reports and downloading your full application

Once you have completed all the required fields on your application, the “My GEMM Calls” page status column will change from “In-progress” to “Submit” (see red circle). Click this green Submit box to submit your application – note that no further changes will be possible once this is done. Once submitted, your application will be marked as ‘Sent’ in the status column (see green circle). Nominees will receive and emailed a summary version of the submitted nomination. Whilst the call is live, nominees will also be able to create a PDF report of the submitted application under the ‘Functions’ column using the ‘PDF Report’ button (see blue arrow).

	2283	2020-12-09 09:36:11.0	Furin - Cassette	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	In-progress	...
	2217	2020-11-27 16:16:34.0	Indel test - Deletion	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	✓ Sent	...
	2213	2020-11-19 13:49:26.0	- Conditional	Nominee	Collaborators	Gene Info	Research Outline	Specific Info	Submit	...

**PLEASE NOTE:** The emailed version does not contain each of the attachments and figures as the PDF building facility requires some time to assemble additional files to the application. To ensure that nominees can check their full submission and keep a record, it is recommended that nominees use the ‘PDF Report button’ to generate their own PDF after submission.