

## Grant write permission to the directory within your labs CRC space

### (Contact your administrator to request access to the CRC space)

Illumina sequencing data is deposited into Notre Dame CRC for transfer to your CRC space. We recommend that the PI establishes a general-purpose called "incoming\_seq\_data" subdirectory within a CRC group space to receive raw data and related files from the Genomics & Bioinformatics Core Facility. Group space has significant benefits over individual CRC space. First, both the PI and laboratory members (with permission) may access the files. Additionally, group space is much larger than individual user space, which is more suited for post-processing and analysis. If your PI would like to establish a group space to receive Illumina data, we can point you in the right direction to get that set up.

Our staff will need permission to read and write to the destination of choice. Instructions of how to grant access and permission are outlined below. Once we have confirmed access, our staff will write your Illumina to subdirectory directory identifiable by a "run ID". After transfer is complete, our staff will send a notification via iLab comment or directly by email. We ask that you immediately review the integrity of the data files and report any irregularity so that we may address it promptly. The Genomics Core will maintain a copy of your Illumina data 30-days post share in the event there is an issue with the file. Illumina data of future projects would be deposited by the same process by the staff member with permission to access the space.

**Comment:** <user\_netID> is the netID of the individual you would like to grant permission to access and copy files to your directory.

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<text> type the information needed without the "< >" surrounding the text such as a pathway, directory, or netID

### Description

Code

example

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### Log into CRC

1. **Log into CRC**  
[https://docs.crc.nd.edu/new\\_user/quick\\_start.html](https://docs.crc.nd.edu/new_user/quick_start.html)  
[https://docs.crc.nd.edu/new\\_user/connecting\\_to\\_crc.html](https://docs.crc.nd.edu/new_user/connecting_to_crc.html)

### Create incoming seq data directory

2. **Change to directory**  
cd <pathway>  
example: cd /afs/crc.nd.edu/group/Your-Lab-Space/
3. **make a new directory**  
mkdir <directory>  
example: mkdir incoming\_seq\_data

Grant permission to access the group space

4. **file system/server set access command**

```
fs sa <pathway> <user_netID> <permissions>
```

example: fs sa /afs/crc.nd.edu/group/Your-Lab-Space/ bharker l

Set permission to subdirectory

5. **Change to directory**

```
cd <directory>
```

example: cd incoming\_seq\_data

6. **File system/server set permission**

```
fs setacl -dir . -acl <user_ID> <permissions>
```

example: fs setacl -dir . -acl bharker rldkwa

Print the full pathway on screen to copy and paste into "iLab comment" to Genomics staff

7. **Print working directory to display the full pathway on the screen**

```
pwd
```

example: /afs/crc.nd.edu/group/Your-Lab-Space/incoming\_seq\_data

The full pathway to the newly created directory appears in the window. Share the pathway with the Genomics and Bioinformatics staff by adding a "comment" to your iLab service request.

Grant access and permission to existing "incoming seq data" subfolder to additional users.

8. **Repeat steps 1 through 7 BUT skip step 3 as there is no need to make a new subdirectory.**