

A close-up photograph of a network switch or patch panel. Numerous white Ethernet cables are plugged into the ports, with some yellow and blue cables also visible. Many of the ports have small yellow indicator lights that are illuminated. The cables are bundled together, and some have white labels attached to them. The background is dark, making the cables and lights stand out.

# Illumina BaseSpace

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Stella Esther Nabirye

# About illumina BaseSpace

BaseSpace: Platform for storage, analysis  
and sharing genetic data



Monitor  
and check  
the quality  
of your Run

Sequencing  
data is  
uploaded to  
BaseSpace and  
becomes a Run

Runs (.bcl) files  
are demultiplexed  
into Samples  
(.FASTq) files

**Sequencing**



**Upload to  
BaseSpace**

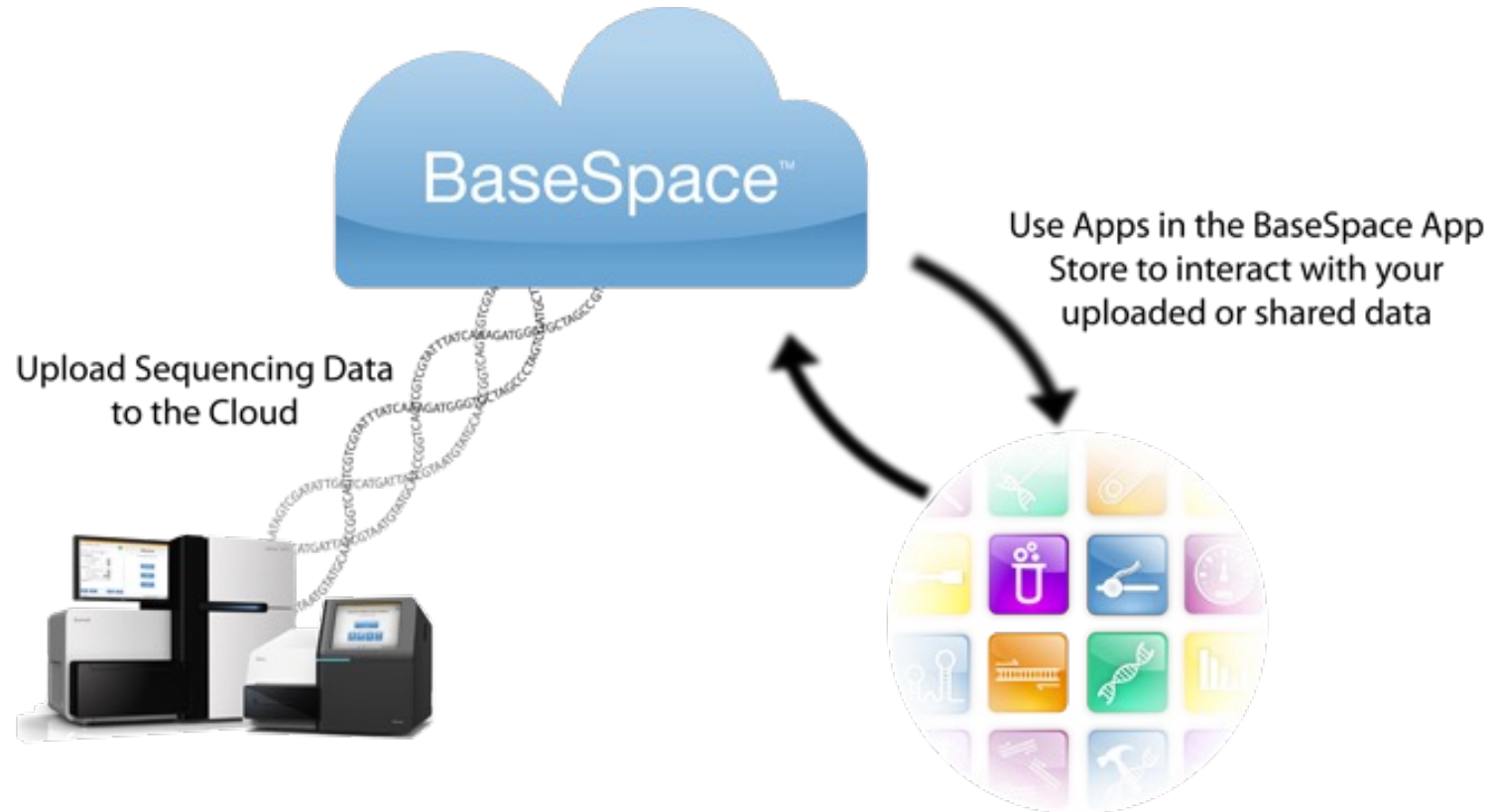
**Runs - .bcl**

**Demultiplexing**



**Samples - .FASTq**

# About Illumina BaseSpace



The logo for BaseSpace Sequence Hub is a green circle with a white border and a white highlight on the left side. Inside the circle, the text "BaseSpace" and "Sequence Hub" are written in white, stacked vertically.

# BaseSpace Sequence Hub



- Enables data management and simplified Bioinformatics for labs getting started and for rapidly scaling NGS operations
- Key Features:
  - Secure
  - Tight instrument Integration
  - Easy sharing and collaboration
  - Public and Private analysis Tools
  - Advanced automation and integration

# Using Base Space sequence hub

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Illumina BaseSpace account required

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Currency is icredits

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Free trial for 30 days – 250 icredits

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Apps – Some free / Some require icredits

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Storage – 1TB available free. Payment for additional storage









# BaseSpace Sequence Hub Interface

The screenshot displays the BaseSpace Sequence Hub interface. At the top, the Illumina logo is on the left, and 'SEQUENCE HUB' is centered. On the right, the user's name 'Stella Esther Na...' is shown next to a profile icon and a grid icon. Below this, a navigation bar contains a search icon, 'HOME', 'RUNS', 'BIOSAMPLES', 'PROJECTS', 'ANALYSES', 'APPS', 'DEMO DATA', a bell icon, a help icon, and a trash icon with a notification badge '83'. The main content area has a purple header with the text 'Hello Stella Esther Nabirye'. Below this is a white box with the message: 'Everything is looking good so far today. Check back later for any incoming items.' The 'Run Insights' section follows, featuring three dropdown filters: 'Sequencing Platform' (No Platforms), 'Instruments' (No Instruments), and 'Sequencing Kits' (No Sequencing Kits). Below the filters are columns for 'Yield', '%>=Q30', '%PF', and '%Aligned to PhiX'. On the right side of this section are time range filters: '1W', '1M', '3M' (selected), '6M', and '12M'. At the bottom left, a chart area is partially visible with a '1 Gbp' label.

<https://basespace.illumina.com/dashboard>


# BaseSpace Sequence Hub Apps


SEQUENCE HUBStella Esther N...


QHOMERUNSBIOSAMPLESPROJECTSANALYSESA**PPS**DEMO DATA


## Accurate, comprehensive, and efficient secondary analysis with DRAGEN


Illumina **DRAGEN** apps provide pushbutton capabilities within BaseSpace Sequence Hub's intuitive and secure environment.

DRAGEN Germline  
Illumina, Inc.

DRAGEN Enrichment  
Illumina, Inc.


DRAGEN Somatic  
Illumina, Inc.



DRAGEN RNA  
Illumina, Inc.







Search Apps



Q



DRAGEN (28) 



DRAGEN Amplicon  
Illumina, Inc. 


DRAGEN Baseline Builder  
Illumina, Inc. 


DRAGEN CNV Baseline Buil...  
BaseSpace Labs 

DRAGEN COVID Lineage  
BaseSpace Labs 

DRAGEN COVIDSeq Test (R...  
Illumina, Inc. 

DRAGEN Differential Expre...  
BaseSpace Labs 

[App Developer Portal](#)

**Bookmarks Empty**  
Get started by bookmarking apps you  
regularly use.


# Getting Started: Install

BaseSpace® **developers**

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Community

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Stella Esther N....

illumina®

## BASESPACE SEQUENCE HUB CLI

Install BaseSpace Sequence  
Hub CLI

- Install:
- Authenticate

Command Structure

Command Summary

Command Discovery

## COMMAND REFERENCE

- Entities and sub-entities

Standalone Commands

- Authenticate

Enterprise Domains & Workgroups

Specify API server and  
Access Token

Scopes

- Whoami

Entity Reference

[Home](#) / [Documentation](#) / CLI Overview

## BaseSpace Sequence Hub CLI

You can work with your BaseSpace Sequence Hub data using the command line interface (CLI). The BaseSpace Sequence Hub CLI supports scripting and programmatic access to BaseSpace Sequence Hub for automation, bulk operations, and other routine functions. It can be used independently or in conjunction with BaseMount.

The BaseSpace Sequence Hub CLI has been updated to support automation features in the latest BaseSpace Sequence Hub.

To see the overall capabilities of the CLI and to help you get started post-installation, we recommend you use the [Worked Examples](#).

## Install BaseSpace Sequence Hub CLI

The BaseSpace Sequence Hub CLI is supported on Linux, Mac, and Windows (32 and 64 bit). It carries a small memory footprint, but for safety it should be installed on a machine with at least 1GB RAM.

For information on the most recent version of BaseSpace Sequence Hub CLI see [Release Notes](#).

### Install:

You can download the latest CLI release using your web browser, the latest release version is: **latest 1.5.3**

- [Mac OS X](#)
- [Linux](#)
- [Windows](#)

feedback



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# Using the BS CLI file

1. Log into your Basespace account
  2. Go to the projects tab, and create a new project.
  3. Once done, log out of Basespace.
  4. Download the BS CLI file from  
<https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-overview>.
  5. Create a new folder on your computer, and save the bs.exe (downloaded in step 4) in this new folder.
  6. Save all your FASTQ files in the same folder.
  7. Open the command prompt in Windows
  8. Change the directory to where the bs.exe file is saved by typing in `cd <file path>`
-

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# Using the BS CLI file

9. Authorize your basespace account as follow:

```
stella-nabirye@latitude:~/Desktop/VSP_Fastq$ bs auth
```

Please go to this URL to authenticate:

<https://basespace.illumina.com/oauth/device?code=HbTQF>

Welcome, Stella Esther Nabirye

10. Copy and paste the URL from above into your web browser and login to your Basespace account to allow BS CLI access to it.

11. Confirm the account is correct by typing in the following:

```
stella-nabirye@latitude:~/Desktop/VSP_Fastq$ bs whoami
```

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## Using the BS CLI file

12. Confirm the projects available in Basespace and obtain the ID for the project that will be used for your FASTQ upload.

**\$ bs list project**

13. Finally, type in the command below to upload the FASTQ files.

**\$ bs upload dataset -p <project ID> --recursive <pathway for folder where fastq files are saved>**

Example: **\$ bs upload dataset -p 366512146 --recursive  
/home/stella-nabirye/Desktop/VSP\_Fastq**

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# Pipelines for VSP data analysis



**Illumina DRAGEN Metagenomics**



**Illumina DRAGEN Microbial  
Enrichment**

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# References

<https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-overview>

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