

BaseSpace™ Sequence Hub Apps Quick Guide




Get a variety of low-cost data analysis apps with BaseSpace Sequence Hub services. All services and DRAGEN™ apps are priced in iCredits. [Learn more.](#)

Quick links







Click on any of the application areas below to quickly view each section.







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| Data Handling, Data Quality Control (QC), and Data Visualization. | Page 4 |
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Biomedical and Basic Research – Genetic Analysis







| App name | Sequencing application(s) | Key functionality | Vendor |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|  DRAGEN Enrichment Demo Data Link | <ul style="list-style-type: none"> • Whole-exome sequencing • Targeted Resequencing | <ul style="list-style-type: none"> • Alignment • Small Variant Calling • Somatic Variant Calling • SV/CNV Calling • Custom Manifest Files | Illumina, Inc. Compute Cost: 2 iCredits per node/hr License Cost: n/a Example Compute Cost: FASTQ to SNVs only 88M reads, 2 x 150 bp Analysis cost = 2.50 iCredits/sample |
|  DRAGEN Germline Demo Data Link | <ul style="list-style-type: none"> • Whole-genome sequencing • Whole-exome sequencing | <ul style="list-style-type: none"> • Alignment • Small variant calling • CNV calling • Somatic variant calling | Illumina, Inc. Compute cost: 7 iCredits per node/hr License cost: n/a Example compute cost: FASTQ to SNVs only 88M reads, 2 x 150 bp Analysis cost = 2.50 iCredits/sample |
|  DRAGEN Joint Genotyping Pipeline Demo Data Link | <ul style="list-style-type: none"> • <i>De novo</i> variant calling | <ul style="list-style-type: none"> • Novel variant identification | Illumina, Inc. Compute cost: 5 iCredits per node/hr License cost: n/a Example compute cost: Input: Trio of gVCFs processed with DRAGEN Germline Analysis cost = 1 iCredits/sample |

Biomedical and Basic Research – Genetic Analysis (continued)





| App name | Sequencing application(s) | Key functionality | Vendor |
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|  <p>DRAGEN Somatic Pipeline Demo Data Link</p> | <ul style="list-style-type: none"> • Whole-genome sequencing • Whole-exome sequencing | <ul style="list-style-type: none"> • Alignment • Somatic variant calling • Tumor-normal and tumor-only analysis | <p>Illumina, Inc.</p> <p>Compute cost: 5 iCredits per node/hr License cost: n/a Example compute cost: 4,750M reads, 2 x 150 bp Analysis cost = 13 iCredits/sample</p> |
|  <p>BWA Aligner Demo Data Link</p> | <ul style="list-style-type: none"> • Whole-genome sequencing • Targeted sequencing | <ul style="list-style-type: none"> • Alignment • Custom reference genome • Batch processing | <p>BaseSpace Labs basespacelabs@illumina.com</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 0.72M reads, 2 x 150 bp Analysis cost = 2 iCredits/sample</p> |
|  <p>DNA Amplicon Demo Data Link 1 Demo Data Link 2</p> | <ul style="list-style-type: none"> • Targeted resequencing (AmpliSeq™ for Illumina) | <ul style="list-style-type: none"> • Alignment • Small variant calling • Annotation | <p>Illumina, Inc.</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: -0.72M reads, 2 x 150 bp Analysis cost = 2 iCredits/sample</p> |
|  <p>EDGC Annotator</p> | <ul style="list-style-type: none"> • Targeted Resequencing | <ul style="list-style-type: none"> • Variant Annotation • Variant Analysis | <p>EONE-DIAGNOMICS Genome Center www.edgc.com/edgcannotator?lang=en</p> <p>Compute Cost: 3 iCredits per node/hr License Cost: n/a</p> |
|  <p>OncoCNV Trainer Demo Data Link</p> | <ul style="list-style-type: none"> • Targeted resequencing (AmpliSeq™ for Illumina) | <ul style="list-style-type: none"> • CNV calling | <p>BaseSpace Labs basespacelabs@illumina.com</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 18M reads, 2 x 150 bp Analysis cost = 1 iCredits/sample</p> |
|  <p>OncoCNV Caller Demo Data Link</p> | <ul style="list-style-type: none"> • Targeted resequencing (AmpliSeq™ for Illumina) | <ul style="list-style-type: none"> • CNV calling | <p>BaseSpace Labs basespacelabs@illumina.com</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 18M reads, 2 x 150 bp Analysis cost = 1.5 iCredits/sample</p> |

| Biomedical and Basic Research – Genetic Analysis (continued) | | | |
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| App name | Sequencing application(s) | Key functionality | Vendor |
|  <p>Pindel Demo Data Link</p> | <ul style="list-style-type: none"> Targeted resequencing (AmpliSeq™ for Illumina) | <ul style="list-style-type: none"> Insertion and deletion breakpoint detection | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 4.1M reads, 2 x 150 bp Analysis cost = 1 iCredits/sample</p> |
|  <p>Pisces Variant Caller Demo Data Link</p> | <ul style="list-style-type: none"> Targeted resequencing | <ul style="list-style-type: none"> Low-frequency somatic variant detection | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 7M reads, 2 x 150 bp Analysis cost = 3 iCredits/sample</p> |
|  <p>TruSeq® Amplicon Demo Data Link</p> | <ul style="list-style-type: none"> Targeted resequencing | <ul style="list-style-type: none"> Alignment Small variant calling Somatic variant calling Annotation Custom manifest files Batch processing | <p>Illumina, Inc. Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: TruSight Myeloid Panel (5000x mean coverage) 2.35M reads, 2 x 150 bp Analysis cost = 0.78 iCredits/sample</p> |
|  <p>TruSight Tumor 15 Demo Data Link</p> | <ul style="list-style-type: none"> Targeted resequencing (TruSight Tumor 15 Panel) | <ul style="list-style-type: none"> Alignment Variant calling | <p>Illumina, Inc. Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: TruSight Tumor 15 Panel (5000x mean coverage) 733K reads, 2 x 150 bp Analysis cost = 0.35 iCredits/sample</p> |
|  <p>TruSight Tumor 170</p> | <ul style="list-style-type: none"> Targeted resequencing (TruSight Tumor 170 Panel) | <ul style="list-style-type: none"> Variant calling SV/CNV calling RNA fusion calling | <p>Illumina, Inc. Compute cost: Free License cost: n/a</p> |
|  <p>UMI Error Correction Demo Data Link Demo Data Link</p> | <ul style="list-style-type: none"> Targeted resequencing (TruSight® Tumor 170) | <ul style="list-style-type: none"> Reduce PCR or sequencing errors for rare and low-frequency somatic variants | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 83M reads, 2 x 125 bp Analysis cost = 2.15 iCredits/sample</p> |

| Data Handling, Data Quality Control (QC), and Data Visualization | | | |
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| App name | Sequencing application(s) | Key functionality | Vendor |
|  <p>FASTQ Toolkit</p> | <ul style="list-style-type: none"> FASTQ manipulation | <ul style="list-style-type: none"> Sub-sampling Adapter trimming Base trimming Quality trimming Read filtering | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com</p> <p>Compute cost: 3 iCredits per node/hr</p> <p>License cost: n/a</p> |
|  <p>FASTQC</p> <p>Demo Data Link</p> | <ul style="list-style-type: none"> Data QC | <ul style="list-style-type: none"> Base QC profile | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com</p> <p>Compute cost: 3 iCredits per node/hr</p> <p>License cost: n/a</p> |
|  <p>Integrative Genomics Viewer</p> | <ul style="list-style-type: none"> Whole-genome sequencing Targeted resequencing ChIP-Seq RNA-Seq | <ul style="list-style-type: none"> Genome browser Visualizations | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com</p> <p>Compute cost: Free</p> <p>License cost: n/a</p> |
|  <p>SRA Import</p> | <ul style="list-style-type: none"> Data import General NGS | <ul style="list-style-type: none"> Imports NGS data from NCBI Sequence Read Archive to BaseSpace Sequence Hub using SRA accession number | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com</p> <p>Compute cost: 3 iCredits per node/hr</p> <p>License cost: n/a</p> |
|  <p>SRA Submission</p> | <ul style="list-style-type: none"> Data export General NGS | <ul style="list-style-type: none"> Submission of data to NCBI SRA | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com</p> <p>Compute cost: 3 iCredits per node/hr</p> <p>License cost: n/a</p> |
|  <p>Variant Calling Assessment Tool</p> <p>Demo Data Link</p> | <ul style="list-style-type: none"> Data QC | <ul style="list-style-type: none"> Comparison of variant call sets SNV and Indel statistics | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com</p> <p>Compute Cost: 3 iCredits per node/hr</p> <p>License Cost: n/a</p> |

| Gene Expression and Regulation | | | |
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| App name | Sequencing application(s) | Key functionality | Vendor |
|  <p>DRAGEN Methylation Pipeline Demo Data Link Demo Data Link</p> | <ul style="list-style-type: none"> Bisulfite sequencing | <ul style="list-style-type: none"> Alignment Methylation calling | <p>Illumina, Inc.</p> <p>Compute cost: 5 iCredits per node/hr License cost: n/a Example compute cost: Targeted methylation 138M reads, 2 x 150 bp Analysis cost = 7.50 iCredits/sample Whole-genome 1,532M reads, 2 x 150 bp Analysis cost = 16.1 iCredits/sample</p> |
|  <p>DRAGEN Reference Builder Demo Data Link</p> | <ul style="list-style-type: none"> Custom genome support | <ul style="list-style-type: none"> Custom reference support | <p>Illumina, Inc.</p> <p>Compute cost: 5 iCredits per node/hr License cost: n/a</p> |
|  <p>DRAGEN RNA Pipeline Demo Data Link</p> | <ul style="list-style-type: none"> Whole-transcriptome gene expression Gene fusion detection | <ul style="list-style-type: none"> Alignment Fusion detection Gene expression | <p>Illumina, Inc.</p> <p>Compute cost: 5 iCredits per node/hr License cost: n/a Example compute cost: 2.6M reads, 2 x 75 bp Analysis cost = 0.5 iCredits/sample</p> |
|  <p>ChIPSeq Demo Data Link</p> | <ul style="list-style-type: none"> DNA-Protein Interactions ChIPSeq | <ul style="list-style-type: none"> Uses MACS for peak identification and HOMER for motif discovery | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a</p> |
|  <p>MethylKit Demo Data Link</p> | <ul style="list-style-type: none"> Methylation profiling Whole-genome sequencing Targeted sequencing | <ul style="list-style-type: none"> Analyze WGBS and targeted bisulfite sequencing data | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a</p> |
|  <p>miRNAs Analysis Demo Data Link</p> | <ul style="list-style-type: none"> Small RNA sequencing miRNA profiling | <ul style="list-style-type: none"> Alignment Differential expression | <p>B&Gu @ University of Torino mirnasanalysisbasespaceapp.blogspot.it Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 5M reads, 1 x 50 bp Analysis cost = 0.78 iCredits/sample</p> |






Gene Expression and Regulation (continued)

| App name | Sequencing application(s) | Key functionality | Vendor |
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|  <p>RNA Amplicon Demo Data Link</p> | <ul style="list-style-type: none"> Targeted gene expression (AmpliSeq™ for Illumina) | <ul style="list-style-type: none"> Alignment Gene counts Fusion detection | <p>Illumina, Inc.</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 2.56M reads, 2 x 150 bp Analysis cost = 1.50 iCredits/sample</p> |
|  <p>RNA-Seq Alignment Demo Data Link Demo Data Link Demo Data Link</p> | <ul style="list-style-type: none"> Transcriptome mining Gene expression | <ul style="list-style-type: none"> Alignment (STAR or TopHat) Gene counts Transcripts counts Annotation Variant calling Fusion detection Novel transcript assembly Batch processing | <p>Illumina, Inc.</p> <p>1.8 License cost: n/a Example compute cost: mRNA: 25M reads, 2 x 75 bp Analysis cost = 6.02 iCredits/sample totalRNA: 50M reads, 2 x 75 bp Analysis cost = 12.04 iCredits/sample</p> |
|  <p>RNA-Seq Differential Expression Demo Data Link</p> | <ul style="list-style-type: none"> Transcriptome mining Gene expression | <ul style="list-style-type: none"> Assembly of novel transcripts Differential expression | <p>Illumina, Inc.</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: mRNA: 25M reads, 2 x 75 bp Analysis cost = 37.64 iCredits/sample totalRNA: 50M reads, 2 x 75 bp Analysis cost = 75.3 iCredits/sample</p> |
|  <p>Small RNA Demo Data Link</p> | <ul style="list-style-type: none"> Small RNA sequencing miRNA profiling | <ul style="list-style-type: none"> Alignment Classification of miRNAs, isomiRs, and piRNAs Novel miRNA & pre-miRNA discovery Differential expression Batch processing | <p>Illumina, Inc.</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a</p> |

Microbial Genomics and Metagenomics

| App name | Sequencing application(s) | Key functionality | Vendor |
|----------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|  <p>16S Metagenomics Demo Data Link</p> | <ul style="list-style-type: none"> 16S rRNA microbial communities profiling | <ul style="list-style-type: none"> Taxonomic classification of microbial communities Batch processing Support for custom databases | <p>Illumina, Inc.</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 100K reads, 2 x 300 bp Analysis cost = 1.28 iCredits/sample</p> |
|  <p>E. coli Serotyping Demo Data Link</p> | <ul style="list-style-type: none"> E. coli serotype identification | <ul style="list-style-type: none"> Serotype identification | <p>GoSeqIt</p> <p>Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: Input: FASTA of E. coli reads Analysis cost = 1 iCredits/sample</p> |
|  <p>IgReC Demo Data Link</p> | <ul style="list-style-type: none"> Targeted sequencing RNA-Seq Immunology | <ul style="list-style-type: none"> Reconstitutes full-length adaptive immune repertoires from Rep-Seq data Alignment | <p>Center for Algorithmic Biotech.</p> <p>yana-safonova.github.io/ig_repertoire_constructor igtools_support@googlegroups.com Compute cost: 3 iCredits per node/hr License cost: n/a</p> |
|  <p>ITS Metagenomics Demo Data Link</p> | <ul style="list-style-type: none"> Fungal rRNA microbial communities profiling | <ul style="list-style-type: none"> Taxonomic classification of microbial communities | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 2.1M reads, 2 x 150 bp Analysis cost = 2 iCredits/sample</p> |
|  <p>Kraken Metagenomics Demo Data Link</p> | <ul style="list-style-type: none"> Shotgun metagenomics | <ul style="list-style-type: none"> Host DNA removal Taxonomic classification | <p>BaseSpace Labs</p> <p>basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 4M reads, 2 x 300 bp Analysis cost = 1.16 iCredits/sample 40M reads, 2 x 300 bp Analysis cost = 11.16 iCredits/sample</p> |
|  <p>MetaPhlAn Demo Data Link</p> | <ul style="list-style-type: none"> Metagenomics | <ul style="list-style-type: none"> Phylogenetic analysis | <p>The Huttenhower Lab</p> <p>huttenhower.sph.harvard.edu/metaphlan Compute cost: 3 iCredits per node/hr License cost: n/a</p> |

Microbial Genomics and Metagenomics (continued)

| App name | Sequencing application(s) | Key functionality | Vendor |
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|  <p>MiXCR Immune Repertoire Analyzer Demo Data Link</p> | <ul style="list-style-type: none"> Targeted resequencing RNA-Seq Immunology | <ul style="list-style-type: none"> Alignment Visualization | <p>MILaboratory milaboratory.com support@milaboratory.com Compute cost: 3 iCredits per node/hr License cost: 10 iCredits/sample</p> |
|  <p>Prokka Genome Annotation Demo Data Link</p> | <ul style="list-style-type: none"> Microbial | <ul style="list-style-type: none"> Prokaryotic genome annotation | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a</p> |
|  <p>Rescaf</p> | <ul style="list-style-type: none"> Microbial | <ul style="list-style-type: none"> Improves quality of scaffold sequences | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a</p> |
|  <p>SPAdes Genome Assembler Demo Data Link</p> | <ul style="list-style-type: none"> Microbial | <ul style="list-style-type: none"> De novo assembly | <p>Algorithmic Biology Lab cab.spbu.ru/spades Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 5MB genome with 100x coverage 833K reads, 2 x 300 bp Analysis cost = 7.30 iCredits/sample</p> |
|  <p>SRST2 Demo Data Link Demo Data Link</p> | <ul style="list-style-type: none"> Microbial ID | <ul style="list-style-type: none"> MLST typing | <p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a</p> |