












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.](#)

Biomedical and Basic Research – Genetic Analysis			
App name	Sequencing application(s)	Key functionality	Vendor
 <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 Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 0.72M reads, 2 x 150 bp 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. Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 100 M reads, 2 x 150 bp cost = 28.10 iCredits/sample</p>
 <p>DRAGEN Enrichment Demo Data Link</p>	<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 	<p>Illumina, Inc. Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: TruSeq Exome (200x mean coverage) 60 M reads, 2 x 75 bp cost = 6.76 iCredits/sample</p>
 <p>DRAGEN Germline Demo Data Link</p>	<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 	<p>Illumina, Inc. Compute cost: 5 iCredits per node/hr License cost: n/a Example compute cost: FASTQ to SNVs only 88M reads, 2 x 150 bp cost = 2.50 iCredits/sample</p>
 <p>DRAGEN Joint Genotyping Pipeline Demo Data Link</p>	<ul style="list-style-type: none"> De novo variant calling 	<ul style="list-style-type: none"> Novel variant identification 	<p>Illumina, Inc. Compute cost: 5 iCredits per node/hr License cost: n/a Example compute cost: Input: Trio of gVCFs processed with DRAGEN Germline cost = 1 iCredits/sample</p>







Biomedical and Basic Research – Genetic Analysis (continued)

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 cost = 7.50 iCredits/sample Whole-genome 1,532M reads, 2 x 150 bp cost = 16.1 iCredits/sample</p>
 <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 cost = 13 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 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 Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 18M reads, 2 x 150 bp 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 Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 18M reads, 2 x 150 bp cost = 1.5 iCredits/sample</p>
 <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 cost = 1 iCredits/sample</p>








Biomedical and Basic Research – Genetic Analysis (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <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 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) 2.35 M reads, 2 x 150 bp 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) 733 K reads, 2 x 150 bp 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 cost = 2.15 iCredits/sample</p>



Data Handling, Data Quality Control (QC), and Data Visualization

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 basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a</p>
 <p>FASTQC Demo Data Link</p>	<ul style="list-style-type: none"> Data QC 	<ul style="list-style-type: none"> Base QC profile 	<p>BaseSpace Labs basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr 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 basespacelabs@illumina.com Compute cost: Free 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 basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr 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 basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a</p>
 <p>Variant Calling Assessment Tool 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 basespacelabs@illumina.com Compute Cost: 3 iCredits per node/hr License Cost: n/a</p>





Gene Expression and Regulation

App name	Sequencing application(s)	Key functionality	Vendor
 <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>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. 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. Compute cost: 5 iCredits per node/hr License cost: n/a Example compute cost: 2.6M reads, 2 x 75 bp cost = 0.5 iCredits/sample</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: 5 M reads, 1 x 50 bp cost = 0.78 iCredits/sample</p>
 <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"> Amplicon gene expression Differential expression 	<p>Illumina, Inc. Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 2.56M reads, 2 x 150 bp 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 detectin Novel transcript assembly Batch processing 	<p>Illumina, Inc. 1.8 License cost: n/a Example compute cost: mRNA: 25 M reads, 2 x 75 bp cost = 6.02 iCredits/sample totalRNA: 50 M reads, 2 x 75 bp cost = 12.04 iCredits/sample</p>






Gene Expression and Regulation (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <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. Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: mRNA: 25M reads, 2 x 75 bp cost = 37.64 iCredits/sample totalRNA: 50M reads, 2 x 75 bp 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. 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 	<p>Illumina, Inc. Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 100 K reads, 2 x 300 bp 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 Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: Input: FASTA of E. coli reads cost = 1 iCredits/sample</p>
 <p>GENIUS Metagenomics: Know Now Demo Data Link</p>	<ul style="list-style-type: none"> • Metagenomics 	<ul style="list-style-type: none"> • Bacterial ID 	<p>CosmosID www.cosmosid.com/basespace-landing Compute cost: 3 iCredits per node/hr License cost: n/a</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. yana-safonova.github.io/ig_repertoire_constructor igtools_support@googlegroups.com 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
 <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 basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 2.1M reads, 2 x 150 bp 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 basespacelabs@illumina.com Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 4 M reads, 2 x 300 bp cost = 1.16 iCredits/sample 40 M reads, 2 x 300 bp 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 huttenhower.sph.harvard.edu/metaphlan Compute cost: 3 iCredits per node/hr License cost: n/a</p>
 <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: n/a</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>QIIME Preprocessing Demo Data Link</p>	<ul style="list-style-type: none"> Microbiome analysis 	<ul style="list-style-type: none"> Taxonomic classification of microbial communities Phylogenetic reconstruction Batch processing 	<p>QIIME Development Team qiime.org Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 100 K reads, 2 x 300 bp cost = 0.04 iCredits/sample</p>
 <p>QIIME Visualizations Demo Data Link</p>	<ul style="list-style-type: none"> Microbiome analysis 	<ul style="list-style-type: none"> Visualization 	<p>QIIME Development Team qiime.org Compute cost: 3 iCredits per node/hr License cost: n/a Example compute cost: 100 K reads, 2 x 300 bp cost = 0.71 iCredits/sample</p>

Microbial Genomics and Metagenomics (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <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</p> <p>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: 5 MB genome with 100x coverage 833 K reads, 2 x 300 bp cost = 7.30 iCredits/sample</p>
 <p>SRST2</p> <p>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>