Specific File Formats

File format	File extension	Read	Write	Comment
ABIF	*.ab1, *.abi, *.abif	+	-	A chromatogram file format. **See also:** *Chromatogram Viewer*
ACE	*.ace,	+	-	A file format for storing data about genomic contigs. **See also:** *Alignment Editor*
Bairoch	*.bairoch	+	+	A file format to store enzymes. **See also:** *Restriction Analysis*
BAM	*.bam	+	-	Binary compressed SAM format. **See also:** *Assembly Browser*
ClustalW	*.aln	+	+	A multiple sequence alignments (MSA) file format. **See also:** *Alignment Editor*
EBWT	*.ebwt	+	+	A Bowtie prebuilt index file. **See also:** *Bowtie*
EMBL	*.em, *.emb, *.embl	+	-	A rich format for storing sequences and their annotations. **See also:** *Sequence View*
FASTA	*.fa, *.mpfa, *.fna, *.fsa, *.fas, *.fasta, *.sef *.seqs	+	+	One of the oldest and simplest sequence file format. **See also:** *Sequence View*
FASTQ	*.fastq	+	+	A file format used to store a sequence and its corresponding quality scores. It was originally developed at the “Wellcome Trust Sanger Institute”. **See also:** *Sequence View*
Genbank	*.gb, *.gbk, *.gen, *.genbank	+	+	A rich format for storing sequences and associated annotations. **See also:** *Sequence View*
GFF	*.gff	+	+	The Gene Finding Format (GFF) format is used to store features and annotations. **See also:** *Sequence View*
HMM	*.hmm	+	+	A file format to store HMM profiles. **See also:** *HMM2*, *HMM3*
MMDB	*.prt	+	-	ASN.1 format used by the Molecular Modeling Database (MMDB). **See also:** *3D Structure Viewer*
MSF	*.msf	+	+	A multiple sequence alignments file format. **See also:** *Alignment Editor*
Mega	*.meg, *.meg.gz	+		A multiple sequence alignments file format. **See also:** *Alignment Editor*
Newick	*.nwk, *.newick	+	+	A tree file format. **See also:** *Building Phylogenetic Tree*, *Phylogenetic Tree Viewer*
Nexus	*.nex *.nxs	+	+	A multiple alignment and phylogenetic trees file format. **See also:** *Alignment Editor*, *Building Phylogenetic Tree*, *Phylogenetic Tree Viewer*
PDB	*.pdb	+	-	The Protein Data Bank (PDB) format allows to view the 3D structure of the sequence. **See also:** *3D Structure Viewer*
pDRAW32	*.pdw	+	-	A sequence file format used by pDRAW32 software. **See also:** *Sequence View*
PFM	*.pfm	+	+	A file format for a position frequency matrix. **See also:** *Weight Matrix*

Phylip	*.phy	+	+	A multiple alignment file format. **See also:** *Alignment Editor*
PWM	*.pwm	+	+	A file format for a position weight matrix. **See also:** *Weight Matrix*
Raw	*.seq	+	+	A raw sequence format. **See also:** *Sequence View*
SAM	*.sam	+	+	The Sequence Alignment/Map (SAM) format is a generic alignment format for storing read alignments against reference sequences. **See also:** *Assembly Browser*, *Bowtie*, *UGENE Genome Aligner*
SCF	*.scf	+	-	It is a Standard Chromatogram Format. **See also:** *Chromatogram Viewer*
SITECON	*.sitecon	+	-	A file format to store TFBS profile. **See also:** *SITECON*
Stockholm	*.sto	+	+	A multiple sequence alignments file format. **See also:** *Alignment Editor*
Swiss-Prot	*.txt *.sw	+	-	An annotated protein sequence in format of the UniProtKB/Swiss-Prot database. **See also:** *Sequence View*
Vector NTI Sequence	*.gb *.gp	+	+	A rich format for storing sequences and associated annotations, produced by Vector NTI software. **See also:** *Sequence View*
VCF	*.vcf	+	+	The VCF specifies the format of a text file used for storing gene sequence variations. **See also:** *Assembly Browser*