

A

Default
YAML

### Setting

**shiny\_db**

**db\_path**

**db\_type**

**shiny\_db\_table**

**output\_file\_table\_name**

**task\_table\_admin\_key**

**task\_table\_name**

**upload\_data\_table\_colnames**

**upload\_data\_table\_name**

**user\_table\_name**

**user\_table\_colnames**

**shiny\_plugins**

**shiny\_plugins\_dir**

**upload\_dir**

**supported\_genome\_version**

**supported\_file\_type**

auto ab1 acedb affybatch afg arff asn1 avinput avinput.gz axt bai bam bcf bed bed12 bed6  
bedgraph bedstrict bgzip bif bigbed bigwig biom1 blastdbd blastdbn blastdbp blastxml bmp btf  
btwisted cai cel charge checktrans chips chrint cism1 clustal cml codata codcmp coderet  
compeq consensusxml cpgplot cpgreport cps cram csfasta csv csv.gz ct cusp customtrack cut  
cxb dan data dbmotif dbn diffseq digest dmnd dreg eigenstratgeno eigenstratpca einverted  
eland elandmulti embl encodepeak epestfind eps equicktandem eset est2genome etandem excel  
fai fasta fastq fastq.gz fastqcscanner fastqillumina fastqsanger fastqsolexa featable featurexml  
fitch flt fped fphe fps fqtoc freak fuzznuc fuzzpro fuzztran garnier gcg geecee genbank  
genetrack gff gff3 gg gif gtf gz h5 hardklor hdt helixturnhelix hennig86 hlf hmm2 hmm3  
hmoment html idpdb idxml ig im inchi interval ipynb isochore jackknifer jackknifernon jpg json  
jsonld kronik laj lav ldepend len linecount lped maf maf.gz mafcustomtrack malist markx0  
markx1 markx10 markx2 markx3 mascotdat match mega meganon memexml mgf mol mol2  
motif mrxs ms2 msp mzdata mzid mzml mzq mxml n3 nametable ncbi ndpi needle neostore  
netcdf newcpgreport newcpgseek nex nexus nexusnon nhdr nhx noreturn nrrd nt obfs obo owl  
oxlicg oxligl oxling oxliss oxlist oxlits pair palindrome pbed pbm pcd pcx pdb pdf pepcoil  
pepinfo pepstats pepxml percin percout pgm phar pheno phylip phylipnon phyloxml pileup pir  
plyscii plybinary png polydot pphe ppm preg prettyseq primersearch protxml psd ptalign  
ptalignca ptalignfiltered ptalignfilteredca ptaligntrimmed ptaligntrimmedca ptortho ptorthocs  
ptphylip pttgf pttree qcml qual qual454 qualillumina qualsolexa qualsolid rast rdata rdf regions  
rexpbase rgb rgenetics sam scf scidx scn score sdf seqtable sf3 sff showfeat showorf sif simple  
sixpack smat smi snpeffdb snpmatrix snpsitdbnsfp snptest splib sqlite sra srs srspair staden stl  
stockholm strider supermatcher svg svslide swiss syco tabix table tabular tagseq tandem  
tar taxonomy textsearch tf2 tf8 tif tiff trackhub trafoxml traml triples tsv ttl twobit txt txt.gz  
uniprotxml vcf vcf.gz vectorstrip velvet vms vmu vtkascii vtkbinary wiff wig wobble wordcount  
xbr xgmml xls xlsx xmfa xml xpm zip

Update

B

Default
YAML

## Setting (YAML)

**BioInstaller YAML**

```

1 shiny_db:
2   db_path: ~/BioInstaller/BioInstaller.shiny.sqlite
3   db_type: sqlite
4 shiny_db_table:
5   output_file_table_name: output_files
6   task_table_admin_key: BioInstaller_admin
7   task_table_name: task_info
8   upload_data_table_colnames:
9     - file_name
10    - file_path
11    - file_size
12    - file_type
13    - genome_version
14    - upload_time
15    - md5

```

Update