Application of Circular visualization of genomic data, based on Parveen *et al* [1].

Tool	Input	Programming language**	OS*	website	Refs.
Circular Genome Viewer (GCView)	FASTA protein sequences, protein GI, UniProt.	J		http://wishart.biology.ualberta.ca/cgview/	[2]
GCView server				http://stothard.afns.ualberta.ca/cgview_server/	[3]
GView				https://www.gview.ca/	[4]
GView server				https://server.gview.ca/	
CGView Comparison Tool (CCT)				http://stothard.afns.ualberta.ca/downloads/CCT/	
BLAST Ring Image Generator (BRIG)				http://sourceforge.net/projects/brig/.	[5]
GenomeDiagram		PY			[6]
GenomeVx	Flat file of GeneBank	C++ program		http://wolfe.ucd.ie/GenomeVx/	[7]
Circos	GFF-style data	PL			[8]
DNAPlotter	Sequence formats	J			[9]
Circoletto	Fasta format	PL			[10]
Circleator	GenBank Sequence Alignment/SAM or BAM format	PL			[11]
RCircos	Specific data frame	R			[12]
Circlize	Specific data frame	R			[13]
OmicCircos	Specified matrix data	R			[14]
Circular Interactive Layout Converter Free Services (clicO FS)	Three type of file: Karyotype, Data, Configuration file.	RU		*http://clicofs.codoncloud.com*	[15]

CIRCUS	SAM, BAM, Annotation, CNV and, variant files.	R			[16]
CircosVCF	VCF file	WT			[17]
J-Circos	Flat file format	JS			
BioCircos.js		JS			[18]
Interactive Protein Sequence Visualization (I-PV)	Protein sequence, conservation and SNV data	PL			[19]
SOFIA		R			[20]
Circos for Genomics and Transcriptomics Data Visualization (CGDV)		WT		https://cgdv-upload.persistent.co.in/cgdv/	[21]
CiVi		PY, JS		http://www.cbs.dtu.dk/services/gwBrowser	[22]

*Programming Language: J – Java; JS – Javascript; PL – Perl; PY – Python; R – R-programming language; RU – Ruby, WT - Webtool
**Operating system: L- Linux, Mo - Mac OS, Wi - Windows, U - Unix

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