

package	source	description	BibTeX key
abacas	abacas	close gaps in genomic alignments from short reads	abacas ³¹
abinit	abinit	package for electronic structure calculations	abinit ³⁰¹
abinit-data	abinit	package for electronic structure calculations (Data files)	abinit ³⁰¹
abinit-doc	abinit	package for electronic structure calculations (Documentation)	abinit ³⁰¹
abyss	abyss	de novo, parallel, sequence assembler for short reads	abyss ³⁸⁴
abyss	abyss	de novo, parallel, sequence assembler for short reads	abyss2009 ⁷⁹³
acedb-other	acedb	retrieval of DNA or protein sequences	acedb1999 ⁸²¹
acedb-other-belvu	acedb	transitional package for belvu	acedb1999 ⁸²¹
acedb-other-dotter	acedb	transitional package for dotter	acedb ⁸⁰³
acedb-other-dotter	acedb	transitional package for dotter	acedb1999 ⁸²¹
aces3	aces3	Advanced Concepts in Electronic Structure III	aces3 ⁵²⁹
aces3	aces3	Advanced Concepts in Electronic Structure III	aces32011 ¹⁹⁰
aces3-data	aces3	Advanced Concepts in Electronic Structure III	aces3 ⁵²⁹
aces3-data	aces3	Advanced Concepts in Electronic Structure III	aces32011 ¹⁹⁰
adapterremoval	adapterremoval	rapid adapter trimming, identification, and read merging of gene sequences	adapterremoval ⁷⁷⁴
adapterremoval-examples	adapterremoval	rapid adapter trimming, identification, and read merging (example data)	adapterremoval ⁷⁷⁴
adun.app	adun.app	Molecular Simulator for GNUstep (GUI)	adun-app ⁴⁰³
adun.app-dbg	adun.app	Molecular Simulator for GNUstep (debugging symbols)	adun-app ⁴⁰³
adun-core	adun.app	Molecular Simulator	adun-app ⁴⁰³
aegean	aegean	integrated genome analysis toolkit	aegean ⁸¹⁶
aegean-dbg	aegean	integrated genome analysis toolkit, with debug symbols	aegean ⁸¹⁶
aevol	aevol	digital genetics model to run Evolution Experiments in silico	aevol ⁵⁸³
aevol	aevol	digital genetics model to run Evolution Experiments in silico	aevol2007 ⁴³⁴
aevol	aevol	digital genetics model to run Evolution Experiments in silico	aevol2010 ⁷⁰
aevol	aevol	digital genetics model to run Evolution Experiments in silico	aevol2010d ⁶⁶¹
aevol	aevol	digital genetics model to run Evolution Experiments in silico	aevol2012 ²⁵⁹
aladin	aladin	Interactive sky atlas for astronomical images and datasets	aladin ⁹²
alfa	alfa	Automated Line Fitting Algorithm	alfa ⁹¹⁷
alien-hunter	alien-hunter	Interpolated Variable Order Motifs to identify horizontally acquired DNA	alien-hunter ⁸⁹⁸
alter-sequence-alignment	alter-sequence-alignment	genomic sequences ALignment Transformation EnviRonment	alter-sequence-align
altree	altree	program to perform phylogeny-based association and localization analysis	altree ⁴⁶
altree-examples	altree	example files for ALTree	altree ⁴⁶
amap-align	amap-align	Protein multiple alignment by sequence annealing	amap-align ⁷⁷⁶
amide	amide	software for Medical Imaging	amide ⁵²²
ampliconnoise	ampliconnoise	removal of noise from 454 sequenced PCR amplicons	ampliconnoise ⁷⁰²
andi	andi	Efficient Estimation of Evolutionary Distances	andi ³³⁶
aoflagger	aoflagger	Find RFI in radio astronomical observations	aoflagger ⁶³⁴
aoflagger-dev	aoflagger	Find RFI in radio astronomical observations (development files)	aoflagger ⁶³⁴
apbs	apbs	Adaptive Poisson Boltzmann Solver	apbs ³⁹
apbs	apbs	Adaptive Poisson Boltzmann Solver	apbs1993 ³⁵⁷
apbs	apbs	Adaptive Poisson Boltzmann Solver	apbs1995 ³⁵⁸
apbs	apbs	Adaptive Poisson Boltzmann Solver	apbs2001 ³⁵⁶
apbs	apbs	Adaptive Poisson Boltzmann Solver	apbs2003 ⁴¹
apbs-data	apbs	data files for APBS (Adaptive Poisson Boltzmann Solver)	apbs ³⁹
apbs-data	apbs	data files for APBS (Adaptive Poisson Boltzmann Solver)	apbs1993 ³⁵⁷
apbs-data	apbs	data files for APBS (Adaptive Poisson Boltzmann Solver)	apbs1995 ³⁵⁸
apbs-data	apbs	data files for APBS (Adaptive Poisson Boltzmann Solver)	apbs2001 ³⁵⁶

apbs-data	apbs	data files for APBS (Adaptive Poisson Boltzmann Solver)	apbs2003 ⁴¹
aragorn	aragorn	tRNA and tmRNA detection in nucleotide sequences	aragorn ⁴⁷⁸
arden	arden	specificity control for read alignments using an artificial reference	arden ²⁸⁹
ariba	ariba	Antibiotic Resistance Identification By Assembly	ariba ³⁷³
artemis	artemis	genome browser and annotation tool	artemis ¹²⁷
artemis	artemis	genome browser and annotation tool	artemis2000 ⁷⁵⁰
artemis	artemis	genome browser and annotation tool	artemis2008 ¹²⁶
artfastqgenerator	artfastqgenerator	outputs artificial FASTQ files derived from a reference genome	artfastqgenerator ²⁵⁷
artfastqgenerator-doc	artfastqgenerator	outputs artificial FASTQ files derived from a reference genome (doc)	artfastqgenerator ²⁵⁷
artfastqgenerator-examples	artfastqgenerator	outputs artificial FASTQ files derived from a reference genome (examples)	artfastqgenerator ²⁵⁷
art-nextgen-simulation-tools	art-nextgen-simulation-tools	simulation tools to generate synthetic next-generation sequencing reads	art-nextgen-simulation-tools
art-nextgen-simulation-tools-profiles	art-nextgen-simulation-tools	profiles for art simulation tools	art-nextgen-simulation-tools
asdftool	python-asdf	Command line tool to manipulate ASDF scientific data files	python-asdf ³¹⁷
asl-doc	asl	documentation for ASL	asl ¹⁵⁷
asl-tools	asl	command-line tools for ASL	asl ¹⁵⁷
assemblytics	assemblytics	detect and analyze structural variants from a genome assembly	assemblytics ⁶⁰⁸
astrometry-data-tycho2	tycho2	Astrometry.net Tycho-2 index files	tycho2 ³⁷⁷
astrometry-data-tycho2-07	tycho2	Astrometry.net Tycho-2 index files (22'-30')	tycho2 ³⁷⁷
astrometry-data-tycho2-07-bigendian	tycho2	Astrometry.net Tycho-2 big endian index files (22'-30')	tycho2 ³⁷⁷
astrometry-data-tycho2-07-littleendian	tycho2	Astrometry.net Tycho-2 little endian index files (22'-30')	tycho2 ³⁷⁷
astrometry-data-tycho2-08	tycho2	Astrometry.net Tycho-2 index files (30'-44')	tycho2 ³⁷⁷
astrometry-data-tycho2-08-bigendian	tycho2	Astrometry.net Tycho-2 big endian index files (30'-44')	tycho2 ³⁷⁷
astrometry-data-tycho2-08-littleendian	tycho2	Astrometry.net Tycho-2 little endian index files (30'-44')	tycho2 ³⁷⁷
astrometry-data-tycho2-09	tycho2	Astrometry.net Tycho-2 index files (44'-60')	tycho2 ³⁷⁷
astrometry-data-tycho2-09-bigendian	tycho2	Astrometry.net Tycho-2 big endian index files (44'-60')	tycho2 ³⁷⁷
astrometry-data-tycho2-09-littleendian	tycho2	Astrometry.net Tycho-2 little endian index files (44'-60')	tycho2 ³⁷⁷
astrometry-data-tycho2-10-19	tycho2	Astrometry.net Tycho-2 index files (60'-2000')	tycho2 ³⁷⁷
astrometry-data-tycho2-10-19-bigendian	tycho2	Astrometry.net Tycho-2 big endian index files (60'-2000')	tycho2 ³⁷⁷
astrometry-data-tycho2-10-19-littleendian	tycho2	Astrometry.net Tycho-2 little endian index files (60'-2000')	tycho2 ³⁷⁷
astrometry.net	astrometry.net	Astrometry plate solver	astrometry-net ⁴⁶⁹
astropy-utils	astropy	Command line tools from astropy	astropy ¹⁵⁵
atac	kmer	genome assembly-to-assembly comparison	kmer ⁹⁰⁵
atac	kmer	genome assembly-to-assembly comparison	kmer2004 ³⁸²
ataqv	ataqv	ATAC-seq QC and visualization	ataqv ⁶⁴⁵
atropos	atropos	NGS read trimming tool that is specific, sensitive, and speedy	atropos ¹⁹⁵
augustus	augustus	gene prediction in eukaryotic genomes	augustus ⁴⁶⁴
augustus	augustus	gene prediction in eukaryotic genomes	augustus2003 ⁸¹⁸
augustus	augustus	gene prediction in eukaryotic genomes	augustus2003f ⁸¹⁷
augustus	augustus	gene prediction in eukaryotic genomes	augustus2006 ⁸¹⁹
augustus	augustus	gene prediction in eukaryotic genomes	augustus2008 ⁸²⁰
augustus	augustus	gene prediction in eukaryotic genomes	augustus2011 ⁴²⁵
augustus-data	augustus	data files for AUGUSTUS	augustus ⁴⁶⁴
augustus-data	augustus	data files for AUGUSTUS	augustus2003 ⁸¹⁸
augustus-data	augustus	data files for AUGUSTUS	augustus2003f ⁸¹⁷
augustus-data	augustus	data files for AUGUSTUS	augustus2006 ⁸¹⁹
augustus-data	augustus	data files for AUGUSTUS	augustus2008 ⁸²⁰
augustus-data	augustus	data files for AUGUSTUS	augustus2011 ⁴²⁵
augustus-doc	augustus	documentation files for AUGUSTUS	augustus ⁴⁶⁴
augustus-doc	augustus	documentation files for AUGUSTUS	augustus2003 ⁸¹⁸
augustus-doc	augustus	documentation files for AUGUSTUS	augustus2003f ⁸¹⁷
augustus-doc	augustus	documentation files for AUGUSTUS	augustus2006 ⁸¹⁹
augustus-doc	augustus	documentation files for AUGUSTUS	augustus2008 ⁸²⁰
augustus-doc	augustus	documentation files for AUGUSTUS	augustus2011 ⁴²⁵

autodocktools	autodocktools	GUI to help set up, launch and analyze AutoDock dockings	autodocktools ⁵⁹²
autodocktools	autodocktools	GUI to help set up, launch and analyze AutoDock dockings	autodocktools2008 ³
autodocktools	autodocktools	GUI to help set up, launch and analyze AutoDock dockings	autodocktools2016 ²
autodock-vina	autodock-vina	docking of small molecules to proteins	autodock-vina ⁸⁷⁸
avogadro	avogadro	Molecular Graphics and Modelling System	avogadro ³³²
avogadro-data	avogadro	Molecular Graphics and Modelling System (Data Files)	avogadro ³³²
avogadro-utils	avogadrolibs	Molecular Graphics and Modelling System (library)	avogadrolibs ³³³
bagel	bagel	Computational Chemistry Package	bagel ⁷⁸³
bagel-data	bagel	Computational Chemistry Package (data files)	bagel ⁷⁸³
baitfisher	baitfisher	software package for designing hybrid enrichment probes	baitfisher ⁵⁶⁷
bali-phy	bali-phy	Bayesian Inference of Alignment and Phylogeny	bali-phy ⁷¹⁵
ballview	ball	free molecular modeling and molecular graphics tool	ball ⁵⁸⁵
ballview	ball	free molecular modeling and molecular graphics tool	ball2010 ³⁵⁰
ballview-dbg	ball	debug symbols for BALL and VIEW libraries	ball ⁵⁸⁵
ballview-dbg	ball	debug symbols for BALL and VIEW libraries	ball2010 ³⁵⁰
bamtools	bamtools	toolkit for manipulating BAM (genome alignment) files	bamtools ⁴⁷
bandage	bandage	Bioinformatics Application for Navigating De novo Assembly Graphs Easily	bandage ⁹¹⁹
bcalm	bcalm	de Bruijn compaction in low memory	bcalm ¹⁴²
bcftools	bcftools	genomic variant calling and manipulation of VCF/BCF files	bcftools ¹⁶⁸
beads	beads	2-DE electrophoresis gel image spot detection	beads ⁴⁷⁰
beagle	beagle	Genotype calling, genotype phasing and imputation of ungenotyped markers	beagle ¹¹¹
beagle	beagle	Genotype calling, genotype phasing and imputation of ungenotyped markers	beagle2013 ¹⁰⁸
beagle	beagle	Genotype calling, genotype phasing and imputation of ungenotyped markers	beagle2016 ¹⁰⁹
beagle	beagle	Genotype calling, genotype phasing and imputation of ungenotyped markers	beagle2018 ¹¹⁰
beagle-doc	beagle	Documentation for Beagle	beagle ¹¹¹
beagle-doc	beagle	Documentation for Beagle	beagle2013 ¹⁰⁸
beagle-doc	beagle	Documentation for Beagle	beagle2016 ¹⁰⁹
beagle-doc	beagle	Documentation for Beagle	beagle2018 ¹¹⁰
beast2-mcmc	beast2-mcmc	Bayesian MCMC phylogenetic inference	beast2-mcmc ⁹⁵
beast2-mcmc-doc	beast2-mcmc	Bayesian MCMC phylogenetic inference - documentation	beast2-mcmc ⁹⁵
beast2-mcmc-examples	beast2-mcmc	Bayesian MCMC phylogenetic inference - example data	beast2-mcmc ⁹⁵
beast-mcmc	beast-mcmc	Bayesian MCMC phylogenetic inference	beast-mcmc ²¹⁰
beast-mcmc-doc	beast-mcmc	Bayesian MCMC phylogenetic inference - documentation	beast-mcmc ²¹⁰
beast-mcmc-examples	beast-mcmc	Bayesian MCMC phylogenetic inference - example data	beast-mcmc ²¹⁰
bedops	bedops	high-performance genomic feature operations	bedops ⁶¹¹
bedops-doc	bedops	high-performance genomic feature operations (documentation)	bedops ⁶¹¹
bedtools	bedtools	suite of utilities for comparing genomic features	bedtools ⁷⁰³
bedtools-test	bedtools	test data for the bedtools package	bedtools ⁷⁰³
belvu	seqtools	multiple sequence alignment viewer and phylogenetic tool	seqtools ⁵⁰
belvu	seqtools	multiple sequence alignment viewer and phylogenetic tool	seqtools1994 ⁸⁰⁴
belvu	seqtools	multiple sequence alignment viewer and phylogenetic tool	seqtools2005 ⁸⁰⁶
berkeley-express	berkeley-express	Streaming quantification for high-throughput sequencing	berkeley-express ⁷²³
berkeley-express	berkeley-express	Streaming quantification for high-throughput sequencing	berkeley-express201
berkeley-express	berkeley-express	Streaming quantification for high-throughput sequencing	berkeley-express201
berkeley-express-doc	berkeley-express	Documentation for RNA-Seq tool eXpress	berkeley-express ⁷²³

berkeley-express-doc	berkeley-express	Documentation for RNA-Seq tool eXpress	berkeley-express201
berkeley-express-doc	berkeley-express	Documentation for RNA-Seq tool eXpress	berkeley-express201
biobambam2	biobambam2	tools for early stage alignment file processing	biobambam2 ⁸⁶⁶
bio-eagle	bio-eagle	Haplotype phasing within a genotyped cohort or using a phased reference panel	bio-eagle ⁵²⁶
bio-eagle	bio-eagle	Haplotype phasing within a genotyped cohort or using a phased reference panel	bio-eagle2016 ⁵²⁵
bio-eagle-examples	bio-eagle	Examples for bio-eagle	bio-eagle ⁵²⁶
bio-eagle-examples	bio-eagle	Examples for bio-eagle	bio-eagle2016 ⁵²⁵
biomaj	biomaj	biological data-bank updater	biomaj ²⁴⁷
biomaj-properties	biomaj	biological data-bank updater - example properties files	biomaj ²⁴⁷
biom-format-tools	python-biom-format	command-line tools for BIOM format	python-biom-format
bioperl	bioperl	Perl tools for computational molecular biology	bioperl ⁸¹³
bio-rainbow	bio-rainbow	clustering and assembling short reads for bioinformatics	bio-rainbow ¹⁴⁵
biosig-tools	biosig4c++	format conversion tools for biomedical data formats	biosig4c- ⁷⁶⁷
biosyntax	biosyntax	Syntax Highlighting for Computational Biology (metapackage)	biosyntax ³⁶
biosyntax-common	biosyntax	Syntax Highlighting for Computational Biology (common files)	biosyntax ³⁶
biosyntax-example	biosyntax	Syntax Highlighting for Computational Biology (example)	biosyntax ³⁶
biosyntax-gedit	biosyntax	Syntax Highlighting for Computational Biology (gedit)	biosyntax ³⁶
biosyntax-less	biosyntax	Syntax Highlighting for Computational Biology (less)	biosyntax ³⁶
biosyntax-vim	biosyntax	Syntax Highlighting for Computational Biology (vim)	biosyntax ³⁶
bio-tradis	bio-tradis	analyse the output from TraDIS analyses of genomic sequences	bio-tradis ⁴⁸
bitseq	bitseq	Bayesian Inference of Transcripts from Sequencing Data	bitseq ³⁴⁵
blasr	blasr	mapping single-molecule sequencing reads	blasr ¹³¹
blimps-examples	blimps	blocks database improved searcher (example data)	blimps ³⁴³
blimps-utils	blimps	blocks database improved searcher	blimps ³⁴³
blixem	seqtools	interactive browser of sequence alignments	seqtools ⁵⁰
blixem	seqtools	interactive browser of sequence alignments	seqtools1994 ⁸⁰⁴
blixem	seqtools	interactive browser of sequence alignments	seqtools2005 ⁸⁰⁶
bodr	bodr	Blue Obelisk Data Repository	bodr ⁶⁰¹
bodr	bodr	Blue Obelisk Data Repository	bodr2006 ³²⁰
bodr	bodr	Blue Obelisk Data Repository	bodr2008 ⁶⁰²
bodr	bodr	Blue Obelisk Data Repository	bodr2011 ⁶³³
bodr	bodr	Blue Obelisk Data Repository	bodr2011e ⁶²⁷
bolt-lmm	bolt-lmm	Efficient large cohorts genome-wide Bayesian mixed-model association testing	bolt-lmm ⁵²⁴
bolt-lmm	bolt-lmm	Efficient large cohorts genome-wide Bayesian mixed-model association testing	bolt-lmm2015 ⁵²³
bolt-lmm-example	bolt-lmm	Examples for bolt-lmm	bolt-lmm ⁵²⁴
bolt-lmm-example	bolt-lmm	Examples for bolt-lmm	bolt-lmm2015 ⁵²³
bowtie	bowtie	Ultrafast memory-efficient short read aligner	bowtie ⁴⁷⁴
bowtie2	bowtie2	ultrafast memory-efficient short read aligner	bowtie2 ⁴⁷³
bowtie2-examples	bowtie2	Examples for bowtie2	bowtie2 ⁴⁷³
bowtie-examples	bowtie	Examples for bowtie, the ultrafast memory-efficient short read aligner	bowtie ⁴⁷⁴
brig	brig	BLAST Ring Image Generator	brig ¹³
busco	busco	benchmarking sets of universal single-copy orthologs	busco ⁷⁸⁰
bustools	bustools	program for manipulating BUS files for single cell RNA-Seq datasets	bustools ⁵⁷⁴
bwa	bwa	Burrows-Wheeler Aligner	bwa ⁵⁰³
caffe	caffe	Tools for fast, open framework for Deep Learning (CPU_ONLY)	caffe ³⁹⁰
caffe-cpu	caffe	Fast, open framework for Deep Learning (Meta)	caffe ³⁹⁰
caffe-cuda	caffe-contrib	Fast, open framework for Deep Learning (Meta)	caffe-contrib ³⁹¹
caffe-doc	caffe	Caffe's doxygen docs and examples	caffe ³⁹⁰
caffe-tools-cpu	caffe	Tools for fast, open framework for Deep Learning (CPU_ONLY)	caffe ³⁹⁰
caffe-tools-cuda	caffe-contrib	Tools for fast, open framework for Deep Learning (CUDA)	caffe-contrib ³⁹¹

caftools	caftools	maintenance of DNA sequence assemblies	caftools ¹⁸¹
cain	cain	simulations of chemical reactions	cain ⁵⁶⁶
cain-examples	cain	examples for cain	cain ⁵⁶⁶
cain-solvers	cain	solvers for cain	cain ⁵⁶⁶
camitk-actionstatemachine	camitk	pipeline replay application for the CamiTK library	camitk ²⁵⁶
camitk-config	camitk	Computer Assisted Medical Intervention Tool Kit - config	camitk ²⁵⁶
camitk-imp	camitk	workbench application for the CamiTK library	camitk ²⁵⁶
canu	canu	single molecule sequence assembler for genomes	canu ⁴⁴³
caret	caret	Computerized Anatomical Reconstruction and Editing Toolkit	caret ²³⁶
cb2bib	cb2bib	extract bibliographic references from various sources	cb2bib ¹⁵⁶
cclib	cclib	Parsers and algorithms for computational chemistry	cclib ⁶²⁹
cclib-data	cclib-data	Parsers and algorithms for computational chemistry (data files)	cclib-data ⁶³⁰
cct	cct	visually comparing bacterial, plasmid, chloroplast, or mitochondrial sequences	cct ³¹⁴
cct	cct	visually comparing bacterial, plasmid, chloroplast, or mitochondrial sequences	cct2017 ⁸³⁰
cct-examples	cct	example data for testing the package cct	cct ³¹⁴
cct-examples	cct	example data for testing the package cct	cct2017 ⁸³⁰
cd-hit	cd-hit	suite of programs designed to quickly group sequences	cd-hit ⁵⁰⁹
centrifuge	centrifuge	rapid and memory-efficient system for classification of DNA sequences	centrifuge ⁴³⁰
cgview	cgview	Circular Genome Viewer	cgview ⁸²⁹
changeo	changeo	Repertoire clonal assignment toolkit (Python 3)	changeo ³²⁴
chemps2	chemps2	Executable to call libchemps2-3 from the command line	chemps2 ¹³⁶
chemps2	chemps2	Executable to call libchemps2-3 from the command line	chemps22014 ⁹⁴¹
chemps2	chemps2	Executable to call libchemps2-3 from the command line	chemps22014c ⁹³⁷
chemps2	chemps2	Executable to call libchemps2-3 from the command line	chemps22014d ⁹³⁹
chemps2	chemps2	Executable to call libchemps2-3 from the command line	chemps22016 ⁹⁴³
chemps2-doc	chemps2	Documentation of the libchemps2-3 package	chemps2 ¹³⁶
chemps2-doc	chemps2	Documentation of the libchemps2-3 package	chemps22014 ⁹⁴¹
chemps2-doc	chemps2	Documentation of the libchemps2-3 package	chemps22014c ⁹³⁷
chemps2-doc	chemps2	Documentation of the libchemps2-3 package	chemps22014d ⁹³⁹
chemps2-doc	chemps2	Documentation of the libchemps2-3 package	chemps22016 ⁹⁴³
chemtool	chemtool	chemical structures drawing program	chemtool ¹¹⁶
chimeraslayer	microbiomeutil	detects likely chimeras in PCR amplified DNA	microbiomeutil ³²⁸
chip-seq	chip-seq	tools performing common ChIP-Seq data analysis tasks	chip-seq ¹⁵
chip-seq-data	chip-seq	tools performing common ChIP-Seq data analysis tasks (data)	chip-seq ¹⁵
chromhmm	chromhmm	Chromatin state discovery and characterization	chromhmm ²³³
chromhmm	chromhmm	Chromatin state discovery and characterization	chromhmm2017 ²³⁵
chromhmm-example	chromhmm	Chromatin state discovery and characterization (example)	chromhmm ²³³
chromhmm-example	chromhmm	Chromatin state discovery and characterization (example)	chromhmm2017 ²³⁵
chromimpute	chromimpute	Large-scale systematic epigenome imputation	chromimpute ²³⁴
circlator	circlator	circularize genome assemblies	circlator ³⁷²
circos	circos	plotter for visualizing data	circos ⁴⁵⁶
clearcut	clearcut	extremely efficient phylogenetic tree reconstruction	clearcut ²³⁷
clonalframe	clonalframe	inference of bacterial microevolution using multi-locus sequence data	clonalframe ¹⁹²
clonalframeml	clonalframeml	Efficient Inference of Recombination in Whole Bacterial Genomes	clonalframeml ¹⁹³
clonalorigin	clonalorigin	inference of homologous recombination in bacteria using whole genome sequences	clonalorigin ¹⁹⁴
clustalo	clustalo	General-purpose multiple sequence alignment program for proteins	clustalo ⁷⁸⁹

clustalo	clustalo	General-purpose multiple sequence alignment program for proteins	clustalo2018 ⁷⁸⁸
clustalw	clustalw	global multiple nucleotide or peptide sequence alignment	clustalw ⁴⁷⁶
clustalx	clustalx	Multiple alignment of nucleic acid and protein sequences (graphical interface)	clustalx ⁴⁷⁷
cluster3	cluster3	Reimplementation of the Eisen-clustering software	cluster3 ¹⁸⁰
cminpack-doc	cminpack	Nonlinear equations and nonlinear least squares problems (doc)	cminpack ¹⁹¹
cmtk	cmtk	Computational Morphometry Toolkit	cmtk ⁷²⁹
cnrun	cnrun	NeuroML-capable neuronal network simulator	cnrun ⁹⁶⁴
cnrun-tools	cnrun	NeuroML-capable neuronal network simulator (tools)	cnrun ⁹⁶⁴
cnvkit	cnvkit	Copy number variant detection from targeted DNA sequencing	cnvkit ⁸⁴⁶
codonw	codonw	Correspondence Analysis of Codon Usage	codonw ⁷⁸²
cod-tools	cod-tools	tools for manipulating CIF format files	cod-tools ³¹⁶
cohomcalg	cohomcalg	sheaf cohomology of line bundles on toric varieties	cohomcalg ⁷⁵
cohomcalg-common	cohomcalg	sheaf cohomology of line bundles on toric varieties (common files)	cohomcalg ⁷⁵
coinor-csdp	coinor-csdp	A software package for semidefinite programming	coinor-csdp ⁹³
coinor-csdp-dbg	coinor-csdp	A software package for semidefinite programming	coinor-csdp ⁹³
coinor-csdp-doc	coinor-csdp	A software package for semidefinite programming	coinor-csdp ⁹³
comet-ms	comet-ms	Tandem mass spectrometry (MS/MS) search engine	comet-ms ³⁹³
comet-ms-dbg	comet-ms	Tandem mass spectrometry (MS/MS) search engine - debug symbols	comet-ms ³⁹³
concavity	concavity	predictor of protein ligand binding sites from structure and conservation	concavity ¹²⁴
concavity-dbg	concavity	predictor of protein ligand binding sites (debug)	concavity ¹²⁴
condor	condor	transitional dummy package	condor ⁵²⁰
condor-dbg	condor	transitional dummy package	condor ⁵²⁰
condor-dev	condor	transitional dummy package	condor ⁵²⁰
condor-doc	condor	transitional dummy package	condor ⁵²⁰
connectagram	connectagram	word unscrambling game	connectagram ³⁰⁶
connectagram-data	connectagram	word unscrambling game - data files	connectagram ³⁰⁶
conservation-code	conservation-code	protein sequence conservation scoring tool	conservation-code ¹²
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k ¹⁶¹
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k1997 ⁵¹⁸
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k1999 ⁵¹⁹
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k2000 ⁴⁴⁸
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k2005 ⁸⁹³
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k2007 ⁴⁵⁷
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k2008 ³²¹
cp2k	cp2k	Ab Initio Molecular Dynamics	cp2k2013 ³⁷⁴
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k ¹⁶¹
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k1997 ⁵¹⁸
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k1999 ⁵¹⁹
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k2000 ⁴⁴⁸
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k2005 ⁸⁹³
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k2007 ⁴⁵⁷
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k2008 ³²¹
cp2k-data	cp2k	Ab Initio Molecular Dynamics (data files)	cp2k2013 ³⁷⁴
cpl-plugin-muse	cpl-plugin-muse	ESO data reduction pipeline for the MUSE instrument	cpl-plugin-muse ⁹¹¹
cpl-plugin-muse-calib	cpl-plugin-muse	ESO data reduction pipeline calibration data downloader for MUSE	cpl-plugin-muse ⁹¹¹
cpl-plugin-muse-doc	cpl-plugin-muse	ESO data reduction pipeline documentation for MUSE	cpl-plugin-muse ⁹¹¹
cpl-plugin-sinfo	cpl-plugin-sinfo	ESO data reduction pipeline SINFONI	cpl-plugin-sinfo ²²⁷
cpl-plugin-sinfo-calib	cpl-plugin-sinfo	ESO data reduction pipeline calibration data downloader for SINFONI	cpl-plugin-sinfo ²²⁷
cpl-plugin-sinfo-doc	cpl-plugin-sinfo	ESO data reduction pipeline documentation for SINFONI	cpl-plugin-sinfo ²²⁷
crac	crac	integrated RNA-Seq read analysis	crac ⁵⁹⁷
crac	crac	integrated RNA-Seq read analysis	crac2013 ⁶⁷⁷
ctn	ctn	Central Test Node, a DICOM implementation for medical imaging	ctn ⁵⁸⁶
ctn-dev	ctn	Development files for Central Test Node, a DICOM implementation	ctn ⁵⁸⁶

cufflinks	cufflinks	Transcript assembly, differential expression and regulation for RNA-Seq	cufflinks ⁸⁷³
cufflinks	cufflinks	Transcript assembly, differential expression and regulation for RNA-Seq	cufflinks2012 ⁸⁷⁴
cutadapt	python-cutadapt	Clean biological sequences from high-throughput sequencing reads	python-cutadapt ⁵⁵⁹
cutemaze	cutemaze	single player maze game	cutemaze ³⁰⁷
cwltool	cwltool	Common Workflow Language reference implementation	cwltool ¹⁶
cython	cython	C-Extensions for Python	cython ⁵⁷
cython3	cython	C-Extensions for Python 3	cython ⁵⁷
cython3-dbg	cython	C-Extensions for Python 3 - debug build	cython ⁵⁷
cython-dbg	cython	C-Extensions for Python - debug build	cython ⁵⁷
cython-doc	cython	C-Extensions for Python - documentation	cython ⁵⁷
daligner	daligner	local alignment discovery between long nucleotide sequencing reads	daligner ⁶⁰³
dawg	dawg	simulate the evolution of recombinant DNA sequences	dawg ¹²⁵
deepnano	deepnano	alternative basecaller for MinION reads of genomic sequences	deepnano ⁹⁹
deepnano-data	deepnano	alternative basecaller for MinION reads of genomic sequences (data)	deepnano ⁹⁹
delly	delly	Structural variant discovery by read analysis	delly ⁷¹⁴
dialign	dialign	Segment-based multiple sequence alignment	dialign ⁵⁹⁰
dialign-tx	dialign-t	Segment-based multiple sequence alignment	dialign-t ⁸³⁸
dialign-tx-data	dialign-t	Segment-based multiple sequence alignment (data files)	dialign-t ⁸³⁸
diamond-aligner	diamond-aligner	accelerated BLAST compatible local sequence aligner	diamond-aligner ¹¹⁷
dicompyler	dicompyler	radiation therapy research platform	dicompyler ⁶⁵³
dict-wn	wordnet	electronic lexical database of English language for dict	wordnet ⁵⁷⁹
dict-wn	wordnet	electronic lexical database of English language for dict	wordnet1998 ²⁴⁴
dict-wn	wordnet	electronic lexical database of English language for dict	wordnet2005 ²⁴⁵
dindel	dindel	determines indel calls from short-read data	dindel ⁹
disulfinder	disulfinder	cysteines disulfide bonding state and connectivity predictor	disulfinder ¹³⁰
disulfinder	disulfinder	cysteines disulfide bonding state and connectivity predictor	disulfinder2002 ²⁵⁸
disulfinder	disulfinder	cysteines disulfide bonding state and connectivity predictor	disulfinder2003 ¹²⁹
disulfinder	disulfinder	cysteines disulfide bonding state and connectivity predictor	disulfinder2004 ⁹⁰²
disulfinder-data	disulfinder	data files for predictor of disulfide bonds in proteins	disulfinder ¹³⁰
disulfinder-data	disulfinder	data files for predictor of disulfide bonds in proteins	disulfinder2002 ²⁵⁸
disulfinder-data	disulfinder	data files for predictor of disulfide bonds in proteins	disulfinder2003 ¹²⁹
disulfinder-data	disulfinder	data files for predictor of disulfide bonds in proteins	disulfinder2004 ⁹⁰²
dnaclust	dnaclust	tool for clustering millions of short DNA sequences	dnaclust ²⁸⁵
dnapi	dnapi	adapter prediction for small RNA sequencing - utils	dnapi ⁸⁸³
dotter	seqtools	detailed comparison of two genomic sequences	seqtools ⁵⁰
dotter	seqtools	detailed comparison of two genomic sequences	seqtools1994 ⁸⁰⁴
dotter	seqtools	detailed comparison of two genomic sequences	seqtools1995 ⁸⁰⁵
dotter	seqtools	detailed comparison of two genomic sequences	seqtools2005 ⁸⁰⁶
drawxtl	drawxtl	crystal structure viewer	drawxtl ²⁴⁹
dssp	dssp	protein secondary structure assignment based on 3D structure	dssp ⁴¹¹
dssp-dbg	dssp	debugging symbols for dssp	dssp ⁴¹¹
ea-utils	ea-utils	command-line tools for processing biological sequencing data	ea-utils ²⁵
edfbrowser	edfbrowser	viewer for biosignal storage files such as bdf and edf	edfbrowser ⁹²⁷
edtsurf	edtsurf	triangulated mesh surfaces for protein structures	edtsurf ⁹⁵¹
eigensoft	eigensoft	reduction of population bias for genetic analyses	eigensoft ⁶⁸⁹

elastix	elastix	toolbox for rigid and nonrigid registration of images	elastix ⁷⁸¹
elastix	elastix	toolbox for rigid and nonrigid registration of images	elastix2010 ⁴³³
elastix-doc	elastix	toolbox for rigid and nonrigid registration of images - docs	elastix ⁷⁸¹
elastix-doc	elastix	toolbox for rigid and nonrigid registration of images - docs	elastix2010 ⁴³³
emboss	emboss	European molecular biology open software suite	emboss ⁷²⁰
emboss-data	emboss	data files for the EMBOSS package	emboss ⁷²⁰
emboss-doc	emboss	documentation for EMBOSS	emboss ⁷²⁰
emboss-lib	emboss	EMBOSS Libraries	emboss ⁷²⁰
emboss-test	emboss	test files for the EMBOSS package	emboss ⁷²⁰
e-mem	e-mem	Efficient computation of Maximal Exact Matches for very large genomes	e-mem ⁴²⁹
emmax	emmax	genetic mapping considering population structure	emmax ⁴¹⁶
epigrass	epigrass	scientific tool for simulations and scenario analysis in network epidemiology	epigrass ¹⁵²
epigrass-doc	epigrass	Documentation for EpiGrass, a network epidemiology tool	epigrass ¹⁵²
ergo	ergo	Quantum chemistry program for large-scale calculations	ergo ⁷⁴⁵
ergo-data	ergo	Quantum chemistry program for large-scale calculations - data package	ergo ⁷⁴⁵
eso-midas	eso-midas	European Southern Observatory Munich Image Data Analysis System	eso-midas ⁴³
eso-midas-test data	eso-midas	Test data files for ESO-MIDAS	eso-midas ⁴³
estscan	estscan	ORF-independent detector of coding DNA sequences	estscan ⁵³⁰
estscan	estscan	ORF-independent detector of coding DNA sequences	estscan1999 ³⁸¹
examl	examl	Exascale Maximum Likelihood (ExaML) code for phylogenetic inference	examl ⁴⁴⁷
exonerate	exonerate	generic tool for pairwise sequence comparison	exonerate ⁷⁹⁵
falcon	falcon	diploid-aware genome assembly of single-molecule sequencing reads	falcon ¹⁴³
fasta3	fasta3	tools for searching collections of biological sequences	fasta3 ⁶⁶⁵
fasta3	fasta3	tools for searching collections of biological sequences	fasta31996 ⁶⁶⁴
fasta3-doc	fasta3	user guide for FASTA tools	fasta3 ⁶⁶⁵
fasta3-doc	fasta3	user guide for FASTA tools	fasta31996 ⁶⁶⁴
fastdnaml	fastdnaml	Tool for construction of phylogenetic trees of DNA sequences	fastdnaml ⁶³⁹
fastlink	fastlink	faster version of pedigree programs of Linkage	fastlink ⁴⁰⁹
fastlink-doc	fastlink	Some papers about fastlink	fastlink ⁴⁰⁹
fastml	fastml	maximum likelihood ancestral amino-acid sequence reconstruction	fastml ²⁸
fastml	fastml	maximum likelihood ancestral amino-acid sequence reconstruction	fastml2000 ⁶⁹⁷
fastml	fastml	maximum likelihood ancestral amino-acid sequence reconstruction	fastml2002 ⁶⁹⁸
fastp	fastp	Ultra-fast all-in-one FASTQ preprocessor	fastp ¹³⁷
fastqtl	fastqtl	Quantitative Trait Loci (QTL) mapper in cis for molecular phenotypes	fastqtl ⁶⁴³
fastqtl-doc	fastqtl	QTL mapper in cis for molecular phenotypes - documentation	fastqtl ⁶⁴³
fasttree	fasttree	phylogenetic trees from alignments of nucleotide or protein sequences	fasttree ⁶⁹¹
fflas-ffpack	fflas-ffpack	Finite field linear algebra subroutines/package	fflas-ffpack ²¹²
fflas-ffpack-common	fflas-ffpack	Finite field linear algebra subroutines/package - common files	fflas-ffpack ²¹²
fflas-ffpack-dev-doc	fflas-ffpack	FFLAS-FFPACK Developer Documentation	fflas-ffpack ²¹²
fflas-ffpack-user-doc	fflas-ffpack	FFLAS-FFPACK User Documentation	fflas-ffpack ²¹²
fitgcp	fitgcp	fitting genome coverage distributions with mixture models	fitgcp ⁵¹⁶
fitscheck	pyfits	transitional package for pyfits-utils	pyfits ⁴⁹
fitsh	fitsh	Software package for astronomical image processing	fitsh ⁶⁵²
fitspng	fitspng	FITS to PNG converter	fitspng ³⁶¹

ftyk	ftyk	general-purpose nonlinear curve fitting and data analysis	ftyk ⁹²⁶
flexbar	flexbar	flexible barcode and adapter removal for sequencing platforms	flexbar ¹⁹⁹
fonts-circos-symbols	circos	plotter for visualizing data - standard fonts	circos ⁴⁵⁶
freebayes	freebayes	Bayesian haplotype-based polymorphism discovery and genotyping	freebayes ²⁷³
freecontact	freecontact	fast protein contact predictor	freecontact ⁴¹²
fsa	fsa	Fast Statistical Alignment of protein, RNA or DNA sequences	fsa ¹⁰⁰
fsl	fsl	transitional dummy package	fsl ³⁸⁸
fsl	fsl	transitional dummy package	fsl2004 ⁷⁹⁶
fsl	fsl	transitional dummy package	fsl2009 ⁹³⁴
fsl-4.1	fsl	analysis tools for FMRI, MRI and DTI brain imaging	fsl ³⁸⁸
fsl-4.1	fsl	analysis tools for FMRI, MRI and DTI brain imaging	fsl2004 ⁷⁹⁶
fsl-4.1	fsl	analysis tools for FMRI, MRI and DTI brain imaging	fsl2009 ⁹³⁴
fsl-5.0	fsl	transitional dummy package	fsl ³⁸⁸
fsl-5.0	fsl	transitional dummy package	fsl2004 ⁷⁹⁶
fsl-5.0	fsl	transitional dummy package	fsl2009 ⁹³⁴
fsl-5.0-core	fsl	analysis tools for FMRI, MRI and DTI brain imaging	fsl ³⁸⁸
fsl-5.0-core	fsl	analysis tools for FMRI, MRI and DTI brain imaging	fsl2004 ⁷⁹⁶
fsl-5.0-core	fsl	analysis tools for FMRI, MRI and DTI brain imaging	fsl2009 ⁹³⁴
fsl-core	fsl	metapackage for the latest version of FSL	fsl ³⁸⁸
fsl-core	fsl	metapackage for the latest version of FSL	fsl2004 ⁷⁹⁶
fsl-core	fsl	metapackage for the latest version of FSL	fsl2009 ⁹³⁴
fsl-doc-4.1	fsl	documentation for FSL	fsl ³⁸⁸
fsl-doc-4.1	fsl	documentation for FSL	fsl2004 ⁷⁹⁶
fsl-doc-4.1	fsl	documentation for FSL	fsl2009 ⁹³⁴
fslview	fslview	viewer for (f)MRI and DTI data	fslview ⁷⁹⁷
fslview-doc	fslview	Documentation for FSLView	fslview ⁷⁹⁷
ftools-fv	ftools-fv	Tool for viewing and editing FITS format files	ftools-fv ⁶⁶⁸
ftools-pow	ftools-fv	Curve plotting and image display interface tool	ftools-fv ⁶⁶⁸
funtools	funtools	Minimal buy-in FITS utility package	funtools ⁵⁴²
gabedit	gabedit	graphical user interface to Ab Initio packages	gabedit ¹⁴
garlic	garlic	visualization program for biomolecules	garlic ⁹⁸⁰
garlic	garlic	visualization program for biomolecules	garlic2005 ⁹⁷⁹
gasic	gasic	genome abundance similarity correction	gasic ⁵¹⁴
gatb-core	gatb-core	Genome Analysis Toolbox with de-Bruijn graph	gatb-core ²⁰⁸
gatb-core-testdata	gatb-core	Genome Analysis Toolbox with de-Bruijn graph (test data)	gatb-core ²⁰⁸
gausssum	gausssum	parse and display Gaussian, GAMESS, and etc's output	gausssum ⁶³¹
gbrowse	gbrowse	GMOD Generic Genome Browser	gbrowse ²⁰²
gbrowse-align	gbrowse	CAlign helper	gbrowse ²⁰²
gbrowse-data	gbrowse	Sample data to use GBrowse	gbrowse ²⁰²
gdc-doc	gdc	Grassroots DICOM documentation	gdc ³⁰²
gdf-tools	libgdf	IO library for the GDF – helper tools	libgdf ⁷⁶⁶
gdl-astrolib	idlastro	Low-level astronomy software for GDL	idlastro ⁴⁶⁸
gdl-coyote	coyote	GDL library from D. Fannings IDL courses	coyote ²³⁹
gdl-mpfit	mpfit	Robust non-linear least squares curve fitting for GDL	mpfit ⁵⁵²
gemma	gemma	Genome-wide Efficient Mixed Model Association	gemma ⁹⁷⁵
gemma	gemma	Genome-wide Efficient Mixed Model Association	gemma2013 ⁹⁷⁷
gemma	gemma	Genome-wide Efficient Mixed Model Association	gemma2014 ⁹⁷⁶
gemma	gemma	Genome-wide Efficient Mixed Model Association	gemma2017 ⁹⁷⁴
gemma-doc	gemma	Example folder for GEMMA	gemma ⁹⁷⁵
gemma-doc	gemma	Example folder for GEMMA	gemma2013 ⁹⁷⁷
gemma-doc	gemma	Example folder for GEMMA	gemma2014 ⁹⁷⁶
gemma-doc	gemma	Example folder for GEMMA	gemma2017 ⁹⁷⁴
genometester	genometester	toolkit for performing set operations on k-mer lists	genometester ⁴²⁰
genometester	genometester	toolkit for performing set operations on k-mer lists	genometester2007 ²⁰
genometester	genometester	toolkit for performing set operations on k-mer lists	genometester2017 ⁶⁵
genomethreader	genomethreader	software tool to compute gene structure predictions	genomethreader ³¹⁸
genometools	genometools	versatile genome analysis toolkit	genometools ³¹⁹

genometools-common	genometools	shared data files for GenomeTools	genometools ³¹⁹
genometools-dbg	genometools	versatile genome analysis toolkit, with debug symbols	genometools ³¹⁹
genometools-doc	genometools	documentation for GenomeTools	genometools ³¹⁹
gentle	gentle	suite to plan genetic cloning	gentle ⁵⁴⁴
getdp	getdp	general environment for the treatment of discrete problems	getdp ²¹¹
getdp-sparskit	getdp	general environment for the treatment of discrete problems	getdp ²¹¹
gff2aplot	gff2aplot	pair-wise alignment-plots for genomic sequences in PostScript	gff2aplot ⁶
gff2ps	gff2ps	produces PostScript graphical output from GFF-files	gff2ps ⁵
giira	giira	RNA-Seq driven gene finding incorporating ambiguous reads	giira ⁹⁷⁸
glam2	glam2	gapped protein motifs from unaligned sequences	glam2 ²⁶⁴
glam2	glam2	gapped protein motifs from unaligned sequences	glam22004 ²⁶³
glueviz	glueviz	Linked data visualization	glueviz ⁵⁵
gmap	gmap	spliced and SNP-tolerant alignment for mRNA and short reads	gmap ⁹⁴⁷
gmap	gmap	spliced and SNP-tolerant alignment for mRNA and short reads	gmap2005 ⁹⁴⁸
gmsh	gmsh	Three-dimensional finite element mesh generator	gmsh ²⁸⁴
gmsh-doc	gmsh	Three-dimensional finite element mesh generator documentation	gmsh ²⁸⁴
gmt	gmt	Generic Mapping Tools	gmt ⁹¹⁶
gmt	gmt	Generic Mapping Tools	gmt1991 ⁹¹³
gmt	gmt	Generic Mapping Tools	gmt1995 ⁹¹⁴
gmt	gmt	Generic Mapping Tools	gmt1998 ⁹¹⁵
gmt-common	gmt	Generic Mapping Tools - Architecture-independent files	gmt ⁹¹⁶
gmt-common	gmt	Generic Mapping Tools - Architecture-independent files	gmt1991 ⁹¹³
gmt-common	gmt	Generic Mapping Tools - Architecture-independent files	gmt1995 ⁹¹⁴
gmt-common	gmt	Generic Mapping Tools - Architecture-independent files	gmt1998 ⁹¹⁵
gmt-dbg	gmt	Generic Mapping Tools Library - Debugging symbols	gmt ⁹¹⁶
gmt-dbg	gmt	Generic Mapping Tools Library - Debugging symbols	gmt1991 ⁹¹³
gmt-dbg	gmt	Generic Mapping Tools Library - Debugging symbols	gmt1995 ⁹¹⁴
gmt-dbg	gmt	Generic Mapping Tools Library - Debugging symbols	gmt1998 ⁹¹⁵
gmt-doc	gmt	Documentation for GMT, the Generic Mapping Tools	gmt ⁹¹⁶
gmt-doc	gmt	Documentation for GMT, the Generic Mapping Tools	gmt1991 ⁹¹³
gmt-doc	gmt	Documentation for GMT, the Generic Mapping Tools	gmt1995 ⁹¹⁴
gmt-doc	gmt	Documentation for GMT, the Generic Mapping Tools	gmt1998 ⁹¹⁵
gmt-doc-pdf	gmt	PDF docs for GMT, the Generic Mapping Tools	gmt ⁹¹⁶
gmt-doc-pdf	gmt	PDF docs for GMT, the Generic Mapping Tools	gmt1991 ⁹¹³
gmt-doc-pdf	gmt	PDF docs for GMT, the Generic Mapping Tools	gmt1995 ⁹¹⁴
gmt-doc-pdf	gmt	PDF docs for GMT, the Generic Mapping Tools	gmt1998 ⁹¹⁵
gmt-examples	gmt	Example scripts illustrating the use of GMT	gmt ⁹¹⁶
gmt-examples	gmt	Example scripts illustrating the use of GMT	gmt1991 ⁹¹³
gmt-examples	gmt	Example scripts illustrating the use of GMT	gmt1995 ⁹¹⁴
gmt-examples	gmt	Example scripts illustrating the use of GMT	gmt1998 ⁹¹⁵
gmt-gshhg	gmt-gshhg	Global Self-consistent Hierarchical High-resolution Geography (GSHHG)	gmt-gshhg ⁹¹²
gmt-gshhg-full	gmt-gshhg	Full resolution coastlines for the Generic Mapping Tools	gmt-gshhg ⁹¹²
gmt-gshhg-high	gmt-gshhg	High resolution coastlines for the Generic Mapping Tools	gmt-gshhg ⁹¹²
gmt-gshhg-low	gmt-gshhg	Low resolution coastlines for the Generic Mapping Tools	gmt-gshhg ⁹¹²
gmt-tutorial-pdf	gmt	Tutorial for GMT, the Generic Mapping Tools (PDF)	gmt ⁹¹⁶

gmt-tutorial-pdf	gmt	Tutorial for GMT, the Generic Mapping Tools (PDF)	gmt1991 ⁹¹³
gmt-tutorial-pdf	gmt	Tutorial for GMT, the Generic Mapping Tools (PDF)	gmt1995 ⁹¹⁴
gmt-tutorial-pdf	gmt	Tutorial for GMT, the Generic Mapping Tools (PDF)	gmt1998 ⁹¹⁵
gnss-sdr	gnss-sdr	Global navigation satellite systems software defined receiver	gnss-sdr ²⁴⁶
gnuastro	gnuastro	GNU Astronomy Utilities programs	gnuastro ⁸
gnudatalanguage	gnudatalanguage	Free IDL compatible incremental compiler	gnudatalanguage ¹⁶⁰
goldendict-wordnet	wordnet	electronic lexical database of English language (goldendict)	wordnet ⁵⁷⁹
goldendict-wordnet	wordnet	electronic lexical database of English language (goldendict)	wordnet1998 ²⁴⁴
goldendict-wordnet	wordnet	electronic lexical database of English language (goldendict)	wordnet2005 ²⁴⁵
gpaw	gpaw	DFT and beyond within the projector-augmented wave method	gpaw ⁵⁹³
grinder	grinder	Versatile omics shotgun and amplicon sequencing read simulator	grinder ²¹
gringo	gringo	grounding tools for (disjunctive) logic programs	gringo ²⁸¹
gringo	gringo	grounding tools for (disjunctive) logic programs	gringo2011 ²⁷⁹
gringo	gringo	grounding tools for (disjunctive) logic programs	gringo2014 ²⁸⁰
gromacs	gromacs	Molecular dynamics simulator, with building and analysis tools	gromacs ³⁴⁹
gromacs	gromacs	Molecular dynamics simulator, with building and analysis tools	gromacs2001 ⁵¹³
gromacs	gromacs	Molecular dynamics simulator, with building and analysis tools	gromacs2005 ⁸⁸⁸
gromacs-data	gromacs	GROMACS molecular dynamics sim, data and documentation	gromacs ³⁴⁹
gromacs-data	gromacs	GROMACS molecular dynamics sim, data and documentation	gromacs2001 ⁵¹³
gromacs-data	gromacs	GROMACS molecular dynamics sim, data and documentation	gromacs2005 ⁸⁸⁸
gromacs-dev	gromacs	Dummy package for libgromacs-dev	gromacs ³⁴⁹
gromacs-dev	gromacs	Dummy package for libgromacs-dev	gromacs2001 ⁵¹³
gromacs-dev	gromacs	Dummy package for libgromacs-dev	gromacs2005 ⁸⁸⁸
gromacs-lam	gromacs	Transition package to gromacs-openmpi	gromacs ³⁴⁹
gromacs-lam	gromacs	Transition package to gromacs-openmpi	gromacs2001 ⁵¹³
gromacs-lam	gromacs	Transition package to gromacs-openmpi	gromacs2005 ⁸⁸⁸
gromacs-mpich	gromacs	Molecular dynamics sim, binaries for MPICH parallelization	gromacs ³⁴⁹
gromacs-mpich	gromacs	Molecular dynamics sim, binaries for MPICH parallelization	gromacs2001 ⁵¹³
gromacs-mpich	gromacs	Molecular dynamics sim, binaries for MPICH parallelization	gromacs2005 ⁸⁸⁸
gromacs-openmpi	gromacs	Molecular dynamics sim, binaries for OpenMPI parallelization	gromacs ³⁴⁹
gromacs-openmpi	gromacs	Molecular dynamics sim, binaries for OpenMPI parallelization	gromacs2001 ⁵¹³
gromacs-openmpi	gromacs	Molecular dynamics sim, binaries for OpenMPI parallelization	gromacs2005 ⁸⁸⁸
gubbins	gubbins	phylogenetic analysis of genome sequences	gubbins ¹⁶³
gwama	gwama	Genome-Wide Association Meta Analysis	gwama ⁶⁰⁴
gwama	gwama	Genome-Wide Association Meta Analysis	gwama2010 ⁶⁰⁵
gwyddion	gwyddion	Scanning Probe Microscopy visualization and analysis tool	gwyddion ⁶¹⁴
gwyddion-common	gwyddion	architecture-independent files for Gwyddion SPM analysis tool	gwyddion ⁶¹⁴
gwyddion-plugins	gwyddion	plugins for Gwyddion SPM analysis tool	gwyddion ⁶¹⁴
gyoto	gyoto	General relativistic geodesic integration and ray-tracing	gyoto ⁸⁹⁹
gyoto-bin	gyoto	General relativistic ray-tracing command-line interface	gyoto ⁸⁹⁹
gyoto-dbg	gyoto	debugging symbols for the Gyoto framework	gyoto ⁸⁹⁹
gyoto-doc	gyoto	documentation for the Gyoto library	gyoto ⁸⁹⁹
harvest-tools	harvest-tools	archiving and postprocessing for reference-compressed genomic multi-alignments	harvest-tools ⁸⁷⁵
hhsuite	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment	hhsuite ⁷¹⁷

hhsuite	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment	hhsuite2005 ⁸⁴⁴
hhsuite	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment	hhsuite2019 ⁸²⁵
hhsuite-data	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment (data)	hhsuite ⁷¹⁷
hhsuite-data	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment (data)	hhsuite2005 ⁸⁴⁴
hhsuite-data	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment (data)	hhsuite2019 ⁸²⁵
hhsuite-dbg	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment (debug)	hhsuite ⁷¹⁷
hhsuite-dbg	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment (debug)	hhsuite2005 ⁸⁴⁴
hhsuite-dbg	hhsuite	sensitive protein sequence searching based on HMM-HMM alignment (debug)	hhsuite2019 ⁸²⁵
hhsuite-doc	hhsuite	documentation for Hhsuite for HMM-HMM comparisons	hhsuite ⁷¹⁷
hhsuite-doc	hhsuite	documentation for Hhsuite for HMM-HMM comparisons	hhsuite2005 ⁸⁴⁴
hhsuite-doc	hhsuite	documentation for Hhsuite for HMM-HMM comparisons	hhsuite2019 ⁸²⁵
hilive	hilive	realtime alignment of Illumina reads	hilive ⁵¹⁷
hinge	hinge	long read genome assembler based on hinging	hinge ⁴¹⁵
hisat2	hisat2	graph-based alignment of short nucleotide reads to many genomes	hisat2 ⁴³¹
hmmer	hmmer	profile hidden Markov models for protein sequence analysis	hmmer ²²¹
hmmer	hmmer	profile hidden Markov models for protein sequence analysis	hmmer1995 ²²⁰
hmmer2	hmmer2	profile hidden Markov models for protein sequence analysis	hmmer2 ²²²
hmmer2-doc	hmmer2	profile hidden Markov models for protein sequence analysis (docs)	hmmer2 ²²²
hmmer2-pvm	hmmer2	HMMER programs with PVM (Parallel Virtual Machine) support	hmmer2 ²²²
hmmer-doc	hmmer	profile hidden Markov models for protein sequence analysis (docs)	hmmer ²²¹
hmmer-doc	hmmer	profile hidden Markov models for protein sequence analysis (docs)	hmmer1995 ²²⁰
hmmer-examples	hmmer	profile hidden Markov models for protein sequence analysis (examples)	hmmer ²²¹
hmmer-examples	hmmer	profile hidden Markov models for protein sequence analysis (examples)	hmmer1995 ²²⁰
hmmer-pvm	hmmer	HMMER programs with PVM (Parallel Virtual Machine) support	hmmer ²²¹
hmmer-pvm	hmmer	HMMER programs with PVM (Parallel Virtual Machine) support	hmmer1995 ²²⁰
htcondor	condor	distributed workload management system	condor ⁵²⁰
htcondor-dbg	condor	distributed workload management system - debugging symbols	condor ⁵²⁰
htcondor-dev	condor	distributed workload management system - development files	condor ⁵²⁰
htcondor-doc	condor	distributed workload management system - documentation	condor ⁵²⁰
htslib-test	htslib	Test data for HTSlib	htslib ⁴⁹⁹
hyphy-common	hyphy	Hypothesis testing using Phylogenies (common files)	hyphy ⁶⁸³
hyphygui	hyphy	Hypothesis testing using Phylogenies (GTK+ gui)	hyphy ⁶⁸³
hyphy-mpi	hyphy	Hypothesis testing using Phylogenies (MPI version)	hyphy ⁶⁸³
hyphy-pt	hyphy	Hypothesis testing using Phylogenies (pthreads version)	hyphy ⁶⁸³
idba	idba	iterative De Bruijn Graph short read assemblers	idba ⁶⁶⁹
idba	idba	iterative De Bruijn Graph short read assemblers	idba2013 ⁶⁷⁰
idba-extra	idba	iterative De Bruijn Graph short read assemblers (extra tools)	idba ⁶⁶⁹
idba-extra	idba	iterative De Bruijn Graph short read assemblers (extra tools)	idba2013 ⁶⁷⁰
igdiscover	igdiscover	analyzes antibody repertoires to find new V genes	igdiscover ¹⁵⁸

igdiscover-doc	igdiscover	analyzes antibody repertoires to find new V genes - doc	igdiscover ¹⁵⁸
igor	igor	infers V(D)J recombination processes from sequencing data	igor ⁵⁴⁹
igv	igv	Integrative Genomics Viewer	igv ⁷²⁵
igv	igv	Integrative Genomics Viewer	igv2012 ⁸⁶²
imagej	imagej	Image processing program with a focus on microscopy images	imagej ⁷⁷²
imview	imview	Image viewing and analysis application	imview ⁸⁴⁵
indelible	indelible	powerful and flexible simulator of biological evolution	indelible ²⁵¹
infernai	infernai	inference of RNA secondary structural alignments	infernai ⁶⁰⁹
infernai-dbg	infernai	debug information for infernai	infernai ⁶⁰⁹
infernai-doc	infernai	inference of RNA secondary structural alignments - documentation	infernai ⁶⁰⁹
inhomog	inhomog	kinematical backreaction and average scale factor evolution	inhomog ⁷⁴⁰
ipig	ipig	integrating PSMs into genome browser visualisations	ipig ⁴⁵⁹
iqtree	iqtree	efficient phylogenetic software by maximum likelihood	iqtree ⁶¹⁹
iraf	iraf	Image Reduction and Analysis Facility	iraf ⁸⁶⁸
iraf-dev	iraf	Image Reduction and Analysis Facility (development files)	iraf ⁸⁶⁸
iraf-fitsutil	iraf-fitsutil	FITS utilities for IRAF	iraf-fitsutil ⁹⁶³
iraf-mscred	iraf-mscred	CCD mosaic reduction package for IRAF	iraf-mscred ⁸⁸⁶
iraf-noao	iraf	IRAF NOAO data reduction package	iraf ⁸⁶⁸
iraf-noao-dev	iraf	IRAF NOAO data reduction package (development files)	iraf ⁸⁶⁸
iraf-rvsao	iraf-rvsao	IRAF package to obtain radial velocities from spectra	iraf-rvsao ⁴⁶²
iraf-wcstools	wcstools	Handle the WCS of a FITS image (IRAF package)	wcstools ⁵⁸¹
itksnap	itksnap	semi-automatic segmentation of structures in 3D images	itksnap ⁹⁵⁷
iva	iva	iterative virus sequence assembler	iva ³⁷⁰
jalview	jalview	multiple alignment editor	jalview ⁹¹⁰
jalview	jalview	multiple alignment editor	jalview2011 ⁸⁷⁷
jellyfish	jellyfish	count k-mers in DNA sequences	jellyfish ⁵⁴⁵
jellyfish1	jellyfish1	count k-mers in DNA sequences	jellyfish1 ⁵⁴⁶
jellyfish-examples	jellyfish	count k-mers in DNA sequences (examples for testing)	jellyfish ⁵⁴⁵
jemboss	emboss	graphical user interface to EMBOSS	emboss ⁷²⁰
jmodeltest	jmodeltest	HPC selection of models of nucleotide substitution	jmodeltest ¹⁷³
jmol	jmol	Molecular Viewer	jmol ³⁴⁸
jmol-applet	jmol	Jmol Java applet	jmol ³⁴⁸
ython-stilts	starjava-ttools	Starlink Tables Infrastructure Library Tool Set (Jython package)	starjava-ttools ⁸⁵³
kalign	kalign	Global and progressive multiple sequence alignment	kalign ⁴⁷⁹
kalign	kalign	Global and progressive multiple sequence alignment	kalign2005 ⁴⁸⁰
kalign	kalign	Global and progressive multiple sequence alignment	kalign2009 ⁴⁸¹
kallisto	kallisto	near-optimal RNA-Seq quantification	kallisto ¹⁰²
kallisto-examples	kallisto	near-optimal RNA-Seq quantification (example data)	kallisto ¹⁰²
kaptive	kaptive	obtain information about K and O types for Klebsiella genome assemblies	kaptive ⁹⁴⁹
kaptive-data	kaptive	reference data for kaptive for Klebsiella genome assemblies	kaptive ⁹⁴⁹
kaptive-example	kaptive	example data for kaptive for Klebsiella genome assemblies	kaptive ⁹⁴⁹
khmer	khmer	in-memory DNA sequence kmer counting, filtering & graph traversal	khmer ¹⁶⁴
khmer	khmer	in-memory DNA sequence kmer counting, filtering & graph traversal	khmer2008 ²⁰³
khmer	khmer	in-memory DNA sequence kmer counting, filtering & graph traversal	khmer2012 ⁶⁶⁷
khmer	khmer	in-memory DNA sequence kmer counting, filtering & graph traversal	khmer2012c ¹⁰⁷

khmer	khmer	in-memory DNA sequence kmer counting, filtering & graph traversal	khmer2014 ⁹⁶⁸
khmer	khmer	in-memory DNA sequence kmer counting, filtering & graph traversal	khmer2015 ⁹⁶⁹
khmer-common	khmer	common files for the khmer project tools	khmer ¹⁶⁴
khmer-common	khmer	common files for the khmer project tools	khmer2008 ²⁰³
khmer-common	khmer	common files for the khmer project tools	khmer2012 ⁶⁶⁷
khmer-common	khmer	common files for the khmer project tools	khmer2012c ¹⁰⁷
khmer-common	khmer	common files for the khmer project tools	khmer2014 ⁹⁶⁸
khmer-common	khmer	common files for the khmer project tools	khmer2015 ⁹⁶⁹
king-probe	king-probe	Evaluate and visualize protein interatomic packing	king-probe ⁹³⁶
kissplice	kissplice	Detection of various kinds of polymorphisms in RNA-seq data	kissplice ⁷⁵²
kleborate	kleborate	tool to screen Klebsiella genome assemblies	kleborate ⁴⁶⁶
kleborate	kleborate	tool to screen Klebsiella genome assemblies	kleborate2018 ⁴⁶⁷
kleborate-examples	kleborate	tool to screen Klebsiella genome assemblies (example data)	kleborate ⁴⁶⁶
kleborate-examples	kleborate	tool to screen Klebsiella genome assemblies (example data)	kleborate2018 ⁴⁶⁷
kma	kma	mapping genomic sequences to raw reads directly against redundant databases	kma ¹⁴⁸
kmc	kmc	count kmers in genomic sequences	kmc ¹⁸⁷
kmer	kmer	suite of tools for DNA sequence analysis	kmer ⁹⁰⁵
kmer	kmer	suite of tools for DNA sequence analysis	kmer2004 ³⁸²
kmer-examples	kmer	sample data for kmer suite of tools for DNA sequence analysis	kmer ⁹⁰⁵
kmer-examples	kmer	sample data for kmer suite of tools for DNA sequence analysis	kmer2004 ³⁸²
kmerresistance	kmerresistance	correlates mapped genes with the predicted species of WGS samples	kmerresistance ¹⁴⁷
kraken	kraken	assigning taxonomic labels to short DNA sequences	kraken ⁹³²
kraken2	kraken2	taxonomic classification system using exact k-mer matches	kraken2 ⁹³³
lagan	lagan	highly parametrizable pairwise global genome sequence aligner	lagan ¹¹²
lamarc	lamarc	Likelihood Analysis with Metropolis Algorithm using Random Coalescence	lamarc ⁴⁵⁸
lambda-align	lambda-align	Local Aligner for Massive Biological Data	lambda-align ³³⁷
lambda-align2	lambda-align2	Local Aligner for Massive Biological Data - v2	lambda-align2 ³³⁸
last-align	last-align	genome-scale comparison of biological sequences	last-align ²⁶⁶
last-align	last-align	genome-scale comparison of biological sequences	last-align2019 ²⁶²
leaff	kmer	biological sequence library utilities and applications	kmer ⁹⁰⁵
leaff	kmer	biological sequence library utilities and applications	kmer2004 ³⁸²
libace-perl	libace-perl	Object-Oriented Access to ACEDB Databases	libace-perl ⁸²²
libajax6	emboss	EMBOSS library for commands	emboss ⁷²⁰
libajax6-dev	emboss	development files for libajax	emboss ⁷²⁰
libaoflagger0	aoflagger	Find RFI in radio astronomical observations (shared lib)	aoflagger ⁶³⁴
libapbs1	apbs	Adaptive Poisson Boltzmann Solver	apbs ³⁹
libapbs1	apbs	Adaptive Poisson Boltzmann Solver	apbs1993 ³⁵⁷
libapbs1	apbs	Adaptive Poisson Boltzmann Solver	apbs1995 ³⁵⁸
libapbs1	apbs	Adaptive Poisson Boltzmann Solver	apbs2001 ³⁵⁶
libapbs1	apbs	Adaptive Poisson Boltzmann Solver	apbs2003 ⁴¹
libapbs-dev	apbs	Adaptive Poisson Boltzmann Solver	apbs ³⁹
libapbs-dev	apbs	Adaptive Poisson Boltzmann Solver	apbs1993 ³⁵⁷
libapbs-dev	apbs	Adaptive Poisson Boltzmann Solver	apbs1995 ³⁵⁸
libapbs-dev	apbs	Adaptive Poisson Boltzmann Solver	apbs2001 ³⁵⁶
libapbs-dev	apbs	Adaptive Poisson Boltzmann Solver	apbs2003 ⁴¹
libarmci-mpi-dev	armci-mpi	ARMCI-MPI (Development version)	armci-mpi ¹⁹⁶
libarrayfire-cpu3	arrayfire	High performance library for parallel computing (CPU backend)	arrayfire ⁹⁵³
libarrayfire-cpu-dev	arrayfire	Development files for ArrayFire (CPU backend)	arrayfire ⁹⁵³
libarrayfire-dev	arrayfire	Common development files for ArrayFire	arrayfire ⁹⁵³
libarrayfire-doc	arrayfire	Common documentation and examples for ArrayFire	arrayfire ⁹⁵³
libarrayfire-ocl3	arrayfire	High performance library for parallel computing (OpenCL backend)	arrayfire ⁹⁵³

libarrayfire-opencl-dev	arrayfire	Development files for ArrayFire (OpenCL backend)	arrayfire ⁹⁵³
libarrayfire-unified3	arrayfire	High performance library for parallel computing (unified backend)	arrayfire ⁹⁵³
libarrayfire-unified-dev	arrayfire	Development files for ArrayFire (unified backend)	arrayfire ⁹⁵³
libasl0	asl	multiphysics simulation software	asl ¹⁵⁷
libasl-dev	asl	development files for ASL	asl ¹⁵⁷
libastrometry0	astrometry.net	Astrometry plate solver (shared lib)	astrometry-net ⁴⁶⁹
libastrometry-dev	astrometry.net	Astrometry plate solver (development files)	astrometry-net ⁴⁶⁹
libavogadro1	avogadro	Molecular Graphics and Modelling System (library)	avogadro ³³²
libavogadro2-1	avogadrolibs	Molecular Graphics and Modelling System (library)	avogadrolibs ³³³
libavogadro-dev	avogadrolibs	Molecular Graphics and Modelling System (development files)	avogadrolibs ³³³
libavogadro-doc	avogadrolibs	Molecular Graphics and Modelling System (lib documentation)	avogadrolibs ³³³
libball1.3	ball	Biochemical Algorithms Library	ball ⁵⁸⁵
libball1.3	ball	Biochemical Algorithms Library	ball2010 ³⁵⁰
libball1.3-dev	ball	Header files for the Biochemical Algorithms Library	ball ⁵⁸⁵
libball1.3-dev	ball	Header files for the Biochemical Algorithms Library	ball2010 ³⁵⁰
libball1.3-doc	ball	Documentation for the BALL library	ball ⁵⁸⁵
libball1.3-doc	ball	Documentation for the BALL library	ball2010 ³⁵⁰
libball1.4	ball	Biochemical Algorithms Library	ball ⁵⁸⁵
libball1.4	ball	Biochemical Algorithms Library	ball2010 ³⁵⁰
libball1.4-data	ball	Biochemical Algorithms Library (data files)	ball ⁵⁸⁵
libball1.4-data	ball	Biochemical Algorithms Library (data files)	ball2010 ³⁵⁰
libball1.4-dev	ball	Header files for the Biochemical Algorithms Library	ball ⁵⁸⁵
libball1.4-dev	ball	Header files for the Biochemical Algorithms Library	ball2010 ³⁵⁰
libball1.4-doc	ball	documentation for the BALL library	ball ⁵⁸⁵
libball1.4-doc	ball	documentation for the BALL library	ball2010 ³⁵⁰
libball1.5	ball	Biochemical Algorithms Library	ball ⁵⁸⁵
libball1.5	ball	Biochemical Algorithms Library	ball2010 ³⁵⁰
libball1.5-data	ball	Biochemical Algorithms Library (data files)	ball ⁵⁸⁵
libball1.5-data	ball	Biochemical Algorithms Library (data files)	ball2010 ³⁵⁰
libball1.5-dev	ball	Header files for the Biochemical Algorithms Library	ball ⁵⁸⁵
libball1.5-dev	ball	Header files for the Biochemical Algorithms Library	ball2010 ³⁵⁰
libball1.5-doc	ball	documentation for the BALL library	ball ⁵⁸⁵
libball1.5-doc	ball	documentation for the BALL library	ball2010 ³⁵⁰
libballview1.3	ball	Biochemical Algorithms Library, VIEW framework	ball ⁵⁸⁵
libballview1.3	ball	Biochemical Algorithms Library, VIEW framework	ball2010 ³⁵⁰
libballview1.3-dev	ball	Header files for the VIEW part of the Biochemical Algorithms Library	ball ⁵⁸⁵
libballview1.3-dev	ball	Header files for the VIEW part of the Biochemical Algorithms Library	ball2010 ³⁵⁰
libballview1.4	ball	Biochemical Algorithms Library, VIEW framework	ball ⁵⁸⁵
libballview1.4	ball	Biochemical Algorithms Library, VIEW framework	ball2010 ³⁵⁰
libballview1.4-dev	ball	Header files for the VIEW part of the Biochemical Algorithms Library	ball ⁵⁸⁵
libballview1.4-dev	ball	Header files for the VIEW part of the Biochemical Algorithms Library	ball2010 ³⁵⁰
libballview1.5	ball	Biochemical Algorithms Library, VIEW framework	ball ⁵⁸⁵
libballview1.5	ball	Biochemical Algorithms Library, VIEW framework	ball2010 ³⁵⁰
libballview1.5-dev	ball	Header files for the VIEW part of the Biochemical Algorithms Library	ball ⁵⁸⁵
libballview1.5-dev	ball	Header files for the VIEW part of the Biochemical Algorithms Library	ball2010 ³⁵⁰
libbamtools2.3.0	bamtools	dynamic library for manipulating BAM (genome alignment) files	bamtools ⁴⁷

libbamtools2.4.0	bamtools	dynamic library for manipulating BAM (genome alignment) files	bamtools ⁴⁷
libbamtools2.5.1	bamtools	dynamic library for manipulating BAM (genome alignment) files	bamtools ⁴⁷
libbamtools-dev	bamtools	C++ API for manipulating BAM (genome alignment) files	bamtools ⁴⁷
libbamtools-doc	bamtools	docs for dynamic library for manipulating BAM (genome alignment) files	bamtools ⁴⁷
libbiojava1.7-java	biojava-live	Java API to biological data and applications (version 1.7)	biojava-live ³⁵⁴
libbiojava-java	biojava-live	Java API to biological data and applications (default version)	biojava-live ³⁵⁴
libbiojava-java-demos	biojava-live	Example programs for BioJava	biojava-live ³⁵⁴
libbiojava-java-doc	biojava-live	[Biology] Documentation for BioJava	biojava-live ³⁵⁴
libbio-perl-perl	bioperl	BioPerl core perl modules	bioperl ⁸¹³
libbiosig1	biosig4c++	I/O library for biomedical data - dynamic library	biosig4c ⁻⁷⁶⁷
libbiosig1-dbg	biosig4c++	I/O library for biomedical data - debug symbols	biosig4c ⁻⁷⁶⁷
libbiosig2	biosig4c++	I/O library for biomedical data - dynamic library	biosig4c ⁻⁷⁶⁷
libbiosig-dev	biosig4c++	I/O library for biomedical data - development files	biosig4c ⁻⁷⁶⁷
libblimps3	blimps	blocks database improved searcher library	blimps ³⁴³
libblimps3-dev	blimps	blocks database improved searcher library (development)	blimps ³⁴³
libblis2	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis2-openmp	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis2-pthread	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis2-serial	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis3	blis	BLAS-like Library Instantiation Software Framework (32bit,meta)	blis ⁸⁹¹
libblis3-openmp	blis	BLAS-like Library Instantiation Software Framework (32bit,openmp)	blis ⁸⁹¹
libblis3-pthread	blis	BLAS-like Library Instantiation Software Framework (32bit,pthread)	blis ⁸⁹¹
libblis3-serial	blis	BLAS-like Library Instantiation Software Framework (32bit,serial)	blis ⁸⁹¹
libblis64-2	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis64-2-openmp	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis64-2-pthread	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis64-2-serial	blis	BLAS-like Library Instantiation Software Framework - shared library	blis ⁸⁹¹
libblis64-3	blis	BLAS-like Library Instantiation Software Framework (64bit,meta)	blis ⁸⁹¹
libblis64-3-openmp	blis	BLAS-like Library Instantiation Software Framework (64bit,openmp)	blis ⁸⁹¹
libblis64-3-pthread	blis	BLAS-like Library Instantiation Software Framework (64bit,pthread)	blis ⁸⁹¹
libblis64-3-serial	blis	BLAS-like Library Instantiation Software Framework (64bit,serial)	blis ⁸⁹¹
libblis64-dev	blis	BLAS-like Library Instantiation Software Framework (dev,64bit,meta)	blis ⁸⁹¹
libblis64-openmp-dev	blis	BLAS-like Library Instantiation Software Framework (dev,64bit,openmp)	blis ⁸⁹¹
libblis64-pthread-dev	blis	BLAS-like Library Instantiation Software Framework (dev,64bit,pthread)	blis ⁸⁹¹
libblis64-serial-dev	blis	BLAS-like Library Instantiation Software Framework (dev,64bit,serial)	blis ⁸⁹¹
libblis-dev	blis	BLAS-like Library Instantiation Software Framework (dev,32bit,meta)	blis ⁸⁹¹
libblis-openmp-dev	blis	BLAS-like Library Instantiation Software Framework (dev,32bit,openmp)	blis ⁸⁹¹
libblis-pthread-dev	blis	BLAS-like Library Instantiation Software Framework (dev,32bit,pthread)	blis ⁸⁹¹
libblis-serial-dev	blis	BLAS-like Library Instantiation Software Framework (dev,32bit,serial)	blis ⁸⁹¹
libbwa-dev	bwa	Burrows-Wheeler Aligner source files	bwa ⁵⁰³

libcaffe1	caffe	library of Caffe, deep learning framework (CPU_ONLY)	caffe ³⁹⁰
libcaffe-cpu1	caffe	library of Caffe, deep learning framework (CPU_ONLY)	caffe ³⁹⁰
libcaffe-cpu-dev	caffe	development files for Caffe (CPU_ONLY)	caffe ³⁹⁰
libcaffe-cuda1	caffe-contrib	library of Caffe, deep learning framework (CUDA)	caffe-contrib ³⁹¹
libcaffe-cuda-dev	caffe-contrib	development files for Caffe (CUDA)	caffe-contrib ³⁹¹
libcaffe-dev	caffe	development files for Caffe (CPU_ONLY)	caffe ³⁹⁰
libcamltk3	camitk	Computer Assisted Medical Intervention Tool Kit - runtime	camitk ²⁵⁶
libcamltk3-data	camitk	Computer Assisted Medical Intervention Tool Kit - data	camitk ²⁵⁶
libcamltk3-dev	camitk	Computer Assisted Medical Intervention Tool Kit - development	camitk ²⁵⁶
libcamltk3-doc	camitk	Computer Assisted Medical Intervention Tool Kit - documentation	camitk ²⁵⁶
libcamltk4	camitk	Computer Assisted Medical Intervention Tool Kit - runtime	camitk ²⁵⁶
libcamltk4-data	camitk	Computer Assisted Medical Intervention Tool Kit - data	camitk ²⁵⁶
libcamltk4-doc	camitk	Computer Assisted Medical Intervention Tool Kit - documentation	camitk ²⁵⁶
libcamltk-dev	camitk	Computer Assisted Medical Intervention Tool Kit - development	camitk ²⁵⁶
libcdk-java	cdk	Chemistry Development Kit (CDK) Java libraries	cdk ⁹²⁵
libexceptions0	cod-tools	C exception handling library	cod-tools ³¹⁶
libexceptions-dev	cod-tools	C exception handling library (development files)	cod-tools ³¹⁶
libcext0	cpl	Commonly used utility functions for C programs	cpl ⁴⁴
libcext-dev	cpl	Commonly used utility functions for C programs (development files)	cpl ⁴⁴
libcext-doc	cpl	API documentation for ESO's C utility library	cpl ⁴⁴
libchemps2-2	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps2 ¹³⁶
libchemps2-2	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22014 ⁹⁴¹
libchemps2-2	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22014c ⁹³⁷
libchemps2-2	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22014d ⁹³⁹
libchemps2-2	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22016 ⁹⁴³
libchemps2-3	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps2 ¹³⁶
libchemps2-3	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22014 ⁹⁴¹
libchemps2-3	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22014c ⁹³⁷
libchemps2-3	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22014d ⁹³⁹
libchemps2-3	chemps2	Spin-adapted DMRG for ab initio quantum chemistry	chemps22016 ⁹⁴³
libchemps2-dev	chemps2	C++ headers, static library, and symlink for libchemps2-3	chemps2 ¹³⁶
libchemps2-dev	chemps2	C++ headers, static library, and symlink for libchemps2-3	chemps22014 ⁹⁴¹
libchemps2-dev	chemps2	C++ headers, static library, and symlink for libchemps2-3	chemps22014c ⁹³⁷
libchemps2-dev	chemps2	C++ headers, static library, and symlink for libchemps2-3	chemps22014d ⁹³⁹
libchemps2-dev	chemps2	C++ headers, static library, and symlink for libchemps2-3	chemps22016 ⁹⁴³
libclassad3	condor	Condor classads expression language - runtime library	condor ⁵²⁰
libclassad7	condor	HTCondor classads expression language - runtime library	condor ⁵²⁰
libclassad8	condor	HTCondor classads expression language - runtime library	condor ⁵²⁰
libclassad-dev	condor	HTCondor classads expression language - development library	condor ⁵²⁰
libclustalo-dev	clustalo	Library to embed Clustal Omega	clustalo ⁷⁸⁹

libclustalo-dev	clustalo	Library to embed Clustal Omega	clustalo2018 ⁷⁸⁸
libclustalo-doc	clustalo	API documentation for library to embed Clustal Omega	clustalo ⁷⁸⁹
libclustalo-doc	clustalo	API documentation for library to embed Clustal Omega	clustalo2018 ⁷⁸⁸
libcminpack1	cminpack	Nonlinear equations and nonlinear least squares problems - runtime	cminpack ¹⁹¹
libcminpack1.0.90	cminpack	Nonlinear equations and nonlinear least squares problems - runtime	cminpack ¹⁹¹
libcminpack-dev	cminpack	Nonlinear equations and nonlinear least squares problems - development	cminpack ¹⁹¹
libcnrun2	cnrun	NeuroML-capable neuronal network simulator (shared lib)	cnrun ⁹⁶⁴
libcnrun2-dev	cnrun	NeuroML-capable neuronal network simulator (development files)	cnrun ⁹⁶⁴
libcodcif2	cod-tools	error-correcting CIF parser - shared library	cod-tools ³¹⁶
libcodcif-dev	cod-tools	error-correcting CIF parser - headers and static libraries	cod-tools ³¹⁶
libcod-cif-parser-bison-perl	cod-tools	error-correcting CIF parser - Perl bindings	cod-tools ³¹⁶
libcod-cif-parser-yapp-perl	cod-tools	error-correcting CIF parser - pure Perl implementation	cod-tools ³¹⁶
libcod-precision-perl	cod-tools	COD precision handling module for Perl language	cod-tools ³¹⁶
libcod-usermessage-perl	cod-tools	COD message formatting module for Perl language	cod-tools ³¹⁶
libcplcore20	cpl	Fundamental CPL data types and functions	cpl ⁴⁴
libcplcore26	cpl	Fundamental CPL data types and functions	cpl ⁴⁴
libcpl-dev	cpl	ESO library for automated astronomical data-reduction	cpl ⁴⁴
libcpldfs20	cpl	CPL functions for Data Flow System compatibility	cpl ⁴⁴
libcpldfs26	cpl	CPL functions for Data Flow System compatibility	cpl ⁴⁴
libcpl-doc	cpl	API documentation for the Common Pipeline Library	cpl ⁴⁴
libcpldrs20	cpl	CPL higher level data processing algorithms	cpl ⁴⁴
libcpldrs26	cpl	CPL higher level data processing algorithms	cpl ⁴⁴
libcplgasgano20	cpl	CPL Java Native Interface library	cpl ⁴⁴
libcplgasgano26	cpl	CPL Java Native Interface library	cpl ⁴⁴
libcplui20	cpl	CPL framework interface library	cpl ⁴⁴
libcplui26	cpl	CPL framework interface library	cpl ⁴⁴
libcv2.1	opencv	computer vision library	opencv ¹⁰¹
libcv2.3	opencv	computer vision library - libcv* translation package	opencv ¹⁰¹
libcv2.4	opencv	computer vision library - libcv* translation package	opencv ¹⁰¹
libcvaux2.1	opencv	computer vision extension library	opencv ¹⁰¹
libcvaux2.3	opencv	computer vision library - libcvaux translation package	opencv ¹⁰¹
libcvaux2.4	opencv	computer vision library - libcvaux translation package	opencv ¹⁰¹
libcvaux-dev	opencv	Translation package for libcvaux-dev	opencv ¹⁰¹
libcv-dev	opencv	Translation package for libcv-dev	opencv ¹⁰¹
libelpa0	elpa	Eigenvalue SoLvers for Petaflop-Applications	elpa ³²
libelpa0	elpa	Eigenvalue SoLvers for Petaflop-Applications	elpa2014 ⁵⁵⁰
libelpa15	elpa	Eigenvalue SoLvers for Petaflop-Applications	elpa ³²
libelpa15	elpa	Eigenvalue SoLvers for Petaflop-Applications	elpa2014 ⁵⁵⁰
libelpa4	elpa	Eigenvalue SoLvers for Petaflop-Applications	elpa ³²
libelpa4	elpa	Eigenvalue SoLvers for Petaflop-Applications	elpa2014 ⁵⁵⁰
libelpa-dev	elpa	Eigenvalue SoLvers for Petaflop-Applications (Development version)	elpa ³²
libelpa-dev	elpa	Eigenvalue SoLvers for Petaflop-Applications (Development version)	elpa2014 ⁵⁵⁰
libfreecontact0	freecontact	fast protein contact predictor library	freecontact ⁴¹²
libfreecontact0-dbg	freecontact	debugging symbols for libfreecontact	freecontact ⁴¹²
libfreecontact0-dev	freecontact	fast protein contact predictor library - development files	freecontact ⁴¹²
libfreecontact0v5	freecontact	fast protein contact predictor library	freecontact ⁴¹²
libfreecontact-dev	freecontact	fast protein contact predictor library - development files	freecontact ⁴¹²
libfreecontact-doc	freecontact	documentation for libfreecontact	freecontact ⁴¹²
libfreecontact-perl	libfreecontact-perl	fast protein contact predictor - binding for Perl	libfreecontact-perl ⁴¹

libfuntools1	funtools	Minimal buy-in FITS library	funtools ⁵⁴²
libfuntools-dev	funtools	Minimal buy-in FITS library (development files)	funtools ⁵⁴²
libgatbcore2	gatb-core	dynamic library of the Genome Analysis Toolbox	gatb-core ²⁰⁸
libgatbcore3	gatb-core	dynamic library of the Genome Analysis Toolbox	gatb-core ²⁰⁸
libgatbcore-dev	gatb-core	development library of the Genome Analysis Toolbox	gatb-core ²⁰⁸
libgbttools0	seqtools	library for visualising sequence alignments	seqtools ⁵⁰
libgbttools0	seqtools	library for visualising sequence alignments	seqtools1994 ⁸⁰⁴
libgbttools0	seqtools	library for visualising sequence alignments	seqtools2005 ⁸⁰⁶
libgbttools-dev	seqtools	library for visualising sequence alignments (devel)	seqtools ⁵⁰
libgbttools-dev	seqtools	library for visualising sequence alignments (devel)	seqtools1994 ⁸⁰⁴
libgbttools-dev	seqtools	library for visualising sequence alignments (devel)	seqtools2005 ⁸⁰⁶
libgdcm2.0	gdcm	Grassroots DICOM runtime libraries	gdcm ³⁰²
libgdcm2.0-dbg	gdcm	Grassroots DICOM runtime libraries, debug version	gdcm ³⁰²
libgdcm2.2	gdcm	Grassroots DICOM runtime libraries	gdcm ³⁰²
libgdcm2.2-dbg	gdcm	Grassroots DICOM runtime libraries, debug version	gdcm ³⁰²
libgdcm2.4	gdcm	Grassroots DICOM runtime libraries	gdcm ³⁰²
libgdcm2.4-dbg	gdcm	Grassroots DICOM runtime libraries, debug version	gdcm ³⁰²
libgdcm2.6	gdcm	Grassroots DICOM runtime libraries	gdcm ³⁰²
libgdcm2.6-dbg	gdcm	Grassroots DICOM runtime libraries, debug version	gdcm ³⁰²
libgdcm2.8	gdcm	Grassroots DICOM runtime libraries	gdcm ³⁰²
libgdcm2-dev	gdcm	Grassroots DICOM development libraries and headers	gdcm ³⁰²
libgdcm3.0	gdcm	Grassroots DICOM runtime libraries	gdcm ³⁰²
libgdcm-cil	gdcm	Grassroots DICOM CLI bindings	gdcm ³⁰²
libgdcm-dev	gdcm	Grassroots DICOM development libraries and headers	gdcm ³⁰²
libgdcm-java	gdcm	Grassroots DICOM Java bindings	gdcm ³⁰²
libgdcm-tools	gdcm	Grassroots DICOM tools and utilities	gdcm ³⁰²
libgdf0	libgdf	IO library for the GDF (general dataformat for biosignals)	libgdf ⁷⁶⁶
libgdf0-dbg	libgdf	IO library for the GDF – debug symbols	libgdf ⁷⁶⁶
libgdf-dev	libgdf	IO library for the GDF – development library	libgdf ⁷⁶⁶
libgenometools0	genometools	versatile genome analysis library	genometools ³¹⁹
libgenometools0-dev	genometools	development files for GenomeTools	genometools ³¹⁹
libgetoptions0	cod-tools	Command line argument processing library for C	cod-tools ³¹⁶
libgetoptions-dev	cod-tools	Command line argument processing library for C (development files)	cod-tools ³¹⁶
libgkarrays1	libgkarrays	library to query large collection of NGS sequences	libgkarrays ⁶⁷⁶
libgkarrays-dev	libgkarrays	library to query large collection of NGS sequences (development)	libgkarrays ⁶⁷⁶
libglobalarrays-dev	ga	Distributed Shared-Memory Programming Environment (development)	ga ⁶²¹
libglobalarrays-dev	ga	Distributed Shared-Memory Programming Environment (development)	ga2012 ⁴⁵⁴
libgmsh2	gmsh	Three-dimensional finite element mesh generator. Shared library	gmsh ²⁸⁴
libgmsh2v5	gmsh	Three-dimensional finite element mesh generator. Shared library	gmsh ²⁸⁴
libgmsh4	gmsh	Three-dimensional finite element mesh generator shared library	gmsh ²⁸⁴
libgmsh4.1	gmsh	Three-dimensional finite element mesh generator shared library	gmsh ²⁸⁴
libgmsh-dev	gmsh	Three-dimensional finite element mesh generator development files	gmsh ²⁸⁴
libgmt4	gmt	Generic Mapping Tools Library	gmt ⁹¹⁶
libgmt4	gmt	Generic Mapping Tools Library	gmt1991 ⁹¹³
libgmt4	gmt	Generic Mapping Tools Library	gmt1995 ⁹¹⁴
libgmt4	gmt	Generic Mapping Tools Library	gmt1998 ⁹¹⁵
libgmt5	gmt	Generic Mapping Tools Library	gmt ⁹¹⁶
libgmt5	gmt	Generic Mapping Tools Library	gmt1991 ⁹¹³
libgmt5	gmt	Generic Mapping Tools Library	gmt1995 ⁹¹⁴
libgmt5	gmt	Generic Mapping Tools Library	gmt1998 ⁹¹⁵
libgmt6	gmt	Generic Mapping Tools Library	gmt ⁹¹⁶
libgmt6	gmt	Generic Mapping Tools Library	gmt1991 ⁹¹³
libgmt6	gmt	Generic Mapping Tools Library	gmt1995 ⁹¹⁴
libgmt6	gmt	Generic Mapping Tools Library	gmt1998 ⁹¹⁵

libgmt-dev	gmt	Generic Mapping Tools Library - Development files	gmt ⁹¹⁶
libgmt-dev	gmt	Generic Mapping Tools Library - Development files	gmt1991 ⁹¹³
libgmt-dev	gmt	Generic Mapping Tools Library - Development files	gmt1995 ⁹¹⁴
libgmt-dev	gmt	Generic Mapping Tools Library - Development files	gmt1998 ⁹¹⁵
libgnuastro1	gnuastro	GNU Astronomy Utilities shared libraries	gnuastro ⁸
libgnuastro10	gnuastro	GNU Astronomy Utilities shared libraries	gnuastro ⁸
libgnuastro6	gnuastro	GNU Astronomy Utilities shared libraries	gnuastro ⁸
libgnuastro9	gnuastro	GNU Astronomy Utilities shared libraries	gnuastro ⁸
libgnuastro-dev	gnuastro	GNU Astronomy Utilities development files	gnuastro ⁸
libgnudatalanguage0	gnudatalanguage	Free IDL compatible incremental compiler shared library	gnudatalanguage ¹⁶⁰
libgromacs2	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs ³⁴⁹
libgromacs2	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs2001 ⁵¹³
libgromacs2	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs2005 ⁸⁸⁸
libgromacs4	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs ³⁴⁹
libgromacs4	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs2001 ⁵¹³
libgromacs4	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs2005 ⁸⁸⁸
libgromacs5	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs ³⁴⁹
libgromacs5	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs2001 ⁵¹³
libgromacs5	gromacs	GROMACS molecular dynamics sim, shared libraries	gromacs2005 ⁸⁸⁸
libgromacs-dev	gromacs	GROMACS molecular dynamics sim, development kit	gromacs ³⁴⁹
libgromacs-dev	gromacs	GROMACS molecular dynamics sim, development kit	gromacs2001 ⁵¹³
libgromacs-dev	gromacs	GROMACS molecular dynamics sim, development kit	gromacs2005 ⁸⁸⁸
libgwyddion2-0	gwyddion	libraries for Gwyddion SPM analysis tool	gwyddion ⁶¹⁴
libgwyddion20-dev	gwyddion	header files for Gwyddion SPM analysis tool	gwyddion ⁶¹⁴
libgwyddion20-doc	gwyddion	HTML library API documentation for Gwyddion SPM analysis tool	gwyddion ⁶¹⁴
libgyoto0	gyoto	General relativistic geodesic integration and ray-tracing	gyoto ⁸⁹⁹
libgyoto0-dev	gyoto	development files for libgyoto	gyoto ⁸⁹⁹
libgyoto2	gyoto	General relativistic geodesic integration and ray-tracing	gyoto ⁸⁹⁹
libgyoto2-dev	gyoto	development files for libgyoto	gyoto ⁸⁹⁹
libgyoto6	gyoto	Gyoto framework main library an standard plugin	gyoto ⁸⁹⁹
libgyoto6-dev	gyoto	development files for libgyoto	gyoto ⁸⁹⁹
libgyoto7	gyoto	Gyoto framework main library an standard plugin	gyoto ⁸⁹⁹
libgyoto7-dev	gyoto	development files for libgyoto	gyoto ⁸⁹⁹
libgyoto8	gyoto	Gyoto framework main library an standard plugin	gyoto ⁸⁹⁹
libgyoto8-dev	gyoto	development files for libgyoto	gyoto ⁸⁹⁹
libhat-trie0	libhat-trie	HAT-trie, an extremely efficient (space and time) modern variant of tries	libhat-trie ²⁹
libhat-trie0	libhat-trie	HAT-trie, an extremely efficient (space and time) modern variant of tries	libhat-trie2005 ³⁰
libhat-trie-dev	libhat-trie	Development headers and static libraries for HAT-trie library	libhat-trie ²⁹
libhat-trie-dev	libhat-trie	Development headers and static libraries for HAT-trie library	libhat-trie2005 ³⁰
libhighgui2.1	opencv	computer vision GUI library	opencv ¹⁰¹
libhighgui2.3	opencv	computer vision library - libhighgui translation package	opencv ¹⁰¹
libhighgui2.4	opencv	computer vision library - libhighgui translation package	opencv ¹⁰¹

libhighgui-dev	opencv	Translation package for libhighgui-dev	opencv ¹⁰¹
libhmm2-dev	hmm2	profile hidden Markov models for protein sequence analysis (devel)	hmm2 ²²²
libhmsbeagle	libhmsbeagle	High-performance lib for Bayesian and Maximum Likelihood phylogenetics	libhmsbeagle ³⁵
libhmsbeagle1v5	libhmsbeagle	High-performance lib for Bayesian and Maximum Likelihood phylogenetics	libhmsbeagle ³⁵
libhmsbeagle-dev	libhmsbeagle	High-performance lib for Bayesian and Maximum Likelihood phylogenetics (devel)	libhmsbeagle ³⁵
libhmsbeagle-java	libhmsbeagle	High-performance lib for Bayesian and Maximum Likelihood phylogenetics (java)	libhmsbeagle ³⁵
libhts1	htslib	C library for high-throughput sequencing data formats	htslib ⁴⁹⁹
libhts2	htslib	C library for high-throughput sequencing data formats	htslib ⁴⁹⁹
libhts3	htslib	C library for high-throughput sequencing data formats	htslib ⁴⁹⁹
libhts-dev	htslib	development files for the HTSlib	htslib ⁴⁹⁹
libhts-private-dev	htslib	private development files for the HTSlib (use with care)	htslib ⁴⁹⁹
libij-java	imagej	Java library for ImageJ	imagej ⁷⁷²
libij-java-doc	imagej	documentation of libij-java	imagej ⁷⁷²
libinhomog0	inhomog	shared library for kin.backreaction/average scale factor	inhomog ⁷⁴⁰
libinhomog-dev	inhomog	static library for kin.backreaction/average scale factor	inhomog ⁷⁴⁰
libispec++1	ispec	Isotopic fine structure calculator (C++ runtime)	ispec ⁵⁶³
libispec++2	ispec	Isotopic fine structure calculator (C++ runtime)	ispec ⁵⁶³
libispec++-dev	ispec	Isotopic fine structure calculator (C++ development files)	ispec ⁵⁶³
libispec++-doc	ispec	Isotopic fine structure calculator (C++ API documentation)	ispec ⁵⁶³
libjava-gmsh2	gmsh	Three-dimensional finite element mesh generator. Java wrapper	gmsh ²⁸⁴
libjellyfish-2.0-2	jellyfish	count k-mers in DNA sequences (dynamic library of jellyfish)	jellyfish ⁵⁴⁵
libjellyfish-2.0-dev	jellyfish	count k-mers in DNA sequences (development files of jellyfish)	jellyfish ⁵⁴⁵
libjellyfish-perl	jellyfish	count k-mers in DNA sequences (Perl bindings of jellyfish)	jellyfish ⁵⁴⁵
libjloda-java	libjloda-java	Java library of data structures and algorithms for bioinformatics	libjloda-java ³⁴⁶
libjmol-java	jmol	Java library for molecular structures	jmol ³⁴⁸
libjmol-java-doc	jmol	API documentation for libjmol-java	jmol ³⁴⁸
libjs-jquery-datatables	datatables.js	jQuery plug-in that makes nice tables from different data sources	datatables.js ¹⁷⁶
libjung-free-java	libjung-free-java	Java Universal Network/Graph Framework	libjung-free-java ⁶⁴⁷
libjung-free-java-doc	libjung-free-java	Java Universal Network/Graph Framework (documentation)	libjung-free-java ⁶⁴⁷
libkmc-dev	kmc	library to access KMC k-mer count files	kmc ¹⁸⁷
libkmer-dev	kmer	suite of tools for DNA sequence analysis (development lib)	kmer ⁹⁰⁵
libkmer-dev	kmer	suite of tools for DNA sequence analysis (development lib)	kmer2004 ³⁸²
libm4ri-0.0.20080521	libm4ri	Method of the Four Russians Inversion library, shared library	libm4ri ¹²
libm4ri-0.0.20140914	libm4ri	Method of the Four Russians Inversion library, shared library	libm4ri ¹²
libm4ri-0.0.20140914-dbg	libm4ri	debugging symbols for libm4ri-0.0.20140914	libm4ri ¹²
libm4ri-0.0.20200125	libm4ri	Method of the Four Russians Inversion library, shared library	libm4ri ¹²
libm4ri-dev	libm4ri	Method of the Four Russians Inversion library, development files	libm4ri ¹²
libm4rie-0.0.20140914	libm4rie	extended Method of the Four Russians Inversion library, shared library	libm4rie ¹¹
libm4rie-0.0.20140914-dbg	libm4rie	debugging symbols for libm4rie-0.0.20140914	libm4rie ¹¹
libm4rie-0.0.20150908	libm4rie	extended Method of the Four Russians Inversion library, shared library	libm4rie ¹¹
libm4rie-0.0.20200125	libm4rie	extended Method of the Four Russians Inversion library, shared library	libm4rie ¹¹

libm4rie-dev	libm4rie	extended Method of the Four Russians Inversion library, development files	libm4rie ¹¹
libmash-dev	mash	development headers and static library for Mash	mash ⁶⁴²
libmathicgb0	mathicgb	Compute Groebner bases (runtime library)	mathicgb ⁷⁴¹
libmathicgb-dev	mathicgb	Compute Groebner bases (developer tools)	mathicgb ⁷⁴¹
libmaxflow0	maxflow	This library provides the maxflow-mincut algorithm	maxflow ⁹⁸
libmaxflow0	maxflow	This library provides the maxflow-mincut algorithm	maxflow2005 ⁴³⁷
libmaxflow0-dbg	maxflow	Debug information for the maxflow-mincut algorithm	maxflow ⁹⁸
libmaxflow0-dbg	maxflow	Debug information for the maxflow-mincut algorithm	maxflow2005 ⁴³⁷
libmaxflow-dev	maxflow	Development files for the maxflow-mincut algorithm	maxflow ⁹⁸
libmaxflow-dev	maxflow	Development files for the maxflow-mincut algorithm	maxflow2005 ⁴³⁷
libmeryl-dev	kmer	in- and out-of-core kmer counting and utilities (development lib)	kmer ⁹⁰⁵
libmeryl-dev	kmer	in- and out-of-core kmer counting and utilities (development lib)	kmer2004 ³⁸²
libmia-2.2-0	mia	library for 2D and 3D gray scale image processing	mia ⁹³⁰
libmia-2.2-0-dbg	mia	Debug information for the MIA library	mia ⁹³⁰
libmia-2.2-dev	mia	library for 2D and 3D gray scale image processing, development files	mia ⁹³⁰
libmia-2.2-doc	mia	library for 2D and 3D gray scale image processing, documentation	mia ⁹³⁰
libmia-2.4-0	mia	library for 2D and 3D gray scale image processing	mia ⁹³⁰
libmia-2.4-4	mia	library for 2D and 3D gray scale image processing	mia ⁹³⁰
libmia-2.4-dev	mia	library for 2D and 3D gray scale image processing, development files	mia ⁹³⁰
libmia-2.4-doc	mia	library for 2D and 3D gray scale image processing, documentation	mia ⁹³⁰
libmialm3	libmialm	Landmark handling for the MIA tool chain	libmialm ⁹²⁹
libmialm3-dbg	libmialm	Debug information for the MIA landmark library	libmialm ⁹²⁹
libmialm-dev	libmialm	Development files for the MIA landmark library	libmialm ⁹²⁹
libmialm-doc	libmialm	Documentation for the MIA landmark library	libmialm ⁹²⁹
libminimap0	minimap	library for approximate mapping of long biosequences	minimap ⁵⁰¹
libminimap2-dev	minimap2	development headers for libminimap	minimap2 ⁵⁰²
libminimap-dev	minimap	development headers for libminimap	minimap ⁵⁰¹
libmodhmm0	libpsortb	library for constructing, training and scoring hidden Markov models	libpsortb ⁹⁵⁵
libmodhmm-dev	libpsortb	library for constructing, training and scoring hidden Markov models (dev)	libpsortb ⁹⁵⁵
libmsnumpress1	libmsnumpress	Numeric data compression for mass spectrometry (runtime)	libmsnumpress ⁸⁵⁵
libmsnumpress-dev	libmsnumpress	Numeric data compression for mass spectrometry (devel files)	libmsnumpress ⁸⁵⁵
libncl1	libncl	NEXUS Class Library	libncl ⁴⁹⁷
libncl2	libncl	NEXUS Class Library	libncl ⁴⁹⁷
libncl-dev	libncl	NEXUS Class Library (static lib and header files)	libncl ⁴⁹⁷
libnfft3-1	nfft	Library for computing Non-uniform Fast Fourier Transforms	nfft ⁴²⁴
libnfft3-2	nfft	library for computing non-uniform Fourier transforms	nfft ⁴²⁴
libnfft3-dbg	nfft	Library for computing Non-uniform Fast Fourier Transforms - debug symbols	nfft ⁴²⁴
libnfft3-dev	nfft	development files for the NFFT library	nfft ⁴²⁴
libnfft3-doc	nfft	documentation for the NFFT library	nfft ⁴²⁴
libnfft3-double2	nfft	library for computing non-uniform Fourier transforms (double precision)	nfft ⁴²⁴
libnfft3-long2	nfft	library for computing non-uniform Fourier transforms (long-double precision)	nfft ⁴²⁴
libnfft3-single2	nfft	library for computing non-uniform Fourier transforms (single precision)	nfft ⁴²⁴
libnucleotidelikelihoodcore0	beast-mcmc	implementation of LikelihoodCore for nucleotides used by beast-mcmc	beast-mcmc ²¹⁰
libnucleus6	emboss	EMBOSS library for molecular sequence analysis	emboss ⁷²⁰
libnucleus6-dev	emboss	development files for libnucleus	emboss ⁷²⁰

liboakleaf0	oakleaf	Robust statistical estimates library (run-time support)	oakleaf ³⁶³
liboakleaf-dev	oakleaf	Robust statistical estimates library (development)	oakleaf ³⁶³
liboakleaf-doc	oakleaf	Robust statistical estimates library (documentation)	oakleaf ³⁶³
liboctave1	octave	Shared libraries of the GNU Octave language	octave ²¹⁸
liboctave2	octave	Shared libraries of the GNU Octave language	octave ²¹⁸
liboctave3v5	octave	Shared libraries of the GNU Octave language	octave ²¹⁸
liboctave6	octave	shared libraries of the GNU Octave language	octave ²¹⁸
liboctave7	octave	shared libraries of the GNU Octave language	octave ²¹⁸
liboctave-dev	octave	development files for the GNU Octave language	octave ²¹⁸
libopencv2.4-java	opencv	Java bindings for the computer vision library	opencv ¹⁰¹
libopencv2.4-jni	opencv	Java jni library for the computer vision library	opencv ¹⁰¹
libopencv3.2-java	opencv	Java bindings for the computer vision library	opencv ¹⁰¹
libopencv3.2-jni	opencv	Java jni library for the computer vision library	opencv ¹⁰¹
libopencv4.1-jni	opencv	Java jni library for the computer vision library	opencv ¹⁰¹
libopencv4.2-java	opencv	Java bindings for the computer vision library	opencv ¹⁰¹
libopencv4.2-jni	opencv	Java jni library for the computer vision library	opencv ¹⁰¹
libopencv-calib3d2.3	opencv	computer vision Camera Calibration library	opencv ¹⁰¹
libopencv-calib3d2.4	opencv	computer vision Camera Calibration library	opencv ¹⁰¹
libopencv-calib3d2.4v5	opencv	computer vision Camera Calibration library	opencv ¹⁰¹
libopencv-calib3d3.2	opencv	computer vision Camera Calibration library	opencv ¹⁰¹
libopencv-calib3d4.1	opencv	computer vision Camera Calibration library	opencv ¹⁰¹
libopencv-calib3d4.2	opencv	computer vision Camera Calibration library	opencv ¹⁰¹
libopencv-calib3d-dev	opencv	development files for libopencv-calib3d4.2	opencv ¹⁰¹
libopencv-contrib2.3	opencv	computer vision contrib library	opencv ¹⁰¹
libopencv-contrib2.4	opencv	computer vision contrib library	opencv ¹⁰¹
libopencv-contrib2.4v5	opencv	computer vision contrib library	opencv ¹⁰¹
libopencv-contrib3.2	opencv	computer vision contrib library	opencv ¹⁰¹
libopencv-contrib4.1	opencv	computer vision contrib library	opencv ¹⁰¹
libopencv-contrib4.2	opencv	computer vision contrib library	opencv ¹⁰¹
libopencv-contrib-dev	opencv	development files for libopencv-contrib4.2	opencv ¹⁰¹
libopencv-core2.3	opencv	computer vision core library	opencv ¹⁰¹
libopencv-core2.4	opencv	computer vision core library	opencv ¹⁰¹
libopencv-core2.4v5	opencv	computer vision core library	opencv ¹⁰¹
libopencv-core3.2	opencv	computer vision core library	opencv ¹⁰¹
libopencv-core4.1	opencv	computer vision core library	opencv ¹⁰¹
libopencv-core4.2	opencv	computer vision core library	opencv ¹⁰¹
libopencv-core-dev	opencv	development files for libopencv-core4.2	opencv ¹⁰¹
libopencv-dev	opencv	development files for opencv	opencv ¹⁰¹
libopencv-dnn4.1	opencv	computer vision Deep neural network module	opencv ¹⁰¹
libopencv-dnn4.2	opencv	computer vision Deep neural network module	opencv ¹⁰¹
libopencv-dnn-dev	opencv	development files for libopencv-dnn4.2	opencv ¹⁰¹
libopencv-features2d2.3	opencv	computer vision Feature Detection and Descriptor Extraction library	opencv ¹⁰¹
libopencv-features2d2.4	opencv	computer vision Feature Detection and Descriptor Extraction library	opencv ¹⁰¹
libopencv-features2d2.4v5	opencv	computer vision Feature Detection and Descriptor Extraction library	opencv ¹⁰¹
libopencv-features2d3.2	opencv	computer vision Feature Detection and Descriptor Extraction library	opencv ¹⁰¹
libopencv-features2d4.1	opencv	computer vision Feature Detection and Descriptor Extraction library	opencv ¹⁰¹
libopencv-features2d4.2	opencv	computer vision Feature Detection and Descriptor Extraction library	opencv ¹⁰¹
libopencv-features2d-dev	opencv	development files for libopencv-features2d4.2	opencv ¹⁰¹
libopencv-flann2.3	opencv	computer vision Clustering and Search in Multi-Dimensional spaces library	opencv ¹⁰¹
libopencv-flann2.4	opencv	computer vision Clustering and Search in Multi-Dimensional spaces library	opencv ¹⁰¹
libopencv-flann2.4v5	opencv	computer vision Clustering and Search in Multi-Dimensional spaces library	opencv ¹⁰¹
libopencv-flann3.2	opencv	computer vision Clustering and Search in Multi-Dimensional spaces library	opencv ¹⁰¹
libopencv-flann4.1	opencv	computer vision Clustering and Search in Multi-Dimensional spaces library	opencv ¹⁰¹
libopencv-flann4.2	opencv	computer vision Clustering and Search in Multi-Dimensional spaces library	opencv ¹⁰¹
libopencv-flann-dev	opencv	development files for libopencv-flann4.2	opencv ¹⁰¹
libopencv-gpu2.3	opencv	computer vision GPU Processing library	opencv ¹⁰¹
libopencv-gpu2.4	opencv	computer vision GPU library	opencv ¹⁰¹

libopencv-gpu2.4v5	opencv	computer vision GPU library	opencv ¹⁰¹
libopencv-gpu-dev	opencv	development files for libopencv-gpu2.4v5	opencv ¹⁰¹
libopencv-highgui2.3	opencv	computer vision High-level GUI and Media I/O library	opencv ¹⁰¹
libopencv-highgui2.4	opencv	computer vision High-level GUI and Media I/O library	opencv ¹⁰¹
libopencv-highgui2.4-deb0	opencv	computer vision High-level GUI and Media I/O library	opencv ¹⁰¹
libopencv-highgui3.2	opencv	computer vision High-level GUI and Media I/O library	opencv ¹⁰¹
libopencv-highgui4.1	opencv	computer vision High-level GUI and Media I/O library	opencv ¹⁰¹
libopencv-highgui4.2	opencv	computer vision High-level GUI and Media I/O library	opencv ¹⁰¹
libopencv-highgui-dev	opencv	development files for libopencv-highgui4.2	opencv ¹⁰¹
libopencv-imgcodecs3.2	opencv	computer vision Image Codecs library	opencv ¹⁰¹
libopencv-imgcodecs4.1	opencv	computer vision Image Codecs library	opencv ¹⁰¹
libopencv-imgcodecs4.2	opencv	computer vision Image Codecs library	opencv ¹⁰¹
libopencv-imgcodecs-dev	opencv	development files for libopencv-imgcodecs4.2	opencv ¹⁰¹
libopencv-imgproc2.3	opencv	computer vision Image Processing library	opencv ¹⁰¹
libopencv-imgproc2.4	opencv	computer vision Image Processing library	opencv ¹⁰¹
libopencv-imgproc2.4v5	opencv	computer vision Image Processing library	opencv ¹⁰¹
libopencv-imgproc3.2	opencv	computer vision Image Processing library	opencv ¹⁰¹
libopencv-imgproc4.1	opencv	computer vision Image Processing library	opencv ¹⁰¹
libopencv-imgproc4.2	opencv	computer vision Image Processing library	opencv ¹⁰¹
libopencv-imgproc-dev	opencv	development files for libopencv-imgproc4.2	opencv ¹⁰¹
libopencv-legacy2.3	opencv	computer vision legacy library	opencv ¹⁰¹
libopencv-legacy2.4	opencv	computer vision legacy library	opencv ¹⁰¹
libopencv-legacy2.4v5	opencv	computer vision legacy library	opencv ¹⁰¹
libopencv-legacy-dev	opencv	development files for libopencv-legacy	opencv ¹⁰¹
libopencv-ml2.3	opencv	computer vision Machine Learning library	opencv ¹⁰¹
libopencv-ml2.4	opencv	computer vision Machine Learning library	opencv ¹⁰¹
libopencv-ml2.4v5	opencv	computer vision Machine Learning library	opencv ¹⁰¹
libopencv-ml3.2	opencv	computer vision Machine Learning library	opencv ¹⁰¹
libopencv-ml4.1	opencv	computer vision Machine Learning library	opencv ¹⁰¹
libopencv-ml4.2	opencv	computer vision Machine Learning library	opencv ¹⁰¹
libopencv-ml-dev	opencv	development files for libopencv-ml4.2	opencv ¹⁰¹
libopencv-objdetect2.3	opencv	computer vision Object Detection library	opencv ¹⁰¹
libopencv-objdetect2.4	opencv	computer vision Object Detection library	opencv ¹⁰¹
libopencv-objdetect2.4v5	opencv	computer vision Object Detection library	opencv ¹⁰¹
libopencv-objdetect3.2	opencv	computer vision Object Detection library	opencv ¹⁰¹
libopencv-objdetect4.1	opencv	computer vision Object Detection library	opencv ¹⁰¹
libopencv-objdetect4.2	opencv	computer vision Object Detection library	opencv ¹⁰¹
libopencv-objdetect-dev	opencv	development files for libopencv-objdetect4.2	opencv ¹⁰¹
libopencv-ocl2.4	opencv	computer vision OpenCL support library	opencv ¹⁰¹
libopencv-ocl2.4v5	opencv	computer vision OpenCL support library	opencv ¹⁰¹
libopencv-ocl-dev	opencv	development files for libopencv-ocl2.4v5	opencv ¹⁰¹
libopencv-photo2.4	opencv	computer vision computational photography library	opencv ¹⁰¹
libopencv-photo2.4v5	opencv	computer vision computational photography library	opencv ¹⁰¹
libopencv-photo3.2	opencv	computer vision computational photography library	opencv ¹⁰¹
libopencv-photo4.1	opencv	computer vision computational photography library	opencv ¹⁰¹
libopencv-photo4.2	opencv	computer vision computational photography library	opencv ¹⁰¹
libopencv-photo-dev	opencv	development files for libopencv-photo4.2	opencv ¹⁰¹
libopencv-shape3.2	opencv	computer vision shape descriptors and matchers library	opencv ¹⁰¹
libopencv-shape4.1	opencv	computer vision shape descriptors and matchers library	opencv ¹⁰¹
libopencv-shape4.2	opencv	computer vision shape descriptors and matchers library	opencv ¹⁰¹
libopencv-shape-dev	opencv	development files for libopencv-shape4.2	opencv ¹⁰¹
libopencv-stitching2.4	opencv	computer vision image stitching library	opencv ¹⁰¹
libopencv-stitching2.4v5	opencv	computer vision image stitching library	opencv ¹⁰¹
libopencv-stitching3.2	opencv	computer vision image stitching library	opencv ¹⁰¹
libopencv-stitching4.1	opencv	computer vision image stitching library	opencv ¹⁰¹
libopencv-stitching4.2	opencv	computer vision image stitching library	opencv ¹⁰¹
libopencv-stitching-dev	opencv	development files for libopencv-stitching4.2	opencv ¹⁰¹

libopencv-superres2.4	opencv	computer vision Super Resolution library	opencv ¹⁰¹
libopencv-superres2.4v5	opencv	computer vision Super Resolution library	opencv ¹⁰¹
libopencv-superres3.2	opencv	computer vision Super Resolution library	opencv ¹⁰¹
libopencv-superres4.1	opencv	computer vision Super Resolution library	opencv ¹⁰¹
libopencv-superres4.2	opencv	computer vision Super Resolution library	opencv ¹⁰¹
libopencv-superres-dev	opencv	development files for libopencv-superres4.2	opencv ¹⁰¹
libopencv-ts2.4	opencv	computer vision ts library	opencv ¹⁰¹
libopencv-ts2.4v5	opencv	computer vision ts library	opencv ¹⁰¹
libopencv-ts-dev	opencv	development files for TS library of OpenCV (Open Computer Vision)	opencv ¹⁰¹
libopencv-video2.3	opencv	computer vision Video analysis library	opencv ¹⁰¹
libopencv-video2.4	opencv	computer vision Video analysis library	opencv ¹⁰¹
libopencv-video2.4v5	opencv	computer vision Video analysis library	opencv ¹⁰¹
libopencv-video3.2	opencv	computer vision Video analysis library	opencv ¹⁰¹
libopencv-video4.1	opencv	computer vision Video analysis library	opencv ¹⁰¹
libopencv-video4.2	opencv	computer vision Video analysis library	opencv ¹⁰¹
libopencv-video-dev	opencv	development files for libopencv-video4.2	opencv ¹⁰¹
libopencv-videoio3.2	opencv	computer vision Video I/O library	opencv ¹⁰¹
libopencv-videoio4.1	opencv	computer vision Video I/O library	opencv ¹⁰¹
libopencv-videoio4.2	opencv	computer vision Video I/O library	opencv ¹⁰¹
libopencv-videoio-dev	opencv	development files for libopencv-videoio4.2	opencv ¹⁰¹
libopencv-videostab2.4	opencv	computer vision video stabilization library	opencv ¹⁰¹
libopencv-videostab2.4v5	opencv	computer vision video stabilization library	opencv ¹⁰¹
libopencv-videostab3.2	opencv	computer vision video stabilization library	opencv ¹⁰¹
libopencv-videostab4.1	opencv	computer vision video stabilization library	opencv ¹⁰¹
libopencv-videostab4.2	opencv	computer vision video stabilization library	opencv ¹⁰¹
libopencv-videostab-dev	opencv	development files for libopencv-videostab4.2	opencv ¹⁰¹
libopencv-viz3.2	opencv	computer vision 3D data visualization library	opencv ¹⁰¹
libopencv-viz4.1	opencv	computer vision 3D data visualization library	opencv ¹⁰¹
libopencv-viz4.2	opencv	computer vision 3D data visualization library	opencv ¹⁰¹
libopencv-viz-dev	opencv	development files for libopencv-viz4.2	opencv ¹⁰¹
libopengm-bin	opengm	command line tools for OpenGM	opengm ¹⁹
libopengm-dev	opengm	C++ template library for discrete factor graph models	opengm ¹⁹
libopengm-doc	opengm	documentation and examples for OpenGM	opengm ¹⁹
libopenmeeg1	openmeeg	library for solving EEG and MEG forward and inverse problems	openmeeg ³¹²
libopenmeeg-dev	openmeeg	openmeeg library – development files	openmeeg ³¹²
libopenms1.11	openms	library for LC/MS data management and analysis - runtime	openms ⁸³⁷
libopenms2.4.0	openms	library for LC/MS data management and analysis - runtime	openms ⁸³⁷
libopenms-dev	openms	library for LC/MS data management and analysis - dev files	openms ⁸³⁷
libopensurgesim	opensurgesim	Free platform for surgical simulation - runtime	opensurgesim ⁴²⁷
libopensurgesim-dev	opensurgesim	Free platform for surgical simulation - development	opensurgesim ⁴²⁷
liborthancclient0.8	orthanc	Orthanc Client runtime library	orthanc ³⁹⁴
liborthancclient-dev	orthanc	Orthanc Client development files	orthanc ³⁹⁴
liborthancclient-doc	orthanc	Orthanc Client documentation	orthanc ³⁹⁴
liboxli1	khmer	in-memory DNA sequence analysis library from the khmer project	khmer ¹⁶⁴
liboxli1	khmer	in-memory DNA sequence analysis library from the khmer project	khmer2008 ²⁰³
liboxli1	khmer	in-memory DNA sequence analysis library from the khmer project	khmer2012 ⁶⁶⁷
liboxli1	khmer	in-memory DNA sequence analysis library from the khmer project	khmer2012c ¹⁰⁷
liboxli1	khmer	in-memory DNA sequence analysis library from the khmer project	khmer2014 ⁹⁶⁸
liboxli1	khmer	in-memory DNA sequence analysis library from the khmer project	khmer2015 ⁹⁶⁹
liboxli-dev	khmer	in-memory DNA sequence analysis dev library	khmer ¹⁶⁴
liboxli-dev	khmer	in-memory DNA sequence analysis dev library	khmer2008 ²⁰³
liboxli-dev	khmer	in-memory DNA sequence analysis dev library	khmer2012 ⁶⁶⁷
liboxli-dev	khmer	in-memory DNA sequence analysis dev library	khmer2012c ¹⁰⁷
liboxli-dev	khmer	in-memory DNA sequence analysis dev library	khmer2014 ⁹⁶⁸
liboxli-dev	khmer	in-memory DNA sequence analysis dev library	khmer2015 ⁹⁶⁹
libpal-java	libpal-java	Phylogenetic Analysis Library	libpal-java ²⁰⁹
libpal-java-doc	libpal-java	Phylogenetic Analysis Library - documentation	libpal-java ²⁰⁹
libpapyrus3-dev	papyrus	DICOM compatible file format library	papyrus ⁷¹³

libpgsbox5	wcslib	Draw and label curvilinear coordinate grids with pgplot	wcslib ¹¹⁹
libpgsbox6	wcslib	Draw and label curvilinear coordinate grids with pgplot	wcslib ¹¹⁹
libpgsbox7	wcslib	Draw and label curvilinear coordinate grids with pgplot	wcslib ¹¹⁹
libpll0	libpll	Phylogenetic Likelihood Library	libpll ³⁸³
libpll-dev	libpll	Phylogenetic Likelihood Library (development)	libpll ³⁸³
libpurify2.0	purify	Routines for radio interferometric imaging (shared lib)	purify ⁶⁸⁷
libpurify-dev	purify	Routines for radio interferometric imaging (development files)	purify ⁶⁸⁷
libpwiz3	libpwiz	library to perform proteomics data analyses (runtime)	libpwiz ¹³²
libpwiz-dev	libpwiz	library to perform proteomics data analyses (development files)	libpwiz ¹³²
libpwiz-doc	libpwiz	set of programs to perform proteomics data analyses (doc)	libpwiz ¹³²
libpwiz-tools	libpwiz	ProteoWizard command line tools	libpwiz ¹³²
libqsopt-ex2	qsopt-ex	Exact linear programming solver – shared library	qsopt-ex ²³
libqsopt-ex-dev	qsopt-ex	Exact linear programming solver – development files	qsopt-ex ²³
libqtpropertybrowser3	camitk	Qt Property Browser Library - runtime	camitk ²⁵⁶
libqtpropertybrowser3-dev	camitk	Qt Property Browser Library - development	camitk ²⁵⁶
libqtpropertybrowser4	camitk	Qt Property Browser Library - runtime	camitk ²⁵⁶
libqtpropertybrowser-dev	camitk	Qt Property Browser Library - development	camitk ²⁵⁶
librandom123-dev	librandom123	parallel random numbers library	librandom123 ⁷⁵⁵
librandom123-doc	librandom123	documentation and examples of parallel random numbers library	librandom123 ⁷⁵⁵
libreion-1.3-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion-1.4-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion-dev	reion	C++ API for RELION (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion-dev-common	reion	C++ API for RELION (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+gui-1.3-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+gui-1.4-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+gui-dev	reion	C++ API for RELION (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+mpi-1.3-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+mpi-1.4-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+mpi-dev	reion	C++ API for RELION (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+mpi+gui-1.3-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+mpi+gui-1.4-1	reion	RELION dynamic library (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
libreion+mpi+gui-dev	reion	C++ API for RELION (3D reconstructions in cryo-electron microscopy)	reion ⁷⁵⁹
librsb0	librsb	recursive sparse blocks matrix computations library	librsb ⁵⁶⁰
librsb-dev	librsb	recursive sparse blocks matrix computations library (development)	librsb ⁵⁶⁰
librsb-doc	librsb	recursive sparse blocks matrix computations library (documentation)	librsb ⁵⁶⁰
libsbml5	libsbml	System Biology Markup Language library	libsbml ⁹⁴
libsbml5-cil	libsbml	System Biology Markup Language library - CLI bindings	libsbml ⁹⁴
libsbml5-cil-doc	libsbml	System Biology Markup Language library – CLI documentation	libsbml ⁹⁴
libsbml5-dbg	libsbml	System Biology Markup Language library - debug symbols	libsbml ⁹⁴
libsbml5-dev	libsbml	System Biology Markup Language library - development files	libsbml ⁹⁴

libsbml5-doc	libsbml	System Biology Markup Language library – documentation	libsbml ⁹⁴
libsbml5-examples	libsbml	System Biology Markup Language library – example files	libsbml ⁹⁴
libsbml5-java	libsbml	System Biology Markup Language library - Java bindings	libsbml ⁹⁴
libsbml5-java-doc	libsbml	System Biology Markup Language library – Java documentation	libsbml ⁹⁴
libsbml5-octave	libsbml	System Biology Markup Language library - Octave bindings	libsbml ⁹⁴
libsbml5-perl	libsbml	System Biology Markup Language library - Perl bindings	libsbml ⁹⁴
libsbml5-perl-doc	libsbml	System Biology Markup Language library – Perl documentation	libsbml ⁹⁴
libsbml5-python	libsbml	System Biology Markup Language library - Python bindings	libsbml ⁹⁴
libsbml5-python-doc	libsbml	System Biology Markup Language library – Python documentation	libsbml ⁹⁴
libsc7	mpqc	Scientific Computing Toolkit (library)	mpqc ⁵⁹⁶
libsc7v5	mpqc	Scientific Computing Toolkit (library)	mpqc ⁵⁹⁶
libsc-data	mpqc	Scientific Computing Toolkit (basis set and atom data)	mpqc ⁵⁹⁶
libsc-dev	mpqc	Scientific Computing Toolkit (development files)	mpqc ⁵⁹⁶
libsc-doc	mpqc	Scientific Computing Toolkit (documentation)	mpqc ⁵⁹⁶
libseqan2-dev	seqan2	C++ library for the analysis of biological sequences (development)	seqan2 ²⁰⁵
libseqan3-dev	seqan3	C++ library for the analysis of biological sequences v3 (development)	seqan3 ²⁰⁶
libseqlib1	libseqlib	C++ htlib/bwa-mem/fermi interface for interrogating sequence data	libseqlib ⁹⁰⁴
libseqlib-dev	libseqlib	C++ htlib/bwa-mem/fermi interface for interrogating sequence data (dev)	libseqlib ⁹⁰⁴
libshark0	shark	Shark machine learning library	shark ³⁷⁹
libshark-dev	shark	development files for Shark	shark ³⁷⁹
libsnp-sites1	snp-sites	Shared libraries of the package snp-sites	snp-sites ⁶⁴⁹
libsnp-sites1-dev	snp-sites	Static libraries and header files for the package snp-sites	snp-sites ⁶⁴⁹
libsopt2.0	sopt	Sparse OPTimisation shared library	sopt ⁶⁸⁶
libsopt3.0	sopt	Sparse OPTimisation shared library	sopt ⁶⁸⁶
libsopt-dev	sopt	Development package for Sparse OPTimisation library	sopt ⁶⁸⁶
libssm1	ssm	macromolecular superposition library - runtime	ssm ⁴⁵⁵
libssm1-dbg	ssm	macromolecular superposition library - debug symbols	ssm ⁴⁵⁵
libssm2	ssm	macromolecular superposition library - runtime	ssm ⁴⁵⁵
libssm-bin	ssm	macromolecular superposition library - binaries	ssm ⁴⁵⁵
libssm-dev	ssm	macromolecular superposition library - development files	ssm ⁴⁵⁵
libssw0	libssw	fast SIMD parallelized implementation of the Smith-Waterman algorithm	libssw ⁹⁷³
libssw-dev	libssw	Development headers and static libraries for libssw	libssw ⁹⁷³
libssw-java	libssw	Java bindings for libssw	libssw ⁹⁷³
libstarlink-ast0	starlink-ast	Handle World Coordinate Systems in Astronomy (main shared lib)	starlink-ast ⁶⁴
libstarlink-ast9	starlink-ast	Handle World Coordinate Systems in Astronomy (main shared lib)	starlink-ast ⁶⁴
libstarlink-ast-dev	starlink-ast	Handle World Coordinate Systems in Astronomy (development package)	starlink-ast ⁶⁴
libstarlink-ast-doc	starlink-ast	Handle World Coordinate Systems in Astronomy (documentation)	starlink-ast ⁶⁴
libstarlink-ast-err0	starlink-ast	Handle World Coordinate Systems in Astronomy (error reporting)	starlink-ast ⁶⁴
libstarlink-ast-err9	starlink-ast	Handle World Coordinate Systems in Astronomy (error reporting)	starlink-ast ⁶⁴
libstarlink-ast-grf3d0	starlink-ast	Handle World Coordinate Systems in Astronomy (dummy 3d routines)	starlink-ast ⁶⁴
libstarlink-ast-grf3d9	starlink-ast	Handle World Coordinate Systems in Astronomy (dummy 3d routines)	starlink-ast ⁶⁴
libstarlink-pal0	starlink-pal	Positional Astronomy Library (shared library)	starlink-pal ³⁸⁹
libstarlink-pal-dev	starlink-pal	Positional Astronomy Library (development files)	starlink-pal ³⁸⁹

libstarlink-pal-doc	starlink-pal	Positional Astronomy Library (documentation)	starlink-pal ³⁸⁹
libsvmloc0	libpsortb	PSORTb adapted library for svm machine-learning library	libpsortb ⁹⁵⁵
libsvmloc-dev	libpsortb	PSORTb adapted library for svm machine-learning library (dev)	libpsortb ⁹⁵⁵
libtfbs-perl	libtfbs-perl	scanning DNA sequence with a position weight matrix	libtfbs-perl ⁴⁹⁶
libtrilinos	trilinos	parallel solver libraries within an object-oriented software framework	trilinos ³⁴⁷
libtrilinos-amesos12	trilinos	direct sparse solver package - runtime files	trilinos ³⁴⁷
libtrilinos-amesos2-12	trilinos	next generation direct sparse solver package - runtime files	trilinos ³⁴⁷
libtrilinos-amesos2-dev	trilinos	next generation direct sparse solver package - development files	trilinos ³⁴⁷
libtrilinos-amesos-dev	trilinos	direct sparse solver package - development files	trilinos ³⁴⁷
libtrilinos-anasazi12	trilinos	large-scale eigenvalue algorithms - runtime files	trilinos ³⁴⁷
libtrilinos-anasazi-dev	trilinos	large-scale eigenvalue algorithms - development files	trilinos ³⁴⁷
libtrilinos-aztecoo12	trilinos	object-oriented interface to the Aztec solver - runtime files	trilinos ³⁴⁷
libtrilinos-aztecoo-dev	trilinos	object-oriented interface to the Aztec solver - development files	trilinos ³⁴⁷
libtrilinos-belos12	trilinos	iterative linear solvers - runtime files	trilinos ³⁴⁷
libtrilinos-belos-dev	trilinos	iterative linear solvers - development files	trilinos ³⁴⁷
libtrilinos-dbg	trilinos	parallel solver libraries within an object-oriented software framework	trilinos ³⁴⁷
libtrilinos-dev	trilinos	parallel solver libraries within an object-oriented software framework	trilinos ³⁴⁷
libtrilinos-doc	trilinos	parallel solver libraries within an object-oriented software framework	trilinos ³⁴⁷
libtrilinos-epetra12	trilinos	basis package for linear algebra - runtime files	trilinos ³⁴⁷
libtrilinos-epetra-dev	trilinos	basis package for linear algebra - development files	trilinos ³⁴⁷
libtrilinos-epetraext12	trilinos	extensions to the Epetra toolkit - runtime files	trilinos ³⁴⁷
libtrilinos-epetraext-dev	trilinos	extensions to the Epetra toolkit - development files	trilinos ³⁴⁷
libtrilinos-galeri12	trilinos	generation of distributed linear systems - runtime files	trilinos ³⁴⁷
libtrilinos-galeri-dev	trilinos	generation of distributed linear systems - development files	trilinos ³⁴⁷
libtrilinos-globipack12	trilinos	1D globalization capabilities - runtime files	trilinos ³⁴⁷
libtrilinos-globipack-dev	trilinos	1D globalization capabilities - development files	trilinos ³⁴⁷
libtrilinos-ifpack12	trilinos	algebraic preconditioners - runtime files	trilinos ³⁴⁷
libtrilinos-ifpack2-12	trilinos	next generation algebraic preconditioners - runtime files	trilinos ³⁴⁷
libtrilinos-ifpack2-dev	trilinos	next generation algebraic preconditioners - development files	trilinos ³⁴⁷
libtrilinos-ifpack-dev	trilinos	algebraic preconditioners - development files	trilinos ³⁴⁷
libtrilinos-intrepid12	trilinos	compatible discretizations of PDEs - runtime files	trilinos ³⁴⁷
libtrilinos-intrepid2-12	trilinos	next generation compatible discretizations of PDEs - runtime files	trilinos ³⁴⁷
libtrilinos-intrepid2-dev	trilinos	next generation compatible discretizations of PDEs - development files	trilinos ³⁴⁷
libtrilinos-intrepid-dev	trilinos	compatible discretizations of PDEs - development files	trilinos ³⁴⁷
libtrilinos-isorropia12	trilinos	partitioning, load balancing, coloring of sparse matrices - runtime files	trilinos ³⁴⁷
libtrilinos-isorropia-dev	trilinos	partitioning, load balancing, coloring of sparse matrices - development files	trilinos ³⁴⁷
libtrilinos-kokkos12	trilinos	Trilinos Kokkos programming model - runtime files	trilinos ³⁴⁷
libtrilinos-kokkos-dev	trilinos	Trilinos Kokkos programming model - development files	trilinos ³⁴⁷
libtrilinos-kokkos-kernels12	trilinos	Kokkos local computational kernels - runtime files	trilinos ³⁴⁷
libtrilinos-kokkos-kernels-dev	trilinos	Kokkos local computational kernels - development files	trilinos ³⁴⁷
libtrilinos-komplex12	trilinos	complex linear solver package - runtime files	trilinos ³⁴⁷
libtrilinos-komplex-dev	trilinos	complex linear solver package - development files	trilinos ³⁴⁷
libtrilinos-ml12	trilinos	multigrid preconditioning - runtime files	trilinos ³⁴⁷
libtrilinos-ml-dev	trilinos	multigrid preconditioning - development files	trilinos ³⁴⁷
libtrilinos-moertel12	trilinos	mortar methods package - runtime files	trilinos ³⁴⁷
libtrilinos-moertel-dev	trilinos	mortar methods package - development files	trilinos ³⁴⁷

libtrilinos-muelu12	trilinos	next generation multilevel preconditioner capabilities - runtime files	trilinos ³⁴⁷
libtrilinos-muelu-dev	trilinos	next generation multilevel preconditioner capabilities - development files	trilinos ³⁴⁷
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libvtkgdcm2.2	gdcm	Grassroots DICOM VTK runtime libraries	gdcm ³⁰²
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libwcs4	wcslib	Implementation of the FITS WCS standard	wcslib ¹¹⁹
libwcs5	wcslib	Implementation of the FITS WCS standard	wcslib ¹¹⁹
libwcs6	wcslib	Implementation of the FITS WCS standard	wcslib ¹¹⁹
libwcs7	wcslib	Implementation of the FITS WCS standard	wcslib ¹¹⁹
libwcstools0	wcstools	Handle the WCS of a FITS image (shared library)	wcstools ⁵⁸¹
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libwcstools-dev	wcstools	Handle the WCS of a FITS image (development files)	wcstools ⁵⁸¹
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libxpa1	xpa	Seamless communication between Unix programs (shared library)	xpa ⁵⁴¹
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lipsia	lipsia	analysis suite for MRI and fMRI data	lipsia ⁵²⁷
lipsia-doc	lipsia	documentation for LIPSIA	lipsia ⁵²⁷
loki	loki	MCMC linkage analysis on general pedigrees	loki ³³⁹
loki	loki	MCMC linkage analysis on general pedigrees	loki2005 ¹⁷⁸
loki-doc	loki	MCMC linkage analysis on general pedigrees (PS manual)	loki ³³⁹
loki-doc	loki	MCMC linkage analysis on general pedigrees (PS manual)	loki2005 ¹⁷⁸
ltrsift	ltrsift	postprocessing and classification of LTR retrotransposons	ltrsift ⁸²³
ltrsift-dbg	ltrsift	postprocessing and classification of LTR retrotransposons, with debug symbols	ltrsift ⁸²³
ltrsift-examples	ltrsift	example data for LTRSift	ltrsift ⁸²³
lua-cnrun	cnrun	NeuroML-capable neuronal network simulator (Lua package)	cnrun ⁹⁶⁴
macs	macs	Model-based Analysis of CHIP-Seq on short reads sequencers	macs ⁹⁷²
macsyfinder	macsyfinder	detection of macromolecular systems in protein datasets	macsyfinder ²
maffilter	maffilter	process genome alignment in the Multiple Alignment Format	maffilter ²¹⁷
maffilter-examples	maffilter	process genome alignment in the Multiple Alignment Format (example data)	maffilter ²¹⁷
mafft	mafft	Multiple alignment program for amino acid or nucleotide sequences	mafft ⁴²²
mafft	mafft	Multiple alignment program for amino acid or nucleotide sequences	mafft2009 ⁴²¹
mapdamage	mapdamage	tracking and quantifying damage patterns in ancient DNA sequences	mapdamage ⁴¹⁰
mapsembler2	mapsembler2	bioinformatics targeted assembly software	mapsembler2 ⁶⁷⁵
maq	maq	maps short fixed-length polymorphic DNA sequence reads to reference sequences	maq ⁵⁰⁴
maqview	maqview	graphical read alignment viewer for short gene sequences	maqview ⁵⁰⁵
mash	mash	fast genome and metagenome distance estimation using MinHash	mash ⁶⁴²
mash-doc	mash	documentation for Mash	mash ⁶⁴²
massxpert	massxpert	linear polymer mass spectrometry software	massxpert ⁷⁴⁸
massxpert-data	massxpert	linear polymer mass spectrometry software - arch-indep data	massxpert ⁷⁴⁸
massxpert-dbg	massxpert	linear polymer mass spectrometry software - debugging symbols	massxpert ⁷⁴⁸
massxpert-doc	massxpert	Linear polymer mass spectrometry software - manual	massxpert ⁷⁴⁸
mathicgb	mathicgb	Compute Groebner bases (command line tool)	mathicgb ⁷⁴¹
matlab-gdf	libgdf	IO library for the GDF – Matlab interface	libgdf ⁷⁶⁶
maude	maude	high-performance logical framework	maude ⁵⁶⁵
mauve-aligner	mauve-aligner	multiple genome alignment	mauve-aligner ¹⁷⁰
mcl	mcl	Markov Cluster algorithm	mcl ⁸⁹⁰
mcl-doc	mcl	documentation for mcl	mcl ⁸⁹⁰
melting	melting	compute the melting temperature of nucleic acid duplex	melting ⁴⁸⁷
melting-gui	melting	graphical interface to compute the melting temperature of nucleic acid duplex	melting ⁴⁸⁷
meryl	kmer	in- and out-of-core kmer counting and utilities	kmer ⁹⁰⁵
meryl	kmer	in- and out-of-core kmer counting and utilities	kmer2004 ³⁸²
meshlab	meshlab	System for processing and editing triangular meshes	meshlab ¹⁴⁶
metaphlan2	metaphlan2	Metagenomic Phylogenetic Analysis	metaphlan2 ⁸⁷⁹
metastudent	metastudent	predictor of Gene Ontology terms from protein sequence	metastudent ³²⁹
metastudent-data	metastudent-data	predictor of Gene Ontology terms from protein sequence - data files	metastudent-data ³³
metastudent-data-2	metastudent-data-2	predictor of Gene Ontology terms from protein sequence - data #2	metastudent-data-2
mglttools-pmv	mglttools-pmv	Python-based Molecular Viewer	mglttools-pmv ²⁹¹
mglttools-pmv-test	mglttools-pmv	Python-based Molecular Viewer (functionality tests)	mglttools-pmv ²⁹¹

mhap	mhap	locality-sensitive hashing to detect long-read overlaps	mhap ⁶³
mia-doctools	mia	Helper scripts for run-time document creation	mia ⁹³⁰
mialmpick	mialmpick	Tools for landmark picking in 3D volume data sets	mialmpick ⁹²⁸
mialmpick-dbg	mialmpick	Debug information landmark picking tool	mialmpick ⁹²⁸
mia-tools	mia	Command line tools for gray scale image processing	mia ⁹³⁰
mia-tools-dbg	mia	Debugging information for the MIA command line tools	mia ⁹³⁰
mia-tools-doc	mia	Cross-referenced documentation of the MIA command line tools	mia ⁹³⁰
microbegps	microbegps	explorative taxonomic profiling tool for metagenomic data	microbegps ⁵¹⁵
microbiomeutil	microbiomeutil	Microbiome Analysis Utilities	microbiomeutil ³²⁸
microbiomeutil-data	microbiomeutil	Reference 16S sequences and NAST-alignments used by microbiomeutil tools	microbiomeutil ³²⁸
minia	minia	short-read biological sequence assembler	minia ¹⁴¹
miniasm	miniasm	ultrafast de novo assembler for long noisy DNA sequencing reads	miniasm ⁵⁰⁰
minimac4	minimac4	Fast Imputation Based on State Space Reduction HMM	minimac4 ¹⁷⁵
minimac4	minimac4	Fast Imputation Based on State Space Reduction HMM	minimac42012 ³⁵⁹
minimac4	minimac4	Fast Imputation Based on State Space Reduction HMM	minimac42014 ²⁶⁷
minimap	minimap	tool for approximate mapping of long biosequences such as DNA reads	minimap ⁵⁰¹
minimap2	minimap2	versatile pairwise aligner for genomic and spliced nucleotide sequences	minimap2 ⁵⁰²
mipe	mipe	Tools to store PCR-derived data	mipe ⁷
mira-assembler	mira	Whole Genome Shotgun and EST Sequence Assembler	mira ¹⁴⁰
mira-doc	mira	documentation for the mira assembler	mira ¹⁴⁰
mira-examples	mira	files to experiment with the mira assembler	mira ¹⁴⁰
mira-rfam-12s-rrna	mira	extract of RFAM 12 rRNA database	mira ¹⁴⁰
mirtop	mirtop	annotate miRNAs with a standard mirna/isomir naming	mirtop ¹⁸⁸
mirtop	mirtop	annotate miRNAs with a standard mirna/isomir naming	mirtop2019 ¹⁸⁹
missfits	missfits	Basic maintenance and packaging tasks on FITS files	missfits ⁵⁵³
mlv-smile	mlv-smile	Find statistically significant patterns in sequences	mlv-smile ⁵⁵⁶
mlv-smile	mlv-smile	Find statistically significant patterns in sequences	mlv-smile1999 ⁸⁹⁴
mlv-smile	mlv-smile	Find statistically significant patterns in sequences	mlv-smile1999d ²⁶
mlv-smile	mlv-smile	Find statistically significant patterns in sequences	mlv-smile2000 ⁸⁹⁵
mmass	mmass	Mass spectrometry tool for proteomics	mmass ⁸³⁶
mmass-doc	mmass	Mass spectrometry tool for proteomics - documentation	mmass ⁸³⁶
mmass-modules	mmass	Mass spectrometry tool for proteomics - extension modules	mmass ⁸³⁶
mmseqs2	mmseqs2	ultra fast and sensitive protein search and clustering	mmseqs2 ⁸²⁴
mmseqs2-examples	mmseqs2	optional resources for the mmseqs2 package	mmseqs2 ⁸²⁴
mobylye	mobylye	Web portal that provides web forms for command-line software	mobylye ⁶¹²
mobylye-utils	mobylye	binary tools used by Mobylye	mobylye ⁶¹²
mocassin	mocassin	MONte Carlo SimulationS of Ionised Nebulae	mocassin ²³⁰
mocassin-benchmarks	mocassin	benchmarks for the photoionisation code MOCASSIN	mocassin ²³⁰
mocassin-data	mocassin	atomic and optical data for the photoionisation code MOCASSIN	mocassin ²³⁰
mocassin-examples	mocassin	Examples for the photoionisation code MOCASSIN	mocassin ²³⁰
montage	montage	Toolkit for assembling FITS images into mosaics	montage ³⁸⁷
montage-gridtools	montage	Create files to run montage on the grid	montage ³⁸⁷
mothur	mothur	sequence analysis suite for research on microbiota	mothur ⁷⁶⁵
mothur-mpi	mothur	mpi-enabled binary for mothur	mothur ⁷⁶⁵
mpgrafic	mpgrafic	MPI version of N-body initial conditions graphic package	mpgrafic ⁶⁹⁴
mpqc	mpqc	Massively Parallel Quantum Chemistry Program	mpqc ⁵⁹⁶

mpqc-openmpi	mpqc	Massively Parallel Quantum Chemistry Program (OpenMPI transitional package)	mpqc ⁵⁹⁶
mpqc-support	mpqc	Massively Parallel Quantum Chemistry Program (support tools)	mpqc ⁵⁹⁶
mptp	mptp	single-locus species delimitation	mptp ⁴¹⁹
mrbytes	mrbytes	Bayesian Inference of Phylogeny	mrbytes ⁷³¹
mrbytes	mrbytes	Bayesian Inference of Phylogeny	mrbytes2001 ³⁶⁹
mrbytes	mrbytes	Bayesian Inference of Phylogeny	mrbytes2003 ⁷³⁰
mrbytes-dbg	mrbytes	Bayesian Inference of Phylogeny - debug symbols	mrbytes ⁷³¹
mrbytes-dbg	mrbytes	Bayesian Inference of Phylogeny - debug symbols	mrbytes2001 ³⁶⁹
mrbytes-dbg	mrbytes	Bayesian Inference of Phylogeny - debug symbols	mrbytes2003 ⁷³⁰
mrbytes-doc	mrbytes	Bayesian Inference of Phylogeny - manual	mrbytes ⁷³¹
mrbytes-doc	mrbytes	Bayesian Inference of Phylogeny - manual	mrbytes2001 ³⁶⁹
mrbytes-doc	mrbytes	Bayesian Inference of Phylogeny - manual	mrbytes2003 ⁷³⁰
mrbytes-mpi	mrbytes	Bayesian Inference of Phylogeny - mpi version	mrbytes ⁷³¹
mrbytes-mpi	mrbytes	Bayesian Inference of Phylogeny - mpi version	mrbytes2001 ³⁶⁹
mrbytes-mpi	mrbytes	Bayesian Inference of Phylogeny - mpi version	mrbytes2003 ⁷³⁰
mrs	mrs	Information Retrieval System for Biomedical databanks	mrs ³⁴²
mrtrix	mrtrix	diffusion-weighted MRI white matter tractography	mrtrix ⁸⁷⁰
mrtrix3	mrtrix3	diffusion-weighted MRI white matter tractography	mrtrix3 ⁸⁶⁹
mrtrix3-doc	mrtrix3	documentation for mrtrix3	mrtrix3 ⁸⁶⁹
mrtrix-doc	mrtrix	documentation for mrtrix	mrtrix ⁸⁷⁰
mssstest	mssstest	Normalisation of disease scores for patients with Multiple Sclerosis	mssstest ⁷⁴²
msxpertsuite	msxpertsuite	mass spectrometry software suite - metapackage	msxpertsuite ⁷⁴⁹
msxpertsuite-massxpert	msxpertsuite	mass spectrometry software suite - massXpert	msxpertsuite ⁷⁴⁹
msxpertsuite-massxpert-data-doc	msxpertsuite	mass spectrometry software suite - massXpert - data and doc	msxpertsuite ⁷⁴⁹
msxpertsuite-minexpert	msxpertsuite	mass spectrometry software suite - mineXpert	msxpertsuite ⁷⁴⁹
msxpertsuite-minexpert-data-doc	msxpertsuite	mass spectrometry software suite - mineXpert - data and doc	msxpertsuite ⁷⁴⁹
multiqc	multiqc	output integration for RNA sequencing across tools and samples	multiqc ²³⁸
mummer	mummer	Efficient sequence alignment of full genomes	mummer ⁴⁶³
mummer-doc	mummer	Documentation for MUMmer	mummer ⁴⁶³
munipack	munipack	Astronomical photometry software package	munipack ³⁶²
munipack-cli	munipack	Command line interface of Munipack	munipack ³⁶²
munipack-core	munipack	Core routines of Munipack	munipack ³⁶²
munipack-doc	munipack	Documentation of Munipack	munipack ³⁶²
munipack-gui	munipack	Graphical user interface of Munipack	munipack ³⁶²
murasaki	murasaki	homology detection tool across multiple large genomes	murasaki ⁶⁸⁴
murasaki-common	murasaki	homology detection tool across multiple large genomes (common files)	murasaki ⁶⁸⁴
murasaki-mpi	murasaki	homology detection tool across multiple large genomes (MPI-version)	murasaki ⁶⁸⁴
muscle	muscle	Multiple alignment program of protein sequences	muscle ²²⁴
muscle	muscle	Multiple alignment program of protein sequences	muscle2004 ²²⁵
mustang	mustang	multiple structural alignment of proteins	mustang ⁴⁴¹
mustang-testdata	mustang	multiple structural alignment of proteins, test data	mustang ⁴⁴¹
nanook	nanook	pre- and post-alignment analysis of nanopore sequencing data	nanook ⁴⁹²
nast-ier	microbiomeutil	NAST-based DNA alignment tool	microbiomeutil ³²⁸
ncbi-cn3d	ncbi-tools6	3-dimensional viewer for biological molecules	ncbi-tools6 ⁹⁰⁸
ncbi-epcr	epcr	Tool to test a DNA sequence for the presence of sequence tagged sites	epcr ⁷⁷⁵
ncbi-epcr	epcr	Tool to test a DNA sequence for the presence of sequence tagged sites	epcr2004 ⁷³⁹
ncbi-seg	ncbi-seg	tool to mask segments of low compositional complexity in amino acid sequences	ncbi-seg ⁹³⁵
ncbi-seg-dbg	ncbi-seg	debug symbols for ncbi-seg	ncbi-seg ⁹³⁵
ncl-tools	libncl	tools to deal with NEXUS files	libncl ⁴⁹⁷
nco	nco	Command-line operators to analyze netCDF files	nco ⁹⁶⁶
ncoils	coils	coiled coil secondary structure prediction	coils ⁵³⁴
neat	neat	Nebular Empirical Analysis Tool	neat ⁹¹⁸
neobio	neobio	computes alignments of amino acid and nucleotide sequences	neobio ¹⁶²

njplot	njplot	phylogenetic tree drawing program	njplot ⁶⁷²
norsnet	norsnet	tool to identify unstructured loops in proteins	norsnet ⁷⁶³
norsp	norsp	predictor of non-regular secondary structure	norsp ⁵²¹
nwchem	nwchem	High-performance computational chemistry software	nwchem ⁸⁸⁷
nwchem-data	nwchem	High-performance computational chemistry software (data files)	nwchem ⁸⁸⁷
obitools	obitools	programs to analyze NGS data in a DNA metabarcoding context	obitools ⁹⁷
octave	octave	GNU Octave language for numerical computations	octave ²¹⁸
octave-biosig	biosig4c++	Octave bindings for BioSig library	biosig4c ⁷⁶⁷
octave-common	octave	architecture-independent files for octave	octave ²¹⁸
octave-dbg	octave	Debug symbols for octave	octave ²¹⁸
octave-divand	octave-divand	n-dimensional interpolation for Octave	octave-divand ⁵²
octave-doc	octave	documentation of the GNU Octave language	octave ²¹⁸
octave-fuzzy-logic-toolkit	octave-fuzzy-logic-toolkit	fuzzy logic toolkit for Octave	octave-fuzzy-logic-t
octave-gdf	libgdf	IO library for the GDF – Octave interface	libgdf ⁷⁶⁶
octave-gmt	gmt	Support of GMT grid files for Octave	gmt ⁹¹⁶
octave-gmt	gmt	Support of GMT grid files for Octave	gmt1991 ⁹¹³
octave-gmt	gmt	Support of GMT grid files for Octave	gmt1995 ⁹¹⁴
octave-gmt	gmt	Support of GMT grid files for Octave	gmt1998 ⁹¹⁵
octave-htmldoc	octave	transitional package for Octave HTML documentation	octave ²¹⁸
octave-info	octave	transitional package for Octave info documentation	octave ²¹⁸
octave-interval	octave-interval	real-valued interval arithmetic for Octave	octave-interval ³⁴¹
octave-interval-doc	octave-interval	real-valued interval arithmetic for Octave (arch-indep files)	octave-interval ³⁴¹
octave-level-set	octave-level-set	level-set toolbox for Octave	octave-level-set ⁴⁴⁹
octave-lassa	octave-lassa	least squares spectral analysis for Octave	octave-lassa ⁵⁶⁴
octave-ltfat	octave-ltfat	Large Time/Frequency Analysis Toolbox	octave-ltfat ⁶⁹⁶
octave-ltfat-common	octave-ltfat	Large Time/Frequency Analysis Toolbox (arch-indep files)	octave-ltfat ⁶⁹⁶
octave-nurbs	octave-nurbs	non-uniform rational B-splines for Octave	octave-nurbs ⁸⁰⁸
octave-nurbs	octave-nurbs	non-uniform rational B-splines for Octave	octave-nurbs2011 ¹⁷⁰
octave-queueing	octave-queueing	Queueing Networks and Markov chains analysis for Octave	octave-queueing ⁵⁶¹
octave-splines	octave-splines	cubic spline functions for Octave	octave-splines ⁴⁵⁰
octave-stk	octave-stk	(not so) Small Toolbox for Kriging	octave-stk ⁵⁶
octave-tisean	octave-tisean	nonlinear time series analysis for Octave	octave-tisean ³⁴⁰
octave-tisean	octave-tisean	nonlinear time series analysis for Octave	octave-tisean2000, ¹³
octave-tisean	octave-tisean	nonlinear time series analysis for Octave	octave-tisean2004 ⁴¹
openbabel	openbabel	Chemical toolbox utilities (cli)	openbabel ⁶³²
opencfu	opencfu	count cell colonies (CFUs) on agar plates by processing digital pictures	opencfu ²⁸²
opencv-data	opencv	development data for opencv	opencv ¹⁰¹
opencv-doc	opencv	OpenCV documentation and examples	opencv ¹⁰¹
openmeeg-tools	openmeeg	openmeeg library – command line tools	openmeeg ³¹²
openmolcas	openmolcas	Quantum chemistry software package	openmolcas ²⁷²
openmolcas-data	openmolcas	Quantum chemistry software package (data files)	openmolcas ²⁷²
openms	openms	package for LC/MS data management and analysis	openms ⁸³⁷
openms-common	openms	package for LC/MS data management and analysis - shared data	openms ⁸³⁷
openms-doc	openms	package for LC/MS data management and analysis - documentation	openms ⁸³⁷
opensurgsim-doc	opensurgsim	Free platform for surgical simulation - documentation	opensurgsim ⁴²⁷
optimir	optimir	Integrating genetic variations in miRNA alignment	optimir ⁸⁶⁰
orthanc	orthanc	Lightweight, RESTful DICOM server for medical imaging	orthanc ³⁹⁴
orthanc-dev	orthanc	Orthanc development files	orthanc ³⁹⁴
orthanc-dicomweb	orthanc-dicomweb	Plugin to extend Orthanc with support of WADO and DICOMweb	orthanc-dicomweb ³⁵
orthanc-doc	orthanc	Documentation of Orthanc	orthanc ³⁹⁴
orthanc-imagej	orthanc-imagej	ImageJ plugin to import images from Orthanc	orthanc-imagej ³⁹⁶
orthanc-mysql	orthanc-mysql	Plugins to use MySQL or MariaDB as a database back-end to Orthanc	orthanc-mysql ³⁹⁷

orthanc-postgresql	orthanc-postgresql	Plugins to use PostgreSQL as a database back-end to Orthanc	orthanc-postgresql ³
orthanc-python	orthanc-python	Develop plugins for Orthanc using the Python programming language	orthanc-python ³⁹⁹
orthanc-webviewer	orthanc-webviewer	Web viewer of medical images for Orthanc	orthanc-webviewer ⁴
orthanc-wsi	orthanc-wsi	Whole-slide imaging support for Orthanc (digital pathology)	orthanc-wsi ⁴⁰¹
otf-symbols-circos	circos	transitional dummy package	circos ⁴⁵⁶
pal2nal	pal2nal	converts proteins to genomic DNA alignment	pal2nal ⁸⁴¹
paleomix	paleomix	pipelines and tools for the processing of ancient and modern HTS data	paleomix ⁷⁷³
palp	palp	Package for Analyzing Lattice Polytopes	palp ⁴⁵³
paml	paml	Phylogenetic Analysis by Maximum Likelihood (PAML)	paml ⁹⁵⁴
paml-doc	paml	Documentation for PAML	paml ⁹⁵⁴
paraclu	paraclu	Parametric clustering of genomic and transcriptomic features	paraclu ²⁶⁵
parsnp	parsnp	rapid core genome multi-alignment	parsnp ⁸⁷⁶
patman	patman	rapid alignment of short sequences to large databases	patman ⁶⁹⁵
pboney	pbsuite	genomic structural variation discovery	pbsuite ²²⁹
pbjelly	pbsuite	genome assembly upgrading tool	pbsuite2012 ²²⁸
pbsim	pbsim	simulator for PacBio sequencing reads	pbsim ⁶⁴⁴
pdb2pqr	pdb2pqr	Preparation of protein structures for electrostatics calculations	pdb2pqr ²⁰¹
pdb2pqr	pdb2pqr	Preparation of protein structures for electrostatics calculations	pdb2pqr2004 ²⁰⁰
pdb2pqr-doc	pdb2pqr	example files accompanying pdb2pqr	pdb2pqr ²⁰¹
pdb2pqr-doc	pdb2pqr	example files accompanying pdb2pqr	pdb2pqr2004 ²⁰⁰
perlprimer	perlprimer	Graphical design of primers for PCR	perlprimer ⁵⁵⁷
perlprimer	perlprimer	Graphical design of primers for PCR	perlprimer2007 ⁵⁵⁸
perlprimer-doc	perlprimer	Tutorial to perlprimer	perlprimer ⁵⁵⁷
perlprimer-doc	perlprimer	Tutorial to perlprimer	perlprimer2007 ⁵⁵⁸
perm	perm	efficient mapping of short reads with periodic spaced seeds	perm ¹³⁸
pftools	pftools	build and search protein and DNA generalized profiles	pftools ⁷⁹⁰
phast	phast	phylogenetic analysis with space/time models	phast ³⁶⁸
phipack	phipack	PHI test and other tests of recombination	phipack ¹¹⁴
php5-gdcm	gdcm	Grassroots DICOM PHP5 bindings	gdcm ³⁰²
php5-vtkgdcm	gdcm	Grassroots DICOM VTK PHP bindings	gdcm ³⁰²
phybin	phybin	binning/clustering newick trees by topology	phybin ⁶¹³
phym1	phym1	Phylogenetic estimation using Maximum Likelihood	phym1 ³²³
phym1	phym1	Phylogenetic estimation using Maximum Likelihood	phym12003 ³²²
physamp	physamp	sample sequence alignment corresponding to phylogeny	physamp ²¹⁶
phyutility	phyutility	simple analyses or modifications on both phylogenetic trees and data matrices	phyutility ⁷⁹⁸
piler	piler	genomic repeat analysis	piler ²²⁶
pilercr	pilercr	software for finding CRISPR repeats	pilercr ²²³
pilon	pilon	automated genome assembly improvement and variant detection tool	pilon ⁹⁰⁶
pirs	pirs	Profile based Illumina pair-end Reads Simulator	pirs ³⁶⁵
pirs-examples	pirs	profile based Illumina pair-end Reads Simulator (example data)	pirs ³⁶⁵
pirs-profiles	pirs	profile based Illumina pair-end Reads Simulator (profile data)	pirs ³⁶⁵
placnet	placnet	Plasmid Constellation Network project	placnet ⁴⁷⁵
plasmidseeker	plasmidseeker	identification of known plasmids from whole-genome sequencing reads	plasmidseeker ⁷³²
plast	plast	Parallel Local Sequence Alignment Search Tool	plast ⁶²⁰
plast-example	plast	Parallel Local Sequence Alignment Search Tool (example data)	plast ⁶²⁰
plink	plink	whole-genome association analysis toolset	plink ⁶⁹⁹
plink1.9	plink1.9	whole-genome association analysis toolset	plink1-9 ¹³³
plink2	plink2	whole-genome association analysis toolset	plink2 ¹³⁴
plip	plip	fully automated protein-ligand interaction profiler	plip ⁷⁵⁴
poa	poa	Partial Order Alignment for multiple sequence alignment	poa ³¹⁵

poretools	poretools	toolkit for nanopore nucleotide sequencing data	poretools ⁵²⁸
poretools-data	poretools	toolkit for nanopore nucleotide sequencing data – sample datasets	poretools ⁵²⁸
pprepair	pprepair	planar partition repair tool	pprepair ²⁷
praat	praat	program for speech analysis and synthesis	praat ⁷⁶
prank	prank	Probabilistic Alignment Kit for DNA, codon and amino-acid sequences	prank ⁵³⁷
predictnls	predictnls	prediction and analysis of protein nuclear localization signals	predictnls ¹⁵³
predictprotein	predictprotein	suite of protein sequence analysis tools	predictprotein ⁷³⁸
prepair	prepair	polygon repair tool	prepair ⁴⁹⁰
prepair	prepair	polygon repair tool	prepair2012 ⁴⁸⁹
prepair-data	prepair	polygon repair tool – example data	prepair ⁴⁹⁰
prepair-data	prepair	polygon repair tool – example data	prepair2012 ⁴⁸⁹
prime-phylo	prime-phylo	bayesian estimation of gene trees taking the species tree into account	prime-phylo ⁹⁸¹
primer3	primer3	tool to design flanking oligo nucleotides for DNA amplification	primer3 ⁷⁴³
primer3-examples	primer3	tool to design flanking oligo nucleotides for DNA amplification (examples)	primer3 ⁷⁴³
prinseq-lite	prinseq-lite	Preprocessing and Information of SEquence data (lite version)	prinseq-lite ⁷⁰⁵
prinseq-lite-examples	prinseq-lite	Preprocessing and Information of SEquence data (example data)	prinseq-lite ⁷⁰⁵
proalign	proalign	Probabilistic multiple alignment program	proalign ⁵³⁶
probabel	probabel	Toolset for Genome-Wide Association Analysis	probabel ³⁴
probabel-examples	probabel	Example files for ProbABEL	probabel ³⁴
probalign	probalign	multiple sequence alignment using partition function posterior probabilities	probalign ⁷³⁴
probcons	probcons	PROBabilistic CONSistency-based multiple sequence alignment	probcons ¹⁹⁷
probcons-extra	probcons	Extra programs from the probcons package	probcons ¹⁹⁷
proda	proda	multiple alignment of protein sequences	proda ⁶⁷⁸
prodigal	prodigal	Microbial (bacterial and archaeal) gene finding program	prodigal ³⁷⁵
profbval	profbval	predictor of flexible/rigid protein residues from sequence	profbval ⁷⁶¹
profbval	profbval	predictor of flexible/rigid protein residues from sequence	profbval2005 ⁷⁶⁰
profsis	profsis	prediction of protein-protein interaction sites from sequence	profsis ⁶³⁶
profnet-bval	profnet	neural network architecture for profbval	profnet ⁷⁶²
profnet-chop	profnet	neural network architecture for profchop	profnet ⁷⁶²
profnet-con	profnet	neural network architecture for profcon	profnet ⁷⁶²
profnet-dbg	profnet	debug files for profnet packages	profnet ⁷⁶²
profnet-isis	profnet	neural network architecture for profsis	profnet ⁷⁶²
profnet-md	profnet	neural network architecture for metadisorder	profnet ⁷⁶²
profnet-norsnet	profnet	neural network architecture for norsnet	profnet ⁷⁶²
profnet-prof	profnet	neural network architecture for profacc	profnet ⁷⁶²
profnet-snapfun	profnet	neural network architecture for snapfun	profnet ⁷⁶²
profphd	profphd	secondary structure and solvent accessibility predictor	profphd ⁷³⁵
profphd	profphd	secondary structure and solvent accessibility predictor	profphd1994 ⁷³⁶
profphd	profphd	secondary structure and solvent accessibility predictor	profphd1995 ⁷³⁷
profphd-net	profnet	neural network architecture for profphd	profnet ⁷⁶²
proftmb	proftmb	per-residue prediction of bacterial transmembrane beta barrels	proftmb ⁷²
proftmb-dbg	proftmb	debugging symbols for proftmb	proftmb ⁷²
progressivemauve	progressivemauve	multiple genome alignment algorithms	progressivemauve ¹⁷
prokka	prokka	rapid annotation of prokaryotic genomes	prokka ⁷⁷⁹
proteinortho	proteinortho	Detection of (Co-)orthologs in large-scale protein analysis	proteinortho ⁴⁸⁸
protest	protest	selection of best-fit models of protein evolution	protest ¹⁷²
pscan-chip	pscan-chip	ChIP-based identification of TF binding sites	pscan-chip ⁹⁵⁹
pscan-chip-data	pscan-chip	auxiliary data for PScan-ChIP	pscan-chip ⁹⁵⁹
pscan-tfbs	pscan-tfbs	search for transcription factor binding sites	pscan-tfbs ⁹⁶⁰
psfex	psfex	Point Spread Function model extractor	psfex ⁶⁹
psi4	psi4	Quantum Chemical Program Suite	psi4 ⁶⁶⁰
psi4-data	psi4	Quantum Chemical Program Suite (data files)	psi4 ⁶⁶⁰

psortb	psortb	bacterial localization prediction tool	psortb ⁹⁵⁶
psychopy	psychopy	environment for creating psychology stimuli in Python	psychopy ⁹⁴⁵
purify	purify	Collection of routines for radio interferometric imaging	purify ⁶⁸⁷
pybedtools-bin	python-pybedtools	Scripts produced for pybedtools	python-pybedtools ¹
pycorrfit	pycorrfit	tool for fitting correlation curves on a logarithmic plot	pycorrfit ⁶⁰⁶
pyfits-utils	pyfits	transitional package for astropy-utils	pyfits ⁴⁹
pyfr	pyfr	flux reconstruction in Python	pyfr ²⁴²
pyfr-doc	pyfr	documentation for PyFR	pyfr ²⁴²
pynast	pynast	alignment of short DNA sequences	pynast ¹²²
python3-apbslib	apbs	Adaptive Poisson Boltzmann Solver	apbs ³⁹
python3-apbslib	apbs	Adaptive Poisson Boltzmann Solver	apbs1993 ³⁵⁷
python3-apbslib	apbs	Adaptive Poisson Boltzmann Solver	apbs1995 ³⁵⁸
python3-apbslib	apbs	Adaptive Poisson Boltzmann Solver	apbs2001 ³⁵⁶
python3-apbslib	apbs	Adaptive Poisson Boltzmann Solver	apbs2003 ⁴¹
python3-asdf	python-asdf	Python 3 library for the Advanced Scientific Data Format	python-asdf ³¹⁷
python3-astrometry	astrometry.net	Astrometry plate solver (Python package)	astrometry-net ⁴⁶⁹
python3-astroml	astroml	Python 3 Machine Learning library for astronomy	astroml ⁸⁹²
python3-astropy	astropy	Core functionality for performing astrophysics with Python	astropy ¹⁵⁵
python3-astrocrappy	astrocrappy	Optimized Cosmic Ray Annihilation in Python	astrocrappy ⁸⁸⁹
python3-avogadro	avogadrolibs	Molecular Graphics and Modelling System (Python 3 module)	avogadrolibs ³³³
python3-ball	ball	Python bindings for the Biochemical Algorithms Library	ball ⁵⁸⁵
python3-ball	ball	Python bindings for the Biochemical Algorithms Library	ball2010 ³⁵⁰
python3-biom-format	python-biom-format	Biological Observation Matrix (BIOM) format (Python 3)	python-biom-format
python3-biopython	python-biopython	Python3 library for bioinformatics	python-biopython ¹⁵
python3-biopython-sql	python-biopython	Biopython support for the BioSQL database schema (Python 3)	python-biopython ¹⁵
python3-biosig	biosig4c++	Python3 bindings for BioSig library	biosig4c ⁷⁶⁷
python3-biotools	python-biotools	Python3 bioinformatics utilities for high-throughput genomic sequencing	python-biotools ⁵¹
python3-brian	brian	simulator for spiking neural networks	brian ³⁰³
python3-brian	brian	simulator for spiking neural networks	brian2009 ³⁰⁴
python3-brian-lib	brian	simulator for spiking neural networks – extensions	brian ³⁰³
python3-brian-lib	brian	simulator for spiking neural networks – extensions	brian2009 ³⁰⁴
python3-caffe	caffe	Python3 interface of Caffe (CPU_ONLY)	caffe ³⁹⁰
python3-caffe-cpu	caffe	Python3 interface of Caffe (CPU_ONLY)	caffe ³⁹⁰
python3-caffe-cuda	caffe-contrib	Python3 interface of Caffe (CUDA)	caffe-contrib ³⁹¹
python3-cclib	cclib	Parsers and algorithms for computational chemistry (Python3 module)	cclib ⁶²⁹
python3-chemps2	chemps2	Python 3 interface for libchemps2-3	chemps2 ¹³⁶
python3-chemps2	chemps2	Python 3 interface for libchemps2-3	chemps22014 ⁹⁴¹
python3-chemps2	chemps2	Python 3 interface for libchemps2-3	chemps22014c ⁹³⁷
python3-chemps2	chemps2	Python 3 interface for libchemps2-3	chemps22014d ⁹³⁹
python3-chemps2	chemps2	Python 3 interface for libchemps2-3	chemps22016 ⁹⁴³
python3-cobra	python-cobra	constraint-based modeling of biological networks with Python 3	python-cobra ²¹⁹
python3-cogent3	python-cogent	framework for genomic biology	python-cogent ⁴³⁵
python3-cpl	python-cpl	Control pipeline recipes from the ESO (Python3)	python-cpl ⁸³²
python3-cutadapt	python-cutadapt	Clean biological sequences from high-throughput sequencing reads (Python 3)	python-cutadapt ⁵⁵⁹
python3-cyvcf2	cyvcf2	VCF parser based on htlib (Python 3)	cyvcf2 ⁶⁶⁶
python3-deeptools	python-deeptools	platform for exploring biological deep-sequencing data	python-deeptools ⁷¹¹
python3-deeptools	python-deeptools	platform for exploring biological deep-sequencing data	python-deeptools20
python3-dendropy	python-dendropy	DendroPy Phylogenetic Computing Library (Python 3)	python-dendropy ⁸³⁹
python3-deprecation	python-deprecation	Library to handle automated deprecations	python-deprecation
python3-dna-jellyfish	jellyfish	count k-mers in DNA sequences (Python bindings of jellyfish)	jellyfish ⁵⁴⁵
python3-dnapi	dnapi	adapter prediction for small RNA sequencing - library	dnapi ⁸⁸³
python3-drizzle	python-drizzle	Dithered image combination for Python	python-drizzle ³⁰⁰

python3-drizzle-dbg	python-drizzle	Python3 binding to libdrizzle - debug symbols	python-drizzle ³⁰⁰
python3-emcee	emcee	Affine-invariant ensemble MCMC sampling for Python 3	emcee ²⁵³
python3-fastcluster	r-cran-fastcluster	Fast hierarchical clustering routines for Python 3	r-cran-fastcluster ⁶⁰⁷
python3-freecontact	python-freecontact	fast protein contact predictor - binding for Python3	python-freecontact ⁴
python3-gammapy	gammapy	Python package for gamma-ray astronomy	gammapy ¹⁸²
python3-gdcm	gdcm	Grassroots DICOM Python bindings	gdcm ³⁰²
python3-gdl	gnudatalanguage	Python interface for the GNU Data Language	gnudatalanguage ¹⁶⁰
python3-genometools	genometools	Python3 bindings for genometools	genometools ³¹⁹
python3-gfapy	gfapy	flexible and extensible software library for handling sequence graphs	gfapy ²⁹⁹
python3-glue	glueviz	Python 3 library for data interaction	glueviz ⁵⁵
python3-gmsh	gmsh	Three-dimensional finite element mesh generator Python 3 wrapper	gmsh ²⁸⁴
python3-gyoto	gyoto	General relativistic geodesic integration for the Python 3 language	gyoto ⁸⁹⁹
python3-hisat2	hisat2	Python scripts accompanying hisat2	hisat2 ⁴³¹
python3-htseq	htseq	Python3 high-throughput genome sequencing read analysis utilities	htseq ¹⁸
python3-isospec	isospec	Isotopic fine structure calculator for Python 3	isospec ⁵⁶³
python3-mia	pymia	Python-3 bindings for the MIA image processing library	pymia ⁹³¹
python3-mia-dbg	pymia	Debug information for Python-3 bindings for MIA	pymia ⁹³¹
python3-mirtop	mirtop	annotate miRNAs with a standard mirna/isomir naming (Python 3)	mirtop ¹⁸⁸
python3-mirtop	mirtop	annotate miRNAs with a standard mirna/isomir naming (Python 3)	mirtop2019 ¹⁸⁹
python3-mofapy	r-bioc-mofa	Multi-Omics Factor Analysis (MOFA) - Python module	r-bioc-mofa ²⁴
python3-montagepy	montage	Python toolkit for assembling FITS images into mosaics	montage ³⁸⁷
python3-nipy	nipy	Analysis of structural and functional neuroimaging data	nipy ⁵⁸⁰
python3-nipy-lib	nipy	Analysis of structural and functional neuroimaging data (compiled modules)	nipy ⁵⁸⁰
python3-nipy-lib-dbg	nipy	Analysis of structural and functional neuroimaging data (debug symbols)	nipy ⁵⁸⁰
python3-nltk	nltk	Python3 libraries for natural language processing	nltk ⁷³
python3-opencv	opencv	Python 3 bindings for the computer vision library	opencv ¹⁰¹
python3-pandas	pandas	data structures for "relational" or "labeled" data	pandas ⁵⁷¹
python3-pandas-lib	pandas	low-level implementations and bindings for pandas	pandas ⁵⁷¹
python3-presto	presto	toolkit for processing B and T cell sequences	presto ⁶⁸⁸
python3-pyani	python-pyani	Python3 module for average nucleotide identity analyses	python-pyani ⁶⁹²
python3-pybedtools	python-pybedtools	Python 3 wrapper around BEDTools for bioinformatics work	python-pybedtools ¹
python3-pybel	pybel	Biological Expression Language	pybel ³⁶⁰
python3-pycodcif	cod-tools	error-correcting CIF parser - Python3 bindings	cod-tools ³¹⁶
python3-pyfaidx	python-pyfaidx	efficient random access to fasta subsequences for Python 3	python-pyfaidx ⁷⁸⁴
python3-pyfits	pyfits	Python3 module for reading, writing, and manipulating FITS files	pyfits ⁴⁹
python3-pymzml	python-pymzml	mzML mass spectrometric data parsing (Python 3.x)	python-pymzml ⁴⁰
python3-pysynphot	pysynphot	Python Synthetic Photometry Utilities	pysynphot ⁵¹²
python3-pywps	pywps	Implementation of OGC's Web Processing Service - Python module	pywps ⁹⁸²
python3-pywps	pywps	Implementation of OGC's Web Processing Service - Python module	pywps2007 ⁹⁸³
python3-qcelestial	qcelestial	Periodic table, physical constants, and molecule parsing for quantum chemistry	qcelestial ⁷⁰¹
python3-qcelestial	qcelestial	Periodic table, physical constants, and molecule parsing for quantum chemistry	qcelestial2014 ⁹⁴²
python3-qcelestial	qcelestial	Periodic table, physical constants, and molecule parsing for quantum chemistry	qcelestial2014c ⁹³⁸
python3-qcelestial	qcelestial	Periodic table, physical constants, and molecule parsing for quantum chemistry	qcelestial2014d ⁹⁴⁴
python3-qcelestial	qcelestial	Periodic table, physical constants, and molecule parsing for quantum chemistry	qcelestial2016 ⁹⁴⁴

python3-requirements-detector	python-requirements-detector	finds and lists the requirements of a Python project	python-requirements-detector
python3-ruffus	python-ruffus	Python3 computation pipeline library widely used in bioinformatics	python-ruffus ³⁰⁵
python3-sbml5	libsbml	System Biology Markup Language library - Python3 bindings	libsbml ⁹⁴
python3-sbml5-doc	libsbml	System Biology Markup Language library - Python3 documentation	libsbml ⁹⁴
python3-shapely	python-shapely	geometric objects, predicates, and operations (Python 3)	python-shapely ²⁹²
python3-spectral-cube	spectral-cube	Manipulate astronomical data cubes with Python	spectral-cube ²⁹³
python3-statsmodels	statsmodels	Python3 module for the estimation of statistical models	statsmodels ⁷⁷⁷
python3-statsmodels-lib	statsmodels	Python3 low-level implementations and bindings for statsmodels	statsmodels ⁷⁷⁷
python3-sunpy	sunpy	Software library for solar physics based on Python	sunpy ⁸⁴⁰
python3-theano	theano	CPU/GPU math expression compiler for Python 3	theano ⁸⁵⁴
python3-vispy	python-vispy	interactive visualization in Python 3	python-vispy ¹²¹
python3-vtkgdc	gdc	Grassroots DICOM VTK/Python bindings	gdc ³⁰²
python3-yade	yade	Platform for discrete element modeling. Python bindings	yade ⁹⁰³
python3-yt	yt	Framework for analyzing and visualizing simulation data (Python 3)	yt ⁸⁸⁴
python-asdf	python-asdf	Python library for the Advanced Scientific Data Format	python-asdf ³¹⁷
python-asdf-doc	python-asdf	Python library for the Advanced Scientific Data Format (documentation)	python-asdf ³¹⁷
python-astrometry	astrometry.net	Astrometry plate solver (Python package)	astrometry-net ⁴⁶⁹
python-astroml	astroml	Python Machine Learning library for astronomy	astroml ⁸⁹²
python-astropy	python-astropy	Core functionality for performing astrophysics with Python	python-astropy ¹⁵⁴
python-astropy-doc	astropy	Core functionality for performing astrophysics with Python (doc)	astropy ¹⁵⁵
python-astrocrappy	astrocrappy	Optimized Cosmic Ray Annihilation in Python 2	astrocrappy ⁸⁸⁹
python-avogadro	avogadro	Molecular Graphics and Modelling System (Python module)	avogadro ³³²
python-ball	ball	Python bindings for the Biochemical Algorithms Library	ball ⁵⁸⁵
python-ball	ball	Python bindings for the Biochemical Algorithms Library	ball2010 ³⁵⁰
python-ballview	ball	Python bindings for VIEW-parts of the Biochemical Algorithms Library	ball ⁵⁸⁵
python-ballview	ball	Python bindings for VIEW-parts of the Biochemical Algorithms Library	ball2010 ³⁵⁰
python-biom-format	python-biom-format	Biological Observation Matrix (BIOM) format (Python 2)	python-biom-format
python-biom-format-doc	python-biom-format	documentation for BIOM format	python-biom-format
python-biopython	python-biopython	Python library for bioinformatics (implemented in Python 2)	python-biopython ¹⁵
python-biopython-doc	python-biopython	Documentation for the Biopython library	python-biopython ¹⁵
python-biopython-sql	python-biopython	Biopython support for the BioSQL database schema (Python 2)	python-biopython ¹⁵
python-biosig	biosig4c++	Python bindings for BioSig library	biosig4c ⁷⁶⁷
python-biotools	python-biotools	Python bioinformatics utilities for high-throughput genomic sequencing	python-biotools ⁵¹
python-brian	brian	simulator for spiking neural networks	brian ³⁰³
python-brian	brian	simulator for spiking neural networks	brian2009 ³⁰⁴
python-brian-doc	brian	simulator for spiking neural networks - documentation	brian ³⁰³
python-brian-doc	brian	simulator for spiking neural networks - documentation	brian2009 ³⁰⁴
python-brian-lib	brian	simulator for spiking neural networks – extensions	brian ³⁰³
python-brian-lib	brian	simulator for spiking neural networks – extensions	brian2009 ³⁰⁴
python-casmoothing	python-casmoothing	Context-aware mesh smoothing for biomedical applications	python-casmoothing
python-cclib	cclib	Parsers and algorithms for computational chemistry (Python module)	cclib ⁶²⁹
python-chemps2	chemps2	Python 2 interface for libchemps2-2	chemps2 ¹³⁶
python-chemps2	chemps2	Python 2 interface for libchemps2-2	chemps22014 ⁹⁴¹
python-chemps2	chemps2	Python 2 interface for libchemps2-2	chemps22014c ⁹³⁷

python-chemps2	chemps2	Python 2 interface for libchemps2-2	chemps22014d ⁹³⁹
python-chemps2	chemps2	Python 2 interface for libchemps2-2	chemps22016 ⁹⁴³
python-cinfony	cinfony	Python abstraction layer to cheminformatics toolkits	cinfony ⁶²⁶
python-cobra	python-cobra	constraint-based modeling of biological networks (Python 2)	python-cobra ²¹⁹
python-cobra-data	python-cobra	constraint-based modeling of biological networks (data)	python-cobra ²¹⁹
python-cogent	python-cogent	framework for genomic biology	python-cogent ⁴³⁵
python-cogent-dbg	python-cogent	debug information for pycogent	python-cogent ⁴³⁵
python-cogent-doc	python-cogent	docs for python3-cogent3	python-cogent ⁴³⁵
python-cpl	python-cpl	Control pipeline recipes from the European Southern Observatory	python-cpl ⁸³²
python-cutadapt	python-cutadapt	Clean biological sequences from high-throughput sequencing reads (Python 2)	python-cutadapt ⁵⁵⁹
python-cyvcf2	cyvcf2	VCF parser based on htlib (Python 2)	cyvcf2 ⁶⁶⁶
python-dendropy	python-dendropy	DendroPy Phylogenetic Computing Library (Python 2)	python-dendropy ⁸³⁸
python-deprecation	python-deprecation	Library to handle automated deprecations - Python 2.x	python-deprecation
python-dipy	dipy	Python library for the analysis of diffusion MRI datasets	dipy ²⁷⁵
python-dipy-doc	dipy	Python library for the analysis of diffusion MRI datasets – documentation	dipy ²⁷⁵
python-dipy-lib	dipy	Python library for the analysis of diffusion MRI datasets – extensions	dipy ²⁷⁵
python-drizzle	python-drizzle	Dithered image combination for Python 2	python-drizzle ³⁰⁰
python-drizzle-dbg	python-drizzle	Python binding to libdrizzle - debug symbols	python-drizzle ³⁰⁰
python-drizzle-doc	python-drizzle	Dithered image combination for Python (API documentation)	python-drizzle ³⁰⁰
python-drizzle-test data	python-drizzle	Dithered image combination for Python (Test data)	python-drizzle ³⁰⁰
python-emcee	emcee	Affine-invariant ensemble MCMC sampling for Python	emcee ²⁵³
python-expyriment	python-expyriment	Python library for cognitive and neuroscientific experiments	python-expyriment ⁴
python-fastcluster	r-cran-fastcluster	Fast hierarchical clustering routines for Python	r-cran-fastcluster ⁶⁰⁷
python-freecontact	python-freecontact	fast protein contact predictor - binding for Python	python-freecontact ⁴
python-gdcm	gdcm	Grassroots DICOM Python bindings	gdcm ³⁰²
python-gdl	gnudatalanguage	Python interface for the GNU Data Language	gnudatalanguage ¹⁶⁰
python-genometools	genometools	Python bindings for genometools	genometools ³¹⁹
python-glue	glueviz	Python 2 library for data interaction	glueviz ⁵⁵
python-gmsh	gmsh	Three-dimensional finite element mesh generator. Python wrapper	gmsh ²⁸⁴
python-gyoto	gyoto	General relativistic geodesic integration for the Python 2 language	gyoto ⁸⁹⁹
python-htseq	htseq	Python high-throughput genome sequencing read analysis utilities	htseq ¹⁸
python-htseq-doc	htseq	documentation for HTSeq (high-throughput genome sequencing)	htseq ¹⁸
python-mia	pymia	Python-2 bindings for the MIA image processing library	pymia ⁹³¹
python-mia-dbg	pymia	Debug information for Python-2 bindings for MIA	pymia ⁹³¹
python-nipy	nipy	Analysis of structural and functional neuroimaging data	nipy ⁵⁸⁰
python-nipy-doc	nipy	documentation and examples for NiPy	nipy ⁵⁸⁰
python-nipy-lib	nipy	Analysis of structural and functional neuroimaging data	nipy ⁵⁸⁰
python-nipy-lib-dbg	nipy	Analysis of structural and functional neuroimaging data	nipy ⁵⁸⁰
python-nipype	nipype	Neuroimaging data analysis pipelines in Python	nipype ²⁸⁶
python-nipype-doc	nipype	Neuroimaging data analysis pipelines in Python – documentation	nipype ²⁸⁶
python-nltk	nltk	Python libraries for natural language processing	nltk ⁷³
python-openbabel	openbabel	Chemical toolbox library (python bindings)	openbabel2008 ⁶²⁸
python-opencv	opencv	Python bindings for the computer vision library	opencv ¹⁰¹
python-opengm	opengm	Python interface to OpenGM	opengm ¹⁹
python-opengm-doc	opengm	documentation for the Python interface to OpenGM	opengm ¹⁹
python-openmeeg	openmeeg	openmeeg library – Python bindings	openmeeg ³¹²
python-pandas	pandas	data structures for "relational" or "labeled" data	pandas ⁵⁷¹

python-pandas-doc	pandas	data structures for "relational" or "labeled" data - documentation	pandas ⁵⁷¹
python-pandas-lib	pandas	low-level implementations and bindings for pandas	pandas ⁵⁷¹
python-pybedtools-doc	python-pybedtools	Documentation for pybedtools library	python-pybedtools ¹
python-pycodcif	cod-tools	error-correcting CIF parser - Python bindings	cod-tools ³¹⁶
python-pyfaidx	python-pyfaidx	efficient random access to fasta subsequences for Python	python-pyfaidx ⁷⁸⁴
python-pyfaidx-examples	python-pyfaidx	example data for efficient random access to fasta subsequences for Python	python-pyfaidx ⁷⁸⁴
python-pyfits	pyfits	Python module for reading, writing, and manipulating FITS files	pyfits ⁴⁹
python-pymzml	python-pymzml	mzML mass spectrometric data parsing (Python 2.x)	python-pymzml ⁴⁰
python-pymzml-doc	python-pymzml	mzML mass spectrometric data parsing - documentation	python-pymzml ⁴⁰
python-pysynphot	pysynphot	Python Synthetic Photometry Utilities	pysynphot ⁵¹²
python-pytrilinos	trilinos	parallel solver libraries within an object-oriented software framework	trilinos ³⁴⁷
python-pywps	pywps	Implementation of OGC's Web Processing Service - Python 2 module	pywps ⁹⁸²
python-pywps	pywps	Implementation of OGC's Web Processing Service - Python 2 module	pywps2007 ⁹⁸³
python-requirements-detector	python-requirements-detector	finds and lists the requirements of a Python project (Python 2)	python-requirements ¹²¹
python-ruffus	python-ruffus	Python computation pipeline library widely used in bioinformatics	python-ruffus ³⁰⁵
python-ruffus-doc	python-ruffus	documentation for python-ruffus computation pipeline library	python-ruffus ³⁰⁵
python-scikits.statmodels	statmodels	transitional compatibility package for statmodels migration	statmodels ⁷⁷⁷
python-shapely	python-shapely	geometric objects, predicates, and operations (Python 2)	python-shapely ²⁹²
python-shapely-doc	python-shapely	geometric objects, predicates, and operations (documentation)	python-shapely ²⁹²
python-spectral-cube	spectral-cube	Manipulate astronomical data cubes with Python 2	spectral-cube ²⁹³
python-statmodels	statmodels	Python module for the estimation of statistical models	statmodels ⁷⁷⁷
python-statmodels-doc	statmodels	documentation and examples for statmodels	statmodels ⁷⁷⁷
python-statmodels-lib	statmodels	low-level implementations and bindings for statmodels	statmodels ⁷⁷⁷
python-sunpy	sunpy	Software library for solar physics based on Python	sunpy ⁸⁴⁰
python-theano	theano	CPU/GPU math expression compiler for Python	theano ⁸⁵⁴
python-visionegg	visionegg	Python library for 2D/3D visual stimulus generation	visionegg ⁸³¹
python-vispy	python-vispy	interactive visualization in Python 2	python-vispy ¹²¹
python-vispy-doc	python-vispy	interactive visualization in Python [documentation]	python-vispy ¹²¹
python-vmtk	vmtk	Python interface for vmtk	vmtk ⁶⁷⁹
python-vtkgdc	gdc	Grassroots DICOM VTK/Python bindings	gdc ³⁰²
python-yade	yade	Platform for discrete element modeling. Python bindings	yade ⁹⁰³
python-yt	yt	Framework for analyzing and visualizing simulation data (Python 2)	yt ⁸⁸⁴
pywps	pywps	Implementation of OGC's Web Processing Service	pywps ⁹⁸²
pywps	pywps	Implementation of OGC's Web Processing Service	pywps2007 ⁹⁸³
pywps-doc	pywps	Implementation of OGC's Web Processing Service - Documentation	pywps ⁹⁸²
pywps-doc	pywps	Implementation of OGC's Web Processing Service - Documentation	pywps2007 ⁹⁸³
pywps-wsgi	pywps	Implementation of OGC's Web Processing Service - WSGI example	pywps ⁹⁸²
pywps-wsgi	pywps	Implementation of OGC's Web Processing Service - WSGI example	pywps2007 ⁹⁸³
q2cli	q2cli	Click-based command line interface for QIIME 2	q2cli ⁸¹
q2-cutadapt	q2-cutadapt	QIIME 2 plugin to work with adapters in sequence data	q2-cutadapt ⁸²
q2-demux	q2-demux	QIIME 2 plugin for demultiplexing of sequence reads	q2-demux ⁸³

q2-feature-classifier	q2-feature-classifier	QIIME 2 plugin supporting taxonomic classification	q2-feature-classifier ⁸⁵
q2-feature-table	q2-feature-table	QIIME 2 plugin supporting operations on feature tables	q2-feature-table ⁸⁵
q2-metadata	q2-metadata	QIIME 2 plugin for working with and visualizing Metadata	q2-metadata ⁸⁶
q2-quality-filter	q2-quality-filter	QIIME2 plugin for PHRED-based filtering and trimming	q2-quality-filter ⁸⁷
q2templates	q2templates	Design template package for QIIME 2 Plugins	q2templates ⁸⁸
q2-types	q2-types	QIIME 2 plugin defining types for microbiome analysis	q2-types ⁸⁹
qiime	qiime	Quantitative Insights Into Microbial Ecology	qiime ⁹⁰
qiime-data	qiime	Quantitative Insights Into Microbial Ecology (supporting data)	qiime ⁹⁰
qiime-doc	qiime	Quantitative Insights Into Microbial Ecology (tutorial)	qiime ⁹⁰
qrisk2	qrisk2	cardiovascular disease risk calculator	qrisk2 ³⁵¹
qsopt-ex	qsopt-ex	Exact linear programming solver	qsopt-ex ²³
qtltools	qtltools	Tool set for molecular QTL discovery and analysis	qtltools ¹⁸⁴
qtltools	qtltools	Tool set for molecular QTL discovery and analysis	qtltools2017 ²⁵⁵
qtltools-example	qtltools	Tool set for molecular QTL discovery and analysis - example	qtltools ¹⁸⁴
qtltools-example	qtltools	Tool set for molecular QTL discovery and analysis - example	qtltools2017 ²⁵⁵
quantum-espresso	espresso	Electronic-Structure and Ab-Initio Molecular Dynamics Suite	espresso ²⁸⁷
quantum-espresso-data	espresso	Electronic-Structure and Ab-Initio Molecular Dynamics Suite (Documentation)	espresso ²⁸⁷
quorum	quorum	QQuality Optimized Reads of genomic sequences	quorum ⁵⁶²
qutemol	qutemol	interactive visualization of macromolecules	qutemol ⁸⁴⁹
raccoon	raccoon	preparation of in silico drug screening projects	raccoon ¹⁵⁹
racon	racon	consensus module for raw de novo DNA assembly of long uncorrected reads	racon ⁸⁹⁶
radiant	radiant	explore hierarchical metagenomic data with zoomable pie charts	radiant ⁶⁴¹
ragout	ragout	Reference-Assisted Genome Ordering UTility	ragout ⁴⁴⁰
ragout	ragout	Reference-Assisted Genome Ordering UTility	ragout2014 ⁴³⁹
ragout-examples	ragout	Reference-Assisted Genome Ordering UTility (example data)	ragout ⁴⁴⁰
ragout-examples	ragout	Reference-Assisted Genome Ordering UTility (example data)	ragout2014 ⁴³⁹
rambo-k	rambo-k	Read Assignment Method Based On K-mers	rambo-k ⁸⁵⁰
rapmap	rapmap	rapid sensitive and accurate DNA read mapping via quasi-mapping	rapmap ⁸⁰⁹
rapmap	rapmap	rapid sensitive and accurate DNA read mapping via quasi-mapping	rapmap2016 ¹⁰³
rapmap-dev	rapmap	rapmap - rapid sensitive and accurate DNA read mapping (some headers)	rapmap ⁸⁰⁹
rapmap-dev	rapmap	rapmap - rapid sensitive and accurate DNA read mapping (some headers)	rapmap2016 ¹⁰³
rapmap-example-data	rapmap	example data for rapmap - rapid sensitive and accurate DNA read mapping	rapmap ⁸⁰⁹
rapmap-example-data	rapmap	example data for rapmap - rapid sensitive and accurate DNA read mapping	rapmap2016 ¹⁰³
rasmol	rasmol	visualization of biological macromolecules	rasmol ⁷⁵⁸
rasmol-doc	rasmol	documentation for rasmol	rasmol ⁷⁵⁸
raster3d	raster3d	tools for generating images of proteins or other molecules	raster3d ⁵⁷⁵
raster3d	raster3d	tools for generating images of proteins or other molecules	raster3d1988 ³⁷
raster3d	raster3d	tools for generating images of proteins or other molecules	raster3d1991 ⁴⁵¹
raster3d	raster3d	tools for generating images of proteins or other molecules	raster3d1994 ⁵⁷⁶
raster3d-doc	raster3d	documents and example files for Raster3D	raster3d ⁵⁷⁵
raster3d-doc	raster3d	documents and example files for Raster3D	raster3d1988 ³⁷
raster3d-doc	raster3d	documents and example files for Raster3D	raster3d1991 ⁴⁵¹
raster3d-doc	raster3d	documents and example files for Raster3D	raster3d1994 ⁵⁷⁶
rate4site	rate4site	detector of conserved amino-acid sites	rate4site ⁵⁶⁸
rate4site-dbg	rate4site	debugging symbols for rate4site-dbg	rate4site ⁵⁶⁸
rawtran	rawtran	RAW photo to FITS converter	rawtran ³⁶⁴

rawtran-doc	rawtran	Documentation of Rawtran	rawtran ³⁶⁴
raxml	raxml	Randomized Axelerated Maximum Likelihood of phylogenetic trees	raxml ⁸¹⁵
raxml	raxml	Randomized Axelerated Maximum Likelihood of phylogenetic trees	raxml2006 ⁸¹⁴
ray	ray	de novo genome assemblies of next-gen sequencing data	ray ⁷⁸
ray	ray	de novo genome assemblies of next-gen sequencing data	ray2012 ⁷⁹
ray-doc	ray	documentation for ray parallel de novo genome assembler	ray ⁷⁸
ray-doc	ray	documentation for ray parallel de novo genome assembler	ray2012 ⁷⁹
ray-extra	ray	Scripts and XSL sheets for post-processing for ray	ray ⁷⁸
ray-extra	ray	Scripts and XSL sheets for post-processing for ray	ray2012 ⁷⁹
r-bioc-affy	r-bioc-affy	BioConductor methods for Affymetrix Oligonucleotide Arrays	r-bioc-affy ²⁷⁷
r-bioc-altcdfenvs	r-bioc-altcdfenvs	BioConductor alternative CDF environments	r-bioc-altcdfenvs ²⁷⁸
r-bioc-aroma.light	r-bioc-aroma.light	BioConductor methods normalization and visualization of microarray data	r-bioc-aroma-light ⁶¹
r-bioc-biobase	r-bioc-biobase	base functions for Bioconductor	r-bioc-biobase ²⁸³
r-bioc-biocgenerics	r-bioc-biocgenerics	generic functions for Bioconductor	r-bioc-biocgenerics ³
r-bioc-biomart	r-bioc-biomart	GNU R Interface to BioMart databases (Ensembl, COSMIC, Wormbase and Gramene)	r-bioc-biomart ²¹⁴
r-bioc-biomart	r-bioc-biomart	GNU R Interface to BioMart databases (Ensembl, COSMIC, Wormbase and Gramene)	r-bioc-biomart2005 ²
r-bioc-bitseq	r-bioc-bitseq	transcript expression inference and analysis for RNA-seq data	r-bioc-bitseq ²⁹⁵
r-bioc-cummerbund	r-bioc-cummerbund	tool for analysis of Cufflinks RNA-Seq output	r-bioc-cummerbund
r-bioc-dada2	r-bioc-dada2	sample inference from amplicon sequencing data	r-bioc-dada2 ¹²⁰
r-bioc-deseq2	r-bioc-deseq2	R package for RNA-Seq Differential Expression Analysis	r-bioc-deseq2 ⁵³¹
r-bioc-dirichletmultinomial	r-bioc-dirichletmultinomial	Dirichlet-Multinomial Mixture Model Machine Learning for Microbiome Data	r-bioc-dirichletmulti
r-bioc-ebseq	r-bioc-ebseq	R package for RNA-Seq Differential Expression Analysis	r-bioc-ebseq ⁴⁹⁵
r-bioc-edger	r-bioc-edger	Empirical analysis of digital gene expression data in R	r-bioc-edger ⁷²⁷
r-bioc-edger	r-bioc-edger	Empirical analysis of digital gene expression data in R	r-bioc-edger2007 ⁷²⁶
r-bioc-genomicalignments	r-bioc-genomicalignments	BioConductor representation and manipulation of short genomic alignments	r-bioc-genomicalignm
r-bioc-genomicfeatures	r-bioc-genomicfeatures	GNU R tools for making and manipulating transcript centric annotations	r-bioc-genomicfeatu
r-bioc-geoquery	r-bioc-geoquery	Get data from NCBI Gene Expression Omnibus (GEO)	r-bioc-geoquery ¹⁷⁷
r-bioc-gviz	r-bioc-gviz	Plotting data and annotation information along genomic coordinates	r-bioc-gviz ⁴⁸³
r-bioc-hilbertvis	r-bioc-hilbertvis	GNU R package to visualise long vector data	r-bioc-hilbertvis ¹⁷
r-bioc-limma	r-bioc-limma	linear models for microarray data	r-bioc-limma ⁸⁰⁰
r-bioc-mergeomics	r-bioc-mergeomics	Integrative network analysis of omics data	r-bioc-mergeomics ⁷⁸
r-bioc-mofa	r-bioc-mofa	Multi-Omics Factor Analysis (MOFA)	r-bioc-mofa ²⁴
r-bioc-multtest	r-bioc-multtest	Bioconductor resampling-based multiple hypothesis testing	r-bioc-multtest ⁶⁸²
r-bioc-pcamethods	r-bioc-pcamethods	BioConductor collection of PCA methods	r-bioc-pcamethods ⁸
r-bioc-phyloseq	r-bioc-phyloseq	GNU R handling and analysis of high-throughput microbiome census data	r-bioc-phyloseq ⁵⁷²
r-bioc-qusage	r-bioc-qusage	qusage: Quantitative Set Analysis for Gene Expression	r-bioc-qusage ⁹⁵²
r-bioc-qvalue	r-bioc-qvalue	GNU R package for Q-value estimation for FDR control	r-bioc-qvalue ⁸²⁸
r-bioc-rtracklayer	r-bioc-rtracklayer	GNU R interface to genome browsers and their annotation tracks	r-bioc-rtracklayer ⁴⁸⁴
r-bioc-shortread	r-bioc-shortread	GNU R classes and methods for high-throughput short-read sequencing data	r-bioc-shortread ⁵⁸⁹
r-bioc-tfbstools	r-bioc-tfbstools	GNU R Transcription Factor Binding Site (TFBS) Analysis	r-bioc-tfbstools ⁸⁴⁷
r-bioc-tximport	r-bioc-tximport	transcript-level estimates for biological sequencing	r-bioc-tximport ⁸⁰²
r-bioc-variantannotation	r-bioc-variantannotation	BioConductor annotation of genetic variants	r-bioc-variantannot
r-cran-ade4	r-cran-ade4	GNU R analysis of ecological data	r-cran-ade4 ²⁰⁷

r-cran-adegetnet	r-cran-adegetnet	GNU R exploratory analysis of genetic and genomic data	r-cran-adegetnet ⁴⁰⁴
r-cran-adephylo	r-cran-adephylo	GNU R exploratory analyses for the phylogenetic comparative method	r-cran-adephylo ⁴⁰⁵
r-cran-alakazam	r-cran-alakazam	Immunoglobulin Clonal Lineage and Diversity Analysis	r-cran-alakazam ³²⁶
r-cran-alakazam	r-cran-alakazam	Immunoglobulin Clonal Lineage and Diversity Analysis	r-cran-alakazam2014
r-cran-apcluster	r-cran-apcluster	Affinity Propagation Clustering	r-cran-apcluster ²⁶⁰
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape ⁶⁵⁷
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape1950 ⁵⁸⁷
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape1973 ¹⁴⁹
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape1981 ¹⁵⁰
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape1985 ¹³⁹
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape1990 ²⁹⁴
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape2004 ⁶⁵⁸
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape2006 ⁶⁵⁶
r-cran-ape	r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution	r-cran-ape2012 ⁶⁸⁵
r-cran-bigmemory	r-cran-bigmemory	Manage Massive Matrices with Shared Memory and Memory-Mapped Files	r-cran-bigmemory ⁵⁷
r-cran-bio3d	r-cran-bio3d	GNU R package for biological structure analysis	r-cran-bio3d ³¹³
r-cran-blockmodeling	r-cran-blockmodeling	Generalized and classical blockmodeling of valued networks	r-cran-blockmodeling
r-cran-blockmodeling	r-cran-blockmodeling	Generalized and classical blockmodeling of valued networks	r-cran-blockmodeling
r-cran-blockmodeling	r-cran-blockmodeling	Generalized and classical blockmodeling of valued networks	r-cran-blockmodeling
r-cran-bms	r-cran-bms	GNU R package for Bayesian model averaging for linear models	r-cran-bms ²⁴³
r-cran-boolnet	r-cran-boolnet	assembling, analyzing and visualizing Boolean networks	r-cran-boolnet ⁵⁹⁸
r-cran-calibrate	r-cran-calibrate	Calibration of Scatterplot and Biplot Axes	r-cran-calibrate ³¹¹
r-cran-cmprsk	r-cran-cmprsk	GNU R subdistribution analysis of competing risks	r-cran-cmprsk ²⁴⁸
r-cran-colorspace	r-cran-colorspace	GNU R Color Space Manipulation	r-cran-colorspace ⁹⁶⁵
r-cran-dosefinding	r-cran-dosefinding	Planning and Analyzing Dose Finding experiments	r-cran-dosefinding ⁶⁸
r-cran-ellipse	r-cran-ellipse	GNU R functions for drawing ellipses and ellipse-like confidence regions	r-cran-ellipse ⁶⁰⁰
r-cran-epi	r-cran-epi	GNU R epidemiological analysis	r-cran-epi ⁶⁸¹
r-cran-evd	r-cran-evd	GNU R Functions for extreme value distributions	r-cran-evd ⁸²⁶
r-cran-expm	r-cran-expm	GNU R Computation of the matrix exponential and related quantities	r-cran-expm ³⁸⁵
r-cran-factominer	r-cran-factominer	Multivariate Exploratory Data Analysis and Data Mining	r-cran-factominer ⁴⁸
r-cran-factominer	r-cran-factominer	Multivariate Exploratory Data Analysis and Data Mining	r-cran-factominer20
r-cran-factominer	r-cran-factominer	Multivariate Exploratory Data Analysis and Data Mining	r-cran-factominer20
r-cran-factominer	r-cran-factominer	Multivariate Exploratory Data Analysis and Data Mining	r-cran-factominer20
r-cran-fastcluster	r-cran-fastcluster	Fast hierarchical clustering routines for GNU R	r-cran-fastcluster ⁶⁰⁷
r-cran-fitdistrplus	r-cran-fitdistrplus	support fit of parametric distribution	r-cran-fitdistrplus ²¹
r-cran-flashclust	r-cran-flashclust	Implementation of optimal hierarchical clustering	r-cran-flashclust ⁴⁷¹
r-cran-genabel	r-cran-genabel	GNU R package for genome-wide SNP association analysis	r-cran-genabel ³³
r-cran-ggplot2	r-cran-ggplot2	implementation of the Grammar of Graphics	r-cran-ggplot2 ⁹²³
r-cran-gprofiler	r-cran-gprofiler	Interface to the 'g:Profiler' Toolkit	r-cran-gprofiler ⁷⁰⁶
r-cran-isospec	isospec	Isotopic fine structure calculator for GNU R	isospec ⁵⁶³
r-cran-kaos	r-cran-kaos	Encoding of Sequences Based on Frequency Matrix Chaos	r-cran-kaos ⁵³⁵

r-cran-knitr	r-cran-knitr	GNU R package for dynamic report generation using Literate Programming	r-cran-knitr ⁹⁵⁰
r-cran-lexrankr	r-cran-lexrankr	extractive summarization of text with the LexRank algorithm	r-cran-lexrankr ²³²
r-cran-maldiquant	r-cran-maldiquant	GNU R package for quantitative analysis of mass spectrometry data	r-cran-maldiquant ²⁸
r-cran-maxlik	r-cran-maxlik	GNU R maximum likelihood estimation	r-cran-maxlik ³⁴⁴
r-cran-metamix	r-cran-metamix	GNU R bayesian mixture analysis for metagenomic community profiling	r-cran-metamix ⁵⁸⁸
r-cran-mixtools	r-cran-mixtools	GNU R tools for analyzing finite mixture models	r-cran-mixtools ⁵⁹
r-cran-msm	r-cran-msm	GNU R Multi-state Markov and hidden Markov models in continuous time	r-cran-msm ³⁸⁶
r-cran-nmf	r-cran-nmf	GNU R framework to perform non-negative matrix factorization	r-cran-nmf ²⁷⁶
r-cran-pcapp	r-cran-pcapp	Robust PCA by Projection Pursuit	r-cran-pcapp ⁸⁶⁷
r-cran-phangorn	r-cran-phangorn	GNU R package for phylogenetic analysis	r-cran-phangorn ⁷⁶⁴
r-cran-phytools	r-cran-phytools	GNU R phylogenetic tools for comparative biology	r-cran-phytools ⁷¹⁹
r-cran-plotrix	r-cran-plotrix	GNU R package providing various plotting functions	r-cran-plotrix ⁴⁹⁴
r-cran-propclust	r-cran-propclust	Propensity Clustering and Decomposition	r-cran-propclust ⁷⁰⁷
r-cran-propclust	r-cran-propclust	Propensity Clustering and Decomposition	r-cran-propclustb ⁷⁰⁸
r-cran-propclust	r-cran-propclust	Propensity Clustering and Decomposition	r-cran-propclustc ⁷⁰⁹
r-cran-pscbs	r-cran-pscbs	R package: Analysis of Parent-Specific DNA Copy Numbers	r-cran-pscbs ⁶⁴⁰
r-cran-pvclust	r-cran-pvclust	Hierarchical Clustering with P-Values via Multi-scale Bootstrap	r-cran-pvclust ⁸⁴²
r-cran-qqman	r-cran-qqman	R package for visualizing GWAS results using Q-Q and manhattan plots	r-cran-qqman ⁸⁸⁵
r-cran-qt1	r-cran-qt1	GNU R package for genetic marker linkage analysis	r-cran-qt1 ¹⁰⁶
r-cran-ranger	r-cran-ranger	Fast Implementation of Random Forests	r-cran-ranger ⁹⁴⁶
r-cran-relsurv	r-cran-relsurv	GNU R relative survival	r-cran-relsurv ⁶⁷¹
r-cran-reshape	r-cran-reshape	Flexibly reshape data	r-cran-reshape ⁹²²
r-cran-rniftilib	r-cran-rniftilib	GNU/R interface to NIFTICLIB	r-cran-rniftilib ³³⁵
r-cran-rocr	r-cran-rocr	GNU R package to prepare and display ROC curves	r-cran-rocr ⁷⁹⁴
r-cran-r.oo	r-cran-r.oo	GNU R object-oriented programming with or without references	r-cran-r-oo ⁶⁰
r-cran-rsvd	r-cran-rsvd	Randomized Singular Value Decomposition	r-cran-rsvd ²³¹
r-cran-scatterplot3d	r-cran-scatterplot3d	GNU R package for Visualizing Multivariate Data	r-cran-scatterplot3d
r-cran-segmented	r-cran-segmented	GNU R segmented relationships in regression models	r-cran-segmented ⁵⁹⁹
r-cran-seqinr	r-cran-seqinr	GNU R biological sequences retrieval and analysis	r-cran-seqinr ¹³⁵
r-cran-seroincidence	r-cran-seroincidence	GNU R seroincidence calculator tool	r-cran-seroincidence
r-cran-seroincidence	r-cran-seroincidence	GNU R seroincidence calculator tool	r-cran-seroincidence
r-cran-seurat	r-cran-seurat	Tools for Single Cell Genomics	r-cran-seurat ⁷⁵⁷
r-cran-seurat	r-cran-seurat	Tools for Single Cell Genomics	r-cran-seurat2015 ⁵³¹
r-cran-shazam	r-cran-shazam	Immunoglobulin Somatic Hypermutation Analysis	r-cran-shazam ³²⁵
r-cran-shazam	r-cran-shazam	Immunoglobulin Somatic Hypermutation Analysis	r-cran-shazam2016 ¹
r-cran-spam	r-cran-spam	GNU R functions for sparse matrix algebra	r-cran-spam ²⁶⁸
r-cran-spatstat	r-cran-spatstat	GNU R Spatial Point Pattern analysis, model-fitting, simulation, tests	r-cran-spatstat ³⁸
r-cran-spp	r-cran-spp	GNU R ChIP-seq processing pipeline	r-cran-spp ⁴²⁸
r-cran-stringi	r-cran-stringi	GNU R character string processing facilities	r-cran-stringi ²⁷⁰
r-cran-surveillance	r-cran-surveillance	GNU R package for the Modeling and Monitoring of Epidemic Phenomena	r-cran-surveillance ³
r-cran-tcr	r-cran-tcr	Advanced Data Analysis of Immune Receptor Repertoires	r-cran-tcr ⁶¹⁰
r-cran-tfmpvalue	r-cran-tfmpvalue	GNU R P-Value Computation for Position Weight Matrices	r-cran-tfmpvalue ⁸⁷¹
r-cran-tidyverse	r-cran-tidyverse	Easily Install and Load the 'Tidyverse'	r-cran-tidyverse ⁹²⁴
r-cran-tigger	r-cran-tigger	Infers new Immunoglobulin alleles from Rep-Seq Data	r-cran-tigger ³²⁷
r-cran-vcd	r-cran-vcd	GNU R Visualizing Categorical Data	r-cran-vcd ⁵⁷⁷
r-cran-wgcna	r-cran-wgcna	Weighted Correlation Network Analysis	r-cran-wgcna ⁴⁷²
rdp-alignment	rdp-alignment	Ribosomal Database Project (RDP) alignment tools package	rdp-alignment ²⁵⁰

rdp-classifier	rdp-classifier	extensible sequence classifier for fungal lsu, bacterial and archaeal 16s	rdp-classifier ⁹⁰⁷
rdp-classifier-doc	rdp-classifier	documentation and examples for rdp-classifier	rdp-classifier ⁹⁰⁷
readseq	readseq	Conversion between sequence formats	readseq ²⁹⁰
reapr	reapr	universal tool for genome assembly evaluation	reapr ³⁷¹
reliion-bin	reliion	toolkit for 3D reconstructions in cryo-electron microscopy	reliion ⁷⁵⁹
reliion-bin+gui	reliion	parallel toolkit for 3D reconstructions in cryo-electron microscopy	reliion ⁷⁵⁹
reliion-bin+mpi	reliion	parallel toolkit for 3D reconstructions in cryo-electron microscopy	reliion ⁷⁵⁹
reliion-bin+mpi+gui	reliion	parallel toolkit for 3D reconstructions in cryo-electron microscopy	reliion ⁷⁵⁹
repeatmasker-recon	repeatmasker-recon	finds repeat families from biological sequences	repeatmasker-recon
resfinder	resfinder	identify acquired antimicrobial resistance genes	resfinder ⁹⁶¹
resfinder-db	resfinder-db	ResFinder database is a curated database of acquired resistance genes	resfinder-db ⁹⁶²
resfinder-example	resfinder	identify acquired antimicrobial resistance genes (example data)	resfinder ⁹⁶¹
rnahybrid	rnahybrid	Fast and effective prediction of microRNA/target duplexes	rnahybrid ⁷¹⁶
rna-star	rna-star	ultrafast universal RNA-seq aligner	rna-star ¹⁹⁸
roary	roary	high speed stand alone pan genome pipeline	roary ⁶⁴⁸
roguenarok	roguenarok	versatile and scalable algorithm for rogue taxon identification	roguenarok ⁴
r-other-curvefdp	r-other-curvefdp	estimation of confidence levels for peptide identifications	r-other-curvefdp ³
r-other-mott-happy	r-other-mott-happy	GNU R package for fine-mapping complex diseases	r-other-mott-happy
r-other-mott-happy.hbrem	r-other-mott-happy	GNU R package for fine-mapping complex diseases	r-other-mott-happy
r-other-mott-happy.hbrem-dbg	r-other-mott-happy	Debug information for Happy R package native library	r-other-mott-happy
r-other-nitpick	r-other-nitpick	peak identification for mass spectrometry data	r-other-nitpick ⁷¹⁸
rsem	rsem	RNA-Seq by Expectation-Maximization	rsem ⁴⁹⁸
rtax	rtax	Classification of sequence reads of 16S ribosomal RNA gene	rtax ⁸⁰¹
saint	saint	Significance Analysis of INteractome	saint ¹⁰⁵
saint	saint	Significance Analysis of INteractome	saint2010 ¹⁴⁴
salmon	salmon	wicked-fast transcript quantification from RNA-seq data	salmon ⁶⁶²
salmon	salmon	wicked-fast transcript quantification from RNA-seq data	salmon2019 ⁸¹⁰
sambamba	sambamba	tools for working with SAM/BAM data	sambamba ⁸⁴⁸
samblaster	samblaster	marks duplicates, extracts discordant/split reads	samblaster ²⁴¹
samtools	samtools	processing sequence alignments in SAM, BAM and CRAM formats	samtools ⁵⁰⁶
samtools-test	samtools	test files for the samtools package	samtools ⁵⁰⁶
saods9	saods9	Image display tool for astronomy	saods9 ⁴⁰⁸
saods9-bl	saods9	BLT subpackage for saods9	saods9 ⁴⁰⁸
saods9-data	saods9	Image display tool for astronomy (shared data)	saods9 ⁴⁰⁸
saods9-doc	saods9	Image display tool for astronomy (help files/documentation)	saods9 ⁴⁰⁸
saods9-tclpackages	saods9	Tcl/Tk packages provided with DS9	saods9 ⁴⁰⁸
sbmltoolbox	sbmltoolbox	libsml toolbox for octave and matlab	sbmltoolbox ⁴²³
scamp	scamp	Compute astrometric and photometric solutions	scamp ⁶⁵
scoary	scoary	pangenome-wide association studies	scoary ¹¹⁵
scrm	scrm	simulator of evolution of genetic sequences	scrm ⁸¹¹
seaview	seaview	Multiplatform interface for sequence alignment and phylogeny	seaview ³⁰⁹
seaview	seaview	Multiplatform interface for sequence alignment and phylogeny	seaview1996 ²⁷¹
seer	seer	genomic sequence element (kmer) enrichment analysis	seer ⁴⁹¹
segemehl	segemehl	short read mapping with gaps	segemehl ³⁵²
segemehl	segemehl	short read mapping with gaps	segemehl2012 ⁶⁴⁶
segemehl	segemehl	short read mapping with gaps	segemehl2014 ³⁵³
seqan3-doc	seqan3	C++ library for the analysis of biological sequences v3 (documentation)	seqan3 ²⁰⁶
seqan-apps	seqan2	C++ library for the analysis of biological sequences	seqan2 ²⁰⁵

seqan-dev	seqan	C++ library for the analysis of biological sequences (development)	seqan ²⁰⁴
seq-gen	seq-gen	simulate the evolution of nucleotide or amino acid sequences	seq-gen ⁷¹⁰
seqsero	seqsero	Salmonella serotyping from genome sequencing data	seqsero ⁹⁷⁰
sextractor	source-extractor	Dummy transitional package for name change	source-extractor ⁶⁷
sga	sga	de novo genome assembler that uses string graphs	sga ⁷⁹²
shapeit4	shapeit4	fast and accurate method for estimation of haplotypes (phasing)	shapeit4 ¹⁸⁵
shapeit4-example	shapeit4	fast and accurate method for estimation of haplotypes (phasing) - example	shapeit4 ¹⁸⁵
shark-doc	shark	documentation for Shark	shark ³⁷⁹
shelxle	shelxle	graphical user interface for SHELXL	shelxle ³⁷⁸
sibelia	sibelia	comparative genomics tool	sibelia ⁵⁸²
sibelia-examples	sibelia	comparative genomics tool (example data)	sibelia ⁵⁸²
sift	sift	predicts if a substitution in a protein has a phenotypic effect	sift ⁴⁶¹
sift	sift	predicts if a substitution in a protein has a phenotypic effect	sift2001 ⁶¹⁵
sift	sift	predicts if a substitution in a protein has a phenotypic effect	sift2002 ⁶¹⁶
sift	sift	predicts if a substitution in a protein has a phenotypic effect	sift2003 ⁶¹⁷
sift	sift	predicts if a substitution in a protein has a phenotypic effect	sift2006 ⁶¹⁸
sigma-align	sigma-align	Simple greedy multiple alignment of non-coding DNA sequences	sigma-align ⁷⁸⁷
sim4	sim4	tool for aligning cDNA and genomic DNA	sim4 ²⁵²
sim4db	kmer	batch spliced alignment of cDNA sequences to a target genome	kmer ⁹⁰⁵
sim4db	kmer	batch spliced alignment of cDNA sequences to a target genome	kmer2004 ³⁸²
simka	simka	comparative metagenomics method dedicated to NGS datasets	simka ⁶²
simkamin	simka	approximate comparative metagenomics method dedicated to NGS datasets	simka ⁶²
skesa	skesa	strategic Kmer extension for scrupulous assemblies	skesa ⁸⁰⁷
skewer	skewer	post-processing of high-throughput DNA sequence reads	skewer ³⁹²
skycat	skycat	Image visualization and access to catalogs and data for astronomy	skycat ¹⁰
skyview	skyview	Image generation from a range of remote databases	skyview ⁵⁷⁰
skyview-java	skyview	Image generation from a range of remote databases (Java package)	skyview ⁵⁷⁰
skyview-java-doc	skyview	Image generation from a range of remote databases (API doc)	skyview ⁵⁷⁰
smalr	smalr	interrogation of the methylation status of nucleotide sequencing reads	smalr ⁵⁴
snakemake	snakemake	pythonic workflow management system	snakemake ⁴⁶⁵
snap	snap	location of genes from DNA sequence with hidden markov model	snap ⁴⁴⁴
snap-aligner	snap-aligner	Scalable Nucleotide Alignment Program	snap-aligner ⁹⁵⁸
sniffles	sniffles	structural variation caller using third-generation sequencing	sniffles ⁷⁷⁸
snpomatic	snpomatic	fast, stringent short-read mapping software	snpomatic ⁵⁴³
snp-sites	snp-sites	Binary code for the package snp-sites	snp-sites ⁶⁴⁹
soapaligner	soapaligner	aligner of short reads of next generation sequencers	soapaligner ⁵⁰⁷
soapdenovo	soapdenovo	short-read assembly method to build de novo draft assembly	soapdenovo ⁵⁰⁸
soapdenovo2	soapdenovo2	short-read assembly method to build de novo draft assembly	soapdenovo2 ⁵³³
soapsnp	soapsnp	resequencing utility that can assemble consensus sequence of genomes	soapsnp ⁷⁰⁴
sortmerna	sortmerna	tool for filtering, mapping and OTU-picking NGS reads	sortmerna ⁴⁴²
source-extractor	source-extractor	Source extractor for astronomical images	source-extractor ⁶⁷

spaced	spaced	alignment-free sequence comparison using spaced words	spaced ⁵⁹¹
spades	spades	genome assembler for single-cell and isolates data sets	spades ⁴²
spades	spades	genome assembler for single-cell and isolates data sets	spades2013 ⁶²³
spades	spades	genome assembler for single-cell and isolates data sets	spades2014 ⁶⁹³
spades	spades	genome assembler for single-cell and isolates data sets	spades2015 ⁸⁹⁷
spades	spades	genome assembler for single-cell and isolates data sets	spades2016 ²²
spades	spades	genome assembler for single-cell and isolates data sets	spades2017 ⁶²⁴
spades	spades	genome assembler for single-cell and isolates data sets	spades2019 ¹¹⁸
spades	spades	genome assembler for single-cell and isolates data sets	spades2019h ⁵⁷³
splash	splash	Visualisation tool for Smoothed Particle Hydrodynamics simulation	splash ⁶⁹⁰
spread-phy	spread-phy	analyze and visualize phylogeographic reconstructions	spread-phy ⁷¹
sra-toolkit	sra-sdk	utilities for the NCBI Sequence Read Archive	sra-sdk ⁴⁹³
sra-toolkit-libs0	sra-sdk	Libraries for the SRA Toolkit	sra-sdk ⁴⁹³
sra-toolkit-libs-dev	sra-sdk	Development files for the NCBI SRA Toolkit's libraries	sra-sdk ⁴⁹³
srst2	srst2	Short Read Sequence Typing for Bacterial Pathogens	srst2 ³⁸⁰
ssake	ssake	genomics application for assembling millions of very short DNA sequences	ssake ⁹⁰⁹
ssake-examples	ssake	example data for SSAKE, a genomic assembler of short reads	ssake ⁹⁰⁹
sspace	sspace	scaffolding pre-assembled contigs after extension	sspace ⁷⁷
ssw-align	libssw	Smith-Waterman aligner based on libssw	libssw ⁹⁷³
stacks	stacks	pipeline for building loci from short-read DNA sequences	stacks ¹²⁸
stacks-web	stacks	web interface for displaying loci from short-read sequences	stacks ¹²⁸
staden	staden	DNA sequence assembly (Gap4/Gap5), editing and analysis tools	staden ⁹¹
staden-common	staden	Architecture independent files for Staden	staden ⁹¹
starlink-table-java	starjava-table	Starlink Tables Infrastructure Library	starjava-table ⁸⁵¹
starlink-table-java-doc	starjava-table	Starlink Tables Infrastructure Library (documentation)	starjava-table ⁸⁵¹
starlink-topcat-java	starjava-topcat	Tool for OPERations on Catalogues And Tables (Java library)	starjava-topcat ⁸⁵²
starlink-topcat-java-doc	starjava-topcat	Tool for OPERations on Catalogues And Tables (JavaDoc)	starjava-topcat ⁸⁵²
starlink-ttools-java	starjava-ttools	Starlink Tables Infrastructure Library Tool Set (Java library)	starjava-ttools ⁸⁵³
starlink-ttools-java-doc	starjava-ttools	Starlink Tables Infrastructure Library Tool Set (Javadoc)	starjava-ttools ⁸⁵³
stiff	stiff	convert scientific FITS images to the TIFF format	stiff ⁶⁶
stilts	starjava-ttools	Starlink Tables Infrastructure Library Tool Set	starjava-ttools ⁸⁵³
stilts-doc	starjava-ttools	Starlink Tables Infrastructure Library Tool Set (documentation)	starjava-ttools ⁸⁵³
stringtie	stringtie	assemble short RNaseq reads to transcripts	stringtie ⁶⁷³
stringtie	stringtie	assemble short RNaseq reads to transcripts	stringtie2016 ⁶⁷⁴
suitename	suitename	categorize each suite in an RNA backbone	suitename ⁷²¹
sumo	sumo	Simulation of Urban MObility (SUMO)	sumo ⁵⁸
sumo-doc	sumo	Simulation of Urban MObility (SUMO), documentation and examples	sumo ⁵⁸
sumo-tools	sumo	Simulation of Urban MObility (SUMO), tools and scripts	sumo ⁵⁸
sumtrees	python-dendropy	Phylogenetic Tree Summarization and Annotation	python-dendropy ⁸³⁹
surankco	surankco	Supervised Ranking of Contigs in de novo Assemblies	surankco ⁴⁶⁰
swarm	swarm-cluster	robust and fast clustering method for amplicon-based studies	swarm-cluster ⁵⁴⁰

swarm	swarm-cluster	robust and fast clustering method for amplicon-based studies	swarm-cluster2014 ⁵⁵
swarp	swarp	Resample and co-add together FITS images	swarp ⁶⁸
sweed	sweed	assessment of SNPs for their evolutionary advantage	sweed ⁶⁶³
synphot-data	pysynphot	Optional data files for pysynphot	pysynphot ⁵¹²
tabix	htslib	generic indexer for TAB-delimited genome position files	htslib ⁴⁹⁹
tandem-mass	tandem-mass	mass spectrometry software for protein identification	tandem-mass ⁹⁶
tandem-mass-dbg	tandem-mass	mass spectrometry software for protein identification - debug symbols	tandem-mass ⁹⁶
tanglet	tanglet	single player word finding game based on Boggle	tanglet ³⁰⁸
tanglet-data	tanglet	single player word finding game based on Boggle - data files	tanglet ³⁰⁸
tantan	tantan	low complexity and tandem repeat masker for biosequences	tantan ²⁶¹
tcl-funtools	funtools	Minimal buy-in FITS library (Tcl interface)	funtools ⁵⁴²
tcliis	saods9	Tcl IIS protocol package	saods9 ⁴⁰⁸
tcl-xpa	xpa	Seamless communication between Unix programs (Tcl interface)	xpa ⁵⁴¹
t-coffee	t-coffee	Multiple Sequence Alignment	t-coffee ⁶²²
t-coffee-doc	t-coffee	PDF and HTML accompanying documents to T-Coffee	t-coffee ⁶²²
t-coffee-examples	t-coffee	annotated examples for the use of T-Coffee	t-coffee ⁶²²
theano-doc	theano	CPU/GPU math expression compiler for Python (docs)	theano ⁸⁵⁴
theseus	theseus	superimpose macromolecules using maximum likelihood	theseus ⁸⁵⁷
theseus	theseus	superimpose macromolecules using maximum likelihood	theseus2006 ⁸⁵⁸
theseus	theseus	superimpose macromolecules using maximum likelihood	theseus2008 ⁸⁵⁹
theseus-examples	theseus	superimpose macromolecules using maximum likelihood (examples)	theseus ⁸⁵⁷
theseus-examples	theseus	superimpose macromolecules using maximum likelihood (examples)	theseus2006 ⁸⁵⁸
theseus-examples	theseus	superimpose macromolecules using maximum likelihood (examples)	theseus2008 ⁸⁵⁹
thesias	thesias	Testing Haplotype Effects In Association Studies	thesias ⁸⁸⁰
thesias	thesias	Testing Haplotype Effects In Association Studies	thesias2002 ⁸⁸²
thesias	thesias	Testing Haplotype Effects In Association Studies	thesias2004 ⁸⁸¹
tigr-glimmer	tigr-glimmer	Gene detection in archea and bacteria	tigr-glimmer ⁷⁵⁶
tigr-glimmer	tigr-glimmer	Gene detection in archea and bacteria	tigr-glimmer2007 ⁸⁶⁵
tigr-glimmer	tigr-glimmer	Gene detection in archea and bacteria	tigr-glimmer2012 ⁴²⁶
tkao	saods9	Tk widgets for astronomical imaging and data visualization	saods9 ⁴⁰⁸
tm-align	tm-align	structural alignment of proteins	tm-align ⁹⁷¹
tnseq-transit	tnseq-transit	statistical calculations of essentiality of genes or genomic regions	tnseq-transit ¹⁸³
toil	toil	cross-platform workflow engine	toil ⁹⁰⁰
topcat	starjava-topcat	Tool for OPERations on Catalogues And Tables	starjava-topcat ⁸⁵²
topcat-doc	starjava-topcat	Tool for OPERations on Catalogues And Tables (documentation)	starjava-topcat ⁸⁵²
tophat	tophat	fast splice junction mapper for RNA-Seq reads	tophat ⁸⁷²
tophat-recondition	tophat-recondition	post-processor for TopHat unmapped reads	tophat-recondition ¹
topp	openms	set of programs implementing The OpenMS Proteomic Pipeline	openms ⁸³⁷
toppred	toppred	transmembrane topology prediction	toppred ⁹⁰¹
trace2dbest	trace2dbest	bulk submission of chromatogram data to dbEST	trace2dbest ⁶⁵⁹
trace2dbest	trace2dbest	bulk submission of chromatogram data to dbEST	trace2dbest2009 ⁷⁶⁸
trace2dbest-doc	trace2dbest	Documentation and sample files for trace2dbest	trace2dbest ⁶⁵⁹
trace2dbest-doc	trace2dbest	Documentation and sample files for trace2dbest	trace2dbest2009 ⁷⁶⁸
tracetuner	tracetuner	interpretation of DNA Sanger sequencing data	tracetuner ²⁶⁹
transrate-tools	transrate-tools	helper for transrate	transrate-tools ⁷⁹⁹
transtermhp	transtermhp	find rho-independent transcription terminators in bacterial genomes	transtermhp ⁴³²
travis	travis	trajectory analyzer and visualizer	travis ¹⁰⁴
travis	travis	trajectory analyzer and visualizer	travis2013 ⁸⁶¹
tree-ppuzzle	tree-puzzle	Parallelized reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle ⁷⁶⁹

tree-ppuzzle	tree-puzzle	Parallelized reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle1996 ⁸³³
tree-ppuzzle	tree-puzzle	Parallelized reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle1997 ⁸³⁴
tree-ppuzzle	tree-puzzle	Parallelized reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle1997d ⁸³⁵
tree-ppuzzle	tree-puzzle	Parallelized reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle2002 ⁷⁷⁰
tree-ppuzzle	tree-puzzle	Parallelized reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle2003 ⁷⁷¹
tree-puzzle	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle ⁷⁶⁹
tree-puzzle	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle1996 ⁸³³
tree-puzzle	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle1997 ⁸³⁴
tree-puzzle	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood	tree-puzzle1997d ⁸³⁵
tree-puzzle-doc	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood (doc)	tree-puzzle ⁷⁶⁹
tree-puzzle-doc	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood (doc)	tree-puzzle1996 ⁸³³
tree-puzzle-doc	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood (doc)	tree-puzzle1997 ⁸³⁴
tree-puzzle-doc	tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood (doc)	tree-puzzle1997d ⁸³⁵
treeview	treeview	Java re-implementation of Michael Eisen's Tree-View	treeview ⁷⁵³
treeviewx	treeviewx	Displays and prints phylogenetic trees	treeviewx ⁶⁵⁰
trilinos-all-dev	trilinos	object-oriented framework for large-scale problems - development files (ALL)	trilinos ³⁴⁷
trilinos-dev	trilinos	object-oriented framework for large-scale problems - development files	trilinos ³⁴⁷
trilinos-doc	trilinos	object-oriented framework for large-scale problems - documentation	trilinos ³⁴⁷
trimmomatic	trimmomatic	flexible read trimming tool for Illumina NGS data	trimmomatic ⁸⁰
trinculo	trinculo	toolkit to carry out genetic association for multi-category phenotypes	trinculo ⁴⁰⁷
trinityrnaseq	trinityrnaseq	RNA-Seq De novo Assembly	trinityrnaseq ³¹⁰
trinityrnaseq-examples	trinityrnaseq	RNA-Seq De novo Assembly common example and testing files	trinityrnaseq ³¹⁰
trnascan-se	trnascan-se	detection of transfer RNA genes in genomic sequence	trnascan-se ⁵³²
trnascan-se-common	trnascan-se	detection of transfer RNA genes in genomic sequence (common files)	trnascan-se ⁵³²
uc-echo	uc-echo	error correction algorithm designed for short-reads from NGS	uc-echo ⁴¹⁸
ugene	ugene	integrated bioinformatics toolkit	ugene ⁶³⁷
ugene	ugene	integrated bioinformatics toolkit	ugene2014 ²⁹⁸
ugene	ugene	integrated bioinformatics toolkit	ugene2018 ⁷³³
ugene-data	ugene	required data for UGENE - integrated bioinformatics toolkit	ugene ⁶³⁷
ugene-data	ugene	required data for UGENE - integrated bioinformatics toolkit	ugene2014 ²⁹⁸
ugene-data	ugene	required data for UGENE - integrated bioinformatics toolkit	ugene2018 ⁷³³
umis	umis	tools for processing UMI RNA-tag data	umis ⁸⁴³
umis-examples	umis	tools for processing UMI RNA-tag data (examples)	umis ⁸⁴³
unicycler	unicycler	hybrid assembly pipeline for bacterial genomes	unicycler ⁹²⁰
unicycler	unicycler	hybrid assembly pipeline for bacterial genomes	unicycler2017 ⁹²¹
unicycler-data	unicycler	hybrid assembly pipeline for bacterial genomes (data package)	unicycler ⁹²⁰
unicycler-data	unicycler	hybrid assembly pipeline for bacterial genomes (data package)	unicycler2017 ⁹²¹
varna	varna	Visualization Applet for RNA	varna ¹⁷⁴
varscan	varscan	variant detection in next-generation sequencing data	varscan ⁴³⁶
vcftools	vcftools	Collection of tools to work with VCF files	vcftools ¹⁶⁹
vdjtools	vdjtools	framework for post-analysis of B/T cell repertoires	vdjtools ⁷⁸⁶

velvet	velvet	Nucleic acid sequence assembler for very short reads	velvet ⁹⁶⁷
velvet-example	velvet	Example data for the Velvet sequence assembler	velvet ⁹⁶⁷
velvet-long	velvet	Nucleic acid sequence assembler for very short reads, long version	velvet ⁹⁶⁷
velvet-tests	velvet	Test data for the Velvet sequence assembler	velvet ⁹⁶⁷
vg	vg	tools for working with genome variation graphs	vg ²⁷⁴
vg-docs	vg	tools for working with genome variation graphs – docs	vg ²⁷⁴
virulencefinder	virulencefinder	identify virulence genes in total or partial sequenced isolates of bacteria	virulencefinder ⁴⁰²
virulencefinder-examples	virulencefinder	example data for virulencefinder	virulencefinder ⁴⁰²
visp-images-data	visp-images	visual servoing library - dataset reference files	visp-images ⁵⁴⁸
visp-images-data	visp-images	visual servoing library - dataset reference files	visp-images2018 ⁸⁶³
vmtk	vmtk	the Vascular Modeling Toolkit	vmtk ⁶⁷⁹
vorop++	vorop++	library for the computation of the Voronoi diagram	vorop- ⁷⁵¹
vorop++-dev	vorop++	library for the computation of the Voronoi diagram (dev files)	vorop- ⁷⁵¹
vorop++-examples	vorop++	library for the computation of the Voronoi diagram (examples)	vorop- ⁷⁵¹
voronota	voronota	Voronoi diagram-based tool to find atom contacts	voronota ⁶³⁸
votca-csg	votca-csg	VOTCA's coarse-graining engine	votca-csg ⁷⁴⁶
votca-csg-scripts	votca-csg	VOTCA's coarse-graining scripts	votca-csg ⁷⁴⁶
votca-csg-tutorials	votca-csg	VOTCA's coarse-graining tutorials	votca-csg ⁷⁴⁶
votca-tools	votca-tools	VOTCA's tools library, helper binaries	votca-tools ⁷⁴⁷
vsearch	vsearch	tool for processing metagenomic sequences	vsearch ⁷²⁸
wannier90	wannier90	Maximally Localized Wannier Functions - executables	wannier90 ⁵⁹⁴
wannier90-data	wannier90	Maximally Localized Wannier Functions - documentation and examples	wannier90 ⁵⁹⁴
wcslib-dev	wcslib	Header files and static library for wcslib and pgsbox	wcslib ¹¹⁹
wcslib-doc	wcslib	API documentation for wcslib	wcslib ¹¹⁹
wcslib-tools	wcslib	Command line tools utilizing wcslib	wcslib ¹¹⁹
wcstools	wcstools	Handle the WCS of a FITS image	wcstools ⁵⁸¹
weightwatcher	weightwatcher	Combine maps and polygon data for astronomical image processing	weightwatcher ⁵⁵⁴
wham-align	wham-align	Wisconsin's High-Throughput Alignment Method	wham-align ⁵¹⁰
wigeon	microbiomeutil	reimplementation of the Pintail 16S DNA anomaly detection utility	microbiomeutil ³²⁸
wise	wise	comparison of biopolymers, like DNA and protein sequences	wise ⁷⁴
wise-data	wise	data files for the wise package	wise ⁷⁴
wise-doc	wise	documentation for the wise package	wise ⁷⁴
wordnet	wordnet	electronic lexical database of English language	wordnet ⁵⁷⁹
wordnet	wordnet	electronic lexical database of English language	wordnet1998 ²⁴⁴
wordnet	wordnet	electronic lexical database of English language	wordnet2005 ²⁴⁵
wordnet-base	wordnet	electronic lexical database of English language (base data)	wordnet ⁵⁷⁹
wordnet-base	wordnet	electronic lexical database of English language (base data)	wordnet1998 ²⁴⁴
wordnet-base	wordnet	electronic lexical database of English language (base data)	wordnet2005 ²⁴⁵
wordnet-dev	wordnet	electronic lexical database of English language (devel)	wordnet ⁵⁷⁹
wordnet-dev	wordnet	electronic lexical database of English language (devel)	wordnet1998 ²⁴⁴
wordnet-dev	wordnet	electronic lexical database of English language (devel)	wordnet2005 ²⁴⁵
wordnet-grind	wordnet	WordNet lexicographer files processor	wordnet ⁵⁷⁹
wordnet-grind	wordnet	WordNet lexicographer files processor	wordnet1998 ²⁴⁴
wordnet-grind	wordnet	WordNet lexicographer files processor	wordnet2005 ²⁴⁵
wordnet-gui	wordnet	electronic lexical database of English language (GUI)	wordnet ⁵⁷⁹
wordnet-gui	wordnet	electronic lexical database of English language (GUI)	wordnet1998 ²⁴⁴
wordnet-gui	wordnet	electronic lexical database of English language (GUI)	wordnet2005 ²⁴⁵
wordnet-sense-index	wordnet	electronic lexical database of English language (index)	wordnet ⁵⁷⁹

wordnet-sense-index	wordnet	electronic lexical database of English language (index)	wordnet1998 ²⁴⁴
wordnet-sense-index	wordnet	electronic lexical database of English language (index)	wordnet2005 ²⁴⁵
wsclean	wsclean	Fast generic widefield interferometric imager	wsclean ⁶³⁵
wsclean-dev	wsclean	Fast generic widefield interferometric imager (development files)	wsclean ⁶³⁵
wtdbg2	wtdbg2	de novo sequence assembler for long noisy reads	wtdbg2 ⁷⁴⁴
xcrysdn	xcrysdn	Crystalline and Molecular Structure Visualizer	xcrysdn ⁴³⁸
xcrysdn-data	xcrysdn	Crystalline and Molecular Structure Visualizer (Data Files)	xcrysdn ⁴³⁸
xmds2	xmds2	eXtensible Multi-Dimensional Simulator	xmds2 ¹⁸⁶
xmds2-doc	xmds2	documentation for the eXtensible Multi-Dimensional Simulator	xmds2 ¹⁸⁶
xpa-tools	xpa	Tools for seamless communication between Unix programs	xpa ⁵⁴¹
yade	yade	Platform for discrete element modeling	yade ⁹⁰³
yade-doc	yade	Platform for discrete element modeling. Documentation	yade ⁹⁰³
yaha	yaha	find split-read mappings on single-end queries	yaha ²⁴⁰
yorick-gyoto	gyoto	General relativistic geodesic integration for the Yorick language	gyoto ⁸⁹⁹
zalign	zalign	parallel local alignment of biological sequences	zalign ⁵³

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