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1	**Package Name**	**Software Description**	**Project URL**
2	Autoconf	An extensible package of M4 macros that produce shell scripts to automatically configure software source code packages	https://www.gnu.org/software/autoconf/
3	Automake		www.gnu.org/software/automake
4	Libtool		www.gnu.org/software/libtool
5	bamtools	BamTools: a C++ API for reading/writing BAM files.	https://github.com/pezmaster31/bamtools
6	Biopython (Python module)	Biopython is a set of freely available tools for biological computation written in Python by an international team of developers	www.biopython.org/
7	blas	The BLAS (Basic Linear Algebra Subprograms) are routines that provide standard building blocks for performing basic vector and matrix operations.	http://www.netlib.org/blas/
8	boost	Boost provides free peer-reviewed portable C++ source libraries.	http://www.boost.org
9	CMake	Cross-platform, open-source build system. CMake is a family of tools designed to build, test and package software	http://www.cmake.org/
10	Cython (Python module)	The Cython compiler for writing C extensions for the Python language	https://www.python.org/
11	Doxygen		http://www.doxygen.org/
12	ffmpeg	FFmpeg is the leading multimedia framework, able to decode, encode, transcode, mux, demux, stream, filter and play pretty much anything that humans and machines have created. It supports the most obscure ancient formats up to the cutting edge. No matter if they were designed by some standards committee, the community or a corporation.	https://www.ffmpeg.org
13	fftw	FFTW is a C subroutine library for computing the discrete Fourier transform (DFT) in one or more dimensions, of arbitrary input size, and of both real and complex data (as well as of even/odd data, i.e. the discrete cosine/sine transforms or DCT/DST).	http://www.fftw.org/download.html
14	git	Git is a distributed version control system designed to handle everything from small to very large projects with speed and efficiency.	http://git-scm.com/
15	gmp	GMP is a free library for arbitrary precision arithmetic, operating on signed integers, rational numbers, and floating-point numbers. There is no practical limit to the precision except the ones implied by the available memory in the machine GMP runs on. GMP has a rich set of functions, and the functions have a regular interface.	https://gmplib.org
16	GNU Compiler Collection (GCC)	The GNU Compiler Collection includes front ends for C, C++, Objective-C, Fortran, Java, Ada, and Go, as well as libraries for these languages (libstdc++, libgcj,...)	https://gcc.gnu.org/
17	GNU Emacs	GNU Emacs is an extensible, customizable text editor—and more. At its core is an interpreter for Emacs Lisp, a dialect of theLisp programming language with extensions to support text editing.	www.gnu.org/software/emacs/
18	gnuplot	Gnuplot is a portable command-line driven graphing utility for Linux, OS/2, MS Windows, OSX, VMS, and many other platforms. The source code is copyrighted but freely distributed (i.e., you don't have to pay for it).	http://www.gnuplot.info
19	Graphviz	Graph Visualization Software	http://www.graphviz.org/
20	hdf5	HDF5 (Hierarchical Data Format version 5) from HDFGroup	http://www.hdfgroup.org/HDF5/
21	imagemagick	ImageMagick® is a software suite to create, edit, compose, or convert bitmap images. It can read and write images in a variety of formats (over 100) including DPX, EXR, GIF, JPEG, JPEG-2000, PDF, PNG, Postscript, SVG, and TIFF. Use ImageMagick to resize, flip, mirror, rotate, distort, shear and transform images, adjust image colors, apply various special effects, or draw text, lines, polygons, ellipses and Bézier curves.	http://imagemagick.org
22	isl	ISL (Integer Set Library) is a library for manipulating sets and relations of integer points bounded by linear constraints.	http://isl.gforge.inria.fr
23	Java	Java is a general-purpose, concurrent, class-based, object-oriented language that is specifically designed to have as few implementation dependencies as possible.	http://java.com/
24	julia	Julia is a high-level, high-performance dynamic programming language for technical computing, with syntax that is familiar to users of other technical computing environments.	http://julialang.org
25	lapack	LAPACK is written in Fortran 90 and provides routines for solving systems of simultaneous linear equations, least-squares solutions of linear systems of equations, eigenvalue problems, and singular value problems.	http://www.netlib.org/lapack/
26	mecurial	Mercurial is a cross-platform, distributed revision control tool for software developers. It is mainly implemented using the Python programming language, but includes a binary diff implementation written in C.	http://en.wikipedia.org/wiki/Mercurial
27	mpc	Gnu Mpc is a C library for the arithmetic of complex numbers with arbitrarily high precision and correct rounding of the result. It extends the principles of the IEEE-754 standard for fixed precision real floating point numbers to complex numbers, providing well-defined semantics for every operation. At the same time, speed of operation at high precision is a major design goal.	http://www.multiprecision.org/index.php?prog=mpc
28	mpfr	The MPFR library is a C library for multiple-precision floating-point computations with correct rounding. MPFR has continuously been supported by the INRIA and the current main authors come from the Caramel and AriC project-teams at Loria (Nancy, France) and LIP (Lyon, France) respectively; see more on the credit page. MPFR is based on the GMP multiple-precision library.	http://www.mpfr.org
29	mpich	MPICH is a high-performance and widely portable implementation of the Message Passing Interface (MPI) standard (MPI-1, MPI-2 and MPI-3).	http://www.mpich.org
30	nose (Python module)	Module for unit testing in Python	https://github.com/nose-devs/nose/
31	octave	GNU Octave is a high-level interpreted language, primarily intended for numerical computations. It provides capabilities for the numerical solution of linear and nonlinear problems, and for performing other numerical experiments.	https://www.gnu.org/software/octave/
32	openmpi	The Open MPI Project is an open source Message Passing Interface implementation that is developed and maintained by a consortium of academic, research, and industry partners.	http://www.open-mpi.org
33	python (+ all the available modules)	Python is an object-oriented, interpreted, and interactive programming language. (version 2)	https://www.python.org/download/releases/2.7.8/
34	python3 (+ all the available modules)	Python is an object-oriented, interpreted, and interactive programming language. (version 3)	https://www.python.org/downloads/release/python-342/
35	root	ROOT, an OO framework for large-scale scientific data analysis and data mining	http://root.cern.ch/drupal/
36	ruby (+ all the available modules)	A dynamic, open source programming language with a focus on simplicity and productivity.	https://www.ruby-lang.org/en/
37	SuiteSparse	Suite of sparse matrix algorithms. Includes UMFPACK, CHOLMOD, SPQR, ordering methods (AMD, CAMD, COLAMD, and CCOLAMD) and more. Can do QR factorization on the GPU	http://faculty.cse.tamu.edu/davis/suitesparse.html
38	torque	Loads the Torque batch computing environment	http://www.adaptivecomputing.com/
39	valgrind	Valgrind is an instrumentation framework for building dynamic analysis tools.	http://valgrind.org
40	zlib	zlib is designed to be a free, general-purpose, legally unencumbered -- that is, not covered by any patents -- lossless data-compression library for use on virtually any computer hardware and operating system.	http://www.zlib.net
41	ddt	Allinea DDT is an advanced debugging tool used for scalar, multi-threaded, and large-scale parallel applications.	http://www.allinea.com/products/downloads/get-support
42	gsl	The GNU Scientific Library (GSL) is a numerical library for C and C++ programmers.	http://www.gnu.org/software/gsl/
43	h5utils	h5utils is a set of utilities for visualization and conversion of scientific data in the free, portable HDF5 format.	http://ab-initio.mit.edu/wiki/index.php/H5utils
44	hypre	Hypre is a massively parallelizable linear solver library written and designed for use in C++. It provides many nice features and objects beyond simple "matrix" or "vector" objects - these include grids, meshes, and stencils. It was developed at Lawrence Livermore National Lab.	http://charlesmartinreid.com/wiki/Hypre, http://acts.nersc.gov/hypre/
45	intel	Intel® Parallel Studio XE 2015 tool suite simplifies the design, development, debug, and tuning of code that utilizes parallel processing to boost application performance. Get more application performance with less effort on compatible Intel® processors and coprocessors.	https://software.intel.com/en-us/intel-compilers, https://software.intel.com/en-us/intel-parallel-studio-xe
46	metis	METIS is a set of serial programs for partitioning graphs, partitioning finite element meshes, and producing fill reducing orderings for sparse matrices. The algorithms implemented in METIS are based on the multilevel recursive-bisection, multilevel k-way, and multi-constraint partitioning schemes developed in our lab.	http://glaros.dtc.umn.edu/gkhome/views/metis
47	mkl	Intel Math Kernel Library	https://software.intel.com/en-us/intel-mkl
48	mpich2	MPICH2 is a high-performance and widely portable implementation of the Message Passing Interface (MPI) standard (MPI-1, MPI-2 and MPI-3).	http://www.mpich.org
49	nco	The netCDF Operator (NCO) toolkit manipulates and analyzes data stored in netCDF-accessible formats	http://nco.sourceforge.net
50	netcdf	NetCDF version 4.3.2 (with NetCDF Fortran Libraries)	http://www.unidata.ucar.edu/software/netcdf/
51	opencv	OpenCV (Open Source Computer Vision Library) is an open source computer vision and machine learning software library. OpenCV was built to provide a common infrastructure for computer vision applications and to accelerate the use of machine perception in the commercial products.	http://opencv.org
52	parmetis	ParMETIS is an MPI-based parallel library that implements a variety of algorithms for partitioning unstructured graphs, meshes, and for computing fill-reducing orderings of sparse matrices.	http://glaros.dtc.umn.edu/gkhome/metis/parmetis/overview
53	petsc	PETSc, pronounced PET-see (the S is silent), is a suite of data structures and routines for the scalable (parallel) solution of scientific applications modeled by partial differential equations.	http://www.mcs.anl.gov/petsc/

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54	pgi	Portland Group Compiler Accelerator Suite (c, c++ and fortran Server x86_64)	https://www.pdc.kth.se/software/compilers/pgi/general.html
55	scalapack	ScaLAPACK is a library of high-performance linear algebra routines for parallel distributed memory machines.	http://www.netlib.org/scalapack/
56	slepc	SLEPc is a software library for the solution of large scale sparse eigenvalue problems on parallel computers. It is an extension of PETSc and can be used for linear eigenvalue problems in either standard or generalized form, with real or complex arithmetic.	http://www.grycap.upv.es/slepc/
57	sundials	SUNDIALS was implemented with the goal of providing robust time integrators and nonlinear solvers that can easily be incorporated into existing simulation codes.	http://computation.llnl.gov/casc/sundials/main.html
58	totalview	TotalView is a GUI-based source code debugger and defect analysis tool that provides unprecedented control over processes and thread execution and visibility into program state and variables.	http://www.roguewave.com/products/totalview.aspx
59	udunits	The UDUNITS package supports units of physical quantities. Its C library provides for arithmetic manipulation of units and for conversion of numeric values between compatible units.	http://www.unidata.ucar.edu/software/udunits/
60	virtualenv	virtualenv is a tool to create isolated Python environments.	http://virtualenv.readthedocs.org/en/latest/virtualenv.html
61	vtk	The Visualization Toolkit (VTK) is an open-source, freely available software system for 3D computer graphics, image processing and visualization.	http://www.vtk.org/VTK/resources/software.html
62	xblas	XBLAS - Extra Precise Basic Linear Algebra Subroutines	http://www.netlib.org/xblas
63	armadillo	Fast C++ matrix library with easy to use functions and syntax, deliberately similar to Matlab. Uses template meta-programming techniques. Also provides efficient wrappers for LAPACK, BLAS and ATLAS libraries, including high-performance versions such as Intel MKL, AMD ACML and OpenBLAS.	http://arma.sourceforge.net
64	bdwgc	The Boehm-Demers-Weiser conservative C/C++ Garbage Collector (libgc, bdwgc, boehmgc)	http://www.hboehm.info/gc/
65	cblas	The reference BLAS is a freely-available software package. It is available from netlib via anonymous ftp and the World Wide Web. Thus, it can be included in commercial software packages (and has been). We only ask that proper credit be given to the authors.	http://www.netlib.org/blas/#_cblas, http://www.prism.gatech.edu/~ndantam3/cblas-doc/doc/html/main.html
66	cloog	CLooG is a free software and library to generate code for scanning Z-polyhedra. That is, it finds a code (e.g. in C, FORTRAN...) that reaches each integral point of one or more parameterized polyhedra.	http://www.cloog.org
67	CUDA Toolkit	The NVIDIA® CUDA® Toolkit provides a comprehensive development environment for C and C++ developers building GPU-accelerated applications. The CUDA Toolkit includes a compiler for NVIDIA GPUs, math libraries, and tools for debugging and optimizing the performance of your applications. You'll also find programming guides, user manuals, API reference, and other documentation to help you get started quickly accelerating your application with GPUs.	https://developer.nvidia.com/cuda-toolkit
68	deal.II	A C++ software library supporting the creation of finite element codes and an open community of users and developers.	http://www.dealii.org
69	Decorator (Python module)	The aim of the decorator module it to simplify the usage of decorators for the average programmer, and to popularize decorators by showing various non-trivial examples	https://pypi.python.org/pypi/decorator
70	dx	OpenDX (IBM Visualization Data Explorer) Data Explorer is a system of tools and user interfaces for visualizing data.	http://www.opendx.org/highlights.php?highlight=inaction/tutorials/
71	Eclipse	Eclipse is famous for our Java Integrated Development Environment (IDE), but our C/C++ IDE and PHP IDE are pretty cool too. You can easily combine language support and other features into any of our default packages, and the Eclipse Marketplace allows for virtually unlimited customization and extension.	http://www.eclipse.org/users/
72	flume	Flume is a distributed, reliable, and available service for efficiently collecting, aggregating, and moving large amounts of log data. It has a simple and flexible architecture based on streaming data flows. It is robust and fault tolerant with tunable reliability mechanisms and many failover and recovery mechanisms. It uses a simple extensible data model that allows for online analytic application.	https://flume.apache.org/
73	gdb	GDB, the GNU Project debugger, allows you to see what is going on `inside' another program while it executes -- or what another program was doing at the moment it crashed.	http://www.gnu.org/software/gdb/
74	gmt	GMT is a collection of public-domain Unix tools that allows you to manipulate x,y and x,y,z data sets (filtering, trend fitting, gridding, projecting, etc.) and produce PostScript illustrations ranging from simple x-y plots, via contour maps, to artificially illuminated surfaces and 3-D perspective views in black/white or full color. Linear, log10, and power scaling is supported in addition to 25 common map projections. The processing and display routines within GMT are completely general and will handle any (x,y) or (x,y,z) data as input.	http://fossies.org/linux/misc/GMT/gmt-4.5.12-src.tar.gz/gmt-4.5.12/src/GMT.1
75	grace	Grace is a WYSIWYG 2D plotting tool for the X Window System and M*tif. Grace runs on practically any version of Unix-like OS. As well, it has been successfully ported to VMS, OS/2, and Win9*/NT/2000/XP (some minor functionality may be missing, though).	http://plasma-gate.weizmann.ac.il/Grace/
76	gstreamer	GStreamer is a library for constructing graphs of media-handling components. The applications it supports range from simple Ogg/Vorbis playback, audio/video streaming to complex audio (mixing) and video (non-linear editing) processing.	http://gstreamer.freedesktop.org
77	guile	Guile is the GNU Ubiquitous Intelligent Language for Extensions, the official extension language for the GNU operating system. Guile is a library designed to help programmers create flexible applications. Using Guile in an application allows the application's functionality to be extended by users or other programmers with plug-ins, modules, or scripts.	https://www.gnu.org/software/guile/download.html
78	harminv	Harminv is a free program (and accompanying library) to solve the problem of harmonic inversion — given a discrete-time, finite-length signal that consists of a sum of finitely-many sinusoids (possibly exponentially decaying) in a given bandwidth, it determines the frequencies, decay constants, amplitudes, and phases of those sinusoids.	http://ab-initio.mit.edu/wiki/index.php/Harminv
79	hdf4	HDF4 (Hierarchical Data Format version 4) from HDFGroup	http://www.hdfgroup.org/products/hdf4/
80	InsightToolkit	ITK is an open-source software toolkit for performing registration and segmentation. Segmentation is the process of identifying and classifying data found in a digitally sampled representation.	http://www.itk.org/ITK/project/project.html
81	jags	JAGS is Just Another Gibbs Sampler. It is a program for analysis of Bayesian hierarchical models using Markov Chain Monte Carlo (MCMC) simulation	http://mcmc-jags.sourceforge.net
82	libctl	ibctl is a free Guile-based library implementing flexible control files for scientific simulations.	http://ab-initio.mit.edu/wiki/index.php/Libctl
83	libffi	A Portable Foreign Function Interface Library - The libffi library provides a portable, high level programming interface to various calling conventions. This allows a programmer to call any function specified by a call interface description at run-time.	https://sourceware.org/libffi/
84	libsbml	LibSBML is a free, open-source programming library to help you read, write, manipulate, translate, and validate SBML files and data streams.	http://sbml.org/Software/libSBML
85	libunistring	libunistring - This library provides functions for manipulating Unicode strings and for manipulating C strings according to the Unicode standard.	https://www.gnu.org/software/libunistring/
86	mpir	Multiple Precision Integers and Rationals (MPIR) is an open-source software multiprecision integer library forked from the GNU Multiple Precision Arithmetic Library (GMP) project. It consists of much code from past GMP releases, and much newer original contributed code	http://mpir.org
87	namsxz	The NASMX Project is a collection of macros, includes and examples, which are meant to help NASM programmers develop 32-bit and 64-bit BSD, Linux, Windows, and XBOX software in a fraction of the time it normally takes.	http://www.nasm.us
88	p4est	The p4est software library enables the dynamic management of a collection of adaptive octrees, conveniently called a forest of octrees. p4est is designed to work in parallel and scales to hundreds of thousands of processor cores.	http://www.p4est.org
89	papi	PAPI - (Performance Application Programming Interface) provides the tool designer and application engineer with a consistent interface and methodology for use of the performance counter hardware found in most major microprocessors.	http://icl.cs.utk.edu/papi/
90	pdt	Program Database Toolkit (PDT) is a framework for analyzing source code written in several programming languages and for making rich program knowledge accessible to developers of static and dynamic analysis tools.	http://www.cs.uoregon.edu/research/pdt/home.php
91	ppl	The Parma Polyhedra Library (PPL) provides numerical abstractions especially targeted at applications in the field of analysis and verification of complex systems.	http://bugseng.com/products/ppl
92	sac	SAC (Seismic Analysis Code) is a general purpose interactive program designed for the study of sequential signals, especially time series data.	https://seiscode.iris.washington.edu/projects/sac
93	scons	SCons is an Open Source software construction tool—that is, a next-generation build tool. Think of SCons as an improved, cross-platform substitute for the classic Make utility with integrated functionality similar to autoconf/automake and compiler caches such as ccache. In short, SCons is an easier, more reliable and faster way to build software.	http://www.scons.org
94	spparks	SPPARKS is a parallel Monte Carlo code for on-lattice and off-lattice models that includes algorithms for kinetic Monte Carlo (KMC), rejection kinetic Monte Carlo (rKMC), and Metropolis Monte Carlo (MMC).	http://spparks.sandia.gov
95	swig	SWIG is a software development tool that connects programs written in C and C++ with a variety of high-level programming languages. SWIG is used with different types of target languages including common scripting languages such as Javascript, Perl, PHP, Python, Tcl and Ruby.	http://www.swig.org
96	tau	TAU Performance System® is a portable profiling and tracing toolkit for performance analysis of parallel programs written in Fortran, C, C++, UPC, Java, Python.	http://www.cs.uoregon.edu/research/tau/home.php
97	tmux	Tmux terminal multiplexer- lets you switch easily between several programs in one terminal, detach them (they keep running in the background) and reattach them to a different terminal.	http://tmux.sourceforge.net

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98	trinity	Trinity is an integrated development/debugging environment (IDE) for Derric, a domain-specific language to declaratively describe binary file formats.	https://github.com/jvdb/trinity
99	visit	VisIt is an Open Source, interactive, scalable, visualization, animation and analysis tool.	https://wci.llnl.gov/simulation/computer-codes/visit
100	matplotlib (Python module)	matplotlib is a python 2D plotting library which produces publication quality figures in a variety of hardcopy formats and interactive environments across platforms	http://matplotlib.org/
101	NumPy (Python module)	Python library that provides a multidimensional array object, various derived objects (such as masked arrays and matrices), and an assortment of routines for fast operations on arrays, including mathematical, logical, shape manipulation, sorting, selecting, I/O, discrete Fourier transforms, basic linear algebra, basic statistical operations, random simulation	http://www.numpy.org/
102	SciPy (Python module)	SciPy contains additional routines needed in scientific work: for example, routines for computing integrals numerically, solving differential equations, optimization, and sparse matrices	www.scipy.org/
103	cdo	Climate Data Operators (CDO) - Command line Operators for Climate and NWP model Data.	https://code.zmaw.de/projects/cdo
104	gdal	GDAL - Geospatial Data Abstraction Library - a translator library for raster and vector geospatial data formats	http://www.gdal.org
105	geos	GEOS (Geometry Engine - Open Source) is a C++ port of the Java Topology Suite (JTS). As such, it aims to contain the complete functionality of JTS in C++. This includes all the OpenGIS Simple Features for SQL spatial predicate functions and spatial operators, as well as specific JTS enhanced topology functions.	http://trac.osgeo.org/geos/
106	grads	The Grid Analysis and Display System (GrADS) is an interactive desktop tool that is used for easy access, manipulation, and visualization of earth science data.	http://iges.org/grads/
107	idl	IDL is the trusted scientific programming language used across disciplines to extract meaningful visualizations out of complex numerical data.	http://exelisvis.com/Home.aspx
108	ncl	NCL - NCAR Command Language - Meteorological Graphics Plotting System	http://www.ncl.ucar.edu
109	ncview	Ncview is a visual browser for netCDF format files.	http://meteora.ucsd.edu/~pierce/ncview_home_page.html
110	panoply	Panoply is a cross-platform application that plots geo-gridded and other arrays from netCDF, HDF, GRIB, and other datasets.	http://www.giss.nasa.gov/tools/panoply/
111	proj	PROJ.4 - Cartographic Projections Library	http://trac.osgeo.org/proj/
112	delft3d	Delft3D is a world leading 3D modeling suite to investigate hydrodynamics, sediment transport and morphology and water quality for fluvial, estuarine and coastal environments. As per 1 January 2011, the Delft3D flow (FLOW), morphology (MOR) and waves (WAVE) modules are available in open source.	http://oss.deltares.nl/web/delft3d
113	sprnt	a river dynamics simulator	https://github.com/frank-y-liu/SPRNT
114	amber	Amber refers to two things: a set of molecular mechanical force fields for the simulation of biomolecules (which are in the public domain, and are used in a variety of simulation programs); and a package of molecular simulation programs which includes source code and demos.	http://ambermd.org
115	bedtools	bedtools utilities are a swiss-army knife of tools for a wide-range of Life Sciences analysis tasks. The most widely-used tools enable genome arithmetic: that is, set theory on the genome.	http://bedtools.readthedocs.org/en/latest/
116	blast	The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or proteinsequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.	http://blast.ncbi.nlm.nih.gov/Blast.cgi
117	bowtie	Bowtie is an ultrafast, memory-efficient short read aligner. It aligns short DNA sequences (reads) to the human genome at a rate of over 25 million 35-bp reads per hour.	http://bowtie-bio.sourceforge.net/manual.shtml
118	bwa	BWA is a program for aligning sequencing reads against a large reference genome (e.g. human genome). It has two major components, one for read shorter than 150bp and the other for longer reads.	http://bio-bwa.sourceforge.net
119	cufflinks	Cufflinks assembles transcripts, estimates their abundances, and tests for differential expression and regulation in RNA-Seq samples. It accepts aligned RNA-Seq reads and assembles the alignments into a parsimonious set of transcripts. Cufflinks then estimates the relative abundances of these transcripts based on how many reads support each one, taking into account biases in library preparation protocols.	http://cufflinks.cbcb.umd.edu
120	express	eXpress is a streaming tool for quantifying the abundances of a set of target sequences from sampled subsequences.	http://bio.math.berkeley.edu/eXpress/
121	fasta	The FASTA programs can be used to search protein and DNA sequence databases, and to confirm the statistical significance of a match by comparing the alignment score to a distribution of scores produced by shuffled sequences.	http://faculty.virginia.edu/wrpearson/fasta/
122	fastqc	A quality control tool for high throughput sequence data	http://www.bioinformatics.babraham.ac.uk/projects/fastqc/
123	freebayes	FreeBayes is a Bayesian genetic variant detector designed to find small polymorphisms, specifically SNPs (single-nucleotide polymorphisms), indels (insertions and deletions), MNPs (multi-nucleotide polymorphisms), and complex events (composite insertion and substitution events) smaller than the length of a short-read sequencing alignment.	http://bioinformatics.bc.edu/marthlab/wiki/index.php/FreeBayes
124	lammps	LAMMPS is a classical molecular dynamics code, and an acronym for Large-scale Atomic/Molecular Massively Parallel Simulator.	http://lammps.sandia.gov
125	namd	NAMD, recipient of a 2002 Gordon Bell Award and a 2012 Sidney Fernbach Award, is a parallel molecular dynamics code designed for high-performance simulation of large biomolecular systems. Based on Charm++ parallel objects, NAMD scales to hundreds of cores for typical simulations and beyond 200,000 cores for the largest simulations.	http://www.ks.uiuc.edu/Research/namd/
126	raxml	RAxML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies	http://sco.h-its.org/exelixis/web/software/raxml/index.html
127	samtools	SAM (Sequence Alignment/Map) format is a generic format for storing large nucleotide sequence alignments.	http://samtools.sourceforge.net
128	schrodinger		http://tech.knime.org/forum/schroedinger-extensions/announcing-schroedinger-software-release-2014-2-0
129	sratoolkit	The Sequence Read Archive (SRA) stores raw sequence data from "next-generation" sequencing technologies including 454, IonTorrent, Illumina, SOLiD, Helicos and Complete Life Sciences.	http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?view=software
130	tophat	TopHat is a fast splice junction mapper for RNA-Seq reads.	http://ccb.jhu.edu/software/tophat/index.shtml
131	vmd	VMD is a molecular visualization program for displaying, animating, and analyzing large biomolecular systems using 3-D graphics and built-in scripting.	http://www.ks.uiuc.edu/Research/vmd/
132	voro++	Voro++ is a software library for carrying out three-dimensional computations of the Voronoi tessellation.	http://math.lbl.gov/voro++/
133	absorb	This software package implements ABSORB: Atlas Building by Self-Organized Registration and Bundling	http://www.nitrc.org/projects/absorb/
134	abyss	ABySS is a de novo, parallel, paired-end sequence assembler that is designed for short reads. The single-processor version is useful for assembling genomes up to 100 Mbases in size. The parallel version is implemented using MPI and is capable of assembling larger genomes.	http://www.bcgsc.ca/platform/bioinfo/software/abyss
135	afni	AFNI (which might be an acronym for Analysis of Functional NeuroImages) is a set of C programs for processing, analyzing, and displaying functional MRI (FMRI) data - a technique for mapping human brain activity.	http://afni.nimh.nih.gov/afni/
136	amos	AMOS is a collection of tools for genome assembly	http://amos.sourceforge.net
137	atsas	A program suite for small-angle scattering data analysis from biological macromolecules	http://www.embl-hamburg.de/biosaxs/software.html
138	auto3dem	AUTO3DEM is an automated image reconstruction system that coordinates the execution of the parallel, numerically-intensive codes P3DR, PCUT, POR, PPFT, and PSF.	http://cryoem.ucsd.edu/programs.shtm
139	bcl2fastq	The Bcl2FastQ conversion software is a tool to handle bcl conversion and demultiplexing. Version 1.8.4 has added ability to mask multiple adapter sequences per read, has standard Illumina adapter sequences included in the bcl2fastq installation, and the stringency of the adapter masking feature is now configurable.	http://support.illumina.com/downloads/bcl2fastq_conversion_software_184.html
140	bedops	BEDOPS is an open-source command-line toolkit that performs highly efficient and scalable Boolean and other set operations, statistical calculations, archiving, conversion and other management of genomic data of arbitrary scale. Tasks can be easily split by chromosome for distributing whole-genome analyses across a computational cluster.	http://bedops.readthedocs.org/en/latest/
141	bioawk	Bioawk is an extension to Brian Kernighan's awk, adding the support of several common biological data formats, including optionally gzip'ed BED, GFF, SAM, VCF, FASTA/Q and TAB-delimited formats with column names.	https://www.biostars.org/p/47751/
142	blat	BLAT on DNA is designed to quickly find sequences of 95% and greater similarity of length 25 bases or more. It may miss more divergent or shorter sequence alignments. It will find perfect sequence matches of 20 bases.	http://genome.ucsc.edu/cgi-bin/hgBlat
143	bsoft	Bsoft is a collection of programs and a platform for development of software for image and molecular processing in structural biology. Problems in structural biology are approached with a highly modular design, allowing fast development of new algorithms without the burden of issues such as file I/O. It provides an easily accessible interface, a resource that can be and has been used in other packages.	http://lsbr.niams.nih.gov/bsoft/bsoft.html
144	cd-hit	CD-HIT is a very widely used program for clustering and comparing protein or nucleotide sequences.	http://weizhong-lab.ucsd.edu/cd-hit/
145	cnvnator	a tool for CNV discovery and genotyping from depth of read mapping.	http://sv.gersteinlab.org

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146	cutadapt	cutadapt is used to remove adapter sequences from high-throughput sequencing data. This is usually necessary when the read length of the sequencing machine is longer than the molecule that is sequenced, for example when sequencing microRNAs.	https://sites.google.com/a/brown.edu/bioinformatics-in-biomed/cutadapt
147	dwgsim	Whole Genome Simulator for Next-Generation Sequencing	https://github.com/nh13/DWGSIM
148	eigensoft	The EIGENSOFT package combines functionality from our population genetics methods (Patterson et al. 2006) and our EIGENSTRAT stratification correction method (Price et al. 2006)	http://genetics.med.harvard.edu/reich/Reich_Lab/Software.html
149	estscan	ESTScan is a program that can detect coding regions in DNA sequences, even if they are of low quality. ESTScan will also detect and correct sequencing errors that lead to frameshifts.	http://estscan.sourceforge.net
150	fastx	The FASTX-Toolkit is a collection of command line tools for Short-Reads FASTA/FASTQ files preprocessing.	http://hannonlab.cshl.edu/fastx_toolkit/index.html
151	freesurfer	An open source software suite for processing and analyzing (human) brain MRI images.	http://freesurfer.net
152	fsl	FSL is a comprehensive library of image analysis and statistical tools for fMRI, MRI and DTI brain imaging data.	http://neuro.debian.net/pkgs/fsl-5.0-complete.html
153	gmap-gsnap	GMAP: A Genomic Mapping and Alignment Program for mRNA and EST Sequences, and GSNAP: Genomic Short-read Nucleotide Alignment Program	http://research-pub.gene.com/gmap/
154	gt	GenomeTools genome analysis system is a set of bioinformatics tools (in the realm of genome informatics) combined into a single binary. more details at GenomeTools.	https://wiki.gacrc.uga.edu/wiki/GenomeTools
155	gview	GView is a Java package used to display and navigate bacterial genomes. GView is useful for producing high-quality genome maps for use in publications and websites, or as a visualization tool in a sequence annotation pipeline.	https://www.gview.ca/wiki/GView/WebHome
156	hmmer	HMMER is used for searching sequence databases for homologs of protein sequences, and for making protein sequence alignments. It implements methods using probabilistic models called profile hidden Markov models (profile HMMs).	http://hmmer.janelia.org/software
157	igv	The Integrative Life Sciences Viewer (IGV) is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.	http://www.broadinstitute.org/igv/
158	igvtools	The Integrative Life Sciences Viewer (IGV) is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.	http://www.broadinstitute.org/igv/
159	ldhat	LDhat is a package written in the C and C++ languages for the analysis of recombination rates from population genetic data.	http://ldhat.sourceforge.net
160	ldhelmet	LDhelmet is a software program for statistical inference of fine-scale crossover recombination rates from population genetic data.	http://sourceforge.net/projects/ldhelmet/
161	meme	MEME is a tool for discovering motifs in a group of related DNA or protein sequences.	http://ebi.edu.au/ftp/software/MEME/
162	migrate	Migration and gene flow estimator	http://popgen.sc.fsu.edu/Migrate/Migrate-n.html
163	mothur	This project seeks to develop a single piece of open-source, expandable software to fill the bioinformatics needs of the microbial ecology community.	http://www.mothur.org
164	mugsy	Mugsy is a multiple whole genome aligner. Mugsy uses Nucmer for pairwise alignment, a custom graph based segmentation procedure for identifying collinear regions, and the segment-based progressive multiple alignment strategy from Seqan::TCoffee. Mugsy accepts draft genomes in the form of multi-FASTA files and does not require a reference genome.	http://mugsy.sourceforge.net
165	mummer	MUMmer is a system for rapidly aligning entire genomes, whether in complete or draft form. For example, MUMmer 3.0 can find all 20-basepair or longer exact matches between a pair of 5-megabase genomes in 13.7 seconds, using 78 MB of memory, on a 2.4 GHz Linux desktop computer.	http://mummer.sourceforge.net
166	pandaseq	PAired-eND Assembler for DNA sequences	https://github.com/neufeld/pandaseq
167	pasa	PASA, acronym for Program to Assemble Spliced Alignments, is a eukaryotic genome annotation tool that exploits spliced alignments of expressed transcript sequences to automatically model gene structures, and to maintain gene structure annotation consistent with the most recently available experimental sequence data.	http://pasa.sourceforge.net
168	repeatmasker	RepeatMasker is a program that screens DNA sequences for interspersed repeats and low complexity DNA sequences. The output of the program is a detailed annotation of the repeats that are present in the query sequence as well as a modified version of the query sequence in which all the annotated repeats have been masked (default: replaced by Ns).	http://www.repeatmasker.org
169	rtax	Taxonomic classifications of single- and paired-end sequences with RTAX	http://qiime.org/tutorials/rtax.html
170	sailfish	Rapid Alignment-free Quantification of Isoform Abundance	http://www.cs.cmu.edu/~ckingsf/software/sailfish/README.html
171	seqtk	Seqtk is a fast and lightweight tool for processing sequences in the FASTA or FASTQ format. It seamlessly parses both FASTA and FASTQ files which can also be optionally compressed by gzip.	https://wiki.gacrc.uga.edu/wiki/Seqtk
172	shrimp	SHRiMP is a software package for aligning genomic reads against a target genome. It was primarily developed with the multitudinous short reads of next generation sequencing machines in mind, as well as Applied Biosystem's colourspace genomic representation.	http://compbio.cs.toronto.edu/shrimp/
173	smalt	SMALT efficiently aligns DNA sequencing reads with a reference genome.	https://www.sanger.ac.uk/resources/software/smalt/
174	smrtanalysis	PacBio's open source software suite for single molecule, real-time sequencing	http://www.pacb.com/devnet/
175	ssake	SSAKE is a de novo assembler for short DNA sequence reads. It is designed to help leverage the information from short sequences reads by assembling them into contigs and scaffolds that can be used to characterize novel sequencing targets.	http://www.bcgsc.ca/platform/bioinfo/software/ssake
176	stacks	Stacks is a software pipeline for building loci from short-read sequences, such as those generated on the Illumina platform. Stacks was developed to work with restriction enzyme-based data, such as RAD-seq, for the purpose of building genetic maps and conducting population Life Sciences and phylogeography.	http://creskolab.uoregon.edu/stacks/
177	structure	The program structure is a free software package for using multi-locus genotype data to investigate population structure.	http://pritchardlab.stanford.edu/structure.html
178	tabix	SAM (Sequence Alignment/Map) is a flexible generic format for storing nucleotide sequence alignment. SAM tools provide efficient utilities on manipulating alignments in the SAM format.	http://samtools.sourceforge.net
179	trimmomatic	Trimmomatic: A flexible read trimming tool for Illumina NGS data	http://www.usadellab.org/cms/index.php?page=trimmomatic
180	velvet	Velvet is a de novo genomic assembler specially designed for short read sequencing technologies	https://www.ebi.ac.uk/~zerbino/velvet/
181	xmipp	Xmipp is a specialized suite of image processing programs, primarily aimed at obtaining the 3D reconstruction of biological specimens from large sets of projection images acquired by transmission electron microscopy	http://xmipp.cnb.csic.es/twiki/bin/view/Xmipp/WebHome
182	abaqus	Abaqus FEA (formerly ABAQUS) is a software suite for finite element analysis and computer-aided Physical Sciences, originally released in 1978.	http://www.simulia.com
183	ansys	ANSYS technology adds real-world value to the Physical Sciences design process. Robust simulation capabilities coupled with a flexible, adaptive architecture deliver efficiency and drive innovation.	http://www.ansys.com
184	campari	Molecular Modeling Software	http://campari.sourceforge.net
185	comsol	Simulation Tool for Electrical, Mechanical, Fluid Flow, and Chemical applications	http://www.comsol.com
186	dl_poly	DL_POLY is a general purpose classical molecular dynamics (MD) simulation software developed at Daresbury Laboratory by I.T. Todorov and W. Smith.	http://www.stfc.ac.uk/SCD/research/app/ccg/software/DL_POLY/44516.aspx
187	dl_poly_classic	DL_POLY Classic is a general purpose molecular dynamics simulation package developed at Daresbury Laboratory	http://www.ccp5.ac.uk/DL_POLY_CLASSIC/
188	Extend-Project	Community contributed extensions to the OpenFOAM CFD toolbox, not approved or endorsed by ESI Group	http://www.extend-project.de/
189	gaussian	Gaussian 09 is the latest in the Gaussian series of programs. It provides state-of-the-art capabilities for electronic structure modeling.	http://www.gaussian.com
190	lsdyna	LS-DYNA is a general-purpose finite element program capable of simulating complex real world problems. It is used by the automobile, aerospace, construction, military, manufacturing, and bioPhysical Sciences industries.	http://www.lstc.com/products/ls-dyna
191	Materials Studio	Materials Studio ® is a software environment that brings the world's most advanced and validated materials simulation technology to desktop computing, solving key problems throughout the R&D process.	https://wiki.csiro.au/display/ASC/Accelrys+Materials+Studio
192	nwchem	ARMCI-MPI is a completely rewritten implementation of the ARMCI one-sided communication interface that uses MPI RMA for one-sided communication.	http://wiki.mpich.org/armci-http://www.nwchem-sw.org/index.php/Download
193	openfoam	OpenFOAM is a free, open source CFD software package developed by OpenCFD Ltd at ESI Group and distributed by the OpenFOAM Foundation	http://www.openfoam.org
194	pointwise	Pointwise is our leading mesh generation software product for CFD, encompassing nearly three decades of technology development. The product features a modern software framework and workflow and provides tools like 64-bit support, multi-threading, and Windows/Linux/Mac portability.	http://www.pointwise.com
195	qchem	Q-Chem is a comprehensive ab initio quantum Physical Sciences package for accurate predictions of molecular structures, reactivities, and vibrational, electronic and NMR spectra.	http://www.q-chem.com
196	qe	Quantum Expresso (QE) is an integrated suite of Open-Source computer codes for electronic-structure calculations and materials modeling at the nanoscale. It is based on density-functional theory, plane waves, and pseudopotentials.	http://www.quantum-espresso.org/download/
197	quantumwise	Simulation software for nanoscience professionals	http://quantumwise.com

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198	starccm+	StarCCM+ is entire Physical Sciences process for solving problems involving flow (of fluids or solids), heat transfer and stress.	http://www.cd-adapco.com/products/star-ccm®
199	tecplot	Tecplot software empowers engineers and scientists working with Physical Sciences (CFD) to discover, analyze, and understand information in complex data.	http://www.tecplot.com/
200	trilinos	The Trilinos Project is an effort to develop algorithms and enabling technologies within an object-oriented software framework for the solution of large-scale, complex multi-Physical Sciences Physical Sciences and scientific problems.	http://trilinos.org
201	vasp5	The Vienna Ab initio Simulation Package (VASP) is a computer program for atomic scale materials modelling, e.g. electronic structure calculations and quantum-mechanical molecular dynamics, from first principles.	http://www.vasp.at
202	xcrysden	Construction and visuazliation of atomistic structures and properties	http://www.xcrysden.org
203	abinit	ABINIT is a package whose main program allows one to find the total energy, charge density and electronic structure of systems made of electrons and nuclei (molecules and periodic solids) within Density Functional Theory (DFT), using pseudopotentials and a planewave or wavelet basis.	http://www.abinit.org
204	atat	ATAT is a generic name that refers to a collection of alloy theory tools	http://alum.mit.edu/www/avdw/atat
205	cantera	Cantera is a suite of object-oriented software tools for problems involving chemical kinetics, thermodynamics, and/or transport processes.	http://www.cantera.org/docs/sphinx/html/index.html
206	eman2		http://ncmi.bcm.edu/ncmi/software/counter_222/software_122
207	gromacs	GROMACS is a versatile package to perform molecular dynamics, i.e. simulate the Newtonian equations of motion for systems with hundreds to millions of particles.	http://www.gromacs.org
208	meep	Meep (or MEEP) is a free finite-difference time-domain (FDTD) simulation software package developed at MIT to model electromagnetic systems, along with our MPB eigenmode package. I	http://ab-initio.mit.edu/wiki/index.php/Meep
209	molden	Molden is a package for displaying Molecular Density from the Ab Initio packages GAMESS-UK , GAMESS-US and GAUSSIAN and the Semi-Empirical packages Mopac/Ampac, it also supports a number of other programs via the Molden Format.	http://www.cmbi.ru.nl/molden/
210	nastran	NASTRAN is a finite element analysis (FEA) program that was originally developed for NASA in the late 1960s under United States government funding for the Aerospace industry.[	http://www.mscsoftware.com/product/msc-nastran, http://en.wikipedia.org/wiki/Nastran
211	nmag	Nmag is a micromagnetic simulation package. It has been developed at the University of Southampton with substantial contributions from Hans Fangohr, Thomas Fischbacher, Matteo Franchin. It is released under the GNU GPL.	http://nmag.soton.ac.uk/nmag/0.2/index.html
212	openbabel	Open Babel is a chemical toolbox designed to speak the many languages of chemical data. It's an open, collaborative project allowing anyone to search, convert, analyze, or store data from molecular modeling, Physical Sciences, solid-state materials, bioPhysical Sciences, or related areas.	http://openbabel.org/wiki/Main_Page
213	patran	Patran is the world's most widely used pre/post-processing software for Finite Element Analysis (FEA), providing solid modeling, meshing, analysis setup and post-processing for multiple solvers including MSC Nastran, Marc, Abaqus, LS-DYNA, ANSYS, and Pam-Crash.	http://www.mscsoftware.com/product/patran
214	phenix	PHENIX is a software suite for the automated determination of molecular structures using X-ray crystallography and other methods.	http://www.phenix-online.org
215	phoebe	PHOEBE stands for Physical Sciences Of Eclipsing BinariEs. It is a tool for modeling eclipsing binary stars based on photometric, spectroscopic, interferometric and/or polarimetric data.	http://phoebe-project.org
216	relion	RELION (for REgularised LIkelihood OptimisatioN, pronounce rely-on) is a stand-alone computer program that employs an empirical Bayesian approach to refinement of (multiple) 3D reconstructions or 2D class averages in electron cryo-microscopy (cryo-EM).	http://www2.mrc-lmb.cam.ac.uk/relion/index.php/Main_Page
217	unitah	The Uintah software suite is a set of libraries and applications for simulating and analyzing complex chemical and physical reactions.	http://www.sci.utah.edu/software/uintah.html
218	WanT	WanT is a GPL open-source scientific software aimed at simulating quantum transport properties (conductance) of nanojunctions (atomistically described) by using a real space Wannier function description of the Hamiltonian of the system.	http://www.wannier-transport.org/wiki/index.php/Main_Page
219	yambo	Yambo is a FORTRAN/C code for Many-Body calculations in solid state and molecular Physical Sciences. Yambo can calculate in an Ab-Initio manner absorption, energy loss and quasiparticles properties.	http://www.yambo-code.org
220	R (+all the modules)	The R Project Statistical Computing Package	http://www.r-project.org
221	ampl	The AMPL system is a sophisticated modeling tool that supports the entire optimization modeling lifecycle: development, testing, deployment, and maintenance.	http://ampl.com
222	cplex	High-performance mathematical programming solver for linear programming, mixed integer programming, and quadratic programming	http://www-01.ibm.com/software/commerce/optimization/cplex-optimizer/
223	gams	The General Algebraic Modeling System (GAMS) is a high-level modeling system for mathematical programming and optimization. It consists of a language compiler and a stable of integrated high-performance solvers. GAMS is tailored for complex, large scale modeling applications, and allows you to build large maintainable models that can be adapted quickly to new situations.	http://www.gams.com
224	gauss		http://www.aptech.com
225	gurobi	Gurobi Optimizer 5.6 - State-of-the-Art Mathematical Programming Solver	http://www.gurobi.com
226	knitro	KNITRO is an ideal tool for solving problems, such as pricing or revenue management, parameter identification in financial and industrial models or design and operation of electricity and gas transportation networks.	http://www.artelys.com/en/optimization-tools/knitro
227	mathematica	Mathematica is a computational software program used in many scientific, Physical Sciences, mathematical and computing fields, based on symbolic mathematics.	http://www.wolfram.com/mathematica/
228	matlab	MATLAB® is a high-level language and interactive environment for numerical computation, visualization, and programming.	www.mathworks.com
229	paraview	ParaView is an open-source, multi-platform data analysis and visualization application. ParaView users can quickly build visualizations to analyze their data using qualitative and quantitative techniques.	http://www.paraview.org/
230	sas		http://www.sas.com/
231	stata	Stata statistical software is a complete, integrated statistical software package that provides everything you need for data analysis, data management, and graphics.	http://www.stata.com
232		The TOMLAB Optimization Environment is a powerful optimization platform and modeling language for solving applied optimization problems in MATLAB.	http://tomopt.com/tomlab/
233	avizo	Avizo is a 3D analysis software for scientific and industrial data.	http://www.fei.com/software/avizo3d/
234	gmtk	The Graphical Models Toolkit (GMTK) is an open source, publicly available toolkit for rapidly prototyping statistical models using dynamic graphical models (DGMs) and dynamic Bayesian networks (DBNs).	http://melodi.ee.washington.edu/gmtk/
235	macaulay2	Macaulay2 is a software system devoted to supporting research in algebraic geometry and commutative algebra, whose creation has been funded by the National Science Foundation since 1992.	http://www.math.uiuc.edu/Macaulay2/
236	maple	Maple combines the world's most powerful mathematical computation engine with an intuitive, clickable user interface.	http://www.maplesoft.com/products/maple/
237	openbugs	BUGS is a software package for performing Bayesian inference Using Gibbs Sampling.	http://www.openbugs.net/w/FrontPage
238	oprofile	OProfile is an open source project that includes a statistical profiler for Linux systems, capable of profiling all running code at low overhead.	http://oprofile.sourceforge.net/about/
239	rdp_classifer	The RDP Classifier is a naive Bayesian classifier that can rapidly and accurately provides taxonomic assignments from domain to genus, with confidence estimates for each assignment.	https://rdp.cme.msu.edu
240	sage	Sage is a free open-source mathematics software system licensed under the GPL. It builds on top of many existing open-source packages: NumPy, SciPy, matplotlib, Sympy, Maxima, GAP, FLINT, R and many more.	http://www.sagemath.org
241	slic3r	Slic3r is the tool you need to convert a digital 3D model into printing instructions for your 3D printer. It cuts the model into horizontal slices (layers), generates toolpaths to fill them and calculates the amount of material to be extruded.	http://slic3r.org
242	spss	IBM SPSS Statistics is an integrated family of products that addresses the entire analytical process, from planning to data collection to analysis, reporting and deployment.	http://www-01.ibm.com/software/analytics/spss/products/statistics/
243	INTERACTIVE - HAMMER		
244	hwloc	The Portable Hardware Locality (hwloc) software package provides a portable abstraction of the hierarchical topology, including NUMA memory nodes, shared caches, processor sockets, processor cores and processing units (logical processors or "threads"). It primarily aims at helping applications with gathering information about modern computing hardware so as to exploit it accordingly and efficiently.	http://www.open-mpi.org/projects/hwloc/
245	mumps	MUMPS: a MUltifrontal Massively Parallel sparse direct Solver	http://mumps.enseeiht.fr/
246	qt	is a cross-platform application and UI framework for developers using C++ or QML, a CSS & JavaScript like language	http://qt-project.org/
247	rstudio	RStudio IDE is a powerful and productive user interface for R	http://www.rstudio.com/
248	cloog-ppl	CLooG is a software which generates loops for scanning Z-polyhedra	https://packages.debian.org/sid/devel/cloog-ppl

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249	fluent	ANSYS Fluent software contains the broad physical modeling capabilities needed to model flow, turbulence, heat transfer, and reactions for industrial applications ranging from air flow over an aircraft wing to combustion in a furnace, from bubble columns to oil platforms, from blood flow to semiconductor manufacturing, and from clean room design to wastewater treatment plants	http://www.ansys.com/Products/Simulation+Technology/Fluid+Dynamics/Fluid+Dynamics+Products/ANSYS+Fluent
250	gridgen	Gridgen is Pointwise's legacy software, used by engineers and scientists worldwide since 1984 to reliably generate high quality grids for CFD.	http://www.pointwise.com/gridgen/
251	hfss	ANSYS HFSS software is the industry standard for simulating 3-D full-wave electromagnetic fields.	http://www.ansys.com/Products/Simulation+Technology/Electronics/Signal+Integrity/ANSYS+HFSS
252	maxwell	The ANSYS Maxwell course will teach the students how to design and analyze 2D and 3D electromagnetic and electromechanical devices such as motors, actuators, transformers, sensors and coils.	http://www.ansys.com/Support/Training+Center/Courses/Introduction+to+ANSYS+Maxwell+2D-3D
253	siwave	ANSYS SIwave is a specialized design platform for power integrity, signal integrity and EMI analysis of electronic packages and PCBs	http://www.ansys.com/Products/Simulation+Technology/Electronics/Signal+Integrity/ANSYS+SIwave
254	spm	The SPM software package has been designed for the analysis of brain imaging data sequences. The sequences can be a series of images from different cohorts, or time-series from the same subject. The current release is designed for the analysis of fMRI, PET, SPECT, EEG and MEG.	http://www.fil.ion.ucl.ac.uk/spm/
255	Adams	Adams is the most widely used multibody dynamics and motion analysis software in the world. Adams helps engineers to study the dynamics of moving parts, how loads and forces are distributed throughout mechanical systems, and to improve and optimize the performance of their products.	http://www.mscsoftware.com/adams-student-edition
256	Adina	DINA System for linear and nonlinear finite element analysis of solids and structures, heat transfer, CFD and electromagnetics. ADINA also offers a comprehensive array of multiphysics capabilities including fluid-structure interaction and thermo-mechanical coupling	http://www.adina.com/index.shtml
257	Advanced Normalized Tools (ANTs)	ANTs extracts information from complex datasets that include imaging (Word Cloud). Paired with ANTsR (answer), ANTs is useful for managing, interpreting and visualizing multidimensional data. ANTs is popularly considered a state-of-the-art medical image registration and segmentation toolkit. ANTsR is an emerging tool supporting standardized multimodality image analysis. ANTs depends on the Insight ToolKit (ITK), a widely used medical image processing library to which ANTs developers contribute.	http://stnava.github.io/ANTs/
258	Ansoft Designer	?	http://www.ansys.com/Support/Platform+Support/ch.Ansoft+Products+14.0.hu
259	Art		
260	Atomic Simulation Environment (ASE)	The Atomistic Simulation Environment (ASE) is a set of tools and Python modules for setting up, manipulating, running, visualizing and analyzing atomistic simulations. The code is freely available under the GNU LGPL license.	https://wiki.fysik.dtu.dk/ase/
261	BCT		
262	Beagle		
263	Beast	BEAST is a cross-platform program for Bayesian analysis of molecular sequences using MCMC. It is entirely orientated towards rooted, time-measured phylogenies inferred using strict or relaxed molecular clock models. It can be used as a method of reconstructing phylogenies but is also a framework for testing evolutionary hypotheses without conditioning on a single tree topology. BEAST uses MCMC to average over tree space, so that each tree is weighted proportional to its posterior probability. We include a simple to use user-interface program for setting up standard analyses and a suit of programs for analysing the results.	http://beast.bio.ed.ac.uk/
264	Blender		
265	ccp4	CCP4 exists to produce and support a world-leading, integrated suite of programs that allows researchers to determine macromolecular structures by X-ray crystallography, and other biophysical techniques. CCP4 aims to develop and support the development of cutting edge approaches to experimental determination and analysis of protein structure, and integrate these approaches into the suit	http://www.ccp4.ac.uk/about.php
266	charmm	is a versatile and widely used molecular simulation program with broad application to many-particle systems	http://www.charmm.org/
267	chimera	UCSF Chimera is a highly extensible program for interactive visualization and analysis of molecular structures and related data, including density maps, supramolecular assemblies, sequence alignments, docking results, trajectories, and conformational ensembles	https://www.cgl.ucsf.edu/chimera/index.html
268	chipmonk	ChIPMonk is a program to enable the visualisation and analysis of ChIP-on-chip data	http://www.bioinformatics.babraham.ac.uk/projects/chipmonk/
269	clustal	Clustal Omega is the latest addition to the Clustal family. It offers a significant increase in scalability over previous versions, allowing hundreds of thousands of sequences to be aligned in only a few hours. It will also make use of multiple processors, where present. In addition, the quality of alignments is superior to previous versions, as measured by a range of popular benchmarks.	http://www.clustal.org/omega/
270	cns_solve	Crystallography & NMR System (CNS) is the result of an international collaborative effort among several research groups. The program has been designed to provide a flexible multi-level hierachical approach for the most commonly used algorithms in macromolecular structure determination. Highlights include heavy atom searching, experimental phasing (including MAD and MIR), density modification, crystallographic refinement with maximum likelihood targets, and NMR structure calculation using NOEs, J-coupling, chemical shift, and dipolar coupling data	http://cns-online.org/
271	comet		
272	compecon	CompEcon is a set of MATLAB functions for solving a variety of problems in economics and finance. The library functions include rootfinding and optimization solvers, a integrated set of routines for function approximation using polynomial, splines and other functional families, a set of numerical integration routines for general functions and for common probability distributions, general solvers for Ordinary Differential Equations (both initial and boundary value problems), routines for solving discrete and continuous time dynamic programming problems, and a general solver for financial derivatives (bonds, futures, options).	http://www4.ncsu.edu/~pfackler/compecon/toolbox.html
273	csim		
274	Data Analysis		
275	desmond	Desmond is a software package developed at D. E. Shaw Research to perform high-speed molecular dynamics simulations of biological systems on conventional commodity clusters. The code uses novel parallel algorithms and numerical techniques to achieve high performance and accuracy on platforms containing a large number of processors, but may also be executed on a single computer.	http://www.mybiosoftware.com/3d-molecular-model/1065
276	dmatlab	Distributed Matlab	
277	eeglab	EEGLAB is an interactive Matlab toolbox for processing continuous and event-related EEG, MEG and other electrophysiological data incorporating independent component analysis (ICA), time/frequency analysis, artifact rejection, event-related statistics, and several useful modes of visualization of the averaged and single-trial data.	http://sccn.ucsd.edu/eeglab/
278	em2em	Program to convert images (2-D images and 3-D volumes) from/to formats typically used in 3-D electron microscopy (3DEM).	https://www.imagescience.de/em2em.html
279	eman	EMAN is a suite of scientific image processing tools aimed primarily at the transmission electron microscopy community	http://blake.bcm.edu/emanwiki/EMAN1
280	emboss	EMBOSS is a free Open Source software analysis package specially developed for the needs of the molecular biology (e.g. EMBnet) user community. The software automatically copes with data in a variety of formats and even allows transparent retrieval of sequence data from the web. Also, as extensive libraries are provided with the package, it is a platform to allow other scientists to develop and release software in true open source spirit.	http://emboss.sourceforge.net/what/
281	fastPHASE	The program fastPHASE implements methods for estimating haplotypes and missing genotypes from population SNP genotype data.	http://c4c.uwc4c.com/express_license_technologies/fastphase
282	feappv	FEAPpv is a general purpose finite element analysis program which is designed for research and educational use	http://www.ce.berkeley.edu/projects/feap/feappv/
283	ferret	Ferret is an interactive computer visualization and analysis environment designed to meet the needs of oceanographers and meteorologists analyzing large and complex gridded data sets. It runs on most Unix systems, and on Windows XP/NT/9x using X windows for display.	http://ferret.pmel.noaa.gov/Ferret/home
284	flex	Flex is a tool for generating scanners. A scanner, sometimes called a tokenizer, is a program which recognizes lexical patterns in text. defines the function yylex(). The file "lex.yy.c" can be compiled and linked to produce an executable. When the executable is run, it analyzes its input for occurrences of text matching the regular expressions for each rule. Whenever it finds a match, it executes the corresponding C code.	http://flex.sourceforge.net/
285	fltk	a cross-platform C++ GUI toolkit for UNIX®/Linux® (X11), Microsoft® Windows®, and MacOS®X. FLTK provides modern GUI functionality without the bloat and supports 3D graphics via OpenGL® and its built-in GLUT emulation.	http://www.fltk.org/index.php
286	frappe		
287	frealign	Frealign is a program for high-resolution refinement of 3D reconstructions from cryo-EM images of single particles	http://grigoriefflab.janelia.org/frealign
288	ftgl	FTGL is a free cross-platform Open Source C++ library that uses Freetype2 to simplify rendering fonts in OpenGL applications. FTGL supports bitmaps, pixmaps, texture maps, outlines, polygon mesh, and extruded polygon rendering modes.	http://sourceforge.net/projects/ftgl/
289	ga		
290	gambit		
291	gc	?	http://www.hboehm.info/gc/gc_source/
292	glpk	The GLPK (GNU Linear Programming Kit) package is intended for solving large-scale linear programming (LP), mixed integer programming (MIP), and other related problems. It is a set of routines written in ANSI C and organized in the form of a callable library.	https://www.gnu.org/software/glpk/

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293	gnat	GNAT is an Ada (including Ada 2005) toolset, integrated into the GCC compiler system.GNAT includes GPS, a visual IDE, a comprehensive toolsuite including a visual debugger, and a set of libraries and bindings	http://www.gnu.org/software/gnat/
294	gpaw	GPAW is a density-functional theory (DFT) Python code based on the projector-augmented wave (PAW) method and the atomic simulation environment (ASE). It uses real-space uniform grids and multigrid methods, atom-centered basis-functions or plane-waves	https://wiki.fysik.dtu.dk/gpaw/
295	Graphics Magick	Provides a robust and efficient collection of tools and libraries which support reading, writing, and manipulating an image in over 88 major formats including important formats like DPX, GIF, JPEG, JPEG-2000, PNG, PDF, PNM, and TIF	http://www.graphicsmagick.org/
296	grass	GRASS GIS, commonly referred to as GRASS (Geographic Resources Analysis Support System), is a free and open source Geographic Information System (GIS) software suite used for geospatial data management and analysis, image processing, graphics and maps production, spatial modeling, and visualization	http://grass.osgeo.org/
297	haskell	Haskell is an advanced purely-functional programming language. An open-source product of more than twenty years of cutting-edge research, it allows rapid development of robust, concise, correct software. With strong support for integration with other languages, built-inconcurrency and parallelism, debuggers, profilers, rich libraries and an active community, Haskell makes it easier to produce flexible, maintainable, high-quality software.	https://www.haskell.org/haskellwiki/Haskell
298	hkl-2000	provides high quality software and hardware solutions for X-ray crystallography laboratories and synchrotron beam lines.	http://www.hkl-xray.com/download-instructions-hkl-2000
299	icewm	IceWM is a window manager for the X Window System (freedesktop,XFree86). The goal of IceWM is speed, simplicity, and not getting in the user's way.	http://www.icewm.org/
300	idba	is a practical iterative De Bruijn Graph De Novo Assembler for sequence assembly in bioinfomatics	http://www.mybiosoftware.com/assembly-tools/7062
301	imagic	IMAGIC is a high end environment for the analysis of images, spectra and other multi-dimensional data-sets. IMAGIC's software package is aimed at processing (huge) data sets from (cryo-) electron microscopy, especially in the field of single particle analyses in Structural Biology.	https://www.imagescience.de/imagic.html
302	impute	IMPUTE is a program for estimating ("imputing") unobserved genotypes in SNP association studies	http://mathgen.stats.ox.ac.uk/impute/impute.html
303	instruct		
304	intlab	INTLAB is the Matlab toolbox for reliable computing and self-validating algorithms	http://www.ti3.tu-harburg.de/intlab/
305	iqr	iqr is a simulation software to graphically design and control large-scale neuronal models. Simulations in iqr can control real-world devices in real-time. iqr can be extended by new neuron, and synapse types, and custom interfaces to hardware.	http://sourceforge.net/projects/iqr/
306	irtk	Image Registration Toolkit	http://www.doc.ic.ac.uk/~dr/software/
307	itksnap	ITK-SNAP is a software application used to segment structures in 3D medical images	http://www.itksnap.org/pmwiki/pmwiki.php
308	j3d	Java 3D API	https://java3d.java.net/binary-builds.html
309	jmol	an open-source Java viewer for chemical structures in 3D	http://jmol.sourceforge.net/
310	jweb		
311	latex	LaTeX is a high-quality typesetting system; it includes features designed for the production of technical and scientific documentation. LaTeX is the de facto standard for the communication and publication of scientific documents.	http://latex-project.org/ftp.html
312	lev00	user friendly packages for DFT codes	http://www.mth.kcl.ac.uk/~lev/codes/lev00/index.html
313	loni/pipeline	The LONI Pipeline is a free workflow application primarily aimed at computational scientists. With the LONI Pipeline, users can quickly create workflows that take advantage of all the greatest tools available in neuroimaging, genomics, bioinformatics, etc	http://pipeline.bmap.ucla.edu/
314	loni/server_library		http://pipeline.loni.usc.edu/learn/server-guide/configuration/
315	mechsys	MechSys is a programming library for the implementation of simulation tools in mechanics. Its source code is mainly written in C++ with parts in Python and Go (under development).	http://mechsys.nongnu.org/index.shtml
316	mercury	Mercury offers a comprehensive range of tools for 3D structure visualization and the exploration of crystal packing.	http://www.ccdc.cam.ac.uk/Solutions/FreeSoftware/Pages/FreeMercury.aspx
317	metavelvet	An extension of Velvet assembler to de novo metagenome assembly from short sequence reads	http://metavelvet.dna.bio.keio.ac.jp/
318	metawatt	The Metawatt binner is a graphical binning tool that makes use of multivariate statistics of tetranucleotide frequencies and interpolated Markov models. It also performs taxonomic assessment of binning quality (via BLAST).	http://sourceforge.net/projects/metawatt/
319	mni		http://www.mccauslandcenter.sc.edu/mricro/mricro/
320	mricro	MRIcro allows Windows and Linux computers view medical images. It is a standalone program, but includes tools to complement SPM (software that allows neuroimagers to analyse MRI, fMRI and PET images). MRIcro allows efficient viewing and exporting of brain images.	http://www.mccauslandcenter.sc.edu/mricro/mricro/mricro.html
321	mricron	MRIcron is a user-friendly and efficient piece of software which aims to assist you in viewing medical imagery with multiple layering, supporting HDR, NII and VOI formats, thus enabling you to analyze scans, X-rays and other similar files with minimal effort.	http://www.mccauslandcenter.sc.edu/mricro/mricron/install.html
322	nastran	MSC Nastran is the world's most widely used Finite Element Analysis (FEA) solver. When it comes to simulating stress, dynamics, or vibration of real-world, complex systems, MSC Nastran is still the best and most trusted software in the world – period. Today, manufacturers of everything from parts to complex assemblies are choosing the FEA solver that is reliable and accurate enough to be certified by the FAA and other regulatory agencies.	http://www.mscsoftware.com/msc-nastran-student-edition
323	netlogo	NetLogo is a programmable modeling environment for simulating natural and social phenomena.NetLogo is particularly well suited for modeling complex systems developing over time	http://ccl.northwestern.edu/netlogo/
324	nltk	Natural Language Toolkit (NLTK) is a Python package for processing natural language text.	http://www.nltk.org/install.html
325	nmoldyn	nMOLDYN is an interactive analysis program for Molecular Dynamics simulations. It is especially designed for the computation and decomposition of neutron scattering spectra, but also computes other quantities.	http://dirac.cnrs-orleans.fr/plone/software/nmoldyn/
326	numactl	numactl is an open source command-line software that implements support for simple NUMA policy. The NUMA (Non-Uniform Memory Access) policy allows you to tune programs by controlling the placement of memory in NUMA systems.	http://linux.softpedia.com/get/Utilities/numactl-8223.shtml
327	opencl	OpenCL™ (Open Computing Language) is a low-level API for heterogeneous computing that runs on CUDA-powered GPUs. Using the OpenCL API, developers can launch compute kernels written using a limited subset of the C programming language on a GPU.	https://developer.nvidia.com/opencl
328	opensees	The Open System for Earthquake Engineering Simulation (OpenSees) is a software framework for simulating the seismic response of structural and geotechnical systems. OpenSees has been developed as the computational platform for research in performance-based earthquake engineering	http://opensees.berkeley.edu/OpenSees/home/about.php
329	optseq2	optseq2 is a tool for automatically scheduling events for rapid-presentation event-related (RPER) fMRI experiments	http://surfer.nmr.mgh.harvard.edu/optseq/
330	ovito	OVITO is a scientific visualization and analysis software for atomistic simulation data	http://www.ovito.org/
331	pcre	The PCRE library is a set of functions that implement regular expression pattern matching using the same syntax and semantics as Perl 5. PCRE has its own native API, as well as a set of wrapper functions that correspond to the POSIX regular expression API. The PCRE library is free, even for building proprietary software.	http://www.pcre.org/
332	phreeqc	PHREEQC version 3 is a computer program written in the C and C++ programming languages that is designed to perform a wide variety of aqueous geochemical calculations	http://wwwbrr.cr.usgs.gov/projects/GWC_coupled/phreeqc/
333	plink	PLINK is a free, open-source whole genome association analysis toolset, designed to perform a range of basic, large-scale analyses in a computationally efficient manner.	http://pngu.mgh.harvard.edu/~purcell/plink/
334	povray	is a ray tracing program which generates images from a text-based scene description, and is available for a variety of computer platforms.	http://www.povray.org/
335	promax		
336	pwgui	PWgui is a GUI for PWscf based programs from Quantum-ESPRESSO integrated suite of codes for electronic structure calculations and materials modeling at the nanoscale	http://www-k3.ijs.si/kokalj/pwgui/
337	pyfoam	pyFoam is a Python front-end to the OpenFOAM (Open Source CFD Toolbox). It introduces interactivity into OpenFOAM, simplifies connection with third-party functionality and streamlines design of custom user solvers	http://openfoamwiki.net/index.php/Contrib/PyFoam
338	pymol	PyMOL is a user-sponsored molecular visualization system on an open-source foundation.	http://www.pymol.org/
339	qhull	Qhull computes the convex hull, Delaunay triangulation, Voronoi diagram, halfspace intersection about a point, furthest-site Delaunay triangulation, and furthest-site Voronoi diagram. It runs in 2-d, 3-d, 4-d, and higher dimensions. It implements the Quickhull algorithm for computing the convex hull. Qhull handles roundoff errors from floating point arithmetic. It can approximate a convex hull.	http://www.qhull.org/
340	qiime	is an open source software package for comparison and analysis of microbial communities, primarily based on high-throughput amplicon sequencing data	http://qiime.org/
341	realvnc	VNC enables you to remotely access and control your devices wherever you are in the world, whenever you need to	https://www.realvnc.com/
342	rnamotif	namotif program [1] searches a database for RNA sequences that match a "motif" describing secondary structure interactions.	http://casegroup.rutgers.edu/casegr-sh-2.5.html

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343	scirun	is a problem solving environment or "computational workbench" in which a user selects software modules that can be connected in a visual programing environment to create a high level workflow for experimentation	http://www.sci.utah.edu/cibc-software/scirun.html
344	sedumi	software for optimization over symmetric cones	http://sedumi.ie.lehigh.edu/
345	seg3D	Seg3D is a free volume segmentation and processing tool developed by the NIH Center	http://www.sci.utah.edu/cibc-software/seg3d.html
346	siesta	SIESTA is both a method and its computer program implementation, to perform efficient electronic structure calculations and ab initio molecular dynamics simulations of molecules and solids. SIESTA's efficiency stems from the use of strictly localized basis sets and from the implementation of linear-scaling algorithms which can be applied to suitable systems. A very important feature of the code is that its accuracy and cost can be tuned in a wide range, from quick exploratory calculations to highly accurate simulations matching the quality of other approaches, such as plane-wave and all-electron methods.	http://departments.icmab.es/leem/siesta/
347	situs	program package for the modeling of atomic resolution structures into low-resolution density maps e.g. from electron microscopy, tomography, or small angle X-ray scattering	http://situs.biomachina.org/
348	socnetv	Social Networks Visualizer (SocNetV) is a cross-platform, user-friendly tool for the analysis and visualization of Social Networks	http://socnetv.sourceforge.net/
349	spider		
350	spm.python		
351	STRanger		
352	teem		
353	Terachem	TeraChem is general purpose quantum chemistry software designed to run on NVIDIA GPU architectures under a 64-bit Linux operating system.	http://www.petachem.com/index.html
354	v_sim	V_Sim visualizes atomic structures such as crystals, grain boundaries and so on (from many file formats, binary or plain text)	http://www-drfmc.cea.fr/L_Sim/V_Sim/
355	veda		
356	virtualgl	VirtualGL is an open source toolkit that gives any Unix or Linux remote display software the ability to run OpenGL applications with full 3D hardware acceleration	http://www.virtualgl.org/
357	wien2k	perform electronic structure calculations of solids using density functional theory (DFT)	http://www.wien2k.at/
358	wordnet	WordNet® is a large lexical database of English	http://wordnet.princeton.edu/wordnet/download/
359	wxDragon	?	http://www.wxdragon.de/
360	XFdtd	XFdtd Release 7 (XF7) is the market's most modern 3D electromagnetic simulation software for FDTD-based modeling and simulation. It's tremendously fast by leveraging NVIDIA's most advanced CUDA-enabled GPUs. And it's easy to use and engineered to replicate real-world processes.	http://www.remcom.com/xf7
361	yalmip	YALMIP is a modelling language for advanced modeling and solution of convex and nonconvex optimization problems. It is implemented as a free (as in no charge) toolbox for MATLAB.	http://users.isy.liu.se/johanl/yalmip/
362			
363	hadoop	Hadoop is an open source data processing framework.	http://hadoop.apache.org/
364	hbase	Hbase is a part of Hadoop, an open source data processing framework.	http://hbase.apache.org/
365	hive	Hive is a part of Hadoop, an open source data processing framework.	http://hive.apache.org/
366	moab	loads the Moab scheduling command environment	http://www.adaptivecomputing.com/
367	pig	Pig is an open source data processing tool.	http://pig.apache.org/
368	sqoop	Sqoop is a part of Hadoop, an open source data processing framework.	http://sqoop.apache.org/
369	apache subversion		
370	acml	ACML is the AMD Core Math Library, which contains functions from BLAS and LAPACK, among other things, optimized for the AMD CPUs	http://developer.amd.com/tools-and-sdks/cpu-development/amd-core-math-library-acml/
371	epd	The Enthought Python Distribution provides scientists with a comprehensive set of tools to perform rigorous data analysis and visualization. Python, distinguished by its flexibility, coherence, and ease-of-use, is rapidly becoming the programming language of choice for researchers worldwide. EPD extends this capacity with a powerful collection of Python libraries to enable interactive technical computing and cross-platform rapid application development. This module also includes pymc.	http://www.enthought.com/
372	flexlm	The Flexlm is a common floating license manager commonly used by applications	http://www.flexerasoftware.com/products/flexnet-publisher.htm
373	g95	Users should use gfortran rather than G95. G95 is a stable, production Fortran 95 compiler available for multiple cpu architectures and operating systems. Innovations and optimizations continue to be worked on. Parts of the F2003 and F2008 standards have been implemented in g95	http://g95.org/
374	h5py	HDF5 for Python (h5py) is a general-purpose Python interface to the Hierarchical Data Format library, version 5. HDF5 is a versatile, mature scientific software library designed for the fast, flexible storage of enormous amounts of data.	http://code.google.com/p/h5py/
375	imsl	?	
376	mpi4py	MPI for Python (mpi4py) provides bindings of the Message Passing Interface (MPI) standard for the Python programming language, allowing any Python program to exploit multiple processors.	http://mpi4py.scipy.org/
377	nag	NAGWARE – f95/f90 fortran compiler	http://www.nag.co.uk/
378	naglib	NAG has over 1,450 tried and tested routines that are both flexible and portable	http://www.nag.co.uk/numeric/numerical_libraries.asp
379	perfexpert	PerfExpert automatically analyzes the performance of programs and suggests optimizations to alleviate the identified bottlenecks. It is intended to make performance assessment easy while providing accurate diagnoses of core, chip, and node-level performance bottlenecks. Because of this focus, it suffices (and is recommended) to use scaled-down data sets and resource configurations to obtain accurate analyses.	http://www.tacc.utexas.edu/perfexpert/
380	Rhadoop	RHadoop is a part of Hadoop, an open source data processing framework.	https://github.com/RevolutionAnalytics/RHadoop/wiki
381	cfour	CFOUR (Coupled-Cluster techniques for Computational Chemistry) is a program package for performing high-level quantum mechanical calculations on atoms and molecules.	http://www.cfour.de/
382	chombo	Chombo provides a set of tools for implementing finite difference methods for the solution of partial differential equations on block-structured adaptively refined rectangular grids. Both elliptic and time-dependent modules are included. Chombo supports calculations in complex geometries with both embedded boundaries and mapped grids, and Chombo also supports particle methods. Most parallel platforms are supported, and cross-platform self-describing file formats are included.	https://commons.lbl.gov/display/chombo/Chombo+-+Software+for+Adaptive+Solutions+of+Partial+Differential+Equations
383	dakota	Dakota — A Multilevel Parallel Object-Oriented Framework for design optimization	http://dakota.sandia.gov/
384	globus	Globus provides the GSI/MyProxy in addition to GridFTP cli tools	http://www.globus.org/
385	gti	GT-SUITE offers the only true virtual engine/powertrain tool, capable of integrated simulations of the total engine and powertrain system	http://www.gtisoft.com/
386	hpctoolkit	HPCToolkit is an integrated suite of tools for measurement and analysis of program performance on computers ranging from multicore desktop systems to the nation's largest supercomputers. By using statistical sampling of timers and hardware performance counters, HPCToolkit collects accurate measurements of a program's work, resource consumption, and inefficiency and attributes them to the full calling context in which they occur.	http://hpctoolkit.org/
387	mongodb	?	
388	mpb	This program computes definite-frequency eigenstates (harmonic modes) of Maxwell's equations in periodic dielectric structures for arbitrary wavevectors, using fully-vectorial and three-dimensional methods. It is especially designed for the study of photonic crystals (a.k.a. photonic band-gap materials), but is also applicable to many other problems in optics, such as waveguides and resonator systems. (For example, it can solve for the modes of waveguides with arbitrary cross-sections.)	http://ab-initio.mit.edu/wiki/index.php/MIT_Photonic_Bands
389	mpcci	Multiphysics Code Coupling Interface	http://www.mpcci.de/multiphysics-engineering.html
390	ncl	NCL is an interpreted language designed specifically for scientific data analysis and visualization. Supports netCDF3 and 4, GRIP1 and 2 HDF-SDS, HDF4-EOS, binary, shapefiles, and ascii files.	http://www.ncl.ucar.edu/
391	octopus	Octopus is a scientific program aimed at the ab initio virtual experimentation on a hopefully ever-increasing range of system types. Electrons are described quantum-mechanically within density-functional theory (DFT), in its time-dependent form (TDDFT) when doing simulations in time. Nuclei are described classically as point particles. Electron-nucleus interaction is described within the pseudopotential approximation.	http://www.tddft.org/programs/octopus/wiki/index.php/Main_Page
392	pbzip	tPBZIP2/MPIBZIP2 is a parallel implementation of the bzip2 block-sorting file compressor that uses pthreads(pbzip2) or MPI (mpibzip2) and achieves near-linear speedup on SMP machines or clusters. Anything compressed with pbzip2/mpibzip2 can be decompressed with bzip2	http://compression.ca/
393	pcp	tPCP: a parallel copy directory copy program for Lustre (/scratch /nobackup)	https://github.com/wtsi-ssg/pcp
394	pigz	Pigz, which stands for parallel implementation of gzip, is a fully functional replacement for gzip that exploits multiple processors and multiple cores to the hilt when compressing data. It does not decompress in parallel.	http://zlib.net/pigz/

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395	tct	Teragrid/Xsede Client Toolkit for connecting with your Teragrid/Xsede portal password to Xsede/Teragrid resources using gsissh myproxy-login and globus-url-copy.	https://www.xsede.org/user-portal
396	wannier90	Maximally-localised Wannier functions (MLWFs) and Wannier90, the computer program that calculates them. Both wannier90.x (the program) and libwannier.a (the library) are built and available.	http://www.wannier.org/
397	wrf	The Weather Research and Forecasting (WRF) Model is a next-generation mesoscale numerical weather prediction system designed to serve both operational forecasting and atmospheric research needs. It features multiple dynamical cores, a 3-dimensional variational (3DVAR) data assimilation system, and a software architecture allowing for computational parallelism and system extensibility.	http://www.wrf-model.org/index.php
398	xsede	Xsede Client Toolkit for connecting with your Xsede portal password to Xsede resources using gsissh myproxy-login and globus-url-copy.	https://www.xsede.org/user-portal
399	cfx	ANSYS CFX is a high-performance, general purpose CFD program that has been applied to solve wide-ranging fluid flow problems.	http://www.ansys.com/Products/Simulation+Technology/Fluid+Dynamics/Fluid+Dynamics+Products/ANSYS+CFX
400	chemkin	Loads the CHEMKIN runtime environment CHEMKIN software enables the simulation of complex chemical reactions	http://www.reactiondesign.com/
401	cubit	loads the CUBIT Mesh Generation Kit	http://cubit.sandia.gov/index.html
402	dytran	Dytran is an explicit finite element analysis (FEA) solution for analyzing complex nonlinear behavior involving permanent deformation of material properties, or the interaction of fluids and structures.	http://www.mscsoftware.com/
403	marc	MARC is a non-linear FEA program	http://www.mscsoftware.com/Products/CAE-Tools/Marc.aspx
404	stata-mp	Stata is a complete, integrated statistical package that provides everything you need for data analysis, data management, and graphics.	http://www.stata.com/
405	converge	Computational fluid dynamics software for complex geometries with moving boundaries. Licensing: This software is licensed for academic, noncommercial use at the University of Michigan	http://convergecfd.com/
406	helios	HELIOS Generalized Geometry Lattice Analysis package. Includes Casmo and Simulate from the Studsvik suite.	http://studsvikscandpower.com/products/helios.php
407	kintecus	Kintecus is chemical modeling software for simulation of combustion, nuclear, biological, enzyme, atmospheric and many other chemical kinetic and equilibrium processes. Kintecus is licensed only for use by specific classes. If you are not in one of those classes, you will not be able to run it.	
408	lahey	loads the Fujitsu Lahey LF95 environment	http://www.lahey.com/
409	mcnp5	loads the mcnp5 environment	https://mcnpx.lanl.gov/
410	molpro	Molpro is a complete system of ab initio programs for molecular electronic structure calculations	http://www.molpro.net/
411	synopsys	Synopsys Synthesis environment	http://www.synopsys.com/home.aspx