What *in silico* molecular docking can do for the 'bench-working biologists'

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Supplementary material

Supplementary table 1. Selected programs, servers and databases used for *in silico* docking

Program/Server/ Database	Docking capabilities*	Website	Observations
Programs			
AutoDock 4 (Morris *et al.* 1998)	RB, FL, FR (*limited side chain flexibility),* LD, BD	*http://autodock.scripps.edu/*	Free, command line program available for Linux, OSX, Windows, Solaris A very god graphical user interface is also available from the program developers: AutoDockTools (ADT); it allows the user to select which atoms of the ligand and the protein are able to be joined by a covalent bound
Glide (Halgren *et al.* 2004; Friesner *et al.* 2004, 2006)	RB, FL, BD	*https://www.schrodinger.com/products/14/5/*	Commercial application available for Linux and Windows
FlexX (Rarey *et al.* 1996; Kramer *et al.* 1999)	RB, FL	*http://www.biosolveit.de/FlexX/*	Commercial program available for Linux and Windows, part of the LeadIT software solution Good user interface Takes account of the metal coordination It allows the user to select which atoms of the ligand and the protein are able to be joined by a covalent bound
Dock 6 (Kuntz *et al.* 1982)	RB, FL, BD, LD	*http://dock.compbio.ucsf.edu/DOCK_6/index.htm*	Free, command line program, available for Unix Linux, Windows, and OSX For preparing the input files and visualization of results the UCSFChimera (Pettersen *et al.* 2004) program can be used
HADDock (Dominguez *et al.* 2003; de Vries *et al.* 2007)	makes use of biochemical and/or biophysical interaction data	*http://www.nmr.chem.uu.nl/haddock/*	Supports up to a total of six separate molecules (proteins, DNA, RNA, oligosaccharides and small ligands) per docking Free for academic, but an license form must be fill-in and sent to the author

			Command line only, available as a collection of scripts.
GOLD(Verdonk *et al.* 2003; Joy *et al.* 2006)	RB, FL, LD,	*http://www.ccdc.cam.ac.uk/products/life_sciences/gold/*	Commercial program available for Linux and Windows which also supports a GUI
			It allows the user to select which atoms of the ligand and the protein are able to be joined by a covalent bound.
ICM (Abagyan and Totrov 1994; Totrov and Abagyan 1997)	FL, FR, BD, PP	*http://www.molsoft.com/docking.html*	Commercial program available for Windows, Linux, SGI, OSX
			Allows automatic preparation of a molecule for a flexible docking
HEXProtein docking (Ritchie and Kemp 2000)	RB, BD	*http://hex.loria.fr/*	Free for academic and governmental users
			Mainly developed for protein–DNA docking but also able to dock an rigid ligand
			Available for Windows, Linux and OSX with a build-in user interface pdb files are directly used as input
			Makes use GPU's when available speeding-up the docking process with factors of up to over 50 (Korb *et al.* 2011)
			A blind global docking takes just a few seconds
Molegro Virtual Docker (Thomsen and Christensen 2006)	FL, FR (side-chain flexibility) LD	*http://www.molegro.com/mvd-product.php*	Commercial program with good graphical user interface (GUI), supported on Linux, Windows and Mac
			An automatic cavity detection
			Algorithm is implemented for prediction of binding sites.
DOT (Mandell *et al.* 2001)	RB, PP	*http://www.sdsc.edu/CCMS/DOT/*	Command line program available for Linux (Red Hat only) OSX, Solaris
			Can dock both proteins, DNA, and RNA
			Automated setup of input files starting with protein coordinate files from the PDB
AutoDock Vina (Trott and Olson 2010)	RB, FL, FR (*limited side chain flexibility),* LD, BD	*http://vina.scripps.edu/*	Open-source command line program with enhanced accuracy offering an more automated docking process
			AutoDockTools (ADT) can also be used for input files preparation and results visualization. Free, available for Linux, OSX, and Windows
DockVison (Hart and Read 1992)	FL, LD	*http://dockvision.com/*	Commercial program with GUI available for only for SGI and Linux
GEMDOCK (Yang and Chen 2004)	FL, FR,	*http://gemdock.life.nctu.edu.tw/dock/*	Free for academic, available for Windows and several Linux distributions
			The new iGEMDOCK also offers a GUI

Fitted (Corbeil *et al.* 2007, 2008)	FL, FR,	*http://fitted.ca/*	Commercial application, web-based graphical interface allowing easy deployment on any operating system.
eHiTs (Zsoldos *et al.* 2006, 2007)	FL, BD	*http://simbiodasys.ca*	Commercial program
			Automatic pocket detection
			Accepts several standard input files
			Includes a specific metal binding term for using metal-containing proteins as receptor
RosettaLigand (Davis and Baker 2009)	BD, FL, FR (full side chain and backbone flexibility,LD	*http://www.rosettacommons.org/software/*	Free for academic, but an on-line license form must be fill-in
			command line only, available as source-code, part of the RosettaCommons software Suite
FiberDock (Mashiach *et al.* 2010)	FL, FR (side-chain and back-bone flexibility) PP	*http://bioinfo3d.cs.tau.ac.il/FiberDock/index.html*	Free for academic, command line only, but also a server version available
ArgusDock and GADock (Oda *et al.* 2007)	RB, PP	*http://www.arguslab.com*	Well integrated into the free ArgusLab molecular modeling, graphics, and drug design program
			Only available for Windows
Escher (NG) (Ausiello *et al.* 1997)	FR (soft docking), PP	*http://www.ddl.unimi.it/escherng/index.htm*	DNA-protein docking capabilities
			Only two PDB files are required as input
			Poorly developed, last version is dated in 2007
			Available for Windows, Linux, IRIX and Amiga OS
GRAMM	RD, PP, BD,	*http://vakser.bioinformatics.ku.edu/main/resources_gramm1.03.php*	Command line only program, available for a variety of platforms and operating systems (including Linux and Windows)
DockIt	FL, BD	*http://www.metaphorics.com/products/dockit.html*	A set of commercial command line programs for docking small molecules into macromolecules
RosettaDock (Chaudhury *et al.* 2011)	RB, FR (side chain flexibility, ensemble docking) BD, PP	*http://www.rosettacommons.org/software/*	Free for academic, but an on-line licence form must be fill-in
			command line only, available as source-code, part of the RosettaCommons software Suite
			Several GUI are available, such as Rosettascripts
PLANTS (Korb *et al.* 2006)	RB, FL, FR(side chain flexibility), BD,	*http://www.tcd.uni-konstanz.de/research/plants.php*	Free for academic, available for Linux, Windows and OSX
			comand line program but free tools are available to preprocess the protein and ligand input structures used for docking (ten Brink and Exner, 2010) and to generate the required input scripts (Zodiac)
Servers			
RosettaDock Server (Lyskov and Gray 2008)	RB, FL (side chain flexibility) PP	*http://rosettadock.graylab.jhu.edu*	Based on RosettaDock program.
ZDOCK Server (Chen *et al.* 2003)	RB, LD, PP	*http://zdock.bu.edu/*	Mainly developed for protein-protein docking, can use .pdb as input files

ClusPro Server (Comeau *et al.* 2004a, b)	RB performed with DOT or ZDOCK, PP	*http://cluspro.bu.edu*	Input can be either the coordinate files of two structures (DNA or RNA) or directly the PDB codes One of the best ranked servers in the CAPRI 2009 and 2010 experiments Janin 2010 Lensink/Wodak 2010 Based on PIPER (Kozakov *et al.* 2006)
PatchDock (Schneidman-Duhovny *et al.* 2005)	RB, BD, LB, PP	*http://bioinfo3d.cs.tau.ac.il/PatchDock*	The input consists of two molecules: proteins, DNA, peptides, drugs The output is a list of potential complexes sorted by shape complementarity Tusing the same method, the SymmDock server is also available for prediction of complexes with *Cn* symmetry
GRAMM-X (Tovchigrechko and Vakser 2006)	LB, BD, PP	*http://vakser.bioinformatics.ku.edu/resources/gramm/grammx*	Designed exclusively for protein-protein docking
RosettaDock Server (Lyskov and Gray 2008)	RB, FL (side chain flexibility) PP	*http://rosettadock.graylab.jhu.edu*	Based on RosettaDock program
Hex Server (Macindoe *et al.* 2010)	RB	*http://hexserver.loria.fr*	The server requires only the two protein structures in PDB format to be uploaded
DockBlaster (Irwin *et al.* 2009)	RB, FL, BD,	*http://blaster.docking.org/*	uses DOCK 3 and PocketPickker (Coleman and Sharp 2010) as a docking engine, and ZINC (Irwin and Shoichet 2005) as a dockable database
Databases			
Worldwide Protein Data Bank (Berman *et al.* 2007		*http://www.wwpdb.org/*	Contains macromolecular structural data that is freely and publicly available to the global community, members are: RCSBPDB (USA), PDBe (Europe), PDBj (Japan), and BMRB (USA)
AffinDB (Block *et al.* 2006)		*http://pc1664.pharmazie.uni-marburg.de/affinity/*	Contains affinity data for protein-ligand complexes from the RCSBPDB
BindingDB (Liu *et al.* 2007		*http://www.bindingdb.org*	Contains data on measured binding affinities for proteins considered as drug-targets
MOAD (Benson *et al.* 2008)		*http://bindingmoad.org/*	A large collection of well solved protein crystal structures with clearly identified ligands and experimentally determined binding data
ChEMBL (Gaulton *et al.* 2012)		*https://www.ebi.ac.uk/chembl/*	Contains 2D structures of bioactive drug-like molecules as well as their calculated properties and bioactivities
ZINC (Irwin and Shoichet 2005)		*http://zinc.docking.org/*	Contains 3D structures of purchasable compounds in ready- to-dock format
PubChem (Wang *et al.* 2009)		*http://pubchem.ncbi.nlm.nih.gov/*	Chemical structures of small organic molecules and information on their biological activities
ChemDB (Chen *et al.* 2007)		*http://cdb.ics.uci.edu/*	Database with chemical structures that provides extensive search criteria
DrugBank (Knox *et al.* 2011)		*http://www.drugbank.ca/*	Combines drug data with drug–target data

*RB, rigid body; FL, flexible ligand; FR, flexible receptor; BD, blind docking; LD, local docking; PP, protein–protein docking.

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