**Supplementary Table S1:** A list of 211 pieces of software for CADD. Software was ranked according to the equation $S_i = \log(10^6.C_i/C_{total})$ where $S_i$ is the score for tool *i*, $C_i$ is the number of citations to tool *i*, and $C_{total}$ is the number of citations to all tools considered. Number of citations was obtained using Google Scholar, last accessed on 14th April 2021.

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 1 | HADDOCK | 26490 | 4.7323 | Docks protein–protein based on biochemical or biophysical information | Free | https://wenmr.science.uu.nl/haddock2.4/ |
| 2 | AutoDock Autodock 1 Autodock 2.4 Autodock 3 Autodock 4 Autodock 4.2 Autodock Vina AutoDockFR AutoDockTools | 22422 | 4.6599 | Automated docking tools | Free | http://autodock.scripps.edu/ |
| 3 | Glide Glide 1.8 Glide 2 Glide 2.5 | 22091 | 4.6535 | Rapid, Accurate Docking and Scoring approach | Subscription | https://www.schrodinger.com/glide |
| 4 | FlexX | 19987 | 4.6100 | Predicts the geometry of the protein-ligand complex and estimates the binding affinity | Free | https://www.biosolveit.de/FlexX/ |
| 5 | LigandFit | 19890 | 4.6079 | Presents a shape-based approach for docking ligands into the active site of the protein | Subscription | https://www.phenix-online.org/documentation/reference/ligandfit.html |
| 6 | AmberTools | 14572 | 4.4728 | A suite of biomolecular simulation programs | Subscription | https://ambermd.org/ |
| 7 | ENCoM | 13145 | 4.4280 | A coarse-grained normal mode analysis method utilized for different residues in proteins or nucleotides in RNA | Free | http://biophys.umontreal.ca/nrg/resources.html |
| 8 | PROCHECK-NMR | 10783 | 4.3420 | Checks the stereochemical quality of a protein structure solved by NMR | Free | https://www.ebi.ac.uk/thornton-srv/software/PROCHECK/ |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 9 | MCDOCK | 10603 | 4.3347 | Allows for a full flexibility of ligands in the docking calculations | Free | DOI: 10.1021/jm990129n |
| 10 | ICM ICM 2.8 ICM-Dock | 10271 | 4.3209 | A new method for protein modelling and design applications to docking and structure prediction | Subscription | http://www.molsoft.com/docking.html |
| 11 | Dock Dock2 Dock3 Dock4 Dock5 Dock6 Dock7 Dock8 Dock9 | 8181 | 4.2221 | Based on Geometric Matching Algorithm | Free | http://dock.compbio.ucsf.edu/ |
| 12 | SOFT Docking | 7474 | 4.1828 | Predicts the sites of interaction between two cognate molecules based on their 3D structures | Subscription | https://doi.org/10.1016/0022-2836(91)90859-5 |
| 13 | FDS | 7188 | 4.1659 | Cluster analysis based on distance similarities | Free | http://www.scfbio-iitd.res.in/dock/fds.jsp |
| 14 | DockVision | 6950 | 4.1512 | Increases capability to generate laudable results | Free | http://dockvision.sness.net/overview/overview.html |
| 15 | PRODOCK | 6442 | 4.1183 | Renders the programming easier and the definition of molecular flexibility straighter forward | Subscription | https://doi.org/10.1002/(SICI)1096-987X(199903)20:4<412::AID-JCC3>3.0.CO;2-N |
| 16 | YASARA YASARA Dynamics YASARA Model YASARA NMR Module YASARA Structure YASARA View YASARA Virtual Reality Workstation YASARA/WHAT IF Twinset | 5870 | 4.0779 | A molecular-graphics, -modeling and -simulation program | Free | http://www.yasara.org/products.htm |
| 17 | KBDOCK | 5820 | 4.0742 | A program that proposes structural templates for protein docking | Free | http://kbdock.loria.fr/ |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 18 | TreeDock | 5796 | 4.0724 | A docking tool that is able explore all clash-free orientations at very fine resolution in a reasonable time | Subscription | https://doi.org/10.1021/ja011240x |
| 19 | LePro | 5639 | 4.0605 | Generates docking input file for LeDock with refined protein atoms within 0.4 nm of any atom of the ligand | Free | http://www.lephar.com/download.htm |
| 20 | DockoMatic | 5594 | 4.0570 | A software that docks secondary ligands used to assist inverse virtual screening | Free | https://doi.org/10.1186/1756-0500-3-289 |
| 21 | SYBYL_ChemScore SYBYL_D-Score SYBYL_F-Score SYBYL_G-Score | 5486 | 4.0485 | A conformational sampling and scoring function | Subscription | https://doi.org/10.1021/jm0203783 |
| 22 | ZDOCK ZDOCKpro | 5415 | 4.0429 | A new scoring function for the initial stage of unbound docking | Subscription | http://zdock.umassmed.edu/ |
| 23 | AADS | 5087 | 4.0157 | An automated active site identification, docking, and scoring protocol | Free | http://www.scfbio-iitd.res.in/dock/ActiveSite_new.jsp |
| 24 | Surflex Dock | 4896 | 3.9991 | An automatic and flexible molecular docking algorithm for rapid in-silico drug-screening applications | Subscription | https://doi.org/10.1007/s10822-007-9114-2 |
| 25 | PyMOL PyMOL 1.4.1 PyMOL 2.1.1 PyMOL 2.4 | 4805 | 3.9910 | An open-source, user-sponsored, molecular visualization system | Subscription | http://www.pymol.org |
| 26 | FlipDock | 4614 | 3.9733 | Allows the automated docking of flexible ligand molecules into active sites of flexible receptor molecules | Free | http://flipdock.scripps.edu/ |
| 27 | SymmDock | 4545 | 3.9668 | A Flexible Induced-fit Backbone Refinement in Molecular Docking | Free | http://bioinfo3d.cs.tau.ac.il/FiberDock/php.php |
| 28 | ClusPro | 4360 | 3.9487 | A widely used tool for protein-protein docking | Free | http://nrc.bu.edu/cluster |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 29 | Surflex | 4180 | 3.9304 | A robust screening tool | Subscription | https://pubmed.ncbi.nlm.nih.gov/12570372/ |
| 30 | ConsDock | 4001 | 3.9114 | A pose within 2 A° RMSD of the X-ray structure can be performed with this software | Subscription | https://doi.org/10.1002/prot.10119 |
| 31 | EADock | 3961 | 3.9071 | A software that is based on "evolutionary algorithms" that generates the good solution through sampling and recognizes this solution as the correct one by its scoring function | Free | http://www.swissdock.ch/ |
| 32 | Fred | 3953 | 3.9062 | A program that docks 70 % of the structures within 2 Å in the cognate docking test | Subscription | https://www.eyesopen.com/oedocking-tk |
| 33 | PASS | 3907 | 3.9011 | A prediction of Activity Spectra for Substances | Free | http://www.way2drug.com/passonline/ |
| 34 | PhDock | 3890 | 3.8992 | A determination of target-based theoretical pharmacophore | Free | http://iscreen.cmu.edu.tw/phdock.php |
| 35 | Robetta | 3545 | 3.8589 | A protein structure prediction service that is continually evaluated through Continuous Automated Model evaluatiOn (CAMEO) | Subscription | http://robetta.bakerlab.org/ |
| 36 | InterEvDock | 3461 | 3.8485 | An expanded server for protein docking using evolutionary and biological information from homology models and multimeric inputs | Free | https://mobyle.rpbs.univ-paris-diderot.fr/cgi-bin/portal.py#forms::InterEvDock2 |
| 37 | FlexDock | 3433 | 3.8449 | An algorithm for Automatic prediction of protein interactions with large scale motion | Subscription | http://bioinfo3d.cs.tau.ac.il/ |
| 38 | RiboDock | 3316 | 3.8299 | A virtual-screening system for automated flexible docking. | Free | https://doi.org/10.1023/B:JCAM.0000035199.48747.1e |
| 39 | GASP | 3271 | 3.8239 | A "Genetic Algorithm Similarity Program" used for testing and investigating methods in statistical genetics by generating samples of | Subscription | https://doi.org/10.1023/A:1008844323931 |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| | | | | family data based on user specified models | | |
| 40 | GOLD | 3208 | 3.8155 | A protein ligand docking software that enables you to make confident binding mode predictions, and achieve high database enrichments | Subscription | https://doi.org/10.1002/prot.10465 |
| 41 | FTDOCK | 3205 | 3.8151 | A tool that performs a global scan of translational and rotational space | Free | http://www.sbg.bio.ic.ac.uk/docking/download.html |
| 42 | QXP | 3186 | 3.8125 | A quick explore (QXP) search algorithm | Subscription | https://doi.org/10.1023/A:1007907728892 |
| 43 | GlamDock | 3150 | 3.8076 | A mapping-based description of the rigid body translation and rotation | Subscription | http://www.chil2.de/Glamdock.html |
| 44 | PSO@AUTODOCK | 3113 | 3.8024 | A Fast and efficient protein ligand docking program based on swarm optimization | Subscription | https://doi.org/10.1111/j.1747-0285.2007.00588.x |
| 45 | SKE-DOCK | 3077 | 3.7974 | A simple geometry docking and a knowledge base scoring function | Subscription | http://www.pharm.kitasato-u.ac.jp/bmd/files/SKE_DOCK.html |
| 46 | Q-Dock(LHM) | 3069 | 3.7963 | A reduced representation mod description | Subscription | DOI: 10.1002/jcc.21395 |
| 47 | PatchDock | 2931 | 3.7763 | An object recognition and image segmentation techniques used in computer vision | Subscription | http://bioinfo3d.cs.tau.ac.il/wk/index.php/Servers_%26_Software |
| 48 | MS-DOCK | 2804 | 3.7570 | All multiple conformations are rigidly docked | Subscription | https://doi.org/10.1186/1471-2105-9-184 |
| 49 | PSI-DOCK | 2638 | 3.7305 | A docking method, Pose-Sensitive Inclined (PSI)-DOCK, for flexible ligand docking | Subscription | https://doi.org/10.1002/prot.20790 |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 50 | PostDOCK | 2559 | 3.7173 | A tool that distinguishes true binding ligand-protein complexes from docking artifacts | Subscription | https://doi.org/10.1021/jm0493360 |
| 51 | MolDock | 2553 | 3.7163 | Combining a differential evolution within a cavity prediction algorithm | Subscription | https://doi.org/10.1021/jm051197e |
| 52 | MEDock | 2510 | 3.7089 | A worldwide search strategy that exploits the highest entropy attribute of the Gaussian probability distribution | Free | https://medock.ee.ncku.edu.tw/ |
| 53 | SwarmDock | 2449 | 3.6982 | A flexible protein-protein docking method | Free | https://bmm.crick.ac.uk/~svc-bmm-swarmdock/submit.cgi |
| 54 | GAsDock | 2373 | 3.6846 | A rapid, accurate, and flexible docking program | Subscription | doi:10.1016/j.bmcl.2004.06.091 |
| 55 | SDOCKER | 2331 | 3.6768 | A method utilizing available x-ray structures to improve docking accuracy | Free | https://github.com/xogeny/sdocker |
| 56 | SOFTDOCK | 2279 | 3.6670 | A model continuity across development lifecycle | Subscription | DOI: 10.1109/DEXA.1999.795265 |
| 57 | DOCK Blaster | 2265 | 3.6643 | A free web-based service for molecular docking and virtual screening | Subscription | http://blaster.docking.org |
| 58 | M-ZDOCK | 2257 | 3.6628 | A symmetric multimer docking | Subscription | http://zdock.umassmed.edu/m-zdock/ |
| 59 | GAPDOCK | 2249 | 3.6612 | A molecular docking methodology explores the behaviour of small molecules in the binding site of a target protein | Subscription | https://doi.org/10.1002/prot.10386 |
| 60 | 3D-QSAR | 2232 | 3.6580 | Simple and advanced tools for developing QSAR models | Free | https://www.3d-qsar.com/ |
| 61 | INVDOCK | 2221 | 3.6558 | A computer-automated identification of potential protein and nucleic acid (RNA or DNA) targets of a small molecule | Subscription | http://bidd.nus.edu.sg/group/softwares/invdock.htm |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 62 | MOE | 2216 | 3.6548 | An integrated computer-aided molecular design platform | Subscription | https://www.chemcomp.com/Products.htm |
| 63 | rDock rDock 3.0 | 2191 | 3.6499 | A docking tool for small molecules against proteins and nucleic acids | Free | http://rdock.sourceforge.net/ |
| 64 | DOCKovalent | 2010 | 3.6125 | Screens large virtual libraries of electrophilic small molecules | Free | http://covalent.docking.org/ |
| 65 | TarFisDock | 1930 | 3.5948 | A web server that docks small molecules with protein structures in the Potential Drug Target Database (PDTD) in an effort to discover new drug targets | Subscription | https://bio.tools/tarfisdock#! |
| 66 | SDOCK | 1927 | 3.5941 | Improves the efficiency and robustness of particle swarm optimization (PSO) for solving flexible protein-ligand docking problems | Subscription | https://onlinelibrary.wiley.com/doi/abs/10.1002/jcc.21839<br>http://mdl.ipc.pku.edu.cn/cgi-bin/down.cgi |
| 67 | FINDSITE-LHM | 1926 | 3.5939 | A homology modelling approach to flexible ligand docking that uses a collection of common molecule substructures derived from evolutionarily related templates as the reference compounds in similarity-based ligand binding pose prediction | Free | http://www.mybiosoftware.com/findsite-lhm-1-0-homology-modeling-approach-flexible-ligand-docking.html |
| 68 | DAIM-SEED-FFLD | 1894 | 3.5866 | DAIM (Decomposition and Identification of Molecules), SEED (Solvation Energy for Exhaustive Docking), and FFLD (Fragment-based Flexible Ligand Docking) | Free | http://www.biochem-caflisch.uzh.ch/movies/0003 |
| 69 | FlexPepDock | 1891 | 3.5859 | Able to refine a coarse starting structure of a peptide-protein complex to a near-native model of the interaction | Free | http://flexpepdock.furmanlab.cs.huji.ac.il/ |
| 70 | VoteDock | 1860 | 3.5788 | Provides fast and accurate prediction method for 3D structure of a protein–ligand complex | Subscription | https://connects.catalyst.harvard.edu/Profiles/display/1104658 |
| 71 | CDocker | 1846 | 3.5755 | Molecular dynamics (MD) simulated-annealing-based algorithm. | Free | https://doi.org/10.1002/jcc.10306 |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 72 | POSIT | 1792 | 3.5626 | A new approach to structure-based drug design (POSIT) rigorously built on the simple concept that pose prediction is intimately coupled to the quality and availability of experimental structural data | Free | https://docs.eyesopen.com/applications/oedocking/posit/posit_overview.html |
| 73 | DynaDock | 1709 | 3.5420 | Used for docking peptides into flexible receptors | Free | https://doi.org/10.1002/prot.22629 |
| 74 | PepCrawler | 1700 | 3.5397 | A fast RRT-based algorithm for high-resolution refinement and binding-affinity estimation of peptide inhibitors | Free | http://bioinfo3d.cs.tau.ac.il/PepCrawler/php.php |
| 75 | GEMDOCK<br>GemDock 1.0<br>GemDock 2.0<br>GemDock 2.1<br>GemDock cent OS5<br>GemDock linux 9<br>GemDock-windos | 1666 | 3.5309 | Uses a Generic Evolutionary Method for molecular docking (GEMDOCK) and an empirical scoring function | Free | http://gemdock.life.nctu.edu.tw/dock/ |
| 76 | FireDock | 1654 | 3.5278 | An efficient method for refinement and re-scoring of rigid-body protein-protein docking solutions | Free | http://bioinfo3d.cs.tau.ac.il/FireDock/ |
| 77 | CovalentDock | 1648 | 3.5262 | Used for covalent bonds | Subscription | https://doi.org/10.1002/jcc.23136 |
| 78 | pyDock | 1644 | 3.5252 | A program which was implemented in order to check the scoring of rigid-body docking poses | Subscription | https://life.bsc.es/pid/pydock/get_pydock.html |
| 79 | DOCKGROUND | 1629 | 3.5212 | Implements a comprehensive database of co-crystallized (bound–bound) protein–protein complexes | Free | http://dockground.bioinformatics.ku.edu/ |
| 80 | SODOCK | 1564 | 3.5035 | Based on particle swarm optimization (PSO) for solving flexible protein–ligand docking problems | Free | http://www.mybiosoftware.com/tag/sodock |
| 81 | SwissDock | 1476 | 3.4783 | A web-server program dedicated to the docking of small molecules on target proteins | Free | http://www.swissdock.ch/docking |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 82 | MedusaDock | 1471 | 3.4769 | Models ligand and receptor flexibility simultaneously with sets of discrete rotamers | Free | https://dokhlab.med.psu.edu/medusadock/#/NewTask |
| 83 | FiberDock | 1427 | 3.4637 | An efficient method for flexible refinement and re-scoring of rigid-body protein-protein docking solutions | Free | http://bioinfo3d.cs.tau.ac.il/FiberDock |
| 84 | VSDMIP | 1426 | 3.4634 | Virtual screening data management on an integrated platform | Free | https://ub.cbm.uam.es/software/vsdmip/ |
| 85 | GalaxySite | 1426 | 3.4634 | An installation of the Galaxy software combined with many common tools and data | Free | http://galaxy.seoklab.org/site |
| 86 | FlexX-Scan | 1365 | 3.4444 | Developed to enhance the speed of the virtual screening process | Subscription | https://pubmed.ncbi.nlm.nih.gov/15382244/ |
| 87 | Kinome Render | 1346 | 3.4383 | Produces customized annotations on the human kinome tree | Free | http://biophys.umontreal.ca/nrg/resources.html |
| 88 | Fleksy | 1333 | 3.4341 | An approach to consider both ligand and receptor flexibility in small molecule docking | Subscription | https://doi.org/10.1021/jm070593p |
| 89 | KinDock | 1319 | 3.4295 | A web server for the analysis of ATP-binding sites of protein kinases | Obsolete | http://abcis.cbs.cnrs.fr/kindock/ |
| 90 | PharmDock | 1306 | 3.4252 | A pharmacophore-based docking program that combines pose sampling and ranking based on optimized protein-based pharmacophore models | Free | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4012150/ |
| 91 | GriDock | 1284 | 3.4178 | Designed to perform the molecular dockings of a large number of ligands stored in a single database (in a format supported by VEGA) | Free | https://www.ddl.unimi.it/cms/index.php?Software_projects:GriDock |
| 92 | ParaDockS | 1282 | 3.4171 | Designed to hold different optimization algorithms and objective functions and provides an accurate prediction of protein–DNA complexes | Subscription | https://doi.org/10.1021/ci900467x |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 93 | EpiDOCK | 1270 | 3.4131 | The first structure-based server that predicts binding to the 23 most frequent MHC class II binding proteins | Free | http://www.ddg-pharmfac.net/epidock/ |
| 94 | MacDOCK | 1248 | 3.4055 | Able to generate orientations consistent with the known covalent binding mode of these complexes | Subscription | DOI: 10.1007/s10822-004-5291-4 |
| 95 | FIPSDock | 1239 | 3.4023 | Implements a variant of the Fully Informed Particle Swarm (FIPS) optimization method | Subscription | http://hub.hku.hk/handle/10722/189104 |
| 96 | Flexidock | 1239 | 3.4023 | Brings the convenience of a HDD docking station, with the performance of a HDD mobile rack | Subscription | http://scholar.dkyobobook.co.kr/searchDetail.laf?barcode=4010024416172 |
| 97 | Smina | 1230 | 3.3992 | A general methodology for designing an empirical scoring function | Free | https://pypi.org/project/docking-py/ |
| 98 | BetaDock | 1228 | 3.3985 | A molecular docking simulation software based on the theory of Beta-complex | Free | DOI: 10.1080/07391102.2011.10507384 |
| 99 | FLOG | 1215 | 3.3938 | Flexible Ligands Oriented on Grid that searches a database of 3D coordinates to explore molecules complementary to a macromolecular receptor of known 3D structure | Subscription | https://doi.org/10.1007/BF00119865 |
| 100 | Combibuild | 1206 | 3.3906 | Builds combinatorial libraries for CRISPR screening | Subscription | https://doi.org/10.1021/jm010338j |
| 101 | MoDock | 1174 | 3.3789 | A main method of structure-based virtual screening | Subscription | https://doi.org/10.1186/s13015-015-0034-8 |
| 102 | CRDOCK | 1173 | 3.3786 | Contains a search engine, several energy minimization algorithms, and different scorings | Free | DOI: 10.1021/ci300194a |
| 103 | FRODOCK | 1154 | 3.3715 | Fast rotational docking based on FRM (Fast Rotational Method) to perform protein-protein docking | Free | http://frodock.chaconlab.org/ |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 104 | GalaxyDock GalaxyDock1 GalaxyDock2 GalaxyDock3 GalaxyDock BP2 | 1154 | 3.3715 | Allows flexibility of pre-selected side-chains of ligand using Conformational Space Annealing | Free | http://galaxy.seoklab.org/softwares/galaxydock.html |
| 105 | SANDOCK | 1153 | 3.3711 | Uses point complementary method that is based on shape and chemical complementarity between interacting molecules | Subscription | DOI: 10.1006/jmbi.1997.1608 |
| 106 | VSDocker | 1143 | 3.3673 | Allows using autodock4 for optimized virtual ligand screening on computer clusters | Subscription | https://www.hsls.pitt.edu/obrc/index.php?page=URL1275058861 |
| 107 | EUDOC | 1114 | 3.3561 | A computer program for identification of drug interaction sites in macromolecules and drug leads from chemical databases | Subscription | https://doi.org/10.1002/jcc.1129 |
| 108 | PyRX PyRX 0.5 PyRX 0.7 PyRX 0.8 PyRX 0.9.6 PyRX 0.9.8 | 1085 | 3.3447 | A tool for Rational Drug Design | Free & Subscription | https://pyrx.sourceforge.io/ |
| 109 | CombDock | 1078 | 3.3419 | A combinatorial docking algorithm for the structural units-assembly problem | Subscription | http://bioinfo3d.cs.tau.ac.il/wk/index.php/Servers_%26_Software |
| 110 | FastDock | 1044 | 3.3280 | Lamarckian genetic algorithm to estimate the binding affinities between the structures | Free | https://pypi.org/project/fastdock/ |
| 111 | Lead finder Leadfinder 2.3 Leadfinder 3.8 | 1029 | 3.3217 | Provides a fast rate of calculations with unique scoring function that provides unsurpassed accuracy of calculations | Subscription | https://www.cresset-group.com/software/lead-finder/ |
| 112 | pyDockTET | 1009 | 3.3131 | A tethered-docking program which uses rigid-body docking system to generate domain-domain poses | Subscription | DOI: 10.1186/1471-2105-9-441 |
| 113 | MADAMM | 1008 | 3.3127 | Utilizes rotamer libraries to produce several combinations of conformers | Subscription | https://doi.org/10.1002/prot.22146 |
| 114 | pyDockRST | 1003 | 3.3106 | Uses the percentage of satisfied restrains | Subscription | DOI: 10.1016/j.jmb.2006.01.001 |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 115 | DOCKTITE | 995 | 3.3071 | Utilized for covalent docking in the Molecular Operating Environment (MOE) | Subscription | https://pubs.acs.org/doi/10.1021/ci500681r |
| 116 | pyDockCG | 992 | 3.3058 | A coarse-grained potential for protein-protein docking scoring and refinement, based on the known UNRES model for polypeptide chains | Subscription | https://doi.org/10.1021/jp112292b |
| 117 | ASEDock | 990 | 3.3049 | Based on a shape similarity assessment between a concave portion and the ligand | Subscription | https://doi.org/10.1021/ci700352q |
| 118 | IsoMIF | 975 | 3.2983 | Allows to identify binding site molecular interaction field (MIF) similarities between pairs of structures | Free | http://biophys.umontreal.ca/nrg/resources.html |
| 119 | LigDockCSA | 975 | 3.2983 | Combines a highly efficient search method with a scoring function based on the autodock energy function with a piecewise linear potential (PLP) torsional energy | Subscription | https://doi.org/10.1002/jcc.21905 |
| 120 | GalaxyPepDock | 946 | 3.2851 | A web server for protein structure prediction, refinement, and related methods Protein-peptide docking based on interaction similarity | Free | http://galaxy.seoklab.org/pepdock |
| 121 | pyDockWEB | 924 | 3.2749 | A web server for the rigid- body docking forecast of protein–protein complex structures using an updated version of the pydock scoring algorithm | Free | https://life.bsc.es/pid/pydockweb |
| 122 | AnchorDock | 912 | 3.2693 | Automatically identifying anchoring spots on the protein surface | Subscription | https://doi.org/10.1016/j.str.2015.03.010 |
| 123 | ArgusLab | 883 | 3.2552 | A molecular modelling graphics and drug design program for Windows OS | Free | http://www.arguslab.com/arguslab.com/ArgusLab.html |
| 124 | idock | 882 | 3.2547 | A multithreaded virtual screening tool for flexible ligand docking for computational drug discovery | Subscription | https://GitHub.com/HongjianLi/idock |
| 125 | HybridDock | 854 | 3.2407 | Significantly improves the performance in both binding affinity and binding mode predictions, compared to the sole mdock program | Subscription | https://doi.org/10.1021/acs.jcim.5b00275 |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 126 | ParaDock | 840 | 3.2335 | Rigid protein flexible DNA Docking | Free | http://bioinfo3d.cs.tau.ac.il/ParaDock/php.php |
| 127 | WinDock | 810 | 3.2177 | Designed to help researchers perform structure-based drug discovery tasks | Subscription | https://doi.org/10.1002/jcc.20756 |
| 128 | OptiDock | 787 | 3.2052 | Involves choosing a representative subset of compounds | Subscription | https://doi.org/10.1021/cc034068x |
| 129 | BiGGER | 765 | 3.1929 | Predicts the mode of binding between two proteins | Free | https://doi.org/10.1002/(SICI)1097-0134(20000601)39:4<372::AID-PROT100>3.0.CO;2-Q |
| 130 | MTiOpenScreen | 759 | 3.1895 | Automated ligand docking into entire protein surface for up to 10 ligands allowing to detect druggable cavities using autodock 4.2 | Free | http://bioserv.rpbs.univ-paris-diderot.fr/services/MTiOpenScreen/ |
| 131 | HomDock | 752 | 3.1855 | Improves docking accuracy and efficiency | Subscription | http://www.chil2.de/HomDock.html |
| 132 | BDOCK | 745 | 3.1814 | An enzyme-inhibitor docking algorithm based on the degree of burial and conservation of surface residues | Free | www.biotec.tu-dresden.de /approximately bhuang/bdock |
| 133 | LiGendock | 730 | 3.1726 | Based on pharmacophore models of binding sites, including a non-enumerative docking calculation | Subscription | https://doi.org/10.1021/ci400079k |
| 134 | DockBench | 726 | 3.1702 | Handles seven docking software packages and offers the possibility to test up to seventeen different protocols | Free | doi: 10.3390/molecules20069977 |
| 135 | AUDocker LE | 673 | 3.1373 | Designed to develop a software tool as a front-end graphical interface | Free | DOI: 10.1186/1756-0500-4-445 |
| 136 | 3dRPC | 667 | 3.1334 | Developed as an automated method for predicting 3D structures of RNA-protein | Free | http://biophy.hust.edu.cn/3dRPC.html |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 137 | DarwinDock | 665 | 3.1321 | Isolates posing and scoring into separate stages to allow complete binding site sampling | Subscription | https://resolver.caltech.edu/CaltechTHESIS:06122017-230026717 |
| 138 | VLifeMDS | 648 | 3.1208 | An integrated platform for Computer Aided Drug Design (CADD) and molecular discovery | Subscription | https://www.vlifesciences.com/products/VLifeMDS/Product_VLifeMDS.php |
| 139 | pDOCK | 630 | 3.1086 | An experimental pygtk docking implementation | Free | https://pypi.org/project/pdock/ |
| 140 | CovalentDock Cloud | 621 | 3.1023 | Provides a simple user-friendly web interface to perform covalent docking | Free | http://docking.sce.ntu.edu.sg/. |
| 141 | SLIM (BSP-SLIM) SLIM21 | 613 | 3.0967 | A blind molecular docking method on low-resolution protein structures | Free | https://zhanglab.ccmb.med.umich.edu/BSP-SLIM/ |
| 142 | 3dRNAscore | 590 | 3.0801 | Developed as an automated method for predicting 3D structures of noncoding RNAs | Free | http://biophy.hust.edu.cn/3dRNAscore.html |
| 143 | FlexAID | 588 | 3.0786 | Can use small-molecules and peptides as ligands while uses proteins/nucleic acids as targets | Free | http://biophys.umontreal.ca/nrg/resources.html |
| 144 | LeDock | 588 | 3.0786 | Can be used for docking of ligands with protein target | Free | http://www.lephar.com/download.htm |
| 145 | MemDock | 585 | 3.0764 | Membrane protein docking algorithm | Free | http://bioinfo3d.cs.tau.ac.il/Memdock/php.php |
| 146 | TagDock | 584 | 3.0757 | Generates 3D models of oligomeric biomolecular complexes | Subscription | https://doi.org/10.1021/bi400158k |
| 147 | MDockPeP | 580 | 3.0727 | Docks the all-atom, flexible peptide onto the whole protein | Free | http://zougrouptoolkit.missouri.edu/mdockpep/ |
| 148 | ASPDock | 578 | 3.0712 | Atomic Solvation Parameters (ASP) model which is used for calculating the | Subscription | http://biophy.hust.edu.cn/ASPDOCK.html |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
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| | | | | binding free energy of protein complexes | | |
| 149 | PythDock | 566 | 3.0621 | Uses Python programming language with a simple scoring function and a population-based search engine | Subscription | https://doi.org/10.1007/s12272-011-0906-5 |
| 150 | HDOCK | 541 | 3.0425 | Predicts the binding complexes between two molecules like proteins and nucleic acids by using a hybrid docking strategy | Free | http://hdock.phys.hust.edu.cn/ |
| 151 | iGEMDOCK | 536 | 3.0384 | Can enrich the hit rate and provide biological insights by deriving the pharmacological interactions from screening compounds | Free | http://gemdock.life.nctu.edu.tw/dock/igemdock.php |
| 152 | DockRank | 528 | 3.0319 | Improves the scoring of docked poses, outperforms several energy-based scoring functions, and prioritizing ligands according to their affinity | Subscription | https://pubmed.ncbi.nlm.nih.gov/23873600/ |
| 153 | ROSIE (Rosetta Online) | 524 | 3.0286 | Provides the 3D structure prediction and high-resolution design of natural and non-natural polymers | Free | https://rosie.rosettacommons.org/ |
| 154 | ISE-Dock | 492 | 3.0012 | Eliminates values that consistently lead to the worst results, thus optimizing the search for docking poses | Subscription | https://pubmed.ncbi.nlm.nih.gov/18058908/ |
| 155 | NRGsuite | 490 | 2.9995 | Gives access to powerful docking simulations that can be used in structure-guided drug design as well as an educational tool | Free | http://biophys.umontreal.ca/nrg/resources.html |
| 156 | evERdock | 488 | 2.9977 | Calculates binding free energy relaying on molecular dynamics (MD) simulations | Subscription | https://doi.org/10.1063/1.5019864 |
| 157 | LeWater | 474 | 2.9850 | Filter docking poses and/or integrated into a scoring function to improve the accuracy of predicted binding affinity | Free | http://www.lephar.com/download.htm |
| 158 | LibDock | 472 | 2.9832 | Enable a safe and efficient loading and unloading while reducing downtime to a minimum | Free | https://www.bioz.com/result/libdock/product/Accelrys |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 159 | bhDock | 463 | 2.9748 | Uses two-step algorithm. First, low-resolution binding sites. Second, molecular dynamics | Free | DOI: 10.1002/jcc.21394 |
| 160 | PLANTS | 462 | 2.9739 | PLANTS (Protein-Ligand ANT System), which is based on ant colony optimization | Subscription | https://doi.org/10.1021/ci800298z |
| 161 | VLifeDock | 460 | 2.9720 | Explores binding mode of ligand over a grid | Subscription | https://www.vlifesciences.com/products/Functional_products/VLifeDock.php |
| 162 | HiPCDock | 432 | 2.9447 | High-performance computing-based molecular docking scheme which is termed hipcdock | Subscription | https://pubmed.ncbi.nlm.nih.gov/19525200/ |
| 163 | eSimDock | 431 | 2.9437 | Employs non-linear machine learning-based scoring functions to improve the accuracy of ligand ranking | Subscription | https://pubmed.ncbi.nlm.nih.gov/24171431/ |
| 164 | DockingApp | 400 | 2.9113 | Explores the behavior of small molecules in the binding site of a target protein | Free | https://doi.org/10.1007/s10822-016-0006-1 |
| 165 | DockDE | 387 | 2.8970 | Showed remarkable performance in terms of convergence speed and robustness regarding the found solution | Subscription | https://link.springer.com/article/10.1023/A:1008202821328 |
| 166 | YUCCA | 352 | 2.8558 | A new algorithm for rigid protein–small-molecule docking | Subscription | https://doi.org/10.1002/cbdv.200590123 |
| 167 | RPDOCK | 348 | 2.8508 | A docking procedure specific to RNA-protein complexes | Subscription | https://www.nature.com/articles/srep01887 |
| 168 | ADAM | 348 | 2.8508 | Predicts a stable binding mode to target flexible ligand molecule macromolecule | Subscription | http://adam.vbi.vt.edu |
| 169 | QSAR-Co | 346 | 2.8483 | Setup classification-based QSAR models that allow mining the response data coming from multiple conditions | Free | https://sites.google.com/view/qsar-co |
| 170 | SymmRef | 315 | 2.8076 | Flexible backbone and side-chain refinement and re-scoring of symmetric rigid-body | Free | http://bioinfo3d.cs.tau.ac.il/SymmRef/php.php |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
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| 171 | DockQ | 310 | 2.8006 | A continuous protein-protein docking model quality measure | Free | http://github.com/bjornwallner/DockQ/ |
| 172 | HSYMDOCK | 280 | 2.7564 | Symmetric protein docking for oligomers with Cn or Dn symmetry from the structure or sequence of a subunit molecule | Free | http://huanglab.phys.hust.edu.cn/hsymdock/ |
| 173 | MEGADOCK | 256 | 2.7175 | A structural bioinformatics software for FFT-grid-based protein-protein docking that takes advantage of CUDA architecture of NVIDIA graphics processing units (GPUs) and multiple computation nodes | Free | http://www.bi.cs.titech.ac.jp/megadock |
| 174 | Molegro | 242 | 2.6931 | Shown to outperform other docking programs with regard to identification of correct binding modes | Free | http://molexus.io/molegro-molecular-viewer/ |
| 175 | LightDock | 240 | 2.6895 | Optimizes the generated docking poses towards those energetically more favourable at every simulation step | Free | https://github.com/brianjimenez/lightdock |
| 176 | MEGADOCK-GPU | 232 | 2.6747 | A fast, improved, protein-protein docking prediction by introducing a simple hydrophobic interaction model | Free | http://www.bi.cs.titech.ac.jp/megadock/gpu/ |
| 177 | GetCleft | 228 | 2.6672 | Built-in and gives the possibility to refine and measure the volume of cavities | Free | http://biophys.umontreal.ca/nrg/resources.html |
| 178 | Snapdock | 224 | 2.6595 | Employs a Geometric Hashing-based structural alignment scheme to align the target proteins to the interfaces of non-redundant protein–protein interface libraries | Subscription | https://doi.org/10.1093/bioinformatics/btx233 |
| 179 | ProQDock | 219 | 2.6497 | Uses support vector machines trained to predict the quality of protein docking models using features that can be calculated from the docking model itself | Free | http://bioinfo.ifm.liu.se/ProQDock |
| 180 | Ligin | 193 | 2.5948 | Uses surface complementarity approach for predicting the structure of ligand-receptor complex | Subscription | https://doi.org/10.1002/(SICI)1097-0134(1997)1+<210::AID-PROT28>3.0.CO;2-Q |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 181 | 2dRNA | 182 | 2.5693 | Predicts RNA secondary structure | Free | http://biophy.hust.edu.cn/2dRNA/download |
| 182 | DockTrina | 177 | 2.5572 | A protein docking technique for demonstrating the 3D structures of nonsymmetrical triangular trimers | Free | https://team.inria.fr/nano-d/software/docktrina/ |
| 183 | FITTED | 175 | 2.5523 | Can deal with both the flexibility of macromolecules (side chains and main chains) and the presence of bridging water molecules | Free | http://mgltools.scripps.edu/documentation/links/fitted |
| 184 | DockThor | 158 | 2.5079 | Performs pose prediction on redocking studies | Free | https://www.dockthor.lncc.br/ |
| 185 | HYBRID | 156 | 2.5024 | The HYBRID program uses a modified version of FRED's algorithm that uses both ligand- and structure-based information to dock molecules | Subscription | https://www.eyesopen.com/oedocking-tk |
| 186 | PATIDOCK | 154 | 2.4968 | Relies solely on the 3D structure of the individual components and the experimentally derived Residual Dipolar Couplings (RDCs) for the complex | Subscription | https://doi.org/10.1021/ja100447p |
| 187 | TCRFlexDock | 147 | 2.4766 | Produces relatively accurate docking models (average interface RMSDs less than 2 A° from bound) | Free | http://www.cbs.dtu.dk/services/TCRpMHCmodels/index.php |
| 188 | mtsslDock<br>mtsslSuite<br>mtsslTrilaterate<br>mtsslWizard | 138 | 2.4491 | Enables the user to dock two macromolecules based on a set of experimental PELDOR distances | Subscription | http://www.mtsslsuite.isb.ukbonn.de/ |
| 189 | Schrödinger | 133 | 2.4331 | Delivers actual creditable and high achievement computational dependent technology to solution in life science and other applied science research | Free | https://www.schrodinger.com/freemaestro |
| 190 | SnugDock | 95 | 2.2870 | Predicts antibody-antigen complexes through optimization of antibody degrees of freedom relevant to binding | Subscription | https://www.rosettacommons.org/docs/latest/application_documentation/antibody/snugdock |
| 191 | ScoreDock | 82 | 2.2231 | Improves the docking accuracy and was shown to be reliable in docking quality assessment | Subscription | DOI: 10.1023/a:1011188704521 |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 192 | DockAFM | 70 | 2.1544 | Establishes a link between topographic images from AFM and molecular dynamics of single proteins | Free | http://biodev.cea.fr/dockafm/ |
| 193 | hint! | 61 | 2.0946 | An empirical molecular modelling system with new methods for de novo drug design and protein or nucleic acid structural analysis | Subscription | https://doi.org/10.1007/BF00135313 |
| 194 | S3DB | 44 | 1.9527 | A database of manually curated target and ligand structures | Free | http://www.swissdock.ch/ |
| 195 | SCIGRESS | 41 | 1.9220 | Computational chemistry integrated platform SCIGRESS | Subscription | https://doi.org/10.11546/cicsj.26.122 |
| 196 | LeFrag | 39 | 1.9003 | Automatically decompose all small molecules in a library into fragments | Free | http://www.lephar.com/download.htm |
| 197 | iMOLSDOCK | 36 | 1.8656 | Uses mutually orthogonal Latin squares (MOLS) to sample the conformation and the docking pose of the ligand and also the flexible residues of the receptor protein | Subscription | https://doi.org/10.1016/j.jmgm.2017.03.008 |
| 198 | molecularforecaster | 35 | 1.8533 | Used for drug discovery, metabolism prediction, combinatorial chemistry, and asymmetric catalyst design | Free | https://www.molecularforecaster.com/ |
| 199 | MpSDock MpSDockZn | 35 | 1.8533 | A metalloprotein-specific docking program, which runs on a scheme similar to consensus scoring consisting | Subscription | http://www.lilab-ecust.cn/home/resource/14.html |
| 200 | Hammerhead | 31 | 1.8006 | Fast, fully automated docking of flexible ligands to protein binding sites | Subscription | doi:10.1016/s1074-5521(96)90093-9 |
| 201 | UDock | 31 | 1.8006 | Interactive protein docking system, intended for both naive and experienced users | Free | http://udock.fr |
| 202 | MEGADOCK-Web | 29 | 1.7717 | A database of protein-protein interactions (ppis) predicted by an FFT-grid-based protein-protein docking software, MEGADOCK | Free | http://www.bi.cs.titech.ac.jp/megadock-web/ |

| No. | Software | No. of citations to published studies | Score | Features | Accessibility | Website |
|---|---|---|---|---|---|---|
| 203 | DockScore | 18 | 1.5645 | Can be utilized to rank protein-protein docked poses | Free | http://caps.ncbs.res.in/dockscore/ |
| 204 | DockAnalyse | 18 | 1.5645 | Analysis of protein-protein interactions | Free | http://bioinf.uab.es/rker/DockAnalyse/DockAnalyse.zip |
| 205 | mApfDock | 13 | 1.4232 | The docking of candidates to atomic property fields derived by co-crystallized ligands | Subscription | https://doi.org/10.4155/fmc.14.113 |
| 206 | mPockDock | 13 | 1.4232 | Reduces the rate of false-negatives in activity prediction by docking flexible 3D models of compounds include multi-conformational docking | Subscription | https://doi.org/10.4155/fmc.14.113 |
| 207 | FlexGAsDock | 13 | 1.4232 | Based on the hierarchical docking strategy | Subscription | http://en.cnki.com.cn/Article_en/CJFDTOTAL-DLLG200802024.htm |
| 208 | ELMDOCK ELMPATIDOCK | 12 | 1.3884 | Relies solely on the 3D structure of the individual components and the overall rotational diffusion tensor of the complex | Subscription | https://onlinelibrary.wiley.com/doi/abs/10.1002/prot.23053 |
| 209 | BDT-AutoDock | 3 | 0.7864 | Using receptor flexibility during docking using a large library of ligands onto one or more receptors without defining one a priori ligand-binding site on them | Free | http://www.quimica.urv.cat/~pujadas/BDT/ |
| 210 | Discovery Studio | 0 | 0.0000 | An interactive package with a broad variety of features for modelling and simulation | Subscription | https://www.bu.edu/tech/support/research/software-and-programming/software-and-applications/rcs-software-packages/discovery-studio/ |
| 211 | 3dRNA-RFSP | 0 | 0.0000 | Constructs a statistical potential for 3D RNA structure evaluation by using an iterative method that circumvents the reference state problem | Free | http://biophy.hust.edu.cn/3dRNA-RFSP.html |