Supplementary information for:

Macromolecular modeling and design in Rosetta: new methods and frameworks

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The main documentation page can be found at https://www.rosettacommons.org/docs/latest/Home.
Tutorials, demos and protocol captures are documented at https://www.rosettacommons.org/demos/latest/Home.

Method	Developer(s)	Lab developed	Documentation	Protocol capture / demo
Protein structure prediction				
fragment picker[1]	Dominik Gront	(formerly David Baker), Dominik Gront	https://www.rosettacommons.org/docs/latest/application_documentation/utilities/app-fragment-picker	Rosetta/demos/public/fragment_picking
RosettaCM[2]	Yifan Song	(formerly David Baker)	https://www.rosettacommons.org/docs/latest/application_documentation/structure_prediction/RosettaCM	Rosetta/demos/public/homology_modeling_threading_basic Supp to [2]
iterative hybridize[3,4]	Sergey Ovchinnikov, Hahnbeom Park	David Baker, Sergey Ovchinnikov	https://www.rosettacommons.org/docs/latest/IterativeHybridize	
RosettaSurface[5–7]	Michael Pacella	Jeffrey Gray	https://www.rosettacommons.org/docs/latest/application_documentation/docking/surface-docking	Rosetta/demos/public/surface_docking_cpp Supp to [5]
Protein-protein docking				
RosettaDock4.0[8]	Nick Marze, Shourya Roy Burman	Jeffrey Gray	https://www.rosettacommons.org/docs/latest/application_documentation/docking/docking-protocol	Rosetta/demos/tutorials/Protein-Protein-Docking https://www.rosettacommons.org/demos/latest/tutorials/Protein-Protein-Docking/Protein-Protein-Docking
Rosetta SymDock2[9]	Shourya Roy Burman	(formerly Ingemar André), Jeffrey Gray	https://www.rosettacommons.org/docs/latest/SymDockProtocol	
Small molecule ligand docking				
RosettaLigand[10–12]	Sam DeLuca, Darwin Fu, Shannon Smith, Rocco Moretti	Jens Meiler	https://www.rosettacommons.org/demos/latest/tutorials/ligand_docking/ligand_docking_tutorial	Rosetta/demos/tutorials/ligand_docking
RosettaLigandEnsemble[13]	Darwin Fu, Rocco Moretti	Jens Meiler	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/HighResEnsembleMover	Rosetta/demos/protocol_capture/rosettaligand_ensemble
pocket optimization[14,15]	David Johnson	John Karanicolas	https://www.rosettacommons.org/docs/latest/application_documentation/utilities/pocket-relax	Supp to [14,15]

			https://www.rosettacommons.org/docs/latest/application_documentation/analysis/pocket-measure	
DARC[16–18]	Ragul Gowthaman, Karen Khar	John Karanicolas	https://www.rosettacommons.org/docs/latest/application_documentation/docking/DARC	Rosetta/demos/public/darc Supp to [16–18]
Protein design				
SEWING[19,20]	Tim Jacobs, Sharon Guffy, Frank Teets	Brian Kuhlmann	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/composite_protocols/sewing/SEWING	
RosettaRemodel[21]	Possu Huang	(formerly David Baker), Possu Huang	https://www.rosettacommons.org/docs/latest/application_documentation/design/rosettaremodel	
LooDo[22]	Kristin Blacklock	Sagar Khare	https://www.rosettacommons.org/demos/latest/protocol_capture/loodo/README	Rosetta/demos/protocol_capture/loodo
RECON[23]	Alex Sevy, Marion Sauer	Jens Meiler	https://www.rosettacommons.org/docs/latest/application_documentation/RECON-multistate-design	https://github.com/sevya/msd_analysis_scripts https://github.com/sevya/parallelized_RECON_protocol_capture Supp to [23]
curved β-sheet design[24]	Enrique Marcos, Benjamin Basanta	David Baker	https://www.rosettacommons.org/docs/latest/application_documentation/design/curvedsheetdesign https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/xsd/filter_StrandCurvatureByLevels_type https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/xsd/filter_HelixBendFilter_type	https://github.com/basantab/DeNovoCurvedSheetDesign
biased forward folding[24]	Daniel Silva, Enrique Marcos	David Baker	https://www.rosettacommons.org/docs/latest/Biased-forward-folding https://github.com/emarcos/biased_forward_folding/	
fold_from_loops[25]	Bruno Correia	formerly David Baker	replaced by FunFolDes below	
FunFolDes[26]	Jaume Bonet, Andreas Scheck	Bruno Correia	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/composite_protocols/fold_from_loops/FunFolDes	https://github.com/lpdi-epfl/FunFolDesData https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/composite_protocols/fold_from_loops/RunningFunFolDes
Protein interface design				
FlexDDG[27]	Kyle Barlow, Shane O'Connor	Tanja Kortemme	https://github.com/Kortemme-Lab/flex_ddG_tutorial	https://github.com/Kortemme-Lab/flex_ddG_tutorial
Coupled Moves[28]	Noah Ollikainen, Rene M. de Jong	Tanja Kortemme & DSM Biotechnology Center	https://www.rosettacommons.org/docs/latest/coupled-moves	Rosetta/main/tests/integration/tests/coupled_moves

Parametric design[29,30]	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/MakeBundleMover https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/BundleGridSamplerMover https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/PerturbBundleMover https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Filters/filter_pages/BundleReporterFilter	Supp to [29]
Peptides and peptidomimetics				
FlexPepDock[31,32]	Barak Raveh, Nir London, Lior Zimmerman	Ora Schueler-Furman	https://www.rosettacommons.org/docs/latest/application_documentation/docking/flex-pep-dock	Rosetta/demos/public/flex_pep_dock_abinitio Rosetta/demos/public/abinitio_fold_and_dock_of_peptides_using_flexpepdock Rosetta/demos/public/global_dock_ssrA_peptide_against_sspB Rosetta/demos/public/peptide_specificity_using_FlexPepBind Rosetta/demos/public/refinement_of_protein_peptide_complex_using_FlexPepDock Supp to [32]
PIPER-FlexPepDock[33]	Nawsad Alam, Alisa Khramushin	Ora Schueler-Furman	https://www.rosettacommons.org/docs/latest/application_documentation/docking/flex-pep-dock	
PeptiDerive[34]	Yuval Sedan, Orly Marcu	Ora Schueler-Furman	https://www.rosettacommons.org/docs/latest/application_documentation/analysis/PeptiDerive	Rosetta/main/tests/integration/tests/peptiderive
simple_cycpep_predict[29,35,36]	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/structure_prediction/simple_cycpep_predict	Rosetta/main/tests/integration/tests/simple_cycpep_predict and many related demos adjacent, Supp to [35,36]
MFPred[37]	Aliza Rubenstein	Sagar Khare	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/analysis/GenMeanFieldMover	Rosetta/main/tests/integration/tests/mf_fixbb_sc Rosetta/main/tests/integration/tests/mf_flexbb_sc
Loop modeling				
NGK (next-generation KIC) [38]	Amelie Stein	Tanja Kortemme	https://www.rosettacommons.org/docs/latest/application_documentation/structure_prediction/loop_modeling/next-generation-KIC https://www.rosettacommons.org/docs/latest/application_documentation/structure_prediction/loop_modeling/loopmodel-kinematic (for -vicinity_sampling)	Rosetta/demos/tutorials/loop_modeling
GenKIC (generalized KIC) [35]	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/composite_protocols/generalized_kic/GeneralizedKIC	https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_1, https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_2,

			https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/GeneralizedKICMover https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/composite_protocols/generalized_kic/GeneralizedKICperturber https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/composite_protocols/generalized_kic/GeneralizedKICfilter https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/composite_protocols/generalized_kic/GeneralizedKICselector https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_1 https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_2 https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_3 https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_4	https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_3, https://www.rosettacommons.org/demos/latest/tutorials/GeneralizedKIC/generalized_kinematic_closure_4 Supp to [29,35]
LoopHashKIC	Xingjie Pan	Tanja Kortemme	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/LoopModelerMover	
Consensus_Loop_Design[24,39]	Enrique Marcos, Tom Linsky	David Baker	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/TaskOperations/taskoperations_pages/ConsensusLoopDesignOperation	Rosetta/main/tests/integration/tests/ConsensusLoopDesign
Modeling of antibodies and proteins in the immune system				
RosettaAntibody[40–43]	Jeliazko Jeliazkov, Nick Marze, Brian Weitzner, Jared Adolf-Bryfogle, Sergey Lyskov, Daisuke Kuroda	Jeffrey Gray	https://www.rosettacommons.org/docs/latest/application_documentation/antibody/antibody-protocol	Rosetta/main/tests/integration/tests/antibody_cc
AbPredict[44,45]	Christoffer Norn, Gideon Lapidoth	Sarel Fleishman	https://www.rosettacommons.org/docs/latest/application_documentation/structure_prediction/AbPredict2	https://www.rosettacommons.org/demos/latest/tutorials/AbPredict/AbPredict
RosettaMHC[46]	Santrupti Nerli	Nik Sgourakis	https://github.com/snerligit/mhc-pep-threader	https://github.com/snerligit/mhc-pep-threader/tree/master/examples
TCRModel[47]	Ragul Gowthaman	Brian Pierce	https://www.rosettacommons.org/docs/latest/application_documentation/structure_prediction/TCRmodel	Rosetta/main/tests/integration/tests/tcrmodel
SnugDock[48]	Jeliazko Jeliazkov, Nick Marze, Brian Weitzner	Jeffrey Gray	https://www.rosettacommons.org/docs/latest/application_documentation/antibody/snugdock	Rosetta/main/tests/integration/tests/SnugDock

RAbD[49] (Rosetta AntibodyDesign)	Jared Adolf-Bryfogle, Brian Weitzner	Bill Schief, Roland Dunbrack	https://www.rosettacommons.org/docs/latest/application_documentation/antibody/RosettaAntibodyDesign	Rosetta/main/tests/integration/tests/antibody_designer
Epitope removal[50,51]	Indigo King	David Baker, Cyrus Biotechnology	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/GreedyOptMutationMover https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/xsd/filter_NMerSVMEnergy_type	
AbDesign[52,53]	Gideon Lapidoth	Sarel Fleishman	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/SpliceOut https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/SpliceOutAntibody https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/SpliceInAntibody https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/SpliceIn https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/SpliceOutTail https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/SpliceInTail	Rosetta/main/tests/integration/tests/splice_out_H1_H2_longer Rosetta/main/tests/integration/tests/splice_out_H1_H2_same Rosetta/main/tests/integration/tests/splice_out_H1_H2_shorter Rosetta/main/tests/integration/tests/splice_out_H3_longer Rosetta/main/tests/integration/tests/splice_out_H3_same Rosetta/main/tests/integration/tests/splice_out_H3_shorter Rosetta/main/tests/integration/tests/splice_out_L1_L2_longer Rosetta/main/tests/integration/tests/splice_out_L1_L2_same Rosetta/main/tests/integration/tests/splice_out_L1_L2_shorter Rosetta/main/tests/integration/tests/splice_out_L3_longer Rosetta/main/tests/integration/tests/splice_out_L3_same Rosetta/main/tests/integration/tests/splice_out_L3_shorter
Modeling with experimental data				
cryoEM *de novo*[54]	Ray Wang	Frank DiMaio, David Baker	https://dimaiolab.ipd.uw.edu/software/	https://dimaiolab.ipd.uw.edu/software/
cryoEM: RosettaES[55]	Brandon Frenz	Frank DiMaio	https://dimaiolab.ipd.uw.edu/software/	https://dimaiolab.ipd.uw.edu/software/
cryoEM: iterative refinement[56,57]	Frank DiMaio, Yifan Song	(formerly David Baker) Frank DiMaio	https://dimaiolab.ipd.uw.edu/software/	https://dimaiolab.ipd.uw.edu/software/
cryoEM: automated refinement[58]	Ray Wang	Frank DiMaio	https://dimaiolab.ipd.uw.edu/software/	https://dimaiolab.ipd.uw.edu/software/
NMR: CS-Rosetta[59]	(formerly Oliver Lange) Santrupti Nerli	Nik Sgourakis	https://csrosetta.chemistry.ucsc.edu/ https://github.com/RosettaCommons/csrosetta3	https://csrosetta.chemistry.ucsc.edu/ https://github.com/RosettaCommons/csrosetta3
NMR: PCS-Rosetta, GPS-Rosetta[60,61]	Christophe Schmitz, Kala Bharath Pilla	Thomas Huber	https://www.rosettacommons.org/demos/latest/protocol_capture/gps_rosetta_pcs_nmr_constraints/README https://github.com/kalabharath/pcs_driven_iterative_resampling	Rosetta/demos/public/gps_rosetta_pcs_nmr_constraints https://github.com/kalabharath/pcs_driven_iterative_resampling/tree/master/sample_run
RosettaNMR framework[62]: using RDC/PRE/PCS/NOE/CS for ab initio, protein-protein docking, ligand	Georg Kuenze, Julia Koehler Leman	Jens Meiler (Richard Bonneau)	https://www.rosettacommons.org/docs/latest/application_documentation/RosettaNMR-with-Paramagnetic-Restraints	Rosetta/demos/public/rosettanmr_w_paramagnetic_restraints Supp to [62]

docking, symmetric assembly				
mass-spec: HRF hydroxyl radical footprinting[63,64]	Melanie Aprahamian	Steffen Lindert	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/ms_expdata_score_terms	Supp to [63]
mass-spec: PyTXMS[65]	Hamed Khakzad	Lars Malmstroem	https://www.rosettacommons.org/docs/latest/scripting_documentation/PyRosetta/PyTXMS	https://zenodo.org/record/1438111#.XIQUoRNKhBw
DNA and RNA				
RNA applications		Rhiju Das	https://www.rosettacommons.org/docs/latest/application_documentation/rna/rna-applications	
SWA (stepwise assembly) [66,67]	Rhiju Das	Rhiju Das	https://www.rosettacommons.org/docs/latest/application_documentation/stepwise/stepwise_assembly/swa-rna-loop https://www.rosettacommons.org/docs/latest/application_documentation/stepwise/stepwise_assembly/swa-protein-long-loop https://www.rosettacommons.org/docs/latest/application_documentation/stepwise/stepwise_assembly/swa-protein-main	Rosetta/demos/public/swa_rna_loop Rosetta/demos/public/swa_protein_long_loop Rosetta/demos/public/swa_protein_main
SWM (stepwise Monte-Carlo) [68]	Caleb Geniesse Andrew Watkins	Rhiju Das	https://www.rosettacommons.org/docs/latest/application_documentation/stepwise/stepwise_monte_carlo/stepwise	Rosetta/demos/public/stepwise_enumerative_assembly Rosetta/demos/public/stepwise_monte_carlo_mini_protein Rosetta/demos/public/stepwise_monte_carlo_protein_loop Rosetta/demos/public/stepwise_monte_carlo_rna_loop Rosetta/demos/public/stepwise_monte_carlo_rna_multiloop
FARFAR (fragment assembly medium resolution structure prediction) [69–71]	Andrew Watkins Kalli Kappel	Rhiju Das	https://www.rosettacommons.org/docs/latest/application_documentation/rna/rna-denovo https://www.rosettacommons.org/docs/latest/application_documentation/rna/rnp-modeling	Rosetta/demos/public/rnp_ddg Rosetta/demos/public/rnp_structure_prediction Rosetta/demos/public/rna_denovo
ERRASER (refinement into EM density maps) [72,73]	Fang-Chieh Chou	Rhiju Das	https://www.rosettacommons.org/docs/latest/application_documentation/rna/erraser	https://www.rosettacommons.org/demos/latest/public/erraser/README
CS-Rosetta-RNA (modeling with NMR data) [74]	Parin Sripakdeevong	Rhiju Das	https://www.rosettacommons.org/docs/latest/application_documentation/rna/CS-Rosetta-RNA	Rosetta/demos/public/cs_rosetta_rna
RECCES (Reweighting of Energy-function Collection with Conformational Ensemble Sampling)	Fang-Chieh Chou	Rhiju Das	https://www.rosettacommons.org/demos/latest/public/recces/README	Rosetta/demos/public/recces

DRRAFTER (*de novo* modeling of protein-RNA complexes into EM densities) [75]	Kalli Kappel	Rhiju Das	https://www.rosettacommons.org/docs/latest/application_documentation/rna/drrafter	https://www.rosettacommons.org/demos/latest/public/drrafter/README
Membrane proteins				
RosettaMP framework[76]: mp_ddg mp_dock mp_relax mp_symdock	Julia Koehler Leman, Rebecca Alford	Jeffrey Gray	https://www.rosettacommons.org/docs/latest/application_documentation/Application%20Documentation#Membrane-Proteins	Rosetta/demos/public/mp_ddg Rosetta/demos/public/mp_dock Rosetta/demos/public/mp_relax Rosetta/demos/public/mp_symdock Supp to [76]
RosettaMP toolkit[77]: mp_score mp_transform mp_mutate_relax helix_from_sequence	Julia Koehler Leman	Jeffrey Gray	https://www.rosettacommons.org/docs/latest/application_documentation/Application%20Documentation#Membrane-Proteins	Rosetta/main/tests/integration/tests/mp_transform Rosetta/demos/protocol_capture/helix_from_sequence Supp to [77]
mp_lipid_acc[78]	Julia Koehler Leman	Richard Bonneau	https://www.rosettacommons.org/docs/latest/application_documentation/Application%20Documentation#Membrane-Proteins	Supp to [78]
mp_domain_assembly[79]	Julia Koehler Leman	Richard Bonneau	https://www.rosettacommons.org/docs/latest/application_documentation/Application%20Documentation#Membrane-Proteins	Rosetta/main/tests/integration/tests/mp_domain_assembly Rosetta/main/tests/integration/tests/mp_domain_assembly_FtsQ Supp to [79]
RosettaCM for membrane proteins[80]	Brian Bender	Jens Meiler	https://www.rosettacommons.org/docs/latest/application_documentation/Application%20Documentation#Membrane-Proteins	Supp to [80]
Carbohydrates				
RosettaCarbohydrate framework[81,82]	Jason W. Labonte, Jared Adolf-Bryfogle	Jeffrey Gray (Bill Schief)	https://www.rosettacommons.org/docs/latest/application_documentation/carbohydrates/WorkingWithGlycans	
Scorefunction				
REF2015 scorefunction[83,84]	Hahnbeom Park, Frank DiMaio	Frank DiMaio, David Baker	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/score-types	
cartesian_ddG[83]	Brandon Frenz, Phil Bradley, Yuan Liu	Frank DiMaio, Phil Bradley	https://www.rosettacommons.org/docs/latest/cartesian-ddG	
HBNet[85,86]	Scott Boyken, Jack Maguire	David Baker, Brian Kuhlman	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/HBNetMover	Rosetta/main/tests/integration/tests/hbnet
HBNetEnergy[85]	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/HBNetEnergy	Rosetta/main/tests/integration/tests/hbnet_energy

				Rosetta/main/tests/integration/tests/hbnet_energy_rosettascripts_linear Rosetta/main/tests/integration/tests/hbnet_energy_symm
AACompositionEnergy	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/AACompositionEnergy	Supp to [36,87]
AARepeatEnergy	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/Repeat-stretch-energy	
VoidsPenaltyEnergy	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/VoidsPenaltyEnergy	
NetChargeEnergy	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/NetChargeEnergy	
BuriedUnsatPenalty	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/rosetta_basics/scoring/BuriedUnsatPenalty	
User interfaces				
PyRosetta[88,89]	Sergey Lyskov, Sidharta Chaudhury, Brian Weitzner, Jason Labonte, Jared Adolf-Bryfogle, Rebecca Alford	Jeffrey Gray	http://www.pyrosetta.org	
RosettaScripts[80,90]	Sarel Fleishman	(formerly David Baker) Sarel Fleishman	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/RosettaScripts	https://www.rosettacommons.org/demos/latest/tutorials/scripting_with_rosettascripts/scripting_with_rosettascripts https://www.rosettacommons.org/demos/latest/tutorials/advanced_scripting_with_rosettascripts/advanced_scripting_with_rosettascripts
InteractiveRosetta[91]	Benjamin Walcott	Chris Bystroff	www.github.com/BystroffLab/InteractiveROSETTA (https://github.com/BystroffLab/InteractiveROSETTA/tree/master/InteractiveROSETTA/help)	
Foldit Standalone[92–95]	Seth Cooper, Firas Khatib	(formerly David Baker) Seth Cooper, Firas Khatib	http://fold.it/standalone	
ROSIE server[96,97]	Sergey Lyskov, Rocco Moretti, Shane O'Connor	Jeffrey Gray	http://rosie.rosettacommons.org/documentation	
Miscellaneous				
Metalloproteins[98,99]	Vikram Mulligan	(formerly David Baker) Richard Bonneau	https://www.rosettacommons.org/docs/latest/rosetta_basics/non_protein_residues/Metals	[99]

			https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/movers_pages/SetupMetalsMover https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/constraint_generators/MetalContactsConstraintGenerator	
Waters[100]	Ryan Pavlovicz	Frank DiMaio	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/Movers/WaterBoxMover	
SimpleMetrics	Jared Adolf-Bryfogle	Bill Schief	https://www.rosettacommons.org/docs/latest/scripting_documentation/RosettaScripts/SimpleMetrics/SimpleMetrics	
AmbRose	Kristin Blacklock, Aliza Rubenstein, Michael Szegedy	Sagar Khare	https://www.rosettacommons.org/docs/latest/AmbRose	Rosetta/tools/AmbRose
RosettaRC	Jared Adolf-Bryfogle	William Schief	https://www.rosettacommons.org/docs/latest/rosetta_basics/running-rosetta-with-options#common-options-and-default-user-configuration	

References:

1. Gront, D., Kulp, D. W., Vernon, R. M., Strauss, C. E. M. & Baker, D. Generalized Fragment Picking in Rosetta: Design, Protocols and Applications. *PLoS One* **6,** e23294 (2011).
2. Song, Y., Dimaio, F., Wang, R. Y.-R. R., Kim, D. E., Miles, C., Brunette, T., Thompson, J. & Baker, D. High-resolution comparative modeling with RosettaCM. *Structure* **21,** 1735–1742 (2013).
3. Ovchinnikov, S., Park, H., Varghese, N., Huang, P.-S., Pavlopoulos, G. A., Kim, D. E., Kamisetty, H., Kyrpides, N. C. & Baker, D. Protein structure determination using metagenome sequence data. *Science (80-.).* **355,** 294–298 (2017).
4. Park, H., Ovchinnikov, S., Kim, D. E., Dimaio, F. & Baker, D. Protein homology model refinement by large-scale energy optimization. *Proc. Natl. Acad. Sci. U. S. A.* **115,** 3054–3059 (2018).
5. Pacella, M. S., Koo, D. C. E., Thottungal, R. A. & Gray, J. J. Using the RosettaSurface algorithm to predict protein structure at mineral surfaces. *Methods Enzymol.* **532,** 343–366 (2013).
6. Lubin, J. H., Pacella, M. S. & Gray, J. J. A Parametric Rosetta Energy Function Analysis with LK Peptides on SAM Surfaces. *Langmuir* **34,** 5279–5289 (2018).
7. Pacella, M. S. & Gray, J. J. A Benchmarking Study of Peptide–Biomineral Interactions. *Cryst. Growth Des.* **18,** 607–616 (2018).
8. Marze, N. A., Roy Burman, S. S., Sheffler, W. & Gray, J. J. Efficient flexible backbone protein–protein docking for challenging targets. *Bioinformatics* **34,** 3461–3469 (2018).
9. Roy Burman, S. S., Yovanno, R. A. & Gray, J. J. Flexible backbone assembly and refinement of symmetrical homomeric complexes. *bioRxiv* 409730 (2018). doi:10.1101/409730
10. Meiler, J. & Baker, D. RosettaLigand: protein-small molecule docking with full side-chain flexibility. *Proteins* **65,** 538–48 (2006).
11. DeLuca, S., Khar, K. & Meiler, J. Fully Flexible Docking of Medium Sized Ligand Libraries with RosettaLigand. *PLoS One* **10,** e0132508 (2015).
12. Davis, I. W. & Baker, D. RosettaLigand Docking with Full Ligand and Receptor Flexibility. *J. Mol. Biol.* **385,** 381–392 (2009).
13. Fu, D. Y. & Meiler, J. RosettaLigandEnsemble: A Small-Molecule Ensemble-Driven Docking Approach. *ACS Omega* **3,** 3655–3664 (2018).

14. Johnson, D. K. & Karanicolas, J. Druggable Protein Interaction Sites Are More Predisposed to Surface Pocket Formation than the Rest of the Protein Surface. *PLoS Comput. Biol.* **9,** e1002951 (2013).
15. Johnson, D. K. & Karanicolas, J. Selectivity by Small-Molecule Inhibitors of Protein Interactions Can Be Driven by Protein Surface Fluctuations. *PLOS Comput. Biol.* **11,** e1004081 (2015).
16. Gowthaman, R., Miller, S. A., Rogers, S., Khowsathit, J., Lan, L., Bai, N., Johnson, D. K., Liu, C., Xu, L., Anbanandam, A., Aubé, J., Roy, A. & Karanicolas, J. DARC: Mapping Surface Topography by Ray-Casting for Effective Virtual Screening at Protein Interaction Sites. *J. Med. Chem.* **59,** 4152–4170 (2016).
17. Khar, K. R., Goldschmidt, L. & Karanicolas, J. Fast Docking on Graphics Processing Units via Ray-Casting. *PLoS One* **8,** e70661 (2013).
18. Gowthaman, R., Lyskov, S. & Karanicolas, J. DARC 2.0: Improved Docking and Virtual Screening at Protein Interaction Sites. *PLoS One* **10,** e0131612 (2015).
19. Jacobs, T. M., Williams, B., Williams, T., Xu, X., Eletsky, A., Federizon, J. F., Szyperski, T. & Kuhlman, B. Design of structurally distinct proteins using strategies inspired by evolution. *Science* **352,** 687–90 (2016).
20. Guffy, S. L., Teets, F. D., Langlois, M. I. & Kuhlman, B. Protocols for Requirement-Driven Protein Design in the Rosetta Modeling Program. *J. Chem. Inf. Model.* **58,** 895–901 (2018).
21. Huang, P.-S., Ban, Y.-E. A., Richter, F., Andre, I., Vernon, R., Schief, W. R. & Baker, D. RosettaRemodel: A Generalized Framework for Flexible Backbone Protein Design. *PLoS One* **6,** e24109 (2011).
22. Blacklock, K. M., Yang, L., Mulligan, V. K. & Khare, S. D. A computational method for the design of nested proteins by loop-directed domain insertion. *Proteins Struct. Funct. Bioinforma.* **86,** 354–369 (2018).
23. Sevy, A. M., Jacobs, T. M., Crowe, J. E. & Meiler, J. Design of Protein Multi-specificity Using an Independent Sequence Search Reduces the Barrier to Low Energy Sequences. *PLoS Comput. Biol.* **11,** e1004300 (2015).
24. Marcos, E., Basanta, B., Chidyausiku, T. M., Tang, Y., Oberdorfer, G., Liu, G., Swapna, G. V. T., Guan, R., Silva, D.-A., Dou, J., Pereira, J. H., Xiao, R., Sankaran, B., Zwart, P. H., Montelione, G. T. & Baker, D. Principles for designing proteins with cavities formed by curved β sheets. *Science* **355,** 201–206 (2017).
25. Correia, B. E., Bates, J. T., Loomis, R. J., Baneyx, G., Carrico, C., Jardine, J. G., Rupert, P., Correnti, C., Kalyuzhniy, O., Vittal, V., Connell, M. J., Stevens, E., Schroeter, A., Chen, M., MacPherson, S., Serra, A. M., Adachi, Y., Holmes, M. A., Li, Y., Klevit, R. E., Graham, B. S., Wyatt, R. T., Baker, D., Strong, R. K., Crowe, J. E., Johnson, P. R. & Schief, W. R. Proof of principle for epitope-focused vaccine design. *Nature* **507,** 201–206 (2014).
26. Bonet, J., Wehrle, S., Schriever, K., Yang, C., Billet, A., Sesterhenn, F., Scheck, A., Sverrisson, F., Veselkova, B., Vollers, S., Lourman, R., Villard, M., Rosset, S., Krey, T. & Correia, B. E. Rosetta FunFolDes - A general framework for the computational design of functional proteins. *PLoS Comput. Biol.* **14,** e1006623 (2018).
27. Barlow, K. A., Ó Conchúir, S., Thompson, S., Suresh, P., Lucas, J. E., Heinonen, M. & Kortemme, T. Flex ddG: Rosetta Ensemble-Based Estimation of Changes in Protein-Protein Binding Affinity upon Mutation. *J. Phys. Chem. B* **122,** 5389–5399 (2018).
28. Ollikainen, N., de Jong, R. M. & Kortemme, T. Coupling Protein Side-Chain and Backbone Flexibility Improves the Re-design of Protein-Ligand Specificity. *PLOS Comput. Biol.* **11,** e1004335 (2015).
29. Dang, B., Wu, H., Mulligan, V. K., Mravic, M., Wu, Y., Lemmin, T., Ford, A., Silva, D.-A., Baker, D. & DeGrado, W. F. De novo design of covalently constrained mesosize protein scaffolds with unique tertiary structures. *Proc. Natl. Acad. Sci. U. S. A.* **114,** 10852–10857 (2017).
30. Lu, P., Min, D., DiMaio, F., Wei, K. Y., Vahey, M. D., Boyken, S. E., Chen, Z., Fallas, J. A., Ueda, G., Sheffler, W., Mulligan, V. K., Xu, W., Bowie, J. U. & Baker, D. Accurate computational design of multipass transmembrane proteins. *Science (80-.).* **359,** 1042–1046 (2018).
31. Raveh, B., London, N. & Schueler-Furman, O. Sub-angstrom modeling of complexes between flexible peptides and globular proteins. *Proteins* **78,** 2029–40 (2010).
32. Raveh, B., London, N., Zimmerman, L. & Schueler-Furman, O. Rosetta FlexPepDock ab-initio: Simultaneous Folding, Docking and Refinement of Peptides onto Their Receptors. *PLoS One* **6,** e18934 (2011).
33. Alam, N., Goldstein, O., Xia, B., Porter, K. A., Kozakov, D. & Schueler-Furman, O. High-resolution global peptide-protein docking using fragments-based PIPER-FlexPepDock. *PLoS Comput. Biol.* **13,** e1005905 (2017).

34. Sedan, Y., Marcu, O., Lyskov, S. & Schueler-Furman, O. Peptiderive server: derive peptide inhibitors from protein-protein interactions. *Nucleic Acids Res.* **44,** W536-41 (2016).
35. Bhardwaj, G., Mulligan, V. K., Bahl, C. D., Gilmore, J. M., Harvey, P. J., Cheneval, O., Buchko, G. W., Pulavarti, S. V. S. R. K., Kaas, Q., Eletsky, A., Huang, P.-S., Johnsen, W. A., Greisen, P. J., Rocklin, G. J., Song, Y., Linsky, T. W., Watkins, A., Rettie, S. A., Xu, X., Carter, L. P., Bonneau, R., Olson, J. M., Coutsias, E., Correnti, C. E., Szyperski, T., Craik, D. J. & Baker, D. Accurate de novo design of hyperstable constrained peptides. *Nature* **538,** 329–335 (2016).
36. Hosseinzadeh, P., Bhardwaj, G., Mulligan, V. K., Shortridge, M. D., Craven, T. W., Pardo-Avila, F., Rettie, S. A., Kim, D. E., Silva, D.-A., Ibrahim, Y. M., Webb, I. K., Cort, J. R., Adkins, J. N., Varani, G. & Baker, D. Comprehensive computational design of ordered peptide macrocycles. *Science (80-.).* **358,** 1461–1466 (2017).
37. Rubenstein, A. B., Pethe, M. A. & Khare, S. D. MFPred: Rapid and accurate prediction of protein-peptide recognition multispecificity using self-consistent mean field theory. *PLOS Comput. Biol.* **13,** e1005614 (2017).
38. Stein, A. & Kortemme, T. Improvements to robotics-inspired conformational sampling in rosetta. *PLoS One* **8,** e63090 (2013).
39. Marcos, E., Chidyausiku, T. M., McShan, A. C., Evangelidis, T., Nerli, S., Carter, L., Nivón, L. G., Davis, A., Oberdorfer, G., Tripsianes, K., Sgourakis, N. G. & Baker, D. De novo design of a non-local β-sheet protein with high stability and accuracy. *Nat. Struct. Mol. Biol.* **25,** 1028–1034 (2018).
40. Sircar, A., Kim, E. T. & Gray, J. J. RosettaAntibody: antibody variable region homology modeling server. *Nucleic Acids Res.* **37,** W474-479 (2009).
41. Weitzner, B. D., Kuroda, D., Marze, N., Xu, J. & Gray, J. J. Blind prediction performance of RosettaAntibody 3.0: Grafting, relaxation, kinematic loop modeling, and full CDR optimization. *Proteins Struct. Funct. Bioinforma.* **82,** 1611–1623 (2014).
42. Weitzner, B. D., Jeliazkov, J. R., Lyskov, S., Marze, N., Kuroda, D., Frick, R., Adolf-Bryfogle, J., Biswas, N., Dunbrack, R. L. & Gray, J. J. Modeling and docking of antibody structures with Rosetta. *Nat. Protoc.* **12,** 401–416 (2017).
43. Sivasubramanian, A., Sircar, A., Chaudhury, S. & Gray, J. J. Toward high-resolution homology modeling of antibody F_v regions and application to antibody-antigen docking. *Proteins Struct. Funct. Bioinforma.* **74,** 497–514 (2009).
44. Norn, C. H., Lapidoth, G. & Fleishman, S. J. High-accuracy modeling of antibody structures by a search for minimum-energy recombination of backbone fragments. *Proteins* **85,** 30–38 (2017).
45. Lapidoth, G., Parker, J., Prilusky, J. & Fleishman, S. J. AbPredict 2: a server for accurate and unstrained structure prediction of antibody variable domains. *Bioinformatics* (2018). doi:10.1093/bioinformatics/bty822
46. Toor, J. S., Rao, A. A., McShan, A. C., Yarmarkovich, M., Nerli, S., Yamaguchi, K., Madejska, A. A., Nguyen, S., Tripathi, S., Maris, J. M., Salama, S. R., Haussler, D. & Sgourakis, N. G. A Recurrent Mutation in Anaplastic Lymphoma Kinase with Distinct Neoepitope Conformations. *Front. Immunol.* **9,** 99 (2018).
47. Gowthaman, R. & Pierce, B. G. TCRmodel: high resolution modeling of T cell receptors from sequence. *Nucleic Acids Res.* **46,** W396–W401 (2018).
48. Sircar, A. & Gray, J. J. SnugDock: Paratope Structural Optimization during Antibody-Antigen Docking Compensates for Errors in Antibody Homology Models. *PLoS Comput. Biol.* **6,** e1000644 (2010).
49. Adolf-Bryfogle, J., Kalyuzhniy, O., Kubitz, M., Weitzner, B. D., Hu, X., Adachi, Y., Schief, W. R. & Dunbrack, R. L. RosettaAntibodyDesign (RAbD): A general framework for computational antibody design. *PLOS Comput. Biol.* **14,** e1006112 (2018).
50. King, C., Garza, E. N., Mazor, R., Linehan, J. L., Pastan, I., Pepper, M. & Baker, D. Removing T-cell epitopes with computational protein design. *Proc. Natl. Acad. Sci. U. S. A.* **111,** 8577–82 (2014).
51. Nivón, L. G., Bjelic, S., King, C. & Baker, D. Automating human intuition for protein design. *Proteins* **82,** 858–66 (2014).
52. Lapidoth, G. D., Baran, D., Pszolla, G. M., Norn, C., Alon, A., Tyka, M. D. & Fleishman, S. J. AbDesign: An algorithm for combinatorial backbone design guided by natural conformations and sequences. *Proteins* **83,** 1385–406 (2015).
53. Baran, D., Pszolla, M. G., Lapidoth, G. D., Norn, C., Dym, O., Unger, T., Albeck, S., Tyka, M. D. & Fleishman, S. J. Principles for computational design of binding antibodies. *Proc. Natl. Acad. Sci. U. S. A.* **114,** 10900–10905 (2017).
54. Wang, R. Y.-R., Kudryashev, M., Li, X., Egelman, E. H., Basler, M., Cheng, Y., Baker, D. & DiMaio, F. De novo protein structure determination from near-atomic-resolution cryo-EM maps. *Nat. Methods* **12,** 335–8 (2015).

55. Frenz, B., Walls, A. C., Egelman, E. H., Veesler, D. & DiMaio, F. RosettaES: a sampling strategy enabling automated interpretation of difficult cryo-EM maps. *Nat. Methods* **14,** 797–800 (2017).
56. DiMaio, F., Echols, N., Headd, J. J., Terwilliger, T. C., Adams, P. D. & Baker, D. Improved low-resolution crystallographic refinement with Phenix and Rosetta. *Nat. Methods* **10,** 1102–4 (2013).
57. DiMaio, F., Song, Y., Li, X., Brunner, M. J., Xu, C., Conticello, V., Egelman, E., Marlovits, T. C., Cheng, Y. & Baker, D. Atomic-accuracy models from 4.5-Å cryo-electron microscopy data with density-guided iterative local refinement. *Nat. Methods* **12,** 361–5 (2015).
58. Wang, R. Y.-R., Song, Y., Barad, B. A., Cheng, Y., Fraser, J. S. & DiMaio, F. Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. *Elife* **5,** (2016).
59. Nerli, S. & Sgourakis, N. G. CS-ROSETTA. *Methods Enzymol.* (2018). doi:10.1016/BS.MIE.2018.07.005
60. Yagi, H., Pilla, K. B., Maleckis, A., Graham, B., Huber, T. & Otting, G. Three-dimensional protein fold determination from backbone amide pseudocontact shifts generated by lanthanide tags at multiple sites. *Structure* **21,** 883–890 (2013).
61. Schmitz, C., Vernon, R., Otting, G., Baker, D. & Huber, T. Protein structure determination from pseudocontact shifts using ROSETTA. *J. Mol. Biol.* **416,** 668–77 (2012).
62. Kuenze, G., Bonneau, R., Leman, J. K. & Meiler, J. Integrative protein modeling in RosettaNMR from sparse paramagnetic restraints. *bioRxiv* 597872 (2019). doi:10.1101/597872
63. Aprahamian, M. L., Chea, E. E., Jones, L. M. & Lindert, S. Rosetta Protein Structure Prediction from Hydroxyl Radical Protein Footprinting Mass Spectrometry Data. *Anal. Chem.* **90,** 7721–7729 (2018).
64. Aprahamian, M. L. & Lindert, S. Utility of Covalent Labeling Mass Spectrometry Data in Protein Structure Prediction with Rosetta. *J. Chem. Theory Comput.* acs.jctc.9b00101 (2019). doi:10.1021/acs.jctc.9b00101
65. Hauri, S., Khakzad, H., Happonen, L., Teleman, J., Malmström, J. & Malmström, L. Rapid determination of quaternary protein structures in complex biological samples. *Nat. Commun.* **10,** 192 (2019).
66. Sripakdeevong, P., Kladwang, W. & Das, R. An enumerative stepwise ansatz enables atomic-accuracy RNA loop modeling. *Proc. Natl. Acad. Sci.* **108,** 20573–20578 (2011).
67. Das, R. Atomic-accuracy prediction of protein loop structures through an RNA-inspired Ansatz. *PLoS One* **8,** e74830 (2013).
68. Watkins, A. M., Geniesse, C., Kladwang, W., Zakrevsky, P., Jaeger, L. & Das, R. Blind prediction of noncanonical RNA structure at atomic accuracy. *Sci. Adv.* **4,** eaar5316 (2018).
69. Das, R., Karanicolas, J. & Baker, D. Atomic accuracy in predicting and designing noncanonical RNA structure. *Nat. Methods* **7,** 291–294 (2010).
70. Cheng, C. Y., Chou, F.-C. & Das, R. Modeling Complex RNA Tertiary Folds with Rosetta. *Methods Enzymol.* **553,** 35–64 (2015).
71. Kappel, K. & Das, R. Sampling Native-like Structures of RNA-Protein Complexes through Rosetta Folding and Docking. *Structure* **27,** 140-151.e5 (2019).
72. Chou, F.-C., Sripakdeevong, P., Dibrov, S. M., Hermann, T. & Das, R. Correcting pervasive errors in RNA crystallography through enumerative structure prediction. *Nat. Methods* **10,** 74–76 (2013).
73. Chou, F.-C., Echols, N., Terwilliger, T. C. & Das, R. in 269–282 (Humana Press, New York, NY, 2016). doi:10.1007/978-1-4939-2763-0_17
74. Sripakdeevong, P., Cevec, M., Chang, A. T., Erat, M. C., Ziegeler, M., Zhao, Q., Fox, G. E., Gao, X., Kennedy, S. D., Kierzek, R., Nikonowicz, E. P., Schwalbe, H., Sigel, R. K. O., Turner, D. H. & Das, R. Structure determination of noncanonical RNA motifs guided by 1H NMR chemical shifts. *Nat. Methods* **11,** 413–416 (2014).
75. Kappel, K., Liu, S., Larsen, K. P., Skiniotis, G., Puglisi, E. V., Puglisi, J. D., Zhou, Z. H., Zhao, R. & Das, R. De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes. *Nat. Methods* **15,** 947–954 (2018).
76. Alford, R. F., Koehler Leman, J., Weitzner, B. D., Duran, A. M., Tilley, D. C., Elazar, A. & Gray, J. J. An Integrated Framework Advancing Membrane Protein Modeling and Design. *PLoS Comput. Biol.* **11,** e1004398 (2015).
77. Koehler Leman, J., Mueller, B. K. & Gray, J. J. Expanding the toolkit for membrane protein modeling in Rosetta. *Bioinformatics* **11,** 1–3 (2016).
78. Koehler Leman, J., Lyskov, S. & Bonneau, R. Computing structure-based lipid accessibility of membrane proteins with mp_lipid_acc in RosettaMP. *BMC Bioinformatics* **18,** 115 (2017).

79. Koehler Leman, J. & Bonneau, R. A novel domain assembly routine for creating full-length models of membrane proteins from known domain structures. *Biochemistry* acs.biochem.7b00995 (2017). doi:10.1021/acs.biochem.7b00995
80. Bender, B. J., Cisneros, A., Duran, A. M., Finn, J. A., Fu, D., Lokits, A. D., Mueller, B. K., Sangha, A. K., Sauer, M. F., Sevy, A. M., Sliwoski, G., Sheehan, J. H., Dimaio, F., Meiler, J. & Moretti, R. Protocols for Molecular Modeling with Rosetta3 and RosettaScripts. *Biochemistry* acs.biochem.6b00444 (2016). doi:10.1021/acs.biochem.6b00444
81. Labonte, J. W., Adolf-Bryfogle, J., Schief, W. R. & Gray, J. J. Residue-centric modeling and design of saccharide and glycoconjugate structures. *J. Comput. Chem.* **38,** 276–287 (2017).
82. Frenz, B., Rämisch, S., Borst, A. J., Walls, A. C., Adolf-Bryfogle, J., Schief, W. R., Veesler, D. & DiMaio, F. Automatically Fixing Errors in Glycoprotein Structures with Rosetta. *Structure* **0,** (2018).
83. Park, H., Bradley, P., Greisen, P., Liu, Y., Mulligan, V. K., Kim, D. E., Baker, D. & DiMaio, F. Simultaneous Optimization of Biomolecular Energy Functions on Features from Small Molecules and Macromolecules. *J. Chem. Theory Comput.* **12,** 6201–6212 (2016).
84. Alford, R. F., Leaver-Fay, A., Jeliazkov, J. R., O'Meara, M. J., Dimaio, F. P., Park, H., Shapovalov, M. V., Renfrew, P. D., Mulligan, V. K., Kappel, K., Labonte, J. W., Pacella, M. S., Bonneau, R., Bradley, P., Dunbrack, R. L., Das, R., Baker, D., Kuhlman, B., Kortemme, T. & Gray, J. J. The Rosetta all-atom energy function for macromolecular modeling and design. *J. Chem. Theory Comput.* **13,** 1–35 (2017).
85. Boyken, S. E., Chen, Z., Groves, B., Langan, R. A., Oberdorfer, G., Ford, A., Gilmore, J. M., Xu, C., DiMaio, F., Pereira, J. H., Sankaran, B., Seelig, G., Zwart, P. H. & Baker, D. De novo design of protein homo-oligomers with modular hydrogen-bond network-mediated specificity. *Science* **352,** 680–7 (2016).
86. Maguire, J. B., Boyken, S. E., Baker, D. & Kuhlman, B. Rapid Sampling of Hydrogen Bond Networks for Computational Protein Design. *J. Chem. Theory Comput.* **14,** 2751–2760 (2018).
87. Rocklin, G. J., Chidyausiku, T. M., Goreshnik, I., Ford, A., Houliston, S., Lemak, A., Carter, L., Ravichandran, R., Mulligan, V. K., Chevalier, A., Arrowsmith, C. H. & Baker, D. Global analysis of protein folding using massively parallel design, synthesis, and testing. *Science* **357,** 168–175 (2017).
88. Chaudhury, S., Lyskov, S. & Gray, J. J. PyRosetta: a script-based interface for implementing molecular modeling algorithms using Rosetta. *Bioinformatics* **26,** 689–691 (2010).
89. Gray, J. J., Chaudhury, S., Lyskov, S., and Labonte, J. W. The PyRosetta Interactive Platform for Protein Structure Prediction and Design: A Set of Educational Modules. (2014). at <http://www.amazon.com/PyRosetta-Interactive-Platform-Structure-Prediction/dp/1500968277>
90. Fleishman, S. J., Leaver-Fay, A., Corn, J. E., Strauch, E.-M. M., Khare, S. D., Koga, N., Ashworth, J., Murphy, P., Richter, F., Lemmon, G., Meiler, J. & Baker, D. RosettaScripts: A scripting language interface to the Rosetta Macromolecular modeling suite. *PLoS One* **6,** 1–10 (2011).
91. Schenkelberg, C. D. & Bystroff, C. InteractiveROSETTA: A graphical user interface for the PyRosetta protein modeling suite. *Bioinformatics* (2015). doi:10.1093/bioinformatics/btv492
92. Kleffner, R., Flatten, J., Leaver-Fay, A., Baker, D., Siegel, J. B., Khatib, F. & Cooper, S. Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. *Bioinformatics* **33,** 2765–2767 (2017).
93. Khatib, F., Cooper, S., Tyka, M. D., Xu, K., Makedon, I., Popovic, Z., Baker, D. & Players, F. Algorithm discovery by protein folding game players. *Proc. Natl. Acad. Sci. U. S. A.* **108,** 18949–53 (2011).
94. Cooper, S., Sterling, A. L. R., Kleffner, R., Silversmith, W. M. & Siegel, J. B. Repurposing citizen science games as software tools for professional scientists. in *Proc. 13th Int. Conf. Found. Digit. Games - FDG '18* 1–6 (ACM Press, 2018). doi:10.1145/3235765.3235770
95. Cooper, S., Khatib, F., Treuille, A., Barbero, J., Lee, J., Beenen, M., Leaver-Fay, A., Baker, D., Popović, Z. & Players, F. Predicting protein structures with a multiplayer online game. *Nature* **466,** 756–760 (2010).
96. Lyskov, S., Chou, F. C., Conch??ir, S. ??, Der, B. S., Drew, K., Kuroda, D., Xu, J., Weitzner, B. D., Renfrew, P. D., Sripakdeevong, P., Borgo, B., Havranek, J. J., Kuhlman, B., Kortemme, T., Bonneau, R., Gray, J. J. & Das, R. Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). *PLoS One* **8,** 5–7 (2013).
97. Moretti, R., Lyskov, S., Das, R., Meiler, J. & Gray, J. J. Web-accessible molecular modeling with Rosetta: The Rosetta Online Server that Includes Everyone (ROSIE). *Protein Sci.* **27,** 259–268 (2018).
98. Mills, J. H., Khare, S. D., Bolduc, J. M., Forouhar, F., Mulligan, V. K., Lew, S., Seetharaman, J., Tong, L., Stoddard, B. L. & Baker, D. Computational Design

of an Unnatural Amino Acid Dependent Metalloprotein with Atomic Level Accuracy. *J. Am. Chem. Soc.* **135,** 13393–13399 (2013).

99. Mulligan, V. K. Manuscript in preparation. (2019).

100. Pavlovicz, R. E., Park, H. & DiMaio, F. Efficient consideration of coordinated water molecules improves computational protein-protein and protein-ligand docking. *bioRxiv* 618603 (2019). doi:10.1101/618603