

BII – Multiscale Simulation, Modelling and Design Publications

***(Publications sorted: Newest – Oldest)*

1.	Kaur H, Jakob RP, Marzinek JK, Green R, Imai Y, Bolla JR, Agustoni E, Robinson CV, Bond PJ, Maier T, Hiller S. The antibiotic darobactin mimics a β-strand to inhibit outer membrane insertase. Nature 2021, doi: 10.1038/s41586-021-03455-w
2.	Raghuvamsi PV, Tulsian NK, Samsudin F, Qian X, Purushotorman K, Yue G, Kozma MM, Hwa WY, Lescar J, Bond PJ, MacAry PA, Anan GS. SARS-CoV-2 S protein:ACE2 interaction reveals novel allosteric targets. Elife, 2021 Feb 8;10:e63646. doi: 10.7554/eLife.63646, PMID: 33554856, doi: 10.7554/eLife.63646
3.	Fibriansah G, Lim EXY, Marzinek JK, Ng TS, Tan JL, Huber RG, Lim XN, Chew VSY, Kostyuchenko VA, Shi J, Anand GS, Bond PJ, Crowe JE Jr, Lok SM. Antibody affinity versus dengue morphology influences neutralization. PLOS Pathogens, 2021, 17(2): e1009331. PMID: 33621239, doi: 10.1371/journal.ppat.1009331
4.	Samsudin F, Gan SKE, Bond PJ. (2020) The impact of Gag non-cleavage site mutations on HIV-1 viral fitness from integrative modelling and simulations. Comput Struct Biotechnol J. 2020 Dec 23;19:330-342. doi: 10.1016/j.csbj.2020.12.022. eCollection 2021.
5.	Chan KF, Su TTC, Krah A, Phua SX, Yeo YJ, Ling WL, Bond PJ, Gan SKE. (2020) An Alternative HIV-1 Non-Nucleoside Reverse Transcriptase Inhibition Mechanism: Targeting the p51 Subunit. Molecules, 2020, Vol: 25, Pg: 5902, doi: 10.3390/molecules25245902
6.	Petruk G, Puthia M, Petrlova J, Samsudin F, Strömdahl AC, Cerps S, Uller L, Kjellström S, Bond PJ, Schmidtchen A. (2020) SARS-CoV-2 Spike protein binds to bacterial lipopolysaccharide and boosts proinflammatory activity. J Mol Cell Biol. 2020 Dec 9:mjaa067. doi: 10.1093/jmcb/mjaa067. Online ahead of print.
7.	Petruk G, Petrlova J, Samsudin F, Giudice RD, Bond PJ, Schmidtchen A. Concentration- and pH-dependent oligomerization of the thrombin-derived C-terminal peptide TCP-25. Biomolecules 2020, 10(11), 1572; doi: 10.3390/biom10111572
8.	Krah A, van der Hoeven B, Mestrom L, Tonin F, Knobel KCC, Bond PJ, McMillan DGG. (2020) A second shell residue modulates a conserved ATP-binding site with radically different affinities for ATP. Biochimica et Biophysica Acta (BBA), Vol 1865, Issue 1, Jan 2021, doi: 10.1016/j.bbagen.2020.129766
9.	Faulkner M, Szabó I, Weetman SL, Sicard F, Huber RG, Bond PJ, Rosta E, Liu LN. (2020) Molecular simulations unravel the molecular principles that mediate selective permeability of carboxysome shell protein. Scientific Reports, 10, Article 17501, 2020, doi: 10.1038/s41598-020-74536-5
10.	Zuzic L, Marzinek JK, Warwicker J, Bond PJ. (2020) A Benzene-Mapping approach for uncovering cryptic pockets in membrane-bound proteins. bioRxiv, 5 Apr 2020, doi: 10.1101/2020.04.04.025163
11.	Shearer J, Marzinek JK, Bond PJ, Khalid S. (2020) Molecular dynamics simulations of bacterial outer membrane lipid extraction: Adequate sampling? J Chem Phys. 2020 Jul 28;153(4):044122. doi: 10.1063/5.0017734. PMID: 32752683

12.	Shivgan AT, Marzinek JK, Huber RG, Krah A, Henschman RH, Matsudaira P, Verma CS, Bond PJ. (2020) Extending the Martini coarse-grained forcefield to N-glycans. Journal of Chemical Information and Modeling, 23 Jul 2020, 60(8):3864-3883, DOI: 10.1021/acs.jcim.0c00495 PMID: 32702979
13.	Krah A, Marzinek JK, Bond PJ. (2020) Characterizing the Hydration Properties of Proton Binding Sites in the ATP Synthase c-Rings of Bacillus Species. J Phys Chem B. 2020 Aug 20;124(33):7176-7183. doi: 10.1021/acs.jpcc.0c03896. Epub 2020 Aug 7. PMID: 32687713
14.	Krah A, Huber RG, McMillan DGG, Bond PJ. (2020) The Molecular Basis for Purine Binding Selectivity in the Bacterial ATP Synthase ϵ Subunit. Chembiochem. 2020 Nov 16;21(22):3249-3254. doi: 10.1002/cbic.202000291. Epub 2020 Aug 4. PMID: 32608105
15.	Huber RG, Marzinek JK, Boon PLS, Yue W, Bond PJ. (2020) Computational modelling of flavivirus dynamics: The ins and outs. Methods. 2020 Jun 8:S1046-2023(19)30326-3. doi: 10.1016/j.ymeth.2020.06.004. PMID: 32526282
16.	Kamariah N, Huber RG, Bond PJ, Müller V, Grüber G. (2020) 3D reconstruction and flexibility of the hybrid engine Acetobacterium woodii F-ATP synthase. Biochem Biophys Res Commun. 2020 Jun 25;527(2):518-524. doi: 10.1016/j.bbrc.2020.04.026. Epub 2020 May 15. PMID: 32423799
17.	Samsudin F, Yeo JY, Gan SK, Bond PJ. (2020) Not all therapeutic antibody isotypes are equal: the case of IgM versus IgG in Pertuzumab and Trastuzumab. Chem Sci. 2020 Feb 12;11(10):2843-2854. doi: 10.1039/c9sc04722k. eCollection 2020 Mar 14. PMID: 32206268
18.	Krah A, Huber RG, Bond PJ. (2020) How Ligand Binding Affects the Dynamical Transition Temperature in Proteins. Chemphyschem. 2020 Mar 3. doi: 10.1002/cphc.201901221. [Epub ahead of print] PMID: 32128947
19.	Petrlova J, Petruk G, Huber RG, McBurnie EW, van der Plas MJA, Bond PJ, Puthia M, Schmidtchen A (2020). Thrombin-derived C-terminal fragments aggregate and scavenge bacteria and their proinflammatory products. Journal of Biological Chemistry, 2020 Mar 13;295(11):3417-3430. doi: 10.1074/jbc.RA120.012741
20.	Marzinek JK, Huber RG, Bond PJ (2020). Multiscale modelling and simulation of viruses. Current Opinion in Structural Biology 2020, 61:146-152, doi: 10.1016/j.sbi.2019.12.019
21.	Tan LK, Wong WY, Yang HT, Huber RG, Bond PJ, Ng LC, Maurer-Stroh S, Hapuarachchi HC. (2019). Flavivirus Cross-Reactivity to Dengue Nonstructural Protein 1 Antigen Detection Assays. Diagnostics, Vol 10, Issue 1, doi: 10.3390/diagnostics10010011
22.	Krah A, Huber RG, Zachariae U, Bond PJ. (2019). On the ion coupling mechanism of the MATE transporter ClbM. BBA - Biomembranes, Vol. 1862, Issue 2, 1 Feb 2020, doi: 10.1016/j.bbamem.2019.183137
23.	Kamariah N, Huber RG, Nartey W, Bhushan S, Bond PJ, Gruber G. (2019). The structural basis for membrane assembly of immunoreceptor signalling complexes. Journal of Molecular Modeling, 2019 Aug 27;25(9):277. doi: 10.1007/s00894-019-4165-6
24.	Kamariah N, Huber RG, Nartey W, Bhushan S, Bond PJ, Gruber G (2019). Structure and subunit arrangement of Mycobacterial F1FO ATP synthase and novel features of the unique mycobacterial subunit ? Journal of Structural Biology, Vol. 207, Issue 2, 1 Aug 2019, Pg 199-208, doi: 10.1016/j.jsb.2019.05.00

25.	Chan KWK, Watanabe S, Jin JY, Pompon J, Teng D, Alonso S, Vijaykrishna D, Halstead SB, Marzinek JK, Bond PJ, Burla B, Torta F, Wenk MR, Ooi EE, Vasudevan SG. (2019). A T164S mutation in the dengue virus NS1 protein is associated with greater disease severity in mice. Science Translational Medicine, 26 Jun 2019, Vol. 11, Issue 498, doi: 10.1126/scitranslmed.aat772
26.	Huber RG, Carpenter TS, Dube N, Holdbrook DA, Ingólfsson HI, Irvine WA, Marzinek JK, Samsudin F, Allison JR, Khalid S, Bond PJ. (2019). Multiscale Modeling and Simulation Approaches to Lipid-Protein Interactions. Methods in Molecular Biology 2019, Vol. 2003, Pg 1-30. doi: 10.1007/978-1-4939-9512-7_1
27.	Holdbrook D, Huber RG, Marzinek JK, Stubbusch AS, Bond PJ. (2019). Multiscale modeling of innate immune receptors: Endotoxin recognition and regulation by host defense peptides. Pharmacological Research 2019 Jul 24;147:104372. doi: 10.1016/j.phrs.2019.104372
28.	Kubankova M, Chambers J, Huber RG, Bond PJ, Marciniak S, Kuimova M. (2019). Linker length affects photostability of protein-targeted sensor of cellular microviscosity. Methods and Applications in Fluorescence, 2019 Sep 26. doi: 10.1088/2050-6120/ab481f
29.	Lim XN, Shan C, Marzinek JK, Dong H, Ng TS, Ooi JSG, Fibriansah G, Wang J, Verma CS, Bond PJ, Shi PY, Lok SM. (2019). Molecular basis of dengue virus serotype 2 morphological switch from 29°C to 37°C. PLOS Pathogens, Sep 2019, Vol. 15, Issue 9, doi 10.1371/journal.ppat.1007996
30.	Gupta A, Marzinek JK, Jefferies D, Bond PJ, Harryson P, Wohland T. (2019). The disordered plant dehydrin Lti30 protects the membrane during water-related stress by cross-linking lipids. Journal of Biological Chemistry, 28 Feb 2019, doi: 10.1074/jbc.RA118.007163
31.	Huber RG, Lim XN, Ng WC, Sim AYL, Poh HX, Shen Y, Lim SY, Sundstrom KB, Sun X, Aw JG, Too HK, Boey PH, Wilm A, Chawla T, Choy MM, Jiang L, de Sessions PF13, Loh XJ, Alonso S, Hibberd M, Nagarajan N, Ooi EE, Bond PJ, Sessions OM, Wan Y. 2019. Structure mapping of dengue and Zika viruses reveals functional long-range interactions. Nature Communications, 2019 Mar 29;10(1):1408. doi: 10.1038/s41467-019-09391-8
32.	Krah A, Marzinek JK, Bond PJ. 2019. Insights into water accessible pathways and the inactivation mechanism of proton translocation by the membrane-embedded domain of V-type ATPases. Biochimica et Biophysica Acta (BBA) - Biomembranes, Vol. 1861, Issue 5, 1 May 2019, Pg 1004-1010, doi: 10.1016/j.bbamem.2019.02.010
33.	Sharma KK, Lim XX, Tantirimudalige SN, Gupta A, Marzinek JK, Holdbrook D, Lim XYE, Bond PJ, Anand GS, Wohland T. (2019). Infectivity of Dengue Virus Serotypes 1 and 2 Is Correlated with E-Protein Intrinsic Dynamics but Not to Envelope Conformations. Structure. 2019 Jan 2. pii: S0969-2126(18)30462-3. doi: 10.1016/j.str.2018.12.006.
34.	Cai S, Lukamto DH, Toh JKC, Huber RG, Bond PJ, Jee JE, Lim TC, Liu P, Chen L, Qu QV, Lee SS, Lee SG. (2019). Directing GDNF-mediated neuronal signaling with proactively programmable cell-surface saccharide-free glycosaminoglycan mimetics. Chem Commun (Camb). 2019 Jan 24;55(9):1259-1262. doi: 10.1039/c8cc09253b.
35.	Ivanov SM, Huber RG, Alibay I, Warwicker J, Bond PJ. (2019). Energetic Fingerprinting of Ligand Binding to Paralogous Proteins: The Case of the Apoptotic Pathway. J Chem Inf Model. 2019 Jan 28;59(1):245-261. doi: 10.1021/acs.jcim.8b00765. Epub 2019 Jan 9.
36.	Ghosh M, Wang LC, Huber RG, Gao Y, Morgan LK, Tulsian NK, Bond PJ, Kenney LJ, Anand GS. (2019). Engineering an Osmosensor by Pivotal Histidine Positioning within Disordered Helices. Structure. 2019 Feb 5;27(2):302-314.e4. doi: 10.1016/j.str.2018.10.012. Epub 2018 Nov 29.

37.	Wirawan M, Fibriansah G, Marzinek JK, Lim XX, Ng TS, Sim AYL, Zhang Q, Kostyuchenko VA, Shi J, Smith SA, Verma CS, Anand G, Crowe JE Jr, Bond PJ, Lok SM. (2019). Mechanism of Enhanced Immature Dengue Virus Attachment to Endosomal Membrane Induced by prM Antibody . Structure. 2019 Feb 5;27(2):253-267.e8. doi: 10.1016/j.str.2018.10.009. Epub 2018 Nov 21.
38.	Lim TC, Cai S, Huber RG, Bond PJ, Siew Chia PX, Khou SL, Gao S, Lee SS, Lee SG. (2018). Facile saccharide-free mimetics that recapitulate key features of glycosaminoglycan sulfation patterns . Chem Sci. 2018 Aug 24;9(41):7940-7947. doi: 10.1039/c8sc02303d. eCollection 2018 Nov 7.
39.	Sharma KK, Marzinek JK, Tantirimudalige SN, Bond PJ, Wohland T. (2018). Single-molecule studies of flavivirus envelope dynamics: Experiment and computation . Prog Biophys Mol Biol. 2018 Sep 14. pii: S0079-6107(18)30181-0. doi: 10.1016/j.pbiomolbio.2018.09.001.
40.	Krah A, Bond PJ. (2018). Single mutations in the ϵ subunit from thermophilic Bacillus PS3 generate a high binding affinity site for ATP . PeerJ. 2018 Sep 5;6:e5505. doi: 10.7717/peerj.5505. eCollection 2018.
41.	Saravanan R, Holdbrook DA, Petrlova J, Singh S, Berglund NA, Choong YK, Kjellstrom S, Bond PJ, Malmsten M, Schmidtchen A. (2018). Structural basis for endotoxin neutralisation and anti-inflammatory activity of thrombin-derived C-terminal peptides . Nat Commun. 2018 Jul 17;9(1):2762. doi: 10.1038/s41467-018-05242-0.
42.	Holdbrook DA, Singh S, Choong YK, Petrlova J, Malmsten M, Bond PJ, Verma NK, Schmidtchen A, Saravanan R. (2018). Influence of pH on the activity of thrombin-derived antimicrobial peptides . Biochim Biophys Acta Biomembr. 2018 Nov;1860(11):2374-2384. doi: 10.1016/j.bbamem.2018.06.002. Epub 2018 Jun 6.
43.	Marzinek JK, Bag N, Huber RG, Holdbrook DA, Wohland T, Verma CS, Bond PJ. (2018). A Funneled Conformational Landscape Governs Flavivirus Fusion Peptide Interaction with Lipid Membranes . J Chem Theory Comput. 2018 Jul 10;14(7):3920-3932. doi: 10.1021/acs.jctc.8b00438. Epub 2018 Jun 20.
44.	Yeow J, Tan KW, Holdbrook DA, Chong ZS, Marzinek JK, Bond PJ, Chng SS. (2018). The architecture of the OmpC-MlaA complex sheds light on the maintenance of outer membrane lipid asymmetry in Escherichia coli . J Biol Chem. 2018 Jul 20;293(29):11325-11340. doi: 10.1074/jbc.RA118.002441. Epub 2018 May 30.
45.	Boon PLS, Saw WG, Lim XX, Raghuvamsi PV, Huber RG, Marzinek JK, Holdbrook DA, Anand GS, Gruber G, Bond PJ. (2018). Partial Intrinsic Disorder Governs the Dengue Capsid Protein Conformational Ensemble . ACS Chem Biol. 2018 Jun 15;13(6):1621-1630. doi: 10.1021/acscchembio.8b00231. Epub 2018 Jun 5.
46.	Huber RG, Berglund NA, Kargas V, Marzinek JK, Holdbrook DA, Khalid S, Piggot TJ, Schmidtchen A, Bond PJ. (2018). A Thermodynamic Funnel Drives Bacterial Lipopolysaccharide Transfer in the TLR4 Pathway . Structure. 2018 Aug 7;26(8):1151-1161.e4. doi: 10.1016/j.str.2018.04.007. Epub 2018 May 17.
47.	Lancaster GI, Langley KG, Berglund NA, Kammoun HL, Reibe S, Estevez E, Weir J, Mellett NA, Pernes G, Conway JRW, Lee MKS, Timpson P, Murphy AJ, Masters SL, Gerondakis S, Bartonicek N, Kaczorowski DC, Dinger ME, Meikle PJ, Bond PJ, Febbraio MA. (2018). Evidence that TLR4 Is Not a Receptor for Saturated Fatty Acids but Mediates Lipid-Induced Inflammation by Reprogramming Macrophage Metabolism . Cell Metab. 2018 May 1;27(5):1096-1110.e5. doi: 10.1016/j.cmet.2018.03.014. Epub 2018 Apr 19.

48.	Chambers JE, Kubankova M, Huber RG, Lopez-Duarte I, Avezov E, Bond PJ, Marciniak SJ, Kuimova MK. (2018). An Optical Technique for Mapping Microviscosity Dynamics in Cellular Organelles . ACS Nano. 2018 May 22;12(5):4398-4407. doi: 10.1021/acsnano.8b00177. Epub 2018 Apr 18.
49.	Latty SL, Sakai J, Hopkins L, Verstak B, Paramo T, Berglund NA, Cammarota E, Cicuta P, Gay NJ, Bond PJ, Klenerman D, Bryant CE. (2018). Activation of Toll-like receptors nucleates assembly of the MyDDosome signaling hub . Elife. 2018 Jan 24;7. pii: e31377. doi: 10.7554/eLife.31377.
50.	Ivanov SM, Cawley A, Huber RG, Bond PJ, Warwicker J. (2017). Protein-protein interactions in paralogues: Electrostatics modulates specificity on a conserved steric scaffold . PLoS One. 2017 Oct 10;12(10):e0185928. doi: 10.1371/journal.pone.0185928. eCollection 2017.
51.	Bond PJ, Verma CS. (2017). Editorial . Prog Biophys Mol Biol. 2017 Sep;128:1-2. doi: 10.1016/j.pbiomolbio.2017.07.005.
52.	Kargas V, Marzinek JK, Holdbrook DA, Yin H, Ford RC, Bond PJ. (2017). A polar SxxS motif drives assembly of the transmembrane domains of Toll-like receptor 4 . Biochim Biophys Acta Biomembr. 2017 Oct;1859(10):2086-2095. doi: 10.1016/j.bbamem.2017.07.010. Epub 2017 Jul 22.
53.	Chang HH, Huber RG, Bond PJ, Grad YH, Camerini D, Maurer-Stroh S, Lipsitch M. (2017). Systematic analysis of protein identity between Zika virus and other arthropod-borne viruses . Bull World Health Organ. 2017 Jul 1;95(7):517-525I. doi: 10.2471/BLT.16.182105. Epub 2016 Jul 18.
54.	Holdbrook DA, Burmann BM, Huber RG, Petoukhov MV, Svergun DI, Hiller S, Bond PJ. (2017). A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone . Structure. 2017 Jul 5;25(7):1079-1088.e3. doi: 10.1016/j.str.2017.05.018. Epub 2017 Jun 22.
55.	Petrova J, Hansen FC, van der Plas MJA, Huber RG, Morgelin M, Malmsten M, Bond PJ, Schmidtchen A. (2017). Aggregation of thrombin-derived C-terminal fragments as a previously undisclosed host defense mechanism . Proc Natl Acad Sci U S A. 2017 May 23;114(21):E4213-E4222. doi: 10.1073/pnas.1619609114. Epub 2017 May 4.
56.	Boags A, Hsu PC, Samsudin F, Bond PJ, Khalid S. (2017). Progress in Molecular Dynamics Simulations of Gram-Negative Bacterial Cell Envelopes . J Phys Chem Lett. 2017 Jun 1;8(11):2513-2518. doi: 10.1021/acs.jpcllett.7b00473. Epub 2017 May 22.
57.	Collins RF, Kargas V, Clarke BR, Siebert CA, Clare DK, Bond PJ, Whitfield C, Ford RC. (2017). Full-length, Oligomeric Structure of Wzz Determined by Cryoelectron Microscopy Reveals Insights into Membrane-Bound States . Structure. 2017 May 2;25(5):806-815.e3. doi: 10.1016/j.str.2017.03.017. Epub 2017 Apr 20.
58.	Santos-Moreno J, East A, Guilvout I, Nadeau N, Bond PJ, Tran Van Nhieu G, Francetic O. (2017). Polar N-terminal Residues Conserved in Type 2 Secretion Pseudopilins Determine Subunit Targeting and Membrane Extraction Steps during Fibre Assembly . J Mol Biol. 2017 Jun 2;429(11):1746-1765. doi: 10.1016/j.jmb.2017.04.005. Epub 2017 Apr 17.
59.	Schonbach C, Verma C, Wee LJ, Bond PJ, Ranganathan S. (2016). Bioinformatics and systems biology research update from the 15th International Conference on Bioinformatics (InCoB2016) . BMC Bioinformatics. 2016 Dec 22;17(Suppl 19):524. doi: 10.1186/s12859-016-1409-7.
60.	Schonbach C, Verma C, Wee LJ, Bond PJ, Ranganathan S. (2016). 2016 update on APBioNet's annual international conference on bioinformatics (InCoB) . BMC Genomics. 2016 Dec 22;17(Suppl 13):1036. doi: 10.1186/s12864-016-3362-2.

61.	Verma C, Bond P. (2016). Introductory note for JBCB special issue. J Bioinform Comput Biol. 2016 Dec;14(6):1602005. doi: 10.1142/S0219720016020054. Epub 2016 Dec 30.
62.	Samsudin F, Ortiz-Suarez ML, Piggot TJ, Bond PJ, Khalid S. (2016). OmpA: A Flexible Clamp for Bacterial Cell Wall Attachment. Structure. 2016 Dec 6;24(12):2227-2235. doi: 10.1016/j.str.2016.10.009. Epub 2016 Nov 17.
63.	Ivanov SM, Huber RG, Warwicker J, Bond PJ. (2016). Energetics and Dynamics Across the Bcl-2-Regulated Apoptotic Pathway Reveal Distinct Evolutionary Determinants of Specificity and Affinity. Structure. 2016 Nov 1;24(11):2024-2033. doi: 10.1016/j.str.2016.09.006. Epub 2016 Oct 20.
64.	Huber RG, Kulemzina I, Ang K, Chavda AP, Surantran S, Teh JT, Kenanov D, Liu G, Rancati G, Szymd R, Kaldis P, Bond PJ, Ivanov D. (2016). Impairing Cohesin Smc1/3 Head Engagement Compensates for the Lack of Eco1 Function. Structure. 2016 Nov 1;24(11):1991-1999. doi: 10.1016/j.str.2016.09.001. Epub 2016 Sep 29.
65.	Huber RG, Marzinek JK, Holdbrook DA, Bond PJ. (2017). Multiscale molecular dynamics simulation approaches to the structure and dynamics of viruses. Prog Biophys Mol Biol. 2017 Sep;128:121-132. doi: 10.1016/j.pbiomolbio.2016.09.010. Epub 2016 Oct 17. Review.
66.	Ortiz-Suarez ML, Samsudin F, Piggot TJ, Bond PJ, Khalid S. (2016). Full-Length OmpA: Structure, Function, and Membrane Interactions Predicted by Molecular Dynamics Simulations. Biophys J. 2016 Oct 18;111(8):1692-1702. doi: 10.1016/j.bpj.2016.09.009.
67.	Lea-Smith DJ, Ortiz-Suarez ML, Lenn T, Nurnberg DJ, Baers LL, Davey MP, Parolini L, Huber RG, Cotton CA, Mastroianni G, Bombelli P, Ungerer P, Stevens TJ, Smith AG, Bond PJ, Mullineaux CW, Howe CJ. (2016). Hydrocarbons Are Essential for Optimal Cell Size, Division, and Growth of Cyanobacteria. Plant Physiol. 2016 Nov;172(3):1928-1940. Epub 2016 Oct 5.
68.	Fukuda Y, Cheong PL, Lynch J, Brighton C, Frase S, Kargas V, Rampersaud E, Wang Y, Sankaran VG, Yu B, Ney PA, Weiss MJ, Vogel P, Bond PJ, Ford RC, Trent RJ, Schuetz JD. (2016). The severity of hereditary porphyria is modulated by the porphyrin exporter and Lan antigen ABCB6. Nat Commun. 2016 Aug 10;7:12353. doi: 10.1038/ncomms12353.
69.	Marzinek JK, Holdbrook DA, Huber RG, Verma C, Bond PJ. (2016). Pushing the Envelope: Dengue Viral Membrane Coaxed into Shape by Molecular Simulations. Structure. 2016 Aug 2;24(8):1410-1420. doi: 10.1016/j.str.2016.05.014. Epub 2016 Jul 7.
70.	Holdbrook DA, Huber RG, Piggot TJ, Bond PJ, Khalid S. (2016). Dynamics of Crowded Vesicles: Local and Global Responses to Membrane Composition. PLoS One. 2016 Jun 16;11(6):e0156963. doi: 10.1371/journal.pone.0156963. eCollection 2016.
71.	Cording A, Gormally M, Bond PJ, Carrington M, Balasubramanian S, Miska EA, Thomas B. (2016). Selective inhibitors of trypanosomal uridylyl transferase RET1 establish druggability of RNA post-transcriptional modifications. RNA Biol. 2017 May 4;14(5):611-619. doi: 10.1080/15476286.2015.1137422. Epub 2016 Jan 20.
72.	Marzinek JK, Lakshminarayanan R, Goh E, Huber RG, Panzade S, Verma C, Bond PJ. (2016). Characterizing the Conformational Landscape of Flavivirus Fusion Peptides via Simulation and Experiment. Sci Rep. 2016 Jan 20;6:19160. doi: 10.1038/srep19160.

73.	East A, Mechaly AE, Huysmans GHM, Bernarde C, Tello-Manigne D, Nadeau N, Pugsley AP, Buschiazzo A, Alzari PM, Bond PJ, Francetic O. (2016). Structural Basis of Pullulanase Membrane Binding and Secretion Revealed by X-Ray Crystallography, Molecular Dynamics and Biochemical Analysis . Structure. 2016 Jan 5;24(1):92-104. doi: 10.1016/j.str.2015.10.023. Epub 2015 Dec 10.
74.	Ortiz-Suarez ML, Bond PJ. (2016). The Structural Basis for Lipid and Endotoxin Binding in RP105-MD-1, and Consequences for Regulation of Host Lipopolysaccharide Sensitivity . Structure. 2016 Jan 5;24(1):200-211. doi: 10.1016/j.str.2015.10.021. Epub 2015 Dec 3.
75.	Paramo T, Tomasio SM, Irvine KL, Bryant CE, Bond PJ. (2015). Energetics of Endotoxin Recognition in the Toll-Like Receptor 4 Innate Immune Response . Sci Rep. 2015 Dec 9;5:17997. doi: 10.1038/srep17997.
76.	Huber RG, Fan H, Bond PJ. (2015). The Structural Basis for Activation and Inhibition of ZAP-70 Kinase Domain . PLoS Comput Biol. 2015 Oct 16;11(10):e1004560. doi: 10.1371/journal.pcbi.1004560. eCollection 2015 Oct.
77.	Berglund NA, Kargas V, Ortiz-Suarez ML, Bond PJ. (2015). The role of protein-protein interactions in Toll-like receptor function . Prog Biophys Mol Biol. 2015 Oct;119(1):72-83. doi: 10.1016/j.pbiomolbio.2015.06.021. Epub 2015 Jul 2.
78.	Berglund NA, Piggot TJ, Jefferies D, Sessions RB, Bond PJ, Khalid S. (2015). Interaction of the antimicrobial peptide polymyxin B1 with both membranes of E. coli: a molecular dynamics study . PLoS Comput Biol. 2015 Apr 17;11(4):e1004180. doi: 10.1371/journal.pcbi.1004180. eCollection 2015 Apr.
79.	Burmann BM, Holdbrook DA, Callon M, Bond PJ, Hiller S. (2015). Revisiting the interaction between the chaperone Skp and lipopolysaccharide . Biophys J. 2015 Mar 24;108(6):1516-1526. doi: 10.1016/j.bpj.2015.01.029.
80.	Strahl H, Turlan C, Khalid S, Bond PJ, Kebalo JM, Peyron P, Poljak L, Bouvier M, Hamoen L, Luisi BF, Carpousis AJ. (2015). Membrane recognition and dynamics of the RNA degradosome . PLoS Genet. 2015 Feb 3;11(2):e1004961. doi: 10.1371/journal.pgen.1004961. eCollection 2015 Feb.
81.	Faustino AF, Guerra GM, Huber RG, Hollmann A, Domingues MM, Barbosa GM, Enguita FJ, Bond PJ, Castanho MA, Da Poian AT, Almeida FC, Santos NC, Martins IC. (2015). Understanding dengue virus capsid protein disordered N-Terminus and pep14-23-based inhibition . PLoS Comput Biol. 2015 Apr 17;11(4):e1004180. doi: 10.1371/journal.pcbi.1004180. eCollection 2015 Apr.
82.	Biggin PC, Bond PJ. (2015). Molecular dynamics simulations of membrane proteins . Methods Mol Biol. 2015;1215:91-108. doi: 10.1007/978-1-4939-1465-4_5.
83.	Marzinek JK, Bond PJ, Lian G, Zhao Y, Han L, Noro MG, Pistikopoulos EN, Mantalaris A. (2014). Free energy predictions of ligand binding to an α-helix using steered molecular dynamics and umbrella sampling simulations . J Chem Inf Model. 2014 Jul 28;54(7):2093-104. doi: 10.1021/ci500164q. Epub 2014 Jul 17.
84.	Paramo T, East A, Garzon D, Ulmschneider MB, Bond PJ. (2014). Efficient Characterization of Protein Cavities within Molecular Simulation Trajectories: trj_cavity . J Chem Theory Comput. 2014 May 13;10(5):2151-64. doi: 10.1021/ct401098b.
85.	Zhao Y, Marzinek JK, Bond PJ, Chen L, Li Q, Mantalaris A, Pistikopoulos EN, Noro MG, Han L, Lian G. (2014). A study on Fe(2+) - α-helical-rich keratin complex formation using isothermal titration calorimetry and molecular dynamics simulation . J Pharm Sci. 2014 Apr;103(4):1224-32. doi: 10.1002/jps.23895. Epub 2014 Feb 11.

86.	Watts CA, Richards FM, Bender A, Bond PJ, Korb O, Kern O, Riddick M, Owen P, Myers RM, Raff J, Gergely F, Jodrell DI, Ley SV. (2013). Design, synthesis, and biological evaluation of an allosteric inhibitor of HSET that targets cancer cells with supernumerary centrosomes. Chem Biol. 2013 Nov 21;20(11):1399-410. doi: 10.1016/j.chembiol.2013.09.012. Epub 2013 Oct 24.
87.	Paramo T, Piggot TJ, Bryant CE, Bond PJ. (2013). The structural basis for endotoxin-induced allosteric regulation of the Toll-like receptor 4 (TLR4) innate immune receptor. J Biol Chem. 2013 Dec 20;288(51):36215-25. doi: 10.1074/jbc.M113.501957. Epub 2013 Oct 30.
88.	Tomasio SM, Harding HP, Ron D, Cross BC, Bond PJ. (2013). Selective inhibition of the unfolded protein response: targeting catalytic sites for Schiff base modification. Mol Biosyst. 2013 Oct;9(10):2408-16. doi: 10.1039/c3mb70234k. Review.
89.	Garzon D, Anselmi C, Bond PJ, Faraldo-Gomez JD. (2013). Dynamics of the antigen-binding grooves in CD1 proteins: reversible hydrophobic collapse in the lipid-free state. J Biol Chem. 2013 Jul 5;288(27):19528-36. doi: 10.1074/jbc.M113.470179. Epub 2013 May 15.
90.	Paramo T, Garzon D, Holdbrook DA, Khalid S, Bond PJ. (2013). The simulation approach to lipid-protein interactions. Methods Mol Biol. 2013;974:435-55. doi: 10.1007/978-1-62703-275-9_19.
91.	Khalid S, Bond PJ. (2013). Multiscale molecular dynamics simulations of membrane proteins. Methods Mol Biol. 2013;924:635-57. doi: 10.1007/978-1-62703-017-5_25. Review.
92.	Beale TM, Allwood DM, Bender A, Bond PJ, Brenton JD, Charnock-Jones DS, Ley SV, Myers RM, Shearman JW, Temple J, Unger J, Watts CA, Xian J. (2012). A-ring dihalogenation increases the cellular activity of combretastatin-templated tetrazoles. ACS Med Chem Lett. 2012 Jan 19;3(3):177-81. doi: 10.1021/ml200149g. eCollection 2012 Mar 8.
93.	Kirchmair J, Williamson MJ, Tyzack JD, Tan L, Bond PJ, Bender A, Glen RC. (2012). Computational prediction of metabolism: sites, products, SAR, P450 enzyme dynamics, and mechanisms. J Chem Inf Model. 2012 Mar 26;52(3):617-48. doi: 10.1021/ci200542m. Epub 2012 Feb 17. Review.
94.	Cross BC, Bond PJ, Sadowski PG, Jha BK, Zak J, Goodman JM, Silverman RH, Neubert TA, Baxendale IR, Ron D, Harding HP. (2012). The molecular basis for selective inhibition of unconventional mRNA splicing by an IRE1-binding small molecule. Proc Natl Acad Sci U S A. 2012 Apr 10;109(15):E869-78. doi: 10.1073/pnas.1115623109. Epub 2012 Feb 6.
95.	Beale TM, Bond PJ, Brenton JD, Charnock-Jones DS, Ley SV, Myers RM. (2012). Increased endothelial cell selectivity of triazole-bridged dihalogenated A-ring analogues of combretastatin A-1. Bioorg Med Chem. 2012 Mar 1;20(5):1749-59. doi: 10.1016/j.bmc.2012.01.010. Epub 2012 Jan 18.
96.	Cisneros DA, Bond PJ, Pugsley AP, Campos M, Francetic O. (2012). Minor pseudopilin self-assembly primes type II secretion pseudopilus elongation. EMBO J. 2012 Feb 15;31(4):1041-53. doi: 10.1038/emboj.2011.454. Epub 2011 Dec 9.
97.	Koutsoukas A, Simms B, Kirchmair J, Bond PJ, Whitmore AV, Zimmer S, Young MP, Jenkins JL, Glick M, Glen RC, Bender A. (2011). From in silico target prediction to multi-target drug design: current databases, methods and applications. J Proteomics. 2011 Nov 18;74(12):2554-74. doi: 10.1016/j.jprot.2011.05.011. Epub 2011 May 18. Review.
98.	Bond PJ, Faraldo-Gomez JD. (2011). Molecular mechanism of selective recruitment of Syk kinases by the membrane antigen-receptor complex. J Biol Chem. 2011 Jul 22;286(29):25872-81. doi: 10.1074/jbc.M111.223321. Epub 2011 May 21.

99.	Bond PJ, Guy AT, Heron AJ, Bayley H, Khalid S. (2011). Molecular dynamics simulations of DNA within a nanopore: arginine-phosphate tethering and a binding/sliding mechanism for translocation. Biochemistry. 2011 May 10;50(18):3777-83. doi: 10.1021/bi101404n. Epub 2011 Apr 13.
100.	Pineiro A, Bond PJ, Khalid S. (2011). Exploring the conformational dynamics and membrane interactions of PorB from C. glutamicum: a multi-scale molecular dynamics simulation study. Biochim Biophys Acta. 2011 Jun;1808(6):1746-52. doi: 10.1016/j.bbamem.2011.02.015. Epub 2011 Feb 24.
101.	Bond PJ, Khalid S. (2010). Antimicrobial and cell-penetrating peptides: structure, assembly and mechanisms of membrane lysis via atomistic and coarse-grained molecular dynamics simulations. Protein Pept Lett. 2010 Nov;17(11):1313-27. Review.
102.	Krah A, Pogoryelov D, Langer JD, Bond PJ, Meier T, Faraldo-Gomez JD. (2010). Structural and energetic basis for H+ versus Na+ binding selectivity in ATP synthase Fo rotors. Biochim Biophys Acta. 2010 Jun-Jul;1797(6-7):763-72. doi: 10.1016/j.bbabbio.2010.04.014. Epub 2010 Apr 21.
103.	Garzon D, Bond PJ, Faraldo-Gomez JD. (2009). Predicted structural basis for CD1c presentation of mycobacterial branched polyketides and long lipopeptide antigens. Mol Immunol. 2009 Dec;47(2-3):253-60. doi: 10.1016/j.molimm.2009.09.029. Epub 2009 Oct 13.
104.	Meier T, Krah A, Bond PJ, Pogoryelov D, Diederichs K, Faraldo-Gomez JD. (2009). Complete ion-coordination structure in the rotor ring of Na+-dependent F-ATP synthases. J Mol Biol. 2009 Aug 14;391(2):498-507. doi: 10.1016/j.jmb.2009.05.082. Epub 2009 Jun 3.
105.	Durrieu MP, Bond PJ, Sansom MS, Lavery R, Baaden M. (2009). Coarse-grain simulations of the R-SNARE fusion protein in its membrane environment detect long-lived conformational sub-states. Chemphyschem. 2009 Jul 13;10(9-10):1548-52. doi: 10.1002/cphc.200900216.
106.	Balali-Mood K, Bond PJ, Sansom MS. (2009). Interaction of monotopic membrane enzymes with a lipid bilayer: a coarse-grained MD simulation study. Biochemistry. 2009 Mar 17;48(10):2135-45. doi: 10.1021/bi8017398.
107.	Bond PJ, Wee CL, Sansom MS. (2008). Coarse-grained molecular dynamics simulations of the energetics of helix insertion into a lipid bilayer. Biochemistry. 2008 Oct 28;47(43):11321-31. doi: 10.1021/bi800642m. Epub 2008 Oct 2.
108.	Psachoulia E, Fowler PW, Bond PJ, Sansom MS. (2008). Helix-helix interactions in membrane proteins: coarse-grained simulations of glycophorin a helix dimerization. Biochemistry. 2008 Oct 7;47(40):10503-12. doi: 10.1021/bi800678t. Epub 2008 Sep 11.
109.	Khalid S, Bond PJ, Holyoake J, Hawtin RW, Sansom MS. (2008). DNA and lipid bilayers: self-assembly and insertion. J R Soc Interface. 2008 Dec 6;5 Suppl 3:S241-50. doi: 10.1098/rsif.2008.0239.focus.
110.	Bond PJ, Parton DL, Clark JF, Sansom MS. (2008). Coarse-grained simulations of the membrane-active antimicrobial Peptide maculatin 1.1. Biophys J. 2008 Oct;95(8):3802-15. doi: 10.1529/biophysj.108.128686. Epub 2008 Jul 18.
111.	Carpenter T, Bond PJ, Khalid S, Sansom MS. (2008). Self-assembly of a simple membrane protein: coarse-grained molecular dynamics simulations of the influenza M2 channel. Biophys J. 2008 Oct;95(8):3790-801. doi: 10.1529/biophysj.108.131078. Epub 2008 Jul 11.
112.	Biggin PC, Bond PJ. (2008). Molecular dynamics simulations of membrane proteins. Methods Mol Biol. 2008;443:147-60. doi: 10.1007/978-1-59745-177-2_8.

113.	Scott KA, Bond PJ, Ivetac A, Chetwynd AP, Khalid S, Sansom MS. (2008). Coarse-grained MD simulations of membrane protein-bilayer self-assembly. Structure. 2008 Apr;16(4):621-30. doi: 10.1016/j.str.2008.01.014.
114.	Sansom MS, Scott KA, Bond PJ. (2008). Coarse-grained simulation: a high-throughput computational approach to membrane proteins. Biochem Soc Trans. 2008 Feb;36(Pt 1):27-32. doi: 10.1042/BST0360027. Review.
115.	Khalid S, Bond PJ, Carpenter T, Sansom MS. (2008). OmpA: gating and dynamics via molecular dynamics simulations. Biochim Biophys Acta. 2008 Sep;1778(9):1871-80. Epub 2007 Jun 2. Review.
116.	Cox K, Bond PJ, Grottesi A, Baaden M, Sansom MS. (2008). Outer membrane proteins: comparing X-ray and NMR structures by MD simulations in lipid bilayers. Eur Biophys J. 2008 Feb;37(2):131-41.
117.	Bond PJ, Sansom MS. (2007). Bilayer deformation by the Kv channel voltage sensor domain revealed by self-assembly simulations. Proc Natl Acad Sci U S A. 2007 Feb 20;104(8):2631-6.
118.	Cuthbertson JM, Bond PJ, Sansom MS. (2006). Transmembrane helix-helix interactions: comparative simulations of the glycophorin a dimer. Biochemistry. 2006 Dec 5;45(48):14298-310.
119.	Bond PJ, Holyoake J, Ivetac A, Khalid S, Sansom MS. (2007). Coarse-grained molecular dynamics simulations of membrane proteins and peptides. J Struct Biol. 2007 Mar;157(3):593-605.
120.	Bond PJ, Derrick JP, Sansom MS. (2007). Membrane simulations of OpcA: gating in the loops? Biophys J. 2007 Jan 15;92(2):L23-5. Epub 2006 Nov 17.
121.	Lee PA, Orriss GL, Buchanan G, Greene NP, Bond PJ, Punginelli C, Jack RL, Sansom MS, Berks BC, Palmer T. (2006). Cysteine-scanning mutagenesis and disulfide mapping studies of the conserved domain of the twin-arginine translocase TatB component. J Biol Chem. 2006 Nov 10;281(45):34072-85.
122.	Psachoulia E, Bond PJ, Sansom MS. (2006). MD simulations of Mistic: conformational stability in detergent micelles and water. Biochemistry. 2006 Aug 1;45(30):9053-8.
123.	Bond PJ, Faraldo-Gomez JD, Deol SS, Sansom MS. (2006). Membrane protein dynamics and detergent interactions within a crystal: a simulation study of OmpA. Proc Natl Acad Sci U S A. 2006 Jun 20;103(25):9518-23.
124.	Bond PJ, Sansom MS. (2006). Insertion and assembly of membrane proteins via simulation. J Am Chem Soc. 2006 Mar 1;128(8):2697-704
125.	Khalid S, Bond PJ, Deol SS, Sansom MS. (2006). Modeling and simulations of a bacterial outer membrane protein: OprF from Pseudomonas aeruginosa. Proteins. 2006 Apr 1;63(1):6-15.
126.	Deol SS, Domene C, Bond PJ, Sansom MS. (2006). Anionic phospholipid interactions with the potassium channel KcsA: simulation studies. Biophys J. 2006 Feb 1;90(3):822-30. Epub 2005 Nov 4.
127.	Sansom MS, Bond PJ, Deol SS, Grottesi A, Haider S, Sands ZA. (2005). Molecular simulations and lipid-protein interactions: potassium channels and other membrane proteins. Biochem Soc Trans. 2005 Nov;33(Pt 5):916-20.
128.	Bond PJ, Cuthbertson J, Sansom MS. (2005). Simulation studies of the interactions between membrane proteins and detergents. Biochem Soc Trans. 2005 Nov;33(Pt 5):910-2.
129.	Law RJ, Capener C, Baaden M, Bond PJ, Campbell J, Patargias G, Arinaminpathy Y, Sansom MS. (2005). Membrane protein structure quality in molecular dynamics simulation. J Mol Graph Model. 2005 Oct;24(2):157-65.

130.	Patargias G, Bond PJ, Deol SS, Sansom MS. (2005). Molecular dynamics simulations of GlpF in a micelle vs in a bilayer: conformational dynamics of a membrane protein as a function of environment. J Phys Chem B. 2005 Jan 13;109(1):575-82.
131.	Bond PJ, Cuthbertson JM, Deol SS, Sansom MS. (2004). MD simulations of spontaneous membrane protein/detergent micelle formation. J Am Chem Soc. 2004 Dec 15;126(49):15948-9.
132.	Deol SS, Bond PJ, Domene C, Sansom MS. (2004). Lipid-protein interactions of integral membrane proteins: a comparative simulation study. Biophys J. 2004 Dec;87(6):3737-49. Epub 2004 Oct 1.
133.	Faraldo-Gomez JD, Forrest LR, Baaden M, Bond PJ, Domene C, Patargias G, Cuthbertson J, Sansom MS. (2004). Conformational sampling and dynamics of membrane proteins from 10-nanosecond computer simulations. Biophys J. 2004 Dec;87(6):3737-49. Epub 2004 Oct 1.
134.	Bond PJ, Sansom MS. (2004). The simulation approach to bacterial outer membrane proteins. Mol Membr Biol. 2004 May-Jun;21(3):151-61. Review.
135.	Domene C, Bond PJ, Deol SS, Sansom MS. (2003). Lipid/protein interactions and the membrane/water interfacial region. J Am Chem Soc. 2003 Dec 10;125(49):14966-7.
136.	Domene C, Bond PJ, Sansom MS. (2003). Membrane protein simulations: ion channels and bacterial outer membrane proteins. Adv Protein Chem. 2003;66:159-93. Review.
137.	Beckstein O, Biggin PC, Bond P, Bright JN, Domene C, Grottesi A, Holyoake J, Sansom MS. (2003). Ion channel gating: insights via molecular simulations. FEBS Lett. 2003 Nov 27;555(1):85-90. Review.
138.	Bond PJ, Sansom MS. (2003). Membrane protein dynamics versus environment: simulations of OmpA in a micelle and in a bilayer. J Mol Biol. 2003 Jun 20;329(5):1035-53.
139.	Bond PJ, Faraldo-Gomez JD, Sansom MS. (2002). OmpA: a pore or not a pore? Simulation and modeling studies. Biophys J. 2002 Aug;83(2):763-75.
140.	Sansom MS, Bond P, Beckstein O, Biggin PC, Faraldo-Gomez J, Law RJ, Patargias G, Tieleman DP. (2002). Water in ion channels and pores--simulation studies. Novartis Found Symp. 2002;245:66-78; discussion 79-83, 165-8. Review.