REFERENCES

Adasme, M., Linnemann, K., Bolz, S., Kaiser, F., Salentin, S., Haupt, V., & Schroeder, M. (2021). PLIP 2021: expanding the scope of the protein–ligand interaction profiler to DNA and RNA. *Nucleic Acids Research*, *49*(W1), W530-W534. doi: 10.1093/nar/gkab294

Ahmed, S., Quadeer, A., & McKay, M. (2022). SARS-CoV-2 T Cell Responses Elicited by COVID-19 Vaccines or Infection Are Expected to Remain Robust against Omicron. *Viruses*, *14*(1), 79. doi: 10.3390/v14010079

Albagi, S., Al-Nour, M., Elhag, M., Abdelihalim, A., Haroun, E., & Essa, M. et al. (2020). A Multiple Peptides Vaccine against nCOVID-19 Designed from the Nucleocapsid phosphoprotein (N) and Spike Glycoprotein (S) via the Immunoinformatics Approach. doi: 10.1101/2020.05.20.106351

Barquera, R., Collen, E., Di, D., Buhler, S., Teixeira, J., & Llamas, B. et al. (2020). Binding affinities of 438 <scp>HLA</scp> proteins to complete proteomes of seven pandemic viruses and distributions of strongest and weakest <scp>HLA</scp> peptide binders in populations worldwide. *HLA*, *96*(3), 277-298. doi: 10.1111/tan.13956

Berger, A., Nsoga, M., Perez-Rodriguez, F., Aad, Y., Sattonnet-Roche, P., & Gayet-Ageron, A. et al. (2021). Diagnostic accuracy of two commercial SARS-CoV-2 antigen-detecting rapid tests at the point of care in community-based testing centers. *PLOS ONE*, *16*(3), e0248921. https://doi.org/10.1371/journal.pone.0248921

Beyerstedt, S., Casaro, E., & Rangel, É. (2021). COVID-19: angiotensin-converting enzyme 2 (ACE2) expression and tissue susceptibility to SARS-CoV-2 infection. European Journal Of Clinical Microbiology & Infectious Diseases, 40(5), 905-919. https://doi.org/10.1007/s10096-020-04138-6

Brown, K., Gubbay, J., Hopkins, J., Patel, S., Buchan, S., Daneman, N., & Goneau, L. (2021). S-Gene Target Failure as a Marker of Variant B.1.1.7 Among SARS-CoV-2 Isolates in the Greater Toronto Area, December 2020 to March 2021. *JAMA*, *325*(20), 2115. doi: 10.1001/jama.2021.5607

Calis, J., Maybeno, M., Greenbaum, J., Weiskopf, D., De Silva, A., & Sette, A. et al. (2013). Properties of MHC Class I Presented Peptides That Enhance Immunogenicity. Plos Computational Biology, 9(10), e1003266. https://doi.org/10.1371/journal.pcbi.1003266

Capule, F., Tragulpiankit, P., Mahasirimongkol, S., Jittikoon, J., Wichukchinda, N., & Alentajan-Aleta, L. et al. (2021). HLA-A*24:07 as a potential biomarker for carbamazepine-induced Stevens–Johnson syndrome/toxic epidermal necrolysis in Filipino patients. Pharmacogenomics, 22(8), 465-472. doi: 10.2217/pgs-2020-0191

Chakraborty, S., Latheef, S., Munjal, A., Tiwari, R., Samad, H., & Karthik, K. et al. (2017). Cytotoxic T cells and Cancer Therapy. *Journal Of Experimental Biology And Agricultural Sciences*. doi: http://dx.doi.org/10.18006/2017.5(4).412.427

Chan, J., Kok, K., Zhu, Z., Chu, H., To, K., Yuan, S., & Yuen, K. (2020). Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. Emerging Microbes & Infections, 9(1), 221-236. https://doi.org/10.1080/22221751.2020.1719902

Chen, H., Tang, L., Yu, X., Zhou, J., Chang, Y., & Wu, X. (2020). Bioinformatics analysis of epitope-based vaccine design against the novel SARS-CoV-2. *Infectious Diseases Of Poverty*, *9*(1). doi: 10.1186/s40249-020-00713-3

Chen, T., Li, M., & Liu, J. (2018). π–π Stacking Interaction: A Nondestructive and Facile Means in Material Engineering for Bioapplications. *Crystal Growth &Amp; Design*, *18*(5), 2765-2783. doi: 10.1021/acs.cgd.7b01503

Chukwudozie, O., Gray, C., Fagbayi, T., Chukwuanukwu, R., Oyebanji, V., Bankole, T., Adewole, R. and Daniel, E., 2021. Immuno-informatics design of a multimeric epitope peptide based vaccine targeting SARS-CoV-2 spike glycoprotein. *PLOS ONE*, 16(3), p.e0248061.

Ciemny, M., Kurcinski, M., Kamel, K., Kolinski, A., Alam, N., Schueler-Furman, O., & Kmiecik, S. (2018). Protein–peptide docking: opportunities and challenges. *Drug Discovery Today*, *23*(8), 1530-1537. doi: 10.1016/j.drudis.2018.05.006

Coronavirus Disease 2019 (COVID-19) Situation Report - 1. Who.int. (2020). Retrieved from https://w
ww.who.int/docs/default-source/searo/indonesia/covid19/who-indonesia-situation-report-
1.pdf.

Coronavirus disease (COVID-19). (2020). Who.int. Retrieved from https://www.who.int/emergencies
/diseases/novel-coronavirus-2019/question-and-answers-hub/q-a-detail/coronavirus-disease
-covid-19.

Coronavirus disease (COVID-19). (2020). Who.int. Retrieved from https://www.who.int/health-
topics/coronavirus.

Chudleigh, H. (2022). 60 Scientists Sign Letter Petitioning FDA for T Cell Recognition | BioSpace.
Retrieved from https://www.biospace.com/article/60-scientists-sign-letter-petitioning-fda-
for-t-cell-recognition/

Douillard, V., Castelli, E., Mack, S., Hollenbach, J., Gourraud, P., Vince, N. and Limou, S., 2021. Current
HLA Investigations on SARS-CoV-2 and Perspectives. *Frontiers in Genetics*, 12.

Ehrenmann, F., Ouaray, Z., & Lefranc, M. (2021). IMGT 'Physicochemical' classes of the 20 common
amino acids. Retrieved from https://www.imgt.org/IMGTeducation/Aide-
memoire/_UK/aminoacids/IMGTclasses.html

Elemans, M., Florins, A., Willems, L., & Asquith, B. (2014). Rates of CTL Killing in Persistent Viral
Infection In Vivo. *Plos Computational Biology*, *10*(4), e1003534. doi:
10.1371/journal.pcbi.1003534

Gasper, D., Tejera, M., & Suresh, M. (2014). CD4 T-Cell Memory Generation and Maintenance. *Critical
Reviews In Immunology*, *34*(2), 121-146. doi: 10.1615/critrevimmunol.2014010373

Gitman, M., Shaban, M., Paniz-Mondolfi, A., & Sordillo, E. (2021). Laboratory Diagnosis of SARS-CoV-2
Pneumonia. *Diagnostics*, *11*(7), 1270. https://doi.org/10.3390/diagnostics11071270

Gonzalez-Galarza, F., McCabe, A., Santos, E., Jones, J., Takeshita, L., & Ortega-Rivera, N. et al. (2019).
Allele frequency net database (AFND) 2020 update: gold-standard data classification, open
access genotype data and new query tools. *Nucleic Acids Research*, *48*(D1), D783–D788.

https://doi.org/10.1093/nar/gkz1029

Gras, S., Nguyen, A., Szeto, C., & Rossjohn, J. (2021). Crystal Structure of HLA A*2402 in complex with YFSPIRVTF, an 9-mer influenza epitope. doi: 10.2210/pdb7jyv/pdb

Gustiananda, M., Sulistyo, B., Agustriawan, D., & Andarini, S. (2021). Immunoinformatics Analysis of SARS-CoV-2 ORF1ab Polyproteins to Identify Promiscuous and Highly Conserved T-Cell Epitopes to Formulate Vaccine for Indonesia and the World Population. *Vaccines*, *9*(12), 1459. https://doi.org/10.3390/vaccines9121459

HLA-A Gene - Major Histocompatibility Complex, Class I, A. Genecards.org. Retrieved from https://www.genecards.org/cgi-bin/carddisp.pl?gene=HLA-A

HLA-A major histocompatibility complex, class I, A [Homo sapiens (human)]. Ncbi.nlm.nih.gov. (2021). Retrieved from https://www.ncbi.nlm.nih.gov/gene/3105.

Hydrogen Bonding. (2020). Retrieved from https://chem.libretexts.org/Bookshelves/Physical_and_Th eoretical_Chemistry_Textbook_Maps/Supplemental_Modules_(Physical_and_Theoretical_C hemistry)/Physical_Properties_of_Matter/Atomic_and_Molecular_Properties/Intermolecula r_Forces/Specific_Interactions/Hydrogen_Bonding

Hydrophobic Interactions. (2020). Retrieved from https://chem.libretexts.org/Bookshelves/Physical_ and_Theoretical_Chemistry_Textbook_Maps/Supplemental_Modules_(Physical_and_Theore tical_Chemistry)/Physical_Properties_of_Matter/Atomic_and_Molecular_Properties/Intermo lecular_Forces/Hydrophobic_Interactions

Immune Epitope Database (IEDB). (2022). Retrieved from http://www.iedb.org

Indonesia Population (2022) - Worldometer. Worldometers.info. (2022). Retrieved from https://www.worldometers.info/world-population/indonesia-population/.

Jabbour, G., Rego, S., Nguyenkhoa, V., & Dakshanamurthy, S. (2021). Design of T cell epitope-based vaccine candidate for SARS-CoV-2 targeting nucleocapsid and spike protein escape variants. doi: 10.1101/2021.09.11.459907

Jakhar, R., & Gakhar, S. (2020). An Immunoinformatics Study to Predict Epitopes in the Envelope

Protein of SARS-CoV-2. *Canadian Journal Of Infectious Diseases And Medical Microbiology*, *2020*, 1-14. https://doi.org/10.1155/2020/7079356

Janse van Rensburg, W., de Kock, A., Bester, C., & Kloppers, J. (2021). HLA major allele group frequencies in a diverse population of the Free State Province, South Africa. *Heliyon*, *7*(4), e06850. doi: 10.1016/j.heliyon.2021.e06850

Karan, M., Tascioglu, C., Erten, N., Ozturk, A., Palanduz, S., & Carin, M. (2002). The Role of HLA Antigens in Chronic Hepatitis B Virus Infection. *Journal Of The Pakistan Medical Association*, *52*(6).

Kishore, A., & Petrek, M. (2018). Next-Generation Sequencing Based HLA Typing: Deciphering Immunogenetic Aspects of Sarcoidosis. Frontiers In Genetics, 9. https://doi.org/10.3389/fgene.2018.00503

Kløverpris, H., Harndahl, M., Leslie, A., Carlson, J., Ismail, N., & van der Stok, M. et al. (2012). HIV Control through a Single Nucleotide on the HLA-B Locus. *Journal Of Virology*, *86*(21), 11493-11500. https://doi.org/10.1128/jvi.01020-12

Kronenberg, D., Knight, R., Estorninho, M., Ellis, R., Kester, M., & de Ru, A. et al. (2012). Circulating Preproinsulin Signal Peptide–Specific CD8 T Cells Restricted by the Susceptibility Molecule HLA-A24 Are Expanded at Onset of Type 1 Diabetes and Kill β-Cells. *Diabetes*, *61*(7), 1752-1759. doi: 10.2337/db11-1520

Kumar, N., Admane, N., Kumari, A., Sood, D., Grover, S., & Prajapati, V. et al. (2021). Cytotoxic T-lymphocyte elicited vaccine against SARS-CoV-2 employing immunoinformatics framework. *Scientific Reports*, *11*(1). https://doi.org/10.1038/s41598-021-86986-6

Kurcinski, M., Jamroz, M., Blaszczyk, M., Kolinski, A., & Kmiecik, S. (2015). CABS-dock web server for the flexible docking of peptides to proteins without prior knowledge of the binding site. *Nucleic Acids Research*, *43*(W1), W419-W424. doi: 10.1093/nar/gkv456

Kuriata, A., Gierut, A., Oleniecki, T., Ciemny, M., Kolinski, A., Kurcinski, M., & Kmiecik, S. (2018). CABS-flex 2.0: a web server for fast simulations of flexibility of protein structures. *Nucleic Acids*

Research, *46*(W1), W338-W343. doi: 10.1093/nar/gky356

Kuzushima, K., Hayashi, N., Kudoh, A., Akatsuka, Y., Tsujimura, K., Morishima, Y., & Tsurumi, T. (2003). Tetramer-assisted identification and characterization of epitopes recognized by HLA A*2402– restricted Epstein-Barr virus–specific CD8+ T cells. *Blood*, *101*(4), 1460-1468. doi: 10.1182/blood-2002-04-1240

La Porta, C., & Zapperi, S. (2020). Estimating the Binding of Sars-CoV-2 Peptides to HLA Class I in Human Subpopulations Using Artificial Neural Networks. Cell Systems, 11(4), 412-417.e2. https://doi.org/10.1016/j.cels.2020.08.011

Lan, N., Kikuchi, M., Huong, V., Ha, D., Thuy, T., & Tham, V. et al. (2008). Protective and Enhancing HLA Alleles, HLA-DRB1*0901 and HLA-A*24, for Severe Forms of Dengue Virus Infection, Dengue Hemorrhagic Fever and Dengue Shock Syndrome. Plos Neglected Tropical Diseases, 2(10), e304. https://doi.org/10.1371/journal.pntd.0000304

Laskowski, R., Jabłońska, J., Pravda, L., Vařeková, R., & Thornton, J. (2017). PDBsum: Structural summaries of PDB entries. *Protein Science*, *27*(1), 129-134. doi: 10.1002/pro.3289

Laskowski R A, MacArthur M W, Thornton J M (2001). PROCHECK: validation of protein structure coordinates, in *International Tables of Crystallography, Volume F. Crystallography of Biological Macromolecules*, eds. Rossmann M G & Arnold E, Dordrecht, Kluwer Academic Publishers, The Netherlands, pp. 722-725.

Li, Q., Guan, X., Wu, P., Wang, X., Zhou, L., & Tong, Y. et al. (2020). Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus–Infected Pneumonia. New England Journal Of Medicine, 382(13), 1199-1207. https://doi.org/10.1056/nejmoa2001316

Liao, S., Du, Q., Meng, J., Pang, Z., & Huang, R. (2013). The multiple roles of histidine in protein interactions. *Chemistry Central Journal*, *7*(1). doi: 10.1186/1752-153x-7-44

Lizbeth, R., Jazmín, G., José, C., & Marlet, M. (2020). Immunoinformatics study to search epitopes of spike glycoprotein from SARS-CoV-2 as potential vaccine. Journal Of Biomolecular Structure And Dynamics, 39(13), 4878-4892. doi: 10.1080/07391102.2020.1780944

Luo, H., Ye, H., Ng, H., Shi, L., Tong, W., Mendrick, D., & Hong, H. (2015). Machine Learning Methods for Predicting HLA-Peptide Binding Activity. Bioinformatics And Biology Insights, 9(S3), 21-29. doi: 10.4137/bbi.s29466

Maier, H., Bickerton, E., & Britton, P. (2015). Coronaviruses (pp. 1-6). New York, NY: Humana Press.

Martz, E., Sussman, J., Decatur, W., Hodis, E., Jiang, Y., & Prilusky, J. (2014). Resolution. Retrieved from https://proteopedia.org/wiki/index.php/Resolution

Montes-Grajales, D., & Olivero-Verbel, J. (2021). Bioinformatics Prediction of SARS-CoV-2 Epitopes as Vaccine Candidates for the Colombian Population. *Vaccines*, *9*(7), 797. https://doi.org/10.3390/vaccines9070797

Moschopoulos, C., Berger, T., & Skevaki, C. (2022). Functional Assessment of T Cells. *Encyclopedia Of Infection And Immunity*, 122-133. doi: 10.1016/b978-0-12-818731-9.00151-8

Moura, R., Agrelli, A., Santos-Silva, C., Silva, N., Assunção, B., & Brandão, L. et al. (2022). Immunoinformatic approach to assess SARS-CoV-2 protein S epitopes recognised by the most frequent MHC-I alleles in the Brazilian population.

Mulpuru, V., & Mishra, N. (2021). Immunoinformatic based identification of cytotoxic T lymphocyte epitopes from the Indian isolate of SARS-CoV-2. *Scientific Reports*, *11*(1). https://doi.org/10.1038/s41598-021-83949-9

Murakoshi, H., Koyanagi, M., Akahoshi, T., Chikata, T., Kuse, N., & Gatanaga, H. et al. (2018). Impact of a single HLA-A*24:02-associated escape mutation on the detrimental effect of HLA-B*35:01 in HIV-1 control. Ebiomedicine, 36, 103-112. doi: 10.1016/j.ebiom.2018.09.022

Naz, A., Shahid, F., Butt, T., Awan, F., Ali, A., & Malik, A. (2020). Designing Multi-Epitope Vaccines to Combat Emerging Coronavirus Disease 2019 (COVID-19) by Employing Immuno-Informatics Approach. *Frontiers In Immunology*, *11*. doi: 10.3389/fimmu.2020.01663

Nguyen, A., Szeto, C., & Gras, S. (2021). The pockets guide to HLA class I molecules. *Biochemical Society Transactions*, *49*(5), 2319-2331. doi: 10.1042/bst20210410

Oakley, A., & Krishnamurthy, K. (2021). Stevens Johnson Syndrome. Retrieved from

https://www.ncbi.nlm.nih.gov/books/NBK459323/

Peng, M., Liu, W., Zheng, J., Lu, C., Hou, Y., & Zheng, C. et al. (2021). Immunological Aspects of SARS-CoV-2 Infection and the Putative Beneficial Role of Vitamin-D. International Journal Of Molecular Sciences, 22(10), 5251. https://doi.org/10.3390/ijms22105251

Pradana, K., Widjaya, M., & Wahjudi, M. (2019). Indonesians Human Leukocyte Antigen (HLA) Distributions and Correlations with Global Diseases. Immunological Investigations, 49(3), 333-363. https://doi.org/10.1080/08820139.2019.1673771

Pylaeva, S., Brehm, M., & Sebastiani, D. (2018). Salt Bridge in Aqueous Solution: Strong Structural Motifs but Weak Enthalpic Effect. *Scientific Reports*, *8*(1). doi: 10.1038/s41598-018-31935-z

PyMOL | pymol.org. Pymol.org. Retrieved from https://pymol.org/.

Qamar, M., Rehman, A., Tusleem, K., Ashfaq, U., Qasim, M., & Zhu, X. et al. (2020). Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics and in silico approaches. *PLOS ONE*, *15*(12), e0244176. https://doi.org/10.1371/journal.pone.0244176

Ramírez, D., & Caballero, J. (2018). Is It Reliable to Take the Molecular Docking Top Scoring Position as the Best Solution without Considering Available Structural Data?. *Molecules*, *23*(5), 1038. doi: 10.3390/molecules23051038

Reynisson, B., Alvarez, B., Paul, S., Peters, B., & Nielsen, M. (2020). NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data. *Nucleic Acids Research*, *48*(W1), W449-W454. doi: 10.1093/nar/gkaa379

Rezaei, N., & Hedayat, M. (2013). Allele Frequency. *Brenner's Encyclopedia Of Genetics*, 77-78. doi: 10.1016/b978-0-12-374984-0.00032-2

Rock, K., Reits, E., & Neefjes, J. (2016). Present Yourself! By MHC Class I and MHC Class II Molecules. *Trends In Immunology*, *37*(11), 724-737. doi: 10.1016/j.it.2016.08.010

Schaap-Johansen, A., Vujović, M., Borch, A., Hadrup, S., & Marcatili, P. (2021). T Cell Epitope Prediction

and Its Application to Immunotherapy. *Frontiers In Immunology*, *12*. doi: 10.3389/fimmu.2021.712488

Schmidt, M., & Varga, S. (2018). The CD8 T Cell Response to Respiratory Virus Infections. *Frontiers In Immunology*, *9*. doi: 10.3389/fimmu.2018.00678

Schrödinger, L., & DeLano, W. (2021). PyMOL. Pymol.org. Retrieved from https://pymol.org.

Shi, Y., Min, F., Zhou, D., Qin, B., Wang, J., & Hu, F. et al. (2017). HLA-A*24:02 as a common risk factor for antiepileptic drug–induced cutaneous adverse reactions. Neurology, 88(23), 2183-2191. doi: 10.1212/wnl.0000000000004008

Smith, C., Swaminathan, S., Lineburg, K., Panikkar, A., Raju, J., & Murdolo, L. et al. (2022). Ablation of CD8+ T-cell recognition of an immunodominant epitope in SARS-CoV-2 Omicron. https://doi.org/10.21203/rs.3.rs-1289622/v1

Sotomayor-Vivas, C., Hernández-Lemus, E., & Dorantes-Gilardi, R. (2022). Linking protein structural and functional change to mutation using amino acid networks. *PLOS ONE*, *17*(1), e0261829. doi: 10.1371/journal.pone.0261829

Sricharoensuk, C., Boonchalermvichien, T., Muanwien, P., Somparn, P., Pisitkun, T., & Sriswasdi, S. (2022). Unsupervised Mining of HLA-I Peptidomes Reveals New Binding Motifs and Potential False Positives in the Community Database. *Frontiers In Immunology*, *13*. doi: 10.3389/fimmu.2022.847756

Srivastava, V., Kaushik, S., Bhargava, G., Jain, A., Saxena, J., & Jyoti, A. (2021). A Bioinformatics Approach for the Prediction of Immunogenic Properties and Structure of the SARS-COV-2 B.1.617.1 Variant Spike Protein. *Biomed Research International*, *2021*, 1-8. doi: 10.1155/2021/7251119

Strong, R., Holmes, M., Li, P., Braun, L., Lee, N., & Geraghty, D. (2003). HLA-E Allelic Variants. *Journal Of Biological Chemistry*, *278*(7), 5082-5090. doi: 10.1074/jbc.m208268200

Sun, Y., & Xi, Y. (2014). Association Between HLA Gene Polymorphism and the Genetic Susceptibility of SARS Infection. *HLA And Associated Important Diseases*. doi: 10.5772/57561

Tan, A., Sodsai, P., Chia, A., Moreau, E., Chng, M., & Tham, C. et al. (2014). Immunoprevalence and Immunodominance of HLA-Cw∗0801-Restricted T Cell Response Targeting the Hepatitis B Virus Envelope Transmembrane Region. *Journal Of Virology*, *88*(2), 1332-1341. doi: 10.1128/jvi.02600-13

The Allele Frequency Net Database - Allele, haplotype and genotype frequencies in Worldwide Populations. (2022). Retrieved from http://www.allelefrequencies.net

Tracking SARS-CoV-2 variants. (2021). Retrieved from https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

Udugama, B., Kadhiresan, P., Kozlowski, H., Malekjahani, A., Osborne, M., & Li, V. et al. (2020). Diagnosing COVID-19: The Disease and Tools for Detection. ACS Nano, 14(4), 3822-3835. https://doi.org/10.1021/acsnano.0c02624

Utomo, D., Ramadhani, A., Hasanah, A., & Fitriah, A. (2018). Cara Mudah Melakukan Docking dengan PyRx (Autodock Vina) (1st ed., pp. 1-4). Global Science.

Vaccines Guidance Document. Extranet.who.int. (2021). Retrieved from https://extranet.who.int/pqweb/sites/default/files/documents/Status_COVID_VAX_29Sept2021_0.pdf.

van Buuren, M., Dijkgraaf, F., Linnemann, C., Toebes, M., Chang, C., & Mok, J. et al. (2013). HLA Micropolymorphisms Strongly Affect Peptide–MHC Multimer–Based Monitoring of Antigen-Specific CD8⁺T Cell Responses. *The Journal Of Immunology*, *192*(2), 641-648. https://doi.org/10.4049/jimmunol.1301770

van Deutekom, H., & Keşmir, C. (2015). Zooming into the binding groove of HLA molecules: which positions and which substitutions change peptide binding most?. *Immunogenetics*, *67*(8), 425-436. https://doi.org/10.1007/s00251-015-0849-y

Warren, R. L., & Birol, I. (2020). HLA predictions from the bronchoalveolar lavage fluid samples of five patients at the early stage of the wuhan seafood market COVID-19 outbreak. *ArXiv*, arXiv:2004.07108v3.

Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., & Gumienny, R. et al. (2018). SWISS-MODEL: homology modelling of protein structures and complexes. Nucleic Acids Research, 46(W1), W296-W303. https://doi.org/10.1093/nar/gky427

Weng, G., Gao, J., Wang, Z., Wang, E., Hu, X., & Yao, X. et al. (2020). Comprehensive Evaluation of Fourteen Docking Programs on Protein–Peptide Complexes. *Journal Of Chemical Theory And Computation*, *16*(6), 3959-3969. doi: 10.1021/acs.jctc.9b01208

WHO Coronavirus (COVID-19) Dashboard. Covid19.who.int. Retrieved from https://covid19.who.int.

Wieczorek, M., Abualrous, E., Sticht, J., Álvaro-Benito, M., Stolzenberg, S., Noé, F., & Freund, C. (2017). Major Histocompatibility Complex (MHC) Class I and MHC Class II Proteins: Conformational Plasticity in Antigen Presentation. Frontiers In Immunology, 8. https://doi.org/10.3389/fimmu.2017.00292

Wiegand, T., Malär, A., Cadalbert, R., Ernst, M., Böckmann, A., & Meier, B. (2020). Asparagine and Glutamine Side-Chains and Ladders in HET-s(218–289) Amyloid Fibrils Studied by Fast Magic-Angle Spinning NMR. *Frontiers In Molecular Biosciences*, *7*. doi: 10.3389/fmolb.2020.582033

wordometer. 2022. *Indonesia Population*. [online] Available at: <https://www.worldometers.info/world-population/indonesia-population/>

Wrapp, D., Wang, N., Corbett, K., Goldsmith, J., Hsieh, C., & Abiona, O. et al. (2020). Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science, 367(6483), 1260-1263. https://doi.org/10.1126/science.abb2507

Wu, Y., Ho, W., Huang, Y., Jin, D., Li, S., & Liu, S. et al. (2020). SARS-CoV-2 is an appropriate name for the new coronavirus. The Lancet, 395(10228), 949-950. https://doi.org/10.1016/s0140-6736(20)30557-2

Xie, N., Du, Q., Li, J., & Huang, R. (2015). Exploring Strong Interactions in Proteins with Quantum Chemistry and Examples of Their Applications in Drug Design. *PLOS ONE*, *10*(9), e0137113. doi: 10.1371/journal.pone.0137113

Yuan, S., Chan, H., & Hu, Z. (2017). Using <scp>PyMOL</scp> as a platform for computational drug

design. *Wires Computational Molecular Science*, *7*(2). doi: 10.1002/wcms.1298

Zhou, P., Jin, B., Li, H., & Huang, S. (2018). HPEPDOCK: a web server for blind peptide–protein docking based on a hierarchical algorithm. *Nucleic Acids Research*, *46*(W1), W443-W450. doi: 10.1093/nar/gky357