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# Supplementary information

# Rapid evaluation of COVID-19 vaccine effectiveness against symptomatic infection with SARS-CoV-2 variants by analysis of genetic distance

In the format provided by the authors and unedited

**Supplementary Information**

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**Table 1: The source of COVID-19 vaccine efficacy or effectiveness (VE) data by December 24, 2021**

| No. | Developers | Vaccine platforms | Vaccine products | Countries | Epidemiological studies | VE source | Data derived from |
|---|---|---|---|---|---|---|---|
| 1 | Bharat Biotech | Inactivated virus | COVAXIN | India | Phase 3 clinical trial | [1] | Table 2 |
| 2 | Sinopharm + China National Biotec Group Co + Beijing Institute of Biological Products | Inactivated virus | Inactivated SARS-CoV-2 vaccine (Vero cell), vaccine name BBIBP-CorV | United Arab Emirates, Bahrain | Phase 3 clinical trial | [2] | Table 2 |
| 3 | Sinopharm + China National Biotec Group Co + Wuhan Institute of Biological Products | Inactivated virus | Inactivated SARS-CoV-2 vaccine (Vero cell) | United Arab Emirates, Bahrain | Phase 3 clinical trial | [2] | Table 2 |
| 4 | Sinovac Research and Development Co. Ltd | Inactivated virus | SARS-CoV-2 vaccine (Inactivated) | Brazil | Phase 3 clinical trial | [3] | Table 2 |
| 5 | | | | Indonesia | Phase 3 clinical trial | [4] | Table 3 |
| 6 | BioNTech / Pfizer + Fosun Pharma | RNA based vaccine | BNT162b2 (3 LNP-mRNAs) | Argentina | Phase 3 clinical trial | [5] | Table 3 |
| 7 | | | | Brazil | Phase 3 clinical trial | [5] | Table 3 |
| 8 | | | | United States of America | Phase 3 clinical trial | [5] | Table 3 |
| 9 | | | | Argentina | Phase 3 clinical trial | [6] | Table 3 |
| 10 | | | | Brazil | Phase 3 clinical trial | [6] | Table 3 |
| 11 | | | | United States of America | Phase 3 clinical trial | [6] | Table 3 |
| 12 | Moderna + National Institute of Allergy and Infectious Diseases (NIAID) | RNA based vaccine | mRNA-1273 | United States of America | Phase 3 clinical trial | [7] | Figure 4 |
| 13 | | | | United States of America | Phase 3 clinical trial | [8] | Figure 3 |
| 14 | Novavax | Protein Subunit | SARS-CoV-2 rS/Matrix M1-Adjuvant (Full length recombinant SARS-CoV-2 glycoprotein nanoparticle vaccine adjuvanted with Matrix M) | Mexico | Phase 3 clinical trial | [9] | Figure 3 |
| 15 | | | | United States of America | Phase 3 clinical trial | [9] | Figure 3 |
| 16 | | | | South Africa (B.1.351) | Phase 3 clinical trial | [10] | Text |
| 17 | | | | United Kingdom (B.1.1.7) | Phase 3 clinical trial | [11] | Figure 4 |
| 18 | | | | United Kingdom (Non-B.1.1.7) | Phase 3 clinical trial | [11] | Figure 4 |
| 19 | CanSino Biological Inc./Beijing Institute of Biotechnology | Viral vector (Non-replicating) | Recombinant novel coronavirus vaccine (Adenovirus type 5 vector) | Argentina | Phase 3 clinical trial | [12] | Table 2 |
| 20 | Gamaleya Research Institute; Health Ministry of the Russian Federation | Viral vector (Non-replicating) | Gam-COVID-Vac Adeno-based (rAd26-S+rAd5-S) | Russia | Phase 3 clinical trial | [13] | Table 2 |
| 21 | Janssen Pharmaceutical | Viral vector (Ad26) | Ad26.COV2.S | Argentina, Chile, Colombia, Mexico, Peru | Phase 3 clinical trial | [14] | Table 3 |
| 22 | | | | Brazil | Phase 3 clinical trial | [14] | Table 3 |
| 23 | | | | South Africa (B.1.351) | Phase 3 clinical trial | [14] | Table 3 |
| 24 | | | | United States of America | Phase 3 clinical trial | [14] | Table 3 |
| 25 | | Viral vector (Non-replicating) | AZD1222 (ChAdOx1-S) | Brazil (B.1.1.28) | Phase 3 clinical trial | [15] | Table 2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 26 | AstraZeneca + University of Oxford | | | Brazil (P.1) | Phase 3 clinical trial | [15] | Table 2 |
| 27 | | | | Brazil (P.2) | Phase 3 clinical trial | [15] | Table 2 |
| 28 | | | | United States of America | Phase 3 clinical trial | [16] | Figure 3 |
| 29 | | | | Chile, Peru | Phase 3 clinical trial | [16] | Figure 3 |
| 30 | | | | Brazil | Phase 3 clinical trial | [17] | Table 2 |
| 31 | | | | United Kingdom | Phase 3 clinical trial | [17] | Table 2 |
| 32 | | | | United Kingdom, Brazil, South Africa | Phase 3 clinical trial | [18] | Table 1 |
| 33 | | | | United Kingdom (B.1.1.7) | Phase 3 clinical trial | [19] | Table 1 |
| 34 | Bharat Biotech | Inactivated virus | COVAXIN | India | Case-control | [20] | Table 2 |
| 35 | | | | India (Vellore) | Cohort | [21] | Text |
| 36 | Sinopharm + China National Biotec Group Co + Beijing Institute of Biological Products<br>Sinovac Research and Development Co. Ltd | Inactivated virus | Inactivated SARS-CoV-2 vaccine (Vero cell), vaccine name BBIBP-CorV<br>SARS-CoV-2 vaccine (Inactivated) | China (Guangzhou) (B.1.617.2) | Cohort | [22] | Table 2 |
| 37 | Sinovac Research and Development Co. Ltd | Inactivated virus | SARS-CoV-2 vaccine (Inactivated) | Brazil (Manaus) | Case-control | [23] | Text |
| 38 | | | | Brazil (São Paulo State) | Case-control | [24] | Table 2 |
| 39 | BioNTech / Pfizer + Fosun Pharma | RNA based vaccine | BNT162b2 (3 LNP-mRNAs) | Italy | Cohort | [25] | Table 3 |
| 40 | | | | Israel | Cohort | [26] | Table 2 |
| 41 | | | | US (Kentucky) | Cohort | [27] | Table 1 |
| 42 | | | | Italy | Cohort | [28] | Table 2 |
| 43 | | | | Israel | Cohort | [29] | Table 2b |
| 44 | | | | Israel | Cohort | [30] | Table |
| 45 | | | | United Kingdom (B.1.1.7) | Case-control | [31] | Table 1 |
| 46 | | | | United Kingdom (B.1.617.2) | Case-control | [31] | Table 1 |
| 47 | | | | United Kingdom (B.1.1.7) | Case-control | [32] | Table 2 |
| 48 | | | | United Kingdom (B.1.617.2) | Case-control | [32] | Table 2 |
| 49 | | | | United States of America (North Carolina) | Cohort | [33] | Text |
| 50 | | | | United States of America | Case-control | [34] | Table 3 |
| 51 | | | | Italy (Treviso) | Cohort | [35] | Table 2 |
| 52 | | | | United Kingdom | Case-control | [36] | Text |
| 53 | | | | Israel | Cohort | [37] | Table 2 |
| 54 | | | | United Kingdom (Scotland) (B.1.1.7) | Test-negative case-control | [38] | Table S5 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 55 | | | | United Kingdom (Scotland) (B.1.617.2) | Test-negative case-control | [38] | Table S5 |
| 56 | | | | Canada | Case-control | [39] | Table 2 |
| 57 | | | | Israel | Cohort | [40] | Table 4 |
| 58 | | | | Israel | Cohort | [41] | Text |
| 59 | Moderna + National Institute of Allergy and Infectious Diseases (NIAID) | RNA based vaccine | mRNA-1273 | United States of America | Case-control | [34] | Table 3 |
| 60 | | | | United States of America (North Carolina) | Cohort | [33] | Text |
| 61 | | | | United States of America (Southern California) | Cohort | [42] | Table 3 |
| 62 | BioNTech / Pfizer + Fosun Pharma | RNA based vaccine | BNT162b2 (3 LNP-mRNAs) | Canada (Ontario) (Earlier variant) | Test-negative case-control | [43] | eTable 6 |
| 63 | Moderna + National Institute of Allergy and Infectious Diseases (NIAID) | | mRNA-1273 | Canada (Ontario) (B.1.1.7) | Test-negative case-control | [43] | eTable 6 |
| 64 | | | | Canada (Ontario) (B.1.351/P.1) | Test-negative case-control | [43] | eTable 6 |
| 65 | | | | France (Earlier variant) | Case-control | [44] | Text |
| 66 | | | | France (B.1.1.7) | Case-control | [44] | Text |
| 67 | | | | France (B.1.351/P.1) | Case-control | [44] | Text |
| 68 | | | | United States of America (33 U.S. sites) | Test-negative case-control | [45] | Table 2 |
| 69 | | | | United States of America (Michigan, Pennsylvania, Texas, Washington, and Wisconsin) | Test-negative case-control | [46] | Table 2 |
| 70 | Janssen Pharmaceutical | Viral vector (Ad26) | Ad26.COV2.S | United States of America (North Carolina) | Cohort | [33] | Text |
| 71 | | | | Brazil (Mato-Grosso do Sul) | Test-negative case-control | [47] | Table 2 |
| 72 | AstraZeneca + University of Oxford | Viral vector (Non-replicating) | AZD1222 (ChAdOx1-S) | United Kingdom (B.1.617.2) | Case-control | [31] | Table 1 |
| 73 | | | | India | Case-control | [48] | Table 2 |
| 74 | | | | United Kingdom (B.1.1.7) | Case-control | [32] | Table 2 |
| 75 | | | | United Kingdom (B.1.617.2) | Case-control | [32] | Table 2 |
| 76 | | | | India (Puducherry) | Test-negative case-control | [49] | Table 2 |
| 77 | | | | United Kingdom (Scotland) (B.1.1.7) | Test-negative case-control | [38] | Table S5 |
| 78 | | | | United Kingdom (Scotland) (B.1.617.2) | Test-negative case-control | [38] | Table S5 |

**Table 2: COVID-19 VE prediction models for different vaccine platforms based on the genetic distance on the RBD**

| Vaccine platforms | | Slope (95% CI) | |
|---|---|---|---|
| mRNA | | -5.2 (-8.0, -2.4) | |
| Viral-vector | | -6.8 (-9.4, -4.2) | |
| Protein subunit | | -14.3 (-19.2, -9.4) | |
| Inactivated | | -15.8 (-19.3, -12.4) | |
| | | | |
| **Random effects variance** | 146.0 | **Two-sided *p*-value for RBD mismatch** | 0.038 |
| **Error variance** | 38.8 | $R^2$ | 86.3% |

**Table 3: COVID-19 VE prediction models for six vaccine products based on the genetic distance on the RBD**

| **Vaccine products** | | **Slope (95% CI)** | |
|---|---|---|---|
| Moderna: mRNA-1273 | | -4.8 (-7.8, -1.9) | |
| Pfizer–BioNTech: BNT162b2 | | -7.5 (-10.9, -4.1) | |
| Oxford–AstraZeneca: AZD1222 | | -5.0 (-7.8, -2.2) | |
| Janssen: Ad26.COV2.S | | -8.5 (-12.1, -4.9) | |
| Sinovac: CoronaVac | | -13.6 (-17.1, -10.1) | |
| Novavax: NVX-CoV2373 | | -14.1 (-18.2, -10.0) | |
| | | | |
| **Random effects variance** | 145.0 | **Two-sided *p*-value for RBD mismatch** | 0.006 |
| **Error variance** | 26.9 | $R^2$ | 87.9% |

**Table 4: COVID-19 VE prediction models for different vaccine platforms based on the genetic distance on the NTD and S protein**

| By genetic distance on the NTD: | | | |
|---|---|---|---|
| **Vaccine platforms** | | **Slope (95% CI)** | |
| mRNA | | -2.5 (-4.6, -0.5) | |
| Viral-vector | | -4.0 (-6.1, -1.8) | |
| Protein subunit | | -5.6 (-9.5, -1.7) | |
| Inactivated | | -7.8 (-10.2, -5.5) | |
| | | | |
| **Random effects variance** | 105.9 | **Two-sided *p*-value for NTD mismatch** | 0.086 |
| **Error variance** | 62.4 | $R^2$ | 75.8% |

| By genetic distance on the S protein: | | | |
|---|---|---|---|
| **Vaccine platforms** | | **Slope (95% CI)** | |
| mRNA | | -0.8 (-1.7, 0.2) | |
| Viral-vector | | -1.6 (-2.6, -0.6) | |
| Protein subunit | | -2.2 (-4.0, -0.5) | |
| Inactivated | | -4.1 (-5.2, -2.9) | |
| | | | |
| **Random effects variance** | 79.6 | **Two-sided *p*-value for S protein mismatch** | 0.082 |
| **Error variance** | 64.3 | $R^2$ | 78.4% |

**Table 5: The source of COVID-19 vaccine efficacy or effectiveness (VE) for validation**

| No. | Vaccine products | Vaccine Platforms | Observed VE | (95%CI) | References |
|---|---|---|---|---|---|
| Alpha (B.1.1.7) | | | | | |
| [1] | BNT162b2 | mRNA | 97 | (96, 98) | 31 |
| [2] | BNT162b2 | mRNA | 93.7 | (91.6, 95.3) | 32 |
| [3] | BNT162b2 | mRNA | 92 | (88, 94) | 38 |
| [4] | BNT162b2 | mRNA | 90 | (85, 94) | 43 |
| [5] | BNT162b2 | mRNA | 86 | (81, 90) | 44 |
| [6] | AZD1222 | Viral vector | 81 | (72, 87) | 38 |
| [7] | AZD1222 | Viral vector | 74.5 | (68.4, 79.4) | 32 |
| [8] | AZD1222 | Viral vector | 70.4 | (43.6, 84.5) | 19 |
| Beta (B.1.351) | | | | | |
| [9] | BNT162b2 | mRNA | 77 | (63, 86) | 44 |
| [10] | Ad26.COV2.S | Viral vector | 52 | (30.3, 67.4) | 14 |
| Gamma (P.1) | | | | | |
| [11] | BNT162b2 | mRNA | 88 | (61, 96) | 43 |
| [12] | AZD1222 | Viral vector | 63.6 | (-2.1, 87) | 15 |
| Delta (B.1.617.2) | | | | | |
| [13] | BNT162b2 | mRNA | 88 | (85.3, 90.1) | 32 |
| [14] | BNT162b2 | mRNA | 84 | (82, 86) | 31 |
| [15] | BNT162b2 | mRNA | 83 | (78, 87) | 38 |
| [16] | AZD1222 | Viral vector | 71 | (66, 74) | 31 |
| [17] | AZD1222 | Viral vector | 67 | (61.3, 71.8) | 32 |
| [18] | AZD1222 | Viral vector | 61 | (51, 70) | 38 |
| [19] | Covaxin | Inactivated | 65.2 | (33.1, 83) | 1 |
| [20] | CoronaVac | Inactivated | 60.4 | (31.8, 88.9) | 22 |
| B.1.1.28 | | | | | |
| [21] | AZD1222 | Viral vector | 72.6 | (46.4, 86) | 15 |
| Zeta (P.2) | | | | | |
| [22] | AZD1222 | Viral vector | 68.7 | (54.9, 78.3) | 15 |
| Omicron (B.1.1.529) | | | | | |
| [23] | mRNA-1273 | mRNA | 13.9 | (10.5, 17.1) | 50 |

**Table 6: SARS-CoV-2 variants tracked by WHO, including variants of concern (VOCs), variants of interest (VOIs), variants under monitoring (VUMs) and formerly monitored variants (March 16, 2022)**

| Pango lineages | WHO label | Nextstrain clade | GISAID clade | VOI or VOC | Earliest documented samples | Mutations in S protein |
|---|---|---|---|---|---|---|
| B.1.1.7 | Alpha | 20I (V1) | GRY | VOC | United Kingdom | 69-70del, 144del, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H |
| B.1.351 | Beta | 20H (V2) | GH/501Y.V2 | VOC | South Africa | D80A, D215G, Δ242-244, K417N, E484K, N501Y, D614G, A701V |
| P.1 | Gamma | 20J (V3) | GR/501Y.V3 | VOC | Brazil | L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, D614G, H655Y, T1027I, V1176F |
| B.1.617.2 | Delta | 21A, 21I, 21J | G/478K.V1 | VOC | India | T19R, 157del, L452R, T478K, D614G, P681R, D950N |
| B.1.1.529 | Omicron | 21K, 21L, 21M | GRA | VOC | Multiple countries | T19I, L24del, P25del, P26del, A27S, A67V, H69del, V70del, T95I, G142D, V143del, Y144del, Y145del , N211I, L212V, V213R, V213G, ins214EP, R214del, R216E, G339D, R346K, S371F, S371L, S373P, S375F, T376A, D405N, R408S, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, Q954H, N969K, N856K and L981F, |
| C.37 | Lambda | 21G | GR/452Q.V1 | VOI | Peru | G75V, T76I, 249del, 251del, 252del, L452Q, F490S, D614G, T859N |
| B.1.621 | Mu | 21H | GH | VOI | Colombia | T95I, Y144S, Y145N, R346K, E484K, N501Y, D614G, P681H, D950N |
| B.1.1.318 | - | - | GR | VUM | Multiple countries | T95I, E484K, D614G,P681H, D796H |
| C.1.2 | - | - | GR | VUM | South Africa | P9L,P25L, C136F, R190S, D215G, Y449H, T478K, E484K, N501Y, D614G, H655Y, N679K, T716I |
| B.1.640 | - | - | GH/490R | VUM | Multiple countries | P9L, E96Q, R190S, I210T, D215H, R346S, N394S, Y449N, E484K, F490R, N501Y, D614G, P681H, T859N, D936H, D1139H |
| AV.1 | - | - | GR | Formerly monitored variants | United Kingdom | D80G, T95I, G142D, N439K, E484K, D614G, P681H, I1130V, D1139H |
| AT.1 | - | - | GR | Formerly monitored variants | Russian Federation | P9L, H245P, E484K, D614G, E780K |
| P.2 | Zeta | 20B/S.484K | GR/484K.V2 | Formerly monitored variants | Brazil | E484K, D614G, V1176F |
| P.3 | Theta | 21E | GR/1092K.V1 | Formerly monitored variants | Philippines | 141-143del, E484K, N501Y, D614G, P681H, E1092K, H1101Y, V1176F |
| R.1 | - | 20B | GR | Formerly monitored variants | Multiple countries | W152L, E484K, D614G, G769V |
| B.1.466.2 | - | - | GH | Formerly monitored variants | Indonesia | N439K, D614G, P681R |
| B.1.1.519 | - | 20B/S.732A | GR | Formerly monitored variants | Multiple countries | T478K, D614G, P681H, T732A |
| C.36.3 | - | - | GR | Formerly monitored variants | Multiple countries | S12F, W152R, R346S, L452R, D614G, Q677H, A899S |
| B.1.214.2 | - | - | G | Formerly monitored variants | Multiple countries | Q414K, N450K, D614G, T716I |
| B.1.427/B.1.429 | Epsilon | 21C | GH/452R.V1 | Formerly monitored variants | California, United States of America | S13I, W152C, L452R, D614G |

| | | | | | | |
|---|---|---|---|---|---|---|
| B.1.1.523 | - | - | GR | Formerly monitored variants | Multiple countries | F306L, E484K, S494P, D614G, E780A, D839V, T1027I |
| B.1.619 | - | 20A/S.126A | G | Formerly monitored variants | | I210T, N440K, E484K, D614G, D936N, S939F, T1027I |
| B.1.620 | - | - | G | Formerly monitored variants | Multiple countries | P26S, V126A, H245Y, S477N, E484K, D614G, P681H, T1027I, D1118H |
| B.1.526 | Iota | 21F | GH/253G.V1 | Formerly monitored variants | New York, United States of America | L5F, T95I, D253G, D614G, A701V |
| B.1.525 | Eta | 21D | G/484K.V3 | Formerly monitored variants | Multiple countries | Q52R, A67V, 69del, 70del, 144del, E484K, D614G, Q677H, F888L |
| B.1.617.1 | Kappa | 21B | G/452R.V3 | Formerly monitored variants | India | T95I, G142D, E154K, L452R, E484Q, D614G, P681R, Q1071H |
| B.1.630 | - | - | GH | Formerly monitored variants | Dominican Republic | P9L, C136F, A222V, A243del, L244del, L452R, T478R, E484Q, H655Y, D614G, D950N |

**Table 7: Randomly selected strains from the variants tracked by WHO to investigate the best candidate vaccine antigens**

| Pango lineages | Accession number | Strain names | Source |
|---|---|---|---|
| B.1.1.7 | EPI_ISL_1718637 | hCoV-19/England/ALDP-15182AD/2021 | GISAID |
| B.1.351 | EPI_ISL_1534311 | hCoV-19/South Africa/NHLS-UCT-GS-B188/2021 | GISAID |
| P.1 | EPI_ISL_1495024 | hCoV-19/Brazil/MG-LBI246/2021 | GISAID |
| B.1.617.2 | EPI_ISL_1704630 | hCoV-19/India/MH-ICMR-NIV-INSACOG-GSEQ-1304/2021 | GISAID |
| BA.1 | EPI_ISL_9215151 | hCoV-19/USA/CA-Curative-120628/2021 | GISAID |
| BA.1.1 | EPI_ISL_7877115 | hCoV-19/India/un-LNHD6/2021 | GISAID |
| BA.2 | EPI_ISL_7971635 | hCoV-19/South Africa/NICD-N23195/2021 | GISAID |
| BA.3 | EPI_ISL_7747499 | hCoV-19/South Africa/CERI-KRISP-K033318/2021 | GISAID |
| C.37 | EPI_ISL_1629764 | hCoV-19/Peru/LIM-UPCH-0372/2021 | GISAID |
| B.1.621 | EPI_ISL_2828025 | hCoV-19/Colombia/BOL-INS-VG-2019/2021 | GISAID |
| B.1.1.318 | EPI_ISL_7335871 | hCoV-19/USA/CA-CDPH-3000035642/2021 | GISAID |
| C.1.2 | EPI_ISL_7456442 | hCoV-19/South Africa/NICD-N21411/2021 | GISAID |
| B.1.640.1 | EPI_ISL_7267558 | hCoV-19/France/CVL-CERBAHC-11681217/2021 | GISAID |
| B.1.640.2 | EPI_ISL_7412265 | hCoV-19/USA/TX-CDC-ASC210487089/2021 | GISAID |
| AT.1 | EPI_ISL_3454818 | hCoV-19/Russia/OMS-RII-MH22451S/2021 | GISAID |
| AV.1 | EPI_ISL_3291235 | hCoV-19/England/PHEC-Q303Q1F8/2021 | GISAID |
| P.2 | EPI_ISL_1240642 | hCoV-19/Brazil/MG-FUNED-49391-21/2021 | GISAID |
| P.3 | EPI_ISL_1122458 | hCoV-19/Philippines/PH-PGC-02772/2021 | GISAID |
| R.1 | EPI_ISL_1793651 | hCoV-19/Japan/YCH0165/2021 | GISAID |
| B.1.466.2 | EPI_ISL_7472531 | hCoV-19/Indonesia/JB-GS-WJHL-ITB-GS-184/2021 | GISAID |
| B.1.1.519 | EPI_ISL_7703862 | hCoV-19/USA/CA-CDPH-3000109212/2021 | GISAID |
| C.36.3 | EPI_ISL_8215718 | hCoV-19/Egypt/NRC-627/2021 | GISAID |
| B.1.214.2 | EPI_ISL_4370585 | hCoV-19/USA/CO-CDC-FG-014845/2021 | GISAID |
| B.1.429 | EPI_ISL_1525760 | hCoV-19/USA/CA-CDC-FG-015454/2021 | GISAID |
| B.1.1.523 | EPI_ISL_8189540 | hCoV-19/Russia/MAG-CRIE-L188T0024u/2021 | GISAID |
| B.1.619 | EPI_ISL_7667718 | hCoV-19/Canada/QC-1nQUP-9969036211/2021 | GISAID |
| B.1.620 | EPI_ISL_7120450 | hCoV-19/Congo/RC-116/2021 | GISAID |
| B.1.525 | EPI_ISL_1729603 | hCoV-19/Germany/BY-RKI-I-095380/2021 | GISAID |
| B.1.526 | EPI_ISL_1200537 | hCoV-19/USA/NY-NYCPHL-003648/2021 | GISAID |
| B.1.617.1 | EPI_ISL_1818634 | hCoV-19/India/KA-NIMH-SEQ-374/2021 | GISAID |
| B.1.630 | EPI_ISL_2828025 | hCoV-19/Colombia/BOL-INS-VG-2019/2021 | GISAID |
| B.1 | EPI_ISL_1473493 | hCoV-19/England/CAMC-145D216/2021 | GISAID |
| B.1.2 | EPI_ISL_1553218 | hCoV-19/USA/IL-S21WGS344/2021 | GISAID |
| B.1.617.3 | EPI_ISL_1704623 | hCoV-19/India/MH-ICMR-NIV-INSACOG-GSEQ-1294/2021 | GISAID |

**Fig. 1: Schematic representation of the SARS-CoV-2 genome**

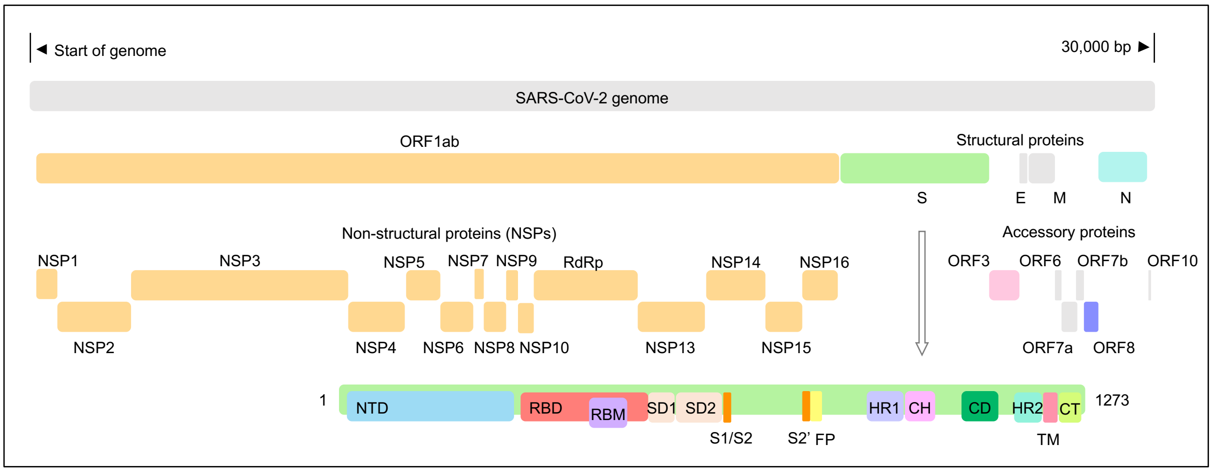
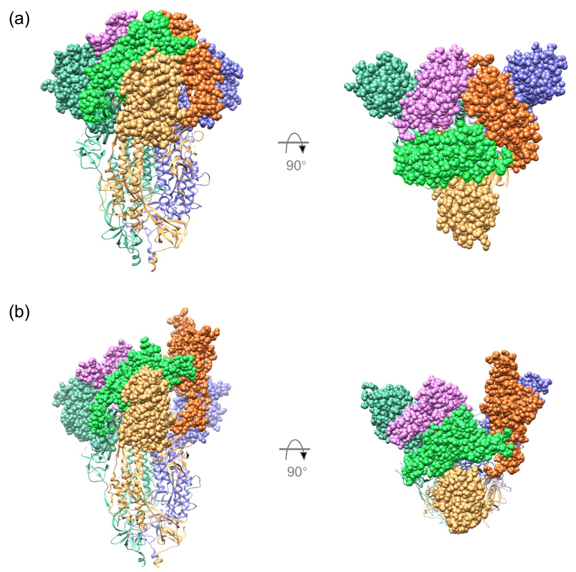


**Fig. 2: Structure of the SARS-CoV-2 Spike protein**




Legend: The location of receptor-binding domain (RBD) and N-terminal domain (NTD) are displayed on the 3D structure of SARS-CoV-2 Spike protein. Panel (a): the conformation of the prefusion trimer; all RBDs in the closed position. Panel (b): the active conformation; one RBD in the open position. The structures are shown from the side view and the top view, respectively. The RBD codons are highlighted in orchid, green and orange spheres. The NTD codons are marked in purple, dark green and yellow. Chimera[51] was used to generate the stereo view of S protein structure with 6VXX[52] and 7DWZ[53] of Protein Data Bank.

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