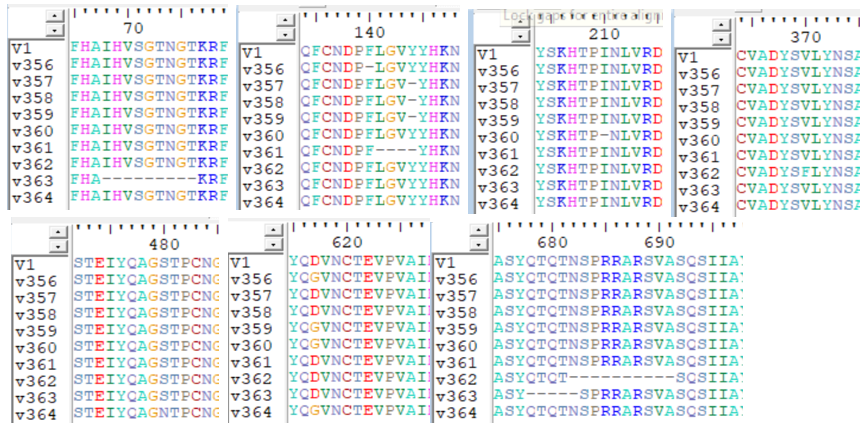
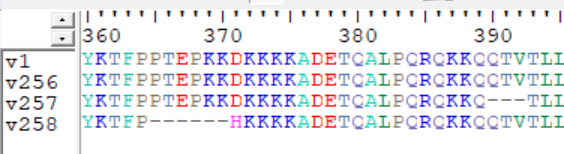
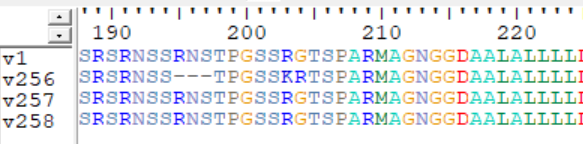
**A study on non-synonymous mutational patterns in structural proteins of SARS-CoV-2**

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**Figure S1. Spike (S) protein sequences alignment comparison. The variant v1 (reference) is compared with other 9 variants (v356-v364), and the several alignment positions are highlighted showing either amino acid substitution or deletion of some amino acid residues.**



**Figure S2. Nucleocapsid (N) protein sequence alignment comparison. The variant v1 (reference) is compared with other 3 variants (v256-v258), and the several alignment positions are highlighted showing deletion of some amino acid residues.**

**Table S1. Number of variant count in different countries for four structural proteins (Spike(S), Nucleocapsid(N), Membrane M), Envelope (E)).**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Country** | **S** | **N** | **M** | **E** | **Country** | **S** | **N** | **M** | **E** |
| AUS | 40 | 42 | 11 | 4 | LKA | 2 | 3 | 2 | 1 |
| BGD | 22 | 14 | 6 | 3 | MAR | 1 | 3 | 2 | 1 |
| BHR | 3 | 2 | 1 | 1 | MYS | 1 | 1 | 1 | 1 |
| BRA | 4 | 3 | 1 | 1 | Morocco | 1 | 1 | 1 | 1 |
| CHL | 2 | 4 | 1 | 1 | NGA | 1 | 1 | 1 | 1 |
| CHN | 16 | 5 | 2 | 3 | NLD | 1 | 2 | 2 | 1 |
| COL | 2 | 2 | 1 | 1 | NPL | 1 | 1 | 1 | 1 |
| CZE | 1 | 2 | 2 | 1 | NZL | 1 | 1 | 1 | 1 |
| DEU | 7 | 6 | 2 | 1 | PAK | 1 | 1 | 1 | 1 |
| EGY | 7 | 6 | 1 | 1 | PER | 1 | 1 | 1 | 1 |
| ESP | 3 | 3 | 2 | 1 | POL | 2 | 3 | 1 | 1 |
| FRA | 15 | 4 | 4 | 1 | RUS | 2 | 2 | 2 | 1 |
| GEO | 1 | 1 | 1 | 1 | SAU | 5 | 6 | 2 | 2 |
| GRC | 11 | 9 | 1 | 2 | SRB | 2 | 4 | 2 | 1 |
| GUM | 1 | 2 | 1 | 1 | SWE | 1 | 1 | 1 | 1 |
| Guangzhou | 1 | 1 | 1 | 1 | THA | 6 | 2 | 2 | 1 |
| HKG | 6 | 4 | 2 | 1 | TLS | 1 | 2 | 1 | 1 |
| IND | 49 | 34 | 5 | 3 | TUN | 5 | 5 | 1 | 1 |
| IRN | 2 | 2 | 1 | 1 | TUR | 3 | 3 | 1 | 1 |
| ISR | 2 | 2 | 1 | 1 | TWN | 6 | 8 | 1 | 1 |
| ITA | 4 | 2 | 3 | 1 | URY | 1 | 1 | 1 | 1 |
| JAM | 2 | 2 | 1 | 1 | USA | 212 | 183 | 35 | 14 |
| KAZ | 2 | 4 | 2 | 1 | VNM | 1 | 1 | 1 | 1 |
| KEN | 1 | 2 | 2 | 2 | ZAF | 1 | 1 | 1 | 1 |
| KOR | 2 | 3 | 1 | 1 |  |  |  |  |  |

**Table S2. Substitutions from different function domains of S protein with the predicted PROVEN score and mutation type.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Substitution | PROVEAN Score | Type | Domain | Substitution | PROVEAN Score | Type | Domain |
| Q314K | -0.634 | Neutral | RBD | Y789D | -1.727 | Neutral | FP |
| Q314L | -2.429 | Neutral | RBD | T791I | -0.896 | Neutral | FP |
| Q314R | -1.209 | Neutral | RBD | K795Q | 0.072 | Neutral | FP |
| T315I | 0.365 | Neutral | RBD | F797C | -2.668 | Deleterious | FP |
| Q321L | -1.042 | Neutral | RBD | L922F | -2.286 | Neutral | HR1 |
| T323I | 0.742 | Neutral | RBD | A924V | -3.742 | Deleterious | HR1 |
| P330S | -1.346 | Neutral | RBD | S929I | -3.335 | Deleterious | HR1 |
| T345S | -0.672 | Neutral | RBD | A930V | -3.727 | Deleterious | HR1 |
| A348S | -0.002 | Neutral | RBD | I931V | -0.758 | Neutral | HR1 |
| A348T | -0.115 | Neutral | RBD | D936Y | -2.602 | Deleterious | HR1 |
| N354K | 0.489 | Neutral | RBD | S939F | -3.094 | Deleterious | HR1 |
| V367F | -1.016 | Neutral | RBD | S939Y | -2.687 | Deleterious | HR1 |
| C379F | -5.187 | Deleterious | RBD | S940F | -3.055 | Deleterious | HR1 |
| V382E | -2.748 | Deleterious | RBD | L981F | 1.754 | Neutral | HR1 |
| V382L | -0.795 | Neutral | RBD | D1163G | -2.279 | Neutral | HR2 |
| P384L | -1.876 | Neutral | RBD | D1168H | -2.257 | Neutral | HR2 |
| T393P | -1.115 | Neutral | RBD | V1176F | -0.161 | Neutral | HR2 |
| R403K | 0.559 | Neutral | RBD | K1181R | -0.522 | Neutral | HR2 |
| R408I | 0.184 | Neutral | RBD | N1187K | -0.467 | Neutral | HR2 |
| L441I | 0.479 | Neutral | RBD | N1187Y | -1.65 | Neutral | HR2 |
| R457K | 0.253 | Neutral | RBD | K1191N | -1.707 | Neutral | HR2 |
| E471Q | 0.445 | Neutral | RBD | N1192T | -2.045 | Neutral | HR2 |
| G476S | -0.203 | Neutral | RBD | E1195Q | -1.047 | Neutral | HR2 |
| S477N | -0.034 | Neutral | RBD | Q1201K | 1.409 | Neutral | HR2 |
| V483A | -0.063 | Neutral | RBD | L1203F | -3.324 | Deleterious | HR2 |
| V483F | -0.372 | Neutral | RBD | K1205N | -0.686 | Neutral | HR2 |
| G485R | -0.035 | Neutral | RBD | G1219C | -0.855 | Neutral | TM |
| S494P | -0.373 | Neutral | RBD | G1219V | -0.54 | Neutral | TM |
| N501Y | -0.09 | Neutral | RBD | V1228L | -0.457 | Neutral | TM |
| H519Q | -0.328 | Neutral | RBD | V1230L | 0.222 | Neutral | TM |
| A520S | -0.044 | Neutral | RBD | M1237I | -1.382 | Neutral | TM |
| A522S | 0.674 | Neutral | RBD | M1237T | -1.999 | Neutral | TM |
| A522V | -0.966 | Neutral | RBD |  |  |  |  |
| K529E | 0.629 | Neutral | RBD |  |  |  |  |

**Table S3. Substitutions from different function domains of N protein with the predicted PROVEN score and mutation type**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Substitution | PROVEAN Score | Type | Domain | Substitution | PROVEAN Score | Type | Domain |
| T247I | -3.167 | Deleterious | CTD | D81Y | -3.664 | Deleterious | NTD |
| S250F | -3.114 | Deleterious | CTD | R89I | -3.626 | Deleterious | NTD |
| T271I | -3.042 | Deleterious | CTD | R92S | -3.718 | Deleterious | NTD |
| D297Y | -3.576 | Deleterious | CTD | R95L | -3.749 | Deleterious | NTD |
| W301C | -2.974 | Deleterious | CTD | A119V | -3.039 | Deleterious | NTD |
| P302S | -4.043 | Deleterious | CTD | P122L | -2.605 | Deleterious | NTD |
| P309L | -8.808 | Deleterious | CTD | D128Y | -4.529 | Deleterious | NTD |
| R319L | -2.562 | Deleterious | CTD | D128H | -2.998 | Deleterious | NTD |
| P326L | -2.816 | Deleterious | CTD | A134V | -2.811 | Deleterious | NTD |
| S327L | -3.022 | Deleterious | CTD | P151L | -4.932 | Deleterious | NTD |
| T334I | -2.72 | Deleterious | CTD | P151S | -3.284 | Deleterious | NTD |
| P344S | -4.031 | Deleterious | CTD | P168Q | -2.71 | Deleterious | NTD |
| K361I | -2.608 | Deleterious | CTD | P46S | -1.589 | Neutral | NTD |
| T247A | -1.69 | Neutral | CTD | G60R | -1.657 | Neutral | NTD |
| K249R | -0.673 | Neutral | CTD | E62V | -1.609 | Neutral | NTD |
| A252S | 0.647 | Neutral | CTD | D63N | -0.609 | Neutral | NTD |
| S255F | -1.685 | Neutral | CTD | P67T | -1.347 | Neutral | NTD |
| S255A | 0.397 | Neutral | CTD | P67S | -1.465 | Neutral | NTD |
| Q260L | -1.543 | Neutral | CTD | Q70H | -1.104 | Neutral | NTD |
| Q260E | -0.935 | Neutral | CTD | S79T | -0.719 | Neutral | NTD |
| V270L | -2.484 | Neutral | CTD | Q83R | -2.007 | Neutral | NTD |
| T282I | -0.444 | Neutral | CTD | A90S | 0.68 | Neutral | NTD |
| G284E | -0.998 | Neutral | CTD | G97S | -1.98 | Neutral | NTD |
| Q289H | -1.27 | Neutral | CTD | S105N | -0.497 | Neutral | NTD |
| Q289L | -1.699 | Neutral | CTD | A119S | -1.628 | Neutral | NTD |
| I292T | -2.017 | Neutral | CTD | G120R | -0.733 | Neutral | NTD |
| Q294L | -0.358 | Neutral | CTD | A125T | 0.85 | Neutral | NTD |
| Y298H | 0.388 | Neutral | CTD | T135I | -1.41 | Neutral | NTD |
| H300Y | -1.577 | Neutral | CTD | L139F | -0.697 | Neutral | NTD |
| A311S | -0.04 | Neutral | CTD | N140T | 1.551 | Neutral | NTD |
| I320V | 0.102 | Neutral | CTD | P142S | -1.348 | Neutral | NTD |
| G321D | 0.964 | Neutral | CTD | D144Y | -1.764 | Neutral | NTD |
| M322V | 0.347 | Neutral | CTD | D144H | -1.536 | Neutral | NTD |
| M322I | -0.041 | Neutral | CTD | H145Y | -0.542 | Neutral | NTD |
| T325I | -1.183 | Neutral | CTD | I146F | -1.44 | Neutral | NTD |
| T325R | 0.154 | Neutral | CTD | A152S | 1.463 | Neutral | NTD |
| P326S | -0.789 | Neutral | CTD | N154Y | -1.017 | Neutral | NTD |
| T329M | 0.924 | Neutral | CTD | A155V | -0.977 | Neutral | NTD |
| W330L | -1.011 | Neutral | CTD | A156S | -0.457 | Neutral | NTD |
| I337F | -1.712 | Neutral | CTD | I157T | -1.31 | Neutral | NTD |
| D340N | -1.602 | Neutral | CTD | Q163K | -0.06 | Neutral | NTD |
| D340G | -2.378 | Neutral | CTD | Q163R | -0.777 | Neutral | NTD |
| K342N | 0.938 | Neutral | CTD | T165I | -0.815 | Neutral | NTD |
| D348Y | -0.588 | Neutral | CTD | T166I | -0.849 | Neutral | NTD |
| D348H | 0.034 | Neutral | CTD | L167F | -1.838 | Neutral | NTD |
| T362I | -1.722 | Neutral | CTD | K169R | -0.589 | Neutral | NTD |