**The unignorable N protein of COVID-19**

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**Supplement Table 1 SARS-CoV Protein conserved domain predicted results**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **Accession** | **Description** | **Interval** | **E-value** |
| Peptidase\_C30 | [pfam05409](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam05409) | Coronavirus endopeptidase C30; Corresponds to Merops family C30. These peptidases are involved ... | 10069-10902 | 1.35E-160 |
| Viral\_protease | [pfam08715](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam08715) | Papain like viral protease; This family of viral proteases are similar to the papain protease ... | 4885-5835 | 1.25E-154 |
| Corona\_nucleoca | [pfam00937](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam00937) | Coronavirus nucleocapsid protein; | 28162-29214 | 5.11E-144 |
| nsp8 | [pfam08717](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam08717) | nsp8 replicase; Viral nsp8 (non structural protein 8) forms a hexadecameric supercomplex with ... | 12022-12615 | 3.18E-112 |
| Corona\_M | [pfam01635](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam01635) | Coronavirus M matrix/glycoprotein; This family consists of various coronavirus matrix proteins ... | 26404-27057 | 7.95E-101 |
| SUD-M | [pfam11633](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam11633) | Single-stranded poly(A) binding domain; This family of proteins represents Nsp3c, the product ... | 4243-4671 | 8.53E-93 |
| Nsp1 | [pfam11501](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam11501) | Non structural protein Nsp1; Nsp1 is the N-terminal cleavage product from the viral replicase ... | 301-645 | 1.14E-73 |
| NSP10 | [pfam09401](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam09401) | RNA synthesis protein NSP10; Non-structural protein 10 (NSP10) is involved in RNA synthesis. ... | 12988-13347 | 3.96E-67 |
| nsp9 | [pfam08710](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam08710) | nsp9 replicase; nsp9 is a single-stranded RNA-binding viral protein likely to be involved in ... | 12616-12954 | 2.13E-55 |
| Corona\_NSP4\_C | [pfam16348](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam16348) | Coronavirus nonstructural protein 4 C-terminus; This is the C-terminal domain of the ... | 9700-9978 | 1.99E-42 |
| DUF3655 super family | [cl13772](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13772) | Protein of unknown function (DUF3655); This domain family is found in viruses, and is ... | 3025-3231 | 7.83E-42 |
| Nsp3\_PL2pro super family | [cl13549](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13549) | Coronavirus polyprotein cleavage domain; This domain is found in SARS coronaviruses, and is ... | 4681-4878 | 2.09E-39 |
| nsp7 | [pfam08716](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam08716) | nsp7 replicase; nsp7 (non structural protein 7) has been implicated in viral RNA replication ... | 11773-12021 | 2.17E-35 |
| Macro | [pfam01661](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam01661) | Macro domain; This domain is an ADP-ribose binding module. It is found in a number of ... | 3370-3693 | 3.08E-23 |
| NAR | [pfam16251](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam16251) | Nucleic acid-binding domain (NAR); This domain, approximately 100 residues in length, is ... | 5914-6252 | 7.97E-13 |
| APA3\_viroporin super family | [cl12831](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl12831) | Coronavirus accessory protein 3a; APA3\_viroporin is a pro-apoptosis-inducing protein. It ... | 25268-26086 | 0.00E+00 |
| SARS\_lipid\_bind | [pfam09399](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam09399) | SARS lipid binding protein; This is a family of proteins found in SARS coronavirus. The ... | 28130-28423 | 1.38E-52 |
| DUF5515 | [pfam17635](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam17635) | Family of unknown function (DUF5515); This is a family of unknown function found in SARS ... | 28583-28792 | 2.77E-32 |
| Sars6 super family | [cl13556](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13556) | Open reading frame 6 from SARS coronavirus; This family is found in Coronaviruses. Proteins in ... | 27074-27259 | 9.51E-26 |
| Corona\_NS8 super family | [cl13520](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13520) | Coronavirus NS8 protein; This family of proteins is functionally uncharacterized. This protein ... | 27779-27895 | 1.34E-07 |
| DUF2873 super family | [cl15597](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl15597) | Protein of unknown function (DUF2873); This viral family of proteins has no known function. | 27638-27766 | 5.96E-06 |
| NSP11 | [pfam06471](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam06471) | NSP11; This region of coronavirus polyproteins encodes the NSP11 protein. | 17976-19754 | 0.00E+00 |
| Corona\_S2 | [pfam01601](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam01601) | Coronavirus S2 glycoprotein; The coronavirus spike glycoprotein forms the characteristic ... | 23433-25247 | 0.00E+00 |
| Corona\_RPol\_N | [pfam06478](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam06478) | Coronavirus RPol N-terminus; This family covers the N-terminal region of the coronavirus ... | 13410-14468 | 0.00E+00 |
| NSP13 | [pfam06460](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam06460) | Coronavirus NSP13; This family covers the NSP13 region of the coronavirus polyprotein. This ... | 20592-21479 | 0.00E+00 |
| Spike\_rec\_bind | [pfam09408](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam09408) | Spike receptor binding domain; Spike is an envelope glycoprotein which aids viral entry into ... | 22443-23198 | 1.81E-90 |
| SARS\_3b super family | [cl13775](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13775) | Severe acute respiratory syndrome coronavirus 3b protein; This family of proteins is found in ... | 25689-26147 | 6.13E-59 |
| SARS\_X4 super family | [cl07404](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl07404) | SARS coronavirus X4 like; The structure of the coronavirus X4 protein (also known as 7a and ... | 27318-27560 | 1.62E-47 |
| Corona\_NS8 super family | [cl13520](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13520) | Coronavirus NS8 protein; This family of proteins is functionally uncharacterized. This protein ... | 27882-28100 | 3.41E-33 |
| DEXXQc\_Upf1-like | [cd17934](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cd17934) | DEXXQ-box helicase domain of Upf1-like helicase; The Upf1-like helicase family includes UPF1, ... | 16980-17495 | 1.36E-19 |
| DNA2 | [COG1112](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=COG1112) | Superfamily I DNA and/or RNA helicase [Replication, recombination and repair]; | 17133-17942 | 9.63E-13 |

**Supplement Table 2 2019-nCoV Protein conserved domain predicted results**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **Accession** | **Description** | **Interval** | **E-value** |
| NSP11 | [pfam06471](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam06471) | NSP11; This region of coronavirus polyproteins encodes the NSP11 protein. | 18046-19824 | 0.00E+00 |
| Corona\_RPol\_N | [pfam06478](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam06478) | Coronavirus RPol N-terminus; This family covers the N-terminal region of the coronavirus ... | 13480-14538 | 0.00E+00 |
| NSP13 | [pfam06460](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam06460) | Coronavirus NSP13; This family covers the NSP13 region of the coronavirus polyprotein. This ... | 20662-21537 | 0.00E+00 |
| APA3\_viroporin super family | [cl12831](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl12831) | Coronavirus accessory protein 3a; APA3\_viroporin is a pro-apoptosis-inducing protein. It ... | 25393-26214 | 1.45E-137 |
| SARS\_X4 super family | [cl07404](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl07404) | SARS coronavirus X4 like; The structure of the coronavirus X4 protein (also known as 7a and ... | 27439-27678 | 8.22E-43 |
| DEXXQc\_Upf1-like | [cd17934](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cd17934) | DEXXQ-box helicase domain of Upf1-like helicase; The Upf1-like helicase family includes UPF1, ... | 17050-17565 | 1.36E-19 |
| Sars6 super family | [cl13556](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13556) | Open reading frame 6 from SARS coronavirus; This family is found in Coronaviruses. Proteins in ... | 27202-27384 | 4.20E-16 |
| DNA2 | [COG1112](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=COG1112) | Superfamily I DNA and/or RNA helicase [Replication, recombination and repair]; | 17203-18012 | 5.39E-13 |
| Corona\_S2 super family | [cl20218](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl20218) | Coronavirus S2 glycoprotein; The coronavirus spike glycoprotein forms the characteristic ... | 23546-25372 | 0.00E+00 |
| Peptidase\_C30 | [pfam05409](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam05409) | Coronavirus endopeptidase C30; Corresponds to Merops family C30. These peptidases are involved ... | 10139-10972 | 1.06E-157 |
| Corona\_nucleoca super family | [cl03023](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl03023) | Coronavirus nucleocapsid protein; | 28313-29377 | 2.15E-133 |
| Viral\_protease super family | [cl09459](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl09459) | Papain like viral protease; This family of viral proteases are similar to the papain protease ... | 4955-5905 | 5.93E-129 |
| nsp8 | [pfam08717](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam08717) | nsp8 replicase; Viral nsp8 (non structural protein 8) forms a hexadecameric supercomplex with ... | 12092-12685 | 1.21E-109 |
| Spike\_rec\_bind super family | [cl09656](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl09656) | Spike receptor binding domain; Spike is an envelope glycoprotein which aids viral entry into ... | 22553-23311 | 3.51E-73 |
| SUD-M super family | [cl13138](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13138) | Single-stranded poly(A) binding domain; This family of proteins represents Nsp3c, the product ... | 4316-4744 | 4.39E-73 |
| NSP10 | [pfam09401](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam09401) | RNA synthesis protein NSP10; Non-structural protein 10 (NSP10) is involved in RNA synthesis. ... | 13058-13417 | 1.65E-65 |
| Nsp1 super family | [cl13018](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13018) | Non structural protein Nsp1; Nsp1 is the N-terminal cleavage product from the viral replicase ... | 302-646 | 5.16E-63 |
| nsp9 | [pfam08710](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam08710) | nsp9 replicase; nsp9 is a single-stranded RNA-binding viral protein likely to be involved in ... | 12686-13024 | 4.16E-54 |
| Corona\_NSP4\_C | [pfam16348](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam16348) | Coronavirus nonstructural protein 4 C-terminus; This is the C-terminal domain of the ... | 9770-10048 | 1.19E-41 |
| nsp7 | [pfam08716](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam08716) | nsp7 replicase; nsp7 (non structural protein 7) has been implicated in viral RNA replication ... | 11843-12091 | 3.94E-35 |
| Nsp3\_PL2pro super family | [cl13549](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13549) | Coronavirus polyprotein cleavage domain; This domain is found in SARS coronaviruses, and is ... | 4757-4948 | 1.99E-27 |
| Macro | [pfam01661](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam01661) | Macro domain; This domain is an ADP-ribose binding module. It is found in a number of ... | 3437-3760 | 3.25E-22 |
| SARS\_3b super family | [cl13775](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13775) | Severe acute respiratory syndrome coronavirus 3b protein; This family of proteins is found in ... | 25814-26275 | 3.83E-22 |
| DUF3655 super family | [cl13772](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13772) | Protein of unknown function (DUF3655); This domain family is found in viruses, and is ... | 3023-3226 | 2.82E-19 |
| NAR super family | [cl24732](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl24732) | Nucleic acid-binding domain (NAR); This domain, approximately 100 residues in length, is ... | 5984-6322 | 1.64E-11 |
| Corona\_M | [pfam01635](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=pfam01635) | Coronavirus M matrix/glycoprotein; This family consists of various coronavirus matrix proteins ... | 26532-27185 | 4.37E-93 |
| SARS\_lipid\_bind super family | [cl09647](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl09647) | SARS lipid binding protein; This is a family of proteins found in SARS coronavirus. The ... | 28284-28574 | 7.89E-35 |
| Corona\_NS8 super family | [cl13520](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl13520) | Coronavirus NS8 protein; This family of proteins is functionally uncharacterized. This protein ... | 27894-28247 | 3.24E-33 |
| DUF5515 super family | [cl38891](https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?ascbin=8&maxaln=10&seltype=2&uid=cl38891) | Family of unknown function (DUF5515); This is a family of unknown function found in SARS ... | 28734-28904 | 4.40E-20 |

**Supplement Table 3 the COACH and COFACTOR calculation result**

**(a) C-score** is the confidence score of the prediction. C-score ranges [0-1], where a higher score indicates a more reliable prediction.

**(b) Cluster size** is the total number of templates in a cluster.

**(c) Lig Name** is the name of possible binding ligand. Click the ligand name to view its information in the BioLiP database.

**(d) Rep** is a single complex structure with the most representative ligand in the cluster, i.e., the one listed in the Lig Name column. Mult is the complex structures with all potential binding ligands in the cluster.

**(e) Ligands** lists all ligands in a cluster. The numbers in the parentheses are the appearing times of the corresponding ligands. Click the ligand name to visualize its detailed information in BioLiP.

**(f)** Templates presents the list of templates in a cluster. The template names are: Click the corresponding template to search the BioLiP database. When the number of templates is >5, click "show all templates" to get the list of all templates in the cluster

**(g) RMSD** the RMSD between residues that are structurally aligned by TM-align.

**(h) IDEN** is the percentage sequence identity in the structurally aligned region.

**(i) Cov** represents the coverage of global structural alignment and is equal to the number of structurally aligned residues divided by length of the query protein.

**(j) BS-score** is a measure of local similarity (sequence & structure) between template binding site and predicted binding site in the query structure. Based on large scale benchmarking analysis, we have observed that a BS-score >1 reflects a significant local match between the predicted and template binding site.

COACH Results:

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Rank** | **C-score** | **Cluster size** | **PDB Hit** | **Lig Name** |  | **Consensus Binding Residues** |
|  | 1 | 0.09 | 5 | [2ckjC](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=2ckj) | [FES](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=FES) |  | 83,84,85,114,115 |
|  | 2 | 0.05 | 3 | [2jxmA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=2jxm) | [HEC](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=HEC) |  | 115,117 |
|  | 3 | 0.05 | 3 | [1m7sA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=1m7s) | [HEM](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=HEM) |  | 352,358 |
|  | 4 | 0.04 | 2 | [4lm7A](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=4lm7) | [U5P](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=U5P) |  | 49,50,51,52,53,54,55,107,109,111,148,156,174 |
|  | 5 | 0.04 | 2 | [3m8dA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=3m8d) | [C8E](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=C8E) |  | 85,86,111 |
|  | 6 | 0.02 | 1 | [1c9uA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=1c9u) | [CA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=CA) |  | 92,116,117,228 |
|  | 7 | 0.02 | 1 | [1mcjB](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=1mcj) | [HIS](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=HIS) |  | 87,110 |
|  | 8 | 0.02 | 1 | N/A | N/A |  | 55,56,66,108,110,159 |
|  | 9 | 0.02 | 1 | N/A | N/A |  | 46,50,51,54,88,90,92,93,104,105,106,107,109,111,149,151,152,176 |
|  | 10 | 0.02 | 1 | [2z3hB](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=2z3h) | [BLO](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=BLO) |  | 123,132 |

TM-SITE result

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Rank** | **C-scorea** | **Cluster sizeb** | **Rep Templc** |  | **Ligandse** | **Predicted binding site residues** |
|  | 1 | 0.18 | 3 | [4cabA\_BS02\_HEM](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/model1/tmsite/complex1_4cabA_BS02_HEM.pdb.gz) |  | [HEM](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=HEM)(3) | 352,358 |
|  | 2 | 0.18 | 2 | [4lm7A\_BS01\_U5P](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/model1/tmsite/complex2_4lm7A_BS01_U5P.pdb.gz) |  | [U5P](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=U5P)(1),[AMP](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=AMP)(1) | 49,50,51,52,53,54,55,107,109,111,148,156,174 |
|  | 3 | 0.17 | 1 | [3wh0A\_BS01\_O4B](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/model1/tmsite/complex3_3wh0A_BS01_O4B.pdb.gz) |  | [O4B](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=O4B)(1) | 86,132 |
|  | 4 | 0.17 | 1 | [1mcjB\_BS01\_HIS](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/model1/tmsite/complex4_1mcjB_BS01_HIS.pdb.gz) |  | [HIS](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=HIS)(1) | 87,110 |
|  | 5 | 0.17 | 1 | [3m8dA\_BS06\_C8E](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/model1/tmsite/complex5_3m8dA_BS06_C8E.pdb.gz) |  | [C8E](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=C8E)(1) | 85,86,111 |

S-SITE Results

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Rank** | **C-scorea** | **Cluster sizeb** | **Templatesc** | **Ligandsd** | **Predicted binding site residues** |
|  | 1 | 0.18 | 3 | [List](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/ssite/templates_1.lst) | [HEC](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=HEC)(1),[CA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=CA)(1),[U](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=U)(1) | 115,116,117 |
|  | 2 | 0.17 | 3 | [List](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/ssite/templates_2.lst) | [GTX](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=GTX)(1),[CU](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=CU)(1),[CA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=CA)(1) | 92,111,112,116,117,160 |
|  | 3 | 0.16 | 3 | [List](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/ssite/templates_3.lst) | [UUU](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=UUU)(1),[PLA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=PLA)(1),[CA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=CA)(1) | 92,112,116,117,148,154,228,277 |
|  | 4 | 0.13 | 1 | [List](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/C-I-TASSER/2019-nCov/COACH/QHD43423/ssite/templates_4.lst) | [BLO](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/sym.cgi?code=BLO)(1) | 123,132 |

COFACTOR Results

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Rank** | **C-scorea** | **PDB Hit** | **TM-score** | **RMSDb** | **IDENc** | **Covd** | **BS-scoree** | **Lig. Name** |  | **Predicted binding site residues** |
|  | 1 | 0.01 | [4k7qA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=4k7q) | 0.364 | 6.98 | 0.030 | 0.599 | 0.81 | ZLD |  | 306,307 |
|  | 2 | -0.04 | [2ckjA](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=2ckj) | 0.336 | 6.94 | 0.045 | 0.542 | 0.86 | FES |  | 83,84,85,114,115 |
|  | 3 | -0.04 | [2ckjD](https://n.ustb.edu.cn/https/77726476706e69737468656265737421eaff4092203c6952300b8aa19a1b2e300e084e0ef7f563b425d119/BioLiP/qsearch_pdb.cgi?pdbid=2ckj) | 0.342 | 6.78 | 0.051 | 0.542 | 0.70 | FES |  | 85,113,114,123,124,134 |

**Supplement Table 4 the SCRIBER calculated results**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Residue  Number | Residue  Type | IntermediatePredictions\_layer1 | | | | FinalPredictions | |
|  |  | DNA-binding-propensity | RNA-binding-propensity | protein-binding-propensity | ligand-binding-propensity | protein-binding-propensity | protein-binding-residues |
| 1 | m | 0.0861 | 0.0821 | 0.2489 | 0.0123 | 0.1974 | 0 |
| 2 | s | 0.0837 | 0.1406 | 0.1932 | 0.018 | 0.1553 | 0 |
| 3 | d | 0.0899 | 0.1484 | 0.181 | 0.0459 | 0.1359 | 0 |
| 4 | n | 0.1016 | 0.2321 | 0.2028 | 0.0668 | 0.1312 | 0 |
| 5 | g | 0.0993 | 0.2045 | 0.1131 | 0.0559 | 0.0931 | 0 |
| 6 | p | 0.0827 | 0.2591 | 0.1941 | 0.0396 | 0.1176 | 0 |
| 7 | q | 0.0809 | 0.3543 | 0.1748 | 0.136 | 0.0986 | 0 |
| 8 | n | 0.0793 | 0.412 | 0.1342 | 0.0962 | 0.0816 | 0 |
| 9 | q | 0.09 | 0.595 | 0.186 | 0.0616 | 0.1117 | 0 |
| 10 | r | 0.0663 | 0.5808 | 0.2445 | 0.0522 | 0.1488 | 0 |
| 11 | n | 0.0762 | 0.4583 | 0.185 | 0.0275 | 0.1149 | 0 |
| 12 | a | 0.0621 | 0.3219 | 0.1196 | 0.0192 | 0.1142 | 0 |
| 13 | p | 0.0666 | 0.4264 | 0.1524 | 0.017 | 0.1249 | 0 |
| 14 | r | 0.0648 | 0.5574 | 0.1993 | 0.0369 | 0.1336 | 0 |
| 15 | i | 0.0738 | 0.2593 | 0.1147 | 0.0246 | 0.1021 | 0 |
| 16 | t | 0.079 | 0.3598 | 0.1819 | 0.0276 | 0.1247 | 0 |
| 17 | f | 0.0632 | 0.1708 | 0.2842 | 0.039 | 0.2081 | 0 |
| 18 | g | 0.081 | 0.2405 | 0.2585 | 0.0193 | 0.1858 | 0 |
| 19 | g | 0.0689 | 0.2467 | 0.1897 | 0.0306 | 0.1509 | 0 |
| 20 | p | 0.0562 | 0.1746 | 0.2803 | 0.0224 | 0.2107 | 0 |
| 21 | s | 0.0703 | 0.3337 | 0.2507 | 0.0392 | 0.1842 | 0 |
| 22 | d | 0.0676 | 0.3014 | 0.2105 | 0.0461 | 0.1676 | 0 |
| 23 | s | 0.0607 | 0.4812 | 0.2042 | 0.0233 | 0.142 | 0 |
| 24 | t | 0.067 | 0.3896 | 0.257 | 0.0269 | 0.1948 | 0 |
| 25 | g | 0.0762 | 0.3615 | 0.2505 | 0.0152 | 0.1818 | 0 |
| 26 | s | 0.0771 | 0.3301 | 0.2053 | 0.0291 | 0.1542 | 0 |
| 27 | n | 0.0815 | 0.2826 | 0.198 | 0.0376 | 0.1735 | 0 |
| 28 | Q | 0.0757 | 0.331 | 0.2752 | 0.0343 | 0.2332 | 1 |
| 29 | n | 0.0943 | 0.3904 | 0.2146 | 0.0311 | 0.1592 | 0 |
| 30 | g | 0.0751 | 0.2363 | 0.1196 | 0.0399 | 0.1061 | 0 |
| 31 | e | 0.1003 | 0.2728 | 0.1775 | 0.1668 | 0.1472 | 0 |
| 32 | r | 0.0981 | 0.3696 | 0.2406 | 0.1689 | 0.1841 | 0 |
| 33 | s | 0.0986 | 0.3716 | 0.1867 | 0.0306 | 0.1308 | 0 |
| 34 | g | 0.1063 | 0.2919 | 0.1642 | 0.0289 | 0.1382 | 0 |
| 35 | a | 0.103 | 0.2779 | 0.1629 | 0.0509 | 0.1183 | 0 |
| 36 | R | 0.0896 | 0.4092 | 0.3027 | 0.1488 | 0.227 | 1 |
| 37 | s | 0.102 | 0.4768 | 0.1778 | 0.0737 | 0.1396 | 0 |
| 38 | k | 0.0849 | 0.625 | 0.2523 | 0.0573 | 0.166 | 0 |
| 39 | q | 0.1075 | 0.5351 | 0.2537 | 0.0578 | 0.1675 | 0 |
| 40 | R | 0.0958 | 0.364 | 0.3277 | 0.0423 | 0.2294 | 1 |
| 41 | R | 0.0824 | 0.4184 | 0.4282 | 0.0413 | 0.3818 | 1 |
| 42 | P | 0.0784 | 0.2892 | 0.2648 | 0.0488 | 0.2385 | 1 |
| 43 | Q | 0.0882 | 0.4368 | 0.3205 | 0.0487 | 0.288 | 1 |
| 44 | G | 0.1118 | 0.3146 | 0.2731 | 0.0134 | 0.2356 | 1 |
| 45 | L | 0.0726 | 0.1629 | 0.3057 | 0.0147 | 0.2592 | 1 |
| 46 | P | 0.063 | 0.1905 | 0.357 | 0.021 | 0.2999 | 1 |
| 47 | N | 0.0684 | 0.255 | 0.3663 | 0.0234 | 0.3161 | 1 |
| 48 | N | 0.0677 | 0.1924 | 0.3239 | 0.0203 | 0.273 | 1 |
| 49 | T | 0.0595 | 0.2234 | 0.2987 | 0.0327 | 0.2489 | 1 |
| 50 | a | 0.045 | 0.1145 | 0.2458 | 0.0236 | 0.1904 | 0 |
| 51 | s | 0.055 | 0.1781 | 0.1922 | 0.0831 | 0.1453 | 0 |
| 52 | W | 0.0527 | 0.1306 | 0.3734 | 0.0801 | 0.3006 | 1 |
| 53 | f | 0.053 | 0.0929 | 0.2989 | 0.0586 | 0.2196 | 0 |
| 54 | T | 0.056 | 0.1946 | 0.3153 | 0.013 | 0.2523 | 1 |
| 55 | a | 0.0568 | 0.1625 | 0.1615 | 0.0171 | 0.1333 | 0 |
| 56 | l | 0.0614 | 0.1143 | 0.1799 | 0.0299 | 0.1689 | 0 |
| 57 | t | 0.0435 | 0.147 | 0.1506 | 0.0134 | 0.1447 | 0 |
| 58 | q | 0.0611 | 0.1827 | 0.1391 | 0.0134 | 0.1137 | 0 |
| 59 | h | 0.0491 | 0.1072 | 0.1767 | 0.0186 | 0.1267 | 0 |
| 60 | g | 0.0546 | 0.0836 | 0.0568 | 0.007 | 0.0709 | 0 |
| 61 | k | 0.0441 | 0.1772 | 0.0828 | 0.0181 | 0.0781 | 0 |
| 62 | e | 0.0559 | 0.1306 | 0.1357 | 0.0109 | 0.0925 | 0 |
| 63 | d | 0.076 | 0.1984 | 0.0916 | 0.0122 | 0.0818 | 0 |
| 64 | l | 0.0664 | 0.1494 | 0.0852 | 0.0039 | 0.078 | 0 |
| 65 | k | 0.0729 | 0.3667 | 0.0837 | 0.0177 | 0.0617 | 0 |
| 66 | f | 0.0664 | 0.114 | 0.0864 | 0.0193 | 0.0782 | 0 |
| 67 | p | 0.0695 | 0.1048 | 0.0896 | 0.0115 | 0.0719 | 0 |
| 68 | r | 0.0716 | 0.2412 | 0.1713 | 0.05 | 0.0975 | 0 |
| 69 | g | 0.0778 | 0.1517 | 0.08 | 0.0426 | 0.0528 | 0 |
| 70 | q | 0.082 | 0.2612 | 0.1518 | 0.0469 | 0.0754 | 0 |
| 71 | g | 0.0969 | 0.1791 | 0.0907 | 0.0912 | 0.063 | 0 |
| 72 | v | 0.0835 | 0.124 | 0.0705 | 0.1461 | 0.0512 | 0 |
| 73 | p | 0.099 | 0.1565 | 0.0733 | 0.0791 | 0.062 | 0 |
| 74 | i | 0.0949 | 0.1229 | 0.1061 | 0.0421 | 0.0676 | 0 |
| 75 | n | 0.0996 | 0.1877 | 0.1232 | 0.0472 | 0.0798 | 0 |
| 76 | t | 0.0844 | 0.1435 | 0.1207 | 0.018 | 0.0903 | 0 |
| 77 | n | 0.0954 | 0.121 | 0.1273 | 0.0481 | 0.1128 | 0 |
| 78 | s | 0.0912 | 0.1808 | 0.1228 | 0.0248 | 0.1287 | 0 |
| 79 | s | 0.0801 | 0.1366 | 0.1074 | 0.0269 | 0.1156 | 0 |
| 80 | p | 0.0719 | 0.1239 | 0.1316 | 0.0236 | 0.1176 | 0 |
| 81 | d | 0.0854 | 0.1164 | 0.1588 | 0.0263 | 0.1248 | 0 |
| 82 | d | 0.1077 | 0.1326 | 0.143 | 0.0234 | 0.0985 | 0 |
| 83 | q | 0.1069 | 0.1731 | 0.153 | 0.0375 | 0.0953 | 0 |
| 84 | i | 0.1013 | 0.1141 | 0.1638 | 0.0306 | 0.1022 | 0 |
| 85 | g | 0.1015 | 0.1038 | 0.0906 | 0.0496 | 0.068 | 0 |
| 86 | y | 0.085 | 0.0981 | 0.1607 | 0.1229 | 0.0847 | 0 |
| 87 | y | 0.1033 | 0.1118 | 0.1705 | 0.108 | 0.0966 | 0 |
| 88 | r | 0.0929 | 0.2291 | 0.2425 | 0.0413 | 0.1375 | 0 |
| 89 | r | 0.0914 | 0.1604 | 0.1916 | 0.0733 | 0.1012 | 0 |
| 90 | a | 0.0924 | 0.124 | 0.086 | 0.0298 | 0.0769 | 0 |
| 91 | t | 0.0935 | 0.2276 | 0.167 | 0.013 | 0.1146 | 0 |
| 92 | r | 0.0999 | 0.3471 | 0.1457 | 0.0683 | 0.0957 | 0 |
| 93 | r | 0.0936 | 0.2981 | 0.1703 | 0.0222 | 0.1149 | 0 |
| 94 | i | 0.1163 | 0.1394 | 0.1261 | 0.0147 | 0.105 | 0 |
| 95 | r | 0.0893 | 0.3459 | 0.2364 | 0.0321 | 0.1599 | 0 |
| 96 | g | 0.1015 | 0.2992 | 0.1528 | 0.0115 | 0.1263 | 0 |
| 97 | g | 0.1095 | 0.376 | 0.1506 | 0.0184 | 0.1348 | 0 |
| 98 | d | 0.1059 | 0.2929 | 0.1565 | 0.0471 | 0.1321 | 0 |
| 99 | g | 0.128 | 0.1318 | 0.0645 | 0.0475 | 0.083 | 0 |
| 100 | k | 0.1216 | 0.3493 | 0.1909 | 0.034 | 0.1453 | 0 |
| 101 | m | 0.1301 | 0.0987 | 0.2117 | 0.0237 | 0.1554 | 0 |
| 102 | k | 0.1114 | 0.3001 | 0.2098 | 0.0191 | 0.1541 | 0 |
| 103 | d | 0.1386 | 0.1081 | 0.2202 | 0.0096 | 0.1718 | 0 |
| 104 | l | 0.1342 | 0.0791 | 0.1746 | 0.0128 | 0.1332 | 0 |
| 105 | s | 0.1116 | 0.102 | 0.1433 | 0.0099 | 0.1225 | 0 |
| 106 | p | 0.1172 | 0.0622 | 0.193 | 0.0048 | 0.1321 | 0 |
| 107 | r | 0.1091 | 0.1147 | 0.2664 | 0.0107 | 0.1479 | 0 |
| 108 | w | 0.0799 | 0.0668 | 0.2539 | 0.0169 | 0.1262 | 0 |
| 109 | y | 0.0787 | 0.0748 | 0.1498 | 0.018 | 0.0749 | 0 |
| 110 | f | 0.0825 | 0.0799 | 0.1842 | 0.0335 | 0.1058 | 0 |
| 111 | y | 0.0897 | 0.0871 | 0.0948 | 0.08 | 0.059 | 0 |
| 112 | y | 0.095 | 0.0742 | 0.1303 | 0.062 | 0.0667 | 0 |
| 113 | l | 0.1034 | 0.0325 | 0.1033 | 0.0267 | 0.0578 | 0 |
| 114 | g | 0.0887 | 0.0489 | 0.082 | 0.0606 | 0.0688 | 0 |
| 115 | t | 0.0948 | 0.0754 | 0.1151 | 0.1568 | 0.0772 | 0 |
| 116 | g | 0.0884 | 0.0584 | 0.071 | 0.0834 | 0.074 | 0 |
| 117 | p | 0.093 | 0.0652 | 0.1156 | 0.0535 | 0.0838 | 0 |
| 118 | e | 0.1207 | 0.0598 | 0.163 | 0.057 | 0.1021 | 0 |
| 119 | a | 0.139 | 0.0955 | 0.0844 | 0.0365 | 0.0826 | 0 |
| 120 | g | 0.1347 | 0.1213 | 0.1 | 0.0298 | 0.0983 | 0 |
| 121 | l | 0.1127 | 0.0821 | 0.0994 | 0.042 | 0.0975 | 0 |
| 122 | p | 0.1074 | 0.0985 | 0.1089 | 0.0147 | 0.1002 | 0 |
| 123 | y | 0.1036 | 0.1034 | 0.1117 | 0.0363 | 0.0977 | 0 |
| 124 | g | 0.1158 | 0.1216 | 0.0384 | 0.0226 | 0.0679 | 0 |
| 125 | a | 0.0978 | 0.0819 | 0.0447 | 0.011 | 0.0699 | 0 |
| 126 | n | 0.0891 | 0.0773 | 0.0519 | 0.0113 | 0.0728 | 0 |
| 127 | k | 0.0697 | 0.159 | 0.0519 | 0.0135 | 0.0672 | 0 |
| 128 | d | 0.0777 | 0.0507 | 0.04 | 0.0153 | 0.0695 | 0 |
| 129 | g | 0.0808 | 0.0322 | 0.0225 | 0.0197 | 0.0544 | 0 |
| 130 | i | 0.0473 | 0.0272 | 0.0539 | 0.0145 | 0.0551 | 0 |
| 131 | i | 0.0477 | 0.0237 | 0.0515 | 0.0102 | 0.0569 | 0 |
| 132 | w | 0.0494 | 0.0323 | 0.0487 | 0.0369 | 0.0568 | 0 |
| 133 | v | 0.0463 | 0.0172 | 0.0293 | 0.0608 | 0.0496 | 0 |
| 134 | a | 0.0465 | 0.0197 | 0.0556 | 0.0287 | 0.0595 | 0 |
| 135 | t | 0.0524 | 0.0245 | 0.1179 | 0.0159 | 0.0787 | 0 |
| 136 | e | 0.0565 | 0.0346 | 0.1408 | 0.0228 | 0.0951 | 0 |
| 137 | g | 0.068 | 0.0597 | 0.0854 | 0.0383 | 0.0881 | 0 |
| 138 | a | 0.0711 | 0.0483 | 0.0695 | 0.0734 | 0.0797 | 0 |
| 139 | l | 0.0678 | 0.0437 | 0.1438 | 0.0331 | 0.1147 | 0 |
| 140 | n | 0.0882 | 0.1388 | 0.1523 | 0.0354 | 0.1158 | 0 |
| 141 | t | 0.0823 | 0.0768 | 0.1038 | 0.0175 | 0.0987 | 0 |
| 142 | p | 0.0982 | 0.0671 | 0.1067 | 0.022 | 0.104 | 0 |
| 143 | k | 0.085 | 0.1952 | 0.1325 | 0.0378 | 0.1124 | 0 |
| 144 | d | 0.1382 | 0.1514 | 0.1252 | 0.0278 | 0.1193 | 0 |
| 145 | h | 0.1322 | 0.2624 | 0.1874 | 0.0721 | 0.1366 | 0 |
| 146 | i | 0.1128 | 0.1886 | 0.1659 | 0.0407 | 0.115 | 0 |
| 147 | g | 0.1068 | 0.1687 | 0.1042 | 0.0592 | 0.0703 | 0 |
| 148 | t | 0.1099 | 0.2065 | 0.139 | 0.09 | 0.0857 | 0 |
| 149 | r | 0.1054 | 0.1781 | 0.1655 | 0.3497 | 0.0927 | 0 |
| 150 | n | 0.0802 | 0.17 | 0.119 | 0.0807 | 0.0705 | 0 |
| 151 | p | 0.0756 | 0.0852 | 0.1201 | 0.0522 | 0.0764 | 0 |
| 152 | a | 0.0637 | 0.0869 | 0.0832 | 0.0457 | 0.0627 | 0 |
| 153 | n | 0.0573 | 0.11 | 0.117 | 0.0412 | 0.081 | 0 |
| 154 | n | 0.0473 | 0.0682 | 0.096 | 0.0188 | 0.0773 | 0 |
| 155 | a | 0.0572 | 0.0516 | 0.0634 | 0.0147 | 0.089 | 0 |
| 156 | a | 0.0386 | 0.0383 | 0.0576 | 0.0226 | 0.0809 | 0 |
| 157 | i | 0.0322 | 0.0366 | 0.0929 | 0.0179 | 0.0868 | 0 |
| 158 | v | 0.0355 | 0.044 | 0.0528 | 0.024 | 0.067 | 0 |
| 159 | l | 0.0312 | 0.0429 | 0.0692 | 0.0276 | 0.0688 | 0 |
| 160 | q | 0.0365 | 0.1225 | 0.0905 | 0.0488 | 0.072 | 0 |
| 161 | l | 0.0476 | 0.0614 | 0.0643 | 0.0809 | 0.0607 | 0 |
| 162 | p | 0.0417 | 0.073 | 0.1281 | 0.0221 | 0.0796 | 0 |
| 163 | q | 0.0588 | 0.1624 | 0.2155 | 0.06 | 0.1036 | 0 |
| 164 | g | 0.0944 | 0.1324 | 0.0874 | 0.0498 | 0.0657 | 0 |
| 165 | t | 0.0971 | 0.1945 | 0.1259 | 0.0363 | 0.0745 | 0 |
| 166 | t | 0.0734 | 0.1569 | 0.1536 | 0.0159 | 0.1043 | 0 |
| 167 | l | 0.0614 | 0.1227 | 0.1161 | 0.0212 | 0.1013 | 0 |
| 168 | p | 0.0575 | 0.1468 | 0.0956 | 0.0192 | 0.0879 | 0 |
| 169 | k | 0.0602 | 0.2644 | 0.1709 | 0.0081 | 0.1208 | 0 |
| 170 | g | 0.0634 | 0.1482 | 0.1026 | 0.0072 | 0.0965 | 0 |
| 171 | f | 0.088 | 0.0921 | 0.2274 | 0.0246 | 0.1747 | 0 |
| 172 | y | 0.0835 | 0.1638 | 0.2526 | 0.0212 | 0.1811 | 0 |
| 173 | a | 0.0742 | 0.1915 | 0.1359 | 0.0117 | 0.1228 | 0 |
| 174 | e | 0.0823 | 0.2603 | 0.1742 | 0.0439 | 0.1277 | 0 |
| 175 | g | 0.092 | 0.2876 | 0.1529 | 0.0229 | 0.1242 | 0 |
| 176 | s | 0.0967 | 0.3954 | 0.2543 | 0.0219 | 0.1914 | 0 |
| 177 | R | 0.0814 | 0.4328 | 0.3438 | 0.0458 | 0.2701 | 1 |
| 178 | g | 0.092 | 0.3269 | 0.169 | 0.029 | 0.1332 | 0 |
| 179 | g | 0.111 | 0.3535 | 0.1736 | 0.0431 | 0.1401 | 0 |
| 180 | s | 0.1049 | 0.5189 | 0.1968 | 0.0791 | 0.1597 | 0 |
| 181 | q | 0.1177 | 0.454 | 0.2903 | 0.0978 | 0.222 | 0 |
| 182 | a | 0.1152 | 0.2992 | 0.1668 | 0.0712 | 0.1245 | 0 |
| 183 | s | 0.1082 | 0.4174 | 0.1799 | 0.1078 | 0.1228 | 0 |
| 184 | s | 0.1229 | 0.3367 | 0.1369 | 0.2729 | 0.1024 | 0 |
| 185 | r | 0.1109 | 0.2888 | 0.285 | 0.3375 | 0.1895 | 0 |
| 186 | s | 0.1218 | 0.2496 | 0.199 | 0.1327 | 0.126 | 0 |
| 187 | s | 0.1197 | 0.2445 | 0.1899 | 0.1013 | 0.1263 | 0 |
| 188 | s | 0.1469 | 0.258 | 0.2075 | 0.2777 | 0.1243 | 0 |
| 189 | R | 0.1327 | 0.2527 | 0.3707 | 0.3052 | 0.2509 | 1 |
| 190 | s | 0.1576 | 0.2275 | 0.2046 | 0.1767 | 0.1399 | 0 |
| 191 | R | 0.1301 | 0.286 | 0.3578 | 0.2019 | 0.2848 | 1 |
| 192 | n | 0.1306 | 0.2551 | 0.2601 | 0.1566 | 0.1792 | 0 |
| 193 | s | 0.1344 | 0.244 | 0.216 | 0.0731 | 0.1555 | 0 |
| 194 | s | 0.1493 | 0.2385 | 0.1724 | 0.109 | 0.1498 | 0 |
| 195 | r | 0.1237 | 0.3353 | 0.2665 | 0.1845 | 0.2068 | 0 |
| 196 | n | 0.1272 | 0.3131 | 0.2251 | 0.0493 | 0.161 | 0 |
| 197 | s | 0.1236 | 0.3051 | 0.1904 | 0.0335 | 0.1582 | 0 |
| 198 | t | 0.1137 | 0.2428 | 0.1723 | 0.1295 | 0.1571 | 0 |
| 199 | p | 0.1188 | 0.2125 | 0.2276 | 0.0371 | 0.1754 | 0 |
| 200 | g | 0.1294 | 0.2437 | 0.1823 | 0.0236 | 0.1433 | 0 |
| 201 | s | 0.1086 | 0.3159 | 0.1885 | 0.0332 | 0.1493 | 0 |
| 202 | s | 0.1191 | 0.3532 | 0.1581 | 0.0649 | 0.1252 | 0 |
| 203 | r | 0.1123 | 0.2982 | 0.2393 | 0.1317 | 0.1704 | 0 |
| 204 | g | 0.101 | 0.2121 | 0.1594 | 0.0115 | 0.1301 | 0 |
| 205 | t | 0.1002 | 0.2634 | 0.2596 | 0.0206 | 0.1827 | 0 |
| 206 | s | 0.0754 | 0.2162 | 0.1512 | 0.0348 | 0.1202 | 0 |
| 207 | p | 0.0757 | 0.1345 | 0.1753 | 0.0121 | 0.1339 | 0 |
| 208 | a | 0.0807 | 0.1329 | 0.1209 | 0.0146 | 0.1016 | 0 |
| 209 | r | 0.0688 | 0.3245 | 0.216 | 0.0273 | 0.1474 | 0 |
| 210 | m | 0.0629 | 0.1911 | 0.1308 | 0.0226 | 0.0941 | 0 |
| 211 | a | 0.0644 | 0.1663 | 0.0905 | 0.0152 | 0.0811 | 0 |
| 212 | g | 0.0454 | 0.1643 | 0.0996 | 0.0111 | 0.0799 | 0 |
| 213 | n | 0.0359 | 0.1515 | 0.1429 | 0.0161 | 0.0851 | 0 |
| 214 | g | 0.0394 | 0.1009 | 0.0823 | 0.0128 | 0.0585 | 0 |
| 215 | g | 0.0298 | 0.0907 | 0.0877 | 0.0124 | 0.0755 | 0 |
| 216 | d | 0.0268 | 0.0534 | 0.0789 | 0.0247 | 0.059 | 0 |
| 217 | a | 0.0269 | 0.036 | 0.0512 | 0.0113 | 0.051 | 0 |
| 218 | a | 0.0233 | 0.0327 | 0.0456 | 0.0149 | 0.0518 | 0 |
| 219 | l | 0.0202 | 0.0229 | 0.0516 | 0.0191 | 0.0535 | 0 |
| 220 | a | 0.0202 | 0.0155 | 0.0293 | 0.0093 | 0.0533 | 0 |
| 221 | l | 0.0223 | 0.0137 | 0.0517 | 0.0051 | 0.0605 | 0 |
| 222 | l | 0.0217 | 0.0131 | 0.0676 | 0.0083 | 0.0486 | 0 |
| 223 | l | 0.0264 | 0.0148 | 0.0745 | 0.0074 | 0.0679 | 0 |
| 224 | l | 0.0249 | 0.0169 | 0.0911 | 0.0096 | 0.0729 | 0 |
| 225 | d | 0.0375 | 0.0274 | 0.0671 | 0.0374 | 0.0712 | 0 |
| 226 | r | 0.0396 | 0.031 | 0.1123 | 0.0393 | 0.0891 | 0 |
| 227 | l | 0.036 | 0.017 | 0.1253 | 0.0119 | 0.0901 | 0 |
| 228 | n | 0.0395 | 0.0549 | 0.1127 | 0.0178 | 0.0984 | 0 |
| 229 | q | 0.0579 | 0.0639 | 0.1439 | 0.0259 | 0.1166 | 0 |
| 230 | l | 0.0635 | 0.0363 | 0.1721 | 0.0184 | 0.1383 | 0 |
| 231 | e | 0.0622 | 0.0672 | 0.2218 | 0.024 | 0.1707 | 0 |
| 232 | s | 0.0729 | 0.0996 | 0.1892 | 0.0109 | 0.1596 | 0 |
| 233 | k | 0.0795 | 0.1541 | 0.2344 | 0.0376 | 0.1676 | 0 |
| 234 | m | 0.0535 | 0.0608 | 0.1999 | 0.0242 | 0.1615 | 0 |
| 235 | s | 0.0553 | 0.1294 | 0.2179 | 0.012 | 0.1654 | 0 |
| 236 | g | 0.0773 | 0.1535 | 0.1859 | 0.0185 | 0.1341 | 0 |
| 237 | k | 0.0748 | 0.3483 | 0.3128 | 0.017 | 0.2068 | 0 |
| 238 | g | 0.0898 | 0.2259 | 0.1693 | 0.0074 | 0.1118 | 0 |
| 239 | q | 0.0783 | 0.2888 | 0.2823 | 0.0181 | 0.1924 | 0 |
| 240 | q | 0.081 | 0.404 | 0.2105 | 0.0324 | 0.1441 | 0 |
| 241 | q | 0.0664 | 0.3198 | 0.1651 | 0.0214 | 0.1236 | 0 |
| 242 | q | 0.073 | 0.3023 | 0.1778 | 0.0238 | 0.1288 | 0 |
| 243 | g | 0.0823 | 0.2323 | 0.1127 | 0.0196 | 0.1038 | 0 |
| 244 | q | 0.077 | 0.3455 | 0.1877 | 0.0203 | 0.1323 | 0 |
| 245 | t | 0.1007 | 0.3632 | 0.2354 | 0.0322 | 0.1661 | 0 |
| 246 | v | 0.0793 | 0.2192 | 0.1532 | 0.0211 | 0.1206 | 0 |
| 247 | t | 0.0667 | 0.2006 | 0.1317 | 0.0537 | 0.1101 | 0 |
| 248 | k | 0.0645 | 0.2328 | 0.1303 | 0.0514 | 0.1157 | 0 |
| 249 | k | 0.0536 | 0.1794 | 0.1527 | 0.0207 | 0.1245 | 0 |
| 250 | s | 0.0538 | 0.1074 | 0.1163 | 0.0125 | 0.114 | 0 |
| 251 | a | 0.0383 | 0.0666 | 0.0642 | 0.0111 | 0.097 | 0 |
| 252 | a | 0.0452 | 0.1257 | 0.086 | 0.0102 | 0.0998 | 0 |
| 253 | e | 0.0564 | 0.1296 | 0.1098 | 0.026 | 0.0999 | 0 |
| 254 | a | 0.0532 | 0.1194 | 0.0767 | 0.0078 | 0.0882 | 0 |
| 255 | s | 0.0595 | 0.1803 | 0.1236 | 0.012 | 0.1039 | 0 |
| 256 | k | 0.0689 | 0.2997 | 0.1149 | 0.0227 | 0.1043 | 0 |
| 257 | k | 0.0719 | 0.347 | 0.0909 | 0.0542 | 0.0871 | 0 |
| 258 | p | 0.0999 | 0.2079 | 0.1219 | 0.0193 | 0.0989 | 0 |
| 259 | r | 0.0861 | 0.3981 | 0.2163 | 0.0479 | 0.1141 | 0 |
| 260 | q | 0.0999 | 0.4402 | 0.2272 | 0.0292 | 0.121 | 0 |
| 261 | k | 0.1011 | 0.7626 | 0.1667 | 0.0689 | 0.0855 | 0 |
| 262 | r | 0.0806 | 0.5561 | 0.268 | 0.074 | 0.1416 | 0 |
| 263 | t | 0.0939 | 0.4141 | 0.227 | 0.0301 | 0.1422 | 0 |
| 264 | a | 0.0841 | 0.3585 | 0.1774 | 0.0153 | 0.1087 | 0 |
| 265 | t | 0.082 | 0.3234 | 0.2282 | 0.0132 | 0.1475 | 0 |
| 266 | k | 0.0792 | 0.4335 | 0.2117 | 0.0297 | 0.1395 | 0 |
| 267 | a | 0.067 | 0.2186 | 0.1594 | 0.0202 | 0.1305 | 0 |
| 268 | Y | 0.0499 | 0.1864 | 0.345 | 0.0244 | 0.2498 | 1 |
| 269 | n | 0.0557 | 0.1951 | 0.2295 | 0.0264 | 0.1786 | 0 |
| 270 | v | 0.0636 | 0.1288 | 0.146 | 0.0558 | 0.121 | 0 |
| 271 | t | 0.0603 | 0.2285 | 0.1752 | 0.0443 | 0.1354 | 0 |
| 272 | q | 0.0734 | 0.2371 | 0.2204 | 0.0589 | 0.1652 | 0 |
| 273 | a | 0.0795 | 0.2519 | 0.1802 | 0.0637 | 0.1128 | 0 |
| 274 | f | 0.0827 | 0.2352 | 0.2373 | 0.2389 | 0.1312 | 0 |
| 275 | g | 0.0957 | 0.2168 | 0.1171 | 0.0908 | 0.0699 | 0 |
| 276 | r | 0.0904 | 0.4067 | 0.32 | 0.0592 | 0.1749 | 0 |
| 277 | r | 0.1078 | 0.4386 | 0.2247 | 0.1751 | 0.1174 | 0 |
| 278 | g | 0.1064 | 0.2949 | 0.1203 | 0.015 | 0.0797 | 0 |
| 279 | p | 0.11 | 0.4108 | 0.2109 | 0.0163 | 0.1145 | 0 |
| 280 | e | 0.1173 | 0.4603 | 0.1982 | 0.0388 | 0.1318 | 0 |
| 281 | q | 0.1143 | 0.4104 | 0.2143 | 0.0183 | 0.1371 | 0 |
| 282 | t | 0.1134 | 0.3802 | 0.1483 | 0.032 | 0.1119 | 0 |
| 283 | q | 0.1133 | 0.3549 | 0.235 | 0.0319 | 0.1671 | 0 |
| 284 | g | 0.1058 | 0.2542 | 0.1561 | 0.0174 | 0.1135 | 0 |
| 285 | n | 0.1031 | 0.2431 | 0.1609 | 0.1135 | 0.1324 | 0 |
| 286 | f | 0.0877 | 0.156 | 0.2012 | 0.1167 | 0.1593 | 0 |
| 287 | g | 0.108 | 0.1365 | 0.1221 | 0.0812 | 0.114 | 0 |
| 288 | d | 0.0989 | 0.1552 | 0.1891 | 0.041 | 0.149 | 0 |
| 289 | q | 0.0947 | 0.2188 | 0.2436 | 0.0204 | 0.1852 | 0 |
| 290 | e | 0.1169 | 0.1294 | 0.1967 | 0.02 | 0.1549 | 0 |
| 291 | l | 0.1008 | 0.1063 | 0.1862 | 0.0126 | 0.1483 | 0 |
| 292 | i | 0.0902 | 0.1115 | 0.1623 | 0.0149 | 0.145 | 0 |
| 293 | r | 0.0714 | 0.1946 | 0.2739 | 0.0261 | 0.2207 | 0 |
| 294 | q | 0.0698 | 0.1911 | 0.1747 | 0.0164 | 0.148 | 0 |
| 295 | g | 0.0907 | 0.1519 | 0.0865 | 0.0314 | 0.0976 | 0 |
| 296 | t | 0.0808 | 0.225 | 0.1765 | 0.0132 | 0.1256 | 0 |
| 297 | d | 0.1037 | 0.2715 | 0.2602 | 0.0121 | 0.1611 | 0 |
| 298 | y | 0.0959 | 0.388 | 0.2473 | 0.0439 | 0.1597 | 0 |
| 299 | k | 0.0991 | 0.4677 | 0.1755 | 0.0252 | 0.1112 | 0 |
| 300 | h | 0.1051 | 0.2048 | 0.2336 | 0.0438 | 0.1544 | 0 |
| 301 | w | 0.1012 | 0.0862 | 0.2639 | 0.0318 | 0.1938 | 0 |
| 302 | p | 0.0893 | 0.0618 | 0.1756 | 0.0154 | 0.144 | 0 |
| 303 | q | 0.1039 | 0.091 | 0.2158 | 0.0319 | 0.16 | 0 |
| 304 | i | 0.0963 | 0.0425 | 0.2031 | 0.03 | 0.159 | 0 |
| 305 | a | 0.0739 | 0.0687 | 0.2132 | 0.0393 | 0.1814 | 0 |
| 306 | Q | 0.0784 | 0.0836 | 0.3071 | 0.0518 | 0.2395 | 1 |
| 307 | F | 0.0831 | 0.038 | 0.3026 | 0.0773 | 0.2523 | 1 |
| 308 | a | 0.0556 | 0.0267 | 0.1552 | 0.0394 | 0.1481 | 0 |
| 309 | p | 0.0604 | 0.0308 | 0.2437 | 0.047 | 0.2052 | 0 |
| 310 | S | 0.0754 | 0.0563 | 0.2567 | 0.0373 | 0.2303 | 1 |
| 311 | a | 0.0764 | 0.0328 | 0.2026 | 0.0244 | 0.167 | 0 |
| 312 | s | 0.0725 | 0.0614 | 0.2957 | 0.0274 | 0.2109 | 0 |
| 313 | a | 0.0748 | 0.0345 | 0.2206 | 0.0397 | 0.1572 | 0 |
| 314 | F | 0.0862 | 0.0396 | 0.4207 | 0.0512 | 0.3068 | 1 |
| 315 | F | 0.0761 | 0.0353 | 0.3621 | 0.0493 | 0.2721 | 1 |
| 316 | g | 0.0759 | 0.0468 | 0.1628 | 0.051 | 0.1169 | 0 |
| 317 | m | 0.0809 | 0.0372 | 0.3078 | 0.0813 | 0.2137 | 0 |
| 318 | s | 0.0819 | 0.0696 | 0.1756 | 0.0909 | 0.1376 | 0 |
| 319 | r | 0.0683 | 0.0869 | 0.2743 | 0.078 | 0.2031 | 0 |
| 320 | i | 0.0632 | 0.0428 | 0.2139 | 0.0406 | 0.1599 | 0 |
| 321 | g | 0.0756 | 0.0801 | 0.1548 | 0.0078 | 0.1224 | 0 |
| 322 | m | 0.0627 | 0.0524 | 0.2754 | 0.0098 | 0.2049 | 0 |
| 323 | e | 0.0807 | 0.048 | 0.1765 | 0.0306 | 0.1476 | 0 |
| 324 | v | 0.0802 | 0.0425 | 0.1106 | 0.0163 | 0.1261 | 0 |
| 325 | t | 0.05 | 0.0622 | 0.1711 | 0.0278 | 0.1535 | 0 |
| 326 | p | 0.0369 | 0.0525 | 0.1764 | 0.0249 | 0.1628 | 0 |
| 327 | s | 0.0603 | 0.0798 | 0.1554 | 0.0676 | 0.1306 | 0 |
| 328 | g | 0.0602 | 0.0482 | 0.1547 | 0.0115 | 0.1184 | 0 |
| 329 | t | 0.056 | 0.0833 | 0.2476 | 0.0222 | 0.1701 | 0 |
| 330 | w | 0.0651 | 0.1067 | 0.2802 | 0.026 | 0.184 | 0 |
| 331 | l | 0.0486 | 0.0522 | 0.1648 | 0.0204 | 0.1176 | 0 |
| 332 | t | 0.0358 | 0.0636 | 0.1503 | 0.0247 | 0.1163 | 0 |
| 333 | y | 0.0337 | 0.0492 | 0.2063 | 0.0551 | 0.1566 | 0 |
| 334 | t | 0.0387 | 0.0364 | 0.144 | 0.0222 | 0.1181 | 0 |
| 335 | g | 0.0409 | 0.0269 | 0.1172 | 0.013 | 0.1026 | 0 |
| 336 | a | 0.043 | 0.017 | 0.1081 | 0.0125 | 0.1029 | 0 |
| 337 | i | 0.0557 | 0.0183 | 0.1278 | 0.0164 | 0.1084 | 0 |
| 338 | k | 0.0515 | 0.0516 | 0.1119 | 0.0195 | 0.099 | 0 |
| 339 | l | 0.0641 | 0.0201 | 0.072 | 0.0282 | 0.0925 | 0 |
| 340 | d | 0.0628 | 0.0248 | 0.0656 | 0.0352 | 0.0863 | 0 |
| 341 | d | 0.0659 | 0.0221 | 0.0808 | 0.0261 | 0.0954 | 0 |
| 342 | k | 0.0709 | 0.0828 | 0.0859 | 0.0322 | 0.0913 | 0 |
| 343 | d | 0.0797 | 0.0402 | 0.0691 | 0.0356 | 0.0841 | 0 |
| 344 | p | 0.1246 | 0.0322 | 0.0675 | 0.0282 | 0.087 | 0 |
| 345 | n | 0.1432 | 0.0589 | 0.0811 | 0.0412 | 0.08 | 0 |
| 346 | f | 0.111 | 0.0229 | 0.0719 | 0.0292 | 0.0744 | 0 |
| 347 | k | 0.0706 | 0.0825 | 0.0802 | 0.0095 | 0.0823 | 0 |
| 348 | d | 0.0712 | 0.0251 | 0.0849 | 0.0063 | 0.0762 | 0 |
| 349 | q | 0.0461 | 0.024 | 0.0669 | 0.0201 | 0.0746 | 0 |
| 350 | v | 0.0353 | 0.0204 | 0.0348 | 0.0079 | 0.062 | 0 |
| 351 | i | 0.0357 | 0.0236 | 0.0608 | 0.0095 | 0.0665 | 0 |
| 352 | l | 0.0326 | 0.0178 | 0.0547 | 0.0112 | 0.0601 | 0 |
| 353 | l | 0.0298 | 0.0116 | 0.0401 | 0.0394 | 0.0566 | 0 |
| 354 | n | 0.0416 | 0.0277 | 0.059 | 0.0473 | 0.0653 | 0 |
| 355 | k | 0.0305 | 0.0561 | 0.0828 | 0.03 | 0.0686 | 0 |
| 356 | h | 0.0358 | 0.0326 | 0.0996 | 0.0614 | 0.0816 | 0 |
| 357 | i | 0.0303 | 0.0251 | 0.0787 | 0.0297 | 0.0765 | 0 |
| 358 | d | 0.0411 | 0.0485 | 0.0876 | 0.0394 | 0.081 | 0 |
| 359 | a | 0.0525 | 0.061 | 0.0727 | 0.0462 | 0.0794 | 0 |
| 360 | y | 0.0624 | 0.1033 | 0.1634 | 0.0525 | 0.124 | 0 |
| 361 | k | 0.0481 | 0.1561 | 0.1665 | 0.0095 | 0.1201 | 0 |
| 362 | t | 0.0628 | 0.0453 | 0.1382 | 0.0075 | 0.1134 | 0 |
| 363 | f | 0.055 | 0.0314 | 0.1484 | 0.0116 | 0.1156 | 0 |
| 364 | p | 0.0497 | 0.0519 | 0.1315 | 0.0071 | 0.1135 | 0 |
| 365 | p | 0.0527 | 0.0565 | 0.141 | 0.0037 | 0.112 | 0 |
| 366 | t | 0.0598 | 0.1022 | 0.13 | 0.0047 | 0.099 | 0 |
| 367 | e | 0.0628 | 0.0605 | 0.1132 | 0.0073 | 0.089 | 0 |
| 368 | p | 0.0725 | 0.0763 | 0.0911 | 0.0046 | 0.0709 | 0 |
| 369 | k | 0.0734 | 0.309 | 0.1021 | 0.0173 | 0.0689 | 0 |
| 370 | k | 0.0633 | 0.4657 | 0.0897 | 0.0289 | 0.0565 | 0 |
| 371 | d | 0.0655 | 0.2392 | 0.0795 | 0.0176 | 0.0582 | 0 |
| 372 | k | 0.0682 | 0.4573 | 0.0624 | 0.0371 | 0.0512 | 0 |
| 373 | k | 0.0673 | 0.4788 | 0.0521 | 0.0358 | 0.0474 | 0 |
| 374 | k | 0.0695 | 0.4486 | 0.0594 | 0.028 | 0.0527 | 0 |
| 375 | k | 0.0665 | 0.302 | 0.0626 | 0.0291 | 0.0599 | 0 |
| 376 | a | 0.0537 | 0.0649 | 0.0796 | 0.0077 | 0.0734 | 0 |
| 377 | d | 0.0583 | 0.0804 | 0.1325 | 0.0106 | 0.0825 | 0 |
| 378 | e | 0.0548 | 0.0503 | 0.1389 | 0.0107 | 0.0981 | 0 |
| 379 | t | 0.0494 | 0.0599 | 0.1347 | 0.0091 | 0.1129 | 0 |
| 380 | q | 0.0427 | 0.146 | 0.1806 | 0.0081 | 0.1462 | 0 |
| 381 | a | 0.049 | 0.0863 | 0.1208 | 0.0039 | 0.1044 | 0 |
| 382 | l | 0.0496 | 0.0764 | 0.1756 | 0.0044 | 0.113 | 0 |
| 383 | p | 0.0474 | 0.4268 | 0.1777 | 0.0085 | 0.1013 | 0 |
| 384 | q | 0.0741 | 0.6016 | 0.2196 | 0.0293 | 0.115 | 0 |
| 385 | r | 0.0697 | 0.6271 | 0.3186 | 0.0318 | 0.1637 | 0 |
| 386 | q | 0.0911 | 0.5394 | 0.2426 | 0.0307 | 0.1254 | 0 |
| 387 | k | 0.0896 | 0.6593 | 0.2105 | 0.0473 | 0.1022 | 0 |
| 388 | k | 0.0783 | 0.6416 | 0.1915 | 0.0689 | 0.0935 | 0 |
| 389 | q | 0.0558 | 0.3709 | 0.207 | 0.0423 | 0.1278 | 0 |
| 390 | q | 0.049 | 0.2401 | 0.2013 | 0.0257 | 0.1387 | 0 |
| 391 | t | 0.0678 | 0.0901 | 0.158 | 0.0244 | 0.1212 | 0 |
| 392 | v | 0.0534 | 0.0388 | 0.1347 | 0.0147 | 0.1081 | 0 |
| 393 | t | 0.0511 | 0.0522 | 0.1669 | 0.0132 | 0.1358 | 0 |
| 394 | l | 0.0435 | 0.0231 | 0.1348 | 0.0171 | 0.1278 | 0 |
| 395 | l | 0.0352 | 0.0173 | 0.1257 | 0.0216 | 0.1123 | 0 |
| 396 | p | 0.0355 | 0.0122 | 0.1124 | 0.0094 | 0.108 | 0 |
| 397 | a | 0.0457 | 0.0075 | 0.059 | 0.0164 | 0.0842 | 0 |
| 398 | a | 0.055 | 0.0092 | 0.0709 | 0.0143 | 0.0856 | 0 |
| 399 | d | 0.0632 | 0.0088 | 0.095 | 0.0224 | 0.0946 | 0 |
| 400 | l | 0.0599 | 0.0052 | 0.0738 | 0.0138 | 0.0829 | 0 |
| 401 | d | 0.1011 | 0.0136 | 0.1166 | 0.023 | 0.0996 | 0 |
| 402 | d | 0.1187 | 0.0083 | 0.0835 | 0.0251 | 0.0842 | 0 |
| 403 | f | 0.0993 | 0.007 | 0.0813 | 0.0596 | 0.084 | 0 |
| 404 | s | 0.1214 | 0.0173 | 0.0503 | 0.0639 | 0.0797 | 0 |
| 405 | k | 0.1172 | 0.0409 | 0.1052 | 0.0899 | 0.0972 | 0 |
| 406 | q | 0.1216 | 0.03 | 0.131 | 0.1081 | 0.1118 | 0 |
| 407 | l | 0.1006 | 0.0141 | 0.1153 | 0.0818 | 0.1048 | 0 |
| 408 | q | 0.0876 | 0.0362 | 0.195 | 0.1012 | 0.1492 | 0 |
| 409 | q | 0.0988 | 0.0482 | 0.1991 | 0.1055 | 0.145 | 0 |
| 410 | s | 0.1152 | 0.0361 | 0.1091 | 0.0836 | 0.1073 | 0 |
| 411 | m | 0.0888 | 0.0296 | 0.1945 | 0.076 | 0.1546 | 0 |
| 412 | s | 0.0923 | 0.0465 | 0.176 | 0.0596 | 0.1387 | 0 |
| 413 | s | 0.112 | 0.0686 | 0.1912 | 0.081 | 0.1508 | 0 |
| 414 | a | 0.0928 | 0.02 | 0.1451 | 0.0301 | 0.1235 | 0 |
| 415 | d | 0.1028 | 0.0225 | 0.226 | 0.0276 | 0.1685 | 0 |
| 416 | s | 0.0901 | 0.0244 | 0.1432 | 0.0167 | 0.1208 | 0 |
| 417 | t | 0.1074 | 0.0162 | 0.1706 | 0.0327 | 0.1513 | 0 |
| 418 | q | 0.0802 | 0.0159 | 0.2062 | 0.0201 | 0.177 | 0 |
| 419 | a | 0.0627 | 0.0104 | 0.1275 | 0.0068 | 0.1339 | 0 |

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All submitters of data may be contacted directly via www.gisaid.org