

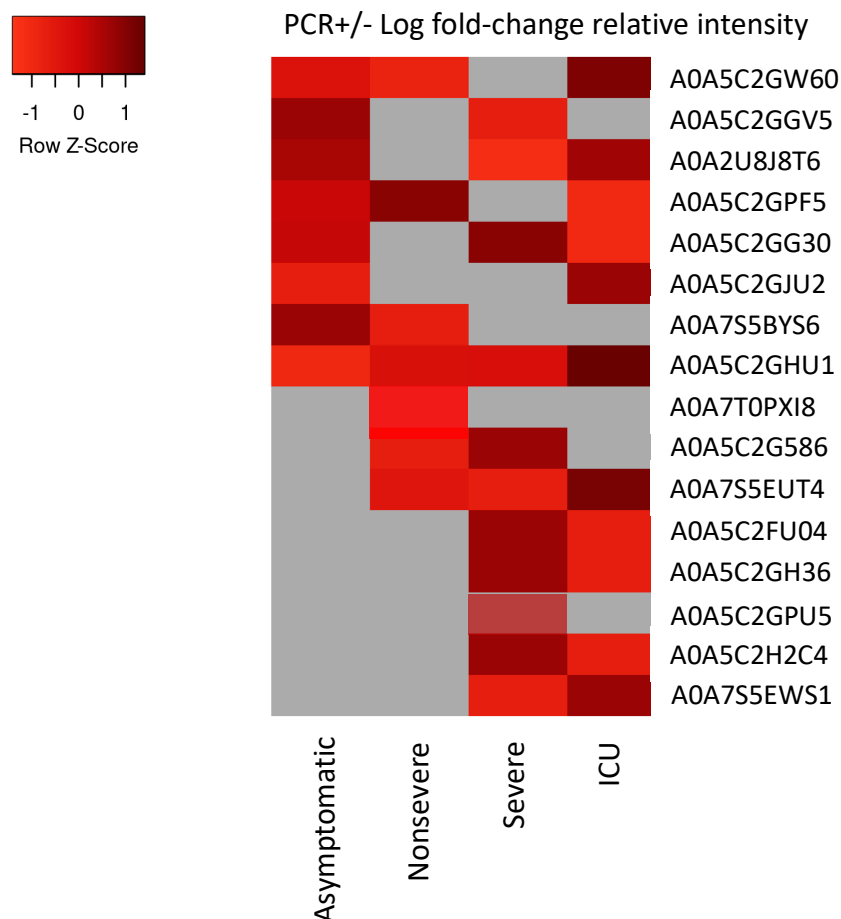
Data file S2. Analysis of immunoglobulin proteins underrepresented and overrepresented in infected cohorts when compared to PCR- individuals.

Part 1. Analysis of immunoglobulin proteins underrepresented in infected cohorts when compared to PCR- individuals.

Analytical workflow

1. Select immunoglobulin protein sequences underrepresented in infected cohorts.
2. Protein BLAST sequence alignment against non-redundant protein database(nr)using compositional matrix adjustment (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome).
3. Identification of anti-SARS-CoV-2 immunoglobulin sequences aligned. Criteria: Score > 160 bits, Identity > 60%.
4. Paratome (<http://www.ofranlab.org>) identification of antigen binding regions.
5. Protein BLAST sequence alignment against SARS-CoV-2 using compositional matrix adjustment (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome).
6. Identification of SARS-CoV-2 sequences aligned. Criteria: Score > 15 bits, Identity > 60%.
7. Identification of correlates of vaccine-induced antibody protective epitopes with emphasis on SARS-CoV-2 Spike S RBD domain.

Input data:



A0A5C2GW60

```
>tr|A0A5C2GW60|A0A5C2GW60_HUMAN IG c1795_light_IGKV3-15_IGKJ4 (Fragment)
OS=Homo sapiens OX=9606 PE=2 SV=1
QIVMTQSPASLSVFPGDSATLFCRASQRIGGNLAWYQQRPGQAPRLLIYGSSNRAAGVPP
RFSGSGSGTDFTLTINSLRSEDYAVYYCQQHHAWPPAFGGGTKVEIK
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2GW60|A0A5C2GW60_HUMAN IG c1795_light_IGKV3-15_IGKJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_811367
Length: 107
```

```
>anti-SARS-CoV-2 immunoglobulin kappa light chain variable region, partial
[Homo sapiens]
```

```
Sequence ID: QJU69756.1 Length: 109
```

```
>immunoglobulin light chain variable region, partial [Homo sapiens]
```

```
Sequence ID: QYF06493.1 Length: 109
```

```
Range 1: 1 to 109
```

```
Score:176 bits(445), Expect:1e-54,
Method:Compositional matrix adjust.,
Identities:83/109(76%), Positives:97/109(88%), Gaps:2/109(1%)
```

```
Query 1 QIVMTQSPASLSVFPGDSATLFCRASQRIGGNLAWYQQRPGQAPRLLIYGSSNRAAGVPP 60
+IVMTQSPA+LSV PG+ ATL CRASQ + NLAWYQQ+PGQAPRLLIYG+S RA G+P
Sbjct 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Query 61 RFSGSGSGTDFTLTINSLRSEDYAVYYCQQHHAWPPA--FGGGTKVEIK 107
RFSGSGSGT+FTLTI+SL+SED+AVYYCQQ++ WPP+ FGGGTKVEIK
Sbjct 61 RFSGSGSGTEFTLTISLQSEDFAVYYCQQYNNWPPSLTFGGGTKVEIK 109
```

Paratome analysis

```
paratome_1_seq_27691_107_bp
ABR L1: QRIGGNLA (27-34)
ABR L2: LLIYGSSNRAA (46-56)
ABR L3: QQHHAWPPA (89-97)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR L1: QRIGGNLA (27-34)
No significant similarity found.
```

```
ABR L2: LLIYGSSNRAA (46-56)
>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UJH96504.1 Length: 1271
Range 1: 751 to 764
```

```
Score:21.4 bits(43), Expect:6037,
Method:,
Identities:9/14(64%), Positives:9/14(64%), Gaps:4/14(28%)
```

```
Query 1 LLIYGSS----NRA 10
LL YGSS NRA
Sbjct 751 LLQYGSSTQLNRA 764
```

```
ABR L3: QQHHAWPPA (89-97)
No significant similarity found.
```

A0A5C2GGV5

```
>tr|A0A5C2GGV5|A0A5C2GGV5_HUMAN IG c110_light_IGKV4-1_IGKJ4 (Fragment)
OS=Homo sapiens OX=9606 PE=2 SV=1
DIVMTQSPDSLAVSLGERATINCKSSQNILYRANNKNYLAWYQQKPGQPPKLLVSWASTR
ESGVPDRFNGSGSGTDFNLTISSLQAEDVAVYSCQQYYSTPLTFGGGTKVEIK
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2GGV5|A0A5C2GGV5_HUMAN IG c110_light_IGKV4-1_IGKJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_252275
Length: 113
```

```
>anti-SARS-CoV-2 immunoglobulin light chain variable region, partial [Homo
sapiens]
```

```
Sequence ID: QTX15727.1 Length: 113
Range 1: 1 to 113
```

```
Score:218 bits(554), Expect:5e-71,
Method:Compositional matrix adjust.,
Identities:102/113(90%), Positives:109/113(96%), Gaps:0/113(0%)
```

```
Query 1 DIVMTQSPDSLAVSLGERATINCKSSQNILYRANNKNYLAWYQQKPGQPPKLLVSWASTR 60
DIVMTQSPDSLAVSLGERATINCKSSQ++L+ +NNKNY+AWYQQKPGQPPKLL+ WASTR
Sbjct 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLHSSNNKNYVAWYQQKPGQPPKLLIYWASTR 60

Query 61 ESGVPDRFNGSGSGTDFNLTISSLQAEDVAVYSCQQYYSTPLTFGGGTKVEIK 113
ESGVPDRF+GSGSGTDF LTISSLQAEDVAVY CQQYYSTPLTFGGGTKVEIK
Sbjct 61 ESGVPDRFSGSGSGTDFLTISSLQAEDVAVYHCQQYYSTPLTFGGGTKVEIK 113
```

Paratome analysis

```
paratome_1_seq_27871_113_bp
ABR L1: QNILYRANNKNYLA (27-40)
ABR L2: LLVSWASTRES (52-62)
ABR L3: QQYYSTPL (95-102)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR L1: QNILYRANNKNYLA (27-40)
>ORF10 protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UDE38504.1 Length: 38
>ORF10 protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UDN73246.1 Length: 38
>ORF10 protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UEF92301.1 Length: 38
>ORF10 protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UEI16040.1 Length: 38
>ORF10 protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UEI16377.1 Length: 38
Range 1: 18 to 28
```

```
Score:24.8 bits(51), Expect:619,
Method:,
Identities:7/11(64%), Positives:7/11(63%), Gaps:0/11(0%)
```

```
Query 4 LYRANNKNYLA 14
LYR N NY A
Sbjct 18 LYRMNSRNYIA 28
```

```
>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UJT26857.1 Length: 1270
```

Range 1: 910 to 918

Score:21.4 bits(43), Expect:10532,
Method:,
Identities:7/10(70%), Positives:8/10(80%), Gaps:1/10(10%)

Query 1 QNILYRANNK 10
QN+LY AN K
Sbjct 910 QNVLY-ANQK 918

ABR L2: LLVSWASTRES (52-62)

>ORF1ab polyprotein, partial [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QZK57390.1 Length: 7077
Range 1: 4948 to 4956

Score:19.7 bits(39), Expect:25032,
Method:,
Identities:6/9(67%), Positives:6/9(66%), Gaps:0/9(0%)

Query 1 LLVSWASTR 9
LL S A TR
Sbjct 4948 LLXSXAATR 4956

ABR L3: QQYYSTPL (95-102)

>ORF3a protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UIJ25215.1 Length: 275
Range 1: 213 to 219

Score:19.7 bits(39), Expect:13007,
Method:,
Identities:6/7(86%), Positives:6/7(85%), Gaps:0/7(0%)

Query 2 QQYYSTPL 8
Q YSTPL
Sbjct 213 QLYSTPL 219

>ORF1ab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QYZ75299.1 Length: 7096
Range 1: 4171 to 4175

Score:18.0 bits(35), Expect:53647,
Method:,
Identities:4/5(80%), Positives:4/5(80%), Gaps:0/5(0%)

Query 3 YYSTP 7
YY TP
Sbjct 4171 YYNTP 4175

AOA2U8J8T6

```
>tr|AOA2U8J8T6|AOA2U8J8T6_HUMAN Ig heavy chain variable region (Fragment)
OS=Homo sapiens OX=9606 GN=IgH PE=2 SV=1
GSGYSFSGYWIVVWRQMPGKGLEWMGLIYPDDSNTRYSPSFQGQVTFSSADKSITTAYLQW
SSLRASDTAIYYCARLSGPNRIMRAHWFDPPWGQGLTVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|AOA2U8J8T6|AOA2U8J8T6_HUMAN Ig heavy chain variable region
(Fragment) OS=Homo sapiens OX=9606 GN=IgH PE=2 SV=1 Query ID:
lcl|Query_416432 Length: 101
```

```
>anti-SARS-CoV-2 immunoglobulin heavy chain variable region, partial [Homo
sapiens]
```

```
Sequence ID: UKB89132.1 Length: 126
```

```
Range 1: 24 to 126
```

```
Score:161 bits(408), Expect:7e-49,
Method:Compositional matrix adjust.,
Identities:82/103(80%), Positives:90/103(87%), Gaps:2/103(1%)
```

```
Query 1 GSGYSFSGYWIVVWRQMPGKGLEWMGLIYPDDSNTRYSPSFQGQVTFSSADKSITTAYLQW 60
        GSGYSF+ YWI VWRQMPGKGLEWMG+IYP DS+TRYSPSFQGQVT SADKSI+TAYLQW
Sbjct 24 GSGYSFTSYWIGWVRQMPGKGLEWMGLIYPGSDSDTRYSPSFQGQVTISADKSISTAYLQW 83

Query 61 SSLRASDTAIYYCAR-LSGPNRIM-RAHWFDPPWGQGLTVTVSS 101
        SSL+ASDTA+YYCAR +SG + WFDPPWGQGLTVTVSS
Sbjct 84 SSLKASDTAMYYCARHMSGTHSSGWYERWFDPPWGQGLTVTVSS 126
```

Paratome analysis

```
paratome_1_seq_28012_101_bp
```

```
Could not find ABR1
```

```
ABR H2: WMGLIYPDDSNTRY (24-37)
```

```
ABR H3: RLSGPNRIMRAHWFDPP (75-90)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H2: WMGLIYPDDSNTRY (24-37)
```

```
>Chain B, S2X303 Fab heavy chain [Severe acute respiratory syndrome
coronavirus 2]
```

```
Sequence ID: 7SOE_B Length: 125
```

```
>Chain E, S2X303 Fab heavy chain [Severe acute respiratory syndrome
coronavirus 2]
```

```
Sequence ID: 7SOE_E Length: 125
```

```
>Chain H, S2X303 Fab heavy chain [Severe acute respiratory syndrome
coronavirus 2]
```

```
Sequence ID: 7SOE_H Length: 125
```

```
Range 1: 49 to 54
```

```
Score:18.9 bits(37), Expect:86006,
Method:,
Identities:4/6(67%), Positives:5/6(83%), Gaps:0/6(0%)
```

```
Query 1 WMGLIY 6
        W+ LIY
Sbjct 49 WLALIY 54
```

```
ABR H3: RLSGPNRIMRAHWFDPP (75-90)
```

```
>ORF1a polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UCK56015.1 Length: 4405
```

Range 1: 3662 to 3668

Score:21.0 bits(42), Expect:20697,

Method:

Identities:6/9(67%), Positives:6/9(66%), Gaps:2/9(22%)

Query 7 RIMRAHWFD 15

RIMR W D

Sbjct 3662 RIMR--WLD 3668

>surface glycoprotein, partial [Severe acute respiratory syndrome
coronavirus 2]

Sequence ID: QTM47912.1 Length: 1259

Range 1: 1086 to 1089

Score:18.9 bits(37), Expect:118712,

Method:

Identities:4/4(100%), Positives:4/4(100%), Gaps:0/4(0%)

Query 11 AHWF 14

AHWF

Sbjct 1086 AHWF 1089

A0A5C2GPF5

```
>tr|A0A5C2GPF5|A0A5C2GPF5_HUMAN IG c1256_heavy_IGHV3-23_IGHD3-3_IGHJ6
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLLESQGGGRLHPGGSLRLSCAASGFTFNYYAMSWVRQAPKGLEWVSAVSGSGASTYY
ADSVKGRFTISRDN SKNTLYLQMSSLRVEDTAVYYCAKVARLTVFGVVNTGHFMDVWGKG
TTVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2GPF5|A0A5C2GPF5_HUMAN IG c1256_heavy_IGHV3-23_IGHD3-3_IGHJ6
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_615149
Length: 127
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76482.1 Length: 124
Range 1: 1 to 124
```

```
Score:204 bits(519), Expect:2e-65,
Method:Compositional matrix adjust.,
Identities:101/127(80%), Positives:109/127(85%), Gaps:3/127(2%)
```

```
Query 1 EVQLLESQGGGRLHPGGSLRLSCAASGFTFNYYAMSWVRQAPKGLEWVSAVSGSGASTYY 60
EVQLL+SGGG + PGGSLRLSCAASGFTF NYAMSWVRQAP KGLEWVSA+SGSG +TYY
Sbjct 1 EVQLLQSGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKLEWVSAISGSGGTYY 60

Query 61 ADSVKGRFTISRDN SKNTLYLQMSSLRVEDTAVYYCAKVARLTVFGVVNTGHFMDVWGKG 120
ADSVKGRFTISRDN SKNTLYLQM+SLR EDTAVYYCAK R+T+ VV D WG+G
Sbjct 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKNERITMLVVVT---LFDYWGGQ 117

Query 121 TTVTSS 127
T VTVSS
Sbjct 118 TLVTSS 124
```

Paratome analysis

```
paratome_1_seq_28214_127_bp
ABR H1: FTFNYYAMS (27-35)
ABR H2: WWSAVSGSGASTYY (47-60)
ABR H3: KVARLTVFGVVNTGHFMDV (98-116)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: FTFNYYAMS (27-35)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UKG54270.1 Length: 7089
Range 1: 4461 to 4467
```

```
Score:20.6 bits(41), Expect:8026,
Method:,
Identities:5/7(71%), Positives:5/7(71%), Gaps:0/7(0%)
```

```
Query 2 TFNYYAM 8
TF NY M
Sbjct 4461 TFSNYQM 4467
```

```
ABR H2: WWSAVSGSGASTYY (47-60)
```

```
>surface glycoprotein, partial [Severe acute respiratory syndrome
coronavirus 2]
Sequence ID: QRX36841.1 Length: 682
Range 1: 256 to 266
```

Score:21.8 bits(44), Expect:7419,
Method:,
Identities:8/11(73%), Positives:8/11(72%), Gaps:2/11(18%)

Query 6 SG--SGASTYY 14
SG SGAS YY
Sbjct 256 SGWTSGASAYY 266

ABR H3: KVARLTVFGVVNTGHFMDV (98-116)

>ORFlab polyprotein, partial [Severe acute respiratory syndrome coronavirus
2]

Sequence ID: UIQ72354.1 Length: 6975

Range 1: 6338 to 6346

Score:28.2 bits(59), Expect:88,
Method:,
Identities:8/9(89%), Positives:8/9(88%), Gaps:0/9(0%)

Query 8 FGVVNTGHF 16
F VVNTGHF
Sbjct 6338 FNVVNTGHF 6346

A0A5C2GG30

```
>tr|A0A5C2GG30|A0A5C2GG30_HUMAN IG c723_heavy_IGHV4-39_IGHD6-6_IGHJ3
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
QVQLQESGPGLVKPSSETLSLTCTVSGYYISSGYYWGCIRQPPGKGLEWIGSIHHSGSTYY
NPSLKSRVTISVDTSKNQFSLKLRSVTATDTAVYYCARRLPEQLVGSDAFDIWGQGTMTV
VSS
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2GG30|A0A5C2GG30_HUMAN IG c723_heavy_IGHV4-39_IGHD6-6_IGHJ3
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_141113
Length: 123
```

```
>anti-SARS-CoV-2 immunoglobulin heavy chain variable region, partial [Homo
sapiens]
```

```
Sequence ID: UKB89162.1 Length: 123
Range 1: 1 to 123
```

```
Score:186 bits(471), Expect:4e-58,
Method:Compositional matrix adjust.,
Identities:105/124(85%), Positives:111/124(89%), Gaps:2/124(1%)
```

```
Query 1 QVQLQESGPGLVKPSSETLSLTCTVsgyyissgyyw-gCIRQPPGKGLEWIGSIHHSGSTY 59
Q+QLQESGPGLVKPSSETLSLTCTVSG ISS Y+ G IRQPPGKGLEWIGSI++SGSTY
Sbjct 1 QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYWGWIWIRQPPGKGLEWIGSIYYSGSTY 60

Query 60 YNPSLKSRVTISVDTSKNQFSLKLRSVTATDTAVYYCARRLPEQLVGSDAFDIWGQGTMTV 119
YNPSLKSRVTISVDTSKNQFSLKL SVTA DTAVYYCAR+ +L G DAFDIWGQGTMTV
Sbjct 61 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARQSSPKL-GDDAFDIWGQGTMTV 119

Query 120 TVSS 123
TVSS
Sbjct 120 TVSS 123
```

Paratome analysis

```
paratome_1_seq_28371_123_bp
ABR H1: YYISSGYYWGC (27-37)
ABR H2: WIGSIHHSGSTYY (48-60)
ABR H3: RRLPEQLVGSDAFDI (98-112)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: YYISSGYYWGC (27-37)
>ORF3a protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QTW51530.1 Length: 275
Range 1: 206 to 212
```

```
Score:20.6 bits(41), Expect:12304,
Method:,
Identities:5/7(71%), Positives:5/7(71%), Gaps:0/7(0%)
```

```
Query 2 YISSGYY 8
YI S YY
Sbjct 206 YITSDYY 212
```

```
ABR H2: WIGSIHHSGSTYY (48-60)
>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UIL01164.1 Length: 1271
Range 1: 64 to 72
```

```
Score:19.7 bits(39), Expect:36472,
Method:,
```

Identities:5/9(56%), Positives:5/9(55%), Gaps:0/9(0%)

```
Query 1  WIGSIHHSG 9
      W  IH SG
Sbjct 64  WXXAIHXSG 72
```

ABR H3: RRLPEQLVGSDAFDI (98-112)

>nucleocapsid phosphoprotein [Severe acute respiratory syndrome coronavirus 2]

Sequence ID: UH063712.1 Length: 419

Range 1: 276 to 284

Score:21.4 bits(43), Expect:12409,

Method:,

Identities:6/9(67%), Positives:6/9(66%), Gaps:0/9(0%)

```
Query 1  RRLPEQLVG 9
      RR PEQ  G
Sbjct 276  RRXPEQXXG 284
```

A0A5C2GJU2

```
>tr|A0A5C2GJU2|A0A5C2GJU2_HUMAN IG c195_heavy_IGHV3-30_IGHD1-26_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
QVQLVESGGGVVQPGRSLRLSCAASGFSFSNYGMHWVRQAPGKGLEWLSVISYDGNIKYY
VDSVKGRFTISRDN SKNTLYLEMNSLRAEDSAVYYCAKGV EWELLKYLD SWGHGTLVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2GJU2|A0A5C2GJU2_HUMAN IG c195_heavy_IGHV3-30_IGHD1-26_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_80258
Length: 121
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76580.1 Length: 120
Range 1: 1 to 120
```

```
Score:212 bits(540), Expect:8e-69,
Method:Compositional matrix adjust.,
Identities:103/121(85%), Positives:110/121(90%), Gaps:1/121(0%)
```

```
Query 1 QVQLVESGGGVVQPGRSLRLSCAASGFSFSNYGMHWVRQAPGKGLEWLSVISYDGNIKYY 60
QVQLVESGGGVVQPGRSLRLSCAASGF+FSNYGMHWVRQAPGKGLEW++VISYDG KYY
Sbjct 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISYDGTNKYY 60

Query 61 VDSVKGRFTISRDN SKNTLYLEMNSLRAEDSAVYYCAKGV EWELLKYLD SWGHGTLVTVS 120
DSVKGRFTISRDN SKNTLYL+MNSLRA+D+AVYYCAKG L + DSWG GTLVTVS
Sbjct 61 ADSVKGRFTISRDN SKNTLYLQMNSLRADDTAVYYCAKG-RGNYLTFFDSWGQGTLVTVS 119

Query 121 S 121
S
Sbjct 120 S 120
```

Paratome analysis

```
paratome_1_seq_6084_121_bp
ABR H1: FSFSNYGMH (27-35)
ABR H2: WLSVISYDGNIKYYV (47-61)
ABR H3: KGV EWELLKYLD S (98-110)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: FSFSNYGMH (27-35)
```

```
>ORF1ab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UFG71429.1 Length: 7096
Range 1: 3156 to 3160
```

```
Score:19.7 bits(39), Expect:16289,
Method:,
Identities:5/5(100%), Positives:5/5(100%), Gaps:0/5(0%)
```

```
Query 2 SFSNY 6
SFSNY
Sbjct 3156 SFSNY 3160
```

```
Range 2: 4469 to 4472
```

```
Score:17.2 bits(33), Expect:139431,
Method:,
Identities:4/4(100%), Positives:4/4(100%), Gaps:0/4(0%)
```

Query 3 FSNY 6
FSNY
Sbjct 4469 FSNY 4472

ABR H2: WLSVISYDGNIKYYV (47-61)
>ORF1a polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UHN63799.1 Length: 4405
Range 1: 1550 to 1557

Score:18.9 bits(37), Expect:102501,
Method:,
Identities:6/9(67%), Positives:6/9(66%), Gaps:1/9(11%)

Query 4 VISYDGNIK 12
VI YD N K
Sbjct 1550 VITYD-NLK 1557

ABR H3: KGVWELLKYLD (98-110)

>ORF1ab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UAT13595.1 Length: 7096
Range 1: 4658 to 4665

Score:26.9 bits(56), Expect:92,
Method:,
Identities:6/8(75%), Positives:8/8(100%), Gaps:0/8(0%)

Query 3 VEWELLKY 10
+EW+LLKY
Sbjct 4658 IEWDLLKY 4665

AOA7S5BYS6

```
>tr|AOA7S5BYS6|AOA7S5BYS6_HUMAN IGH c384_heavy_IGHV1-69_IGHD4-23_IGHJ6
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
QVQLVQSAAEVKKPGSSVKVSKASGGTFSGYTVSWVRQAPGQGLEWMGAVIPVYGTAQY
AWKFQGRVTISADESTSTAYLDLSRLTSED TAVYYCARGDNGGLGYWYFYMDVWGRGTTIVSS
```

BLAST Sequence alignment against nr

```
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76551.1 Length: 124
Range 1: 1 to 124
```

```
Score:193 bits(490), Expect:6e-61,
Method:Compositional matrix adjust.,
Identities:95/124(77%), Positives:105/124(84%), Gaps:0/124(0%)
```

```
Query 1 QVQLVQSAAEVKKPGSSVKVSKASGGTFSGYTVSWVRQAPGQGLEWMGAVIPVYGTAQY 60
Sbjct 1 QVQLVQS AEVKKPGSSVKVSKASGGTF Y +SWVRQAPGQGLEWMG IP+ GT Y 60

Query 61 AWKFQGRVTISADESTSTAYLDLSRLTSED TAVYYCARGDNGGLGYWYFYMDVWGRGTTV 120
Sbjct 61 A QKFQGRVTI+ADESTSTAY++LS L SEDTAVYYCAR + G+ +Y+ MDVWG+GTTV 120

Query 121 IVSS 124
Sbjct 121 TVSS 124
```

Paratome analysis

```
paratome_1_seq_6446_124_bp
ABR H1: GTFSGYTVS (27-35)
ABR H2: WMGAVIPVYGTAQY (47-60)
ABR H3: RGDNGGLGYWYFYMDV (98-113)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: GTFSGYTVS (27-35)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UFU96319.1 Length: 7096
Range 1: 1334 to 1339
```

```
Score:19.7 bits(39), Expect:16424,
Method:,
Identities:5/6(83%), Positives:5/6(83%), Gaps:0/6(0%)
```

```
Query 3 FSGYTV 8
Sbjct 1334 FNGYTV 1339
```

```
ABR H2: WMGAVIPVYGTAQY (47-60)
>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UAJ56903.1 Length: 1270
Range 1: 149 to 160
```

```
Score:21.0 bits(42), Expect:15102,
Method:,
Identities:6/12(50%), Positives:6/12(50%), Gaps:0/12(0%)
```

```
Query 1 WMGAVIPVYGTA 12
Sbjct 149 WMESVFRVYSSA 160
```

ABR H3: RGDNGGLGYWYFYMDV (98-113)
>nucleocapsid phosphoprotein, partial [Severe acute respiratory syndrome
coronavirus 2]
Sequence ID: UBE05898.1 Length: 416
Range 1: 95 to 111

Score:22.7 bits(46), Expect:5107,
Method:,
Identities:7/17(41%), Positives:9/17(52%), Gaps:4/17(23%)

Query	1	RGDNGGLGY----	WYFY	13
		RG +G +	WYFY	
Sbjct	95	RGGDGXMXXXXXR	WYFY	111

AOA5C2GHU1

QLRLVQSGGEVRKPGASVKVSCQTSYGYSFTNFAVSWVRQAPGHGLEWMGRISGSNGVADYAQDFQDRVMTTDDTV
TSTAYMEMRSLTSDDTAIYYCARDRLDYYENSAYFLGHDGFDIWGQGTMTVTVLS

Ig Heavy variable >tr|AOA5C2GHU1|AOA5C2GHU1_HUMAN IG c789_heavy_IGHV1-
18_IGHD3-22_IGHJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1

BLAST Sequence alignment against nr

Query: tr|AOA5C2GHU1|AOA5C2GHU1_HUMAN IG c789_heavy_IGHV1-18_IGHD3-22_IGHJ3
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_540851
Length: 130

>anti-SARS-CoV-2 immunoglobulin heavy chain variable region, partial [Homo
sapiens]

Sequence ID: UKB89114.1 Length: 131

Range 1: 1 to 131

Score:161 bits(408), Expect:3e-48,

Method:Compositional matrix adjust.,

Identities:89/131(68%), Positives:105/131(80%), Gaps:1/131(0%)

Query	1	QLRLVQSGGEVRKPGASVKVSCQTSYGYSFTNFAVSWVRQAPGHGLEWMGRISGSNGVADY	60
		Q++LVQSG EV+KPGASVKVSC+ SGY+FT++ +SWVRQAPG GLEWMG IS NG +Y	
Sbjct	1	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
Query	61	AQDFQDRVtmtdtvtstAYMEMRSLTSDDTAIYYCARDRLDYYENSAYF-LGHDGFDI	119
		AQ Q RVTMTTDT TSTAYME+RSL SDDTA+YYCARD YY++S Y+ + FD	
Sbjct	61	AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDGTSHYYDSSGYYGADRNWFDP	120
Query	120	WGQGTMTVTVLS	130
		WGQGT+VTV S	
Sbjct	121	WGQGTLVTVSS	131

>anti-SARS-CoV-2 immunoglobulin heavy chain variable region, partial [Homo
sapiens]

Sequence ID: QTX15776.1 Length: 122

Range 1: 1 to 122

Score:161 bits(407), Expect:3e-48,

Method:Compositional matrix adjust.,

Identities:89/130(68%), Positives:102/130(78%), Gaps:8/130(6%)

Query	1	QLRLVQSGGEVRKPGASVKVSCQTSYGYSFTNFAVSWVRQAPGHGLEWMGRISGSNGVADY	60
		+++LVQSG EV+KPGASVKVSC+ SGY+FT++ +SWVRQAPG GLEWMG IS NG +Y	
Sbjct	1	EVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY	60
Query	61	AQDFQDRVtmtdtvtstAYMEMRSLTSDDTAIYYCARDRLDYYENSAYFLGHDGFDIW	120
		AQ Q RVTMTTDT TSTAYME+RSL SDDTA+YYCARD R GHD FDIW	
Sbjct	61	AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDTRGR-----GGHDAFDIW	112
Query	121	GQGTMTVTVLS	130
		GQGTMTV+ S	
Sbjct	113	GQGTMTVISS	122

>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]

Sequence ID: QKY76564.1 Length: 128

Range 1: 1 to 128

Score:160 bits(404), Expect:9e-48,

Method:Compositional matrix adjust.,

Identities:89/130(68%), Positives:102/130(78%), Gaps:2/130(1%)

```

Query   1      QLRLVQSGGEVRKPGASVKVSCQTSGYSFTNFAVSWVRQAPGHGLEWMGRISGSNGVADY  60
          Q++LVQSG EV+KPGASVKVSC+ SGY+FT++ +SWVRQAPG GLEWMG IS  NG  +Y
Sbjct   1      QVQLVQSGAEVKKPGASVKVSCASGYTFTSYVISWVRQAPGQGLEWMGWISAYNGNTNY  60

Query   61     AQDFQDRVtmtdtvtstAYMEMRSLTSDDTAIYYCARDRLDYYENSAYFLGHDGFDIW  120
          AQ  Q RVTMTTDT TSTAYME+RSL SDDTA+YYCARD+  YY  S      H G D+W
Sbjct   61     AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDQGPTYYYGSG--SPHYGMDVW  118

Query   121    GQGTMTVTVLS  130
          GQGT VTV S
Sbjct   119    GQGTTVTVSS  128

```

Paratome analysis

```

paratome_1_seq_12087_130_bp
ABR H1: YSFTNFAVS (27-35)
ABR H2: WMGRISGSNGVADY (47-60)
ABR H3: RDRRLDYYENSAYFLGHDGFDI (98-119)

```

BLAST Sequence alignment against SARS-CoV-2

```

ABR H1:
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UFC29138.1 Length: 7096
Range 1: 2351 to 2356

```

```

Score:19.7 bits(39), Expect:16334,
Method:,
Identities:5/6(83%), Positives:5/6(83%), Gaps:0/6(0%)

```

```

Query    3      FTNFAV  8
          F NFAV
Sbjct   2351  FSNFAV  2356

```

Range 2: 4811 to 4817

```

Score:17.2 bits(33), Expect:139818,
Method:,
Identities:5/7(71%), Positives:6/7(85%), Gaps:0/7(0%)

```

```

Query    3      FTNFAVS  9
          F +FAVS
Sbjct   4811  FYDFAVS  4817

```

ABR H2

```

>surface glycoprotein, partial [Severe acute respiratory syndrome
coronavirus 2]
Sequence ID: QRX29628.1 Length: 682
Range 1: 357 to 365

```

```

Score:24.0 bits(49), Expect:1281,
Method:,
Identities:8/11(73%), Positives:8/11(72%), Gaps:2/11(18%)

```

```

Query    4      RISGSNGVADY  14
          RIS  N VADY
Sbjct   357  RIS--NXVADY  365

```

ABR H3

```

>ORFla polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QWC82475.1 Length: 4405
Range 1: 1893 to 1907

```


Score:26.5 bits(55), Expect:522,
Method:
Identities:10/16(63%), Positives:11/16(68%), Gaps:4/16(25%)

Query	2	DRRLD-YY--ENSAYF	14
		DR LD YY +NS YF	
Sbjct	1893	DRKLDNYYKKDNS-YF	1907

AOA7T0PXI8

```
>tr|AOA7T0PXI8|AOA7T0PXI8_HUMAN Immunglobulin heavy chain variable region
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLVESGGGVVVRPGGSLRLSCAASGFSFDDYAMTWVRQAPGKGLEWVSGITYNGGSTGY
ADSVKGRFTISRDNAKNSLYLQMTNLRAGDTAVYFCARDATYCGGDCYLDYWGQGALVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|AOA7T0PXI8|AOA7T0PXI8_HUMAN Immunglobulin heavy chain variable
region (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID:
lcl|Query_52619 Length: 122
```

```
>anti-SARS-CoV-2 immunoglobulin heavy chain variable region, partial [Homo
sapiens]
```

```
Sequence ID: QKY76690.1 Length: 125
```

```
Range 1: 1 to 125
```

```
Score:197 bits(502), Expect:8e-63,
Method:Compositional matrix adjust.,
Identities:98/125(78%), Positives:107/125(85%), Gaps:3/125(2%)
```

```
Query 1 EVQLVESGGGVVVRPGGSLRLSCAASGFSFDDYAMTWVRQAPGKGLEWVSGITYNGGSTGY 60
EVQLVESGGGVV+PG SLRLSCAASGF+FDDYAM WVRQAPGKGLEWVSGI++N GS GY
Sbjct 1 EVQLVESGGGLVQPGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY 60

Query 61 ADSVKGRFTISRDNAKNSLYLQMTNLRAGDTAVYFCARDATYCGG---DCYLDYWGQGAL 117
ADSVKGRFTISRDNAKNSLYLQM +LRA DT +Y+CA+D Y G Y DYWGQG L
Sbjct 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTGLYYCAKDINYDSGGYHKNYFDYWGQGTL 120

Query 118 VTVSS 122
VTVSS
Sbjct 121 VTVSS 125
```

Paratome analysis

```
paratome_1_seq_6561_122_bp
ABR H1: FSFDDYAMT (27-35)
ABR H2: WVSGITYNGGSTGY (47-60)
ABR H3: RDATYCGGDCYLDY (98-111)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: FSFDDYAMT (27-35)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QYV18445.1 Length: 7096
Range 1: 1087 to 1090
```

```
Score:18.0 bits(35), Expect:68513,
Method:,
Identities:4/4(100%), Positives:4/4(100%), Gaps:0/4(0%)
```

```
Query 3 FDDY 6
FDDY
Sbjct 1087 FDDY 1090
```

```
ABR H2: WVSGITYNGGSTGY (47-60)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UKT45678.1 Length: 7093
Range 1: 4731 to 4735
```

```
Score:18.0 bits(35), Expect:179260,
Method:,
Identities:5/5(100%), Positives:5/5(100%), Gaps:0/5(0%)
```

Query 10 GSTGY 14
GSTGY
Sbjct 4731 GSTGY 4735

ABR H3: RDATEYCGGDCYLDY (98-111)
>ORF1a polyprotein, partial [Severe acute respiratory syndrome coronavirus
2]
Sequence ID: QRX11300.1 Length: 3727
Range 1: 187 to 196

Score:21.0 bits(42), Expect:15118,
Method:
Identities:6/10(60%), Positives:7/10(70%), Gaps:0/10(0%)
Query 2 DATEYCGGDCY 11
D +CG DCY
Sbjct 187 DNNFCGPDCY 196

A0A5C2G586

```
>tr|A0A5C2G586|A0A5C2G586_HUMAN IGH c149_heavy__IGHV3-20_IGHD3-10_IGHJ6
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLVESGGSVVRPGGSLRLSCAASGFTFDDYAMTWVRQAPGKGLEWVCGINWNGGSTGY
ADSVKGRFTISRDNAKNSLYLQMNSLRADDTALYYCARNGALYYPGSEWPTLPLKYYYGMDVWGQGTTVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2G586|A0A5C2G586_HUMAN IGH c149_heavy__IGHV3-20_IGHD3-
10_IGHJ6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID:
lcl|Query_19769 Length: 133
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76519.1 Length: 129
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76525.1 Length: 129
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76528.1 Length: 129
Range 1: 1 to 129
```

```
Score:209 bits(531), Expect:4e-67,
Method:Compositional matrix adjust.,
Identities:109/133(82%), Positives:114/133(85%), Gaps:4/133(3%)
```

```
Query 1 EVQLVESGGSVVRPGGSLRLSCAASGFTFDDYAMTWVRQAPGKGLEWVCGINWNGGSTGY 60
Sbjct 1 EVQLVESGGSVVRPGGSLRLSCAASGFTFDDY M+WVRQAPGKGLEWV INWNGGSTGY 60

Query 61 ADSVKGRFTISRDNAKNSLYLQMNSLRADDTALYYCARNGALYYPGSEWPTLPLKYYYGM 120
Sbjct 61 ADSVKGRFTISRDNAKNSLYLQMNSLRA+DTALY+CAR + S W YYY M 116

Query 121 DVWGQGTTVTVSS 133
Sbjct 117 DVWGKGTTVTVSS 129
```

Paratome analysis

```
paratome_1_seq_6688_133_bp
ABR H1: FTFDDYAMT (27-35)
ABR H2: WVCINWNGGSTGY (47-60)
ABR H3: RYGALYYPGSEWPTLPLKYYYGMDV (98-122)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: FTFDDYAMT (27-35)
>ORF1ab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QYV18445.1 Length: 7096
Range 1: 1087 to 1090
```

```
Score:18.0 bits(35), Expect:68513,
Method:,
Identities:4/4(100%), Positives:4/4(100%), Gaps:0/4(0%)
```

```
Query 3 FDDY 6
Sbjct 1087 FDDY 1090
```

```
>ORF3a protein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QZU11999.1 Length: 275
```

Range 1: 207 to 212

Score:18.5 bits(36), Expect:48026,
Method:,
Identities:5/6(83%), Positives:5/6(83%), Gaps:0/6(0%)

Query 1 FTFDDY 6
FT DDY
Sbjct 207 FTSDDY 212

ABR H2: WVCGINWNGGSTGY (47-60)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UHE81962.1 Length: 7096
Range 1: 4402 to 4406

Score:19.3 bits(38), Expect:62036,
Method:,
Identities:4/5(80%), Positives:5/5(100%), Gaps:0/5(0%)

Query 1 WVCGI 5
WVCG+
Sbjct 4402 WVCGV 4406

>membrane glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UKO22082.1 Length: 222
Range 1: 73 to 79

Score:19.7 bits(39), Expect:43115,
Method:,
Identities:6/7(86%), Positives:6/7(85%), Gaps:1/7(14%)

Query 5 INWN-GG 10
INWN GG
Sbjct 73 INWNTGG 79

ABR H3: RNGALYYPGSEWPTLPLKYYYGMDV (98-122)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QKM77286.1 Length: 7096
Range 1: 5620 to 5634

Score:23.1 bits(47), Expect:10988,
Method:,
Identities:9/21(43%), Positives:9/21(42%), Gaps:9/21(42%)

Query 4 ALYYPGSEWPTLPLK---YYY 21
ALYYP K YYY
Sbjct 5620 ALYYP-----XXKEYXYYY 5634

AOA7S5EUT4

```
>tr|AOA7S5EUT4|AOA7S5EUT4_HUMAN IGH c1335_heavy_IGHV3-11_IGHD4-23_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
QVQLVESGGGLVKPGGSLRLSCAASGLTFSDYFMSWVRQAPGKGLEWLSYINNRGGHIYY
ADSVKGRFTISRDNQNSLYLQMNSLRAEDTAVYYCASVPTFDGNFRRPLYFYFDSWGQGT
LVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|AOA7S5EUT4|AOA7S5EUT4_HUMAN IGH c1335_heavy_IGHV3-11_IGHD4-
23_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID:
lcl|Query_51035 Length: 126
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76453.1 Length: 120
Range 1: 1 to 120
```

```
Score:202 bits(513), Expect:1e-64,
Method:Compositional matrix adjust.,
Identities:101/126(80%), Positives:107/126(84%), Gaps:6/126(4%)
```

```
Query 1 QVQLVESGGGLVKPGGSLRLSCAASGLTFSDYFMSWVRQAPGKGLEWLSYINNRGGHIYY 60
      QVQLVESGGGLVKPGGSLRLSCAASG TFSDY+MSW+RQAPGKGLEW+SYI++ G IYY
Sbjct 1 QVQLVESGGGLVKPGGSLRLSCAASGTFSDYYMSWIRQAPGKGLEWVSIISSSGITIYY 60

Query 61 ADSVKGRFTISRDNQNSLYLQMNSLRAEDTAVYYCASVPTFDGNFRRPLYFYFDSWGQGT 120
      ADSVKGRFTISRDNQNSLYLQMNSLRAEDTAVYYC V P YF WGQGT
Sbjct 61 ADSVKGRFTISRDNQNSLYLQMNSLRAEDTAVYYCTGV-----VAAPAEYFQHWGQGT 114

Query 121 LVTVSS 126
      LVTVSS
Sbjct 115 LVTVSS 120
```

```
>anti SARS-CoV-2 immunoglobulin heavy chain, partial [Homo sapiens]
Sequence ID: QNT09657.1 Length: 129
Range 1: 1 to 129
```

```
Score:201 bits(512), Expect:3e-64,
Method:Compositional matrix adjust.,
Identities:102/129(79%), Positives:111/129(86%), Gaps:3/129(2%)
```

```
Query 1 QVQLVESGGGLVKPGGSLRLSCAASGLTFSDYFMSWVRQAPGKGLEWLSYINNRGGHIYY 60
      QVQLVESGGGLVKPGGSLRLSCAASG TFSDY+M+W+RQAPGKGLEW+SYI++ G IYY
Sbjct 1 QVQLVESGGGLVKPGGSLRLSCAASGTFSDYYMTWIRQAPGKGLEWVSIISSSGSTIYY 60

Query 61 ADSVKGRFTISRDNQNSLYLQMNSLRAEDTAVYYCASVPTFDGNFR---RPLYFYFDSWG 117
      ADSVKGRFTISRDNQNSLYLQMNSLRAEDTAVYYCA G +R R +FD WG
Sbjct 61 ADSVKGRFTISRDNQNSLYLQMNSLRAEDTAVYYCARARGSSGWYRIGTRWGNWFDWPWG 120

Query 118 QGTLVTVSS 126
      QGTLVTVSS
Sbjct 121 QGTLVTVSS 129
```

Paratome analysis

```
paratome_1_seq_22986_126_bp
ABR H1: LTFSDYFMS (27-35)
ABR H2: WLSYINNRGGHIYYA (47-61)
ABR H3: ASVPTFDGNFRRPLYFYFDS (97-115)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: LTFSDYFMS (27-35)
```

>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UHX88987.1 Length: 7096
Range 1: 5547 to 5550

Score:19.3 bits(38), Expect:23321,
Method:,
Identities:4/4(100%), Positives:4/4(100%), Gaps:0/4(0%)

Query 5 DYFM 8
DYFM
Sbjct 5547 DYFM 5550

Range 2: 4468 to 4472

Score:17.6 bits(34), Expect:97565,
Method:,
Identities:4/5(80%), Positives:5/5(100%), Gaps:0/5(0%)

Query 2 TFSDY 6
TFS+Y
Sbjct 4468 TFSNY 4472

ABR H2: WLSYINNRGGHIYYA (47-61)

Query: unnamed protein product Query ID: lc1|Query_15311 Length: 15

>ORFla polyprotein, partial [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UCW21460.1 Length: 4288
Range 1: 15 to 19

Score:19.7 bits(39), Expect:50869,
Method:,
Identities:5/5(100%), Positives:5/5(100%), Gaps:0/5(0%)

Query 9 GGHIY 13
GGHIY
Sbjct 15 GGHIY 19

>nucleocapsid phosphoprotein, partial [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UDJ53547.1 Length: 266
Range 1: 177 to 181

Score:19.3 bits(38), Expect:71485,
Method:,
Identities:4/5(80%), Positives:4/5(80%), Gaps:0/5(0%)

Query 1 WLSYI 5
WL YI
Sbjct 177 WLT YI 181

ABR H3: ASVPTFDGNFRRPLYFDS (97-115)

Query: unnamed protein product Query ID: lc1|Query_52520 Length: 19

>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UJR43981.1 Length: 7092
Range 1: 5169 to 5176

Score:21.4 bits(43), Expect:22123,

Method:
Identities:6/8(75%), Positives:6/8(75%), Gaps:0/8(0%)

Query 9 NFRRLPLY 16
NFR LYY
Sbjct 5169 NFRSVLXY 5176

>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UBE13906.1 Length: 1273
Range 1: 26 to 38

Score:19.3 bits(38), Expect:123128,
Method:
Identities:6/13(46%), Positives:7/13(53%), Gaps:0/13(0%)

Query 4 PTFDGNFRRLPLY 16
P + FRR YY
Sbjct 26 PAYTNSFRRGVYY 38

A0A5C2FU04

```
>tr|A0A5C2FU04|A0A5C2FU04_HUMAN IGL c441_light_IGKV3D-15_IGKJ1 (Fragment)
OS=Homo sapiens OX=9606 PE=2 SV=1
EILMTQSPATLSVSPGERVTLSQWASQSISSYLAWYQQKPGQAPRLLFYGASTRATGIPA
RFSASGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRAFGQGTVEIK
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2FU04|A0A5C2FU04_HUMAN IGL c441_light_IGKV3D-15_IGKJ1
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_4889
Length: 107
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin light chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76193.1 Length: 107
>anti-SARS-CoV-2 spike protein immunoglobulin light chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76252.1 Length: 107
Range 1: 1 to 107
```

```
Score:197 bits(501), Expect:3e-63,
Method:Compositional matrix adjust.,
Identities:97/107(91%), Positives:99/107(92%), Gaps:0/107(0%)
```

```
Query 1 EILMTQSPATLSVSPGERVTLSQWASQSISSYLAWYQQKPGQAPRLLFYGASTRATGIPA 60
        EI+MTQSPATLSVSPGER TLSC ASQS+SS LAWYQQKPGQAPRLL YGASTRATGIPA
Sbjct 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Query 61 RFSASGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRAFGQGTVEIK 107
        RFS SGSGTEFTLTISSLQSEDFAVYYCQQYNNWP FGQGT VEIK
Sbjct 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPGTFGQGTKVEIK 107
```

Paratome analysis

```
paratome_1_seq_6875_107_bp
ABR L1: QSISSYLA (27-34)
ABR L2: LLFYGASTRAT (46-56)
ABR L3: QQYNNWPRA (89-97)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR L1: QSISSYLA (27-34)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UFC70978.1 Length: 7091
Range 1: 1021 to 1027
```

```
Score:18.9 bits(37), Expect:26492,
Method:,
Identities:5/7(71%), Positives:5/7(71%), Gaps:0/7(0%)
```

```
Query 1 QSISSYL 7
        Q IS YL
Sbjct 1021 QTISGYL 1027
```

```
>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QZI78246.1 Length: 1271
Range 1: 688 to 693
```

```
Score:19.3 bits(38), Expect:18584,
Method:,
Identities:5/6(83%), Positives:5/6(83%), Gaps:0/6(0%)
```

Query 1 QSISSY 6
QSI Y
Sbjct 688 QSISAY 693

ABR L2: LLFYGASTRAT (46-56)
>ORF1ab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QS013661.1 Length: 7096
Range 1: 4763 to 4768

Score:18.9 bits(37), Expect:51342,
Method:,
Identities:5/6(83%), Positives:5/6(83%), Gaps:0/6(0%)

Query 1 LLFYGA 6
LLFY A
Sbjct 4763 LLFYAA 4768

ABR L3: QQYNNWPRA (89-97)

>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UFD05785.1 Length: 1271
Range 1: 1205 to 1211

Score:21.4 bits(43), Expect:3979,
Method:,
Identities:5/7(71%), Positives:6/7(85%), Gaps:0/7(0%)

Query 1 QQYNNWP 7
+QY NWP
Sbjct 1205 EQYINWP 1211

A0A5C2GH36

```
>tr|A0A5C2GH36|A0A5C2GH36_HUMAN IG c401_light_IGKV3-20_IGKJ4 (Fragment)
OS=Homo sapiens OX=9606 PE=2 SV=1
EIVLMQSPGTLSPGERATLSCRPSQSVSSNHLAWYQQKPGQAPRLLIYGASVRATGIP
DRFSGSGSGTDFTLTISRLEPEDFAVYYCHQYGRSPTFGGGTRVEIK
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2GH36|A0A5C2GH36_HUMAN IG c401_light_IGKV3-20_IGKJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_18782
Length: 107
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin light chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76187.1 Length: 108
>anti-SARS-CoV-2 spike protein immunoglobulin light chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76198.1 Length: 108
Range 1: 1 to 108
```

```
Score:198 bits(503), Expect:1e-63,
Method:Compositional matrix adjust.,
Identities:100/108(93%), Positives:101/108(93%), Gaps:1/108(0%)
```

```
Query 1 EIVLMQSPGTLSPGERATLSCRPSQSVSSNHLAWYQQKPGQAPRLLIYGASVRATGIP 60
        EIVL QSPGTLSPGERATLSCR S QSVSSN LAWYQQKPGQAPRLLIYGAS RATGIP
Sbjct 1 EIVLTQSPGTLSPGERATLSCRASQSVSSNFLAWYQQKPGQAPRLLIYGASSRATGIP 60

Query 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCHQYGRSP-TFGGGTRVEIK 107
        DRFSGSGSGTDFTLTISRLEPEDFAVYYC QYGRSP TFG GTR+EIK
Sbjct 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGRSPITFGQGRLEIK 108
```

Paratome analysis

```
paratome_1_seq_6953_107_bp
ABR L1: QSVSSNHLA (27-35)
ABR L2: LLIYGASVRAT (47-57)
ABR L3: HQYGRSP (90-96)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR L1: QSVSSNHLA (27-35)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QNN88284.1 Length: 7096
Range 1: 3739 to 3744
```

```
Score:18.5 bits(36), Expect:47890,
Method:,
Identities:5/6(83%), Positives:5/6(83%), Gaps:0/6(0%)
```

```
Query 2 SVSSNH 7
        SV SNH
Sbjct 3739 SVTSNH 3744
```

```
ABR L2: LLIYGASVRAT (47-57)
>surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UDB79764.1 Length: 1273
Range 1: 1012 to 1020
```

```
Score:17.6 bits(34), Expect:150151,
Method:,
Identities:5/9(56%), Positives:6/9(66%), Gaps:0/9(0%)
```

Query 2 LIYGASVRA 10
LI A +RA
Sbjct 1012 LIXXAXIRA 1020

ABR L3: HQYGRSP (90-96)

>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]

Sequence ID: UGC79169.1 Length: 7108

Range 1: 96 to 100

Score:19.3 bits(38), Expect:14481,

Method:

Identities:5/5(100%), Positives:5/5(100%), Gaps:0/5(0%)

Query 2 QYGRS 6
QYGRS
Sbjct 96 QYGRS 100

A0A5C2GPU5

```
>tr|A0A5C2GPU5|A0A5C2GPU5_HUMAN IG c893_heavy_IGHV3-15_IGHD3-16_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLVESGGGLVKPGGSLRLSCAASGFSFSNAWMSWVRQAPGKGLEWVGHISKADGGTT
DYAVPVKPIFTISRDDSKNTLYLQLNSLKTEDTAMYICTTG GALSIFYDYWGQGLTVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2GPU5|A0A5C2GPU5_HUMAN IG c893_heavy_IGHV3-15_IGHD3-16_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_90911
Length: 121
```

```
>cross-reactive anti-SARS-CoV-2 immunoglobulin heavy chain variable region,
partial [Homo sapiens]
```

```
Sequence ID: QRG26521.1 Length: 127
```

```
Range 1: 1 to 127
```

```
Score:206 bits(524), Expect:3e-66,
Method:Compositional matrix adjust.,
Identities:105/127(83%), Positives:112/127(88%), Gaps:6/127(4%)
```

```
Query 1 EVQLVESGGGLVKPGGSLRLSCAASGFSFSNAWMSWVRQAPGKGLEWVGHISKADGGTT 60
      +VQLVESGGGLVKPGGSLRLSCAASGF+FSNAWMSWVRQAPGKGLEWVG IKSK DGGTT
Sbjct 1 QVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKSKTDGGTT 60

Query 61 DYAVPVKPIFTISRDDSKNTLYLQLNSLKTEDTAMYICTT---GGGALSIFY---DYWGQG 114
      DYA PVK FTISRDDSKNTLYLQ+NSLKTEDTA+YYCTT G G+L Y+ D WG+G
Sbjct 61 DYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTTEEPGAGSLYYYYYMDVWGKG 120

Query 115 TLVTVSS 121
      T VTVSS
Sbjct 121 TTVTVSS 127
```

```
>anti-SARS-CoV-2 immunoglobulin gamma heavy chain variable region, partial
[Homo sapiens]
```

```
Sequence ID: QJU69707.1 Length: 127
```

```
Range 1: 1 to 127
```

```
Score:213 bits(541), Expect:1e-68,
Method:Compositional matrix adjust.,
Identities:107/127(84%), Positives:111/127(87%), Gaps:6/127(4%)
```

```
Query 1 EVQLVESGGGLVKPGGSLRLSCAASGFSFSNAWMSWVRQAPGKGLEWVGHISKADGGTT 60
      EVQLVESGGGLVKPGGSLRLSCAASGF+FSNAWMSWVRQAPGKGLEWVG IKSK DGGTT
Sbjct 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKSKTDGGTT 60

Query 61 DYAVPVKPIFTISRDDSKNTLYLQLNSLKTEDTAMYICTTG-----GALSIFYDYWGQG 114
      DYA PVK FTISRDDSKNTLYLQ+NSLKTEDTA+YYCTT G+ Y DYWGQG
Sbjct 61 DYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTDRVYDIWGSYRYLDYWGQG 120

Query 115 TLVTVSS 121
      TLVTVSS
Sbjct 121 TLVTVSS 127
```

Paratome analysis

```
paratome_1_seq_7036_121_bp
ABR H1: FSFSNAWMS (27-35)
ABR H2: WVGHIKSKADGGTTDY (47-62)
ABR H3: TGGGALSIFYDY (100-110)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: FSFSNAWMS (27-35)
```

No significant similarity found.

ABR H2: WVGHIKSKADGGTTDY (47-62)

>ORF1a polyprotein [Severe acute respiratory syndrome coronavirus 2]

Sequence ID: UKR34990.1 Length: 4401

Range 1: 1301 to 1311

Score:19.3 bits(38), Expect:84318,

Method:,

Identities:7/11(64%), Positives:8/11(72%), Gaps:0/11(0%)

Query 5 IKSKADGGTTD 15

I K DGGTT+

Sbjct 1301 IPTKKDGGTTE 1311

ABR H3: TGGGALSYFDY (100-110)

>ORF1ab polyprotein [Severe acute respiratory syndrome coronavirus 2]

Sequence ID: UDG47217.1 Length: 7096

Range 1: 4838 to 4847

Score:21.0 bits(42), Expect:8671,

Method:,

Identities:6/10(60%), Positives:7/10(70%), Gaps:0/10(0%)

Query 2 GGGALSYFDY 11

G A SY+DY

Sbjct 4838 GNAAISYYDY 4847

>ORF3a protein [Severe acute respiratory syndrome coronavirus 2]

Sequence ID: UHP61412.1 Length: 275

Range 1: 204 to 211

Score:19.7 bits(39), Expect:25152,

Method:,

Identities:6/8(75%), Positives:6/8(75%), Gaps:2/8(25%)

Query 6 LSYF--DY 11

LSYF DY

Sbjct 204 LSYFTSDY 211

A0A5C2H2C4

```
>tr|A0A5C2H2C4|A0A5C2H2C4_HUMAN IG c1116_light_IGKV3-20_IGKJ2 (Fragment)
OS=Homo sapiens OX=9606 PE=2 SV=1
EIVLTQSPGTLSSLPGDRATLSCRASRSVSSAQLTWYQQRPGQAPRLLLYATSTRATGVP
DRFSGSGSGTDFTLTISKVQPEDFAVYFCHQYESSPRTFGQGTKLEIK
```

BLAST Sequence alignment against nr

```
Query: tr|A0A5C2H2C4|A0A5C2H2C4_HUMAN IG c1116_light_IGKV3-20_IGKJ2
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID: lcl|Query_10487
Length: 108
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin light chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76271.1 Length: 108
Range 1: 1 to 108
```

```
Score:188 bits(478), Expect:1e-59,
Method:Compositional matrix adjust.,
Identities:89/108(82%), Positives:101/108(93%), Gaps:0/108(0%)
```

```
Query 1 EIVLTQSPGTLSSLPGDRATLSCRASRSVSSAQLTWYQQRPGQAPRLLLYATSTRATGVP 60
      EIVLTQSPGTLSSLPG+RATLSCRAS+SVSS L WYQQ+PGQAPRLL++ S+RATG+P
Sbjct 1 EIVLTQSPGTLSSLPGERATLSCRASQSVSSTFLAWYQQKPGQAPRLLIFGASSRATGIP 60

Query 61 DRFSGSGSGTDFTLTISKVQPEDFAVYFCHQYESSPRTFGQGTKLEIK 108
      DRFSGSGSGTDFTLTIS+++PEDFAVY+CHQY +SP TFGQGTKLEIK
Sbjct 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCHQYGTSPYTFGQGTKLEIK 108
```

Paratome analysis

```
paratome_1_seq_7482_108_bp
ABR L1: RSVSSAQLT (27-35)
ABR L2: LLLYATSTRAT (47-57)
ABR L3: HQYESSPR (90-97)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR L1: RSVSSAQLT (27-35)
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UBU25355.1 Length: 7096
Range 1: 4404 to 4412
```

```
Score:18.9 bits(37), Expect:33499,
Method:,
Identities:6/9(67%), Positives:6/9(66%), Gaps:0/9(0%)
```

```
Query 1 RSVSSAQLT 9
      R VS A LT
Sbjct 4404 RGVSAARLT 4412
```

```
ABR L2: LLLYATSTRAT (47-57)
```

```
>ORFla polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: QO094433.1 Length: 4405
Range 1: 2176 to 2186
```

```
Score:19.7 bits(39), Expect:24963,
Method:,
Identities:6/11(55%), Positives:6/11(54%), Gaps:0/11(0%)
```

Query 1 LLLYATSTRAT 11
LL T TR T
Sbjct 2176 LLXXXTXTRST 2186

ABR L3: HQYESSPR (90-97)
No significant similarity found.

A0A7S5EWS1

```
>tr|A0A7S5EWS1|A0A7S5EWS1_HUMAN IGH c768_heavy_IGHV3-48_IGHD4-17_IGHJ3
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLEESGGGLVQPGGSLRLSCEVSGFTFRNYEMNWVRQAPGKGLEWVAYIGSFSSPTHY
AGSVRGRFTISRDNKNSLYLQMNSLRADDTALYYCARTRKSDYGDYSEDEGMDVWGRGT
MVTVSS
```

BLAST Sequence alignment against nr

```
Query: tr|A0A7S5EWS1|A0A7S5EWS1_HUMAN IGH c768_heavy_IGHV3-48_IGHD4-
17_IGHJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1 Query ID:
lcl|Query_71519 Length: 126
```

```
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76471.1 Length: 126
>anti-SARS-CoV-2 spike protein immunoglobulin heavy chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76492.1 Length: 126
Range 1: 1 to 126
```

```
Score:192 bits(488), Expect:1e-60,
Method:Compositional matrix adjust.,
Identities:94/126(75%), Positives:104/126(82%), Gaps:0/126(0%)
```

```
Query 1 EVQLEESGGGLVQPGGSLRLSCEVSGFTFRNYEMNWVRQAPGKGLEWVAYIGSFSSPTHY 60
        EVQL ESGGGLVQPGGSLRLSC SGFTF +YEMNWVRQAPGKGLEWV+YI S S +Y
Sbjct 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYEMNWVRQAPGKGLEWVS YISSSGSAIYY 60

Query 61 AGSVRGRFTISRDNKNSLYLQMNSLRADDTALYYCARTRKSDYGDYSEDEGMDVWGRGT 120
        A SV+GRFTISRDNKNSLYLQMNSLR +DTA+YYCAR +S Y D+ D WG+GT
Sbjct 61 ADSVKGRFTISRDNKNSLYLQMNSLRVEDTAVYYCAREARSRYFDWLPSYYFDYWGGQT 120

Query 121 MVTVSS 126
        +VTVSS
Sbjct 121 LVTVSS 126
```

Paratome analysis

```
paratome_1_seq_7559_126_bp
ABR H1: FTFRNYEMN (27-35)
ABR H2: WVAYIGSFSSPTHY (47-60)
ABR H3: RTRKSDYGDYSEDEGMDV (98-115)
```

BLAST Sequence alignment against SARS-CoV-2

```
ABR H1: FTFRNYEMN (27-35)
```

```
>ORFlab polyprotein [Severe acute respiratory syndrome coronavirus 2]
Sequence ID: UKG54270.1 Length: 7089
Range 1: 4461 to 4467
```

```
Score:21.4 bits(43), Expect:3973,
Method:,
Identities:5/7(71%), Positives:6/7(85%), Gaps:0/7(0%)
```

```
Query 2 TFRNYEM 8
        TF NY+M
Sbjct 4461 TFSNYQM 4467
```

```
ABR H2: WVAYIGSFSSPTHY (47-60)
```

```
>ORFla polyprotein [Severe acute respiratory syndrome coronavirus 2]
```

Sequence ID: QWU48698.1 Length: 4402
Range 1: 2593 to 2600

Score:22.3 bits(45), Expect:5258,
Method:,
Identities:6/8(75%), Positives:7/8(87%), Gaps:0/8(0%)

Query 3 AYIGSFSS 10
AY+G FSS
Sbjct 2593 AYVGTFSS 2600

ABR H3: RTRKSDYGDYSEDEGMDV (98-115)

>ORFlab polyprotein, partial [Severe acute respiratory syndrome coronavirus
2]

Sequence ID: UFZ21166.1 Length: 7070
Range 1: 5500 to 5505

Score:22.3 bits(45), Expect:9684,
Method:,
Identities:6/6(100%), Positives:6/6(100%), Gaps:0/6(0%)

Query 4 KSDYGD 9
KSDYGD
Sbjct 5500 KSDYGD 5505

Part 2. Analysis of immunoglobulin proteins overrepresented in infected cohorts when compared to PCR- individuals.

Analytical workflow

1. Select immunoglobulin protein sequences overrepresented with highest PCR+/- Log fold-change relative intensity exclusively in each infected asymptomatic, nonsevere and severe cohorts.
2. Protein BLAST sequence alignment against non-redundant protein database(nr)using compositional matrix adjustment (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome).
3. Identification of immunoglobulin sequences aligned with known function. Criteria: Score > 160 bits, Identity > 60%.
4. Identification of correlates of identified proteins with protective or disease associated capacity.

Input data:

Protein ID	Severe
A0A5C2GIT4	0.977
A0A5C2GDW3	0.795
A0A7S5C115	0.731

Protein ID	Nonsevere
A0A5C2G7I4	0.343
A0A5C2GPZ0	0.328
A0A7S5EYL7	0.296

Protein ID	Asymptomatic
A0A5C2GJF4	1.240
A0A5C2FZ03	0.793
A0A5C2G410	0.730

Severe patients

A0A5C2GIT4

BLAST Sequence alignment against nr

```
>tr|A0A5C2GIT4|A0A5C2GIT4_HUMAN IG c17_heavy_IGHV5-51_IGHD5-12_IGHJ6
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLVQSGAEMKKPGESLRISCRGSGYTFTKYWIGWVRLMPGRGLEWMGIIFPRDSETRY
SPSFQGGQVTISADKSIRTAYLQWTSLNVSDSATYYCARAKGIEAPGHYYGMDVWGHGTTV
TVSS
```

```
>anti-peanut 2S albumin immunoglobulin heavy chain variable region, partial
[Homo sapiens]
```

```
Sequence ID: QVG74243.1 Length: 124
```

```
Range 1: 1 to 124
```

```
Score:196 bits(497), Expect:4e-62,
Method:Compositional matrix adjust.,
Identities:93/124(75%), Positives:105/124(84%), Gaps:0/124(0%)
```

```
Query 1 EVQLVQSGAEMKKPGESLRISCRGSGYTFTKYWIGWVRLMPGRGLEWMGIIFPRDSETRY 60
Sbjct 1 EVQLVQSGAE+KKPGESL+ISC GSG+ FT YWI WVR MPG+GLEWMG I+P D++T Y 60

Query 61 SPSFQGGQVTISADKSIRTAYLQWTSLNVSDSATYYCARAKGIEAPGHYYGMDVWGHGTTV 120
Sbjct 61 SPSFQGGQVTISADKSI TAYLQW+SL SD+A+YYCAR + +YYGMDVWG GTTV 120

Query 121 TVSS 124
Sbjct 121 TVSS 124
```

Correlate: Risk of allergy

A0A5C2GDW3

```
>tr|A0A5C2GDW3|A0A5C2GDW3_HUMAN IGH + IGL c109_heavy_IGHV3-11_IGHD3-
10_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
QVQLVESGGGLVKPGGSLRLSCAASGFTFSDDYYMSWVRQAPGKGLEWISYIRNRGNMGYY
ADSVKGRFTISRDNAKNSLYLQMSSLQADDTAVYYCARISGFYSGSEVFDYWGQGTLTIVS
S
```

BLAST Sequence alignment against nr

```
>anti-peanut 2S albumin immunoglobulin heavy chain variable region, partial
[Homo sapiens]
```

```
Sequence ID: QVG74146.1 Length: 122
```

```
Range 1: 1 to 122
```

```
Score:202 bits(514), Expect:1e-64,
Method:Compositional matrix adjust.,
Identities:101/122(83%), Positives:110/122(90%), Gaps:1/122(0%)
```

```
Query 1 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDDYYMSWVRQAPGKGLEWISYIRNRGNMGYY 60
Sbjct 1 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDDYYMSW+RQAPGKGLEW+SYI + G+ +YY 60

Query 61 ADSVKGRFTISRDNAKNSLYLQMSSLQADDTAVYYCAR-ISGFYSGSEVFDYWGQGTLTIV 119
Sbjct 61 ADSVKGRFTISRDNAKNSLYLQM+SL+A+DTAVYYCAR G FDYWGQGTL+TV 120
```

```
Query 120 SS 121
      SS
Sbjct 121 SS 122
```

Correlate: Risk of allergy

A0A7S5C115

```
>tr|A0A7S5C115|A0A7S5C115_HUMAN IGH c1867_heavy_IGHV3-49_IGHD2-2_IGHJ6
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLVESGGGLVQPGRSLRLSCTGSGFTFGDFAMSWVRQAPGKGLEWVSLIRSNAYGGTT
EHAASVKGRFTISRDNKSIAYLQMDSLQTEDTAVYYCTRGLPAIIGYYMDVWAKGTTVT
VSS
```

BLAST Sequence alignment against nr

```
>anti-GPIIb/IIIa immunoglobulin heavy chain variable region, partial [Homo
sapiens]
Sequence ID: AAK77548.1 Length: 122
Range 1: 1 to 122
```

```
Score:206 bits(525), Expect:2e-66,
Method:Compositional matrix adjust.,
Identities:102/122(84%), Positives:108/122(88%), Gaps:0/122(0%)
```

```
Query 1 EVQLVESGGGLVQPGRSLRLSCTGSGFTFGDFAMSWVRQAPGKGLEWVSLIRSNAYGGTT 60
        EVQLVESGGGLVQPGRSLRLSCT SGFTFGD+AMSWVRQAPGKGLEWV IRS AYGGTT
Sbjct 1 EVQLVESGGGLVQPGRSLRLSCTASGFTFGDYAMSWVRQAPGKGLEWVGFIIRSKAYGGTT 60

Query 61 EHAASVKGRFTISRDNKSIAYLQMDSLQTEDTAVYYCTRGLPAIIGYYMDVWAKGTTVT 120
        E+AASVKGRFTISR+SKSIAYLQM+SL+TEDTAVYYCT P Y MDVW +GT VT
Sbjct 61 EYAASVKGRFTISRDDSKSIAYLQMNLSLKTEDTAVYYCTVRSPGYYYYGMDVWGQGLT 120

Query 121 VS 122
        VS
Sbjct 121 VS 122
```

Correlate: Chronic idiopathic thrombocytopenic purpura (ITP) caused by an antibody reactive with platelet-associated antigens

```
>anti-GPIIb/IIIa immunoglobulin heavy chain variable region, partial [Homo
sapiens]
Sequence ID: AAK77548.1 Length: 122
Range 1: 1 to 122
```

```
Score:206 bits(525), Expect:2e-66,
Method:Compositional matrix adjust.,
Identities:102/122(84%), Positives:108/122(88%), Gaps:0/122(0%)
```

```
Query 1 EVQLVESGGGLVQPGRSLRLSCTGSGFTFGDFAMSWVRQAPGKGLEWVSLIRSNAYGGTT 60
        EVQLVESGGGLVQPGRSLRLSCT SGFTFGD+AMSWVRQAPGKGLEWV IRS AYGGTT
Sbjct 1 EVQLVESGGGLVQPGRSLRLSCTASGFTFGDYAMSWVRQAPGKGLEWVGFIIRSKAYGGTT 60

Query 61 EHAASVKGRFTISRDNKSIAYLQMDSLQTEDTAVYYCTRGLPAIIGYYMDVWAKGTTVT 120
        E+AASVKGRFTISR+SKSIAYLQM+SL+TEDTAVYYCT P Y MDVW +GT VT
Sbjct 61 EYAASVKGRFTISRDDSKSIAYLQMNLSLKTEDTAVYYCTVRSPGYYYYGMDVWGQGLT 120

Query 121 VS 122
        VS
Sbjct 121 VS 122
```

Correlate: Autoantibodies anti-platelet GPIIb/IIIa

Nonsevere patients

A0A5C2G7I4

```
>tr|A0A5C2G7I4|A0A5C2G7I4_HUMAN IGH c572_heavy__IGHV3-21_IGHD5-18_IGHJ5
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLVESGGGLVKPGGSLKLSCAASGFPFSAYTMTWVRQAPGKGLEWVSIISGSDSYISY
VDSVKGRFTISRDNANNALYLQMNSLRAEDTAVYYCARVEGLDPIDRWGQGTPVTVSS
```

BLAST Sequence alignment against nr

```
>myosin-reactive immunoglobulin heavy chain variable region, partial [Homo sapiens]
```

```
Sequence ID: AAD56259.1 Length: 118
```

```
Range 1: 1 to 117
```

```
Score:171 bits(432), Expect:3e-52,
Method:Compositional matrix adjust.,
Identities:92/117(79%), Positives:100/117(85%), Gaps:0/117(0%)
```

```
Query 1 EVQLVESGGGLVKPGGSLKLSCAASGFPFSAYTMTWVRQAPGKGLEWvsiiisgdsyisy 60
EVQLVESGGGLV+PGGSL+LSCAASGF FS+Y+M WVRQAPGKGLEWVS IS + I Y
Sbjct 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSTIITIYY 60

Query 61 vdsvkGRFTISRDNANNALYLQMNSLRAEDTAVYYCARVEGLDPIDRWGQGTPVTVSS 117
DSVKGRFTISRDN N+LYLQMNSLRAEDTAVYYCAR + + D WGQGT VTVS
Sbjct 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGDSSEAFDIWGQGTMTVTVS 117
```

```
>anti-SARS-CoV-2 immunoglobulin gamma heavy chain, partial [Homo sapiens]
```

```
Sequence ID: QUX33738.1 Length: 116
```

```
Range 1: 1 to 116
```

```
Score:169 bits(428), Expect:8e-52,
Method:Compositional matrix adjust.,
Identities:93/118(79%), Positives:102/118(86%), Gaps:2/118(1%)
```

```
Query 1 EVQLVESGGGLVKPGGSLKLSCAASGFPFSAYTMTWVRQAPGKGLEWvsiiisgdsyisy 60
EVQL+ESGGGLV+PGGSL+LSCAASGF FS+YTM WVRQAPGKGLEWVS I+ S I Y
Sbjct 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYTMNWVRQAPGKGLEWVSYITSDSSTIYY 60

Query 61 vdsvkGRFTISRDNANNALYLQMNSLRAEDTAVYYCARVEGLDPIDRWGQGTPVTVSS 118
DSVKGRFTISRDN N+LYLQMNSLRAEDTAVYYCAR + +D D WG+GT VTVSS
Sbjct 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARNKAMD--DYWGRGTLVTVSS 116
```

Correlate: Protective capacity against SARS-CoV-2 and autoantibodies-mediated risk of myasthenia gravis

A0A5C2GPZ0

```
>tr|A0A5C2GPZ0|A0A5C2GPZ0_HUMAN IG c650_heavy_IGHV3-23_IGHD4-11_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVQLLDSGGGSVQPGGSLRLSCAASGFYFSNYAMNWVRQAPGKGLQWVARISGTGGDTFY
ADSVKGRFTISRDN SKNILSLQMDSLRDEDTAVYFCAKDRLSSPKVSEAYFDYWGPGLTV
TVSS
```

BLAST Sequence alignment against nr

```
>anti-SARS-CoV-2 immunoglobulin gamma heavy chain, partial [Homo sapiens]
```

```
Sequence ID: QUX33727.1 Length: 121
```

```
Range 1: 1 to 121
```

```
Score:199 bits(506), Expect:2e-63,
```

Method:Compositional matrix adjust.,

Identities:100/124(81%), Positives:109/124(87%), Gaps:3/124(2%)

```
Query 1 EVQLLDSEGGGSVQPGGSLRLSCAASGFFYSNYAMNWVRQAPGKGLQWVARISGTGGDTFY 60
Sbjct 1 EVQLL+SGGG VQPGGSLRLSCAASGF FS+YAM+WVRQAPGKGL+WV+ ISG+GG T+Y 60

Query 61 ADSVKGRFTISRDN SKNILSLQMDSLRDEDTAVYFCAKDR LSSPKVSEAYFDYWGP GTLV 120
Sbjct 61 ADSVKGRFTISRDN SKN L LQM+SLR EDTAVY+CAKDR SS YFDYWG GTLV 117

Query 121 TVSS 124
Sbjct 118 TVSS 121
```

>anti-peanut 2S albumin immunoglobulin heavy chain variable region, partial
[Homo sapiens]

Sequence ID: QVG74500.1 Length: 122

Range 1: 1 to 122

Score:197 bits(502), Expect:7e-63,

Method:Compositional matrix adjust.,

Identities:100/124(81%), Positives:110/124(88%), Gaps:2/124(1%)

```
Query 1 EVQLLDSEGGGSVQPGGSLRLSCAASGFFYSNYAMNWVRQAPGKGLQWVARISGTGGDTFY 60
Sbjct 1 EVQLL+SGGG VQPGGSLRLSCAASGF FS+YAM+WVRQAPGKGL+WV+ ISG+GG T+Y 60

Query 61 ADSVKGRFTISRDN SKNILSLQMDSLRDEDTAVYFCAKDR LSSPKVSEAYFDYWGP GTLV 120
Sbjct 61 ADSVKGRFTISRDN SKN L LQM+SLR EDTAVY+CAKDR SS +S FDYWG GTLV 118

Query 121 TVSS 124
Sbjct 119 TVSS 122
```

>anti-hepatitis B surface antigen immunoglobulin heavy chain variable
region, partial [Homo sapiens]

Sequence ID: AAL57837.1 Length: 121

Range 1: 1 to 121

Score:196 bits(499), Expect:2e-62,

Method:Compositional matrix adjust.,

Identities:96/124(77%), Positives:109/124(87%), Gaps:3/124(2%)

```
Query 1 EVQLLDSEGGGSVQPGGSLRLSCAASGFFYSNYAMNWVRQAPGKGLQWVARISGTGGDTFY 60
Sbjct 1 EVQL++SGGG VQPGGSLRLSCAASGF FS+YAM+WVRQAPGKGL+WV+ IS GG T+Y 60

Query 61 ADSVKGRFTISRDN SKNILSLQMDSLRDEDTAVYFCAKDR LSSPKVSEAYFDYWGP GTLV 120
Sbjct 61 ADSVKGRFTISRDN SKN L LQM+SLR EDTAVY+CAKDR +++ A+FDYWG GTLV 117

Query 121 TVSS 124
Sbjct 118 TVSS 121
```

>Diabody 305 complex with EpoR [Homo sapiens]

Sequence ID: 4Y5X_J Length: 136

Range 1: 8 to 131

Score:195 bits(496), Expect:9e-62,

Method:Compositional matrix adjust.,

Identities:95/124(77%), Positives:106/124(85%), Gaps:0/124(0%)

```
Query 1 EVQLLDSEGGGSVQPGGSLRLSCAASGFFYSNYAMNWVRQAPGKGLQWVARISGTGGDTFY 60
Sbjct 1 EVQLL+SGGG VQPGGSLRLSCAASGF FS+YAM+WVRQAPGKGL+WV+ ISG+GG T+Y
```

```

Sbjct  8      EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY  67
Query  61      ADSVKGRFTISRDN SKNILSLQMDSLRDEDTAVYFCAKDR LSSPKVSEAYFDYWGPGTLV  120
          ADSVKGRFTISRDN SKN L LQM+SLR EDTAVY+C KDR++          YFD WG GT V
Sbjct  68      ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVKDRVAVAGKGSYYFDSWGRGTTV  127
Query  121     TVSS      124
          TVSS
Sbjct  128     TVSS      131

```

Correlate: Protective capacity against SARS-CoV-2 and Hepatitis B virus, risk of allergy and autoantibodies protein binding/immune system

A0A7S5EYL7

```

>tr|A0A7S5EYL7|A0A7S5EYL7_HUMAN IGH c4094_heavy_IGHV3-21_IGHD5-18_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
EVHLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKGLEWVSSISSSSRSIYY
ADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCASPLSRGYSYIFDYWGQGT LVTVSS

```

BLAST Sequence alignment against nr

>anti-SARS-CoV-2 immunoglobulin heavy chain variable region, partial [Homo sapiens]

Sequence ID: QTX15853.1 Length: 125

Range 1: 1 to 125

Score:199 bits(507), Expect:1e-63,
Method:Compositional matrix adjust.,
Identities:107/125(86%), Positives:114/125(91%), Gaps:4/125(3%)

```

Query  1      EVHLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKGLEWVssisssrsiYY  60
          EV LVESGGG+VKPGGSLRLSCAASGFTFS+YSMNWVRQAPGKGLEWVSSISSSS I+Y
Sbjct  1      EVQLVESGGGVVKPGGSLRLSCAASGFTTFSTYSMNWVRQAPGKGLEWVSSISSSSSTDIHY  60

Query  61      ADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCASPLSRGY----SYIFDYWGQGT L  116
          ADS+KGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCA      RG+      +YIFD+WGQGT L
Sbjct  61      ADSMKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCARDFHRGWYDHSAYIFDFWGQGT L  120

Query  117     VTVSS      121
          VTVSS
Sbjct  121     VTVSS      125

```

>anti-SARS-CoV-2 immunoglobulin gamma, partial [Homo sapiens]

Sequence ID: QTI96680.1 Length: 126

Range 1: 1 to 126

Score:197 bits(502), Expect:8e-63,
Method:Compositional matrix adjust.,
Identities:107/126(85%), Positives:110/126(87%), Gaps:5/126(3%)

```

Query  1      EVHLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKGLEWVssisssrsiYY  60
          EV LVESGGGLV+PGGSLRLSCAASGFTTFSSY MNWVRQAPGKGLEWVS ISSS +IYY
Sbjct  1      EVQLVESGGGLVQPGGSLRLSCAASGFTTFSSYEMNWVRQAPGKGLEWVS YISSSGSTIYY  60

Query  61      ADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCASPLS-----RGYSYIFDYWGQGT  115
          ADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCA      S      Y+ IFDYWGQGT
Sbjct  61      ADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCARDYSYCSSTSCYTSIFDYWGQGT  120

Query  116     LVTVSS      121
          LVTVSS
Sbjct  121     LVTVSS      126

```

>anti-peanut 2S albumin immunoglobulin heavy chain variable region, partial [Homo sapiens]

Sequence ID: QVG74488.1 Length: 120
Range 1: 1 to 120

Score:196 bits(499), Expect:2e-62,
Method:Compositional matrix adjust.,
Identities:106/121(88%), Positives:111/121(91%), Gaps:1/121(0%)

```
Query 1 EVHLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVssisssrsiYY 60
        EV LVESGGGLV+PGGSLRLSCAASGFTFSSY MNWVRQAPGKGLEWVS ISSSS +IYY
Sbjct 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYCMNWVRQAPGKGLEWVSyiSSSSNTIYY 60

Query 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCASPLSRGYSYIFDYWGQGLTVTVSS 121
        ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY+CA + G+ Y FDYWGQGLTVTVSS
Sbjct 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYFCARDKTSGWY-FDYWGQGLTVTVSS 120
```

Correlate: Protective capacity against SARS-CoV-2 and risk of allergy

Asymptomatic cases

A0A5C2GJF4

```
>tr|A0A5C2GJF4|A0A5C2GJF4_HUMAN IG c470_heavy_IGHV3-33_IGHD1-26_IGHJ4
(Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1
QVQLVQSGGGVVPQGGSLRLSCAASGFTFSSYGIHWVRQAPGKGLDWVAFIRSDGSNKYY
ADSVRGRFIIIRDNSKNTLYLQMNSLRRTDDAAVYYCAKGGDEWDLWGAHFDYWGQGLTVT
VSS
```

BLAST Sequence alignment against nr

```
>anti-SARS-CoV-2 immunoglobulin heavy chain variable region, partial [Homo
sapiens]
Sequence ID: UKB89119.1 Length: 123
Range 1: 19 to 123
```

```
Score:181 bits(459), Expect:3e-56,
Method:Compositional matrix adjust.,
Identities:88/105(84%), Positives:94/105(89%), Gaps:0/105(0%)
```

```
Query 19 RLSCAASGFTFSSYGIHWVRQAPGKGLDWVAFIRSDGSNKYYADSVRGRFIIIRDNSKNT 78
          RLSCAASGFTFSSYG+HWVRQAPGKGL+WVA I DGSNKYYADSV+GRF ISRDNSKNT
Sbjct 19 RLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTIIRDNSKNT 78

Query 79 LYLQMNSLRRTDDAAVYYCAKGGDEWDLWGAHFDYWGQGLTVTVSS 123
          LYLQMNSLR +D AVYYCAKGG +D G +FDYWGQGLTVTVSS
Sbjct 79 LYLQMNSLRAEDTAVYYCAKGGGWYDYKGYFFDYWGQGLTVTVSS 123
```

```
>anti-glycoprotein VI immunoglobulin heavy chain variable region antibody,
partial [Homo sapiens]
Sequence ID: AAN15190.1 Length: 119
Range 1: 19 to 119
```

```
Score:178 bits(452), Expect:2e-55,
Method:Compositional matrix adjust.,
Identities:88/105(84%), Positives:92/105(87%), Gaps:4/105(3%)
```

```
Query 19 RLSCAASGFTFSSYGIHWVRQAPGKGLDWVAFIRSDGSNKYYADSVRGRFIIIRDNSKNT 78
          RLSCAASGFTFSSYG+HWVRQAPGKGL+WVAFIR DGSNKYYADSV+GRF ISRDNSKNT
Sbjct 19 RLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTIIRDNSKNT 78

Query 79 LYLQMNSLRRTDDAAVYYCAKGGDEWDLWGAHFDYWGQGLTVTVSS 123
          LYLQMNSLR +D AVYYCAKG A FDYWGQGLTVTVSS
Sbjct 79 LYLQMNSLRAEDTAVYYCAKG----PRIAASFYWGQGLTVTVSS 119
```

Correlate: Protective capacity against SARS-CoV-2 and thrombosis.

A0A5C2FZ03

```
>tr|A0A5C2FZ03|A0A5C2FZ03_HUMAN IGL c497_light_IGKV1D-17_IGKJ1 (Fragment)
OS=Homo sapiens OX=9606 PE=2 SV=1
DIQMTQSPSAMSASVGDRVTITCRASQGISNYLAWFQQKPGKVPKRLIYAASNLSQSGVPS
RFSGSGSGTEFTLTISLQSEDFATYYCLQHNSYPRTFGQGTKVEIK
```

BLAST Sequence alignment against nr

```
anti-SARS-CoV-2 immunoglobulin light chain variable region, partial [Homo
sapiens]
Sequence ID: QKK35737.1 Length: 107
>immunoglobulin light chain variable region, partial [Homo sapiens]
Sequence ID: QXE98237.1 Length: 107
```

Range 1: 1 to 107

Score:204 bits(519), Expect:6e-66,
Method:Compositional matrix adjust.,
Identities:98/107(92%), Positives:103/107(96%), Gaps:0/107(0%)

```
Query 1 DIQMTQSPSAMSASVGDRVTITCRASQGISNYLAWFQQKPGKVPKRLIYAASNLSQSGVPS 60
        DIQ+TQSPSAMSASVGDRVTITCRASQGI++ LAWFAQKPGKVPKRLIYAASNLSQ+GVPS
Sbjct 1 DIQLTQSPSAMSASVGDRVTITCRASQGINDLAWFQQKPGKVPKRLIYAASNLSQNGVPS 60

Query 61 RFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPRTFGQGTKVEIK 107
        RFSGSGSGTEFTLTISSLQ EDFATYYCLQHNSYP TFG GTK+EIK
Sbjct 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKLEIK 107
```

>anti-ZIKV immunoglobulin light chain variable region, partial [Homo sapiens]

Sequence ID: AOT82813.1 Length: 110
Range 1: 1 to 107

Score:202 bits(513), Expect:5e-65,
Method:Compositional matrix adjust.,
Identities:97/107(91%), Positives:101/107(94%), Gaps:0/107(0%)

```
Query 1 DIQMTQSPSAMSASVGDRVTITCRASQGISNYLAWFQQKPGKVPKRLIYAASNLSQSGVPS 60
        DI MTQSPS++SASVGDRVTITCRASQGI N L W+QQKPGK PKRLIYAAS+LSQSGVPS
Sbjct 1 DIVMTQSPSSLSASVGDRVTITCRASQGINDLGWYQQKPGKAPKRLIYAASSLSQSGVPS 60

Query 61 RFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPRTFGQGTKVEIK 107
        RFSGSGSGTEFTLTISSLQ EDFATYYCLQHNSYPRTFGQGTKVEIK
Sbjct 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPRTFGQGTKVEIK 107
```

>anti HBs antibody light-chain Fab fragment, partial [Homo sapiens]

Sequence ID: BAB18259.1 Length: 214
Range 1: 1 to 107

Score:202 bits(514), Expect:1e-63,
Method:Compositional matrix adjust.,
Identities:95/107(89%), Positives:101/107(94%), Gaps:0/107(0%)

```
Query 1 DIQMTQSPSAMSASVGDRVTITCRASQGISNYLAWFQQKPGKVPKRLIYAASNLSQSGVPS 60
        DI++TQSPSAM+ASVGDRVTITCRASQGI NYL WFQQKPGKVPKRLIYAAS+LSQSGVPS
Sbjct 1 DIELTQSPSAMAASVGDRVTITCRASQGIGNYLVWFQQKPGKVPKRLIYAASSLSQSGVPS 60

Query 61 RFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPRTFGQGTKVEIK 107
        RFSGSGSGTEFTLTISSLQ EDFATYYCL HN+YP +FG GTKVEIK
Sbjct 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLHHNNYPLSFGGGTKVEIK 107
```

Correlate: Protective capacity against SARS-CoV-2, Zika virus and Hepatitis B virus

A0A5C2G410

>tr|A0A5C2G410|A0A5C2G410_HUMAN IGL c4031_light_IGKV3-15_IGKJ1 (Fragment)
OS=Homo sapiens OX=9606 PE=2 SV=1
EIVMTQSPATVSVYPGERATLSCRASQSVSTNLAWYQQKPGQAPRLLMYGASTRATDIPL
RFSGSGSGTEFTLTISSLQSEDFAVYYCQHYHNPRTFGQGTKVESE

BLAST Sequence alignment against nr

>rotavirus-specific intestinal-homing antibody light chain variable region,
partial [Homo sapiens]

Sequence ID: AAW67418.1 Length: 109
Range 1: 3 to 107

Score:201 bits(512), Expect:8e-65,
Method:Compositional matrix adjust.,
Identities:96/105(91%), Positives:101/105(96%), Gaps:0/105(0%)

```
Query 1 EIVMTQSPATVSVYPGERATLSCRASQSVSTNLAWYQQKPGQAPRLLMYGASTRATDIPL 60
Sbjct 3 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 62

Query 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQHYHNWPRTFGQGTKVE 105
Sbjct 63 RFSGSGSGTEFTLTISSLQSEDFAVYYCQYNNWPRTFGQGTKVD 107
```

>anti-SARS-CoV-2 spike protein immunoglobulin light chain variable region,
partial [Homo sapiens]
Sequence ID: QKY76147.1 Length: 107
Range 1: 1 to 105

Score:199 bits(506), Expect:5e-64,
Method:Compositional matrix adjust.,
Identities:95/105(90%), Positives:100/105(95%), Gaps:0/105(0%)

```
Query 1 EIVMTQSPATVSVYPGERATLSCRASQSVSTNLAWYQQKPGQAPRLLMYGASTRATDIPL 60
Sbjct 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Query 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQHYHNWPRTFGQGTKVE 105
Sbjct 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQYNNWPRTFGQGNRVE 105
```

Correlate: Protective capacity against SARS-CoV-2 and rotavirus