1. AAW65588.1 HBsAg-adr [Hepatitis B virus]

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| HBsAg-adr [Hepatitis B virus] | AAW65588.1 | 50.00% | 5 | 1 (**PGTNTSN**) |



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**QJT73034.1 Gene S SARS-Cov-2**  **595VSVITPGTNTSN606**

**AAW65588.1 HBsAg-adr [Hepatiti** **106.CPLL...S.TS117**

1. Hib2. WP\_015702013.1 capsular polysaccharide biosynthesis protein [Haemophilus influenzae serotype b]

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| capsular polysaccharide biosynthesis protein [Haemophilus influenzae serotype b] | | WP\_015702013.1 | 23.16% | 7 | 1 | **KNLNES** |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | | Accession |
| 17.7 | 34.6 | 6% | 3.5 | 23.16% | | Query\_40591 |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 22/95(23%) | 31/95(32%) | 19/95(20%) |



10 20 30 40 50 60 70 80 90 100

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**QJT73034.1 Gene S SARS-Cov-2**  **501NGVGYQPYRVVVLSFELLHAPATVCGPKKSTN----------------LVKNKCV---NFNFNGLTGTGVLNESNKKFLPFQQFGRDIADTTDAV576**

**WP\_015702013.1 Haemophilus inf** **099.NFD..SSSSIPNEVGVW.KSL..KV..NCS.AWFRIYVGIEKDAGEL.I..IFISEN..D.IY.NNLFYH..D.DT.SLLSD.KENYIEKCND.193**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/13(46%) | 10/13(76%) | 0/13(0%) |



10 20

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**QJT73034.1 Gene S SARS-Cov-2**  **1186LNEVAKNLNESLI1198**

**WP\_015702013.1 Haemophilus inf** **0205V.SII..I.D.A.217**

1. AEO88919.1 capsular polysaccharide biosynthesis protein [Streptococcus pneumoniae serotype 19F]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | Accession |
| 20.4 | 87.4 | 10% | 0.15 | 23.15% | Query\_18695 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| capsular polysaccharide biosynthesis protein [Streptococcus pneumoniae serotype 19F] | AEO88919.1 | 23.15% | 18 | **2 ('LGFIAGLI'/'NSVAYS')** |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 25/108(23%) | 48/108(44%) | 17/108(15% |



10 20 30 40 50 60 70 80 90 100

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**QJT73034.1 Gene S SARS-Cov-2]**  **946GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL----------DKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA----EIRASANLAATK**

**AEO88919.1 capsular polysaccha** **062.EKSGLT..DL..GSS...DYREIILS-QD..EEVV.D.KLDLTPKDLAN.IKVT.PV.TR.VS--V.VSDR.PEEAS.I.NSLR.VA.QKIISI.R**

110

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**QJT73034.1 Gene S SARS-Cov-2]**  **MSECVLGQSKR1039**

**AEO88919.1 capsular polysaccha** **V.DVTTLEEA.166**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/17(35%) | 13/17(76%) | 0/17(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **1218LGFIAGLIAIVMVTIML1234**

**AEO88919.1 capsular polysaccha** **0182I..L..V.GTSVIVLI.198**

## **Range 3**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/17(35%) | 11/17(64%) | 0/17(0%) |



10 20

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**QJT73034.1 Gene S SARS-Cov-2]**  **703NSVAYSNNSIAIPTNFT719**

**AEO88919.1 capsular polysaccha** **033S...FAYSTFV.KPE..49**

## **Range 4**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 5/11(45%) | 9/11(81%) | 0/11(0%) |



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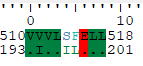
....|....|....|..

**QJT73034.1 Gene S SARS-Cov-2]**  **508YRVVVLSFELL518**

**AEO88919.1 capsular polysaccha** **082..EII..QDV.92**

## **Range 5**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/9(67%) | 7/9(77%) | 0/9(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **510VVVLSFELL518**

**AEO88919.1 capsular polysaccha** **193.I..IL...201**

# CAI33577.1 capsular polysaccharide biosynthesis protein Wzd [Streptococcus pneumoniae serotype 18C]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | Accession |
| 20.4 | 85.8 | 9% | 0.18 | 35.29% | Query\_50549 |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/17(35%) | 13/17(76%) | 0/17(0%) |



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**QJT73034.1 Gene S SARS-Cov-2**  **1218LGFIAGLIAIVMVTIML1234**

**CAI33577.1 Streptococcus pneum** **0182I..L..V.GTSVIVLL.198**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 23/84(27%) | 38/84(45%) | 16/84(19%) |



10 20 30 40 50 60 70 80 90

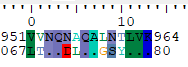
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

**QJT73034.1 Gene S SARS-Cov-2**  **703NSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVK786**

**CAI33577.1 Streptococcus pneum** **033S...FAYSTFV.KPE..--S..R.YV.NRN.E----------EKSGLT.QD..A..YLVKDY.E---.ILS..V-LE..VSDL.100**

## **Range 3**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 7/14(50%) | 10/14(71%) | 0/14(0%) |



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**QJT73034.1 Gene S SARS-Cov-2**  **951VVNQNAQALNTLVK964**

**CAI33577.1 Streptococcus pneum** **067LT..DL..GSY...80**

## **Range 4**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/9(67%) | 7/9(77%) | 0/9(0%) |



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**QJT73034.1 Gene S SARS-Cov-2**  **510VVVLSFELL518**

**CAI33577.1 Streptococcus pneum** **193.I..LL...201**

# CAI33319.1 capsular polysaccharide biosynthesis protein Wzd [Streptococcus pneumoniae serotype 14]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | Accession |
| 19.2 | 70.0 | 16% | 0.37 | 27.38% | Query\_57655 |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 23/84(27%) | 39/84(46%) | 16/84(19%) |



10 20 30 40 50 60 70 80 90

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

**QJT73034.1 Gene S SARS-Cov-2]**  **703NSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVK786**

**CAI33319.1 capsular polysaccha** **033S...FAYSTFV.KPE..--S..R.YV.NRDQ----------.EKSGLT.QD..A..YLVKDY.E---.ILS..V-LE..VSDL.100**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 25/108(23%) | 47/108(43%) | 17/108(15%) |



10 20 30 40 50 60 70 80 90 100

....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

**QJT73034.1 Gene S SARS-Cov-2]**  **46GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL----------DKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA----EIRASANLAATKM**

**CAI33319.1 capsular polysaccha** **62.EKSGLT..DL..GSY...DYREIILS-QD..EEVV.D.KLDLTPKGLAN.IKVT.PV.TR.VS--V.VNDR.PEEAS.I.NSLR.VA.QKIISI.RV**

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**QJT73034.1 Gene S SARS-Cov-2]**  **SECVLGQSKR1039**

**CAI33319.1 capsular polysaccha** **.DVTTLEEA.166**

## **Range 3**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 5/17(29%) | 11/17(64%) | 0/17(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **1218LGFIAGLIAIVMVTIML1234**

**CAI33319.1 capsular polysaccha** **0182I..L..VSGTSVIVFL.198**

## **Range 4**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 5/11(45%) | 9/11(81%) | 0/11(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **508YRVVVLSFELL518**

**CAI33319.1 capsular polysaccha** **082..EII..QDV.92**

# CAI32924.1 capsular polysaccharide biosynthesis protein Wzd [Streptococcus pneumoniae serotype 7F]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | Accession |
| 20.4 | 88.1 | 16% | 0.18 | 35.29% | Query\_20879 |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/17(35%) | 13/17(76%) | 0/17(0%) |



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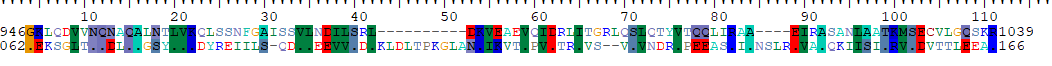
....|....|....|....|....|

**QJT73034.1 Gene S SARS-Cov-2]**  **1218LGFIAGLIAIVMVTIML1234**

**CAI32924.1 capsular polysaccha** **0182I..L..V.GTSVIVLL.198**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 25/108(23%) | 47/108(43%) | 17/108(15%) |



10 20 30 40 50 60 70 80 90 100

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**QJT73034.1 Gene S SARS-Cov-2]**  **946GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL----------DKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA----EIRASANLAATK**

**CAI32924.1 capsular polysaccha** **062.EKSGLT..DL..GSY...DYREIILS-QD..EEVV.D.KLDLTPKGLAN.IKVT.PV.TR.VS--V.VNDR.PEEAS.I.NSLR.VA.QKIISI.R**

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**QJT73034.1 Gene S SARS-Cov-2]**  **MSECVLGQSKR1039**

**CAI32924.1 capsular polysaccha** **V.DVTTLEEA.166**

## **Range 3**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 23/84(27%) | 38/84(45%) | 16/84(19%) |



10 20 30 40 50 60 70 80 90

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**QJT73034.1 Gene S SARS-Cov-2]**  **703NSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVK786**

**CAI32924.1 capsular polysaccha** **033S...FVYSTFV.KPE..--S..R.YV.NRDQ----------.EKSGLT.QD..A..YLVKDY.E---.ILS..V-LE..VSDL.100**

## **Range 4**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 5/11(45%) | 9/11(81%) | 0/11(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **508YRVVVLSFELL518**

**CAI32924.1 capsular polysaccha** **082..EII..QDV.92**

## **Range 5**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/9(67%) | 7/9(77%) | 0/9(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **510VVVLSFELL518**

**CAI32924.1 capsular polysaccha** **193.I..LL...201**

# >CAI32793.1 capsular polysaccharide biosynthesis protein Wzd [Streptococcus pneumoniae serotype 5]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | Accession |
| 22.7 | 73.1 | 10% | 0.030 | 29.76% | Query\_38215 |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 25/84(30%) | 40/84(47%) | 16/84(19%) |



10 20 30 40 50 60 70 80 90

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**QJT73034.1 Gene S SARS-Cov-2]**  **703NSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVK786**

**CAI32793.1 capsular polysaccha** **033S...FAYSTFV.KPE..--S..R.YV..RDQ----------.EKSGLT.QD..A..YL.KDY.E---.ILS..V-LE..VSDL.100**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 7/17(41%) | 12/17(70%) | 0/17(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **1218LGFIAGLIAIVMVTIML1234**

**CAI32793.1 capsular polysaccha** **0182I..LV...V.NVTVLL.198**

## **Range3**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 5/11(45%) | 9/11(81%) | 0/11(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **508YRVVVLSFELL518**

**CAI32793.1 capsular polysaccha** **082..EII..QDV.92**

## **Range 4**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 7/23(30%) | 13/23(56%) | 0/23(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **567RDIADTTDAVRDPQTLEILDITP589**

**CAI32793.1 capsular polysaccha** **083.E.ILSQ.VLEEVVSDLK..L..105**

# >COS99248.1 capsular polysaccharide biosynthesis protein Cps14C [Streptococcus pneumoniae serotype 1]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | Accession |
| 20.4 | 87.4 | 16% | 0.17 | 35.29% | Query\_29961 |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/17(35%) | 13/17(76%) | 0/17(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **1218LGFIAGLIAIVMVTIML1234**

**COS99248.1 capsular polysaccha** **0182I..L..V.GTSVIVLL.198**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 22/84(26%) | 38/84(45%) | 16/84(19%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **703NSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVK786**

**COS99248.1 capsular polysaccha** **033S...FAYSTFV.KPE..--S..R.YV.NRNQ----------.EKPGLT.QD..A.AYLVKDY.E---.VLS..V-LE..ISDL.100**

## **Range 3**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 25/108(23%) | 46/108(42%) | 17/108(15%) |



10 20 30 40 50 60 70 80 90 100

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**QJT73034.1 Gene S SARS-Cov-2]**  **946GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL----------DKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA----EIRASANLAATK**

**COS99248.1 capsular polysaccha** **062.EKPGLT..DL..GAY...DYREIVLS-QD..EEVI.D.KLDLMPKGLAN.IKVT.PV.TR.VS--V.VSDR.PEEAS.I.NSLR.VA.QKIISI.R**

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**QJT73034.1 Gene S SARS-Cov-2]**  **MSECVLGQSKR1039**

**COS99248.1 capsular polysaccha** **V.DVTTLEEA.166**

## **Range 4**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/11(55%) | 9/11(81%) | 0/11(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **508YRVVVLSFELL518**

**COS99248.1 capsular polysaccha** **082YREIVLSQDVL92**

## **Range 5**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/9(67%) | 7/9(77%) | 0/9(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **510VVVLSFELL518**

**COS99248.1 capsular polysaccha** **193.I..LL...201**

# AAK20668.1 Wzd [Streptococcus pneumoniae serotype 4]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| [Max Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=1&HSP_SORT=1) | [Total Score](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=2&HSP_SORT=1) | [Query Cover](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=4&HSP_SORT=0) | [E value](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=0&HSP_SORT=0) | [Per. Ident](https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ADV_VIEW=yes&ADV_VIEW=on&ALIGNMENTS=100&ALIGNMENT_VIEW=Pairwise&BLAST_SPEC=blast2seq&DATABASE_SORT=0&DESCRIPTIONS=100&DYNAMIC_FORMAT=on&FIRST_QUERY_NUM=0&FORMAT_OBJECT=Alignment&FORMAT_PAGE_TARGET=&FORMAT_TYPE=HTML&GET_SEQUENCE=yes&I_THRESH=&LINE_LENGTH=60&MASK_CHAR=2&MASK_COLOR=1&NEW_VIEW=yes&NUM_OVERVIEW=100&PAGE=Proteins&QUERY_INDEX=0&QUERY_NUMBER=0&RESULTS_PAGE_TARGET=&RID=CUEJNBY0114&SHOW_LINKOUT=yes&SHOW_OVERVIEW=yes&STEP_NUMBER=&WORD_SIZE=3&ADV_VIEW=on&DISPLAY_SORT=3&HSP_SORT=3) | Accession |
| 18.9 | 84.3 | 12% | 0.52 | 35.29% | Query\_56593 |

## **Range 1**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/17(35%) | 12/17(70%) | 0/17(0%) |



10 20

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**QJT73034.1 Gene S SARS-Cov-2]**  **1218LGFIAGLIAIVMVTIML1234**

**AAK20668.1 Wzd [Streptococcus**  **0183IGFLAGVIGTSVIVLHL199**

## **Range 2**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 24/103(23%) | 44/103(42%) | 17/103(16%) |



## **Range 3**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 12/48(25%) | 19/48(39%) | 7/48(14%) |



10 20 30 40 50

....|....|....|....|....|....|....|....|....|....|....

**QJT73034.1 Gene S SARS-Cov-2]**  **773EQDKNTQEVFAQVKQIYK-------TPPIKDFGGFNFSQILPDPSKPS813**

**AAK20668.1 Wzd [Streptococcus**  **004..NTIEID..QL..SLW.RKLMILIVALVTGA.A.AY.TFIVK.EYT.51**

## **Range 4**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 6/9(67%) | 7/9(77%) | 0/9(0%) |



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**QJT73034.1 Gene S SARS-Cov-2]**  **510VVVLSFELL518**

**AAK20668.1 Wzd [Streptococcus**  **194.I..HL...202**

## **Range 5**

|  |  |  |
| --- | --- | --- |
| Identities | Positives | Gaps |
| 5/11(45%) | 9/11(81%) | 0/11(0%) |



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....|....|....|..

**QJT73034.1 Gene S SARS-Cov-2]**  **508YRVVVLSFELL518**

**AAK20668.1 Wzd [Streptococcus**  **083..EII..QDV.93**