

Product Data Sheet



Recombinant SARS-CoV-2 Spike Protein

Product Code: 39502

Sengenics Corporation Pte Ltd

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Description:

Recombinant SARS-CoV-2 Spike protein lysates, full length. Protein is expressed in baculovirus expression system in insect cells using the patented KREX™ functional proteomics technology.

Expression System:

Insect cell

GenBank Accession:

YP_009724390.1

Synonym:

COVID-19, 2019-nCoV, SARS Coronavirus 2, S protein

Protein Length:

1273aa

Expected Molecular Weight:

141.2kDa calculated from the sequence below
(https://www.bioinformatics.org/sms/prot_mw.html)

Form:

Liquid (Crude lysates)

Lysis Buffer:

25mM HEPES, 50mM KCl, 4mM CaCl₂, 20mM MgCl₂, 20% Glycerol, 0.2% Triton X-100, 0.2% BSA, 2mM DTT, 1 tablet Protease inhibitor (in 5mL buffer)

Storage Conditions:

-80°C, Avoid Freeze/Thaw Cycles

Stability:

Lysates are stable for up to 18 months from production date

Shipping:

Frozen shipment in dry ice

Authorised Uses:

For Research Use Only*

Applications:

Identification, development or production of a high-affinity vaccine; Development of an antigen-based COVID-19 sero-diagnostic test; Characterisation of full-length, correctly folded and functional SARS-CoV-2 antigens.

Sequence:

>SARS-CoV-2-SP

```
1 MFVFLVLLPL VSSQCVNLTT RTQLPPAYTN SFTRGVYYPD KVFRSSVLHS TQDLFLPFFS
61 NVTWFHAIHV SGTNGTKRFD NPVLPFNDGV YFASTEKSNIRGWIFGTTL DSKTQSLLIIV
121 NNATNVVIKV CEFQFCNDPF LGVYHYKNNK SWMESEFRVY SSANNCTFEY VSQPFMLDLE
181 GKQGNFKNLR EBFVKNIDGY FKIYSKHTPI NLVRDLDPQGF SALEPLVDLP IGINITRFQT
241 LLALHRSYLT PGDSSSGWTA GAAAYVGYL QPRTFLKYN ENGTITDAVD CALDPLSETK
301 CTLKSFTVEK GIYQTSNFRV QPTESI VRFP NITNLCPFGE VFNATRFASV YAWNKRKRISN
361 CVADYSVLYN SASFSTFKCY GVSPTKLNLD CFTNVYADSF VIRGDEV RQI APGQTGKIAD
421 YNYKLPDDFT GCVIAWNSNN LDSKVGNYN YLYRLFRKSN LKPFERDIST EIYQAGSTPC
481 NGVEGFNCYF PLQSYGFQPT NGVGYQPYRV VVLSFELLHA PATVCGPKKS TNLVKNKCVN
541 FNFNGLTGTG VLTESNKKFL PFQQFGRDIA DTTDAVRDPQ TLEILDITPC SFGGVSVITP
601 GTNTSNQVAV LYQDVNCTEV PVAIHADQLT PTWRVYSTGS NVFQTRAGCL IGAEHVNNSY
661 ECDIPIGAGI CASYQTQTN PRRARSVASQ SIIAYTMSLG AENSVAYSNN SIAIPTNFTI
721 SVTTEILPVS MTKTSVDC TM YICGDSTEC S NLLLQYGSFC TQLNRALTGI AVEQDKNTQE
781 VFAQVKQIYK TPIIKDFGGF NFSQILPDPS KPSKRSFIED LLFNKVTLAG AGFIKQYGDG
841 LGDIAARDLI CAQKFNGLTV LPPLLTDEMI AQYTSALLAG TITSGWTFGA GAALQIPFAM
901 QMAYRFNGIG VTQNVLYENQ KLIANQFN SA IGKIQDSLSS TASALGKLQD VVNQNAQALN
961 TLVKQLSSNF GAISSVLNDI LSRLDKVEAE VQIDRLITGR LQSLQTYVTQ QLIRAAEIRA
1021 SANLAATKMS ECVLGQSKRV DFCGKGYHLM SFPQSAPHGV VFLHVTVVPA QEKNFTTAPA
1081 ICHDGAHFP REGVFSNGT HWFVTQRNFY EPQIITDNT FVSGNCDVVI GIVNNTVYDP
1141 LQPELDSFKE ELDKYFKNHT SPDVDLGDIS GINASVVNIQ KEIDRLNEVA KNLNESLIDL
1201 QELGKYEQYI KWPWYIWLGF IAGLIAIVMV TIMLCMTSC CSCLKGCCSC GSCKFDEDD
1261 SEPVLKGVKL HYT
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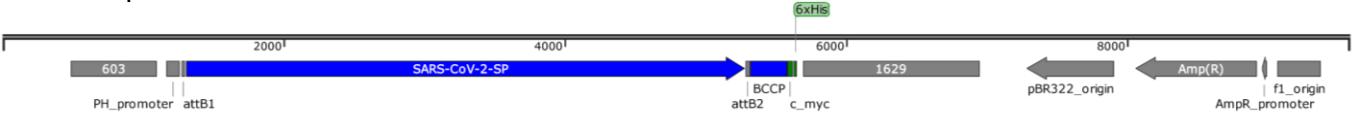
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Vector Map:



Sequence alignment with reference sequence (YP_009724390.1):

```
SARS-CoV-2-SP      MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS 60
YP_009724390.1    MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS 60
*****

SARS-CoV-2-SP      NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWI FGTTLDSKTQSLIV 120
YP_009724390.1    NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWI FGTTLDSKTQSLIV 120
*****

SARS-CoV-2-SP      NNATNVVIVKVEFQFCNDPFLGVYYHKNKNSWMESEFRVYSSANNCTFEYVSQPFLMDLE 180
YP_009724390.1    NNATNVVIVKVEFQFCNDPFLGVYYHKNKNSWMESEFRVYSSANNCTFEYVSQPFLMDLE 180
*****

SARS-CoV-2-SP      GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLPIGINITRFQT 240
YP_009724390.1    GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDL PQGFSALEPLVDLPIGINITRFQT 240
*****

SARS-CoV-2-SP      LLALHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK 300
YP_009724390.1    LLALHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK 300
*****

SARS-CoV-2-SP      CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISN 360
YP_009724390.1    CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISN 360
*****

SARS-CoV-2-SP      CVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIAD 420
YP_009724390.1    CVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIAD 420
*****

SARS-CoV-2-SP      YNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPC 480
YP_009724390.1    YNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPC 480
*****

SARS-CoV-2-SP      NGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN 540
YP_009724390.1    NGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN 540
*****

SARS-CoV-2-SP      FNFNGLTGTGVLTESNKKFLFPQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP 600
YP_009724390.1    FNFNGLTGTGVLTESNKKFLFPQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP 600
*****

SARS-CoV-2-SP      GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNSY 660
YP_009724390.1    GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGNSNVFQTRAGCLIGAEHVNSY 660
*****

SARS-CoV-2-SP      ECDIPIGAGICASYQTQTN SPRARSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTI 720
YP_009724390.1    ECDIPIGAGICASYQTQTN SPRARSVASQSI IAYTMSLGAENSVAYSNN SIAIPTNFTI 720
*****
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SARS-CoV-2-SP YP_009724390.1	SVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDKNTQE 780 SVTTEILPVSMTKTSVDCTMYICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDKNTQE 780 *****
SARS-CoV-2-SP YP_009724390.1	VFAQVKQIYKTPPIKDFGGFNFSQILPDPSPKRSFIEDLLFNKVTLADAGFIKQYGDC 840 VFAQVKQIYKTPPIKDFGGFNFSQILPDPSPKRSFIEDLLFNKVTLADAGFIKQYGDC 840 *****
SARS-CoV-2-SP YP_009724390.1	LGDIARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAM 900 LGDIARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAM 900 *****
SARS-CoV-2-SP YP_009724390.1	QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDLSSTASALGKLDVVNQNAQALN 960 QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDLSSTASALGKLDVVNQNAQALN 960 *****
SARS-CoV-2-SP YP_009724390.1	TLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTVQQLIRAAEIRA 1020 TLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTVQQLIRAAEIRA 1020 *****
SARS-CoV-2-SP YP_009724390.1	SANLAATKMSECVLGQSKRVDFCGKYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA 1080 SANLAATKMSECVLGQSKRVDFCGKYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA 1080 *****
SARS-CoV-2-SP YP_009724390.1	I CHDGAHF PREGV FVSN GTHWFV TQRNFYEPQIIITDNTFVSGNCDVIGIVNNTVYDP 1140 I CHDGAHF PREGV FVSN GTHWFV TQRNFYEPQIIITDNTFVSGNCDVIGIVNNTVYDP 1140 *****
SARS-CoV-2-SP YP_009724390.1	LQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL 1200 LQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL 1200 *****
SARS-CoV-2-SP YP_009724390.1	QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCTSCCSCCKGCCSCGSCCKFDEDD 1260 QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCTSCCSCCKGCCSCGSCCKFDEDD 1260 *****
SARS-CoV-2-SP YP_009724390.1	SEPV LKGVKLHYT 1273 SEPV LKGVKLHYT 1273 *****

References:

1. Sengenics KREX™ proteomics technology [<https://www.sengenics.com/krex/>]
2. KREX™ is protected by multiple international patents worldwide [<https://www.sengenics.com/list-of-patents/>]
3. Blackburn, Jonathan M, and Aubrey Shoko. 2011. "Protein Function Microarrays for Customised Systems-Oriented Proteome Analysis." Methods in molecular biology (Clifton, N.J.) 785: 305–30
4. Beeton-Kempen, Natasha et al. 2014. "Development of a Novel, Quantitative Protein Microarray Platform for the Multiplexed Serological Analysis of Autoantibodies to Cancer-Testis Antigens." International journal of cancer 135(8): 1842–51
5. Other References [<https://www.sengenics.com/sengenics-krex-publications/>]
6. Walls, A. C., Tortorici, M. A., Bosch, B. J., Frenz, B., Rottier, P. J. M., DiMaio, F., ... Velesler, D. 2016. "Cryo-electron microscopy structure of a coronavirus spike glycoprotein trimer." Nature, 531(7592): 114–117.
7. Wrapp, D., Wang, N., Corbett, K. S., Goldsmith, J. A., Hsieh, C.-L., Abiona, O., ... McLellan, J. S. 2020. "Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation." Science (New York, N.Y.).

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