COVID-19 patient #8 Protein score: 33

1	MSSSSWLLLS	LVAVTAAQST	IEEQAKTFLD	KFNHEAEDLF	YQSSLASWNY
51	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA	QMYPLQEIQN	LTVKLQLQAL
101	QQNGSSVLSE	DESERINTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLMN
251	AYPSYISPIG	CLPAHLLGDM	NGREWTNLYS	LTVPFGQKPN	IDVTDAMVDQ
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWD
351	LGKGDFRILM	CTKVTMDDFL	TANNEMGHIQ	YDMAYAAQPF	LLRNGANEGF
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL
451	PFTYMLEKWR	WMVFKGEIPK	DOWNKKWNEM	KREIVGVVEP	VPHDETYCDP
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTEA
551	GOKLENMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK
601	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFRSSVAYA
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSRSR	INDAFRINDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVEGVVM
751	GVIVVGIVIL	IFTGIRDRKK	KNKAR SGENP	YASIDISKGE	NNPGFQNTDD
801	VQTSF				

COVID-19 patient #11

Protein score: 41

-	100000000000000000000000000000000000000	atter analysis	TOO BURLED	111 11111111111111111111111111111111111	1500100000
51	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA	QMYPLQEIQN	LTVKLQLQAL
101	QQNGSSVLSE	DKSKRLNTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLMN
251	AYPSYISPIG	CLPAHLLGDM	WGRFWTNLYS	LTVPFGQKPN	IDVTDAMVDQ
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWD
351	LGKGDFRILM	CTKVTMDDFL	TAHHEMGHIQ	YDMAYAAQPF	LLRNGANEGF
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL
451	PFTYMLEKWR	WMVFKGEIPK	DQWMKKWWEM	KREIVGVVEP	VPHDETYCDP
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTEA
551	GQKLFNMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK
601	NSEVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFRSSVAYA
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSRSR	INDAFRLNDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVM
751	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFONTDD
801	VOTSE				

Healthy control #5 Protein score: 15

1	MSSSSWLLLS	LVAVTAAQST	IEEQAKTFLD	KFNHEAEDLF	YQSSLASWNY
51	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA	QMYPLQEIQN	LTVKLQLQAL
101	QQNGSSVLSE	DKSKRLNTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLMN
251	AYPSYISPIG	CLPAHLLGDM	WGRFWTNLYS	LTVPFGQKPN	IDVTDAMVDQ
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWD
351	LGKGDFRILM	CTKVTMDDFL	TAHHEMGHIQ	YDMAYAAQPF	LLR NGANEGF
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL
451	PFTYMLEKWR	WMVFKGEIPK	DQWMKKWWEM	KREIVGVVEP	VPHDETYCDP
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAK HEGPLH	KCDISNSTEA
551	GQK LFNMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK
601	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFRSSVAYA
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPR IS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSRSR.	INDAFRLNDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVM
751	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFQNTDD
801	VOTSF				

Healthy control #7 (No ACE2 detected)

Expanded View Figures

COVID-19 patient #9 Protein score: 57

1	MSSSSWLLLS	LVAVTAAQST	IEEQAK TFLD	KFNHEAEDLF	YQSSLASWNY
51	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA	QMYPLQEIQN	LTVK LQLQAL
101	QQNGSSVLSE	DKSKRLNTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLMN
251	AYPSYISPIG	CLPAHLLGDM	WGRFWTNLYS	LTVPFGQKPN	IDVTDAMVDQ
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWD
351	LGKGDFRILM	CTKVTMDDFL	TANNEMGHIQ	YDMAYAAQPF	LLRNGANEGF
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL
451	PFTYMLEKWR	WMVFKGEIPK	DQWMKKWWEM	KREIVGVVEP	VPHDETYCDP
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTEA
551	GQKLFNMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK
601	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFR SSVAYA
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSRSR	INDAFRLNDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVM
751	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFONTDD
801	VQTSF				

COVID-19 patient #12 Protein score: 29

1	MSSSSWLLLS	LVAVTAAQST	IEEQAKTFLD	KFNHEAEDLF	YQSSLASWNY
51	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA	QMYPLQEIQN	LTVKLQLQAL
101	QQNGSSVLSE	DKSKRLNTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLMN
251	AYPSYISPIG	CLPAHLLGDM	WGRFWTNLYS	LTVPFGQKPN	IDVTDAMVDQ
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWD
351	LGKGDFRILM	CTKVTMDDFL	TAHHEMGHIQ	YDMAYAAQPF	LLRNGANEGF
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL
451	PFTYMLEKWR	WMVFKGEIPK	DQWMKKWWEM	KREIVGVVEP	VPHDETYCDP
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTEA
551	GQKLFNMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK
601	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFRSSVAYA
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSR SR	INDAFR LNDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVM
751	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFQNTDD
801	VQTSF				

Healthy control #10 Protein score: 29

Healthy control #8

(No ACE2 detected)

-	W2222MTTT2	LANALANÖ21.	TEEQAKTFLD	RENHEAEDLE	IÖPPTVPMUI
51	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA	QMYPLQEIQN	LTVKLQLQAI
101	QQNGSSVLSE	DESERLITIL	NTMSTIYSTG	K VCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYC
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLM
251	AYPSYISPIG	CLPAHLLGDM	WGRFWTNLYS	LTVPFGQKPN	IDVTDAMVD
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWE
351	LGKGDFRILM	CTKVTMDDFL	TAHHEMGHIQ	YDMAYAAQPF	LLRNGANEGI
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTI
451	PFTYMLEKWR	WMVFKGEIPK	DQWMKKWWEM	KREIVGVVEP	VPHDETYCDI
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTE
551	GQKLFNMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNF
601	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFRSSVAY/
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSRSR	INDAFRLNDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVN
751	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFQNTDI
801	VQTSF				

COVID-19 patient #10 Protein score: 53

1	MSSSSWLLLS	LVAVTAAQST	IEEQAKTFLD	KENHEAEDLE	YQSSLASWNY
51	NTNITEENVQ	NMNNAGDKWS	AFLKEQSTLA	QMYPLQEIQN	LTVKLQLQAL
101	QQNGSSVLSE	DKSKRLNTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLMN
251	AYPSYISPIG	CLPAHLLGDM	WGRFWINLYS	LTVPFGQKPN	IDVTDAMVDQ
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAWD
351	LGKGDFRILM	CTKVTMDDFL	TAHHEMGHIQ	YDMAYAAQPF	LLENGANEGE
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL
451	PFTYMLEKWR	WMVFKGEIPK	DOWNKKWWEM	KREIVGVVEP	VPHDETYCDP
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTEA
551	GQKLFNMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK
601	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFRSSVAYA
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSRSR	INDAFRLNDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVM
751	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFQNTDD
801	VQTSF				

COVID-19 patient #13 Protein score: 37

1	MSSSSWLLLS	LVAVTAAQST	IEEQAKTFLD	KFNHEAEDLF	YQSSLASWNY
51	NTNITEENVQ	NMNNAGDK WS	AFLKEQSTLA	QMYPLQEIQN	LTVKLQLQAL
101	QQNGSSVLSE	DKSKRLNTIL	NTMSTIYSTG	KVCNPDNPQE	CLLLEPGLNE
151	IMANSLDYNE	RLWAWESWRS	EVGKQLRPLY	EEYVVLKNEM	ARANHYEDYG
201	DYWRGDYEVN	GVDGYDYSRG	QLIEDVEHTF	EEIKPLYEHL	HAYVRAKLMN
251	AYPSYISPIG	CLPAHLLGDM	WGRFWTNLYS	LTVPFGQKPN	IDVTDAMVDQ
301	AWDAQRIFKE	AEKFFVSVGL	PNMTQGFWEN	SMLTDPGNVQ	KAVCHPTAND
351	LGKGDFRILM	CTK VTMDDFL	TAHHEMGHIQ	YDMAYAAQPF	LLRNGANEGF
401	HEAVGEIMSL	SAATPKHLKS	IGLLSPDFQE	DNETEINFLL	KQALTIVGTL
451	PFTYMLEKWR	WMVFKGEIPK	DQWMKKWWEM	KREIVGVVEP	VPHDETYCDP
501	ASLFHVSNDY	SFIRYYTRTL	YQFQFQEALC	QAAKHEGPLH	KCDISNSTEA
551	GQKLFNMLRL	GKSEPWTLAL	ENVVGAKNMN	VRPLLNYFEP	LFTWLKDQNK
601	NSFVGWSTDW	SPYADQSIKV	RISLKSALGD	KAYEWNDNEM	YLFRSSVAYA
651	MRQYFLKVKN	QMILFGEEDV	RVANLKPRIS	FNFFVTAPKN	VSDIIPRTEV
701	EKAIRMSRSR	INDAFRLNDN	SLEFLGIQPT	LGPPNQPPVS	IWLIVFGVVM
751	GVIVVGIVIL	IFTGIRDRKK	KNKARSGENP	YASIDISKGE	NNPGFONTDD
801	VOTSF				

Healthy control #6 (No ACE2 detected)

Healthy control #9 (No ACE2 detected)

Figure EV1. ACE2 proteins are detected in the serum exosomes of all six COVID-19 patients.

The identified peptide sequences (red color) of endogenous ACE2 by mass spectrometry analyses using exosomes isolated from the sera of six COVID-19 patients and six healthy controls (Cohort #3). All six COVID-19 patients but only two of six healthy controls showed exosomal ACE2 proteins in the serum exosomes. Exosomes were sequentially isolated using ExoQuick kits and then ExoQuick ULTRA columns. Exosomes were further purified by immunoprecipitation using a combination of anti-CD9, anti-CD63, and anti-CD81 magnetic beads. The protein score is the sum of the highest ions score of MS/MS search for each distinct peptide.

A UBR4 protein sequence

1	MATSGGEEAA	AAAPAPGTPA	TGADTTPGWE	VAVRPLLSAS	YSAFEMKELP
51	QLVASVIESE	SEILHHEKQY	EPFYSSFVAL	STHYITTVCS	LIPRNOLOSV
101	AAACKVLIEF	SLLRLENPDE	ACAVSQKHLI	LLIKGLCTGC	SRLDRTEIIT
151	FTAMMKSAKL	PQTVKTLSDV	EDQKELASPV	SPELRQKEVQ	MNFLNQLTSV
201	FNPR TVASQP	ISTQTLVEGE	NDEQSSTDQA	SAIKTKNVFI	AQNVASLQEL
251	GGSEKLLRVC	LNLPYFLRYI	NRFQDAVLAN	SFFIMPATVA	DATAVRNGFH
301	SLVIDVTMAL	DTLSLPVLEP	LNPSRLQDVT	VLSLSCLYAG	VSVATCMAIL
351	HVGSAQQVRT	GSTSSKEDDY	ESDAATIVQK	CLEIYDMIGQ	AISSSRRAGG
401	EHYQNFQLLG	AWCLLNSLFL	ILNLSPTALA	DKGK EKDPLA	ALRVRDILSR
451	TKEGVGSPKL	GPGK GHQGFG	VLSVILANHA	IKLLTSLFQD	LQVEALHKGW
501	ETDGPPAALS	IMAQSTSIQR	IQRLIDSVPL	MNLLLTLLST	SYR KACVLQR
551	QRKGSMSSDA	SASTDSNTYY	EDDFSSTEED	SSQDDDSEPI	LGQWFEETIS
601	PSKEK AAPPP	PPPPPPLESS	PRVKSPSKQA	PGEKGNILAS	RKDPELFLGL
651	ASNILNFITS	SMLNSRNNFI	RNYLSVSLSE	HHMATLASII	KEVDKDGLKG
701	SSDEEFAAAL	YHFNHSLVTS	DLQSPNLQNT	LLQQLGVAPF	SEGPWPLYIH
751	PQSLSVLSRL	LLIWQHKASA	QGDPDVPECL	KVWDRFLSTM	KQNALQGVVP
801	SETEDLNVEH	LQMLLLIFHN	FTETGRRAIL	SLFVQIIQEL	SVNMDAQMRF
851	VPLILARLLL	IFDYLLHQYS	KAPVYLFEQV	QHNLLSPPFG	WASGSQDSNS
901	RRATTPLYHG	FKEVEENWSK	HFSSDAVPHP	RFYCVLSPEA	SEDDLNRLDS
951	VACDVLFSKL	VKYDELYAAL	TALLAAGSQL	DTVRRKENKN	VTALEACALQ
1001	YYFLILWRIL	GILPPSKTYI	NQLSMNSPEM	SECDILHTLR	WSSRLRISSY
11051	POSIDOTAL	QGMKAEHASS	LLELASTIKC	SSVRIDVEIV	EEIFARQISS
1151	SSEITKNLLP	ATLOLIDTYA	SETRAVILON	FNEEGTTEKP	SKEKLOGEAA
1201	VLAIGSSRCK	ANTLOPTLVO	NLPSSVOTVC	ESWNNINTNE	FPNIGSWRNA
1251	FANDTIPSES	YISAVOAAHL	GTLCSOSLPL	AASLKHTLLS	LVRLTGDLIV
1301	WSDEMNPPQV	IRTLLPLLLE	SSTESVAEIS	SNSLERILGP	AESDEFLARV
1351	YEKLITGCYN	ILANHADPNS	GLDESILEEC	LQYLEKQLES	SQARKAMEEF
1401	FSDSGELVQI	MMATANENLS	AKFCNRVLKF	FTKLFQLTEK	SPNPSLLHLC
1451	GSLAQLACVE	PVR LQAWLTR	MTTSPPK DSD	QLDVIQENRQ	LLQLLTTYIV
1451 1501	RENSQVGEGV	PVRLQAWLTR CAVLLGTLTP	MTTSPPK DSD MATEMLANGD	QLDVIQENRQ GTGFPELMVV	LLQLLTTYIV MATLASAGQG
1451 1501 1551	GSLAQLACVE RENSQVGEGV AGHLQLHNAA	PVRLQAWLTR CAVLLGTLTP VDWLSRCKKY	MTTSPPK DSD MATEMLANGD LSQKNVVEKL	QLDVIQENRQ GTGFPELMVV NANVMHGKHV	LLQLLTTYIV MATLASAGQG MILECTCHIM
1451 1501 1551 1601	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL	PVRLQAWLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH	MTTSPPK DSD MATEMLANGD LSQKNVVEKL LSVDGEERAI	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEEDSQAE
1451 1501 1551 1601 1651	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK	PVRLQAWLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTFTITQKE	MTTSPPK DSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMVDGVGV	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK
1451 1501 1551 1601 1651 1701	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG	PVRLQAWLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTFTITQKE SFFCDCGAKE	MTTSPPK DSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMVDGVGV TPSSGMSSTM	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR
1451 1501 1551 1601 1651 1701 1751	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS	PVRLQAWLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMVDGVGV TPSSGMSSTM EKPKKSSLCR	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ
1451 1501 1551 1601 1651 1701 1751 1801	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL	PVRLQAWLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCK MVDGVGV TPSSGMSSTM EKPK KSSLCR AVGSSSRAQQ	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK
1451 1501 1551 1601 1651 1701 1751 1801 1851	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV ULSSPHCRPO	PURLQAWLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF HLAVSHERCK	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC
1451 1501 1551 1601 1651 1701 1751 1801 1851 1901 1951	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SVLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRRQ PFTVLSLTGN	PVRLQANLTR CAVLLGTLTP VDMLSRCKKY SQSNQQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF HLAVSHEKGK PCKEDYLAVC	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVLQLSALL GLKDCHVLTF	QLDVIQENRQ GTGFPELMVV NANVMHCKHV EVDSDWVEEL TCKMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKRKL SSSGSVSDHL	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAKC AHVLRRVAKC VLHPOLATGN
1451 1501 1551 1601 1651 1701 1751 1801 1851 1901 1951 2001	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVENTDQLMV VLSSPHGRRQ PFTVLSLTGN FIIKAVWLPG	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLSSQEGAF HLAVSHEKGK PCKEDYLAVC SQTELALVTA	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVLQLSALL GLKDCHVLTF DFVKIYDLCV	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCSMUDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKRKL SSSGSVSDHL DALSPTFYFL	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC TLTRLASAPV VLHQLATGN LPSSKIRDVT
1451 1501 1551 1601 1651 1701 1751 1801 1851 1901 1951 2001 2051	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVENTDQLMV VLSSPHGRRQ PFTVLSLTGM FIIKAVWLPG FLFNEEGKNI	PVRLQAWLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTTTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLCSQEGAF HLAVSHEKGK PCKEDYLAVC IVIMSSAGYI IVIMSSAGYI	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVLQLSALL GLKDCHVLTF DFVKIYDLCV YTQLMEEASS	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCSMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKRKL SSSGSVSDHL DALSPTFYFL DALSPTFYFL	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC TLTRLASAPV VLHQLATGN LPSSKIRDVT VLEINHEDLK
1451 1501 1551 1601 1651 1701 1751 1801 1851 1901 1951 2001 2051 2101	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVENTDQLMV VLSSPHGRRQ PFTVLSLTGM FIIKAVWLPG FLFNEEGKNI DSNSQVAGGG	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTTTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF HLAVSHEKGK PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYYSHVLQ	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVQLSALL GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCSMVDGGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKKKL SSSGSVSDHL DALSPTFYFL DALSPTFYFL SFAATISKTT	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRVAMC TLTRLASAPV VLHQLATGM LPSSKIRDVT VLEINHEDLK LEVLQLFPIN
1451 1501 1551 1601 1651 1701 1751 1801 1951 2001 2051 2101 2151	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRRQ PFTVLSLTGM FIIKAVWLPG FLFNEEGKNI DSNSQVAGGG IKSSNGGSKT	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF HLAVSHEKGK PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYYSHVLQ SPALCQWSEV	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAL FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVLQLSALL GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNHPGLVCCV	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCSMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKRKL SSGSVSDHL DALSPTFYFL DALSPTFYFL SFAATISRTT QQTTGVPLVV	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRVAMC TLTRLASAPV VLHPQLATGN LPSSKIRDVT LPSSKIRDVT VLEINHEDLK LEVLQLFPIN MVKPDTFLIQ
1451 1501 1551 1601 1651 1701 1751 1801 1851 1901 1951 2001 2051 2101 2151 2201	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRRQ PFTVLSLTGM FIIKAVWLPG FLFNEEGKNI DSNSQVAGGG IKSSNGGSKT EIKTLPAKAK	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF HLAVSHEKGK PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYYSHVLQ SPALCQWSEV IQDMVAIRHT	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAL LSVDGEERAL DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVLQLSALL GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNHPGLVCCV ACNEQQRTTM	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCSMVDGVV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKKKL SSGSVSDHL DALSPFYFL AQQGFYVTN SFAATISRT QQTTGVFLVV ILLCEDGSLR	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC TLTRLASAPV VLHPQLATGN LPSSKIRDVT VLEINHEDLK LEVLQLFPIN MVKPDTFLIQ IYMANVENTS
1451 1501 1551 1601 1651 1701 1751 1801 1851 1901 1951 2001 2051 2101 2151 2201 2251	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRRQ PFTVLSLTGN FIIKAVWLPG FLFNEEGKNI DSNSQVAGGG EIKTSNGGSKT EIKTLPAKAK YWLQPSLQPS	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNGQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF HLAVSHEKGK PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYYSHVLQ SPALCQMSEV IQDMVAIRHT SVISIMKPVR	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI SMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVLQLSALL GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNHFGLVCCV ACNEQQRTTM KRKTATITTR	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKRKL SSSGVSDHL DALSPFFYEL AQQGFYVTN SFAATISRTT QQTTGVPLVV ILLCEDGSLR TSSQVTFPID	LLQLLTTIV MATLASAQQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC TLTRLASAPV VLHPQLATGN LPSSKIRDVT VLEINHEDLK LEVLQLFPIN MVKPDTFLIQ IYMANVENTS FFEHNQQLTD
1451 1501 1551 1601 1751 1801 1851 1901 1951 2001 2051 2101 2151 2201 2251 2301	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRQ PFTVLSLTGN FIIKAVWLPG FLFNEEGKNI DSNSQVAGGG IKSSNGGSKT EIKTLPAKAK YWLQPSLQPS VEFGGNDLLQ	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNQQGFSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDNLNFLMD PTLGSQEGAF HLAVSHEKGK PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYSHVLQ SPALCQWSEV IQDMVAIRHT SVISIMKPVR VYNAQQIKHR	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAL LSVDGEERAL DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD ITVLQLSALL GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNHPGLVCCV ACNEQQRTTM KRKTATITTR LNSTGMYVAN	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVELL TCKMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKRKL SSGSVSDHL DALSFFYFL AQQGFYVTN SFAATISRTT QQTTGVPLVV ILLCEDGSLR TSSQVTFPID TKPGGFTIEI	LLQLLTTYIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC TLTRLASAPV VLHPQLATGN LPSSKIRDVT VLEINHEDLK LEVLQLFPIN MVKPDTFLIQ IYMANVENTS FFEHNQQLTD SNNNSTMVMT
1451 1501 1551 1601 1651 1701 1751 1801 1951 2001 2051 2101 2151 2201 2251 2301 2351	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRQ FITVLSITGN FIIKAVWLPG FLFNEEGKNI DSNSQVAGGG IKSSNGGSKT EIKTLPAKAK YWLQPSLQPS VEFGGNDLLQ GMRIQIGTQA	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNQQGFSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDNLNFLMD PTLGSQEGAF PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYSHVLQ SPALCQWSEV IQDMVAIRHT SVISIMKPVR VYNAQQIKHR	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNHPGLVCCV ACNEQQRTTM KRKTATITTR LNSTGMYVAN FGRTMQLNLS	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS SSGSVSDHL DALSPTFYFL AQQGPFYVTN SFAATISRTT QQTTGVPLVV ILLCEDGSLR TSSQVTFPID TKPGGFTIEI RSRWFDFPFT	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC LPSSKIRDVT VLHPQLATGN MVKPDTFLIQ IYMANVENTS FFEINQQLTD SNNNSTMVMT REEALQADKK
1451 1501 1551 1601 1651 1701 1801 1951 2001 2051 2101 2151 2201 2251 2301 2351 2401	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV ULSSPHGRRQ PFTVLSLTGN FILKAVWLPG FLFNEEGKNI DSNSQVAGGG IKSSNGGSKT EIKTLPAKAK YWLQPSLQPS VEFGGNDLLQ GMRIQIGTQA LNLFIGASVD	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNQQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYSHVLQ SPALCQMSEV IQDMVAIRHT SVISIMKPVR VYNAQQIKHR IERAPSYIEI PAGVTMIDAV	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNHPGLVCCV ACNEQQRTTM KRKTATITTR LNSTGMVVAN FGRTMQLNLS KIYGKTKEQF	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMDGGGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS SSSGSVSDHL DALSPTFYFL AQQGPFYVTN SFATISRTT QQTTGVLVV ILLCEDGSLR TSSQVTFPID TKPGGFTIEI RSRWFDFPFT GWPDEPPEEF	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC ULTRLASAPV VLHPQLATGN ULEINHEDLK LEVLQLFFIN MVKPDTFLIQ IYMANVENTS SINNSTMVMT REEALQADKK PSASVSNICP
1451 1501 1551 1601 1651 1701 1751 1801 1951 2001 2051 2101 2251 2201 2251 2301 2351 2401 2451	GSLAQLACCE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRRQ FITVJSLTGN FILKAVWLPG FLFNEEGKNI DSNSQVAGGG IKSSNGGSKT EIKTLPAKAK YWLQPSLQPS VEFGGNDLLQ GMRIQIGTQA SNLNQSNGTG	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNQQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDNLNFLMD PTLGSQEGAF PTLGSQEGAF PCKEDYLAVC SQTELAIVTA IVIMSSAGYI VSVYSHVLQ SPALCQMSEV IQDMVAIRHT SVISIMKPVR VYNAQQIKHR IERAPSYIEI PAGVTMIDAV DSDSAAPTTT	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNHPGLVCCV ACNEQQRTTM KRKTATITTR LNSTGMYVAN FGRTMQLNLS KIYGKTKEQF SGTVLERLVV	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL EVDSDWVEEL TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS SSSGSVSDHL DALSPTFYFL AQQGPFYVTN SFAATISRTT QQTTGVFLVV ILLCEDGSLR TSSQVTFPID TKPGGFTIEI RSRWFDFPFT GWPDEPPEEF SSLEALESCF	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC TLTRLASAPV VLHPQLATGN VLEINHEDLK LEVLQLFPIN MVKPDTFLIQ IYMANVENTS FFEHNQQLTD SNNNSTMVMT REEALQADKK PSASVSNICP
1451 1501 1551 1601 1751 1801 1951 2001 2051 2101 2251 2201 2251 2301 2351 2401 2451 2551	GSLAQLACVE RENSQVGEGV AGHLQLHNAA SYLADVTNAL DSDEDSLCNK DHEISYAKYG ISESLVRHAS NQANFSFAPL AVEMTDQLMV VLSSPHGRRQ FITVISLTGN FIIKAVWLPG FLFNEEGKNI DSNSQVAGGG IKSSNGGSKT EIKTLPAKAK YWLQPSLQPS UPEGGNDLLQ GMRIQIGTQA LNLFIGASVD SNLNQSNGTG NKNAAQELAT	PVRLQANLTR CAVLLGTLTP VDWLSRCKKY SQSNQQGPSH LCTFTITQKE SFFCDCGAKE TSSPADKAKV VLDMLNFLMD PTLGSQEGAF HLAVSHEKGK PCKEDYLAVC SQTELATVTA IVIMSSAGYI VSVYSHVLQ SPALCQMSEV IQDMVAIRHT SVISIMKPVR VYNAQQIKHR IERAPSVIEI PAGVTMIDAV DSDSAAPTTT LLLSLPAPAS	MTTSPPKDSD MATEMLANGD LSQKNVVEKL LSVDGEERAI FMNQHWYHCH DGSCLALVKR TISDGKVADE AIQTNFQQAS ENVRMNYSGD GLKDCHVLTF DFVKIYDLCV YTQLMEEASS MLFFSYCQGK MNH9GLVCCV ACNEQQRTTM KRKTATITTR LNSTGMYVAN FGRTMQLNLS KIYGKTKEQF SGTVLERLVV VQQQSKSLLA	QLDVIQENRQ GTGFPELMVV NANVMHGKHV EVDSDWVEEL TCKMVDGVGV TPSSGMSSTM EKPKKSSLCR AVGSSSRAQQ QGQTIRQLIS KQADSSKRKL DALSPTFYFL AQQGPFYVTN SFAATISRTT QQTTGVPLVV ILLCEDGSLR TSSQVTFPID TKPGGFTIEI RSSWFDFPFT GWPDEPPEF SSLEALESCF SLHTSRSAYH	LLQLLTTIV MATLASAGQG MILECTCHIM AVEEEDSQAE CTVCAKVCHK KESAFQSEPR TVEGCREELQ ALSELHTVEK AHVLRRVAMC TLTRLASAPV VLEINHEDLK LEVLQLFPIN MVKPDTFLIQ IYMANVENTS FFEHNQLTD SNNNSTMYMT REEALQADKK PSASVSNICP AVGPIIEKER SHKQQALDSK
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2951	GSEGEGEGET	EGDVHTSNRL	HMVRLMLLER	LLQTLPQLRN	VGGVRAIPYM
3001	QVILMLTTDL	DGEDEKDKGA	LDNLLSQLIA	ELGMDKKDVS	KKNERSALNE
3051	VHLVVMR LLS	VFMSRTKSGS	KSSICESSSL	ISSATAAALL	SSGAVDYCLH
3101	VLKSLLEYWK	SQQNDEEPVA	TSQLLKPHTT	SSPPDMSPFF	LRQYVKGHAA
3151	DVFEAYTQLL	TEMVLRLPYQ	IKKITDTNSR	IPPPVFDHSW	FYFLSEYLMI
3201	QQTPFVRRQV	RKLLLFICGS	K EKYRQLR DL	HTLDSHVRGI	KKLLEEQGIF
3251	LR ASVVTASS	GSALQYDTLI	SLMEHLKACA	EIAAQR TINW	QKFCIKDDSV
3301	LYFLLQVSFL	VDEGVSPVLL	QLLSCALCGS	KVLAALAASS	GSSSASSSSA
3351	PVAASSGQAT	TQSKSSTKKS	KKEEKEK ekd	GETSGSQEDQ	LCTALVNQLN
3401	KFADKETLIQ	FLRCFLLESN	SSSVR WQAHC	LTLHIYRNSS	KSQQELLLDL
3451	MWSIWPELPA	YGR KAAQFVD	LLGYFSLKTP	QTEKK LKEYS	QKAVEILRTQ
3501	NHILTNHPNS	NIYNTLSGLV	EFDGYYLESD	PCLVCNNPEV	PFCYIKLSSI
3551	KVDTRYTTTQ	QVVKLIGSHT	ISK VTVKIGD	LKRTK MVRTI	NLYYNNRTVQ
3601	AIVELKNKPA	RWHKAK KVQL	TPGQTEVKID	LPLPIVASNL	MIEFADFYEN
3651	YQASTETLQC	PRCSASVPAN	PGVCGNCGEN	VYQCHKCRSI	NYDEKDPFLC
3701	NACGFCKYAR	FDFMLYAKPC	CAVDPIENEE	DRKK AVSNIN	TLLDKADRVY
3751	HQLMGHRPQL	ENLLCKVNEA	APEKPQDDSG	TAGGISSTSA	SVNRYILQLA
3801	QEYCGDCKNS	FDELSKIIQK	VFASRKELLE	YDLQQREAAT	KSSRTSVQPT
3851	FTASQYRALS	VLGCGHTSST	KCYGCASAVT	EHCITLLRAL	ATNPALRHIL
3901	VSQGLIRELF	DYNLRRGAAA	MREEVRQLMC	LLTR DNPEAT	QQMNDLIIGK
3951	VSTALKGHWA	NPDLASSLQY	EMLLLTDSIS	KEDSCWELRL	RCALSLFLMA
4001	VNIKTPVVVE	NITLMCLRIL	QKLIKPPAPT	SKKNKDVPVE	ALTTVKPYCN
4051	EIHAQAQLWL	KRDPKASYDA	WKKCLPIRGI	DGNGKAPSKS	ELRHLYLTEK
4101	YVWRWKQFLS	RRGKR TSPLD	LK LGHNNWLR	QVLFTPATQA	ARQAACTIVE
4151	ALATIPSRKQ	QVLDLLTSYL	DELSIAGECA	AEYLALYQKL	ITSAHWKVYL
4201	AAR GVLPYVG	NLITKEIARL	LALEEATLST	DLQQGYALKS	LTGLLSSFVE
4251	VESIKRHFKS	RLVGTVLNGY	LCLRKLVVQR	TKLIDETQDM	LLEMLEDMTT
4301	GTESETKAFM	AVCIETAKRY	NLDDYRTPVF	IFERLCSIIY	PEENEVTEFF
4351	VTLEKDPQQE	DFLQGRMPGN	PYSSNEPGIG	PLMRDIKNKI	CQDCDLVALL
4401	EDDSGMELLV	NNKIISLDLP	VAEVYKKVWC	TTNEGEPMRI	VYRMRGLLGD
4451	ATEEFIESLD	STTDEEEDEE	EVYKMAGVMA	QCGGLECMLN	RLAGIRDFKQ
4501	GRHLLTVLLK	LFSYCVKVKV	NRQQLVKLEM	NTLNVMLGTL	NLALVAEQES
4551	KDSGGAAVAE	QVLSIMEIIL	DESNAEPLSE	DKGNLLLTGD	KDQLVMLLDQ
4601	INSTFVRSNP	SVLQGLLRII	PYLSFGEVEK	MQILVERFKP	YCNFDKYDED
4651	HSGDDKVFLD	CFCKIAAGIK	NNSNGHQLKD	LILQKGITQN	ALDYMKKHIP
4701	SAKNLDADIW	KKFLSRPALP	FILRLLRGLA	IQHPGTQVLI	GTDSIPNLHK
4751	LEQVSSDEGI	GTLAENLLEA	LREHPDVNKK	IDAARRETRA	EKKRMAMAMR
4801	QKALGTLGMT	TNEKGQVVTK	TALLKQMEEL	IEEPGLTCCI	CREGYKFQPT
4851	KVLGIYTFTK	RVALEEMENK	PRKQQGYSTV	SHFNIVHYDC	HLAAVRLARG
4901	REEWESAALQ	NANTKCNGLL	PVWGPHVPES	AFATCLARHN	TYLQECTGQR
4951	EPTYQLNIHD	IK LLFLRFAM	EQSFSADTGG	GGRESNIHLI	PYIIHTVLYV
5001	LNTTRATSRE	EKNLQGFLEQ	PK EKWVESAF	EVDGPYYFTV	LALHILPPEQ
5051	WRATRVEILR	RIJUTSOARA	VAPCCATRLT	DKAVKDYSAY	RSSLLEWALV
		Kunt 10grade	THEOGRATICE		NOODDL WADY
5101	DLIYNMFKKV	PTSNTEGGWS	CSLAEYIRHN	DMPIYEAADK	ALKTFQEEFM



Figure EV2. UBR4 is identified as an ACE2-interacting protein by mass spectrometry.

- A The identified peptide sequences (red color) of endogenous UBR4 by mass spectrometry analyses using ACE2 immunocomplexes. ACE2-overexpressing HEK293T cells were treated with the proteasome inhibitor MG132 (25 μM) for 2 h.
- B Besides Lys26, Lys112, and Lys114 residues, Lys94 residue was also identified as an ACE2 ubiquitination site. Mass spectrometry analysis of the ACE2 peptide containing the ubiquitination residue Lys94 from ACE2-transfected HEK293T cells treated with MG132.





Figure EV3. GLK-induced ACE2 phosphorylation blocks the ACE2-UBR4 interaction and subsequent ACE2 ubiquitination.

A In situ PLA assays of the interaction between Flag-tagged ACE2 and Myc-tagged UBR4 proteins in HEK293T cells. Cells were co-transfected with Flag-ACE2 and Myc-UBR2 plus either GFP-GLK (green) or GFP-GLK (K45E) kinase-dead mutant (green) plasmids. Nuclei were stained with DAPI. Red dots represent direct interaction signals. Yellow color represents the co-existence of PLA signal (red) and GLK (K45E) mutant protein (green). Original magnification, x200. Scale bars, 20 µm.

B *In vitro* ubiquitination assays using Myc-tagged UBR4 and Flag-tagged ACE2 proteins with E1 ubiquitin-activating enzyme, E2 ubiquitin-conjugating enzyme, and His-tagged ubiquitin. ACE2 ubiquitination and ACE2 were detected by immunoblotting with anti-His and anti-Flag antibodies, respectively. Data shown are representative results of three independent experiments.



Figure EV4. Infection of hACE2 knockin mice and EF1α-hACE2 transgenic mice with SARS-CoV-2 pseudovirus or live SARS-CoV-2.

A PCR analyses of hACE2 knockin allele in the genomic DNA from mouse tails. The PCR product of the 2,379-bp band indicates the hACE2 knockin allele.

- B Real-time PCR analyses of knockin human ACE2 (hACE2) mRNA levels in the lymph nodes, kidneys, liver, heart, lungs, small intestine, brain, and muscle from wildtype or hACE2 KI mice. The human ACE2 mRNA levels were normalized to mouse GAPDH mRNA levels. *n* = 2 (technical replicates) per group.
- C Immunoblotting analyses of GLK, tubulin, and human ACE2 proteins in the lungs, kidneys, spleen, and lymph nodes of wild-type and hACE2 KI mice.
- D Immunoblotting of ACE2, GLK, and CD9 proteins in the exosomes isolated from the sera of the SARS-CoV-2 pseudovirus-infected mice. Exosomes were isolated sequentially using ExoQuick kits and then ExoQuick ULTRA columns. Arrowheads denote glycosylated ACE2 proteins; asterisk denotes unglycosylated ACE2 proteins.
- E, F EF1α-hACE2 Tg and wild-type mice were infected intranasally with 2 × 10⁵ pfu of live SARS-CoV-2. n = 4 (biological replicates) per group. EF1α-hACE Tg mice were treated intranasally with PBS (Mock) as controls. On day 3 postinfection, the mice were sacrificed, and the lung tissues were homogenized for the TCID₅₀ assay (E). The survival rate of EF1α-hACE2 Tg mice challenged with live SARS-CoV2 was monitored (F). WT, wild-type mice; KI, hACE2 knockin mice; Tg, EF1α-hACE2 transgenic mice. The number of infected mice was less than 3 from day 7 due to deaths; thus, the statistical analysis of panel F was only performed on data up to day 6 postinfection.

Data information: In (B), data are presented as means \pm SD. In (E), data are presented as means \pm SEM. **P*-value < 0.05 (Kruskal–Wallis test). In (F), data are presented as means \pm SEM. **P*-value < 0.05 (Mann–Whitney test).



Figure EV5. GLK inhibitor attenuates ACE2 protein levels, ACE2-containing exosomes, and SARS-CoV-2 pseudovirus infection.

A–D Human ACE2 KI mice were intranasally infected with SARS-CoV-2 pseudovirus on Day 0 and Day 1. Mice were also treated with the GLK inhibitor verteporfin on Day 0 after infection. n = 3 (biological replicates) per group. Infection efficiencies of SARS-CoV-2 pseudovirus in mouse tissues were measured by IVIS and presented as luminescence counts on Day 2 (A). Immunoblotting of ACE2 and vinculin in the lung tissues of the infected hACE2 KI mice with/without the GLK inhibitor verteporfin (10 μ M in 100 μ) treatment (B). Immunoblotting of ACE2 and CD9 in exosomes isolated from the sera (C) and BALF (D) of the infected mice with/without the GLK inhibitor verteporfin (10 μ M in 100 μ) treatment. Arrowhead denotes glycosylated ACE2 proteins; asterisk denotes unglycosylated ACE2 proteins.

Data information: WT, wild-type mice; KI, hACE2 knockin mice.