

SARS-CoV-2	1	MSDNGPQ-NQRMAPRITFGGPDSTGSDNQNGERSGARSKQRRPQGLPNNTASWFTALTQH
SARS-CoV	1	MSDNGPQSNQRSAPRITFGGPDSTDMNQNGGRNGARPKQRRPQGLPNNTASWFTALTQH
SARS-CoV-2	60	GKEELRFPRGQGVPIINTNSSPDDQIGYYRRATRRIRGGDGKMKELSPRWYFYLLGTGPEA
SARS-CoV	61	GKEELRFPRGQGVPIINTNSCPDDQIGYYRRATRRIRGGDGKMKELSPRWYFYLLGTGPEA
SARS-CoV-2	120	GLPYGANKDGIWVATEGALNTPKDHIGTRNPANNAATVLQLPQGTTLPKGFYAEGRGG
SARS-CoV	121	SLPYGANKEGIWVATEGALNTPKDHIGTRNPANNAATVLQLPQGTTLPKGFYAEGRGG
SARS-CoV-2	180	SQASSRSSSRSRNSSRNSTPGSSRGTSPTARMAGNGGLAALALLLLDRLNQLESKMSGKGQ
SARS-CoV	181	SQASSRSSSRSRGNSRNSTPGSSRGNSPTARMASGGGTALALLLLDRLNQLESKMSGKGQ
SARS-CoV-2	240	QQQGQTVTKKSAAEASKKPRQKRTATKAYNVVTQAFGRRGPEQTQGNFGDQELIRQGTDYK
SARS-CoV	241	QQQGQTVTKKSAAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQELIRQGTDYK
SARS-CoV-2	300	HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDA
SARS-CoV	301	HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPNFKDQVILLNKHIDA
SARS-CoV-2	360	YKTFPPTEPKKDKKKKADETOALPQRQKKQPTVTLLPAADLDDFSKQLQCSMS--SADST
SARS-CoV	361	YKTFPPTEPKKDKKKKTDEAQLPQRQKKQPTVTLLPAADMDDFSQQLQNSMSGASADST
SARS-CoV-2	418	QA
SARS-CoV	421	QA

Total sites= 422 aa

Conserved sites= 382 aa

Variable sites= 37 aa

Deleted sites= 3 aa

Supplemental Figure 1: Protein Alignment of N-Protein from SARS-CoV and SARS-CoV-2.
Alignment was performed using MEGA-X and aligned using ClustalW with the default settings.
Conserved sites are highlighted in black; substitutions of biochemically similar amino acids are highlighted in grey. Alignment is with accession's SARS-CoV: NP_828858.1 and SARS-CoV-2: YP_009724397.2

SARS-CoV	1	APITKGVTFGDDTVWEVQGYKNNRITFELDERMDKVLNEKCSVYTVESGTEVTEFACVVAE
SARS-CoV-2	1	APTK-VTFGDDTVIEVQGYKSVNITFELDERMDKVLNEKCSAYTVELGTEVNEFACVVAD
SARS-CoV	61	AVVKTLPVSDLLTNMGIDLDEWSVATFYLFDDAGEENFSSRMYSFYPPDEEEEDAFEC
SARS-CoV-2	60	AVVKTLPVSELLTPIGIDLDEWSVATFYLFDESSEGFKLASHMYCSFYPPDEEEEDGDC
SARS-CoV	121	EEEEIDEICEHEYGTEDDYQGLPLEFGASAETVRVEEEEEEDWLDDTTEQSE-----
SARS-CoV-2	119	EEEEFEPSTQYEGTEDDYQGKPLEFGASAAQPEEEEQEEDWLDDDSQQIVGQQDGSED
SARS-CoV	173	-----IEPEPEPTPEEP-----VNOFTGYLKLTDNVAIKCVDIVKEAQSANPMV
SARS-CoV-2	179	NQTTTIQTIVEVQPLEMELTPVVQTIENVNSESGLYKLTDNVYIKNADIVEEAKKVKPTV
SARS-CoV	217	IVNAANTHLKHGGGVAGALNKATNGAMQKESDDYIKLNGPLTVGGSCVLSGHNLAKECLH
SARS-CoV-2	239	VVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVGGSCVLSGHNLAKECLH
SARS-CoV	277	VVGPNINAGEDIQLLKAAYENFNFSQDILLAPLLSAGIFGAKPIQSLQVCVQTVRTOVYLA
SARS-CoV-2	299	VVGPNVNGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSLRVCVDTVRTRNVYLA
SARS-CoV	337	VNDKALYEQVMDYLLNLKPEVEAPKQEEPPNTEDS--KTEKSVVQKPVDPKPIKACI
SARS-CoV-2	359	VFDKNLYDKIVSSLEMKSEKQVEQKIAETPKKEEVKPEETESKPSVEQRKQDDKKIKACV
SARS-CoV	395	DEVTTTLEETKFLTNKLLLEADINGKLYHDSQNMIRGEDMSFLEKDAPYVVGDTVITSGDI
SARS-CoV-2	419	BEVTTTLEETKFLTENLLLEIDINGNLHPDSATLVSDIDITFLKKDAPYVVGDTVQEGVL
SARS-CoV	455	TCVVIPSKKAGGTTEMLSALEKVPVDEYITTPGQGCAGYTLEEAKTALKKCKSAFYVL
SARS-CoV-2	479	TAVVIPKKKAGGTTEMLAKALEKVPEDNYITTPGQGLNGYTVEEAKTVLKKCKSAFYIL
SARS-CoV	515	PSEAPNAKEEILGTVSWNLREMLAHAEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIV
SARS-CoV-2	539	PSIISNEKQEEILGTVSWNLREMLAHAEETRKLMPVCVETKAIMSTIQRKYKGIKIQEGVV
SARS-CoV	575	DYGVREFFYTSKEPVASITTKLNSLNEPIVMTPIGYVTHGFENLEEAARCMRSLKAPAVVS
SARS-CoV-2	599	DYGAREFYTSKTTVASIINTLNDLNETLVMTPIGYVTHGLNLEEAARYMRSLKVPATVS
SARS-CoV	635	VSSPDAVTYNGYLTSSSKTSEEHFVETVSLAGSYKDWSSYSGQRTGLGHEFLKRGDKIVY
SARS-CoV-2	659	VSSPDAVTAYNGYLTSSSKTPEEHFTETVSLAGSYKDWSSYSGQSTGLGHEFLKRGDKSVY
SARS-CoV	695	HTLESPVEFHLDGEVLSLDKLSLLSLREVETIKVFTTVDNINLHTQIVDMSMTYGQQFG
SARS-CoV-2	719	YTSN-PTTFHLDGEVITFDNLKLLSLREVETIKVFTTVDNINLHTQIVDMSMTYGQQFG
SARS-CoV	755	PTYLDGADVTKIKPHVNEHGKTFEVLPSDDTLRSEAFEYYHTLDESFLGRYMSALNHTKK
SARS-CoV-2	778	PTYLDGADVTKIKPHNSHEGKTFEVLPNDDTLRVEAFEYYHTTDPSEFLGRYMSALNHTKK
SARS-CoV	815	WKEPQVGGLTSLKWADNNCYLSSVLLALQQLLEKFNPPALQDAYYRARAGAAANFCALIL
SARS-CoV-2	838	WKMPQVNGLTSLKWADNNCYLATAALLTLQQLLEKFNPPALQDAYYRARAGAAANFCALIL
SARS-CoV	875	AYSNTKTVGELGDVRETMTIHLLOHANLSSAKRVLNVVCKHCGQKTTTLTGVEAVMYMGTLIS
SARS-CoV-2	898	AYCNKTVGELGDVRETMSYLFQHANLSSCKRVLNVVCKTCGQQQTTLKGVEAVMYMGTLIS
SARS-CoV	935	YDNLKTCVSIQCVCGRDATQYLVQQESSFVMSAPPAEYKLLQQTFLCANEYTGNYQCGH
SARS-CoV-2	958	YEQFKKGVOIPCTCGKQATKYLVQQESSFVMSAPPAQYELKHGTFTCASEYTGNYQCGH
SARS-CoV	995	YTHITAKETLYRIDGAHLTKMSEYKGPVTDVFYKETSYTTTIKPVSYKLDGVITYTEIEPK
SARS-CoV-2	1018	YKHTISKETLYCIDGALLTKSSEYKGPVTDVFYKENSYTTTIKPVYKLDGVVCTEIDPK
SARS-CoV	1055	LDGYKKDNAYYTEQPIDLVPTQPIPNASFDNFKLTCSTNKFADDLNQMTGETKPASREL
SARS-CoV-2	1078	LDNYKKDNSYYTEQPIDLVENQPYPNASFDNFKFVCDNFKFADDLNQMTGYKKPASREL
SARS-CoV	1115	SVTFFPDNLNGDVVAIDYRHYSSAFKKGAKLLHKPIVWHINQATTKTTEKPNTWCIRCLWS
SARS-CoV-2	1138	KVTFFPDNLNGDVVAIDYRHYTPSEKKGAKLLHKPIVWHINNATNKATKPNTWCIRCLWS

SARS-CoV	1175	TKPVDTSNSFEVLAVEDTQGMNDLACE	SQQPTSEEVENPTIQKEVLECDVKTTEVVGNV
SARS-CoV-2	1198	TKPVEITSNSFDVLKSEDAQGMNDLACE	DLKEVSEEVENPTIQKDVLECNVKTTEVVGDI
SARS-CoV	1235	ILKPSDEGVKVTQELGHEDLMAAYVENTS	TIKKPNELSLAIGLKTATHGIAAINSVPW
SARS-CoV-2	1258	ILKPAANNSIKITEEVGHTDLMAAYVNS	STIKKPNELSRVIGLKTATHGIAAINSVPW
SARS-CoV	1295	SKLLAYVVKPFLGQAAITTSNCAKRLA	QRFVNNYPYVFTLLFQLCTFTKSTNSRIEASLP
SARS-CoV-2	1318	DTIANYAKPFLNKVVSTTINIVTRCL	NRVCTNYMPYFETLLQLCTFTKSTNSRIKASMP
SARS-CoV	1355	TTIAKNVKSVAKLCLDAGINVKSPKFSK	LEFTIANWLLLLSLCLGSLICVTAAGVLLS
SARS-CoV-2	1378	TTIAKNIVKSVCKFCLEASFNLIKSPNFS	KLINIIWFLLLSVCLGSLIYSTAALGVLS
SARS-CoV	1415	NFCAPSYCNCVRELYLNSNVTMDCEG	SFPCTCLSGLDSDSYPALETIQVTISSMK
SARS-CoV-2	1438	NLCMPSYCTGYREGYLNSNVTIATVCT	GSIPCSVCLSGLDSDIYPSLETIQVTISSEK
SARS-CoV	1475	LDLTILGLAAEWFLAYLLETFEFLYL	LGLSAIMQMFEGYFASHFISNSWLMWFIISIVQMA
SARS-CoV-2	1498	WDLTAEGLVAEWFLAYLLETFEFLYL	GLAAIMQMFESYFAWHFISNSWLMWLIINIVQMA
SARS-CoV	1535	PVSAMVRMYIFFASFYYIWKSYVHIMD	GCTSSSTCMCYKRNRA TRVECTTIVNGMKRSFY
SARS-CoV-2	1558	PIVSAMVRMYIFFASFYYIWKSYVHV	DGCNSSTCMCYKRNRA TRVECTTIVNGVRRSFY
SARS-CoV	1595	VYANGGKGFKTHNWNCLNCDTFCTG	STFISDEVARDLSLQFKRPINPTDQSSYIVDSVA
SARS-CoV-2	1618	VYANGGKGFKLHNWNCNCDTFCA	GSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVT
SARS-CoV	1655	VKNGAHLHYFDKAGQKTYERHPL	LSHFVNLDNLRANNTKGS LPINVIVFDGKSKCEDESASK
SARS-CoV-2	1678	VKNGSHLHYFDKAGQKTYERHSL	LSHFVNLDNLRANNTKGS LPINVIVFDGKSKCEDSSAK
SARS-CoV	1715	SASVYYSQLMCQPILLLDQALVSDV	GDSTEVSVKMFDAYVDTFSATFSVPMEKLKALVAT
SARS-CoV-2	1738	SASVYYSQLMCQPILLLDQALVSDV	GDSEVAVKMFDAYVNTFSSTFNVPMEKLKTLVAT
SARS-CoV	1775	AHSELAKGVALDGVLTSTFSAARQ	GVVDVDTKDVTECLKLSHSDIEVTGDSCNNFML
SARS-CoV-2	1798	AEAEELAKNVSLDNVLTSTFSAARQ	GFVDSVDTKDVTECLKLSHQSDIEVTGDSCNNVML
SARS-CoV	1835	TYNKVENMTPRDLGACIDCNARH	INAQVAKSHNVS LIWNVKDMMSLSEQLRKQIRSAACK
SARS-CoV-2	1858	TYNKVENMTPRDLGACIDCSARH	INAQVAKSHNIALI WNVKDMMSLSEQLRKQIRSAACK
SARS-CoV	1895	NNLPFRLTCATTRQVVNVTTTKI	SLKGG
SARS-CoV-2	1918	NNLPFKLTCATTRQVVNVTTKIAL	KGG

Total sites= 1948 aa

Conserved sites= 1477 aa (75.8%)

Variable sites= 442 aa

Deleted sites= 29 aa

Supplemental Figure 2: Protein Alignment of PLPro Protease from SARS-CoV and SARS-CoV-2. Alignment was performed using MEGA-X and aligned using ClustalW with the default settings. Conserved sites are highlighted in black; substitutions of biochemically similar amino acids are highlighted in grey. Alignment is with accession's SARS-CoV: NP_828862.2 and SARS-CoV-2: YP_009725299.1.