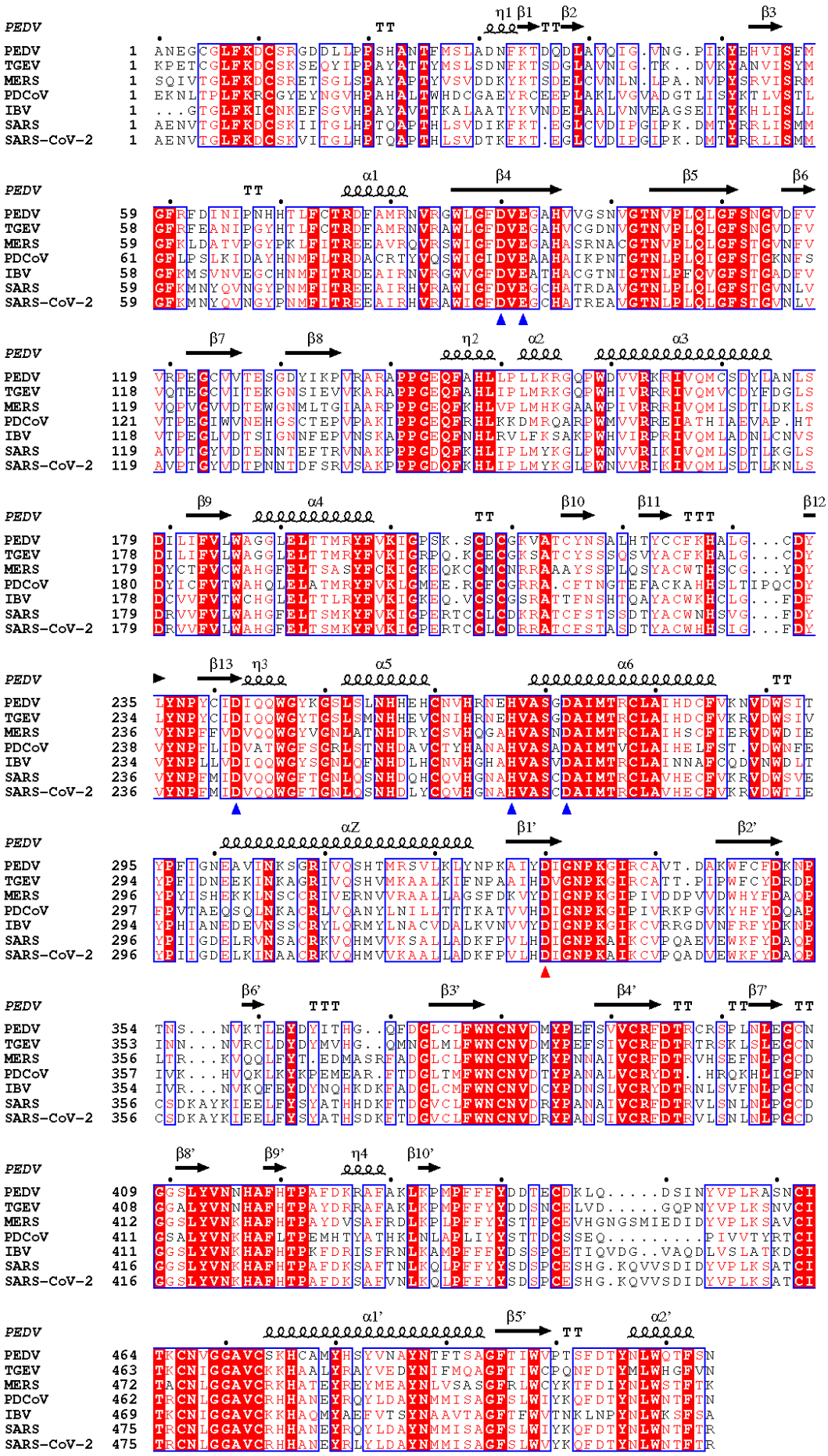
Legend for supplementary figure

Supplementary Figure 1. Structure-based sequence alignment of representative coronavirus nsp14. (A) sequence alignment of CoV nsp14 proteins. PEDV nsp14 (gi: 557844763) and its homologs from *Alphacoronavirus* genus TGEV (gi: 110746821), *Betacoronavirus* genus SARS-CoV (gi: 40795428) and SARS-CoV-2 (gi: 1806553187), *Deltacoronavirus* genus PDCoV (gi: 668361756), and *Gammacoronavirus* genus IBV (gi: 9626535) were chosen for alignment by ClustalW2. Identical residues are shown in boxes with solid red background, and conserved residues are highlighted in red square. The catalytic residues D90, E92, D242, H267 and D272 of the ExoN domain are indicated with blue triangles. The SAM binding residue D330 of the G-N-7 MTase domain is marked with red triangle. The predicted secondary structure of PEDV nsp14 is displayed on the top. For the G-N-7 MTase domain, the secondary elements were labelled with new ranking number and followed the SAM-MT fold way. The figure was generated by ESPript Version3.0. **(B) Predicted tertiary structure of PEDV nsp14.** Ribbon representation of the tertiary structure of PEDV nsp14 generated with MODELLER 9.15 using SARS-CoV nsp14 (PDB ID: 5C8S) as template. Ribbon representation of the full-length PEDV nsp14. ExoN domain was shown in cyan color and G-N-7 MTase domain was shown in red color. The SAM binding motif was highlighted by yellow. **(C) Ribbon representation of the G-N-7 MTase domain of PEDV nsp14**. The N and C terminus are indicated. The amino acid residues (D330, G332, and D350) involved in the SAM binding was labeled.

Fig.S1

(A)


PEDV
PEDV 1 ANEGCGLFKDCSRGDDLLPPSHANTFMSLADNFKTDQDLAVQIG.VNG.PIKYEHVISFM
TGEV 1 KPETCGLFKDCSKSEQYIPPAYATTYMSLSDNFKTSDGLAVNIG.TK..DVKYANVISYM
MERS 1 SQIVTGLFKDCSRETSGLSPAYAPTYVSVDDKYKTSDELCVNLN.LPA.NVPYSRVISRM
PDCoV 1 EKNLTPLFKRCGYEYNGVHPAHALTWHDCGAEYRCEEPLAKLVGVADGTLISYKTLVSTL
IBV 1 ...GTGLFKICNKEFSGVHPAYAVTTKALAATYKVNDELAALVNVEAGSEITYKHLISLL
SARS 1 AENVTGLFKDCSKIITGLHPTQAPTHLSVDIKFKT.EGLCVDIPGIPK.DMTYRRLISMM
SARS-CoV-2 1 AENVTGLFKDCSKVITGLHPTQAPTHLSVDTKFKT.EGLCVDIPGIPK.DMTYRRLISMM
PEDV
PEDV 59 GFRFDINIPNHHTLFCTRDFAMRNVRGWLGFDVEGAHVVGSNVGTNVPLQLGFSNGVDFV
TGEV 58 GFRFEANIPGYHTLFCTRDFAMRNVRAWLGFDVEGAHVCGDNVGTNVPLQLGFSNGVDFV
MERS 59 GFKLDATVPGYPKLFITREEAVRQVRSWIGFDVEGAHASRNACGTNVPLQLGFSTGVNFV
PDCoV 61 GFLPSLKIDAYHNMFLTRDACRTYVQSWIGIDVEAAHAIKPNTGTNLPLQIGFSTGKNFS
IBV 58 GFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPFQVGFSTGADFV
SARS 59 GFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLGFSTGVNLV
SARS-CoV-2 59 GFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATREAVGTNLPLQLGFSTGVNLV
PEDV
PEDV 119 VRPECCVVTESGDYIKPVRARAPPGEQFAHLLPLLKRGQPWDVVRKRIVQMCSDYLANLS
TGEV 118 VQTECCVITEKGNSIEVVKARAPPGEQFAHLIPLMRKGQPWHIVRRRIVQMVCDYFDGLS
MERS 119 VQPVCVVDTEWGNMLTGIAARPPGEQFKHLVPLMHKGAAWPIVRRRIVQMLSDTLDKLS
PDCoV 121 VTPECIWVNEHGSCTEPVPAKIPPGEQFRHLKKDMRQARPWMVVRREIATHIAEVAP.HT
IBV 118 VTPECLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIVQMLADNLCNVS
SARS 119 AVPTCYVDTENNNTEFTRVNAKPPGDQFKHLIPLMYKGLPWNVVRIKIVQMLSDTLKGLS
SARS-CoV-2 119 AVPTCYVDTPNNTDFSRVSAKPPGDQFKHLIPLMYKGLPWNVVRIKIVQMLSDTLKNLS
PEDV
PEDV 179 DILIFVLWAGGLELTTMRYFVKIGPSK.SCDCGKVATCYNSALHTYCCFKHALG...CDY
TGEV 178 DILIFVLWAGGLELTTMRYFVKIGRPQ.KCECGKSATCYSSSQSVYACFKHALG...CDY
MERS 179 DYCTFVCWAHGFELTSASYFCKIGKEQKCCMCNRRAAAYSSPLQSYACWTHSCG...YDY
PDCoV 180 DYICFVTWAHQLELATMRYFVKLGMEE.RCFCGRRA.CFTNGTEFACKAHHSLTIPQCDY
IBV 178 DCVVFVTWCHGLELTTLRYFVKIGKEQ.VCSCGSRATTFNSHTQAYACWKHCLG...FDF
SARS 179 DRVVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNHSVG...FDY
SARS-CoV-2 179 DRVVFVLWAHGFELTSMKYFVKIGPERTCCLCDRRATCFSTASDTYACWHHSIG...FDY
PEDV
PEDV 235 LYNPYCIDIQQWGYKGSLSLNHHEHCNVHRNEHVASGDAIMTRCLAIHDCFVKNVDWSIT
TGEV 234 LYNPYCIDIQQWGYTGSLSMNHHEVCNIHRNEHVASGDAIMTRCLAIHDCFVKRVDWSIV
MERS 236 VYNPFFVDVQQWGYVGNLATNHDRYCSVHQGAHVASNDAIMTRCLAIHSCFIERVDWDIE
PDCoV 238 VYNPFLIDVATWGFSGRLSTNHDAVCTYHANAHVASADAIMTVCLAIHELFST.VDWNFE
IBV 234 VYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAHVASVDAIMTRCLAINNAFCQDVNWDLT
SARS 236 VYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWSVE
SARS-CoV-2 236 VYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIE
PEDV
PEDV 295 YPFIGNEAVINKSGRIVQSHTMRSVLKLYNPKAIYDIGNPKGIRCAVT.DAKWFCFDKNP
TGEV 294 YPFIDNEEKINKAGRIVQSHVMKAALKIFNPAAIHDVGNPKGIRCATT.PIPWFCYDRDP
MERS 296 YPYISHEKKLNSCCRIVERNVVRAALLAGSFDKVYDIGNPKGIPIVDDPVVDWHYFDAQP
PDCoV 297 FPVTAEQSQLNKACRLVQANYLNILLTTTKATVVHDIGNPKGIPIVRKPGVKYHFYDQAP
IBV 294 YPHIANEDEVNSSCRYLQRMYLNACVDALKVNVVYDIGNPKGIKCVRRGDVNFRFYDKNP
SARS 296 YPIIGDELRVNSACRKVQHMVVKSALLADKFPVLHDIGNPKAIKCVPQAEVEWKFYDAQP
SARS-CoV-2 296 YPIIGDELKINAACRKVQHMVVKAALLADKFPVLHDIGNPKAIKCVPQADVEWKFYDAQP
PEDV
PEDV 354 TNS...NVKTLEYDYITHG..QFDGLCLFWNCNVDMYPEFSVVCRFDTRCRSPLNLEGCN
TGEV 353 INN...NVRCLDYDYMVHG..QMNGLMLFWNCNVDMYPEFSIVCRFDTRTRSKLSLEGCN
MERS 356 LTR...KVQQLFYT.EDMASRFADGLCLFWNCNVPKYPNNAIVCRFDTRVHSEFNLPGCD
PDCoV 357 IVK...HVQKLKYKPEMEAR.FTDGLTMFWNCNVDTYPANALVCRYDT..HRQKHLIGPN
IBV 354 IVR...NVKQFEYDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRFDTRNLSVFNLPGCN
SARS 356 CSDKAYKIEELFYSYATHSDKFTDGVCLFWNCNVDRYPANSIVCRFDTRVLSNLNLPGCD
SARS-CoV-2 356 CSDKAYKIEELFYSYATHSDKFTDGVCLFWNCNVDRYPANSIVCRFDTRVLSNLNLPGCD
PEDV
PEDV 409 GGSLYVNNHAFHTPAFDKRAFAKLKPMPFFFYDDTECDKLQ.....DSINYVPLRASNCI
TGEV 408 GGALYVNNHAFHTPAYDRRAFAKLKPMPFFYYDDSNCELVD.....GQPNYVPLKSNVCI
MERS 412 GGSLYVNKHAFHTPAYDVSAFRDLKPLPFFYYSTTPCEVHGNGSMIEDIDYVPLKSAVCI
PDCoV 411 GSALYVNKHAFLTPEMHTYATHKLNLAPLIYYSTTDCSSEQ.........PIVVTYRTCI
IBV 411 GGSLYVNKHAFHTPKFDRISFRNLKAMPFFFYDSSPCETIQVDG..VAQDLVSLATKDCI
SARS 416 GGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHG.KQVVSDIDYVPLKSATCI
SARS-CoV-2 416 GGSLYVNKHAFHTPAFDKSAFVNLKQLPFFYYSDSPCESHG.KQVVSDIDYVPLKSATCI
PEDV
PEDV 464 TKCNVGGAVCSKHCAMYHSYVNAYNTFTSAGFTIWVPTSFDTYNLWQTFSN
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MERS 472 TACNLGGAVCRKHATEYREYMEAYNLVSASGFRLWCYKTFDIYNLWSTFTK
PDCoV 462 TRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTN
IBV 469 TKCNLGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSA
SARS 475 TRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTR
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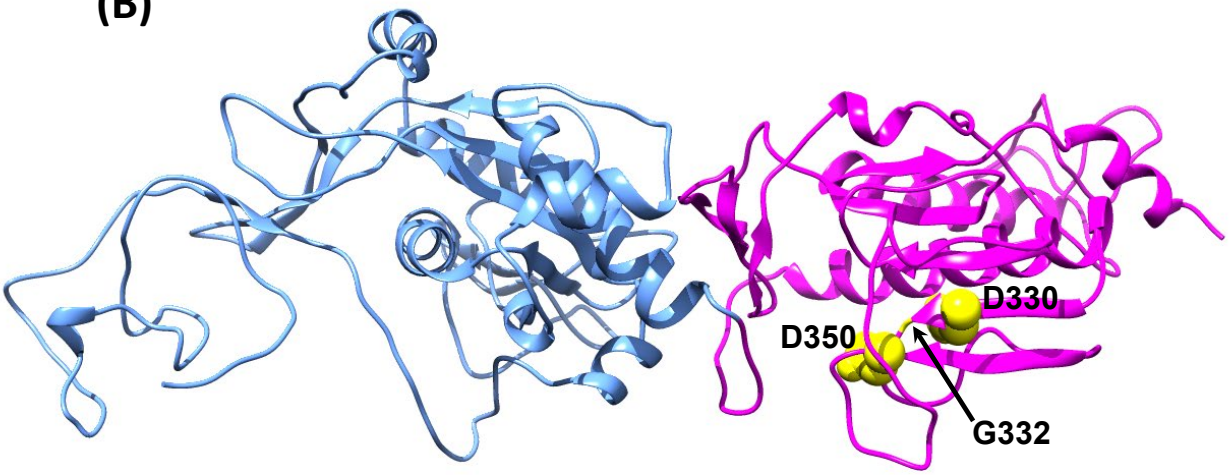
Fig.S1

(B)



(C)