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Supplemental Material to:

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Cholesterol sensitivity of KIR2.1 depends on functional interlinks between the N and C termini

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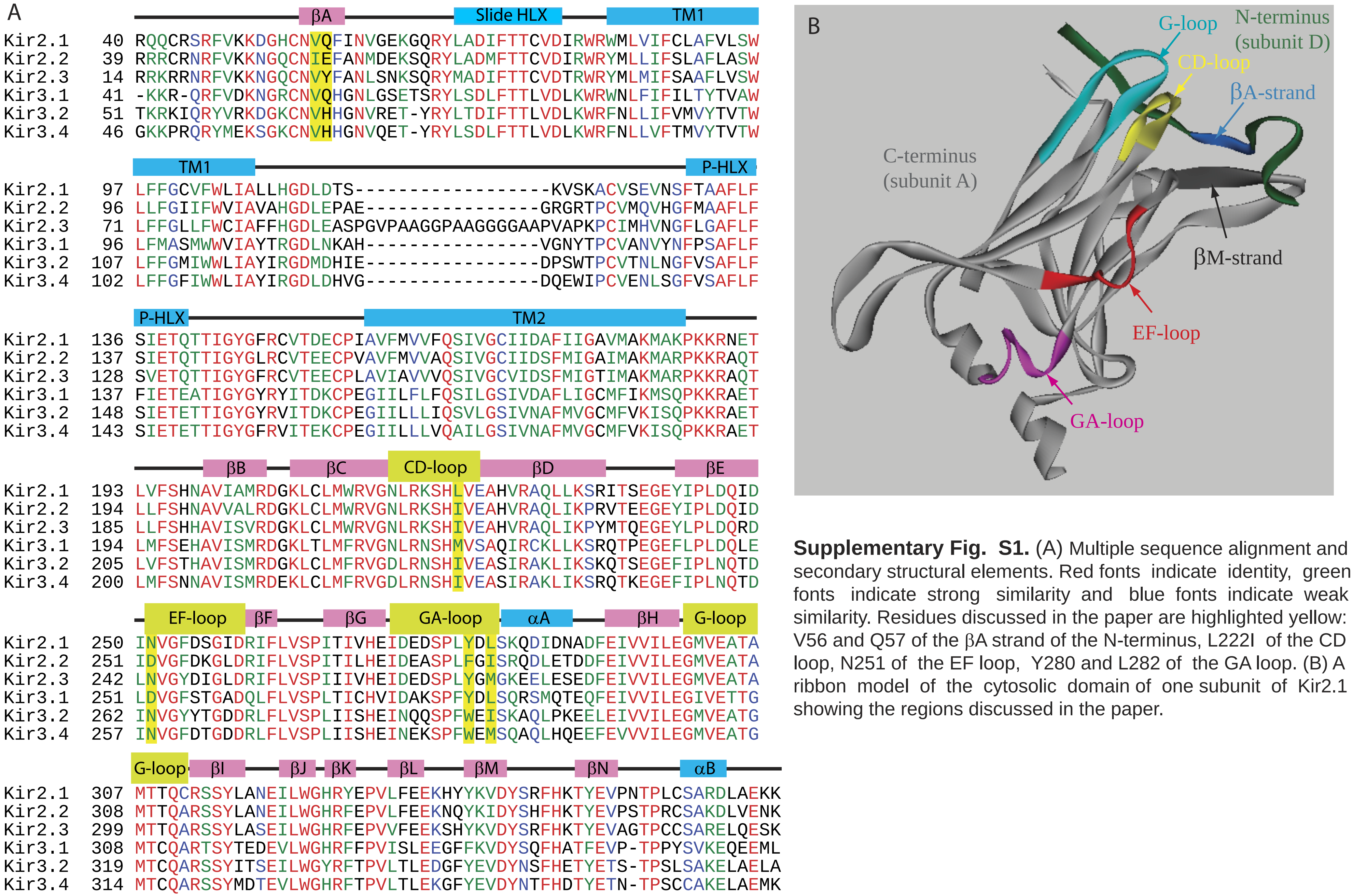

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Kir2.1   40 RQQCRSRFVKKDGHCNVQFINVGEKGQRYLADIFTTCVDIRWRWMLVIFCLAFVLSW
Kir2.2   39 RRRCRNRFVKKNGQCNIEFANMDEKSQRYLADMFTTCVDIRWRYMLLIFSLAFLASW
Kir2.3   14 RRKRRNRFVKKNGQCNVYFANLSNKSQRYMADIFTTCVDTRWRYMLMIFSAAFLVSW
Kir3.1   41 -KKR-QRFVDKNGRCNVQHGNLGSETSRYLSDLFTTLVDLKWRWNLFIFILTYTVAW
Kir3.2   51 TKRKIQRYVRKDGKCNVHHGNVRET-YRYLTDIFTTLVDLKWRFNLLIFVMVYTVTW
Kir3.4   46 GKKPRQRYMEKSGKCNVHHGNVQET-YRYLSDLFTTLVDLKWRFNLLVFTMVYTVTW

Kir2.1   97 LFFGCVFWLIALLHGDLDTS-----------------KVSKACVSEVNSFTAAFLF
Kir2.2   96 LLFGIIFWVIAVAHGDLEPAE----------------GRGRTPCVMQVHGFMAAFLF
Kir2.3   71 LFFGLLFWCIAFFHGDLEASPGVPAAGGPAAGGGGAAPVAPKPCIMHVNGFLGAFLF
Kir3.1   96 LFMASMWWVIAYTRGDLNKAH----------------VGNYTPCVANVYNFPSAFLF
Kir3.2  107 LFFGMIWWLIAYIRGDMDHIE----------------DPSWTPCVTNLNGFVSAFLF
Kir3.4  102 LFFGFIWWLIAYIRGDLDHVG----------------DQEWIPCVENLSGFVSAFLF

Kir2.1  136 SIETQTTIGYGFRCVTDECPIAVFMVVFQSIVGCIIDAFIIGAVMAKMAKPKKRNET
Kir2.2  137 SIETQTTIGYGLRCVTEECPVAVFMVVAQSIVGCIIDSFMIGAIMAKMARPKKRAQT
Kir2.3  128 SVETQTTIGYGFRCVTEECPLAVIAVVVQSIVGCVIDSFMIGTIMAKMARPKKRAQT
Kir3.1  137 FIETEATIGYGYRYITDKCPEGIILFLFQSILGSIVDAFLIGCMFIKMSQPKKRAET
Kir3.2  148 SIETETTIGYGYRVITDKCPEGIILLLIQSVLGSIVNAFMVGCMFVKISQPKKRAET
Kir3.4  143 SIETETTIGYGFRVITEKCPEGIILLLVQAILGSIVNAFMVGCMFVKISQPKKRAET

Kir2.1  193 LVFSHNAVIAMRDGKLCLMWRVGNLRKSHLVEAHVRAQLLKSRITSEGEYIPLDQID
Kir2.2  194 LLFSHNAVVALRDGKLCLMWRVGNLRKSHIVEAHVRAQLIKPRVTEEGEYIPLDQID
Kir2.3  185 LLFSHHAVISVRDGKLCLMWRVGNLRKSHIVEAHVRAQLIKPYMTQEGEYLPLDQRD
Kir3.1  194 LMFSEHAVISMRDGKLTLMFRVGNLRNSHMVSAQIRCKLLKSRQTPEGEFLPLDQLE
Kir3.2  205 LVFSTHAVISMRDGKLCLMFRVGDLRNSHIVEASIRAKLIKSKQTSEGEFIPLNQTD
Kir3.4  200 LMFSNNAVISMRDEKLCLMFRVGDLRNSHIVEASIRAKLIKSRQTKEGEFIPLNQTD

Kir2.1  250 INVGFDSGIDRIFLVSPITIVHEIDEDSPLYDLSKQDIDNADFEIVVILEGMVEATA
Kir2.2  251 IDVGFDKGLDRIFLVSPITILHEIDEASPLFGISRQDLETDDFEIVVILEGMVEATA
Kir2.3  242 LNVGYDIGLDRIFLVSPIIIVHEIDEDSPLYGMGKEELESEDFEIVVILEGMVEATA
Kir3.1  251 LDVGFSTGADQLFLVSPLTICHVIDAKSPFYDLSQRSMQTEQFEIVVILEGIVETTG
Kir3.2  262 INVGYYTGDDRLFLVSPLIISHEINQQSPFWEISKAQLPKEELEIVVILEGMVEATG
Kir3.4  257 INVGFDTGDDRLFLVSPLIISHEINEKSPFWEMSQAQLHQEEFEVVVILEGMVEATG

Kir2.1  307 MTTQCRSSYLANEILWGHRYEPVLFEEKHYYKVDYSRFHKTYEVPNTPLCSARDLAEKK
Kir2.2  308 MTTQARSSYLANEILWGHRFEPVLFEEKNQYKIDYSHFHKTYEVPSTPRCSAKDLVENK
Kir2.3  299 MTTQARSSYLASEILWGHRFEPVVFEEKSHYKVDYSRFHKTYEVAGTPCCSARELQESK
Kir3.1  308 MTCQARTSYTEDEVLWGHRFFPVISLEEGFFKVDYSQFHATFEVP-TPPYSVKEQEEML
Kir3.2  319 MTCQARSSYITSEILWGYRFTPVLTLEDGFYEVDYNSFHETYETS-TPSLSAKELAELA
Kir3.4  314 MTCQARSSYMDTEVLWGHRFTPVLTLEKGFYEVDYNTFHDTYETN-TPSCCAKELAEMK
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Supplementary Fig. S1. (A) Multiple sequence alignment and secondary structural elements. Red fonts indicate identity, green fonts indicate strong similarity and blue fonts indicate weak similarity. Residues discussed in the paper are highlighted yellow: V56 and Q57 of the βA strand of the N-terminus, L222I of the CD loop, N251 of the EF loop, Y280 and L282 of the GA loop. (B) A ribbon model of the cytosolic domain of one subunit of Kir2.1 showing the regions discussed in the paper.