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Supporting information for article:

Crystal structure of the antigen-binding fragment of a monoclonal antibody specific for the multidrug-resistance-linked ABC transporter human P-glycoprotein

Lothar Esser, Suneet Shukla, Fei Zhou, Suresh V. Ambudkar and Di Xia

UIC2/Fab - heavy chain

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      10      20      30      40      50
UIC2      EVQLQESGPE LVKTGASVKI SCKASGYSFS NYIIHWVKQS HGKLSLEWIGF ISCYNGATFY
UIC2-tmp  EVILVESGGG LVKPGGSLKL SCAASGAAAA AAAAAWVRQT PEKRLWEVAT AAAAAAAAAA
MRK16     EVILVESGGG LVKPGGSLKL SCAASGFTFS SYTMSWVRQT PEKRLWEVAT ISSGGGNTYY
3HI5     EVQLLESGGG LVQPGGSLRL SCAASGFTFS RYVMWVRQA PGKGLEWVSY IWPSGGNTYY

      60      70      80      90     100     110
UIC2      .          .          . |ABC          .          |ABCDE          .
UIC2      NQKFKGKATF TVDNSSSTAY MKFNLSLTFED SAVYYCARLP IQFGNFYPMD YWGQGTTVTV
UIC2-tmp  AASVKGRFTI SRDNAKNNLY LQMSSLRSED TALYYCARAA AAAAAAAAAA AWGQGTLVTV
MRK16     PDSVKGRFTI SRDNAKNNLY LQMSSLRSED TALYYCARYY RYEAWFAS-- -WGQGTLVTV
3HI5     ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCASSY DFWSNAPD-- -IWGQGTMTV

      120     130     140     150     160     170
UIC2      SAAKTTAPSV YPLAPVCGDT TGSSVTLGCL VKGYFPEPVT LTWNSGSLSS GVHTFPAVLQ
UIC2-tmp  SAAKTTAPSV YPLAPVCGDT TGSSVTLGCL VKGYFPEPVT LTWNSGSLSS GVHTFPAVLQ
MRK16     SAAKTTAPSV YPLAPVCGDT TGSSVTLGCL VKGYFPEPVT LTWNSGSLSS GVHTFPAVLQ
3HI5     SAAKTTAPSV YPLAPVCGDT TGSSVTLGCL VKGYFPEPVT LTWNSGSLSS GVHTFPAVLQ

      180     190     200     210
UIC2      S-DLYTLSSSV TVTSTWPSQ SITCNVAHPA SSTKVDDKIE PRGPT
UIC2-tmp  S-DLYTLSSSV TVTSTWPSQ SITCNVAHPA SSTKVDDKIE P
MRK16     S-DLYTLSSSV TVTSTWPSQ SITCNVAHPA SSTKVDDKIE P
3HI5     SGLYLSLSSVV TVPSSSLGK TYTCNVDHKP SNTKVDDKRVE S

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UIC2/Fab - light chain

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      10      20      30      40      50
UIC2      QVVMTQSPLS LPVSLGDQAS ISCRSSQSLH HSNNGTYLHW YLQKPGQSPK LLIYKVSNRF
UIC2-tmp  DVLMTQTPVS LSVSLGDQAS ISCAAAAAA AAAAAAAAW YLQKPGQSPK LLIYAAAAAA
MRK16     DVLMTQTPVS LSVSLGDQAS ISCRSSQSIH HSTGNTYLEW YLQKPGQSPK LLIYKISNRF
3HI5     QDIQMTQSPSS LSASVGRVDT ITCRASQSIG -----SYLNW YQKQTGKAPK ALIYAASSLQ

      60      70      80      90     100     110
UIC2      SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YFCSSQSTHIP PWTFGGGTKL DIKRADAAPT
UIC2-tmp  AGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YYCAAAAAA AAAPFGGGTKL EIKRADAAPT
MRK16     SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YYCFQASHAP -RTFGGGTKL EIKRADAAPT
3HI5     SGVPSRFSGS GSGTDFTLTI SSLQLEDFAT YYCQQSYSTP --SFGQGTQV EIKRTVAAPS

      120     130     140     150     160     170
UIC2      VSIFPPSSEQ LTSGGASVVC FLNNFYPKDI NVKWKIDGSE RQNGVLNSWT DQDSKDYTS
UIC2-tmp  VSIFPPSSEQ LTSGGASVVC FLNNFYPKDI NVKWKIDGSE RQNGVLNSWT DQDSKDYTS
MRK16     VSIFPPSSEQ LTSGGASVVC FLNNFYPKDI NVKWKIDGSE RQNGVLNSWT DQDSKDYTS
3HI5     VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAL QSGNSQESVT EQDSKDYTS

      180     190     200     210
UIC2      MSSTLTITKD EYERHNSYTC EATHKTSTSP IVKSFNRNEC
UIC2-tmp  MSSTLTITKD EYERHNSYTC EAT-----SP IVKSFNRNEC
MRK16     MSSTLTITKD EYERHNSYTC EAT-----SP IVKSFNRNEC
3HI5     LSSTLTLSKA DYEKHKVYAC EVT-HQGLSS PVTKSFNRG

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Figure S1 Sequence of UIC2 aligned to that of related antibodies.

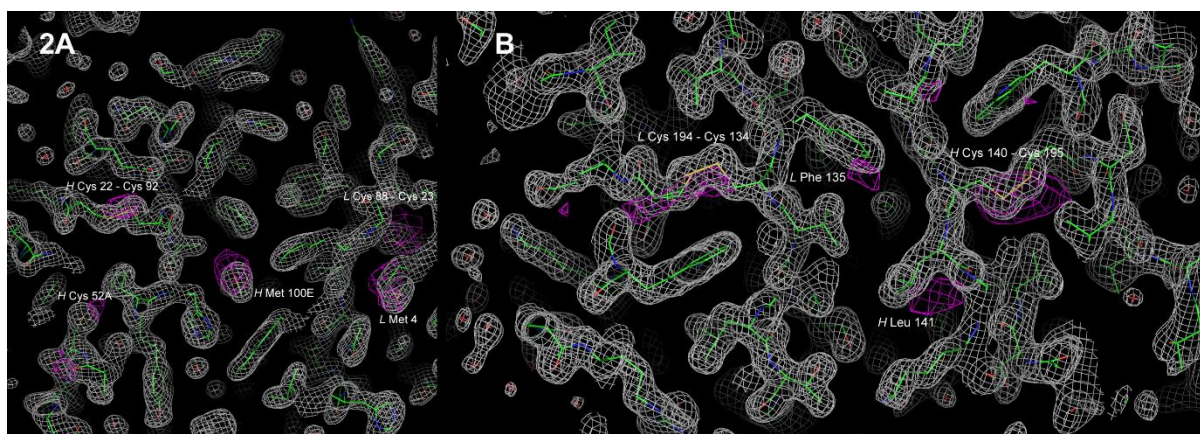


Figure S2 The anomalous difference density around selected sulfur atoms was calculated at 4.5 Å and is here shown in magenta. The contour level is 3.2 sigma. The overall quality of the anomalous map is good but note that there is still noise for instance at Phe135 and Leu141.

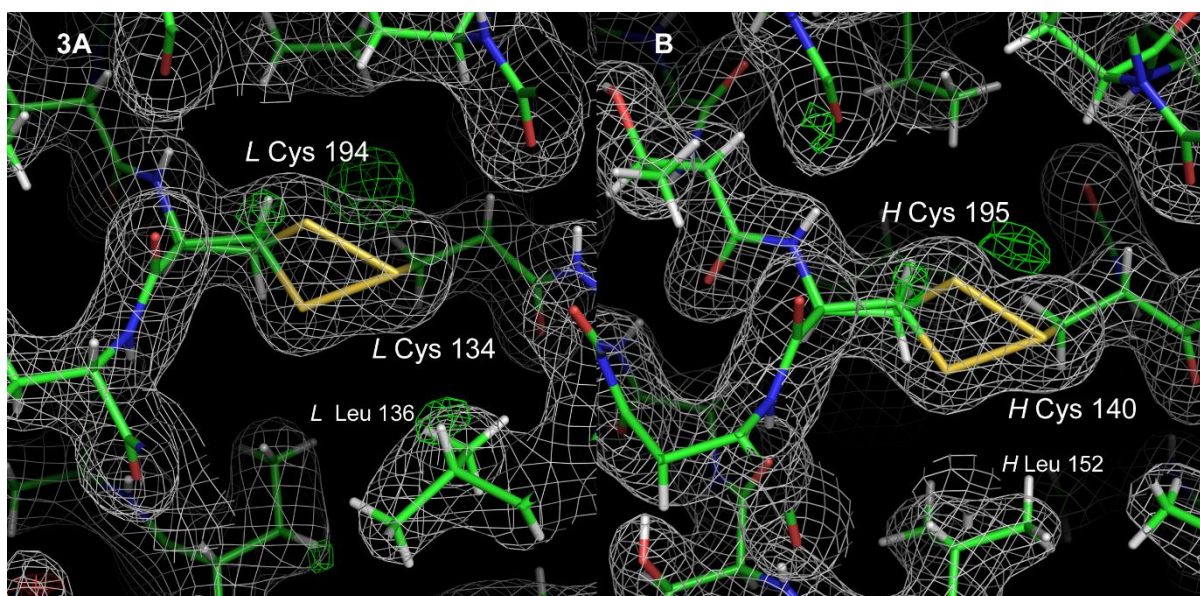


Figure S3 Cys194 of the light chain and Cys195 of the heavy chain were modeled with two rotamers, which refined to nearly equal occupancy in each case. All other disulfides refined with each cysteine exhibiting a single rotamer.

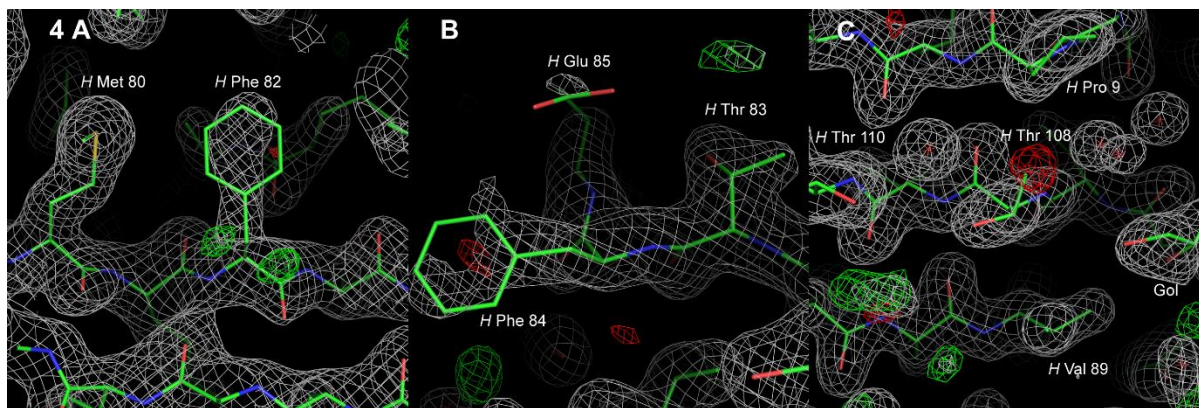


Figure S4 Sequenced heavy chain residues F82, T83, F84 and T108 are shown with their weighted 2Fo-Fc (light gray) and Fo-Fc density. Residues F82, F84 and T108 show the greatest disagreement with their 2Fo-Fc density. T83 seemed to have improved towards the end of refinement.