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Supporting information for article:

Structural insight into arginine methylation by the mouse protein arginine methyltransferase 7: a zinc finger freezes the mimic of the dimeric state into a single active site

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Table S1 RMSD values among PRMT catalytic modules, calculated using superpose Cα atoms.

Table S2 RMSD values among the PRMT AdoMet-binding domains

Table S3 RMSD values among the PRMT β -barrel domains

ANM7_MOUSE 310 WRDHWMOCVYFILEQEE P[V . Q[GSPRCVAHHDDYC[VWYSLQRTSPDENDS[A[YQVRPV[CDCQAH
 ANM7_HUMAN 310 WRDHWMOCVYFILEQEE P[V . Q[GSPALYI[VAHHDDYC[VWYSLQRTSPKNER[V[RQMRPV[CDCQAH
 ANM7_XENLA 306 WRDHWMOCVYFILEKEC S[V . Q[GEVCC[TAHQHDDYC[VWYSLNKKSSA.ENDP[VCRERPT[CHCGAH
 ANM7_DANRE 306 WRDHWMOSVYFILEAEE N[V . E[GEEELMLMVSHDDYS[LWYSLTHSEQ.NDVRV[AFFRPC[CCTCQAH
 ANM7_DROME 321 WRDHWMOCVYFILEKPL Q[LLEAGKSFH[LSCHHDEYS[LWFDAREEAPTKS . . . VRRHT[CCTCDLH
 ANM7_CAEEL 297 WRDHWMOCVYFILEKK K[V.E[MNQTFEI[VCVNHDEFSLWFSNVGKD KSRSY[CVCGLH
 ANM16_ARATH 348 WCDHW[KOCVWFTP[GTV VSISK[GEVKHL[HASHTCTN[IY[NLKKTQSLLTHER.T[HFP[LSTGDLH
 ANM7_TRYB2 326 RDMQW[GQALQLIDASN.GPLPTPV[VTE[GKNYNFECNFSGD R[VILHMQL[CPESGN
 K4E9B9_TRYCR 336 RDMQW[GQALQLIDAAAN.GPFPTPV[VTE[GEEELKF[KCHFSSD R[VTAHIHL[CPTAEE
 A4H4P9_LEIBR 356 RDMQW[GQALQLIDAGSTARMPTEL[SMSS[GESYKPECALSSD R[VMSLRV[GGGTA
 THWxQ

ANM7_MOUSE 372 ILWNR[PRFGEIN[DQDR[T[DHYAQALRT[VLL..PGSVC[CVSDGSI[LSM[LAHHLGAEQVFTVESSVAS...Y
 ANM7_HUMAN 372 ILWNR[PRFGEIN[DQDR[T[DHYAQALRT[VLK..PDSVC[LCVSDGSI[LSV[LAHHLGVEQVFTVESSAAS...H
 ANM7_XENLA 367 ITWNR[ARFGELND[RHR[TQQYFEALKK[VVT..PSSTCL[CVSDGSI[LPV[LAHSLGAKQIYTLESSSSIA...Q
 ANM7_DANRE 367 I[VWTR[PRFGEIN[DQDR[TESVYSLARS[IK..PDSVC[LSVSDGSI[LPV[FAHLLGSKKVFSLESGGMA..K
 ANM7_DROME 380 MTYSRSRIGQLN[SPRNLKRYLRL[ESEA.EKSNVL[VL[GNGCL[GLASSALGAASVLLHEPHRFS..R
 ANM7_CAEEL 351 SMLSR[QT[VYHV[NE[MFE[NQFKDEVDK[LSK..GLHVAT[V[GEGSF[GLLAAKTAKRVTIIDGNFRFR...R
 ANM16_ARATH 409 ITLPP[PERVATY[GDTYRQSI[FEATRK[AIQGKSY[PQCL[VI[DDSLI[LPMALHISNRSRVLSLSPGLQENAA
 ANM7_TRYB2 380 GEMTE[CEGKTT..
 K4E9B9_TRYCR 390 AASP[KTTPTD[ND[AIKTE..NEACEK[VNK[GKK..
 A4H4P9_LEIBR 411 TAP[SK[VDT..[SEAE..[SEPQ..

ANM7_MOUSE 437 RLMKRIFKVNHLEDKISVINKRPELLTAADLEGKKVSL[LG[E[PFTT..SLL[PW[HNL[F[WYVRTS[V[DQHL
 ANM7_HUMAN 437 KLLRKIFKANHLEDKINIIKRPPELLTNEDLQGRKVS[L[G[E[PFTT..SLL[PW[HNL[F[WYVRTA[V[DQHL
 ANM7_XENLA 432 HLMKKLFQVNHLGEKIQVLHKSADSLITADFEDRKIST[LIG[E[PFTT..NLL[PW[HNL[F[WYSRTA[LSTNL
 ANM7_DANRE 432 QVIEQVLHTNSLKDGVQLLGIRAEQQLSIALLDGQNQISV[LMG[E[PFTT..SLL[PW[HNL[F[WYCRTA[V[AQLL
 ANM7_DROME 446 RLIESIVKHNQKLNV.QFLDKVEE..LEDSRLAALITH[FA[E[PFTL..AIL[PW[DNFY[F[GTL[LT[KIKDRL
 ANM7_CAEEL 414 DIFFKYIHYYKLTVN.EIIEKVTS..L..TDSPDI[VLA[E[PFTM..AMN[PW[NHLRF[L[YDVEV[L[KMMH
 ANM16_ARATH 479 RYFEAIADSNGFSKD.RFEYFRDGKTNLAKAYPGKIDL[LIG[E[PFTSGL[GL[PW[QNLRF[WKDRTL[LDSVL
 ANM7_TRYB2 ..
 K4E9B9_TRYCR ..
 A4H4P9_LEIBR ..

ANM7_MOUSE 505 APGAV[VMP[QAA[SHAVIVEF[RDI[WRIRSPC[GDC[E[GFD[VHIMDDMIKHSLDFRESREAEPHPL[W[E[YPC..
 ANM7_HUMAN 505 GPGAV[VMP[QAA[SHAVIVEF[RDI[WRIRSPC[GDC[E[GFD[VHIMDDMIKRALDFRESREAEPHPL[W[E[YPC..
 ANM7_XENLA 500 AKDCT[LP[PLS[SHVVAVEEF[KDI[WRIRSPC[GMC[E[GFD[VSIMDDMIKMNLSNFRESQEAEPHPL[W[E[YPC..
 ANM7_DANRE 500 QPDAT[LP[PRAT[LYVAVEEF[KDI[WRIRSPC[GTC[E[GFD[VSPMDEMIORSLDFRESWEAEPHPL[W[E[YPC..
 ANM7_DROME 510 PEGVK[IS[PCSARI[YALPVEF[LDI[HKIRAPV[GSC[E[GFD[LRLFDEMVERSAEQAVS.LVEAQPL[W[E[YPC..
 ANM7_CAEEL 474 GDELR[V[E[PHMGV[LP[KAIPEKEFED[DI[QNIASDV[GTVN[GFD[LSFFFDEISTKARTAT.DAIVDEQSL[W[E[YAG..
 ANM16_ARATH 548 SEDA[VMP[YKGV[LPDI[WKSRCCL[GSEV[E[GFD[HTLVNTTLGGCGDLP[GKDS[PCLPFF[E[IW[QCGET
 ANM7_TRYB2 ..
 K4E9B9_TRYCR ..
 A4H4P9_LEIBR ..

ANM7_MOUSE 572 RSLSKPQE[IT[TFDFQQPI[PQQPMQSKGT[ME[LTRPGKSHG[A[V[LWM[E[YQLTPDS..T[IS[T[G[LINPAEDKG
 ANM7_HUMAN 572 RSLEPWQ[IT[TFDFQQPV[LP[QLCAEGT[VELRRPGQSHA[A[V[LWM[E[YHLPPEC..T[LST[G[LLEPADPEG
 ANM7_XENLA 567 RALSEPIQ[VM[TFNFTEPVPTEEIRASGS[LNLVRSGQCHG[A[V[LWM[E[YELTKEI..T[VST[G[LIGISEEMG
 ANM7_DANRE 567 RALT[KPCP[VM[TFDFTQCVPEQPISSDGA[VPTGRGRCHG[V[LWM[E[YQLTDDI..S[VSM[G[LTKAVSQEG
 ANM7_DROME 576 RALSEPOQE[VI[SVDFSNFG..QEHSLKGSI[ELKHPRICCNG[V[LWD[WOLVEDNSPRSI[V[S[G[PSEPVVPGE
 ANM7_CAEEL 540 IVKGDAVE[IRFPIDGRVSS...QKCV[NIDNMSSNA[IP[MWM[E[WEFGGIN..L[ST[G[LLSI.SSAG
 ANM16_ARATH 618 KILSKEFT[VME[FD[FSKPI[.GPCSGEVQ[IEFIKPGVCHG[IA[LWM[D[WVMDENST.V[IS[T[G[PDD..
 ANM7_TRYB2 ..
 K4E9B9_TRYCR ..
 A4H4P9_LEIBR ..

ANM7_MOUSE 638 DCCWNPHC[KQA[YFLSTTLDR.VPLNGPRSV.SYVVEFHPL.T[GDI[TMEFRLADTLS
 ANM7_HUMAN 638 GCCWNPHC[KQA[YFFSPAPDPR.ALLGGPRTV.SYAVEFHPL.T[GDI[IMEFRRADTPD
 ANM7_XENLA 633 ECQWYPHRK[QOG[VFSSILNPQTIPAQSPSSV.SYSVTFIPK.EGD[IRMCFEPDF..
 ANM7_DANRE 633 ACEWNPHRK[QOG[FFF[RSAKET..SGDGREDL.SYSLT[FE[PH.SGD[IKMDF[SITES..
 ANM7_DROME 644 FVKWDMFV[RQG[HFP[RRPK..EAITHL.EWSTVFKPL.IGE[I[TFSFGQKKL..
 ANM7_CAEEL 600 VPEWNKG[YQG[YPITAL..RNDKSL.CLHALFDKS.T[GDI[INFQFGKSEDS..
 ANM16_ARATH 679 ..[K[YW[KQG[V[LLGKPVTVR..MEGPSSSIGI[QASLDLSSNS[EL[IVTHTIS..
 ANM7_TRYB2 ..
 K4E9B9_TRYCR ..
 A4H4P9_LEIBR ..

Figure S1 Multiple sequence alignment of PRMT7 from selected organisms. Sequences are from *Mus musculus* (ANM7_MOUSE), *Homo sapiens* (AMN7_HUMAN), *Xenopus laevis* (AMN7_XENLA), *Danio rerio* (AMN7_DANRE), *Drosophila melanogaster* (AMN7_DROME), *Caenorhabditis elegans* (AMN7_CAEEL), *Arabidopsis thaliana* (AMN16_ARATH), *Trypanosoma brucei* (AMN7_TRYB2), *Trypanosoma cruzi* (K4E9B9_TRYCR) and *Leishmania braziliensis* (A4H4P9_LEIBR). The alignment was drawn with Esprint (Gouet *et al.*, 1999) and the conserved sequences are framed. The position of the Zinc coordinating residues are indicated by inverted red stars.

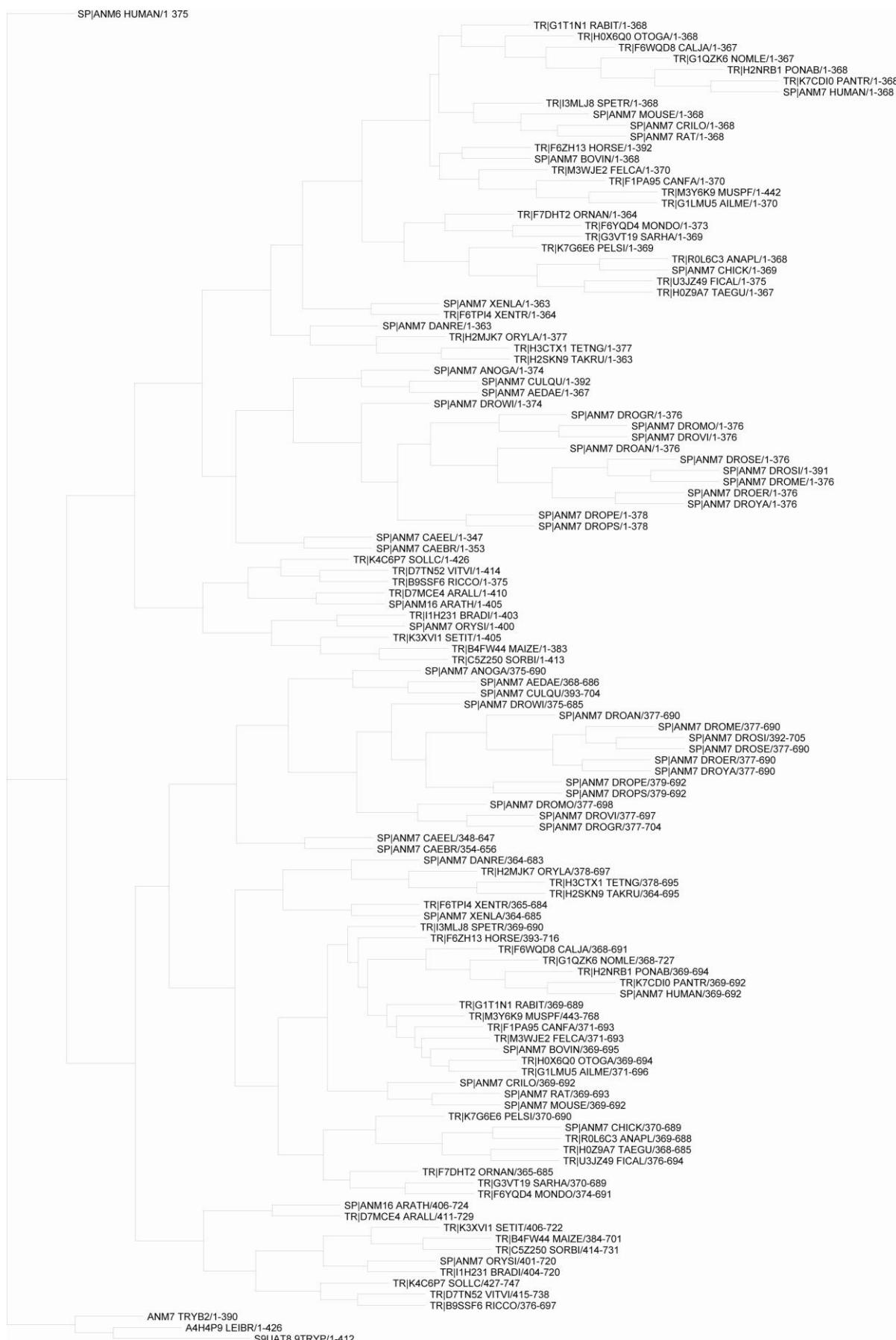


Figure S2 Phylogenetic tree of PRMT7 individual modules. 61 PRMT7 sequences were selected and aligned to identify the boundaries of the PRMT modules and separate the two modules for the 58 PRMT7 with tandem repeats. The individual modules were then realigned using Clustal Omega (McWilliam *et al.*, 2013) and human PRMT6 sequence was added as an outgroup. All gap-containing columns were removed, resulting in an alignment of 208 residues. This alignment was used to compute a distance matrix with *protdist* (Felsenstein, 1989) and a bootstrapping value of 100 replicates. A Neighbor Joining consensus tree was built with *neighbors* (Felsenstein, 1989) and rendered with *drawtree* (Felsenstein, 1989). All steps were performed on the Mobyle@pasteur online platform (Neron *et al.*, 2009).

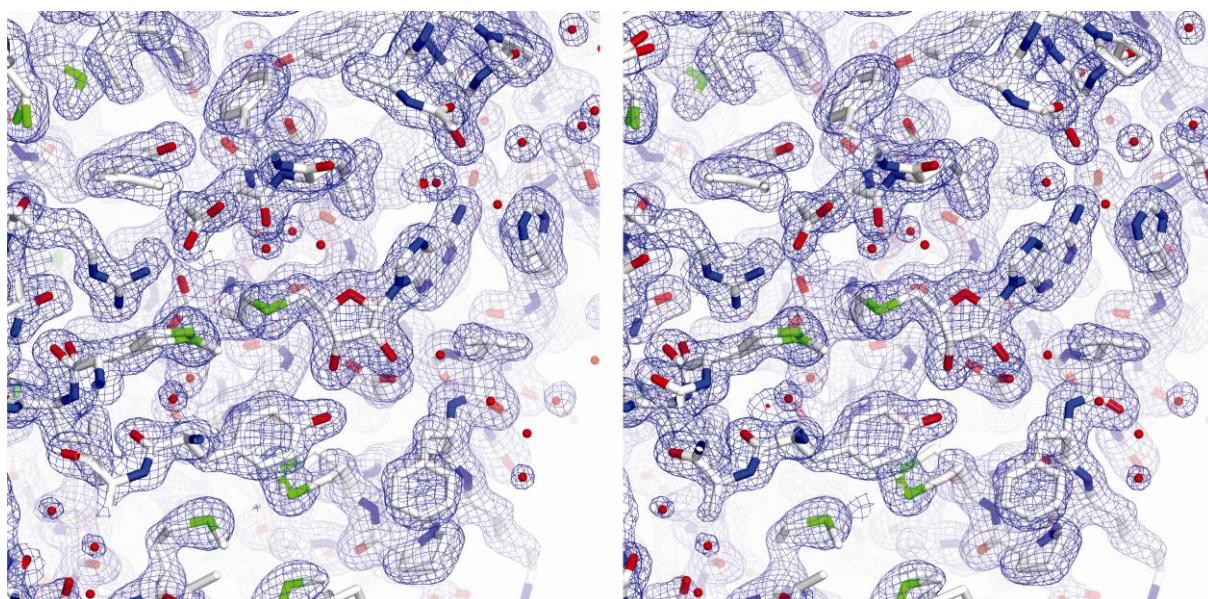


Figure S3 Stereo view of the electron density map of PRMT7 in the area of the AdoHcy molecule. The protein and cofactor are drawn as stick models. The 2mFo-DF_C electron density map is drawn as blue mesh contoured at 0.355 e/Å³ (1.3 σ).

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