

6OMT Group1

	I	II	
Bkor60MT3	SALINECKDKFQGI NSLVDVGGGTGTAA RNLVKAFPHLKC	CTVYDLPHV	IADSPVYPE IQ 232
Cro60MT4	SALVNECKGVFGVKVKT	LDVVG	GGGTGTAVMNI AKAFPSIQCSVYDLAHV IADSNAPFE INR 233
Cro60MT3	SAFLNCKDKF	IGITSLVDVAGGTGTAVMNI	AKAFPHIKCTLYDLPHV IADSPAYPE IDR 229
Cro60MT5	SALVNECKDKF	IGITSLVDVGGGTGTAVMNI	AKAFPHIKCTVFDLPHV IADSVAYPE INR 230
Cro60MT6	SALVNECKDKF	IGITSLVDVGGGTGTAVMNI	AKAFPHIKCTVFDLPHV IADSVAYPE INR 89
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	III	IV	
Bkor60MT3	VPGDMF	KV	IPYADAILMKCILHWDGDECI ELKKCKEALPKEGGKV IVDIVLDVKSEH 292
Cro60MT4	VAGDMF	FEH	IPNADAILMKCILHWDSEECIQILKKCKKAVPKNGGKV IVDIVLDVESQH 293
Cro60MT3	VAGDMF	KY	IPSADAILMKYILHDYDEKCIQILKKCKKAVSEDEGGKV I IDIVLNVD SKH 289
Cro60MT5	VAGDMF	NY	IPSADAILMKSILHGFDDAECTQILKKCKKAVPKDEGGKV IVDIVLNGESEH 290
Cro60MT6	VAGDMF	NY	IPSADAILKYILHDFDDEECTQILKKCKKAVPKDEGGK I IDIVLNVESEH 149
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	V		
Bkor60MT3	PYTKLRLTLDVDMMLNT	GGGKERT	EEEWKKL IQDAGFSYNITQISALQSVIEAFPY 349
Cro60MT4	PYTKMRLTLDLDMMLNT	GGGKERT	EEEWKKL IYAAGFSYNITQISAAQSVIEAFPY 350
Cro60MT3	PLTKFRVSSDLDMMLTT	GGGKERT	KEEWKKLFKAAGYKGYNITEISALQSVIEAFPY 346
Cro60MT5	PYTKMRVTMDMDMM	IAT	EGGKERT EEEWKLLF DAVGRSYKISQISALQSVIEAFPY 347
Cro60MT6	PYTNMRVTMD	IDMM	IGTGGGKERT EEEWKLLF GAAGFRSYNISQISALQSVIEAFPY 206
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6OMT Group II

	I	II
Bkor60MT1	SHTSMVTDVAVVGKEFDHVLDMGTS L I DVGGS GTGVAARA I AKAFPE-VKC AVFDLPHV I A	218
Bkor60MT6	SHTSMVTDVAVVGKEFDHVLDMGTS L I DVGGS GTGVAARA I AKAFPE-VKC AVFDLPHV I A	218
Bkor60MT2	SHTMFV I PAVVGGLMKSKI LDDVKS LVDVGGS GTGAAAKG I ADGFPH-VKC FVMDLAHV I E	224
Bkor60MT7	SHTMFV I PAVVGGLMKSKI LDDVKS LVDVGGS GTGAAAKG I ADGFPH-VKC FVMDLAHV I E	224
Cro60MT2	SHTKCMVPALVTGLVKEKVLDDVTS LVDVGGS SEGI AAKAIKE I ASH-VKC VMDLAHV I E	230
Cro60MT1	SHTKCMVSAVLVGLTKERVLDDVT I LVDVGGS SEGVASKA I VDAASH-VKC I VMDLSHV I E	229
Bkor60MT4	SHTMCMVPALVSGLTKENVLADVAS LMDVGGS SEGI ASKAV I QVVSII VKC I I MDLAHV I D	146
Bkor60MT5	SHTMCMVPALVSGLTKENVLADVAS LMDVGGS SEDI I SWL-----	125
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	III	IV
Bkor60MT1	TAPECEPV TRI EGDVF VSLPKTDLVFMKSVLHDWGDEDCVK I LNKCKEA I ADS KQKG I VL	278
Bkor60MT6	TAPECEPV TRI EGDVF VSLPKTDLVFMKSVLHDWGDEDCVK I LNKCKEA I ADS KQKG I VL	278
Bkor60MT2	SVPKDGGL NFVAGDMF SF I PKADA I FLKSVLHNYDDVCLK I LAKCKEA I PL- TKGKV I L	283
Bkor60MT7	SVPKDGGL NFVAGDMF SF I PKADA I FLKSVLHNYDDVCLK I LAKCKEA I PL- TKGKV I L	283
Cro60MT2	TVPKDARL EYVLAGDMF AS I PQTDAVLLKSVLHNYDGRGLE I LGCKVA I PA- TKGKV I L	289
Cro60MT1	SVPKDPRL DFLAGDMF AFV PQTDAVLLKS I LHNYDDHCVK I LTMCKEA I HS- TRGKV I I	288
Bkor60MT4	TVPNDRPL DFLAGDMF DFVPKADAVLLKS I LHNYDDENCLK I LTKCKEA I PT- KGKGV I	205
Bkor60MT5	----- VTFD VPKADAVLLKS I LHNYDDENCLK I LTKCKEA I PT- KGKGV I	171
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	V	
Bkor60MT1	VE I VMDAVSTDEEFSAKLGMEMDMLVT VAGKER SEQEWQSLFKAAGYSRYH I TPIVA I E	338
Bkor60MT6	VE I VMDAVSTDEEFSAKLGMEMDMLVT VAGKER SEQEWQSLFKAAGYSRYH I TPIVA I E	338
Bkor60MT2	VE I VVDVE-TLPEFSARCCMDMEMML- MGGKERT KQEWVLLDKAGFSHHE I I PVMA--	339
Bkor60MT7	VE I VVDVE-TLPEFSARCCMDMEMML- MGGKERT KQEWVLLDKAGFSHHE I I PVMA--	339
Cro60MT2	VE I VLETE-NLAEFAPGRLGVDQM I C- MGGKERT KQEWECLLHKAGFTLHNI I PIMANE	347
Cro60MT1	VE I I DTE-NLQEFSSARLGLDMEMLC- MGGKERT KQEWKCLDKVGFSHHDI I PIRAI E	346
Bkor60MT4	VE I VIDTQ-NLPEFSARLGLDMEM I C- MGGQERT KQEWATLLHKAGFDHHT I I PIRAI E	263
Bkor60MT5	VE I VIDTQ-NLPEFSARLGLDMEM I C- MGGQERT KQEWATLLHKAGFDHHT I I PIRAI E	229
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Supplementary Figure S1. Sequence comparison of the group 1 and group II of 6OMTs of *C. robustum* and *B. koreana*. The conserved motif sequences are highlighted with red. The motifs I and IV are S-adenosyl-L-methionine binding (conserved region I) and metal binding (conserved region IV) sites, respectively.