

Supplementary Figure 2

DmGry 347 HFGIYYHKAEE-FVMKRRD-AAMEYAA--MQASSEATPTPI-QNPLSLYTEF--FGIRAVKTKDL-----VAEQQA-----
HsGry 345 NPGFYQAAAY-VAQERKQ-LAKTLCNH--EASVMYNDPDL-ETQTG-VLDF--YQORSWRQCILSFLSDPEKSKVG-----
DrGry 345 NPGFYQAAAY-VAQERKQ-QAGQLCSH--EPGVGYPADPL-ETTSG-ALDF--YQORPWRQCQSIDPPDEKSKQG-----
AtGry 365 YPYYVQLAAH-VLKDKKS-ALELLLSM--SEIAQEDSSSA-SITPSVYVGO--FA-QLEKCEAI-TLHSITDEYT-----
CeGry 361 NPGTHLDDAAASISAANTE-IAALKRNA--PQNVYPSDDPF--ANSS--STVF--FGQRPWRINHEGLA--TAEVAAA-----
Dm130 371 CAPIW-----N-LAKDKLY-ELGKLCGL--LPG-CTPTEQD--HIVVQ-LSSG--IGDAPSEQHQFLQATPQLRDRSPN-----
At130 495 ASLSTGNIPEMFDGRPSFTEGSGLEASPRTPSSLKVOAQPMSRTNSS--PGNFESPLDRPMLAEIFVA--A--HAL-----
Hs130 385 TVGLW-----S-VAIEKLR-SLGLCGL--VSE-KGPNSEDL--NRTVD-LLAG--LGAERPET-----
Tn130 377 TVGLW-----V-VAIEKLR-SLGLCGL--MSE-KGPNSEDL--NRTVD-LLAG--LGAERPETGFFSD-ETLLSDDTLGLACNHFNRFIHFKLSY

DmGry 412 ---NMQLCDQERSYNHSA-----AIHAIISQMAQFKIYKCLRFK-KLAIDMEEELKSGDHAKALTLYSMLPDPYRQEKWTTFDVLK
HsGry 416 ---ILAIQLKERNVVHSE-----IIITLISNVAQFKKYPKRMKS-HLMVMGEEYAKDYTKALKLLDYVMCDYRSEGWNTLLASVLT
DrGry 416 ---ILALQVKERDLVHSE-----LIITLISNVAQFKKYPKRMKS-HLMVMGEEYAKDYTKALKLLDYVMCDYRTERWNTLLASVLT
AtGry 435 ---RYTIS-EAKRVQDSI-----QITAWLKRYSYESTNLKAQRMAA-LCAFEVAREFDLADPNNAKFFFDIAANLYRQEGVTLNEVIGY
CeGry 430 ---VTA--IQRLLVNH-----GVSTLSALAAQYQKYGLRMMK-KVMEMEMANTCANNIEQRLRNFGLVVKDNL--PYSIRKDMHR
Dm130 436 ---RKPCKS-GAEOLKEAGSNQAFQKLYLELAELAISTYKHVTRLSAR-LVGLDLGNFCALNEPHKAVGFDTLLRELKAGNWHMSSQTFE
At130 567 ---RLT--ISDHDLLKTSIIQDFENKYLNTKGAENHRSWKRHGVLVDGETAVCFKHGYDAAANSYKCVALVAGEGWODLAEVLPN
Hs130 434 ---ANTAQS-PYKLLKEAASSVEAFERHYLDSHATIEMTSIGRIRSAK-FVGGDLAEFMRKKAPOKAEIYLQGALKNYLAGEWALPTGHTTRKQ
Tn130 457 FTVNSLQS-PYKLLKEAASSVEAFERHYLDSHATIEMTSIGRIRSAK-FVGGDLAEFMRKKAPOKAEIYLQGALKNYLAGEWALPTGHTTRKQ

DmGry 495 TLRCALLSQAADVIACSVEALSLR-HQSDQSERILILENLWQ-----VFOGVPPM--PKTQLT---PEAQLWTSALANV-KSPIQIDL
HsGry 499 ALKCSYLMAQLKDYITYSLEELGRA-STLKDDQKSRIEKNLIN-----VLMNESPD--PEPDCDILAVKTAQKLWADRISLAGSNIFTIGV
DrGry 499 ALKCSYLMAQLKDYITYSLEELGRA-STLKDDQKSRIEKNLIN-----VLMNESPD--PEPDCDILAVKTAQKLWADRISLAGSNIFTIGV
AtGry 517 LRECSRNLDAKDFVEFSELEMVALP-VTSYENSGNLRNKNYGP--GGPATISGRESIHQEVFLLVCREAELLSSTEG--SGFKLATDSPLHTEI
CeGry 509 ATWAAAYATSIQDVAKCCMQMCPAY--SEVLPSDCVKGLD-----VLDGKPPGSPFFNDDISQEQQLHTYQLQWQHVLO--EHPFAVQVA
Dm130 527 LANCYRKMCDSLATKTKCSSISCCA-ELET-LVRFYFDFELKSLKTLKTLTSAQPSIE--N-----ANVCVTE
At130 626 LAQCOKILDDQAGMSSCVRLSLDKGLFSSKERQAFQSEVVT-----LAHSEMKN-----PVPPLDV
Hs130 525 LAECOKHLQEIENLQTSLSLASHD-HLT-EEERKHFCQELD-----PASQPSDS--P-----GHKIVLPM
Tn130 551 VAECCOKLLERTDEQLQTSLSLASHD-HLT-EEERKHFCQELD-----PASQPSDS--P-----GHKIVLPM

DmGry 573 DKVND---VVMCATFER--VQLSNDLLOQLIVRVLTDIPLRIRSFHVILADAGNP
HsGry 582 QDFVP---FVQCKAKFHA--PSFHVVPVQFDIYLKADCPHPFRFSKICVSNQ--E
DrGry 582 QDFVP---FVQCKAKFHA--PSFHVVPVQFDIYLKADCPHPFRFSKICVSNQ--E
AtGry 606 DLVSLRPLRVLLASVAFHD--QMIKPHALCSFTLSLLSHLELPEVIDHEVQFNQS--T
CeGry 591 SKIAE--LFLTETRVSLDQ-QTVEQDQSKVAVRVEIVSKIEQVIRLNDVSVHLKAKKF-
Dm130 592 DHF-RIL--D--IEVVKPII--QDDYILVQLKVESLYERGVVAENVKLCYELEASS
At130 713 SSLIT---PSG--NTGPPL--QLCDGDPGNLSVTVMSSGFFDDITLDSLSLTLVATNN-
Hs130 503 HSFAQ--LRD--LHFDPNSAVVHVGVLCVEITMYSQMPVPHVEQIVUNVHFSI-E
Tn130 608 DNLSH---LRD--LHFDPNSAVVHVGVLCVEITMYSQMPVPHVEQIVUNVHFSI-E

DmGry 1175 NPSAVPIFGVFCIRWRANCKEENE-----SKFVIRGLDIAEPLNINYCTIEEK-MFVKMPMAFKVVLKKNPT
HsGry 973 IEGGV-ATGHYIISWKRKTSAMENIPIIT-----TVIITPHVIVENIPLHVNADLPSF-GRVRESLPVKYHLQNKTT
DrGry 973 GTSTV-ASGHYIISWKRKTSAMENIPIIT-----TVIITPHVIVENIPLYVHAEVSPF-GRVRESLPVRYHLENRT
AtGry 1033 RTPKL-GLGSIHLKWRREGGNITEAYVS-----TKHKLPEVNVVEASPLVMSLDSPPY-AILGEPFTYAVRICNQT
CeGry 952 DESET-PLGRMSVWRRAVP--NSCPVR-----SVAPICRIPVLACPLISISSHKTNPAIVROPIECFCEFKSHS
Dm130 986 HFVIKYASLSQPDVWRTYGCAFDLV-----DYTIFKLOAQLP-----NELCLRTVCNMNLKTKV-
At130 1123 DHSET-DTEGRDL---VFK--SAIVLQ-----RPVLDPCLTGFLP-----LPSDGLRUGKLTIMQWRVERLK
Hs130 1003 SR-QS-VFFVWELKWTTEPPPSLHCRFSVGFSPASEEQLSISLKPYTEFKVENFFLYNVKAEIIP-----PSGMEYCRTGSLCSLEVLITRLS
Tn130 1062 SK-HS-VFCLWEVRWKDNLPSCLQCFVSTDFSPLNQDV-SV-FKLHGHQFQLERVTLLYSVRADILP-----PAGEQHCRCGLLCKLEVFITRLS

DmGry 1241 THVLHL-----IANLS-ISKTDNFCISGKQLDI--SIMAYEEKELVYNYLPLQVCGWQELPVLSTIENY--KADPOKK-D-----
HsGry 1041 DVQD-----VEIS-VEPSDAFMPSGLKQIRL--RILPGTEQEMLYNFYPLMACYQQLPSLNINLLR--FPNFT-----
DrGry 1041 DVQD-----VEIS-VEPSDAFMPSGLKQIRL--RILPGTEQEMLYNFYPLMACYQQLPSLNINLLR--FPNFT-----
AtGry 1101 QLQD-----AKFG-LADAQSFVLSGSHSNTV--SVLPKSEHVLSYKLVPLTCEQOOLPKITTSAR--YAA-----
CeGry 1019 KEAVE-----ISTN-FDLNDVFMPSGERKVTM--TVLPGARTRRVTVVVMALSAARLNFPKISIKSPQ--ISDQT-----
Dm130 1044-----HENPYTDLMYEVLNDQNLWAVCGRSAGVVM--KDVDSHSISLDMVPLSTCFPLMPSIRITSKYT--AGGKS-----
At130 1180 EFKLEVDK-DEALTESDEHFSTKLMYEVVDNNSNNAVCGKSSCGVIMSPVAARATHRKHVHEVMPLFAGLYLPLFDVRVFKYLPHSHAHSSQOLDADSWI
Hs130 1091 DFKLEVDK-DEALTESDEHFSTKLMYEVVDNNSNNAVCGKSSCGVIMSPVAARATHRKHVHEVMPLFAGLYLPLFDVRVFKYLPHSHAHSSQOLDADSWI
Tn130 1148 EPAEGEMAEERSRSLDGLKTKMLYQVADSNNSNNAVCGKSSCGVIMSPVAARATHRKHVHEVMPLFAGLYLPLFDVRVFKYLPHSHAHSSQOLDADSWI

DmGry 1310-----S-----Q-----N-----ALLDELVORALPKRVFVLPPLKO-----DTS-IAAA
HsGry 1105-----NQLLRRFIPSTFVKPQGRMD-----DTS-IAAA
DrGry 1105-----SOLLRRFIPSTFVKPQGRNG-----DAS-IEAA
AtGry 1163-----EFQPSAVASSVVFVSAPOA-----EKAISTSK
CeGry 1083-----LQSLRTEAAIFVLPKAKD-----L-APHP
Dm130 1111-----K-----TDGHSKVFHFPFGQVYNSTRSMQIHVIASVAGDQ
At130 1256-----SN-----PSGHLVGVLPQLSS-----SYC-LPVK
Hs130 1185 ENDSLVSVDKGGDDQPDSSSLKRSVSHSACSSEH--KGLPMPRLQALPAGQVFNSSSGTQVLVLSQDDH-----VLE-VSVT
Tn130 1243 ENDSLVSVDKGGDDQPDSSSLKRSVSHSACSSEH--KGLPMPRLQALPAGQVFNSSSGTQVLVLSQDDH-----VLE-VSVT