

S2 Fig

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                *           20           *           40           *           60           *           80           *           100
PxGATad : MCNLPKPFHSVCRCLCSFCGDNCSVDKLPIDRDRDKKSRLESEMIMSYLSIMVSPADPLPQV-VCGSCAHLDEPHTFRELSHKSERLLEQFLQY----- : 93
BmGATad : MCNLPKPYHSVCRCLCSFCGDNCSVDKLPIDRDRDKKSRLEWEMITTDLSMMVSPEDMLPQV-VCGSCAQLDEPHTFRELSHKSERLLEQFLQY----- : 93
TcGATad : ----- : -
AaGATad : -----MCLYCYWKLWQHRYRILEILSQSSEKLEHLIASSPASIAAKASAEQDA-IAALQALRNNNHHTAKSVTVLTKTHLQNLQLEANSVSVI : 86
HsapGATad : ----- : -
PhcGATad : MSNVLPKPFYELCRCLCSGCDG----VKLSLFGEEAISRKFLFKIMCLSIMVREITLNFVMVGFSSLSVRIAVYSTLHKVSKSDSLPSPICHRCVYKLD : 95
DmGATad : MNNVPHKFRQVCRCLCLTLVN-ECDVAVLQIYDNNSSHNSAPDRISADFRGVANRANCFSCALSPPNCSCIVDNPVLSANKNERRQGTVPVPIPIPVSVF : 99

                *           120          *           140          *           160          *           180          *           200
PxGATad : ---ANSLSPKPEEIVVKTGAKLEEMRPLEPEGEYEAR----YSER-SPDSTDTEK-AESRRAAVALLQIKNYDPTKYQVK-EQDSDHIVFNSVGLPAPA-- : 181
BmGATad : ---AFSLSPKPEEILSITAAKLEEITKPLNDNDYEHATKHKYABIGSPDSTEEMKNLESQAAVTLQIKNYDPSKYVVKTEEPRTFNPSVSLPSPS-- : 188
TcGATad : -----MKRSNAVLESMMN-----ASTILKABDTFNSITISLRTPEPES- : 37
AaGATad : PIESMKITSSSNQQQQQHPISITQTIHLHHPQQQQQVFPQQQIQQLPKQQQQQQQQQQQLIQVKNLTQLQEHLETAALVLMDISKVIISPPSSNPQSP- : 185
HsapGATad : ----- : -
PhcGATad : VLHDFREVSRRKSEVILKQVLYGMDQLKNGKANPENVECLPTTKDLVTVLPETGEDNCLSQEPLKEESEKMFETINKNLFEEEDKDTITLNSILEPTKLLK : 195
DmGATad : VFPVSPQIQSTLHHHQNTKIHYPSPVPSAADKASERERQCQLESIDIAERSTVFKQSQSSDHEHIEHISGETPSPSASLSQSQKSEPMREEEHHQHNN : 199

                *           220          *           240          *           260          *           280          *           300
PxGATad : -----ERAREVMHCNAVIDIISKAVAVK-----REQEE-----TLYKRVSEKYPNAEFSDEQFP--YTP--HTP : 236
BmGATad : -----ERASEVMHCNAVIDIINKAVEVAQ-----RENEESQKFTDYTGVIDRTHANVTVDVYTYREYTDHNA : 253
TcGATad : -----AKEQNPHTTEPTDLR-----YPP : 56
AaGATad : -----SLIAEQQQQKQQSHQQYQHSINNNNQ-----PQLQSKSVIKPHEVYLLNSLKRSPSSEEMDLTKRVRKVEP : 253
HsapGATad : ----- : -
PhcGATad : KSLVSLLENSNVGKTKSNDLESDVVEKIK-----ESDKEEVKINDKSKELSKDDSLKLEKCLLNGSNGVYK : 267
DmGATad : NQQSGRETSVNTNITSGTDNYGKEHGRDSSSPHLTPQIFNCLSIKALPNDGLPNVVGDCRQKLDSEKFRMMAHNSQIALKEFLINISKNLRPDPNDL : 299

                *           320          *           340          *           360          *           380          *           400
PxGATad : LAPHPAPTPPD-DDRAEKEMDLSVYSAVKNEPAE-----EKELDRDITYRSIAHNEASNYSEESKERTHPH----KSKDNNVSDDCSLSSS----- : 320
BmGATad : VYVFNQATSPCSLDRENRREIDSHYSSGKNEIAEKTEQTRDQSRSPFKMTMHNKVSFVDEYKQHIYDQSVNKMMLTKDTASVVEECSSQSS----- : 348
TcGATad : DSEFNISIPSPSIAPSPGEGAMQDDCPNQPADLSN-----KKPENLTCVPEIDFIKEEVN-----DNASYSN----- : 119
AaGATad : NILSPPLPATLVKKNVIKREHMDDMAVDDQASQHSADSSDSGRQMDISSQDAGSECTTDDLKRSNNNNNNNNHHHHHHHHHQHQHQMD----- : 348
HsapGATad : ----- : -
PhcGATad : SNNEPSKYQNEENKNTESDIEGNEINALEKEVQKIEIKDIYENGLDNTLNTYRRTVTIVLNEKCKVENEENDI DIKKENNLVENEDESSD----- : 362
DmGATad : ETKLDAILKASSEIAAKALTEISTFSKVYDHSKLDSSIQPLDRKIEISNQEMPAHSLYPSLFSKITMKSQKSKAMSGSSHSQSDSKLQKDSIEKY : 399

                *           420          *           440          *           460          *           480          *           500
PxGATad : ESDPDRLQMDISQMSQDDPEETQSARSTQSSPQPNHEDNTDKESLWQALHRQNN---GRGG-ATQLRRRLINSHLGMTVSP----- : 399
BmGATad : GSDPDRLQMDISQMSQDDPEETQSARSTQSSPQPHDGEQDKESLWQALHRQNN---GRSG-ATQLRRRLINSHLGMTVSP----- : 426
TcGATad : SSDPERLEVDMSQGVBEHSN---STTASATSPVDNVPDDEEASLWRALSHNGYNPNVPLSG-ASQLRRLITCKLGMSTIP----- : 199
AaGATad : HHIGRETPDSMNSLEEQHLLQQAQIHLSSQFGALADGADPATTQWLQALQNTNLVINGAGNATQLRKLINAATLGLQFSPSIQTTPGVLKQTESN : 448
HsapGATad : -----MFDDFSREB-----CVNCGAMSTELWRDGTGHYLCNACGLYHKMN--GINRPLIKPQRRLSAS----- : 59
PhcGATad : EGQLVIADGGIDAGGKMTVVVVTPEGKYIEFGRNRIYGEREREAAEVLQAINSYQLGPPKGLASNLRLKTLFCNNRNTRENSVLM----- : 447
DmGATad : ENLQQLETAAVLMDISKRIVISPPCSNPFCSAAVDTSIKSVIKSKRPSNQNEIQDGVIDLSLKKQKNDYSNQRNAARHHPFCQTPMLDIQSHLR : 499

                *           520          *           540          *           560          *           580          *           600
PxGATad : -----LRA---APPAPHQPANGVNSPNGD----- : 420
BmGATad : -----LRASTSP-TPSAVQPPVNGSVSPNGE----- : 451
TcGATad : -----APPFVLDRVSSSPSEPLINMETNPK----- : 223
AaGATad : RNSGQS-----GRRKQSCPSRTPEVGENSPNTMEALKLITTSNKASGVGVPTIVTNNNR : 501
HsapGATad : ----- : -
PhcGATad : -----NCTNFQKNDIEKNGSTIYNKRKRS----- : 471
DmGATad : SEEDFNQYSITINQVGGSDFKSKAPKASTGSLDSDSDSHKLEMDITSSINDRKTDPDLSSDHATDAATTLQNLQALARSAAKSKEDNPAQOIFRNMMS : 599

                *           620          *           640          *           660          *           680          *           700
PxGATad : -----WSSG-RG-AVAGTARRKQSFPARAQVPEAAPP--PPWPQNNASENQEPSDS-TTASNAYRGG---NRVELSCSN : 487
BmGATad : -----WPASGRGSNVAGTARRKQSFPARAQVTPQDPSTNNSTWQQ-AAADNQEGETEVGSGVGGNRS---ARVELSCSN : 522
TcGATad : -----PSTGRRKQSYPTKASIEDRSRPARDDGEDYIPDFTGNSPWCNLQIIVKGGKGAGM-ARVLDLSCTN : 288
AaGATad : SSSSPVHLDAASQLNRRANILFRKTTDGSPPGVLLPGVIDQNSGAVSQLVAAQQAQQAQQQQQQSQSPQQQQQQQGNHNSQKDMTCN : 601
HsapGATad : -----YPVKTVQEINGKVPNTYDEIAGEDDEIGEEIHIPEFGIPSTESSHPFPRIDFPNLIKAKDKSKD-IKRTDLSCTN : 67
PhcGATad : QPFAPVPVSTVFTKVPPEPIALLKDLSEAGSKSKPCRRKQSFPTKDCIDVVNENVTDYTTSEAPPDCKKRRNINIFNAIPG---AQKDMSCSN : 546
DmGATad : ----- : -

                *           720          *           740          *           760          *           780          *           800
PxGATad : CGTHHTTIWRRDARGEMVNCAGLYYKLGVPVPRPTAMRRDTITRRRRKFRD-PTNRKRRGNTACAEPVEIAPVPGEGTTEDDYPRRTGEEQDYRRGR : 586
BmGATad : CGTHHTTIWRRDTRGEMVNCAGLYYKLGVPVPRPTAMRRDTITRRRRKFRD-SKHSRNRKRRSGSAMTNPEVS-----EGG-----AA : 600
TcGATad : CGTQTTTIWRRNRGEMVNCAGLYYKLGIDRPHMRRDTITRRRRKRAAEARNEKDKREYPTINNQFKAP-----KKG-----HGN : 368
AaGATad : CGTHTTTIWRNRIRGEMVNCAGLYYKLGIVNRPHMRRDTITRRRRKGDKATRRRNIKQEGAEVIDNGVMEG----AADLHALQNHLLIALRDA : 696
HsapGATad : CGTHTTTIWRNRNAGEPVCNACGLYKMLHGVPVPRPLAMRKEGITRRRRKMLNLSKTPAAPSGSESPPASGASS-----NSSNATTSSEEM : 155
PhcGATad : CGTCTTTIWRNRNALGEMVNCAGLYYKLGIVNRPMNRRDTITRRRRKAGEKPSRRRSANSITNGDGPDEMLA-----AL : 623
DmGATad : CGTLTTTIWRRSVRGEMVNCAGLYYKLGIVNRPHSMRRDTITRRRRKELERSKHKHKQMSSCSIETTKQDFLT-----AR : 773

                *           820          *           840          *           860          *           880
PxGATad : GGEAEBAVLAALRRQLQPHLLAALHAHSARPP-----HAQVGS-TADYDEAPLNLVAVHV--TEETH- : 646
BmGATad : GAEGTEAVLAALRRQLQPHLLAALHAHTTRPH-----RHQVGTNAQEYDEAPLNLVAVHVPAAEETH- : 663
TcGATad : AETADTEVLSALRRQLQPHLVVALQGHKTTAYPHLQAANFAHFLLPSTSGSPGGSAPVESDEESIADPLNLSVQMTETESH-- : 451
AaGATad : RATPPNPFMSPAFQHYLRVTONFDPNGATSGGVIVG-----GGEIDAGDSDSPENDIDSCNPLNLVAVQLGGSDNSQH : 770
HsapGATad : RPIKTEFGSSHYGHSSSVSTFTFSVAMSGHGPSIHP---VLSALKLSPQGYAPVSPVSPQTSKQSDSWNSVLWLDASHGDIITA : 236
PhcGATad : RRQISPLDLASLQHNQVPOQTHSNVITVNPFGPP-----ASYSAHIQTAEASDGEDDDMDMSELPLNLSVSLDDDDDES-- : 700
DmGATad : ESLAISGLVFNKFKKIDDTETPAALAKDILSRKK-----SNLPAFNDTCEADLSAPLNLSVENNAKLT-- : 842
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