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EXO70A1    QIFRGFD--SLSDQCFAEVTVS-SVSMLLSFGDAIA----RSKRSPEKLFVLLDM    364
EXO70A2    QILDGVE--SLRDQCFGEVTVN-SVAVLLSFGEAIA----KSKRSPEKLFVLLDM    338
EXO70A3    QILDGVE--PFRDQSFAEITTI-SFGMLLSFGYAIA----ISRRSPEKVFVILDM    292
EXO70B1    RVF--FGFSSAADLSFMEVCRG-STIQLLNFADAIA----IGSRSPERLFKVLDV    335
EXO70B2    RVFSDLPVSSVTDLSFMEVCRG-TTTQLLNFADAIA----LGSRLPERLFKVVDL    319
EXO70C1    AVFPDQDHSSVRKRLFTGLVSA-VTIRFLDFSGAVV----LTKRSSEKLFKFLDM    345
EXO70C2    RIFPGDE-----GNLFCIVTHG-LAIQFLGFAEAVA----MTRRSTEKLFKILDI    390
EXO70D1    HVFESVGAVNIHEACFMETVKG-PAIQLFNFAEAIS----ISRRSPEKLFKILDL    319
EXO70D2    QIFEG----TMEETCFMEIVKT-SALQLFNFPEAIS----ISRRSPEKLFKILDL    307
EXO70D3    QLFDGI-CTAMDETCFMETVKA-SALRLFTFPEAIS----ISRRSPEKLFKILDL    313
EXO70E1    QIFGDLN--EIGLTCFVDTVKA-PMMQLLNFGEAVS----LGPRQPEKLLRILEM    336
Exo70E2    QILGDFE--SISTACFIEISKD-AILSLLNFGEAVV----LRSCKPEMLERFLSM    343
EXO70F1    EIFSSSE--SSKEVCFNETTKS-CVMQLLNFGEAVA----IGRRSSEKLFRILDM    374
EXO70G1    DVFERLG-LNVWMDCFSKIAAQAGMLAFLQFGKTVT----DSKKDPIKLLKLLDI    366
EXO70G2    DVFEDIG-EDVPLRCFGEIASNSVILQLLRFGSRIS----KCKREPPKLIKLLDC    326
EXO70H1    HVFSAS--NSTRESCFYEIANE-AATNLFKFPEFVA----KEKKSHERIFPLMDL    315
EXO70H2    HVFSAS--STIRESCFYEIVNE-AGINLFKFPELVA----EKKPSPERIFRLMDL    314
EXO70H3    EIFESS--VSLREFCFRDISKE-GALLLFGFPETITLRD-KKNPHPEKIFPLLDM    301
EXO70H4    HVFESS--DAIRESCFSDISRD-GALLLFGFPEIINTKTSKKHSPPEKVFRLLDM    307
EXO70H5    HVFSPS--VSVAESCFTEITLD-SALTLFIFPVSVA----RCKKTVEKIFLTLDI    288
EXO70H6    HIFS----SSVAESCFVDITLQ-SALNLFIFSLTVA----KSRKTAEKIFPTLDV    306
EXO70H7    HVFSSS--GLIVESSFTEITQE-GALILFTFPEYASK---IKKLTPEKMFRFLDM    299
EXO70H8    HVFSSSS-STIRESAFAEITSQ-TALALFTFPEKMA----KCRKSPEKIFLTLDV    281
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Fig. S3- Alignment of Arabidopsis EXO70 protein sequences in the region of the exo70a2-2 G319E mutation

Clustal Omega multiple sequence alignment of the whole proteins sequences were trimmed to the region of interest. The EXO70A2 G319 position is marked with red highlight. Conserved residues are marked with "*", ":" marks positions with conservation of amino acids with strongly similar properties, "." marks conservation between weakly similar amino acid properties.