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                 10        20        30        40        50        60        70        80        90       100
Amy1 V1  MKFFLLLSLIGFCWAQYDPHTQYGRTAIVHLFEWRWVDIAKECERYLAPNGFAGVQVSPPNENIVVHSPSRPWWERYQPISYKICSRSGNEDEFRDMVNR
Amy1 V2  MKFFLLLSLIGFCWAQYDPHTQYGRTAIVHLFEWRWVDIAKECERYLAPNGFAGVQVSPPNENIVVHSPSRPWWERYQPISYKICSRSGNEDEFRDMVNR
Amy2a1   MKFVLLLSLIGFCWAQYDPHTSDGRTAIVHLFEWRWVDIAKECERYLAPKGFGGVQVSPPNENVVVHNPSRPWWERYQPISYKICTRSGNEDEFRDMVTR
Amy2a2   MKFVLLLSLIGFCWAQYDPHTSDGRTAIVHLFEWRWVDIAKECERYLAPKGFGGVQVSPPNENVVVHNPSRPWWERYQPISYKICTRSGNEDEFRDMVTR
Amy2a3   MKFVLLLSLIGFCWAQYDPHTSDGRTAIVHLFEWRWVDIAKECERYLAPKGFGGVQVSPPNENVVVHNPSRPWWERYQPISYKICTRSGNEDEFRDMVTR
Amy2a4   MKFVLLLSLIGFCWAQYDPHTSDGRTAIVHLFEWRWVDIAKECERYLAPKGFGGVQVSPPNENVVVHNPSRPWWERYQPISYKICTRSGNEDEFRDMVTR
Amy2a5   MKFVLLLSLIGFCWAQYDPHTSDGRTAIVHLFEWRWVDIAKECERYLAPKGFGGVQVSPPNENVVVHNPSRPWWERYQPISYKICTRSGNEDEFRDMVTR
Amy2b    MKFVLLLSLIGFCWAQYDPHTSDGRTAIVHLFEWRWVDIAKECERYLAPKGFGGVQVSPPNENIVIHNPSRPWWERYQPISYKICTRSGNEDEFRDMVTR

                110       120       130       140       150       160       170       180       190       200
Amy1 V1  CNNVGVRIYVDAVINHMCGVGAQAGQSSTCGSYFNPNNRDFPGVPYSGFDFNDGKCRTASGGIENYQDAAQVRDCRLSGLLDLALEKDYVRTKVADYMNH
Amy1 V2  CNNVGVRIYVDAVINHMCGVGAQAGQSSTCGSYFNPNNRDFPGVPYSGFDFNDGKCRTASGGIENYQDAAQVRDCRLSGLLDLALEKDYVRTKVADYMNH
Amy2a1   CNNVGVRIYVDAVINHMCGAGNPAGTSSTCGSYLNPNNRREFPAVPYSAWDFNDNKCN---GEIDNYNDAYQVRNCRLTGLLDLALEKDYVRTKVADYMNH
Amy2a2   CNNVGVRIYVDAVINHMCGAGNPAGTSSTCGSYLNPNNRREFPAVPYSAWDFNDNKCN---GEIDNYNDAYQVRNCRLTGLLDLALEKDYVRTKVADYMNH
Amy2a3   CNNVGVRIYVDAVINHMCGAGNPAGTSSTCGSYLNPNNRREFPAVPYSAWDFNDNKCN---GEIDNYNDAYQVRNCRLTGLLDLALEKDYVRTKVADYMNH
Amy2a4   CNNVGVRIYVDAVINHMCGAGNPAGTSSTCGSYLNPNNRREFPAVPYSAWDFNDNKCN---GEIDNYNDAYQVRNCRLTGLLDLALEKDYVRTKVADYMNH
Amy2a5   CNNVGVRIYVDAVINHMCGAGNPAGTSSTCGSYLNPNNRREFPAVPYSAWDFNDNKCN---GEIDNYNDAYQVRNCRLTGLLDLALEKDYVRTKVADYMNH
Amy2b    CNNVGVRIYVDAVINHMCGSGNPAGTSSTCGSYLNPNNRREFPAVPYSAWDFNDNKCN---GEISNYNDAYQVRNCRLSGLLDLALEKDYVRTK-------

                210       220       230       240       250       260       270       280       290       300
Amy1 V1  LIDIGVAGFRLDASKHMWPGDIKAILDKLHNLNTKWFSQGSRPFIFQEVIDLGGEAVSSNEYFGNGRVTEFKYGAKLGKVMRKWDGEKMSYLKNWGEGWG
Amy1 V2  LIDIGVAGFRLDASKHMWPGDIKAILDKLHNLNTKWFSQGSRPFIFQEVIDLGGEAVSSNEYFGNGRVTEFKYGAKLGKVMRKWDGEKMSYLKNWGEGWG
Amy2a1   LIDIGVAGFRLDAAKHMWPGDIKAVLDKLHNLNTKWFSQGSRPFIFQEVDQYIIFKILILLFNYSVSSFPPFIPPHTSMYLSAVT
Amy2a2   LIDIGVAGFRLDAAKHMWPGDIKAVLDKLHNLNTKWFSQGSRPFIFQEVIDLGGEAIKGSEYFGNGRVTEFKYGAKLGTVIRKWNGEKMSYLKNWGEGWG
Amy2a3   LIDIGVAGFRLDAAKHMWPGDIKAVLDKLHNLNTKWFSQGSRPFIFQEVIDLGGEAIKGSEYFGNGRVTEFKYGAKLGTVIRKWNGEKMSYLKNWGEGWG
Amy2a4   LIDIGVAGFRLDAAKHMWPGDIKAVLDKLHNLNTKWFSQGSRPFIFQEVIDLGGEAIKGSEYFGNGRVTEFKYGAKLGTVIRKWNGEKMSYLKNWGEGWG
Amy2a5   LIDIGVAGFRLDAAKHMWPGDIKAVLDKLHNLNTKWFSQGSRPFIFQEVIDLGGEAIKGSEYFGNGRVTEFKYGAKLGTVIRKWNGEKMSYLKNWGEGWG
Amy2b    ----------------------------------------------------VIDLGGEAIKGSEYFGNGRVTEFKFGAKLGTVIRKWNGEKMSYLKNWGEGWG

                310       320       330       340       350       360       370       380       390       400
Amy1 V1  LMPSDRALVFVDNHDNQRGHGAGGASILTFWDARLYKMAVGFMLAHPYGFTRVMSSYYWPRNFQNGKDVNDWVGPPNNNGKTKEVSINPDSTCGNDWICE
Amy1 V2  LMPSDRALVFVDNHDNQRGHGAGGASILTFWDARLYKMAVGFMLAHPYGFTRVMSSYYWPRNFQNGKDVNDWVGPPNNNGKTKEVSINPDSTCGNDWICE
Amy2a1   
Amy2a2   LVPSDRALVFVDNHDNQRGHGAGGSSILTFWDARMYKMAVGFMLAHPYGFTRVMSSYRWNRNFQNGKDQNDWIGPPNNNGVTKEVTINADTTCGNDWVCE
Amy2a3   LVPSDRALVFVDNHDNQRGHGAGGSSILTFWDARMYKMAVGFMLAHPYGFTRVMSSYRWNRNFQNGKDQNDWIGPPNNNGVTKEVTINADTTCGNDWVCE
Amy2a4   LVPSDRALVFVDNHDNQRGHGAGGSSILTFWDARMYKMAVGFMLAHPYGFTRVMSSYRWNRNFQNGKDQNDWIGPPNNNGVTKEVTINADTTCGNDWVCE
Amy2a5   LVPSDRALVFVDNHDNQRGHGAGGSSILTFWDARMYKMAVGFMLAHPYGFTRVMSSYRWNRNFQNGKDQNDWIGPPNNNGVTKEVTINADTTCGNDWVCE
Amy2b    LVPSDRALVFVDNHDNQRGHGAGGSSILTFWDARMYKMAVGFMLAHPYGFTRVMSSYRWNRNFQNGKDQNDWIGPPNNNGVTKEVTINADTTCGNDWVCE

                410       420       430       440       450       460       470       480       490       500
Amy1 V1  HRWRQIRNMVAFRNVVNGQPFANWWDNDSNQVAFGRGNKGFIVFNNDDWALSETLQTGLPAGTYCDVISGDKVDGNCTGIKVYVGNDGKAHFSISNSAED
Amy1 V2  HRWRQIRNMVAFRNVVNGQPFANWWDNDSNQVAFGRGNKGFIVFNNDDWALSETLQTGLPAGTYCDVISGDKVDGNCTGIKVYVGNDGKAHFSISNSAED
Amy2a1   
Amy2a2   HRWRQIRNMVAFRNVVNGQPFSNWWDNNSNQVAFSRGNRGFIVFNNDDWALSATLQTGLPAGTYCDVISGDKVDGNCTGLRVNVGSDGKAHFSISNSAED
Amy2a3   HRWRQIRNMVAFRNVVNGQPFSNWWDNNSNQVAFSRGNRGFIVFNNDDWALSATLQTGLPAGTYCDVISGDKVDGNCTGLRVNVGSDGKAHFSISNSAED
Amy2a4   HRWRQIRNMVAFRNVVNGQPFSNWWDNNSNQVAFSRGNRGFIVFNNDDWALSATLQTGLPAGTYCDVISGDKVDGNCTGLRVNVGSDGKAHFSISNSAED
Amy2a5   HRWRQIRNMVAFRNVVNGQPFSNWWDNNSNQVAFSRGNRGFIVFNNDDWALSATLQTGLPAGTYCDVISGDKVDGNCTGLRVNVGSDGKAHFSISNSAED
Amy2b    HRWRQIRNMVAFRNVVNGQPFANWWDNNSNQVAFSRGNRGFIVFNNDDWALSATLQTGLPAGTYCDVISGDKVDGNCTGLKVNVGSDGKAHFSISNSAED

                510
Amy1 V1  PFIAIHAESKI
Amy1 V2  PFIAIHAESKI
Amy2a1   
Amy2a2   PFIAIHADSKL
Amy2a3   PFIAIHADSKL
Amy2a4   PFIAIHADSKL
Amy2a5   PFIAIHADSKL
Amy2b    PFIAIHADSKL
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Supplemental Figure 1. ClustalW alignments of predicted protein sequences of mouse amylase proteins: Amy1 V1 (NP_031472.2), Amy1 V2 (NP_001110505.1), Amy2a1 (XP_011238675.1), Amy2a2 (NP_001153624.1), Amy2a3 (NP_001153623.1), Amy2a4 (NP_001153622.1), Amy2a5 (NP_001036176.1) and Amy2b (NP_001177332.1). Bold indicates mis-aligned residues. 53 non-identical residues between Amy1 and the full-length Amy2 proteins (Amy2a2, Amy2a3, Amy2a4 and Amy2a5), including a 3 residue deletion in Amy2 proteins. All full-length Amy2 proteins are of identical sequence. Amy2b is of identical sequence except for deletion of 55 internal residues, plus a single residue substitution (A for S). Amy2a1 is a 3'-end truncated protein with an additional 35 residues at its 3'-end. ClustalW multiple alignment parameters: open gap penalty, 30; extend gap penalty, 5.0; delay divergent, 30%; gap distance, 4; similarity matrix, gonnet.