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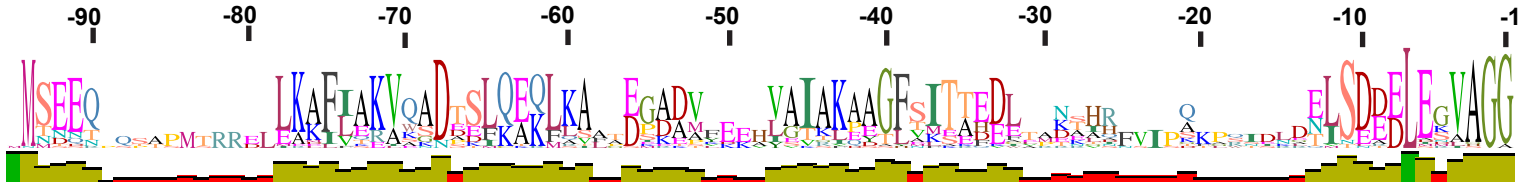


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LahA1     MNEN----------LEKFFQKVSADEKIQAKMKSFTDIDEAYD--YAVSIQDGYSKEEFEAVMVEIT----K-GSAENDEISDDDLENVAGG   IISEARGLKAVNGNSDNLTNFAAGAI
LahA2     MNEN----------LKMFLQKVAADEKIQAKMKSFTDIDEAYE--YAVSIQDGYSKEEFEAVMAKSA----K-GSTINDEISDTDLESVAGG   TITEGAKGFR-ASAGDEVDYSLFAATAI
LahA3     MNDS----------LKEFLKKLSEDEELCAKLESAGDSDKAYE--IAKTIQEGFTKEEFVDAMTRINNSISA-----DGEINDDDLISVAGG   LTTDEETLLMDGTFLGSAIVAASSAGAV
LahA4     MNEN----------LKMFLQKVAADEEKQAKMQSFTDMDEAYE--YAATVQEGFTKEEFTELMTKIK----DFASQNNDEINDDDLANVAGG   TSTSACIARAATAATAAVTMSLLAV
LahA5     MNEN----------LKLFLQKVAADKEIQAKMQSFDDIDEAYK--YAVTVQDGFTKEEFEELMTKLS----K-ATSESDEISDADLSRVAGG   MTTTDEAGLIGSLTTVASVAALSLSLSAM
LahA6      MNER----------IKDLFTEIEKNPELKKKLQALPDEDASKDKAIEIAKEYGFVLTREDL--EGDI----N------GEISNEELMMVAGG   LRMEDYARDASGSGFVLTAIRKALM
LahA7   MNSNEN----------LKKFLEEASKNEELKTKLAALTDKDTAVEKAIEIGKEYGFNLTAEDF--ETTD----G------AEVSLDELEQIAGG   WCHYAASGGLKYPCPCSIVGQGLLH
LahA8     MNEN----------MKKFLEEASKNEKLKTKLAALTDKDTAVEKAIEIGKEYGFNLTTEDF--ETTD----G------EEVSDDDLKTVGGG   VIANGREFAGLLKIPIIYGGVN
LahA9     MSEN----------MRKFLKEVENNAELKARLSALPDEEESKKKVVEIAKEYGFTLTAEDC--EVGN----A------ENISDDELEAVAGG   SCLFGGVENGCGCIFAGVGGA

ProcA 1.1 MSEEQ----------LKAFIAKVQADTSLQEQLKA--EGADV----VAIAKAAGFSITTEDLE-KEHR----Q-------TLSDDDLEGVAGG   FFCVQGTANRFTINVC
ProcA 1.2 MSEEQ----------LKAFIAKVQADPSLQEQLKA--EGADV----VSIAKAAGFSITTEDL--NSHI----T----TKLNLSEEELEGVAGA   MDCVSSTAQQTECRPGGPRASYCWDDLR
ProcA 1.3 MSEEQ----------LKGFLSKVQSDASLQEQLKV--EGADV----VAIAKAAGFSITTEDL--NSHR----Q-------NLSEDELEGVAGG   GLCTLTSNLAAVCCGGCRRATSE
ProcA 1.4 MSEEQ----------LKAFLTKVQADTSLQEQLKA--EGADP----VAIAKAAGFAITTEDL--NSHR----Q-------NLSDDELEGVAGG   GSSYRNGKCTFGPACPS
ProcA 1.5 MSEEQ----------LKAFIAKVQADTSLQEQLKV--EGADV----VAIAKAAGFSITTEDL--NTHR----Q-------NLSDDELEGLHGA   GPGCTGGWWAFTDCTAGGGSCEG
ProcA 1.6 MSEEQ----------LKAFIAKVQADTSLQEQLKV--EGADV----VAIAKAAGFSITTDDFERNTHR----Q-------TLSDDELEGVAGG   KSTNGCGCKPGHTLSSFLCTLECWL
ProcA 1.7 MSEEQ----------LKAFIAKVQADTSLQEQLKV--EGADV----VAIAKASGFAITTEDL--KAHQ----A---NSQKNLSDAELEGVAGG   TIGGTIVSITCETCDLLVGKMC
ProcA 2.1 MSEEQ----------LKAFIAKVQADSSLQEQLKA--EGADV----VAIAKAAGFSITTEDWDQRPVR----------TLSDEELEGAAGG   CCITGESPGSAPTNDYKCTKGRGPGGCY
ProcA 2.2 MSEEQ----------LKAFIAKVQADPSLQEQLKA--EGADT----VAIAKAAGFSITTEDL--KEHR----Q-------TLSDDELESVAGG   GNDTVITKEYSCYVTSDKGCC
ProcA 2.3 MSEEQ----------LKAFLEKVKADTSLKEKLKAAKSPEDV----VGIAKEHGHEFTADKI----------S-------QLSEEELEGVAGG   MQAGSCNWICFVNGVYINDGRMANKAI
ProcA 2.4 MSEEQ----------LKAFLAKVQADASLQEQLKA--EGADV----VAIAKAAGFSITTEDL--NSHR----QI------EMTDDELEGVAGG   GCGLGARRETAQCWLSH
ProcA 2.5 MSEEQ----------LKAFIAKVQGDTSLQEQLKA--EGADV----VAIAKAAGFAITEAEV--KAYQ----T------RNLSDEELDEVAGG   APCRPFTDPIYCWRKGEQTIIGRGRSCLYPE
ProcA 2.6 MSEEQ----------LKAFIAKVQADTSLQEQLKA--EGADV----VAIAKAAGFAISTEDL--NNHR----Q-------NLSDDELEGVAGG   GICVYVNCVLSIRETPSVI
ProcA 2.7 MSEEQ----------LKAFIAKVQADTSLQEQLKA--EGADV----VAIAKAAGFSIATEDL--KTHR----Q-------TLSDDDLEGVAGG   AGCYPICDWTSPTRS
ProcA 2.8 MSEEQ----------LKAFLTKVQADTSLQEQLKI--EGADV----VAIAKAAGFSITTEDL--NSHR----Q-------NLSDDELEGVAGG   AACHNHAPSMPPSYWEGEC
ProcA 2.9 MSEEQ----------LKAFIAKVQADPSLQEQLKA--EGADV----VAIAKAAGFTITTEDL--KTAR----Q-------TLSDDDLEGVAGG   YEDGDYTKSISIVVACCRF
ProcA 2.10 MSEEQ----------LKAFIAKVQADSSLQEQLKA--EGADP----VSIAKAAGFTITTEDL--NSHR----Q-------NLSDEELEGAAGG   AGGTIPSLMTGCGWLTGLCVR
ProcA 2.11 MSEEQ----------LKAFIAKVQADTSLQEQLKA--EGADV----VAIAKAAGFAITKEDL--NSHR----Q-------TLSEDELESVAGG   GRIDTCPAGGGTSEQTGTCC
ProcA 3.1 MSEEQ----------LKAFIAKVQADASLQEQLRT--EGADV----VAIAKAAGFSITTEDL--NSHR----Q-------NLSDDELEGVAGG   GGKMTVRGRDMSCGCQDYWEDDY
ProcA 3.2 MSEEQ----------LKAFIAKVQADASLQEQLRT--EGADV----VAIAKAAGFSITTEDL--NSHR----Q-------NLSDDELEGVAGG   GGGCDGIRITDKQTVADNTIVPCSCFHQ
ProcA 3.3 MSEEQ----------LKAFIAKVQGDSSLQEQLKA--EGADV----VAIAKAAGFTIKQQDL--NAAA----S-------ELSDEELEAASGG   GDTGIQAVLHTAGCYGGTKMCRA
ProcA 3.4 MSEEQ----------LKAFIAKVQGDTSLQEQLKA--EGADV----VAIAKAAGFSITTEDL--NTHR----Q-------TLSDRELEGVAGG   TTAFTGVDTESIAFCCS
ProcA 3.5 MSEEQ----------LKAFLEKVKADTSLQEKLKAAADSDAV----LVIAKDAGFSISADDL--KNAQ----S-------EISEEELESVAGG   AGVTEATIDAGGGCTFNPCCR
ProcA 4.1 MSEEQ----------LKALIAKVQADTSLQEQLKA--EGADV----VAIAKAAGFSITTEDL--KEHR----QTLSVGRQTLSESELEGLAGG   GGGARTKTANVPSDLPVRAPAMSTFAENQT
ProcA 4.2 MSEEQ----------LKAFIAKVQADTSLQEQLKA--EGADP----VAIAKAAGFSITTEDL--KEHR----Q-------ALSDDDLEGVAGG   TIVTVTGALISIAAEC
ProcA 4.3 MSEEQ----------LKAFIAKVQADTSLQEQLKA--EGADV----VAIAKAAGFTITTEDL--NSHR----Q-------NLTDDELEGVAGG   TASGGCDTSMFCY
ProcA 4.4 MSEEQ----------LKAFLEKVKGDTSLQEKLQAAADSDAV----LAIAKEAGFMISADEL--KKAQ----S-------EISEEELESAAGG   RLKSGCHCGTVIRSYSKYC
ProcA s.1 MSEEQ----------LKAFLEKVKADTSLQEKLKAAADSDAV----LVIAKDAGFSISADDL--KNAQ----S-------EISEEELESVAGG   AQSAGGCGICECDNRQSTSCHYPSHG
ProcA s.2 MSEEQ----------LKAFLEKVKADTSLQEKLKAAAGSDAV----LAIAKAAGLMISADDL--TKAQ----S-------EISDAELEDAAGG   GAQGPACCAAMESSDTRCGWVSWVLSEVVPPQ
ProcA t.1                 MQEQLKA--EGADV----IAIAKAAGFSITIEDL--KEHR----K-------TLSDAELEGLAGG   AFNHDWGQTTRNYKCETSYCC

XY33a     MSEEQ----------LKAFLTKVQADTSLQEQLKI--EGADV----VAIAKAAGFSITTEDL--NSHR----Q-------NLSDDELEGVAGG   AACHFLLFSMPPSHVLDIC

AzoA1     MSNDL-AGTPMTRRELEAKIVARAWSDDTFKAKFLA--DPRAMFEEHLGTRFPEALTMTAHEETPDALHFVIPAKPQIDLDELSDEDLEKVAGG   VDLVVTACAVSIVATAAGMLATLSAMQISMYLDLKLNKKPW
AzoA2     MTTET-QTAPMSRRELEAKIVARAWSDEDFKAKFLA--DPKAMFEEHLGTKLPETLVMTAHEETADALHFVIPAKPQIDLDELSDEDLEKVAGG   VDVSLTVFVATVAITAGLSAGVASIGSLLGGLAIPRKW
AzoA3     MTDQT-QSTSMTRRELEAKIVARAWSDEDFKAKFLA--DPKAMLEEHLGTRLPETLVIAAHEETADALHFVIPAKPWSDLDELSDEDLEKVAGG   VDVAEWMLRLRSSPPCPSLPSPPRLRQQ
AzoA4     MTTQTPSSAPMTRRDLEAKIVARAWSDDEFKAKFLA--DPKAMFEEHLGTKLPETLVMTAHEETADAIHFVIPAKPQIDLDELSDEDLEKVAGG   VDVSVTIFTAVMASALSAAATVAVSATATAGLIKW
AzoA5     MTDQT-QSAPMTRRDLEAKIVARAWSDDDFKAKFLA--DPKAMFEEHLGTKLPETLVMTAHEETPDTIHFVIPAKPQIDLDELSDEDLEKVAGG   VDAITTAAIGTALFTLVTGLAASAVTAGVFTYIGGTMAATHKGSW
AzoA6     MTNET-QPTPMSRRELEAKIVARAWSDDDFKAKFLA--DPKAMFEEHLGTKLPETLVMTAHEETPDTIHFVIPAKPRIDLDELSDEDLEKVAGG   VDFVTSIIATAIITASASALVTAPAAAILGTRKW
AzoA7     MTDQT-QSAPMTRRDLEAKIVARAWSDDDFKAKFLA--DPKAMFEEHLGTKLPASLVMTAHEETADTIHFVIPAKPRIDLDELSDEDLEKVAGG   VDIVTTITVTAIISAGVGGAAFSAVATVLAAGGIRGVCAKW
AzoA8     MTNDT-QTAPMTRRELEAKIVARAWSDDAFKAKFLA--DPKAMFEEHLGTKLPETLEITAHEETAEALHFVIPAKPRIDLDELSEEDLEKVAGG   VDALATALVTITISIASMVGTAASAGGVTYLTAKGAKW

HalA2                                                  MVNSKDLRNPEFRKAQGLQFVDEVNEKELSSLAGS   GDVHAQTTWPCATVGVSVALCPTTKCTSQC
LctA                                                     MKEQNSFNLLQEVTESELDLILGA   KGGSGVIHTISHECNMNSWQFVFTCCS
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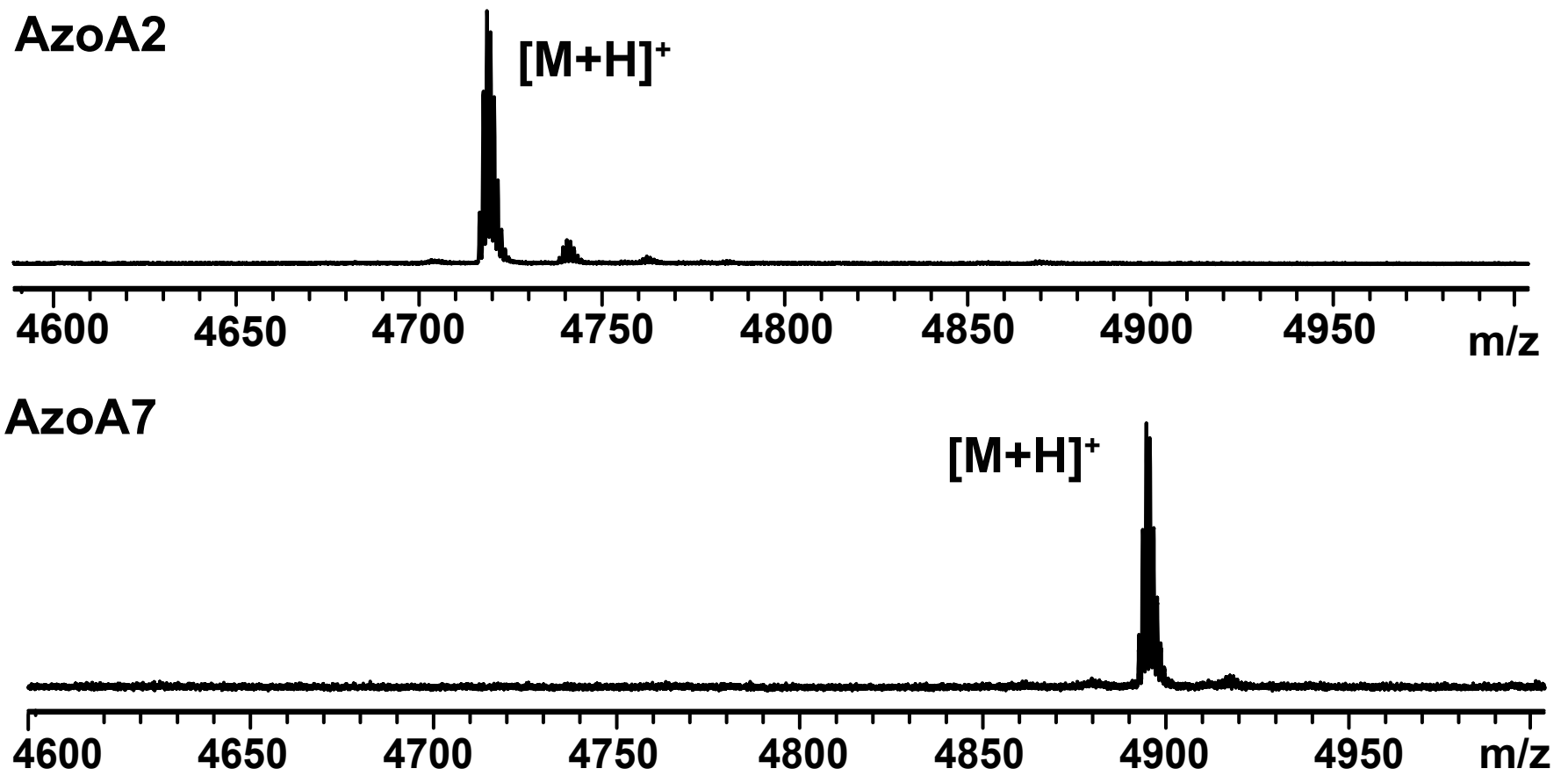
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