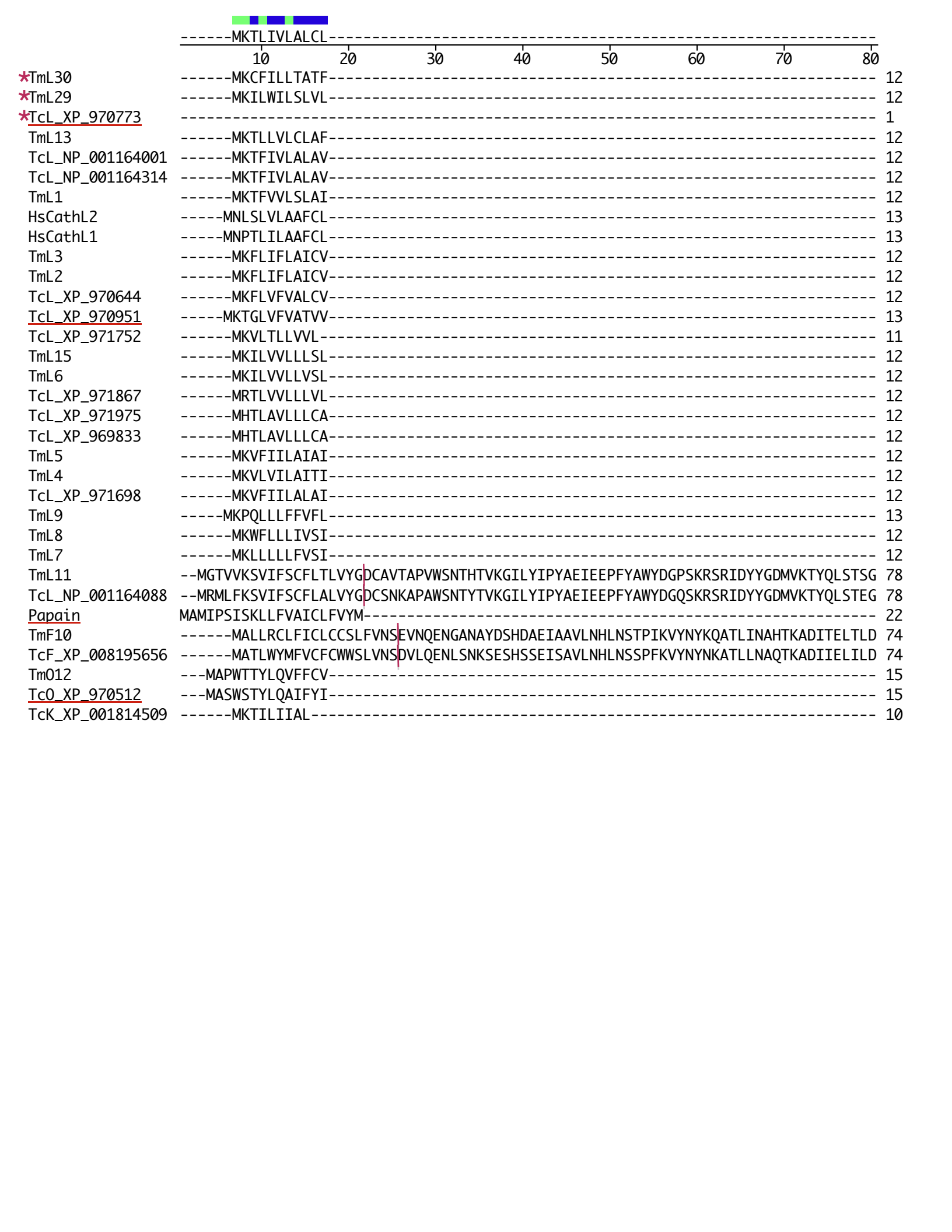
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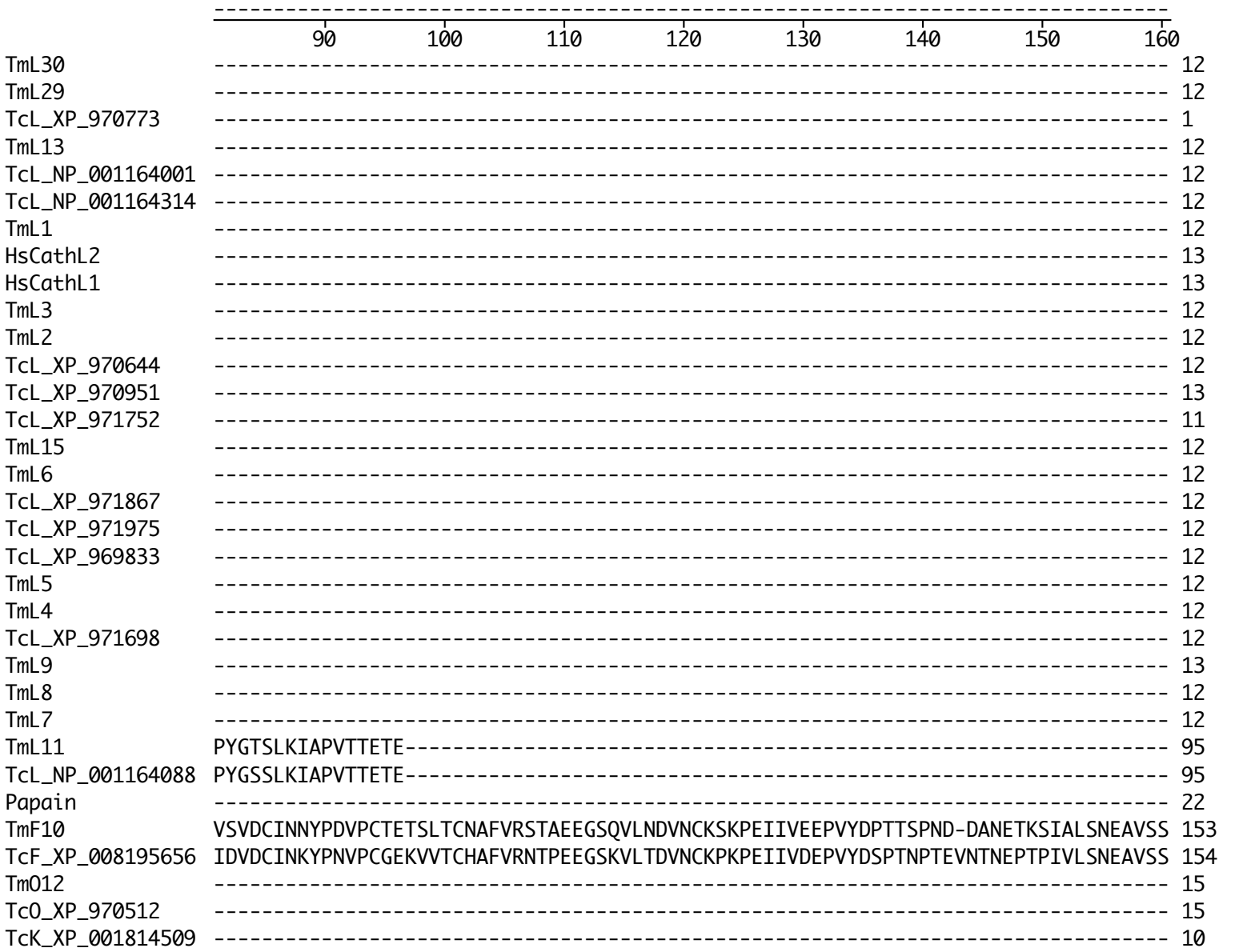
*TmL29 ------MKILWILSLVL---------- 12
*TcL_XP_970773 ---------- 1
TmL13 ------MKTLLVLCLAF---------- 12
TcL_NP_001164001 ------MKTFIVLALAV---------- 12
TcL_NP_001164314 ------MKTFIVLALAV---------- 12
TmL1 ------MKTFVVLSLAI---------- 12
HsCathL2 -----MNLSLVLAAFCL---------- 13
HsCathL1 -----MNPTLILAAFCL---------- 13
TmL3 ------MKFLIFLAICV---------- 12
TmL2 ------MKFLIFLAICV---------- 12
TcL_XP_970644 ------MKFLVFVALCV---------- 12
TcL_XP_970951 -----MKTGLVFVATVV---------- 13
TcL_XP_971752 ------MKVLTLLVVL---------- 11
TmL15 ------MKILVVLLLSL---------- 12
TmL6 ------MKILVVLLVSL---------- 12
TcL_XP_971867 ------MRTLVVLLLVL---------- 12
TcL_XP_971975 ------MHTLAVLLLCA---------- 12
TcL_XP_969833 ------MHTLAVLLLCA---------- 12
TmL5 ------MKVFIILAIAI---------- 12
TmL4 ------MKVLVILAITI---------- 12
TcL_XP_971698 ------MKVFIILALAI---------- 12
TmL9 -----MKPQLLLFFVFL---------- 13
TmL8 ------MKWFLLLIVSI---------- 12
TmL7 ------MKLLLLLFVSI---------- 12
TmL11 --MGTVVKSVIFSCFLTLVYGDCAVTAPVWSNTHTVKGILYIPYAEIEEPFYAWYDGPSKRSRIDYYGDMVKTYQLSTSG 78
TcL_NP_001164088 --MRMLFKSVIFSCFLALVYGDCSNKAPAWSNTYTVKGILYIPYAEIEEPFYAWYDGQSKRSRIDYYGDMVKTYQLSTEG 78
Papain MAMIPSISKLLFVAICLFVYM---------- 22
TmF10 ------MALLRCLFICLCCSLFVNSEVNQENGANAYDSHDAEIAAVLNHLNSTPIKVYNYKQATLINAHTKADITELTLD 74
TcF_XP_008195656 ------MATLWYMFVCFCWWSLVNSDVLQENLSNKSESHSSEISAVLNHLNSSPFKVYNYNKATLLNAQTKADIIELILD 74
TmO12 ---MAPWTTYLQVFFCV---------- 15
TcO_XP_970512 ---MASWSTYLQAIFYI---------- 15
TcK_XP_001814509 ------MKTILIIAL---------- 10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TmL29 12
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TmL13 12
TcL_NP_001164001 12
TcL_NP_001164314 12
TmL1 12
HsCathL2 13
HsCathL1 13
TmL3 12
TmL2 12
TcL_XP_970644 12
TcL_XP_970951 13
TcL_XP_971752 11
TmL15 12
TmL6 12
TcL_XP_971867 12
TcL_XP_971975 12
TcL_XP_969833 12
TmL5 12
TmL4 12
TcL_XP_971698 12
TmL9 13
TmL8 12
TmL7 12
TmL11 PYGTSLKIAPVTTETE 95
TcL_NP_001164088 PYGSSLKIAPVTTETE 95
Papain 22
TmF10 VSVDCINNYPDVPCTETSLTCNAFVRSTAEEGSQVLNDVNCKSKPEIIVEEPVYDPTTSPND-DANETKSIALSNEAVSS 153
TcF_XP_008195656 IDVDCINKYPNVPCGEKVVTCHAFVRNTPEEGSKVLTDVNCKPKPEIIVDEPVYDSPTNPTEVNTNEPTPIVLSNEAVSS 154
TmO12 15
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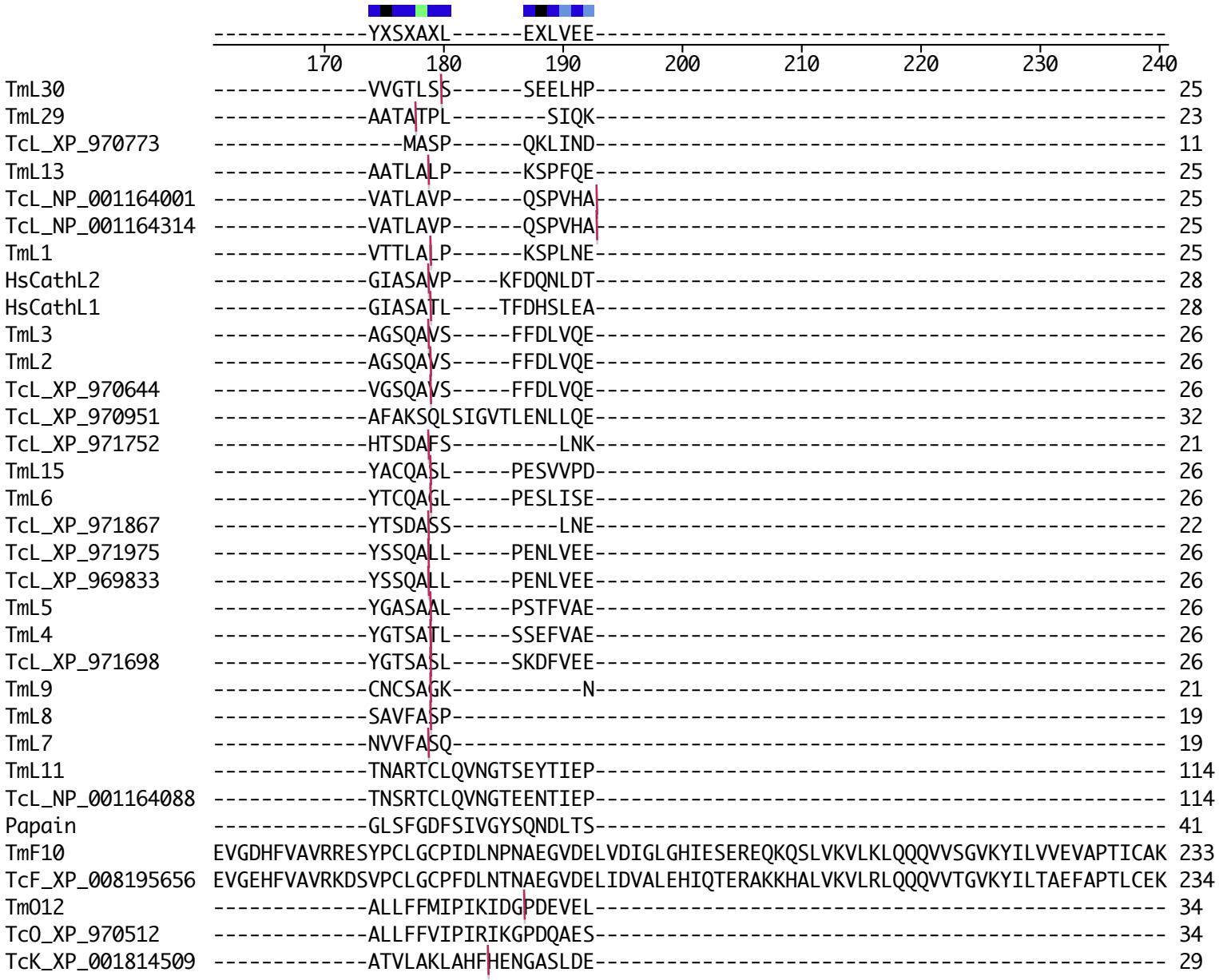
TcK_XP_001814509 10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TmL29 ----------AATATPL--------SIQK---------- 23
TcL_XP_970773 ----------MASP------QKLIND---------- 11
TmL13 ----------AATLALP------KSPFQE---------- 25
TcL_NP_001164001 ----------VATLAVP------QSPVHA---------- 25
TcL_NP_001164314 ----------VATLAVP------QSPVHA---------- 25
TmL1 ----------VTTLALP------KSPLNE---------- 25
HsCathL2 ----------GIASAVP----KFDQNLDT---------- 28
HsCathL1 ----------GIASATL----TFDHSLEA---------- 28
TmL3 ----------AGSQAVS-----FFDLVQE---------- 26
TmL2 ----------AGSQAVS-----FFDLVQE---------- 26
TcL_XP_970644 ----------VGSQAVS-----FFDLVQE---------- 26
TcL_XP_970951 ----------AFAKSQLSIGVTLENLLQE---------- 32
TcL_XP_971752 ----------HTSDAFS---------LNK---------- 21
TmL15 ----------YACQASL-----PESVVPD---------- 26
TmL6 ----------YTCQAGL-----PESLISE---------- 26
TcL_XP_971867 ----------YTSDASS---------LNE---------- 22
TcL_XP_971975 ----------YSSQALL-----PENLVEE---------- 26
TcL_XP_969833 ----------YSSQALL-----PENLVEE---------- 26
TmL5 ----------YGASAAL-----PSTFVAE---------- 26
TmL4 ----------YGTSATL-----SSEFVAE---------- 26
TcL_XP_971698 ----------YGTSASL-----SKDFVEE---------- 26
TmL9 ----------CNCSAGK----------N---------- 21
TmL8 ----------SAVFASP---------- 19
TmL7 ----------NVVFASQ---------- 19
TmL11 ----------TNARTCLQVNGTSEYTIEP---------- 114
TcL_NP_001164088 ----------TNSRTCLQVNGTEENTIEP---------- 114
Papain ----------GLSFGDFSIVGYSQNDLTS---------- 41
TmF10 EVGDHFVAVRRESYPCLGCPIDLNPNAEGVDELVDIGLGHIESEREQKQSLVKVLKLQQQVVSGVKYILVVEVAPTICAK 233
TcF_XP_008195656 EVGEHFVAVRKDSVPCLGCPFDLNTNAEGVDELIDVALEHIQTERAKKHALVKVLRLQQQVVTGVKYILTAEFAPTLCEK 234
TmO12 ----------ALLFFMIPIKIDGPDEVEL---------- 34
TcO_XP_970512 ----------ALLFFVIPIRIKGPDQAES---------- 34
TcK_XP_001814509 ----------ATVLAKLAHFHENGASLDE---------- 29

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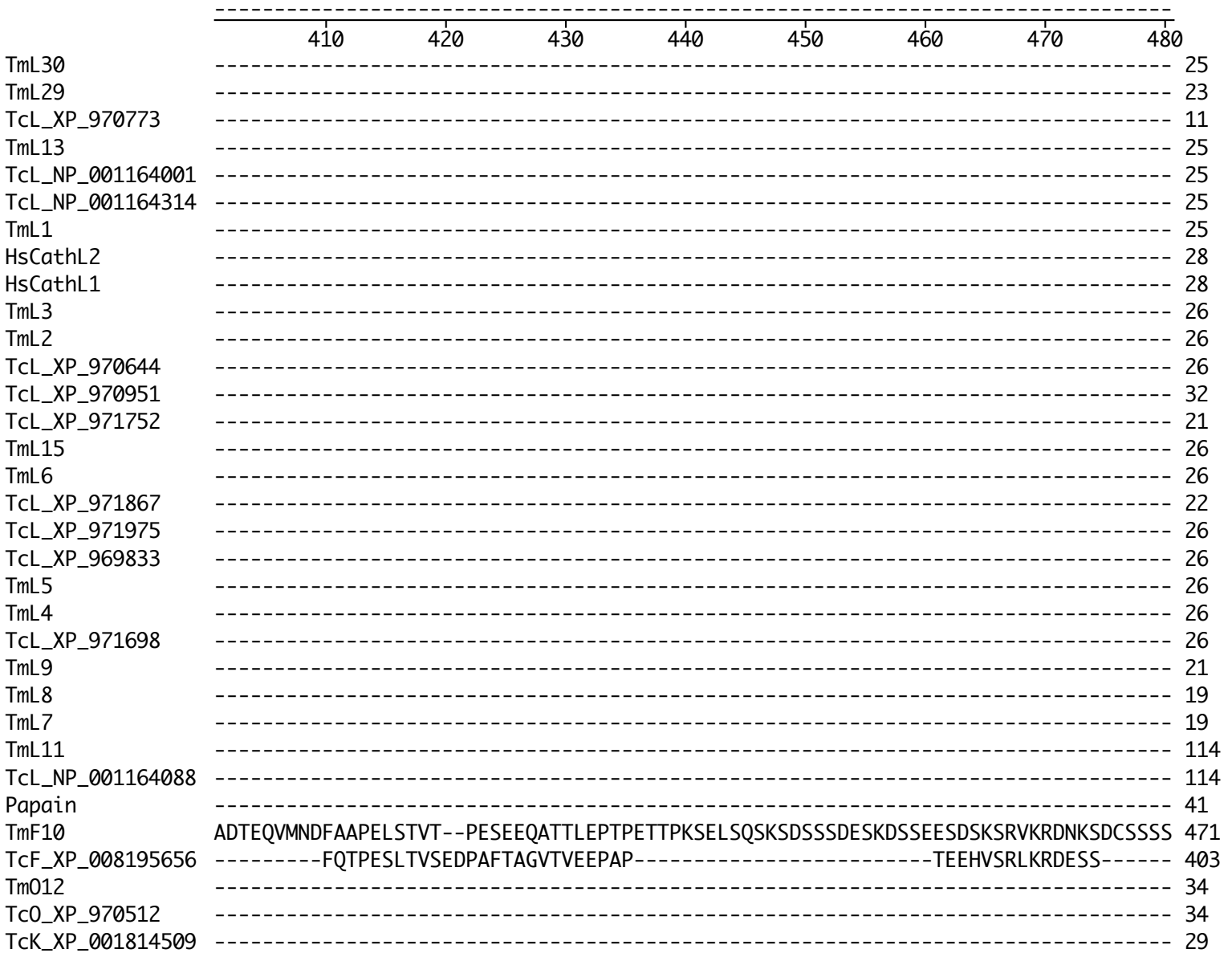
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TmL29 23
TcL_XP_970773 11
TmL13 25
TcL_NP_001164001 25
TcL_NP_001164314 25
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HsCathL2 28
HsCathL1 28
TmL3 26
TmL2 26
TcL_XP_970644 26
TcL_XP_970951 32
TcL_XP_971752 21
TmL15 26
TmL6 26
TcL_XP_971867 22
TcL_XP_971975 26
TcL_XP_969833 26
TmL5 26
TmL4 26
TcL_XP_971698 26
TmL9 21
TmL8 19
TmL7 19
TmL11 114
TcL_NP_001164088 114
Papain 41
TmF10 ADTEQVMNDFAAPELSTVT--PESEEQATTLEPTPETTPKSELSQSKSDSSSDESKDSSEESDSKSRVKRDNKSDCSSSS 471
TcF_XP_008195656 ---------FQTPESLTVSEDPAFTAGVTVEEPAP----------TEEHVSRLKRDESS------ 403
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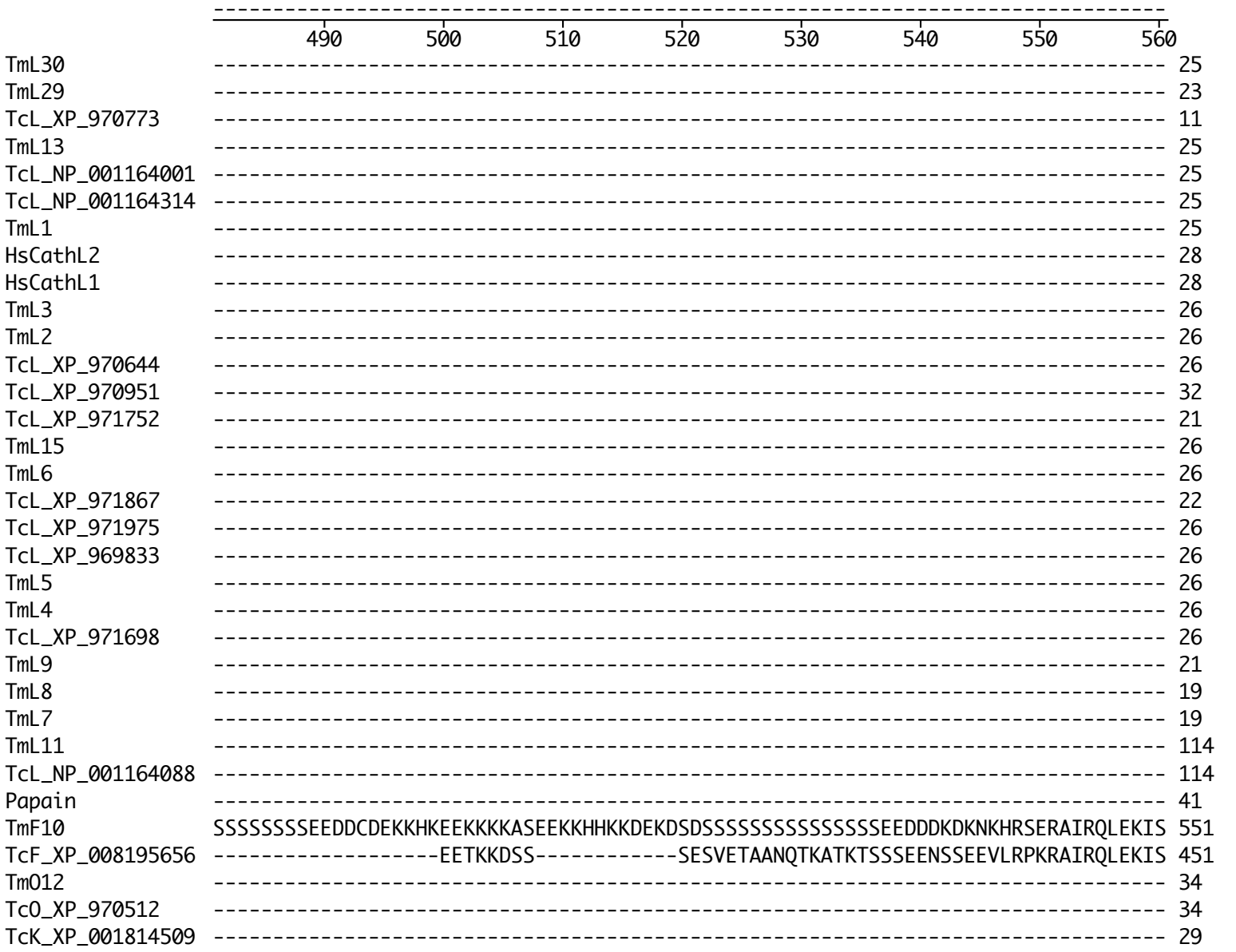
TcK_XP_001814509 29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TmL29 23
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TmL13 25
TcL_NP_001164001 25
TcL_NP_001164314 25
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HsCathL2 28
HsCathL1 28
TmL3 26
TmL2 26
TcL_XP_970644 26
TcL_XP_970951 32
TcL_XP_971752 21
TmL15 26
TmL6 26
TcL_XP_971867 22
TcL_XP_971975 26
TcL_XP_969833 26
TmL5 26
TmL4 26
TcL_XP_971698 26
TmL9 21
TmL8 19
TmL7 19
TmL11 114
TcL_NP_001164088 114
Papain 41
TmF10 SSSSSSSSEEDDCDEKKHKEEKKKKASEEKKHHKKDEKDSDSSSSSSSSSSSSSSSEEDDDKDKNKHRSERAIRQLEKIS 551
TcF_XP_008195656 EETKKDSS SESVETAANQTKATKTSSSEENSSEEVLRPKRAIRQLEKIS 451
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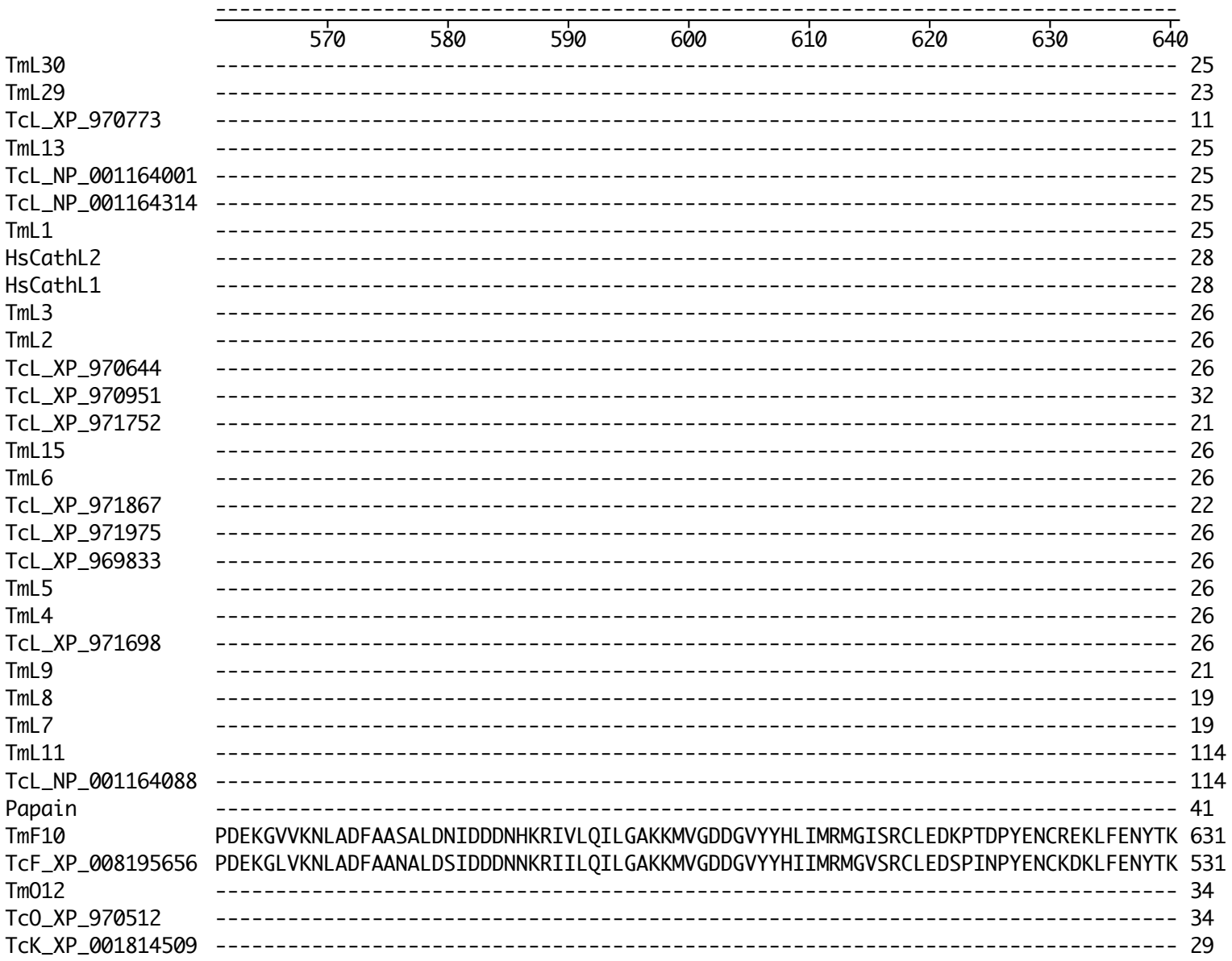
TcO_XP_970512 34
TcK_XP_001814509 29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TmL29 23
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TmL13 25
TcL_NP_001164001 25
TcL_NP_001164314 25
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HsCathL2 28
HsCathL1 28
TmL3 26
TmL2 26
TcL_XP_970644 26
TcL_XP_970951 32
TcL_XP_971752 21
TmL15 26
TmL6 26
TcL_XP_971867 22
TcL_XP_971975 26
TcL_XP_969833 26
TmL5 26
TmL4 26
TcL_XP_971698 26
TmL9 21
TmL8 19
TmL7 19
TmL11 114
TcL_NP_001164088 114
Papain 41
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TcF_XP_008195656 PDEKGLVKNLADFAANALDSIDDDNNKRIILQILGAKKMVGDDGVYYHIIMRMGVSRCLEDSPINPYENCKDKLFENYTK 531
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TcK_XP_001814509 29

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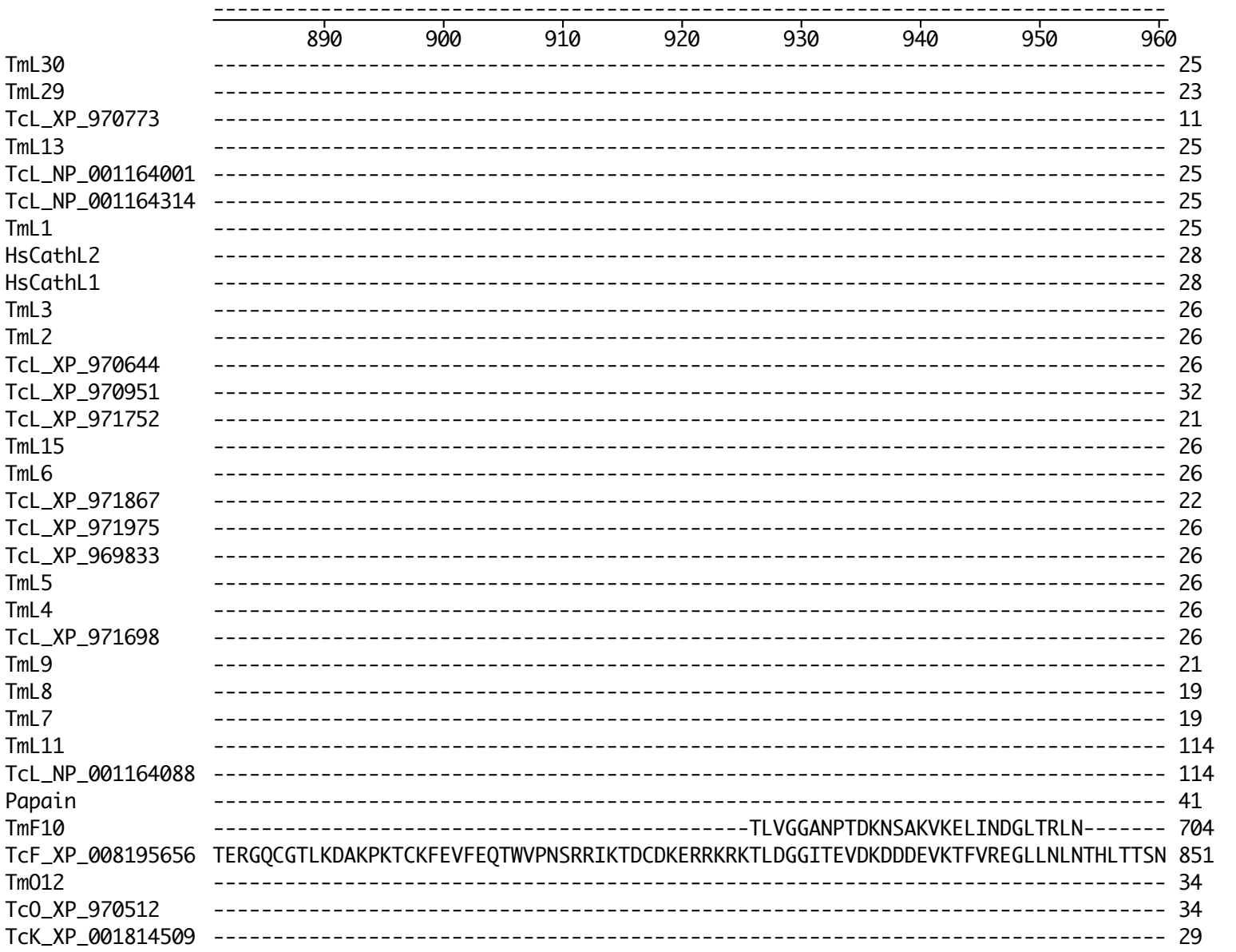
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TmL29 23
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TcL_NP_001164314 25
TmL1 25
HsCathL2 28
HsCathL1 28
TmL3 26
TmL2 26
TcL_XP_970644 26
TcL_XP_970951 32
TcL_XP_971752 21
TmL15 26
TmL6 26
TcL_XP_971867 22
TcL_XP_971975 26
TcL_XP_969833 26
TmL5 26
TmL4 26
TcL_XP_971698 26
TmL9 21
TmL8 19
TmL7 19
TmL11 114
TcL_NP_001164088 114
Papain 41
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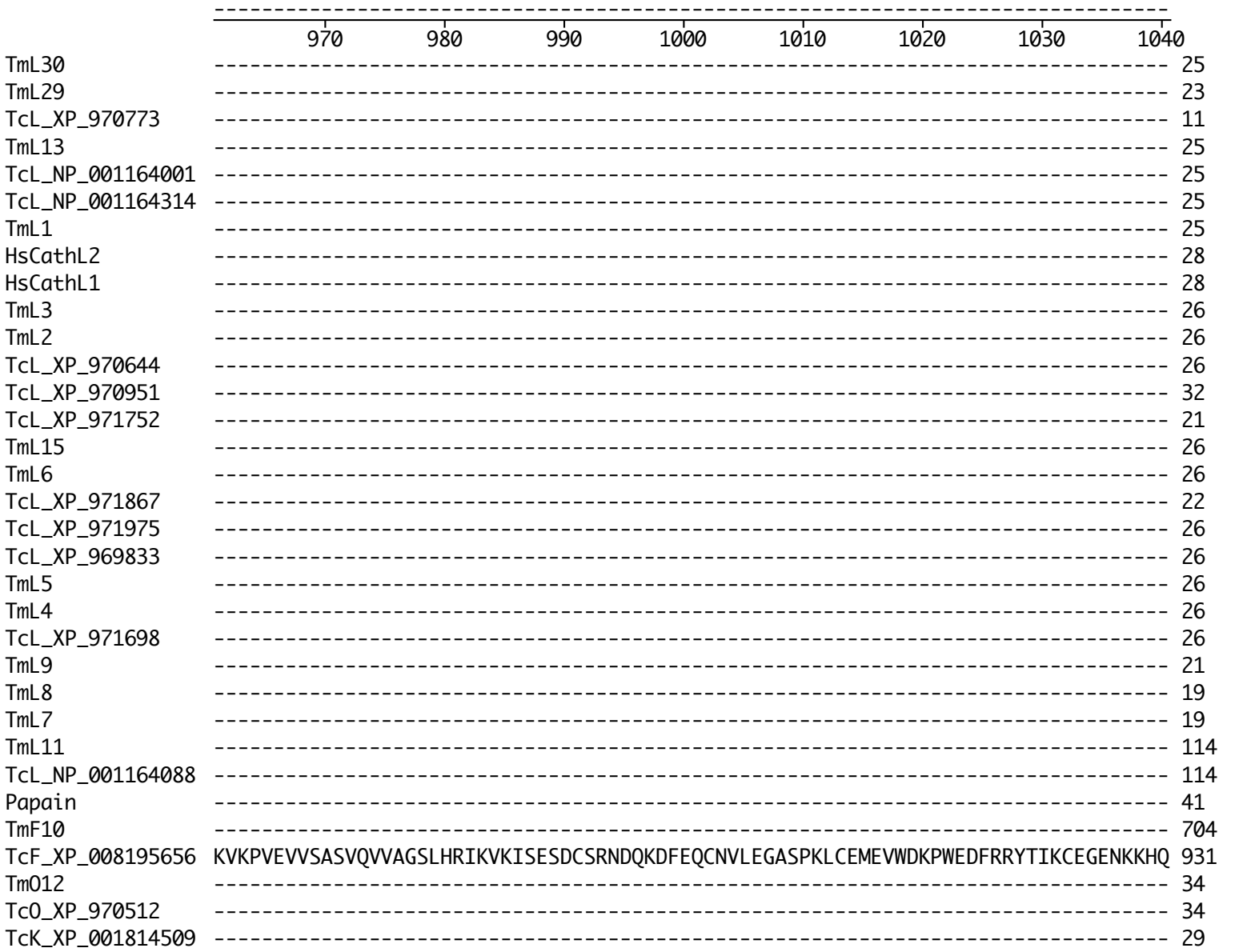
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TmL29 23
TcL_XP_970773 11
TmL13 25
TcL_NP_001164001 25
TcL_NP_001164314 25
TmL1 25
HsCathL2 28
HsCathL1 28
TmL3 26
TmL2 26
TcL_XP_970644 26
TcL_XP_970951 32
TcL_XP_971752 21
TmL15 26
TmL6 26
TcL_XP_971867 22
TcL_XP_971975 26
TcL_XP_969833 26
TmL5 26
TmL4 26
TcL_XP_971698 26
TmL9 21
TmL8 19
TmL7 19
TmL11 114
TcL_NP_001164088 114
Papain 41
TmF10 704
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TmO12 34
TcO_XP_970512 34
TcK_XP_001814509 29

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                1050       1060       1070       1080       1090       1100       1110       1120
TmL30           ------------------------------------------------------------------------------------------ 25
TmL29           ------------------------------------------------------------------------------------------ 23
TcL_XP_970773   ------------------------------------------------------------------------------------------ 11
TmL13           ------------------------------------------------------------------------------------------ 25
TcL_NP_001164001 ------------------------------------------------------------------------------------------ 25
TcL_NP_001164314 ------------------------------------------------------------------------------------------ 25
TmL1            ------------------------------------------------------------------------------------------ 25
HsCathL2        ------------------------------------------------------------------------------------------ 28
HsCathL1        ------------------------------------------------------------------------------------------ 28
TmL3            ------------------------------------------------------------------------------------------ 26
TmL2            ------------------------------------------------------------------------------------------ 26
TcL_XP_970644   ------------------------------------------------------------------------------------------ 26
TcL_XP_970951   ------------------------------------------------------------------------------------------ 32
TcL_XP_971752   ------------------------------------------------------------------------------------------ 21
TmL15           ------------------------------------------------------------------------------------------ 26
TmL6            ------------------------------------------------------------------------------------------ 26
TcL_XP_971867   ------------------------------------------------------------------------------------------ 22
TcL_XP_971975   ------------------------------------------------------------------------------------------ 26
TcL_XP_969833   ------------------------------------------------------------------------------------------ 26
TmL5            ------------------------------------------------------------------------------------------ 26
TmL4            ------------------------------------------------------------------------------------------ 26
TcL_XP_971698   ------------------------------------------------------------------------------------------ 26
TmL9            ------------------------------------------------------------------------------------------ 21
TmL8            ------------------------------------------------------------------------------------------ 19
TmL7            ------------------------------------------------------------------------------------------ 19
TmL11           ------------------------------------------------------------------------------------------ 114
TcL_NP_001164088 ------------------------------------------------------------------------------------------ 114
Papain          ------------------------------------------------------------------------------------------ 41
TmF10           ------------------------------------------------------------------------------------------ 704
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TcK_XP_001814509 ------------------------------------------------------------------------------------------ 29
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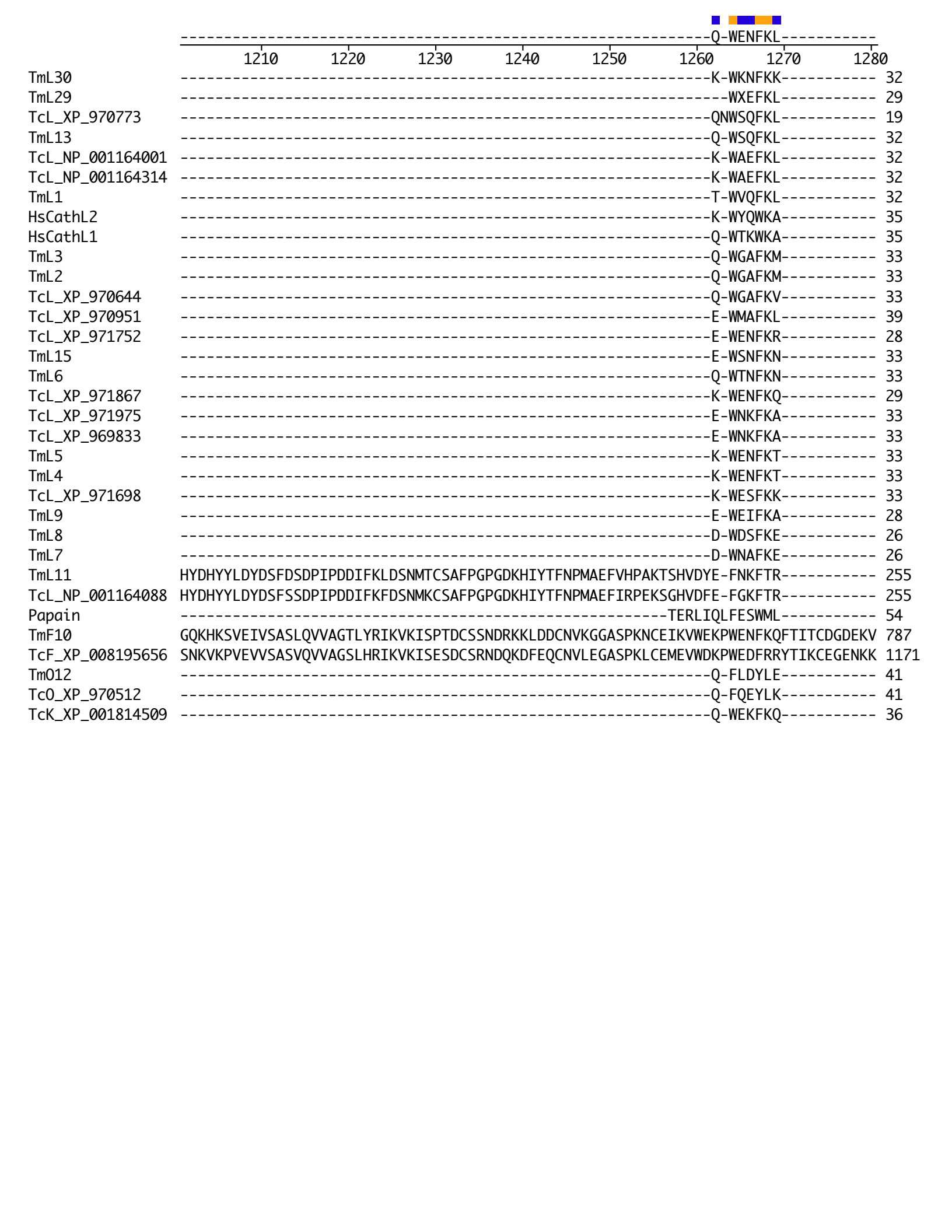
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1240
1250
1260
1270
1280
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TmL29 -WXEFKL 29
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TmL13 Q-WSQFKL 32
TcL_NP_001164001 K-WAEFKL 32
TcL_NP_001164314 K-WAEFKL 32
TmL1 T-WVQFKL 32
HsCathL2 K-WYQWKA 35
HsCathL1 Q-WTKWKA 35
TmL3 Q-WGAFKM 33
TmL2 Q-WGAFKM 33
TcL_XP_970644 Q-WGAFKV 33
TcL_XP_970951 E-WMAFKL 39
TcL_XP_971752 E-WENFKR 28
TmL15 E-WSNFKN 33
TmL6 Q-WTNFKN 33
TcL_XP_971867 K-WENFKQ 29
TcL_XP_971975 E-WNKFKA 33
TcL_XP_969833 E-WNKFKA 33
TmL5 K-WENFKT 33
TmL4 K-WENFKT 33
TcL_XP_971698 K-WESFKK 33
TmL9 E-WEIFKA 28
TmL8 D-WDSFKE 26
TmL7 D-WNAFKE 26
TmL11 HYDHYYLDYDSFDSDPIPDDIFKLDSNMTCSAFPGPGDKHIYTFNPMAEFVHPAKTSHVDYE-FNKFTR 255
TcL_NP_001164088 HYDHYYLDYDSFSSDPIPDDIFKFDSNMKCSAFPGPGDKHIYTFNPMAEFIRPEKSGHVDFE-FGKFTR 255
Papain TERLIQLFESWML 54
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TcF_XP_008195656 SNKVKPVEVVSASVQVVAGSLHRIKVKISESDCSRNDQKDFEQCNVLEGASPKLCEMEVWDKPWEDFRRYTIKCEGENKK 1171
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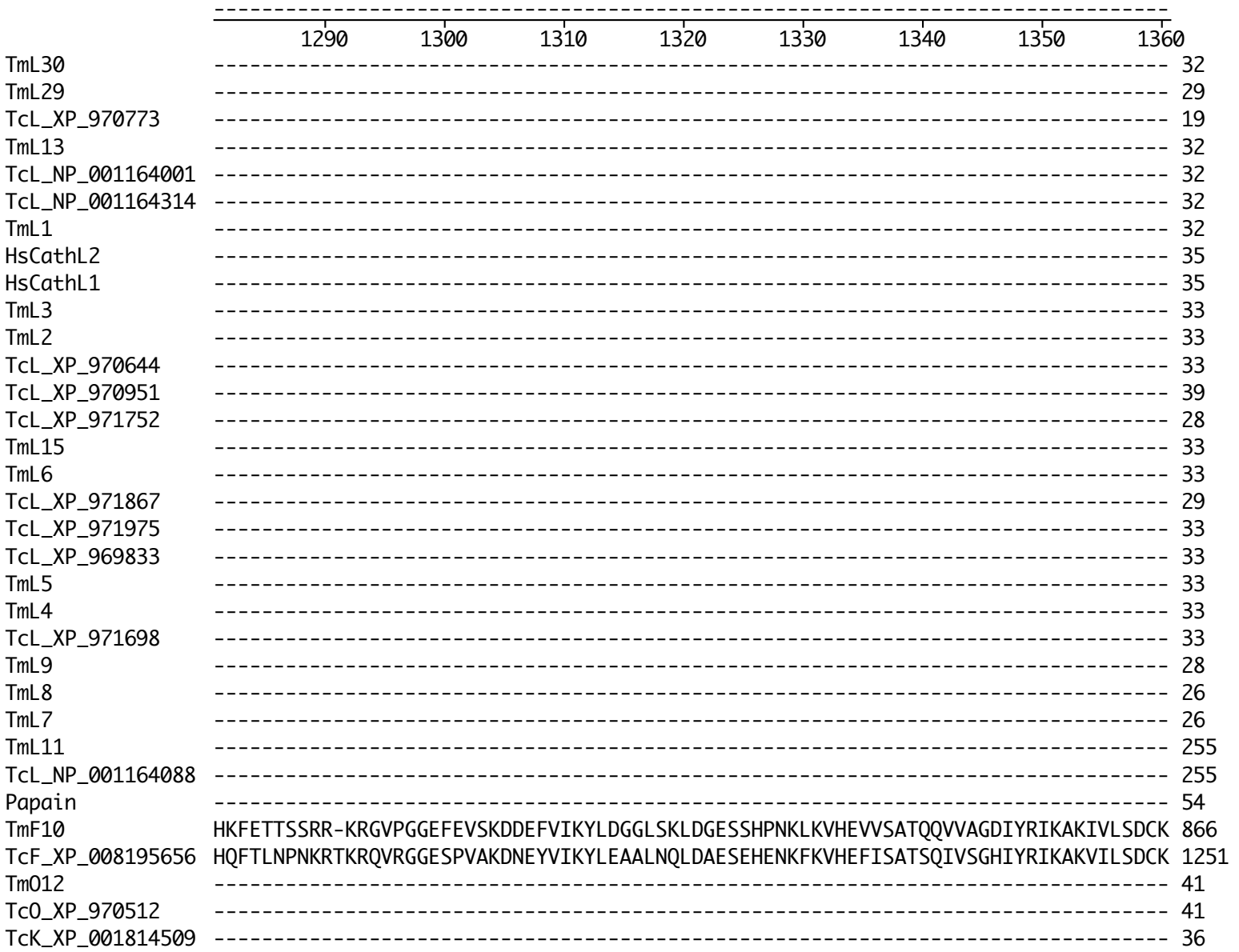
TcK_XP_001814509 Q-WEKFKQ 36


1290 1300 1310 1320 1330 1340 1350 1360
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TmL29 29
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TmL13 32
TcL_NP_001164001 32
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HsCathL1 35
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TcL_XP_970644 33
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TcL_XP_971752 28
TmL15 33
TmL6 33
TcL_XP_971867 29
TcL_XP_971975 33
TcL_XP_969833 33
TmL5 33
TmL4 33
TcL_XP_971698 33
TmL9 28
TmL8 26
TmL7 26
TmL11 255
TcL_NP_001164088 255
Papain 54
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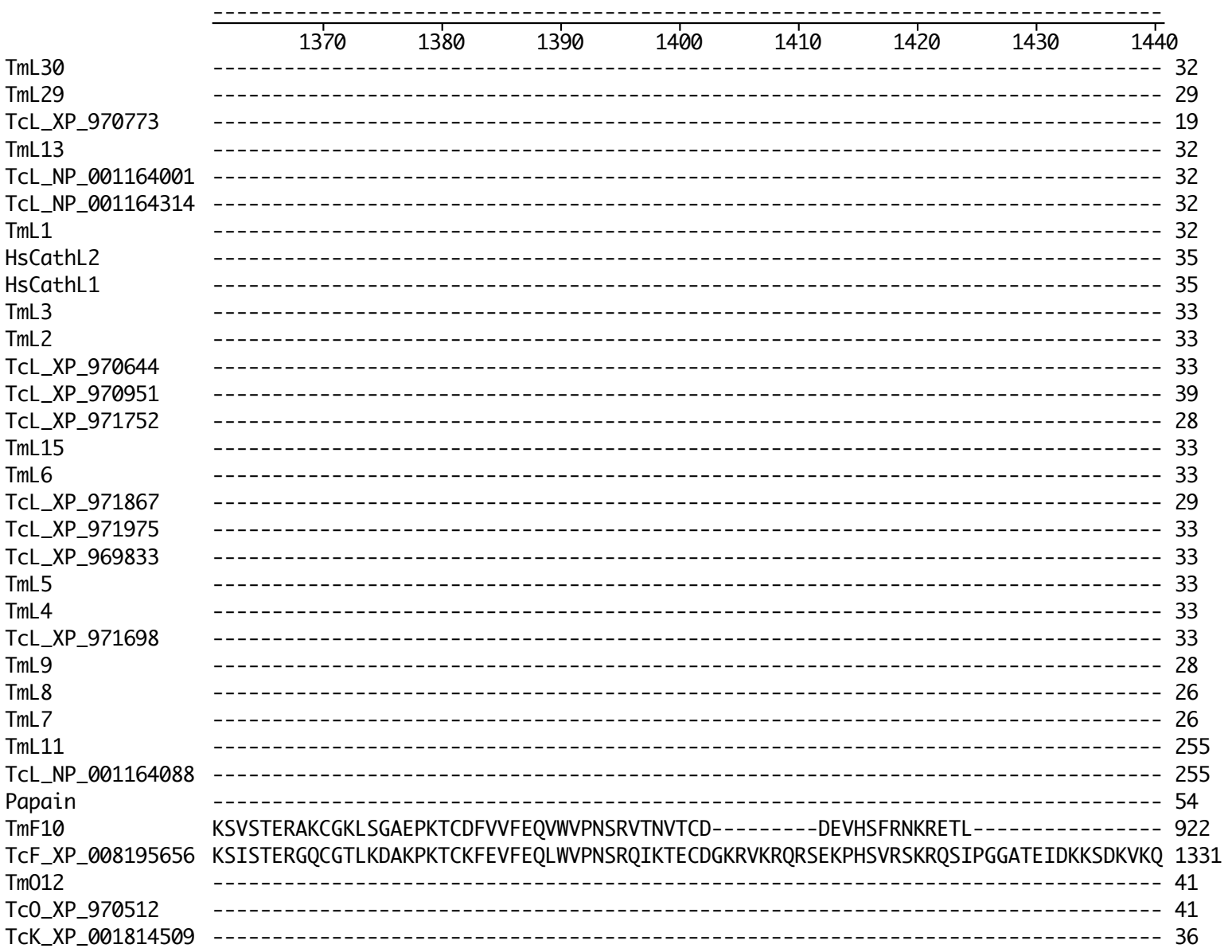
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1380
1390
1400
1410
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1440
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TmL29 29
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TmL13 32
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TcL_NP_001164314 32
TmL1 32
HsCathL2 35
HsCathL1 35
TmL3 33
TmL2 33
TcL_XP_970644 33
TcL_XP_970951 39
TcL_XP_971752 28
TmL15 33
TmL6 33
TcL_XP_971867 29
TcL_XP_971975 33
TcL_XP_969833 33
TmL5 33
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TmL9 28
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TmL7 26
TmL11 255
TcL_NP_001164088 255
Papain 54
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TcF_XP_008195656 KSISTERGQCGTLKDAKPKTCKFEVFEQLWVPNSRQIKTECDGKRVKRQRSEKPHSVRSKRQSIPGGATEIDKKSDKVKQ 1331
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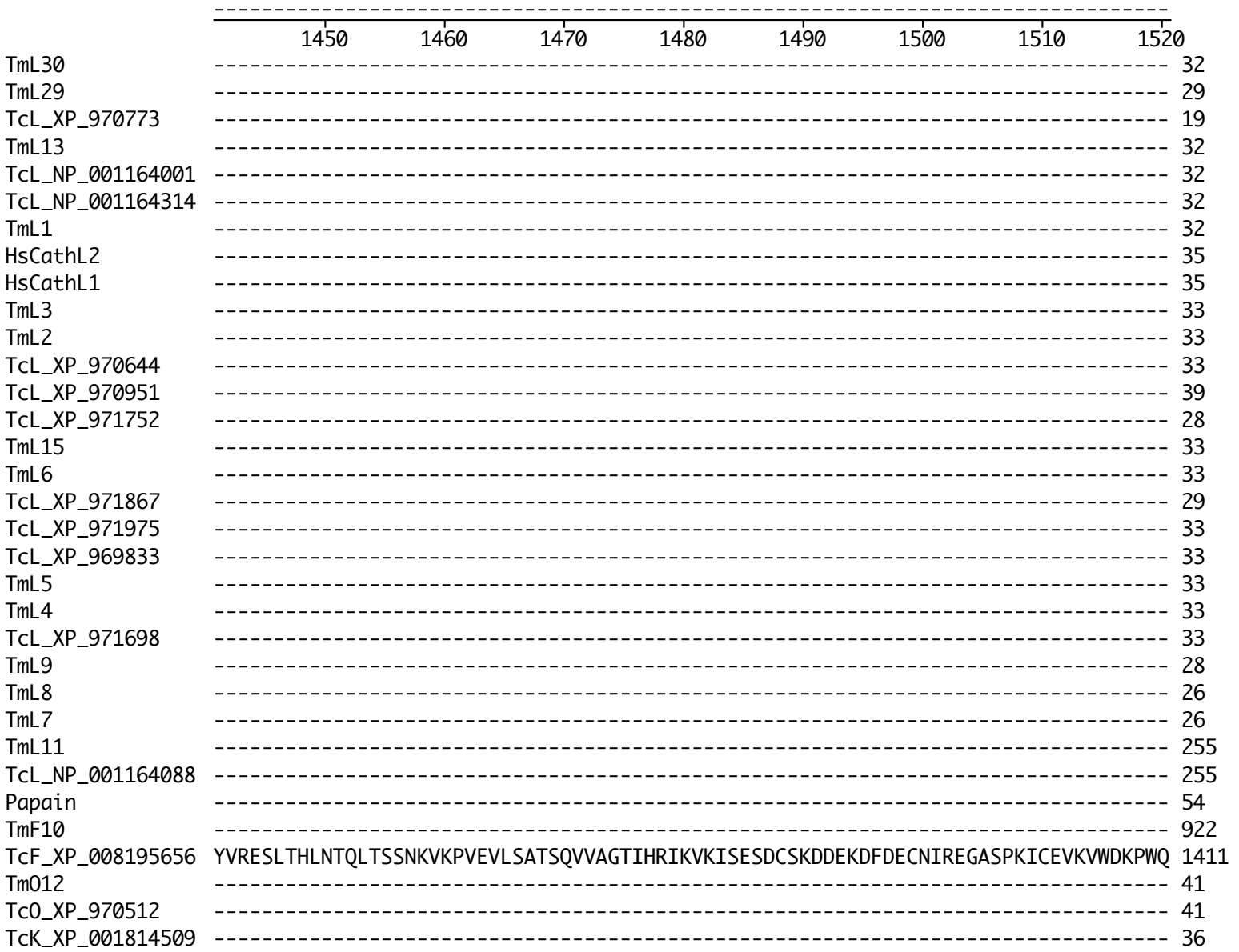
1450 1460 1470 1480 1490 1500 1510 1520
TmL30 32
TmL29 29
TcL_XP_970773 19
TmL13 32
TcL_NP_001164001 32
TcL_NP_001164314 32
TmL1 32
HsCathL2 35
HsCathL1 35
TmL3 33
TmL2 33
TcL_XP_970644 33
TcL_XP_970951 39
TcL_XP_971752 28
TmL15 33
TmL6 33
TcL_XP_971867 29
TcL_XP_971975 33
TcL_XP_969833 33
TmL5 33
TmL4 33
TcL_XP_971698 33
TmL9 28
TmL8 26
TmL7 26
TmL11 255
TcL_NP_001164088 255
Papain 54
TmF10 922
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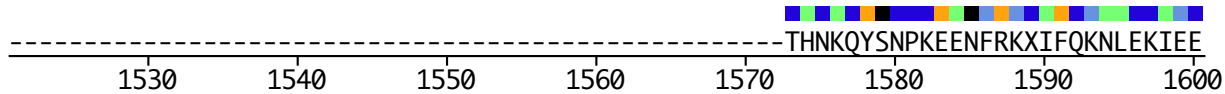
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1550
1560
1570
1580
1590
1600

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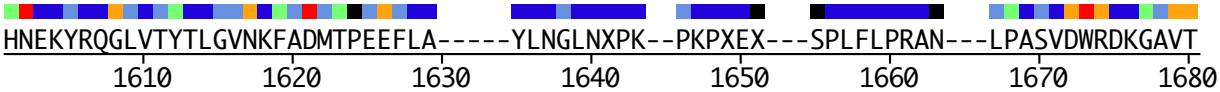


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TmL29             HNVRYEKGEVTYSKAMNKFGDWTAEEFLA-----FVNSTRFQK--PRLTKA--PPKLHLNRRL---AEDEVDWRSKGAVT 124
TcL_XP_970773     HNTKYRNGEVTYFKAMNKFGDLTTDEFLA-----FVNRNKLTK--REKNEK--HTKLNTTKIE---YETQVDWRANGLVS 114
TmL13             HNAKFEKGEVTYSKAMNQFGDMSKEEFLA-----YVNRGKAQK--PKHPEN-LRMPYVSSKKP---LAASVDWRSN-AVS 127
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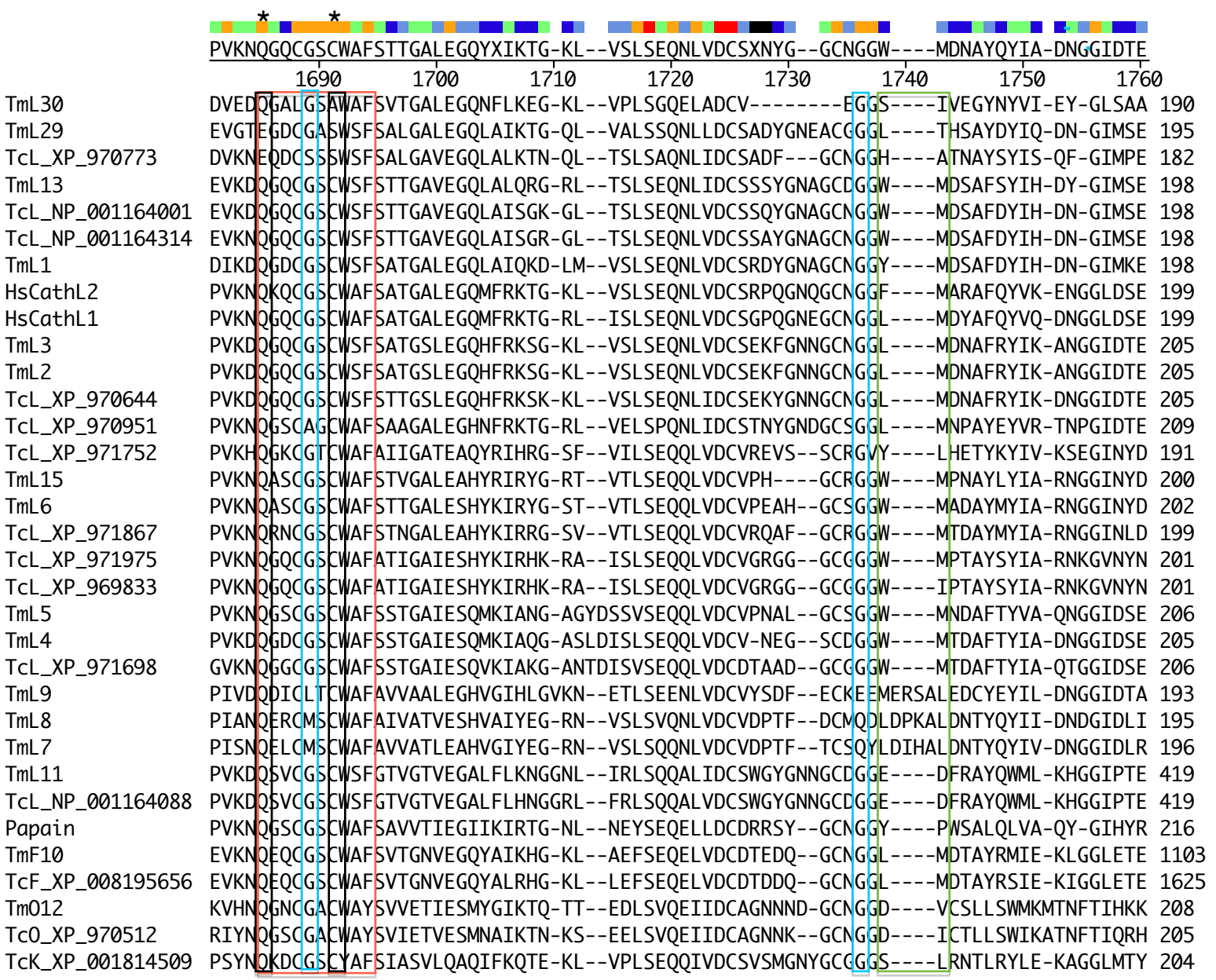
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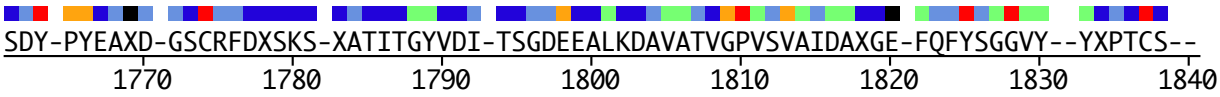


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TcL_NP_001164314 SAY-PYTASE-GSCRFNPSES-VTSLQGYYDL-PSGDENALKSAVANNGPIAVALDATDE-LQFYSGGVL--YDTTCS-- 270
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