```
                 10        20        30        40        50        60        70        80        90       100       110
         ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_Hes6  MAPPAAPGRDRVGR---------------EDEDGWETRGD----RKARKPLVEKKRRARINESLQELRLLLAGAE-----VQAKLENAEVLELTVRRVQGVLRGRA----
Mm_Hes6  MAPSQAPSRDRAGQ---------------EDEDRWEARGD----RKARKPLVEKKRRARINESLQELRLLLAGTE-----VQAKLENAEVLELTVRRVQGALRGRA----
Gg_Hes6.1 MAPSFRHGKGRAPRGGSGGADRRVSGGRGAERGGWGARADGAVCPQARKPLVEKKRRARINESLRELRRLLAGG-------EAKLENAEVLELTVRRVQAVLERRA----
Xt_Hes6.1 ------------------------------------MERRE----RQMRKPLVEKRRRARINESLQDLRGILSDTE-----FQSKMENAEVLELTVKRVERILRNRT----
Dr_Her13 MVHAAELR----NNLG------------VGEYACYGFK-G---DRKTRKPIVEKKRRARINESLQDLRTLLTNND-----LQTKMENAEVLELTVKRVESILQSRS----
Ol_Her13.1 ----MSRR--------------------PGADGGPADRKI----MMRRKPLVEKRRRARINDSLHELRLLVADAD-----LHAKMENAEVLEVTVNRVESVMQNRD----
Fr_Her13.1 MAPLRSNA--------------------DGTDRGDGLESD----RKARKPLVEKKRRARINKSLEELRLLVAEPD-----LQSKLENAELLAMTVKRVENILQDPT----
Dr_Hes6  MAPASR------SNT--------------HDEDNYGIK-----DRKTRKPLVEKKRRARINESLQELRLLLADPD-----AQVKMENAEVLEMTVKRVESILQNKA----
Fr_Her13.2 MAPSAR-----SSHTELD---------MDGDEFDFGRQKT---DRKIRKPLVEKKRRARINESLRELRTLLADTD-----IHSKMENAEVLEMTVKKVEDVLKDQT----
Ol_Her13.2 MAPSVQPSSSSSSSSDVC---------TEDDE-PYGIQRA---DRKVRKPLVEKKRRARINESLQELRTLLADAD-----FNSKMENAEVLEVTVKKVEDILKSRS----
Gg_Hes6.2 MTAAAMGGG---------------------AHKLSSTKEE----RKLRKPLIERKRRERINNCLDQLKETVVGAF---HLDQSKLEKADILEMTVKHLQNIQNSKL---M
Xt_Hes6.2 MSGAGRSQL----------------------KACSAKEE----RKLRKPLIERKRRERINTCLEQLKETVIKAF---HLDQSKLEKADILEMTVRHLQNIQKSKS---T
Dr_Her8a MTASNMGNG---------------------PEKNFNAKEE----RKLRKPLIEKKRRERINSSLEQLKGIMVDAY---NLDQSKLEKADVLEITVQHMENLQRGHGQGGS
Dr_Her8.2 MTATKLQQNS-------------------CQLHISSKEE----RKLRKPLIERKRRERINLCLDQLRETVVAVF---KPDQSKLEKADILEMTVKHLQNIQSSR----V
Fr_Her8  MTASSMEHS---------------------SGKHSRAKEE----RKMRKPLIERKRRERINNCLDQLKEAVIGAF---QLDQSKLEKADILEMTVRHLQNIQSSK----R
Ol_Her8  MTASSVVQD----------------------VDKHPSAKEE----RKMRKPLIERKRRERINNCLDQLKETVIGAF---RLDQSKLEKADILEMTVKHLQNIQNSQ----M
Mm_Hes5  MAPSTVAVEM-----------------------------LSPKEK----NRLRKPVVEKMRRDRINSSIEQLKLLLEQEFARHQP-NSKLEKADILEMAVSYLK---HSKAF---
Mm_Hes1  MPADIMEKNSSSPVAATPASVNTTP---------DKPKTA-SEHRKSSKPIMEKRRRARINESLSQLKTLILDALKKDSSRHSKLEKADILEMTVKHLRNLQRAQMT---

                 120       130       140       150       160       170       180       190       200       210       220
         ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_Hes6  REREQLQAEASERFAAGYIQCMHEVHTFVSTCQAIDATVAAELLNHLDESMPLREGSSFQDLLGDALAG-------------PPRAPGRSGWPAGGAP---------GSP
Mm_Hes6  REREQLQAEASERFAAGYIQCMHEVHTFVSTCQAIDATVSAELLNHLDESMPLREGSSFQDLLGDSLAG-------------LPGGSGRSSWPPGGSP---------ESP
Gg_Hes6.1 LEGGRLHREASERFAAGYIQCMHEVHTFVSGCPGIDATTAAELLNHLDESMPLSEGG-LRDLMADVLAE-------------PWPG-GDAALPLAEAA---------LGL
Xt_Hes6.1 AEADRLQREASERFAAGYIQCMHEVHTFVSSCPGIDASLAAELLNHLDESMPLSEGS-LQDLVMDVLLD-------------STSSEEGCGLGVLGS-------------
Dr_Her13 QETGTVTQEASERFAAGYIQCMHEVHTFVSTCPGIEARVAAELLNHLDESMPLN-ENHLHEMIKDLISEPSSSGD--SWQSGEAQNPGRHCVSGMSS----------ELP
Ol_Her13.1 QDVDAVNREACERFAAGYIQCMHDVHTFMSSCPGIDQELSAELLNHLDESLPLNEQNLVPDAASHHPGR-------------NSTYAPHDRLQMAGVS------------
Fr_Her13.1 PDAEASSREACERFTAGYIQCMHDVHTFVSTCPGVDQTFAAELLHHLMESMPLNDQ----ERQRGIPDA-------------LSTRPPCGGGSAAWGS------------
Dr_Her6  KEADSVNREANERFAAGYIQCMHEVHTFVSSCPGIDATIAADLLNHLLECMPLNDEERFQDILSDLISDSNNSGTWPGEAAYATLSPGGTSVANGGSS----------ALS
Fr_Her13.2 QETEALNREANERFAAGYIQCMHEVHMFVSSCPGIDATVAAELLNHLLECMPLN-EDHLQDTLMDLIADTSGS------DGSTWHG-GGESLCVTLESPRGRSGLSAVLS
Ol_Her13.2 QEKDALNREASERFAAGYIQCMHEVHTFVTSCPGIDAAVAAELLNHLLECMPMN-EDHLQDVMMDLITDTSAC------NSSTLASPGGGSLSGCEAS----------ALS
Gg_Hes6.2 ADSKVG-LEAQQRYSTGYIQCMHEVHNLLLTCEWMDKTLGARLLNHLLKSLRRSSEDTSKAALSSSSPSQQPLLT-----AKTPLGPKGNTTGTNPSQEH----------
Xt_Hes6.2 GEPSQGSVDAQQRFSTGYIQCMHELHSLLLTCDWMDPALGARLLNHLLKSLRRPEG--------------RTAFL-----IQDYEGDTGRTMSPSLSD------------
Dr_Her8a NSPGTG-FESRQRYSSGYIQCMHEVHNLLLSCPGMDKTLGARLLNHLLKSLRHISTE----PSGTSSAGTSSPLP-----LSPTQSPINLPSSLQPHALH----------
Dr_Her8.2 SDPVLN-TGARQRYSTGYIQCMQEVHNLLHSCDWMDKTLGSRLLNHLFKSLRLSAKDCPRLPKTSLTSVPSDHSE-----YSSFHVDETASPKPCSSSP------------
Fr_Her8  GEVTSG-LEAQQKYSTGYIQCVHEVHNMLLTCEWMDKTLGSRLLNHLLKSLRRSAD---------HCPPQSELQQ-----DFLPHADQGTSVALSGES------------
Ol_Her8  PDPTLG-LEAQQRYSTGYIQCMHEVHNMLLTCDWMDKTLGSRLLNHLLKSLRRSTD----------DSSRNQPRH-----DALLDVPLRSVLATPLRG----------
Mm_Hes5  -AAAAGPKSLHQDYSEGYSWCLQEAVQFLTLHAAS--DTQMKLLYHFQ-----------------------------------RPPAPAAPAKEPPAP----------GAA
Mm_Hes1  -AALSTDPSVLGKYRAGFSECMNEVTRFLSTCEGVNTEVRTRLLGHLANCMTQINAMTYPGQAHPALQAPPPP---------PPSGPAGPQHAPFAPPPPPLVPIPGGAA

                 230       240       250       260       270       280       290       300
         ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_Hes6  IPSPPGPGDDLCSDLEEAP----------------------------EAELSQAPAEGPDLVPAALGSLTTAQIARSVWRPW--
Mm_Hes6  LSSPPGPGDDLCSDLEEIP----------------------------EAELNRVPAEGPDLVSTSLGSLTAARRAQSVWRPW--
Gg_Hes6.1 ALPSPSSGEETCSDSDEA-----------------------------EAEPVQTPAHG--LEAAQTRAVPSPGSPKSMWRPW--
Xt_Hes6.1 ------SSEDSCSDMEES-----------------------------EGEK---AGMGSVQDSGRTPEIQPP--TPTMWRPW--
Dr_Her13 QFLSNPFQDDLCSDLDET----------------------------ETEERSASAEDTLDFSM------VTHSKFMWRPW--
Ol_Her13.1 PSPFASSTDDLSSDLDET----------------------------DSEHSQRSNSEEGRESHGT--PHGVHFSKVLWRPW--
Fr_Her13.1 PAP--SSSDHPYSDLDET----------------------------ESEQNHFSSLDEAESQDLS--FFSGAPSKPTWRPW--
Dr_Her6  PAPSTTSSDDICSDLDDT----------------------------DTEHSRISVDAGDQAPVVP----TLYTNKSIWRPW--
Fr_Her13.2 PAPSTTSSEDLCSDLDDT----------------------------DSEHNQSSTEGLEHREG------LMTSSRSMWRPW--
Ol_Her13.2 PATSP-SSEDSCSDLDEV----------------------------DGEHHQSSTEVAAGSRGGL-SMPTVAYPRFMWRPW--
Gg_Hes6.2 -FYPAEHKQALKNSFQPPSLLGFGQ----------------------VDAVPPRQVLQPNFSHNNPSMG------SLDMWRPW--
Xt_Hes6.2 ---CEAEQTSVP---------------------------------LHSDVAQGKT----QCSLLR-------SLQMWRPW--
Dr_Her8a -LSPSPPSSPTHSLVRPR-------------------------------EQFSPPSSPSP---QSPASLPPFFPGVDPSMWRPW--
Dr_Her8.2 -FLCKRPNQSQNQ-----------------------------------HFTPIRMPHD---VESSHLS------VLQMWRPW--
Fr_Her8  ---VARHLQRKR----PP-----------------------------AHVADPSQSPPP----HGPQLG------LLEMWRPW--
Ol_Her8  --LPKKPRQKEGS---PP-----------------------------LLGGQQERPE---LHSSHLS------MMEMWRPW--
Mm_Hes5  PQPARSSAKA-------------------------------------------------AAAAVSTSRQPACGLWRPW--
Mm_Hes1  PPPGSAPCKLGSQAGEAAKVFGGFQVVPAPDGQFAFLIPNGAFAHSGPVIPVYTSNSGTSVGPNAVSPSSGSSLTSDSMWRPWRN
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