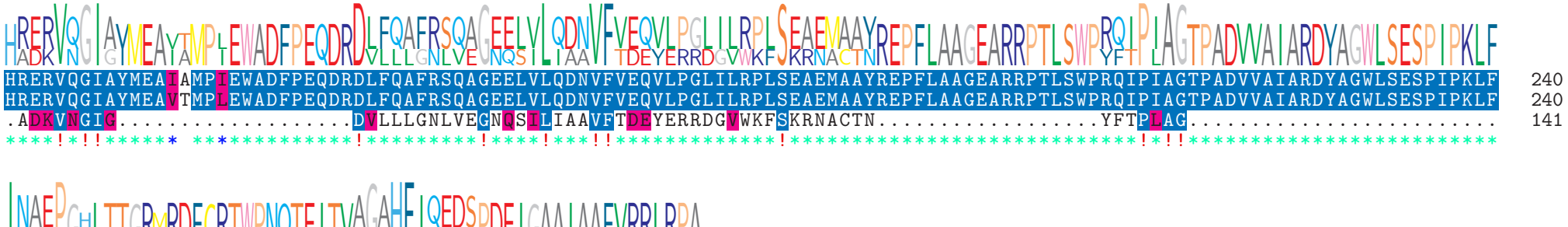
MSLGAKPFGEKKFIEIKGRRMAYIDEGTGDPILFQHGNPTSSYLWRNIMPHCAGLGRLIACDLIGMGDSDKLDPSGPERYAYAEHRDYLDALWEALDLGDRVVLVVHDWGSALGFDWARR 120
MSLGAKPFGEKKFIEIKGRRMAYIDEGTGDPILFQHGNPTSSYLWRNIMPHCAGLGRLIACDLIGMGDSDKLDPSGPERYTYAEHRDYLDALWEALDLGDRVVLVVHDWGSVLGFDWARR 120
MSDLDRLASRAAIQDLYSDKLIAVDK.....RQEGRLASIWWDDAEWTIEGIG.....TYKGPEGALDLAN.....NVLWPMFHE.....CIHYGTNLRLEFVS. 84


HRERVQGIAYMEAIAMPIEWADFPEQDRDLFQAFRSQAGEELVLQDNVFVEQVLPGLILRPLSEAEMAAYREPFLAAGEARRPTLSWPRQIPIAGTPADVVAIARDYAGWLSESPIPKLF 240
HRERVQGIAYMEAVTMPLEWADFPEQDRDLFQAFRSQAGEELVLQDNVFVEQVLPGLILRPLSEAEMAAYREPFLAAGEARRPTLSWPRQIPIAGTPADVVAIARDYAGWLSESPIPKLF 240
.ADKVNGIG.....DVLLLGNLVEGNQSILIAAVFTDEYERRDGVWKFSKRNACTN.....YFTPLAG..... 141

INAEPGALTTGRMRDFCRTWPNQTEITVAGAHFIQEDSPDEIGAAIAAFVRRLRPA 296
INAEPGHLTTGRIRDFCRTWPNQTEITVAGAHFIQEDSPDEIGAAIAAFVRRLRPA 296
IHFAP.....PGIHFAPSGA..... 156