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gi|114572323|ref|XP_514159.2| MGASSPRSPPEVGPAPGLPFCCGSSLAVVLLALPVANGOCNAPEWLPFARPTNLDEFEFFIGTYLNYECPGYSGRPFISIILKNSVWTGAKDRCKRKS CRNPPDPVNGMVHVIKDIQFGSQIKYSCTKGYRLIGSSSATCIISGD 150
gi|73960701|ref|XP_851667.1| -----
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gi|86793109|ref|NP_000642.3| TVIWDNETPICDRIPCGLPPIITNGDFISTNRENPHYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCPGFVMKGPRRVKQALNKWPELPSCSRVCQPP 300
gi|114572323|ref|XP_514159.2| TVIWDNETPICDRIPCGLPPIITNGDFISTNRENPHYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCPGFVMKGPRRVKQALNKWPELPSCSRVCQPP 300
gi|73960701|ref|XP_851667.1| -----
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gi|73960701|ref|XP_851667.1| -----
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gi|114572323|ref|XP_514159.2| -----
gi|73960701|ref|XP_851667.1| -----
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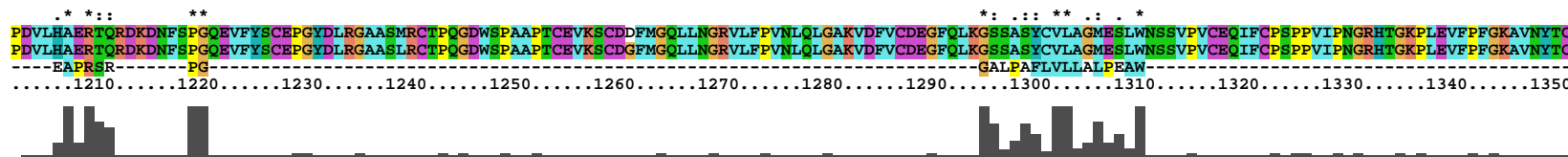
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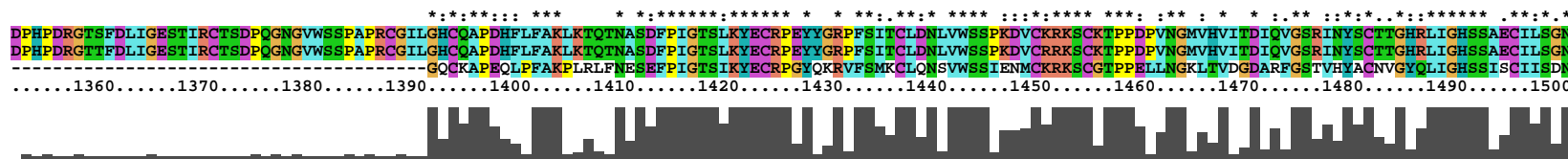
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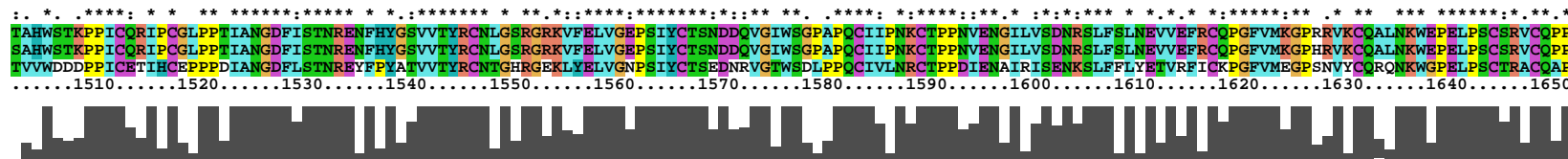
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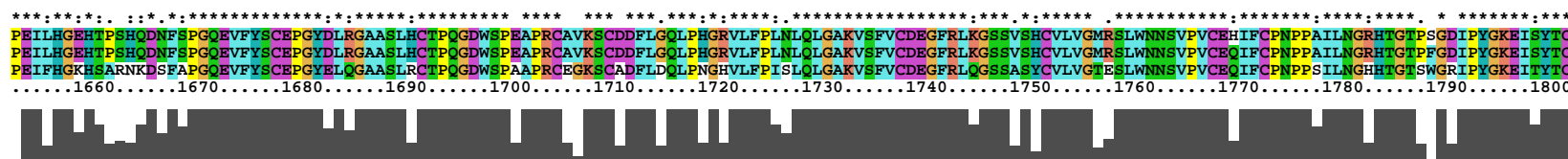
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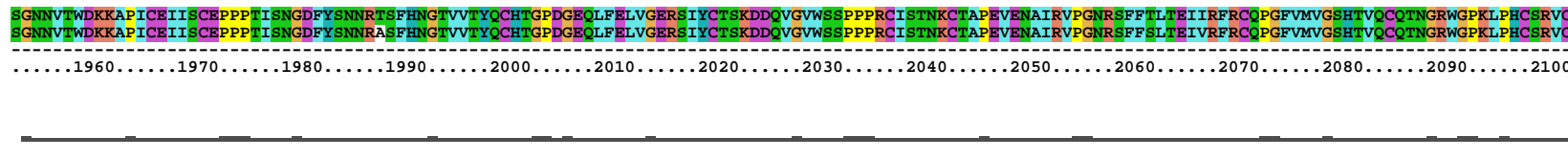
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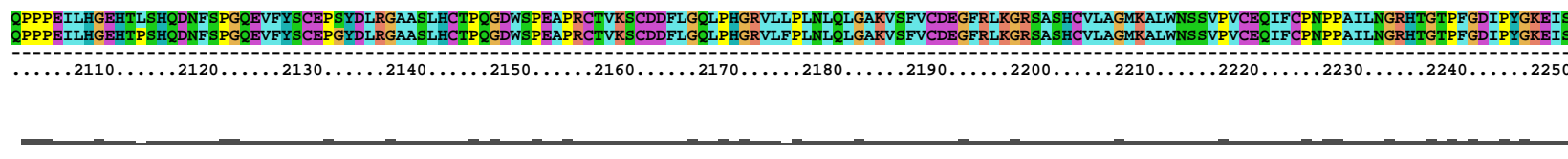
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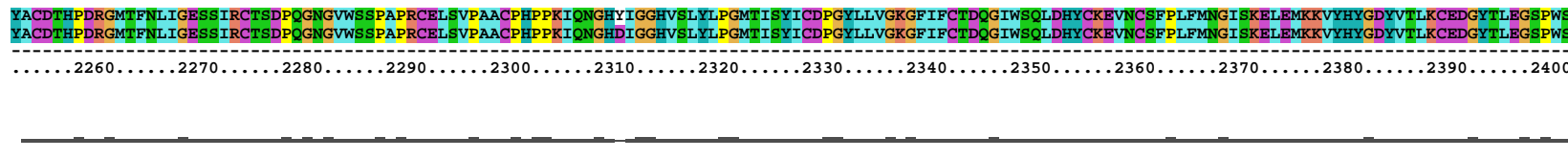
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