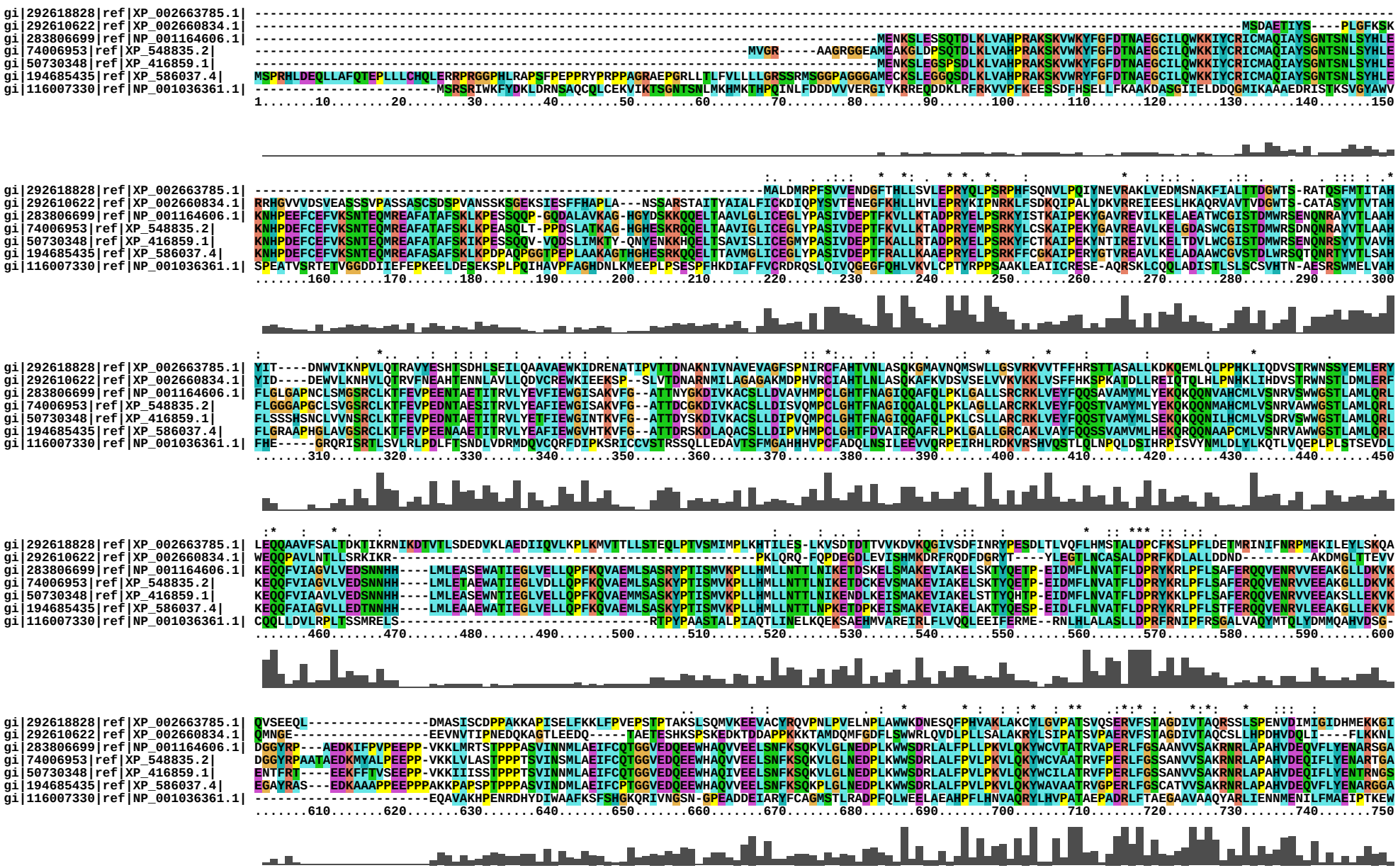
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gi|116007330|ref|NP_001036361.1|

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gi|292618828|ref|XP_002663785.1| TQLSNDWMVGVEQKKETHRRNSGDILKDLELRKQIGMDHMEKKGITHLSIDWIIGIEHVVEQGNTPQ   578
gi|292610622|ref|XP_002660834.1| ------------------------------------------------------------------   517
gi|283806699|ref|NP_001164606.1| EAEPEDQDEGEWGLDQEQVFSLGDGVSGG--FFGIRDSSFL-------------------------   694
gi|74006953|ref|XP_548835.2|     EAEPEDEDEGEWGLDHEQVFPLGDAVHAG--FFGIRDSGFV-------------------------   709
gi|50730348|ref|XP_416859.1|     EAEPEDEDEGEWGLEQEQIFNLNDSVNVNNNFFNIRDSGFV-------------------------   695
gi|194685435|ref|XP_586037.4|    DAELEDEDEGEWGLDHEQAFAPGEAAHAG--FFGVRDGSFV-------------------------   779
gi|116007330|ref|NP_001036361.1| QL----------------------------------------------------------------   661
                                 .......760.......770.......780.......790.......800.......810.......
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