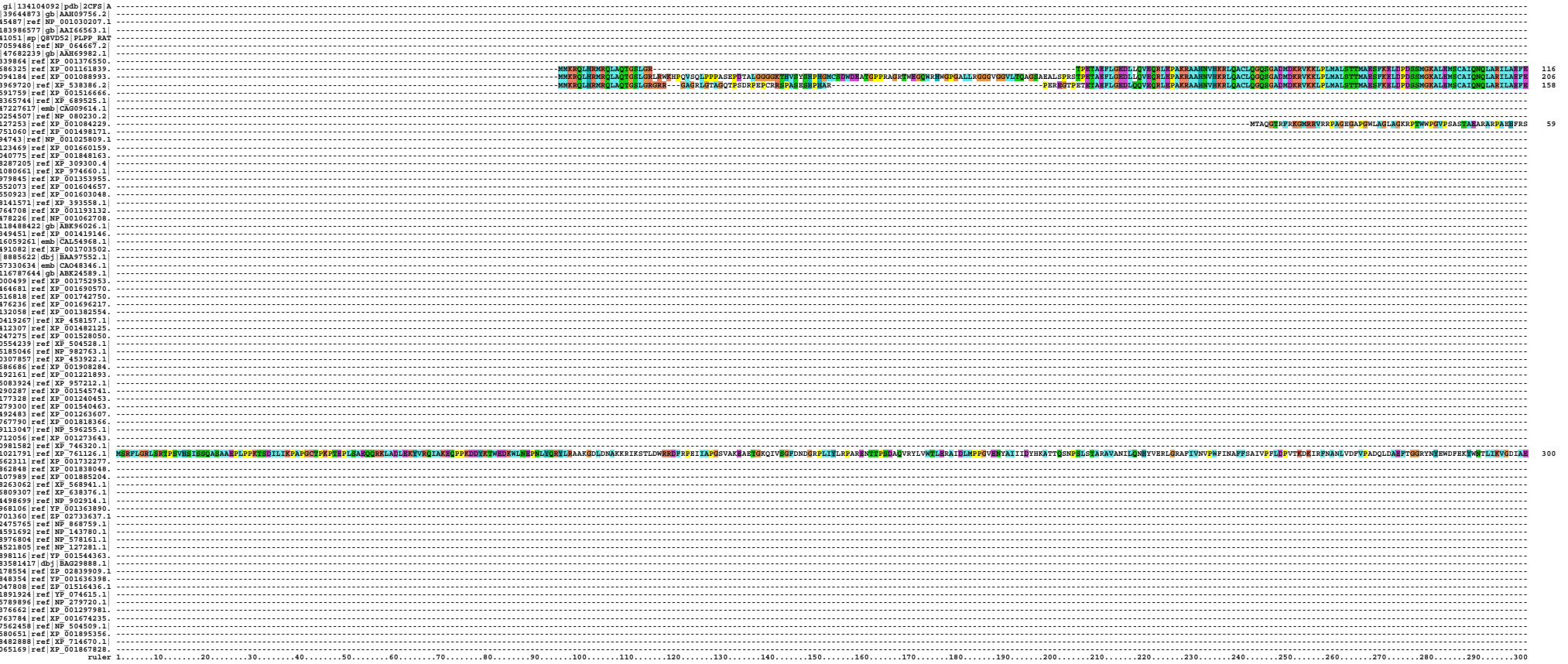


# CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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# CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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gi 134104092 pdb 2CF5 A	..MAMRGERLRAAARDVLRGACG	..VLPDGVVGNRRAVPAFLRLRLAQA	..KALVFNRRRRAAR	..PELALFARLQ	..PQGRABELLALCALARLRLRQPPDPAPG	..AVVFLVGGELR-AR	123
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gi 183948577 gb AAI66563.1	..MARGERLRAAARDVLRGACG	..VLPDGVVGNRRAVPAFLRLRLAQA	..KALVFNRRRRAAR	..PELALFARLQ	..PQGRABELLALCALARLRLRQPPDPAPG	..AVVFLVGGELR-AR	121
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26339864 ref XP_001376550	..MARGERLRAAARDVLRGACG	..VLPDGVVGNRRAVPAFLRLRLAQA	..KALVFNRRRRAAR	..PELALFARLQ	..PQGRABELLALCALARLRLRQPPDPAPG	..AVVFLVGGELR-AR	120
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45349451 ref XP_001419146	..MARGERLRAAARDVLRGACG	..VLPDGVVGNRRAVPAFLRLRLAQA	..KALVFNRRRRAAR	..PELALFARLQ	..PQGRABELLALCALARLRLRQPPDPAPG	..AVVFLVGGELR-AR	123
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21712056 ref XP_001273643	..MARGERLRAAARDVLRGACG	..VLPDGVVGNRRAVPAFLRLRLAQA	..KALVFNRRRRAAR	..PELALFARLQ	..PQGRABELLALCALARLRLRQPPDPAPG	..AVVFLVGGELR-AR	119
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50307897|ref|XP_453822.1 309
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85083924|ref|XP_957212.1 306
54290287|ref|XP_001545741 319
19177328|ref|XP_001240453 306
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69767790|ref|XP_001818366 306
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21712056|ref|XP_001273643 333
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52968106|ref|YP_001363890 259
68701360|ref|XP_0217637.1 282
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14521805|ref|NP_127281.1 262
59898116|ref|YP_001544363 266
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51891924|ref|YP_074615.1 257
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23766662|ref|XP_001297981 322
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17862458|ref|NP_504509.1 322
70580651|ref|XP_001895356 301
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