

ATATGAAGGC G CCGCAGC GGAG A T T A ACCC G C T T GGCAC G G T CC GGGGGG CGC CGCCACCAGGACCACCAAT AAACC T T T

ATGCAGTGGCAACAGGCAGACAAACAAATAAACTTACAACCTCAACAACGGATCCGGCTGGCATGATGAAGAACGCAGCGAAATGGATACGTAT

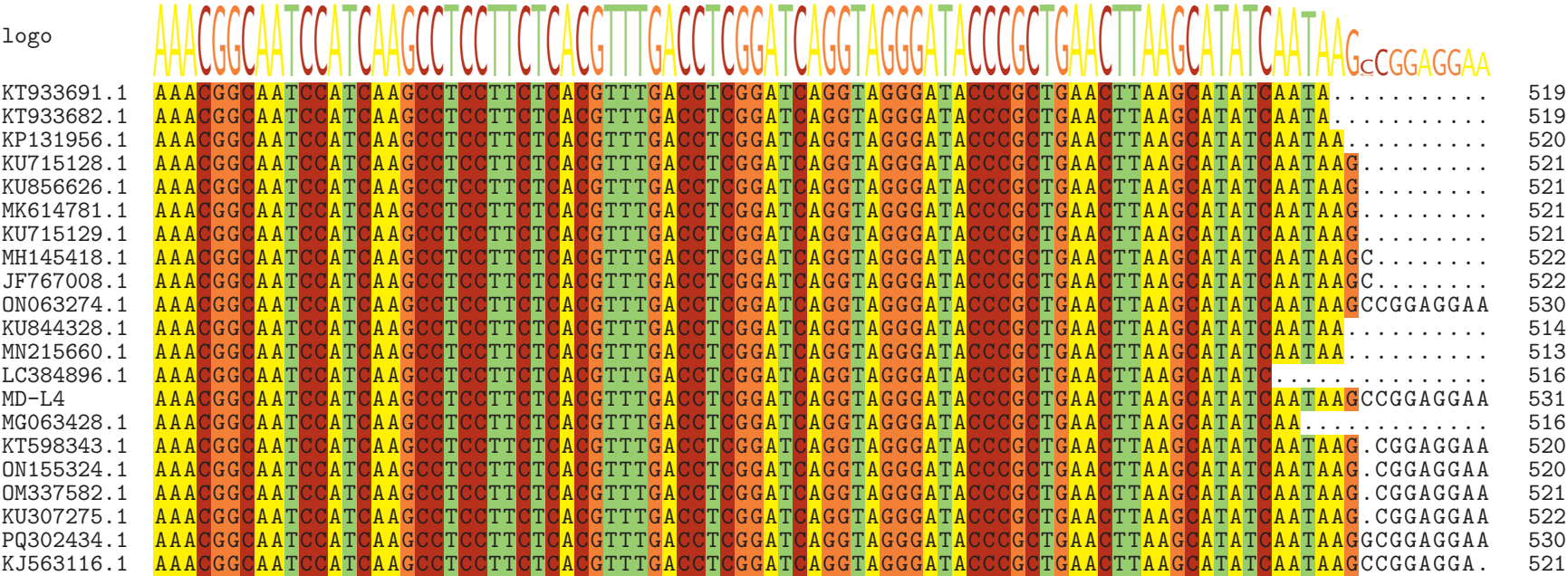
KT933691.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	218
KT933682.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	218
KP131956.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	218
KU715128.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	218
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JF767008.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	218
ON063274.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	218
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MN215660.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	211
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PQ302434.1	TATGCAGTTGCAATCAGCGTCAGTACAAA	CAATGTAATAATCATTTACAACTTTCAA	CAACGGATCTCTTGGTTCTGGCATCGATGAAGAA	CGCAGCGAAATGCGATACGTA	218
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GGG GGGGG G C GG CGCCAAAGAC CGCC AAAG GAT GGCAGCCGGCC T C GG CGCAGCGCAGCACA TTTT GCGC GCCA CAGCA

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KP131956.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	438
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ON063274.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	438
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MN215660.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	431
LC384896.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	439
MD-L4	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	439
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ON155324.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	429
OM337582.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	430
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PQ302434.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	438
KJ563116.1	TTGGTGTTGGGCGTTTTGTCTTTGGTGGCCAAAGACTCGCCTTAAAGTGATTGGCAGCCGGCCTTTCTGGTTTGCAGCGCAGCACATTTTTGCGCTTGCCATCAGCA	430

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- X 13.9 (C); Accessible sidechain area (Å²)
- X 23.0 (I); 23.5 (V); 25.2 (G)
- X 28.7 (F); 29.0 (L); 30.5 (M); 31.5 (A)
- X 41.7 (W); 44.2 (S); 46.0 (T); 46.7 (H)
- X 53.7 (P)
- X 59.1 (Y); 60.9 (D); 62.2 (N)
- X 72.3 (E); 74.0 (Q)
- X 93.8 (R)
- X 110.3 (K)