

V3 Loop Amino Acids

The following pages present amino acid alignments of the V3 loop, arranged by phylogenetic subtype. For each subtype, the number of sequences used to construct the alignment is indicated. The top line in each alignment represents the consensus sequence for that subtype, where “consensus” simply means the most common amino acid found in each position among the sequences of the given subtype. The subscripts record the frequency with which that amino acid is observed at that location among members of the subtype. An amino acid which is conserved 100% is shown with no subscript. Directly beneath the most common amino acid in each position are the other amino acids observed in that position, listed from most common to least common. An asterisk (*) subscript means less than 0.5% of the sequences had the indicated amino acid at that location. A dash (-) indicates a gap inserted to maintain the alignment. Percentages were rounded to the nearest whole number.

For this year’s alignment, the HMMER (version 1.8) hidden Markov model software (Sean Eddy, Dept. of Genetics, Washington U. School of Medicine, St. Louis, MO 63110; eddy@genetics.wustl.edu <http://hmmmer.wustl.edu/>) was used to objectively align all 3,826 sequences. The frequency counts are derived from this alignment.

Both the HMMER alignment of nucleotide sequences, and an edited version translated to amino acid sequences, will be available from the LANL HIV database (<http://hiv-web.lanl.gov>). Questions about these alignments should be directed to Brian Foley btbf@t10.lanl.gov (505) 665-1970.

C subtype (443 sequences)

V₅₈ C₁₀₀ T₈₇ R₉₉ P₉₉ N₇₅ N₉₉ N₉₉ T₉₉ R₉₉ K₇₈ S₉₈ I₆₃ R₅₇ I₉₉ G₉₉ P₁₀₀ G₁₀₀ Q₉₉ T₇₈ F₉₈ Y₉₄ A₉₈ T₉₃ G₈₃ D₆₅ I₉₆ I₉₅ G₁₀₀ D₈₅ I₉₉ R₉₉ Q₈₉ A₉₉ H₈₀ C₁₀₀ N₉₂
 N₂₁ R₁ I₀ T₉₉ T₉₉ G₁₂ S₉₉ T₉₉ K₉₉ K₁ E₁₁ G₂₁ M₂₁ G₃ V₁ R₁ I₁ R₉₉ I₁ R₉₉ K₉₉ R₁ A₁₈ L₁ F₆ T₁ N₁₁ E₁₂ V₃ T₂ E₉ N₁₄ M₉₉ K₉₉ K₄ D₉₉ Y₁₉ L₉₉ T₃
 E₉ Y₉₉ A₃ R₉₉ S₁₁ D₉₉ I₉₉ V₉₉ G₉₉ R₉₉ G₉₉ R₉₉ V₂ S₉₉ H₉₉ A₂ D₂ G₁₀ E₃ R₃ T₉₉ R₃ E₃ R₃ N₁ S₂
 T₄ M₂ H₉₉ H₁ K₉₉ Y₉₉ H₉₉ S₉₉ R₁ T₁ A₇ M₉₉ G₉₉ E₉ T₉₉ R₃ T₉₉ D₉₉ I₁
 M₂ M₁ Y₉₉ A₉₉ T₉₉ S₁ V₉₉ E₉ M₉₉ K₁ Q₁ L₁ H₉₉ R₉₉ Q₉₉ D₁
 K₂ I₁ R₁ K₉₉ Y₉₉ D₉₉ K₉₉ M₉₉ H₉₉ R₉₉ R₉₉ R₉₉ V₉₉ H₁
 I₁ R₁ K₉₉ Y₉₉ T₉₉ P₉₉ A₉₉ K₉₉ K₉₉ E₉₉
 L₉₉ R₉₉ E₉₉ T₉₉ M₉₉ N₉₉ E₉₉
 D₉₉ D₉₉ A₉₉ S₉₉ -
 A₉₉ S₉₉ -

D subtype (182 sequences)

N₇₅ C₁₀₀ T₇₀ R₉₉ P₉₉ Y₆₂ N₇₅ K₆ K₁₀ N₈₃ N₈₃ T₇₃ I₁₀ I₁₀ K₆ S₁ R₁₅ R₂₅ Q₆₁ S₄₁ T₆₅ H₆₀ I₉₀ G₉₉ P₉₉ G₇₀ Q₇₀ A₈₅ L₃₅ Y₇₀ T₈₉ T₆₂ T₃₉ K₂₁ I₆₉ I₆₀ G₃₃ D₇₆ I₉₆ R₉₀ Q₈₁ A₉₉ H₆₇ C₉₉ N₈₈
 T₁₅ I₁₀ W₁ L₁ A₅ V₄ S₃ L₁ M₁ E₁ I₁
 D₃ A₅ S₉ E₄ R₄ R₁ N₁ R₂ E₂ Q₂ V₂ A₁ S₁ H₁ M₁ Y₁ -
 K₂ Y₂ T₁ D₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 S₁ G₃ R₄ T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 H₁ I₂ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 R₁ A₁ S₂ A₁ Y₂ S₁ T₂ D₁ H₁
 E₁ I₁ Y₂ S₁ T₂ D₁ H₁
 I₁ A₁ S₂ A₁ Y₂ S₁ T₂ D₁ H₁
 T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 R₁ A₁ S₂ A₁ Y₂ S₁ T₂ D₁ H₁
 E₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 R₁ A₁ S₂ A₁ Y₂ S₁ T₂ D₁ H₁
 E₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
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 E₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 R₁ A₁ S₂ A₁ Y₂ S₁ T₂ D₁ H₁
 E₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 R₁ A₁ S₂ A₁ Y₂ S₁ T₂ D₁ H₁
 E₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
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 T₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 R₁ A₁ S₂ A₁ Y₂ S₁ T₂ D₁ H₁
 E₁ I₁ V₁ Q₁ V₁ Q₁ V₁ Y₁ Y₁ L₁ N₁
 T₁

H subtype (11 sequences)

N₅₅ C₁₀₀ T₈₂ R₁₀₀ P₈₂ N₁₀₀ N₁₀₀ N₁₀₀ T₉₁ R₉₁ K₆₄ S₈₂ I₉₁ H₆₄ I₇₃ I₉₁ G₉₁ P₉₁ G₁₀₀ Q₇₃ A₉₁ F₇₃ Y₈₂ A₈₂ T₈₂ G₆₄ D₈₂ I₁₀₀ I₁₀₀ G₁₀₀ D₇₃ I₁₀₀ R₁₀₀ Q₇₃ A₁₀₀ H₈₂ C₁₀₀ N₁₀₀
 T₄₅ I₉ L₉ G₂₇ H₉ E₉ R₁₈ G₁₈ M₉ R₁₈ F₉ G₉ I₉ A₉ R₉ R₂₇ T₉ I₁₈ H₉ T₁₈ E₉ V₁₈ E₁₈ V₁₈ N₂₇ I₁₀₀ G₁₀₀ D₇₃ I₁₀₀ R₁₀₀ Q₇₃ A₁₀₀ H₈₂ C₁₀₀ N₁₀₀
 A₉ T₉ A₉ T₉ A₉ E₉ T₉ P₉ L₉ P₉ L₉ I₉ N₉ A₉ R₉ K₉ Y₁₈

J subtype (3 sequences)

V₆₇ C₁₀₀ T₃₃ R₁₀₀ P₁₀₀ N₁₀₀ N₁₀₀ N₁₀₀ T₁₀₀ R₁₀₀ K₁₀₀ G₁₀₀ I₁₀₀ M₆₇ G₁₀₀ P₁₀₀ G₁₀₀ Q₁₀₀ V₁₀₀ I₁₀₀ Y₁₀₀ A₁₀₀ T₁₀₀ G₁₀₀ E₁₀₀ I₁₀₀ G₁₀₀ D₆₇ I₁₀₀ R₁₀₀ E₃₃ A₆₇ H₆₇ C₁₀₀ N₁₀₀
 E₃₃ V₃₃ A₃₃ I₃₃ H₁₀₀ M₆₇ G₁₀₀ P₁₀₀ G₁₀₀ Q₁₀₀ V₁₀₀ I₁₀₀ Y₁₀₀ A₁₀₀ T₁₀₀ G₁₀₀ E₁₀₀ I₁₀₀ G₁₀₀ D₆₇ I₁₀₀ R₁₀₀ E₃₃ A₆₇ H₆₇ C₁₀₀ N₁₀₀
 Y₃₃

K subtype (5 sequences)

N₆₀ C₁₀₀ T₈₀ R₁₀₀ P₁₀₀ N₁₀₀ N₁₀₀ N₁₀₀ T₁₀₀ R₁₀₀ K₆₀ S₆₀ I₁₀₀ H₆₀ I₈₀ I₆₀ G₁₀₀ P₁₀₀ G₁₀₀ K₄₀ A₄₀ F₈₀ Y₁₀₀ A₈₀ T₁₀₀ G₈₀ D₆₀ I₁₀₀ I₁₀₀ G₁₀₀ D₆₀ I₁₀₀ R₁₀₀ Q₆₀ K₄₀ A₁₀₀ H₈₀ C₁₀₀ N₁₀₀
 T₂₀ I₂₀ G₂₀ R₂₀ G₄₀ R₄₀ M₂₀ R₄₀ V₄₀ V₂₀ T₂₀ D₂₀ A₂₀ R₁₀₀ D₆₇ I₁₀₀ R₁₀₀ Q₆₀ K₄₀ A₁₀₀ H₈₀ C₁₀₀ N₁₀₀
 V₂₀ S₂₀ Q₂₀ T₂₀

CRF02(AG) form (57 sequences)

N₈₀ C₁₀₀ T₈₁ R₁₀₀ P₁₀₀ N₁₀₀ N₁₀₀ N₁₀₀ T₁₀₀ R₁₀₀ K₈₆ S₈₄ V₈₁ R₇₉ I₉₆ I₉₆ G₁₀₀ P₁₀₀ G₁₀₀ Q₆₆ T₈₂ F₁₀₀ Y₉₈ A₁₀₀ T₇₇ G₈₄ D₇₅ I₁₀₀ I₉₆ G₁₀₀ D₈₂ I₁₀₀ R₉₈ Q₉₁ A₁₀₀ H₉₆ C₁₀₀ N₉₁
 T₅ I₁₁ G₃₉ K₂ Y₂ R₄ N₄ Q₇ G₁₂ I₁₈ H₁₈ M₂ K₂ A₁₆ L₂ I₁₁ E₁₁ M₂ N₁₈ I₉₆ G₁₀₀ D₈₂ I₁₀₀ R₉₈ Q₉₁ A₁₀₀ H₉₆ C₁₀₀ N₉₁
 I₂ S₁₄ S₁₄ D₂ K₂ S₂ R₄ N₄ L₂ P₄ T₂ R₉ D₄ R₅ T₂ K₂ K₉ Y₄ T₄ K₂
 S₂ V₄ Y₂ H₂ K₄ D₂ E₂
 K₂ P₂ A₂ C₄ N₂

CRF03(AB) form (42 sequences)

N₁₀₀ C₁₀₀ T₉₈ R₉₈ P₁₀₀ N₁₀₀ N₁₀₀ N₁₀₀ T₁₀₀ R₉₈ K₁₀₀ G₁₀₀ I₁₀₀ H₁₀₀ I₉₈ I₁₀₀ G₁₀₀ P₁₀₀ G₁₀₀ R₁₀₀ A₁₀₀ F₁₀₀ Y₁₀₀ A₁₀₀ T₉₅ G₉₈ D₁₀₀ I₉₅ T₉₀ G₁₀₀ D₉₈ I₁₀₀ R₉₈ Q₁₀₀ A₁₀₀ H₉₀ C₁₀₀ N₁₀₀
 X₂ T₂ X₂ G₂ I₅ R₂ M₂ I₅ E₂ V₂ P₂ K₂ L₂

