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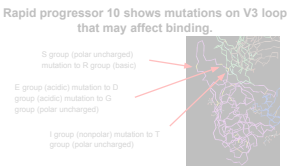
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# Analysis of HIV-1 Amino Acid

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## Outline

- The HIV virus attacks CD4 T cells in the human body and can mutate its genetic structure through changes in amino acids
- Markham et al. 1988 concluded that there was higher diversity among rapid progressor groups
- Amino acid sequences of the first and last visits of four subjects from Markham et al. 1988 were analyzed
- No significant difference was observed between number of mutations observed in rapid versus nonprogressors
- Certain types of mutations may affect the structure of gp120 more drastically than others
- Future studies consisting of subjects with larger numbers of data points are needed to determine higher rates of diversity among rapid progressors

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## When the HIV virus enters a human host it attacks and infects CD4 T cells.

- HIV viruses infect CD4 T cells in human hosts enabling them to proliferate
  - A CD4 T cell's role is to protect the body from infection
  - When a CD4 T cell is infected with an HIV virus, it cannot fight infections
- The V3 loop on the gp120 of a HIV-1 virus helps to infect the host cell by binding to a cytokine receptor

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## Amino acid mutations can change the structure of the HIV virus.

- HIV viruses actively mutate their genetic structure in the body making it difficult to create drugs to kill the virus
- Amino acids are most often categorized into four sections
  - Nonpolar, Polar, Basic, and Acidic

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- The HIV virus attacks CD4 T cells in the human body and can mutate its genetic structure through changes in amino acids
- Markham et al. 1988 concluded that there was higher diversity among rapid progressor groups based on nucleotide sequences
- Amino acid sequences of the first and last visits of four subjects from Markham et al. 1988 were analyzed
- No significant difference was observed between number of mutations observed in rapid versus nonprogressors
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## Markham et al. 1988 showed results concluding higher diversity was found among rapid progressors compared to nonprogressors.

- 16 subjects were compared and placed into categories of nonprogressors, moderate progressors, and rapid progressors based on CD4 T cell decline
- Diversity between the clones of each subject was determined by comparing the number of nucleotide sequence mutations
- Rapid progressors were determined to have a higher diversity

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## Does diversity increase within the amino acid sequences over time more within the rapid progressors compared to nonprogressors?

- Hypothesis: Since diversity increases over time within the DNA sequences for all progressor types, and more so within the rapid progressors, we would expect to see more diversity within the amino acid sequences over time within the rapid progressors.
  - The amino acid sequences in the first and last visits for four subjects were analyzed
  - Using the multiple sequence alignment and ClustalW tool within