

Hypervariable Region I

Hypervariable Region II

Multiple sequence alignment for Hypervariable Region I, showing amino acid sequences for various strains such as MK906026, KF15525, and others, with positions 10 to 240 indicated at the top.

Conservation



Consensus

Consensus sequence for Hypervariable Region I: GAGKRRARRSGATTVAGRAPARETQAKKHEVAGANKAHLKHYSPFAEGNCWCISIAIANRVMNSKFTETLPERVRRPDDIATDELVNTIQRLPALDRNGACASAKYVLKLEGEHNTVSTVGHSPFLPLCEVGGCCHEKGGDPAVDFVSGDFACLDRLAEVHMLPSSAIPAAALAEHMSDGNRP+SPAATVNTVSGFYARHSGGHPDQVCLQKILSLCOVIEDCCCS

Occupancy



Hypervariable Region II

Multiple sequence alignment for Hypervariable Region II, showing amino acid sequences for various strains, with positions 250 to 480 indicated at the top.

Conservation



Consensus

Consensus sequence for Hypervariable Region II: QNKTNRVTFEAAKLDLVLRGATSLAEELAKRPPSVLDTSFDDWVILPGVAAQAQTKLPLVWQRCARVPPVVTQ+SLDKDSVPLTAFSLSNCPYAQDGEVRRHRLNSVLSKLEEVREYGLMSTGGPPFPLPSGLDELKQKHELDLKLNAQATSEHMAAAQVLDLKAWKWYRWPVPPPPRVPQAKTKVSKSLFEGKVPAPRRKRVSDGSPVLMGDNVPSWEDL

Occupancy



Hypervariable Region II

Multiple sequence alignment for Hypervariable Region II, showing amino acid sequences for various strains, with positions 490 to 720 indicated at the top.

Conservation



Consensus

Consensus sequence for Hypervariable Region II: AVGGDLPDPTPEPMTSPSEVLPVFA+RVRPVPVPLSGAPPAPRRTVSRVYPLSEPVPVPRRRKQVQVGAANLTLTQDEPLDLSASSQTEYEAAPLPPQNEGLVEVEQAEVLSIDLININAPVSSSSLSVETRPKYSQAQI1DGGGCGCGLQVKEKYLWSHREACATKLDPAQTQWLSRHWDRVDMLTWNVTSYQAPFLADKFKLPMILTEFP

Occupancy



Hypervariable Region II

Multiple sequence alignment for Hypervariable Region II, showing amino acid sequences for various strains, with positions 730 to 960 indicated at the top.

Conservation



Consensus

Consensus sequence for Hypervariable Region II: VPCGFLVMPRTAPVSGAESDLTIGSVAEDVPRILGKVEVDGTEQDQPLFADQVDDPDKPDRPSSRESDESTQAPPAGTGGALVLDSDGVEVDSCE+STTEK+EDDFVINGASQTSPEFTDLPSSDG+ADGGGLRTVKKKARLFDQLSRQVFLVSHLVPFRRFLKSDGQVSPDQWGAFFTLCLFLVSYVFAFJAPLJLFGSSVSRVRRMVFQGCWLAIVGLFK

Occupancy

