Sheet1

SUPPLEMENTARY TABLE 1

| SUITLEVIENTANT TABLE T | |
|---|--|
| Торіс | Question |
| Source / Purification | Cloned or native |
| | Storage requirements |
| | Describe truncation |
| | Tagged |
| | Tag Name |
| | Full length or truncated |
| Accessory Proteins/Complexes | Nucleotide incorporation accessory protein(s) |
| | Exonuclease accessory protein(s) |
| | Other accessory protein(s) |
| Historical Protein Properties (MW, pl,) | Molecular Weight |
| | Extinction Coefficient |
| | Specific Activity |
| | Isoelectric Point |
| | Sequence URL |
| Nucleotide Incorporation | With Strand Displacement |
| | Processivity |
| | Gap Filling |
| | Maximum Product Length |
| | Nick Extension |
| | With 5' exonuclease activity |
| Nucleotide Analogs / Template Lesions | Incorporation of non-standard nucleotides |
| Nucleolide Analogs / Template Lesions | Template lesions |
| Exonuclease Activity | 3-5' Exo Specific Activity |
| Exonuclease Activity | |
| | 5-3' Exonuclease processivity |
| | 3-5' Exonuclease (proofreading) |
| | 5-3' Exonuclease |
| RNase H Activity | RNase H |
| Terminal Transferase | Terminal Transferase |
| Reverse Transcriptase | Reverse Transcriptase Activity |
| Other Enzymatic Activities | Extension from RNA primer |
| Kinetic Parameters | k _{cat} |
| | K _p |
| | K _M |
| | M |
| | V _{max} |
| Fidelity | Nucleotide Substitution Rate |
| | Frameshift Error Rate |
| | Overall Error Rate |
| Modulators/Inhibitors | K |
| | Percent/Fold Effect |
| Structure and Structure/Function | RNase H Catalytic Triad |
| | 5'-3' Exo Catalytic Triad |
| | 3'-5' Exo Catalytic Triad |
| | Amino Acids Contacting NTP |
| | Amino Acids Contacting Template |
| | Amino Acids Contacting Template Amino Acids Contacting Primer |
| | Polymerase Catalytic Triad Amino Acids |
| | Other Important Residues |
| | Other important Residues |

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Health/Disease Biotech Applications Methods Associated condition Application name Methods Featured