Molecular Biology Protocols /a /l

Error Rates for Thermal Resistant DNA Polymerases

This list was originally compiled by Eric First (erfi@eel.sunet.se) and later posted to the reagnts newsgroup by Paul Hengen (pnh@fcsparc6.ncifcrf.gov). Except where indicate total errors (e.g. base substitutions, frameshifts, etc.). Due to differences in the methods polymerase fidelity it is best to directly compare values for different enzymes only if the same authors. Vent, Deep Vent, and Pfu all possess 3'-5' exonuclease (proofreading) ac

Error Rates

1. Taq (Thermus aquaticus)

1.1×10^{-4} base substitutions/bp	(Tindall and Kunkel
2.4×10^{-5} frameshift mutations/bp	(Tindall and Kunkel
2.1×10^{-4} errors/bp	(Keohavang and Thil
7.2×10^{-5} errors/bp	(Ling et al., 1991)
8.9×10^{-5} errors/bp	(Cariello et al., 1
2.0×10^{-5} errors/bp	(Lundberg et al., 1
1.1×10^{-4} errors/bp	(Barnes, 1992)

2. KlenTaq (Thermus aquaticus, N-terminal deletion mut

5.1×10^{-5} errors/bp	(Barnes, 1992)

3. Vent (Thermococcus litoralis)

2.4×10^{-5} errors/bp	(Cariello et al., 1
4.5×10^{-5} errors/bp	(Ling et al., 1991)
5.7 x 10-5 errors/bp	(Matilla et al., 19

4. Vent(exo-) (Thermococcus litoralis)

1.9×10^{-4} errors/bp	(Matilla et al., 19

5. Deep Vent (Pyrococcus species GB-D)

No published literature. New England Biolabs claims i is equal to or greater than that of Vent.

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fidelity

6. Deep Vent(exo-)
No published literature.

7. Pfu (Pyrococcus furiosus)
1.6 x 10^{-6} errors/base (Lundberg et al., 1

8. Replinase (Thermus flavis)
1.03 x 10^{-4} errors/base (Matilla et al., 19

References:

1. Barnes, W.M. (1992) Gene 112(1), p29-35.
"The Fidelity of Taq polymerase catalyzing PCR is impr
an N-terminal deletion."
Assay: loss of LacZ function.

2. Cariello, N.F., Swenberg, J.A., and Skopek, T.R. (1
Acids
Res 19(15), p4193-4198.
"Fidelity of Thermococcus Litoralis DNA Polymerase (Ve
determined by denaturing gradient gel electrophoresis.
Assay: denaturing gradient gel electrophoresis

3. Eckert, K.A., and Kunkel, T.A. (1990) Nucleic Acids
p3739-
3744.
"High Fidelity DNA synthesis by the Thermus aquaticus
polymerase."
Assay: see Tindall and Kunkel (1988)

4. Eckert, K.A., and Kunkel, T.A. (1991) PCR Methods A
24.
"DNA polymerase fidelity and the polymerase chain reac

5. Keohavong, P., and Thilly, W.G. (1989) Proc Natl Ac
86(23),
p9253-9257.

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1991) Nucleic

ent) in PCR
."

s Res 18(13)

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Appl 1(1) p17-

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Assay: denaturing gradient gel electrophoresis

6. Kong, H., Kucera, R.B., and Jack, W.E. (1993) J Bic
p1965-1975.
"Characterization of a DNA polymerase from the hyperth
archaea Thermococcus litoralis. Vent DNA polymerase,
kinetics, thermal stability, processivity, strand disp
and exonuclease activities."

7. Ling, L.L., Keohavong, P., Dias, C., and Thilly, W.
PCR Methods Appl 1(1) p63-69.
"Optimization of the polymerase chain reaction with re
fidelity: modified T7, Taq, and Vent DNA polymerases."

8. Lundberg, K.S., Shoemaker, D.D., Adams, M.W., Short
J.A.,
and Mathur, E.J. (1991) Gene 108(1), p1-6.
"High-fidelity amplification using a thermostable DNA
isolated from Pyrococcus furiosus."
Assay: loss of LacI (repressor) activity

9. Matilla, P., Korpela, J., Tenkanen, T., and Pitkane
Nucleic Acids Res 19(18), p4967-4973.
"Fidelity of DNA synthesis by the Thermococcus litoral
polymerase--an extremely heat stable enzyme with proof
activity."
Assay: reversion of opal suppressor in LacZ (base sub
forward mutation assay (measures all mutations
The mutation frequencies quoted above were ca
the reversion assay, so they only indicate bas
mutations. No sequence analysis was done in t
determine the relative frequency of base subst
frameshift mutations (as was done in Tindall a

10. Tindall, K.R., and Kunkel, T.A. (1988) Biochemistr
6013.
"Fidelity of DNA synthesis by the Thermus aquaticus DN
Assay: reversion of opal suppressor in LacZ (base sub
forward mutation assay (measures all mutations
sequence analysis of randomly selected mutants

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that 32/42 mutations were base substitutions,
were T to C mutations. Combined results of se
analysis and forward mutation assay to calcula
of base substitution and frameshift mutations.

More recently, there were several discussions in bionet.molbio.methds-reagnts regardin
polymerases for PCR and isolation of home-grown Taq polymerase, which were then r

P. N. Hengen, 1995. Methods and reagents - Fidelity of DNA polymerases for P
Biochemical Sciences 20 (8): 324-325

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