REBASE—restriction enzymes and methylases

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ABSTRACT

REBASE is a comprehensive database of information about restriction enzymes and their associated methylases, including their recognition and cleavage sites and their commercial availability. Also included is a listing of homing endonucleases. Information from REBASE is distributed via monthly electronic mailings as well as through anonymous ftp and the World Wide Web. The REBASE web site (http://www.neb.com/ rebase) contains a web page for every enzyme, reference and supplier. Additionally, there is a search facility, help and NEWS pages, and a complete description of our various services. Specialized files are available that can be used directly by many software packages.

INTRODUCTION

The restriction enzyme database, REBASE, is a comprehensive collection of information about restriction enzymes and DNA methylases. Since the last description of the contents of REBASE (1), 99 new restriction enzymes have been added. These include nine Type II enzymes with new specificities as shown in Table 1. Among the 3015 restriction enzymes now known, there are 19 fully characterized Type I specificities, 221 different Type II specificities and four different Type III specificities. A total of 484 different Type II restriction enzymes are commercially available representing 143 different specificities. Homing endonucleases (2) are also listed in REBASE and seven of the 37 known are commercially available. REBASE currently stores 4692 published references, with abstracts, and 562 unpublished observations.

REBASE is updated daily. Each month, a set of REBASE data files are released publicly and distributed to the scientific community, at no charge, via Email. They can also be retrieved by anonymous ftp (www.neb.com, in pub/rebase) or through the World Wide Web (http://www.neb.com/rebase) or through the World Wide Web (http://www.neb.com/rebase). On the web, each enzyme, reference and supplier have their own page, with links to all related information. A sample enzyme page is shown in Figure 1. Also, we provide datafiles designed for use with a variety of software packages such as GCG, IGSuite, GENEPRO, Staden, DNA Strider, Pro-Cite, PC/Gene, SEQAIDII, GENE-TYX, DNASIS, CAD Gene, Gene Runner, MacVector, EndNote, Readasoft Plasmid, Molecular Biology Insights' OLIGO Primer Analysis Software, PREMIER Biosoft International's Primer Premier and Plasmid Premier, Clone Manager, and Reference Manager. Other data files include a complete set of references, including abstracts, to papers on restriction enzymes and methylases; a list of all commercial suppliers of restriction enzymes and methylases, complete with contact information and a listing of enzymes they currently sell. New data files are constantly being added and each release of REBASE includes a monthly newsletter indicating that the files at the www and ftp sites have been updated, and listing new enzymes, newly available formats, enzyme name changes, etc. To join the mailing list or for more information, contact either author (Email: macelis@neb.com or roberts@neb.com; telephone, +1 978 927 3382; fax, +1 978 921 1527).

Table 1. New Type II restriction enzymes

Enzyme ^a	Recognition sequence ^b	Reference ^c
BbvCI\$	CC^TCA_GC	Ge,L., Krotee,S., Ganatra,M. and Grandoni,R.
BseSI	GKGCMC	Steponaviciene,D., Petrusyte,M., Kairaitiene,R., Kiuduliene,E., Butkus,V. and Janulaitis,A.
BtrI ^{\$}	CAC↓GTC	Abdurashitov,M.A., Belichenko,O.A., Lebedeva,N.A., Dedkov,V.S. and Degtyarev,S.K.
BtsI	GCAGTG	Pan,X.S. and Morgan,R.
HaeIV	GAYNNNNRTC	Piekarowicz,A.
Hpy178III	TCNNGA	Xu,Q. and Blaser,M.
Hpy188IX	TCNGA	Xu,Q. and Blaser,M.
PpiI	GAGNNNNNGTTC	Vitkute,J., Kairaitiene,R., Kiuduliene,E., Petrusyte,M., Butkus,V. and Janulaitis,A.
PsiI ^{\$}	TTATAA	Abdurashitov,M.A., Belichenko,O.A., Lebedeva,N.A. and Degtyarev,S.K.

^aThe endonucleases are named in accordance with the proposal of Smith and Nathans (3). \$ means the enzyme is commercially available.

^bCleavage sites are indicated as \downarrow when cleavage is at the identical position on both strands, ^ indicates cleavage on the strand shown and _ indicates cleavage on the complementary strand. K = G or T; M =A or C; N = any base; Y = C or T; R = A or G.

^cAll references are currently unpublished.

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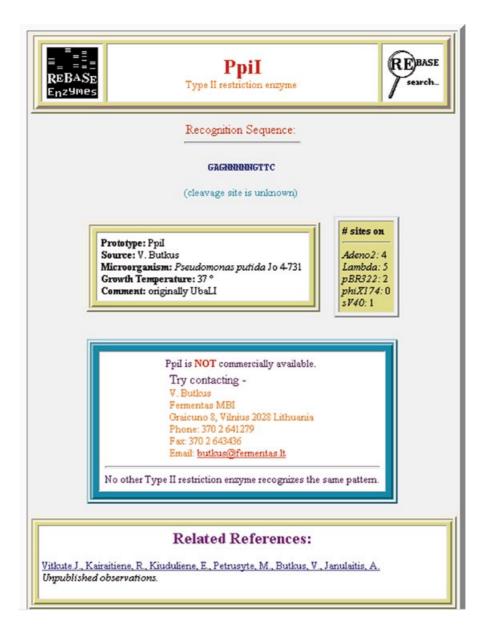


Figure 1. The home page for PpiI (http://www.neb.com/rebase/enz/PpiI.html).

We request that authors use this article to cite REBASE as a general reference for the complete listing that is available electronically.

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REFERENCES

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- 3 Smith,H.O. and Nathans,D.J. (1973) Mol. Biol., 81, 419–423.