CORRESPONDENCE

A universal nomenclature for subunits of the RNA polymerase III transcription initiation factor TFIIB

Ian M. Willis¹

Department of Biochemistry, Albert Einstein College of Medicine, Bronx, New York 10461, USA

At the Cold Spring Harbor Laboratory Meeting on Mechanisms of Eukaryotic Transcription held last summer, László Tora initiated a discussion about the increasingly bewildering nomenclature used to refer to TATA-binding protein-associated factors (TAFs) in different organisms. This problem was most acute for TAFs involved in transcription by RNA polymerase (Pol) II because of the large (and growing) number of these proteins. However, the existing nomenclature was also problematic for TAFs used in transcription by RNA polymerases I and III. In particular, the frequent naming of TAFs according to their molecular mass, which varies among orthologs, created considerable confusion. Recently, a unified and systematic nomenclature for the Pol II TAFs has been adopted (Tora 2002).

Researchers working on RNA polymerase III have now agreed on a universal nomenclature for the proteins that, together with the TATA-binding factor, TBP, comprise the various forms of the Pol III initiation factor TFIIB (Table 1). In considering a universal nomenclature for the subunits of TFIIB, it was widely agreed that the TAF3 designation (where the number denotes Pol III) was not suitable because (1) the B" component is not associated with TBP to any significant degree and (2) the TFIIB-related factor (Brf1), although associated with TBP in most, but not all systems (Hamada et al. 2001), is functionally analogous to a general transcription factor, rather than to any Pol II TAF. The universal nomenclature that has been adopted for TFIIB subunits addresses these and other issues as follows:

1. The BRF nomenclature has been retained for orthologs and paralogs of Brf1.
2. Orthologs of the B" component have been renamed Bdp1 for TFIIB double prime, the name given originally to the biochemical fraction containing this polypeptide (Kassavetis et al. 1991).
3. Genes (denoted by all upper-case italicized letters)

or their protein products (denoted by nonitalicized letters with only the first letter being upper-case) can be additionally annotated when referring to orthologs by applying the two-letter species prefix (Hs, Dm, Ce, Sc, Sp, etc.) as proposed in the unified Pol II TAF nomenclature (Tora 2002).

4. Spliced variants of the subunits, which have been described for *HsBRF1* (McCulloch et al. 2000) and *HsBDP1* (Kelter et al. 2000; Schramm et al. 2000), are designated by a suffix comprising an underscore, a lower-case 'v,' and a number to denote the variant in accordance with the recommendations of the Human Gene Nomenclature Committee. Thus, the fourth variant of human Brf1 to be identified is designated Brf1_v4.
5. The new TFIIB subunit nomenclature conforms to the Guidelines for Human Gene Nomenclature (<http://www.gene.ucl.ac.uk/nomenclature/guidelines.html>) while satisfying the three-letter naming convention used for *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*. Aside from improved communication between researchers, an important benefit of annotations under the same name is the greatly facilitated cross-referencing of entries in different genome databases.

Table 1. Nomenclature for subunits of TFIIB^a

Former name for protein	New protein name
Brf1, TFIIB70 (yeast), Brf, hBRF, hTFIIB90, TAF3C, GTF3B, TAF3B2	Brf1
BRF2	Brd1_v2
BRF3	Brf1_v3
BRF4	Brf1_v4
BRFU, TFIIB50, FLJ11052	Brf2
Tfc5, B", TFIIB90 (yeast), TFIIB150 (human), TAF3B1, TFNR	Bdp1
TFNR exon 15 alternate splicing variant	Bdp1_v2

^aThis nomenclature has been endorsed by the following people: E. Peter Geiduschek, Steven Hahn, Nouria Hernandez, George Kassavetis, Richard Maraia, Robert G. Roeder, Susan Lobo-Ruppert, Michael Schultz, André Sentenac, Martin Teichmann, and Robert J. White.

¹E-MAIL willis@aecom.yu.edu; FAX (718) 430-8565.

Article and publication are at <http://www.genesdev.org/cgi/doi/10.1101/gad.998102>.

Willis

Acknowledgments

On behalf of the Pol III community, I thank Ruth Lovering from the Human Genome Gene Nomenclature Committee for her advice on guidelines and Stephen Bustin, who kindly agreed to rename butyrate response factors 1 and 2 so that the Brf name could be retained for Pol III transcription factors.

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Genes Dev. 2002, **16**:

Access the most recent version at doi:[10.1101/gad.998102](https://doi.org/10.1101/gad.998102)

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