CORRESPONDENCE

A unified nomenclature for TATA box binding protein (TBP)-associated factors (TAFs) involved in RNA polymerase II transcription

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Initiation of transcription by RNA polymerase II (Pol II) requires general transcription factors to assemble the Pol II pre-initiation complex (PIC) (Hampsey 1998). PIC assembly on both TATA-containing and TATA-less promoters can be nucleated by the general transcription factors TFIID or B-TFIID, which are comprised of the TATA-binding protein (TBP) and TBP-associated factors (TAF_{II}s) (Bell and Tora 1999; Albright and Tjian 2000). More than 10 years ago, the first TAF_{II}s were discovered in *Drosophila* and in human cells (Dynlacht et al. 1991; Tanese et al. 1991). These proteins were identified in biochemically stable complexes with TBP and named after their electrophoretic mobility in polyacrylamide gels. Subsequently, many TAF_{II}s from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Caenorhabditis elegans*, *Drosophila melanogaster*, and *Homo sapiens* have been identified. They are distinguished by a number, which indicates their apparent or predicted molecular weight. Cross-species comparisons show a strong sequence conservation of TAF_{II}s (Sanders and Weil 2000; Gangloff et al. 2001; Walker et al. 2001). Availability of genome sequences has accelerated the identification of TAF_{II}-orthologous and -related genes, resulting in uncertainty whether the gene in question encodes a genuine TAF_{II}. From a discussion initiated at the 2001 Cold Spring Harbor Laboratory meeting on Mechanisms of Eukaryotic Transcription it became clear that the current TAF_{II} nomenclature is unsatisfactory. To clarify the relationship between orthologs and paralogs of TAF_{II}s and to avoid confusion stemming from molecular weights we propose a new unified nomenclature for the Pol II TAF_{II}s. We believe that this will (1) aid cross-species comparisons in the literature and sequence databases, (2) facilitate interactions between various laboratories and scientists, (3) expedite literature searches, and (4) avoid confusion caused by similarity in the names of unrelated TAF_{II}s.

The unified nomenclature is based on the following considerations:

1. It now appears evident from a comparison of *Drosophila*, human, and yeast TFIID that there is an essential or "core" set of TAFs that are conserved across many species. These 13 evolutionarily conserved TAFs (Sanders and Weil 2000) have been aligned with their orthologs from different species and designated TAF1 to TAF13 (see Table 1). After extensive discussions this nomenclature was chosen because of its simplicity and because it complies with guidelines endorsed by both the *Saccharomyces* Genome Database (SGD) and the human HUGO Gene Nomenclature Committees.
2. In the new nomenclature the suffix (II) to indicate TAFs involved in Pol II transcription will no longer be used. Discussions are currently underway in the research communities working with other respective TBP-containing complexes, that is, SL1/TIF-1B and TFIIB, to also abandon the suffices (I) and (III) in the Pol I and Pol III literature.
3. If one organism harbors two genes or more belonging to the same TAF family and they have been shown to encode TBP-associated factors in biochemical experiments, these genes will be called, for example, TAF4 and TAF4b. At present, two bona fide paralogous TAF genes have been described belonging to the TAF4 family (human TAF_{II}135 and TAF_{II}105), the TAF5 family (*S. pombe* TAF_{II}72 and TAF_{II}73), and the TAF10 family (*D. melanogaster* TAF_{II}24 and TAF_{II}16) (see Table). This conforms to the SGD, which has used this exception previously (for example, for the ribosomal proteins).

The following scientists have endorsed the use of this nomenclature system: David Auble, Arnie Berk, Keith Blackwell, Martine Collart, Irwin Davidson, Rivka Dikstein, Alberto Ferrús, Jim Goodrich, Patrick Grant, Steve Hahn, Tetsuro Kokubo, Tony Kouzarides, Ruth Lovering (HUGO), James Manley, Ernest Martinez, Michael Meisterernst, Hiroshi Mitsuzawa, Yoshihiro Nakatani, Thomas Oelgeschläger, Frank Pugh, Joseph Reese, Robert Roeder, Georges-André Sentenac, Stephen Smale, Michel Strubin, Kevin Struhl, Naoko Tanese, Marc Timmers, Robert Tjian, Peter Verrijzer, Amy Walker, Edith Wang, David Wassarman, Tony Weil, Fred Winston, and Jerry Workman.

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Table 1. New Pol II TAF nomenclature including the corresponding known orthologs and paralogs

New name	<i>H. sapiens</i> (hs)	<i>D. melanogaster</i> (dm)	<i>C. elegans</i> (ce)		<i>S. cerevisiae</i> (sc)	<i>S. pombe</i> (sp)
			previous name	new name		
TAF1	TAF _{II} 250	TAF _{II} 230	<i>taf-1</i> (W04A8.7)	<i>taf-1</i>	Taf145/130	TAF _{II} 111
TAF2	TAF _{II} 150	TAF _{II} 150	<i>taf-2</i> (Y37F11B.4)	<i>taf-2</i>	Taf150 or TSM1	(T38673)
TAF3	TAF _{II} 140	TAF _{II} 155 or BIP2	(C11G6.1)	<i>taf-3</i>	Taf47	
TAF4	TAF _{II} 130/135	TAF _{II} 110	<i>taf-5</i> (R119.6)	<i>taf-4</i>	Taf48 or MPT1	(T50183)
TAF4b	TAF _{II} 105					
TAF5	TAF _{II} 100	TAF _{II} 80	<i>taf-4</i> (F30F8.8)	<i>taf-5</i>	Taf90	TAF _{II} 72
TAF5b						TAF _{II} 73
TAF5L	PAF65β	Cannonball				
TAF6	TAF _{II} 80	TAF _{II} 60	<i>taf-3.1</i> (W09B6.2)	<i>taf-6.1</i>	Taf60	(CAA20756)
TAF6L	PAF65α	(AAF52013)	<i>taf-3.2</i> (Y37E11AL.8)	<i>taf-6.2</i>		
TAF7	TAF _{II} 55	(AAF54162)	<i>taf-8.1</i> (F54F7.1)	<i>taf-7.1</i>	Taf67	TAF _{II} 62/PTR6
TAF7L	TAF2Q		<i>taf-8.2</i> (Y111B2A.16)	<i>taf-7.2</i>		
TAF8	(BAB71460)	Prodos	(ZK1320.12)	<i>taf-8</i>	Taf65	(T40895)
TAF9	TAF _{II} 32/31	TAF _{II} 40	<i>taf-10</i> (T12D8.7)	<i>taf-9</i>	Taf17	(S62536)
TAF9L	TAF _{II} 31L (AAG09711)					
TAF10	TAF _{II} 30	TAF _{II} 24	<i>taf-11</i> (K03B4.3)	<i>taf-10</i>	Taf25	(T39928)
TAF10b		TAF _{II} 16				
TAF11	TAF _{II} 28	TAF _{II} 30β	<i>taf-7.1</i> (F48D6.1)	<i>taf-11.1</i>	Taf40	(CAA93543)
TAF11L			<i>taf-7.2</i> (K10D3.3)	<i>taf-11.2</i>		
TAF12	TAF _{II} 20/15	TAF _{II} 30α	<i>taf-9</i> (Y56A4.3)	<i>taf-12</i>	Taf61/68	(T37702)
TAF13	TAF _{II} 18	(AAF53875)	<i>taf-6</i> (C14A4.10)	<i>taf-13</i>	Taf19 or FUN81	(CAA19300)
TAF14					Taf30	
TAF15	TAF _{II} 68					
<i>B-TFIID</i>						
BTAF1	TAF _{II} 170/TAF-172	Hel89B	(F15D4.1)	<i>btaf-1</i>	Mot1	(T40642)

- The species from which the TAF gene originates will be indicated by two letters (e.g., hsTAF1 for TAF_{II}250 from *H. sapiens*).
- Paralogous genes, which are found in the same organism to encode factors with homology to known Pol II TAFs, but which have not (yet) shown to be associated in stable complexes with TBP, will be called TAF-like genes, for example, TAF5L. This is the case for human PAF65α, PAF65β, TAF2Q and their orthologs.
- The *C. elegans* TAFs will use a nomenclature originally suggested by the Blackwell laboratory (Walker et al. 2001; i.e., *taf-1* instead of TAF1, but they will keep the proposed numbering between 1 and 13. Furthermore, for reasons that are related to nomenclature recommendations in this organism the TAF-like genes will be called, for example, *taf-6.2*, *taf-7.2*, etc. For all other organisms we propose to follow the unified nomenclature.
- For factors that show significant homology to either group ("essential TAF" or "TAF-like"), but have not been published or for which no biochemical characterization has been performed, accession numbers indicating their existence in the databases have been included in brackets. An empty box means that no orthologs or paralogs have been identified yet.
- For specific TAFs, which do not seem to have a TAF ortholog in other species, TAF14 (*S. cerevisiae*

TAF30) and TAF15 (*H. sapiens* TAF_{II}68) numbers have been assigned.

- The TAF_{II}170/TAF172/89B helicase/MOT1 genes present a special case. These proteins have been identified in biochemically stable complexes with TBP, which can support Pol II transcription in vitro. The *S. cerevisiae* MOT1 gene was first identified genetically and its name has gained wide acceptance in the yeast community. Therefore, we suggest to maintain MOT1 for the yeast gene. For other organisms we propose to use BTAF1 to testify that the protein resides in a complex distinct from TFIID.

The proposed new nomenclature establishes a set of rules and a systematic way to name genes and proteins belonging to the TAF family of nuclear proteins playing a role in Pol II transcription regulation. The nomenclature is flexible enough to accommodate any species-specific subunits as they arise. Thus, the numbering of the essential core TAFs from 1 to 13 should make it easier to recall and to facilitate communication at all levels between researchers working inside and outside of the transcription field.

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