# Unified nomenclature for the winged helix/forkhead transcription factors

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The winged helix/forkhead class of transcription factors is characterized by a 100-amino-acid, monomeric DNA-binding domain. The structure of the DNA-binding domain of one of the class members, hepatocyte nuclear factor 3  $\gamma$  (HNF3 $\gamma$ ), in a complex with a DNA target has been solved (Clark et al. 1993). The DNA-binding domain folds into a variant of the helix–turn–helix motif and is made up of three  $\alpha$  helices and two characteristic large loops, or "wings." Therefore, the DNA-binding motif has been named the winged helix DNA-binding domain.

Over the past 9 years since the identification of the first member of this class, the Drosophila melanogaster gene Fork head, >100 members of this gene family have been identified (for review, see Kaufmann and Knöchel 1996) in species ranging from yeast to human. The rapid accumulation of sequences by many different laboratories has led to the use of multiple names and classification systems, making it very difficult to follow the literature and to name newly characterized winged helix/ forkhead transcription factors. This problem was recognized and discussed at the first International Meeting on Forkhead/Winged Helix Proteins, held in La Jolla, California, in November 1998. At that time a proposal was developed to standardize the nomenclature for these proteins. Fox (Forkhead box) was adopted as the unified symbol for all chordate winged helix/forkhead transcription factors. A winged helix/forkhead nomenclature committee was elected to implement this proposal, in consultation with the community at large. This final proposal has been endorsed by >20 scientists<sup>1</sup> as well as the Human and Mouse Gene Nomenclature Committees.

#### The Fox subclasses

All Fox proteins contain the characteristic 100-aminoacid winged helix domain, that defines this class of tran-

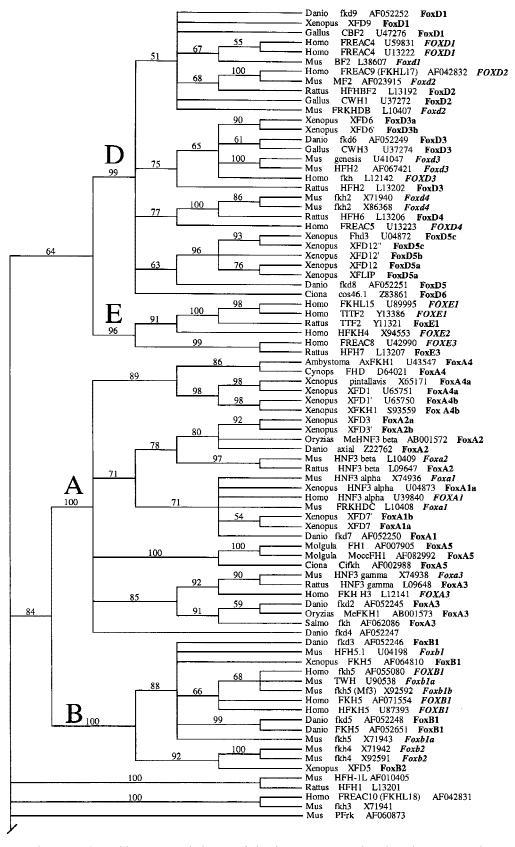
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scription factors. Other portions of the Fox proteins, which encode, for instance, transactivation or trans-repression domains, are highly divergent. We have utilized phylogenetic analysis to delineate 15 subclasses for all known chordate Fox proteins. The analysis included chordate sequences obtained from GenBank and sequences submitted directly to the nomenclature committee. The Fox domains of the proteins were aligned using Clustal W (Thompson et al. 1994), and a neighborjoining tree was generated using PAUP\* 4.0 (Swofford 1999); (Fig. 1). This phylogenetic tree will be updated regularly as new sequences are discovered and may be downloaded from http://www.biology.pomona.edu/fox. html. A complete phylogenetic analysis of all known forkhead proteins will be published elsewhere (D. Martínez and J.E. Signorovitch, pers. comm.).

## Numbering

Fox proteins were assigned to individual subclasses based on the phylogenetic analysis described above. Subclasses were designated by a letter, and within each subclass proteins were given an Arabic numeral. Therefore, the actual name of any Fox protein is "Fox, subclass N, member X'', or for example, Foxd3. Abbreviations for the chordate Fox proteins will contain all uppercase letters for human (e.g., FOXD3); only the first letter capitalized for mouse (e.g., Foxd3); and the first and subclass letters capitalized for all other chordates (e.g., FoxD3). Current assignments for the chordate Fox proteins are listed in Table 1, together with previously used names. Whenever possible we have assigned the same name to ortholog proteins from different species. In a few cases where the phylogenetic affinities were not well resolved by the tree in Figure 1 (e.g., Foxd1 and Foxd2), a within-class phylo-

<sup>1</sup>The following scientists have endorsed the use of this nomenclature system: Frederic G. Barr, William Biggs, Peter Carlsson, James E. Darnell, Sven Enerbäck, Peter Gruss, Brigid Hogan, Andrew D. Hollenbach, Robert Hromas, Tsutomu Kume, Trish Labosky, Eseng Lai, Suzanne C. Li, Naoyuki Miura, Sally A. Moody, Sharon Plon, Hiroshi Sasaki, Günther Schütz, Mathias Treier, Malcolm Whitman, Jeffrey Whitsett, Stella Zannini, and Ken Zaret.



**Figure 1.** (Continued on p. 144) Neighbor-joining phylogeny of chordate Fox proteins based on the amino acid sequence of the Fox domain. The distance measure used was mean character difference. The tree was rooted using *Homo* QRF1 (AF086040) as the outgroup. The numbers in the interior branches are bootstrap percentages. For each protein we indicate the organism (genus), the name, the accession number, and the proposed Fox name.

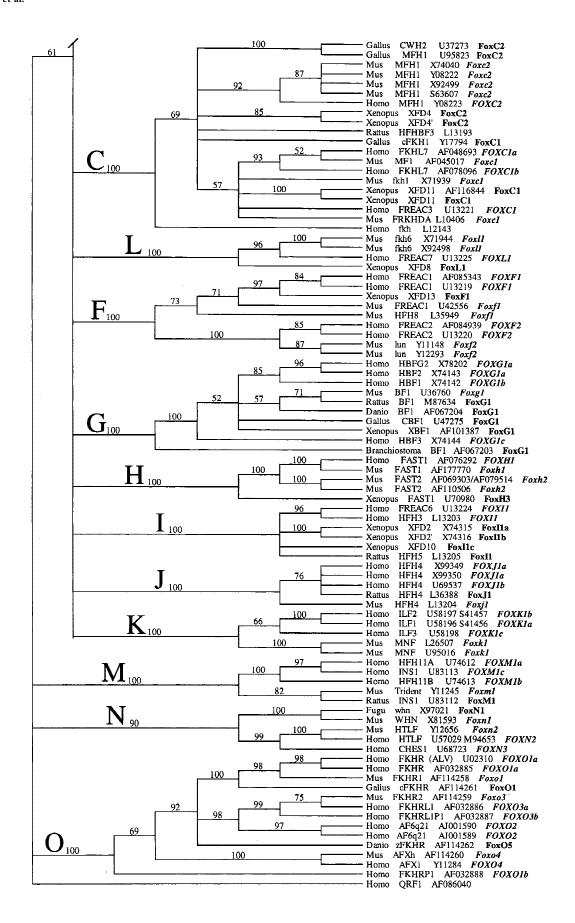


Table 1. A proposed nomenclature for chordate winged helix proteins

Ambystoma mexicanus							4	MUS HIDSCHUS			
Branchiostoma floridae		AF067203	FoxG1	Homo sapiens	hs FREAC10 (FKHL18)	AF042831		Mus musculus	mm (DNA)	Y12294	Fox72
Ciona infestinalis	a Cifkh	AF002988	FoxA5	Homo sapiens	hs HBF1		FOXG1b	Mus musculus	mm MF1	AF045017	Foxe1
Ciona intestinalis	ci cos46.1	Z83861	FoxD6	Homo sapiens	hs HBF2	X74143	FOXG1a	Mus musculus	mm Mf2	AF023915	Foxd2
Cynops pyrrhogaster	<b>\$</b> FHD	D64021	FoxA4	Homo sapiens	hs HBF3	X74144	FOXG1c	Mus musculus	mm MFH1	S63607	Foxc2
Danio rerio	dr axial	222762	FoxA2	Homo sapiens	hs HBFG2	X78202	FOXG18	Mus musculus	mm MFH1	X92499	Foxc2
Danio rerio	dr BF1	AF067204	FoxG1	Homo sapiens	hs HFH3	L13203	FOXIT	Mus musculus	mm MFH1	X74040	Foxc2
Danio rerio	dr fkd2	AF052245	FoxA3	Homo sapiens	he HFH4	U69537	FOXJ16	Mus musculus	mm MFH1	Y08222	Foxe2
Danio rerio	dr Red3	AF052246	FoxB1	Homo sapiens	ns HFH4	X99349 X00350	FOXUL	Mus musculus	LAN EE	/0697	Foxk?
Danio rerio	or fkd4	Ar05224/	;	ното sapiens	ns HFH4	X99350	FOX.13	Mus musculus	JUM EE	910080	-oxx
Danio rerio	dr fkd5	AF052248	FoxB1	Homo sapiens	hs HFH4 (DNA)	X99351	FOXJ18	Mus musculus	mm Ptr	AF060873	•
Danio rerio	dr fkd6	AF052249	FoxD3	Homo sapiens	hs HFH11A	U74812	FOXM1a	Mus musculus	mm Trident	Y11245	Foxm1
Danio rerio	dr fkd7	AF052250	FoxA1	Homo sapiens	hs HFH118	U74613	FOXM18	Mus musculus	HM I mm	090538	Foxb1a
Danio rerio	dr fkd8	AF052251	FoxD5	Homo sapiens	hs HFKH4	X94553	FOXE2	Mus musculus	MM WHIN	X81593	Foxn1
Danio rerio	dr fkd9	AF052252	FoxD	Homo sapiens	ns HFKH5	U87393	FOXB1	Molgula oculata	mo FH1	AF007905	FoxA5
Danio reno	dr FKH5	AF052651	FoxB1	Homo sapiens	US HNF30	039840	FOXA1	Molgura ocurata	mo Mocci H1	AF082992	FoxA5
Danio rerio	dr zFKHR	AF114282	FoxO5	Homo sapiens	hs HTLF	U57029 M94653	FOXNZ	Oryzias latipes	ol Mefkh1	AB001573	FoxA3
Fugu rubripes	fr whn	X97021	FoxN1	Homo sapiens	hs II.F1	U58196 S41456	FOXK12	Onyzias latipes	of MeHNF33	AB001572	FoxA2
Gallus gallus	9g CBF1	U47275	Fox G1	Homo sapiens	hs ILF2	U58197 S41457	FOXK1b	Rattus norvegicus	E :	M87634	Fox G1
Gallus gallus	gg CBF2	U47276	FoxD1	Homo sapiens	hs ILF3	U58198	FOXK1c	Rattus norvegicus	m fkh2 (DNA)	AA956527	
Gallus gallus	gg cFKH	Y17794	FoxCi	Homo sapiens	hs INS1	U83113	FOXM1c	Rattus norvegicus	m FREAC1 (DNA)	AA817785	
Gallus gallus	gg cFKHR	AF114261	Fox01	Homo sepiens	hs MFH1	Y08223	FOXC2	Raffus norvegious	m FREAC1 (DNA)	AA819437	
Gallus gallus	99 CWH1	U37272	FoxD2	Homo sapiens	hs QRF1 (DNA)	AF086040		Rattus norvegicus	a HFH1	L13201	
Gallus gallus	gg CWH2	U37273	FoxC2	Homo sapiens	hs TITF2	Y13386	FOXE1	Raffus norvegicus	m HFH2	L13202	FoxD3
Gallus gallus	gg CWH3	U37274	FoxD3	Mus musculus	mm AFXh	AF114260	Foxo4	Rattus norvegicus	m HFH4	L36388	FoxJ1
Gallus gallus	9g MFH1	U95823	FoxC2	Mus musculus	mm BF1 (HMbf1)	U36760	Foxg1	Rattus norvegicus	m HFH5	L13205	Fox1
Homo sapiens	hs AF6q21	AJ001589	FOX02	Mus musculus	mm BF2	L38607	Foxd1	Raffus norvegicus	m HFH6	L13206	FoxD4
Homo sapiens	hs AF6q21 (exon 1)	AJ001590	FOX02	Mus musculus	mm FAST1	AF177770	Foxh1	Raffus norvegicus	m HFH7	L13207	FoxE3
Homo sapiens	hs AFX1	Y11284	FOXO4	Mus musculus	mm FAST2	AF069303	Foxh2	Rattus norvegicus	m HFHBF2	L13192	FoxD2
Homo sapiens	hs AFX1 (DNA exon 2)	Y11285	FOXO4	Mus musculus	mm FAST2	AF079514	Foxh2	Ratfus norvegicus	m HFHBF3	L13193	
Homo sapiens	hs AFX1 (partial)	U10072	FOXO4	Mus musculus	mm FAST2	AF110506	Foxth2	Rattus norvegicus	HNF36	L09647	FoxA2
Homo sapiens	he AFX1(DNA exon 3)	Y11286	FOXO4	Mus musculus	mm fikh1	X71939	Foxe1	Raffus norvegicus	∃ HNF3γ	L09648	FoxA3
Homo sapiens	hs ALV (PAX3-FKHR)	U02368	FOX01a	Mus musculus	mm fkh2	X86368	Foxd4	Raffus norvegicus	INS!	U83112	FoxM1
Homo sapiens	hs ALV (PAX3-FKHR)	U02308	FOXO1a	Mus musculus	mm fkh2	X71940	Foxd4	Raffus norvegicus	m TTF2	Y11321	FoxE1
Homo sapiens	hs CHES!	U68723	FOXN3	Mus musculus	THE TRAS	X/1941	;	Salmo salar	SSTKI	AF-062086	FOXA3
Homo sepiens	13 1 A3 1	117147	EOVD3	Mus misoulus	mm feba	X02501	Forch?	Yenome feerie	- F- G- S-	104872	EovD5.
Homo seniens	he feb (DNA)	112143	P. CARLO	Mus musculus	mm 645	X71943	Foxb1s	Xenoms facus	A FKH5	AFD64810	FoyR1
Homo caniene	hs FKH H3	112141	FOX43	Mus musculus	mm fkh5 (Mf3)	X92592	Foxb1b	Xenopus faevis	x HNF3a	1104873	Fox A1a
Homo sapiens	hs fkh5	AF055080	FOXB1	Mus musculus	mm fkh6	X71944	Foxt7	Xenopus laevis	xl pintallavis	X65171	FoxA4a
Homo sapiens	ha FKH5	AF071554	FOXB1	Mus musculus	mm fkh6	X92498	Foxd	Xenopus laevis	xl XBF1	AF101387	FoxG1
Homo sapiens	hs FKHL7	AF048693	FOXC1a	Mus musculus	mm Fkh10	AF093879		Xenopus laevis	xl XFD1	U65751	FoxA4a
Homo sapiens	hs FKHL7	AF078096	FOXC1b	Mus musculus	mm FKHR1	AF114258	Foxo1	Xenopus laevis	xl XFD1'	U65750	FoxA4b
Homo sapiens	hs FKHL15	089995	FOXE1	Mus musculus	mm FKHR2	AF114259	Foxo3	Xenopus faevis	xi XFD2	X74315	FoxI1a
Homo sapiens	hs FKHR (ALV)	U02310	FOX018	Mus musculus	mm FREAC1	U42556	Foxfi	Xenopus laevis	xi XFD2'	X74316	FoxHb
Ното заріелз	ha FKHR	U37332	FOX01e	Mus musculus	mm FRKHDA	L10406	Foxe1	Xenopus laevis	X XFD3	*	FoxA2a
Homo sapiens	hs FKHR	AF032885	FOX01a	Mus musculus	mm FRKHDB	L10407	Foxd2	Xenopus laevis	X XFD3'	*	FoxA2b
Homo sapiens	IS FKHK (UNA)	03/335	-cxc1a	Mus musculus	MM FKKHUC	L10408	FOX87	Xenopus laevis	X AFD4	* 3	10XC7
Homo saplens	HE FIXTHEL I PT (DNA)	AF032887	FOXO36	Mus musculus		O4104/	San	Xenous faevis	M XFD5		ForB?
Homo sepiens	hs FKHRP1 (DNA)	AF032888	FOX01b	Mus musculus	mm HFH2	AF067421	Foxe3	Xenopus faevis	X XFD6	*	FoxD3a
Homo sapiens	hs FREAC1	U13219	FOXF1	Mus musculus	mm HFH4	L13204	Foxi1	Xenopus laevis	xl XFD6'	*	FoxD3b
Homo sapiens	hs FREAC1	AF085343	FOXF1	Mus musculus	mm HFH4 (DNA)	AF006200	Foxit	Xenopus laevis	xi XFD7	*	FoxA1a
Homo sapiens	hs FREAC1(DNA exen1)		FOXF1	Mus musculus	mm HFH5.1	004198	Foxb1	Xenopus laevis	xl XFD7"	*	FoxA1b
Homo sapiens	hs FREAC2	U13220	FOXF2	Mus musculus	mm HFH8	L35949	Foxf1	Xenopus laevis	xt XFD8	*	FoxL1
Homo sapiens	hs FREAC2		FOXF2	Mus musculus	mm HNF3g	X74936	Foxa1	Xenopus laevis	X XFD9	*	FoxD
Homo sapiens	hs FREACZ (DNA exon1)		FOXF2	Mus musculus	(ANC) SELVED THE	X/5584	-oxa1	Xenopus laevis	א אינויא א	*	PoxITC
Homo sapiens	ns rkcACs	013221	C COX CO	Mus musculus	mm HNE3a (DNA)	CDDDYX	Foxer	Venopus faevis	N YEDA	*	) ()
Homo sapiens	hs FREACA	1159831	EOXO1	Mus musculus	mm HNF36	104197	Foxe2	Xenopus laevis	X XFD12	÷ *	FoxD5a
Homo sapiens	hs FREAC4	U59832	FOXD1	Mus musculus	mm HNF3ß	L10409	Foxa2	Xenopus laevis	xl XFD12'	*	FoxD5b
Homo sapiens	hs FREAC5	U13223	FOXD4	Mus musculus	mm HNF38	X74937	Foxa2	Xenopus laevis	xl XFD12"	*	FoxD5c
Homo sapiens	hs FREAC6	U13224	FOXI1	Mus musculus	mm HNF3y	X74938	Foxa3	Xenopus faevis	x XFD13	*	FoxF1
Homo sapiens	hs FREAC7	U13225	FOXL1	Mus musculus	mm HTLF	Y12656	Foxn2	Xenopus laevis	X XFKH1	593559	FoxA4b
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Accession nos. submitted to the Fox Nomenclature Committee by W. Knöchel (\*) and S.A. Sullivan and S. Molly (\*\*).

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genetic analysis was performed using the full sequence of the proteins (data not shown). We have used lowercase letters to distinguish between virtually identical proteins (e.g., Foxa4a and Foxa4b), presumably derived from duplicated genes, a case commonly found in polyploid species like *Xenopus laevis*. Please note that the phylogenetic tree includes several proteins that have not received a Fox designation because as yet, their phylogenetic relationships remain unclear due to limited sequence information.

# Naming new sequences

A new Fox protein is defined as a fully sequenced gene, cDNA, or protein that belongs to the Fox family of proteins based on sequence homology of its winged helix DNA-binding domain. We have established a Fox Nomenclature web site (http://www.biology.pomona.edu/fox.html) that provides a form for submitting protein sequences to the Fox Nomenclature Committee. We encourage investigators who have discovered new Fox sequences to submit them to the committee for assignment of the proper Fox name. These sequences will be kept confidential until publication of the sequence by the investigators. We recommend that this new system of nomenclature be used in all future publications.

## References

- Clark, K.L., E.D. Halay, E. Lai, and S.K. Burley. 1993. Co-crystal structure of the HNF-3/fork head DNA-recognition motif resembles histone H5. *Nature* **364:** 412–420.
- Kaufmann, E. and W. Knöchel. 1996. Five years on the wings of fork head. *Mech. Dev.* 57: 3–20.
- Swofford, D.L. 1999. *PAUP\*: Phylogenetic analysis using par*simony and other methods. Sinauer, Sunderland, MA.
- Thompson, J.D., D.G. Higgins, and T.J. Gibson. 1994. CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighing, position specific gap penalties and weight matrix choice. *Nucleic Acid Res.* 22: 4673–4680.