

Table 1 from Hahn *et al.* (2006) *Journal of Experimental Zoology* (in press)
 “Unexpected diversity of aryl hydrocarbon receptors in non-mammalian vertebrates: Insights from comparative genomics”

Table 1. Metazoan PAS and bHLH-PAS genes

Gene symbol ¹	HUGO name	other names ¹	domains ¹	<i>H. sapiens</i>	<i>C. intestinalis</i>	<i>D. melanogaster</i>	<i>C. elegans</i>
AHR	AHR	dioxin receptor	bHLH, PAS	7p21	Ci-AHR	spineless (ss)	ahr-1
AHR2	not assigned		bHLH, PAS	not found			
AHRR	AHRR	KIAA1234, (AHR2, AHR3) ²	bHLH, PAS	5p15			
ARNT	ARNT	HIF-1 β	bHLH, PAS	1q21	Ci-ARNT	tango (tgo)	aha-1
ARNT2	ARNT2		bHLH, PAS	15q24			
HIF-1 α	HIF1A	MOP1	bHLH, PAS, ODD	14q21-24	Ci-HIF	similar (sima)	hif-1
HIF-2 α	EPAS1	EPAS1, HLF, MOP2	bHLH, PAS, ODD	2p21-p16			
HIF-3 α	HIF3A	MOP7, iPAS (splice variant)	bHLH, PAS, ODD	19q13			
SIM1	SIM1		bHLH, PAS	6q21	Ci-Sim	single-minded (sim)	T01D3.2 ³
SIM2	SIM2	SIM	bHLH, PAS	21q22			
CLOCK	CLOCK		bHLH, PAS	4q12	not found	clock (clk)	not found
CLOCK2	NPAS2	NPAS2, MOP4	bHLH, PAS	2q11			
NPAS1	NPAS1	MOP5, TRH1	bHLH, PAS	19q13	Ci-Trh	trachealess (trh)	T01D3.2 ³
NPAS3	NPAS3	MOP6, TRH2	bHLH, PAS	14q12-q13			
NCOA1	NCOA1	SRC1, NRC1, RIP160, HIN-2	bHLH, PAS	2p23	ci0100137333 ⁴	taiman (tai)	not found
NCOA2	NCOA2	NRC2, TIF2, GRIP1	bHLH, PAS	8q13			
NCOA3	NCOA3	NRC3, RAC3, p/CIP, ACTR, AIB1	bHLH, PAS	20q12			
BMAL1	ARNTL	MOP3, JAP3, TIC, ARNTL, ARNT3	bHLH, PAS	11p15	not found	cycle (cyc)	not found
BMAL2	ARNTL2	MOP9, CLIF	bHLH, PAS	12p11			
NXF	NPAS4	MOP22, LE-PAS, dysfusion, PASD10, NPAS4, cranky, (AHR2, AHR4) ²	bHLH, PAS	11q13	Ci-cranky	dysfusion (dys) (cranky, cry)	NXFL (C15C8.2)
Met	not assigned	Rst (JH resistance), gce, CG6211	bHLH, PAS	not found	not found	Met, MetL (2 genes)	not found
KCNH1	KCNH1	EAG1, HERG, ERG1	PAS, ion_tr, CRP	1q32-q41	250019, 261512	ether-a-go-go (eag) (KCNAE)	egl-2
KCNH5	KCNH5	EAG2, HERG2	PAC, ion_tr, CRP	14q23			
KCNH2	KCNH2	ERG1, HERG1	PAS, ion_tr, CRP	7q35-q36			
KCNH6	KCNH6	EAG2, ERG2, HERG2	PAS, ion_tr, CRP	17q23			
KCNH7	KCNH7	HERG3, ERG3	PAS, ion_tr, CRP	2q24			
PDE8A	PDE8A	phosphodiesterase-8A	PAS, PDEase, HDc	15q25	240595	phosphodiesterase 8 (pde8, CG5411)	pde-6
PDE8B	PDE8B	phosphodiesterase-8B	PAS, PDEase, HDc	5q14			
PER1	PER1	period	PAS	17p12	not found	period (per)	not found
PER2	PER2	period	PAS	2q37			
PER3	PER3	period	PAS	1p36			
PASK	PASK	PASkin	PAS, protein kinase	2q37	262860	CG3105	not found

Legend:

A listing of known members of the PAS gene family in *H. sapiens*, *C. intestinalis*, *D. melanogaster*, and *C. elegans*, compiled from our previous work (1-3), other surveys (4-7), and from our recent analysis of completed genomes. For *H. sapiens*, chromosomal locations are given; for other species, gene names are listed. Accession numbers indicate hypothetical (predicted) proteins. Genes are grouped by subfamily (indicated by shading) to illustrate evolutionary (orthologous and paralogous) relationships.

¹Abbreviations of gene names and domains: AHR: aryl hydrocarbon receptor; AHRR: AHR repressor; ARNT: AHR nuclear translocator; HIF: hypoxia-inducible factor; SIM: single-minded; CLK: clock: circadian locomotor output cycles kaput; NPAS: neuronal PAS domain-containing; NCOA: nuclear receptor co-activator; BMAL: brain and muscle ARNT-like; ODD, oxygen-dependent degradation domain; PDE: phosphodiesterase; PER: period; PASK: PAS kinase; Met: methoprene-tolerant; MOP: member of PAS; PDEase: 3',5'-cyclic-nucleotide phosphodiesterase, KCNH: potassium voltage-gated channel, subfamily H; EAG: ether-a-go-go potassium channel; HERG: human ether-a-go-go-related gene; egl-2: egg laying defective family member; bHLH: basic helix-loop-helix; PAS: Per-ARNT-SIM; CRP: cAMP receptor protein domain; HDc: metal dependent phosphohydrolase domain; PAC: PAS-associated, C-terminal domain. HUGO names from: <http://www.gene.ucl.ac.uk/cgi-bin/nomenclature/searchgenes.pl>

²These designations are from previous surveys of bHLH genes in *H. sapiens*, *D. melanogaster*, and *C. elegans* (4-6). As we note in the text, AHRR is a member of the AHR subfamily, while NXF is part of a distinct subfamily of bHLH-PAS genes.

³For this *C. elegans* predicted gene, orthology to specific *Drosophila* and vertebrate genes is uncertain.

⁴A fragment encoding 50 aa of sequence with high % identity to vertebrate NCoA2.

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