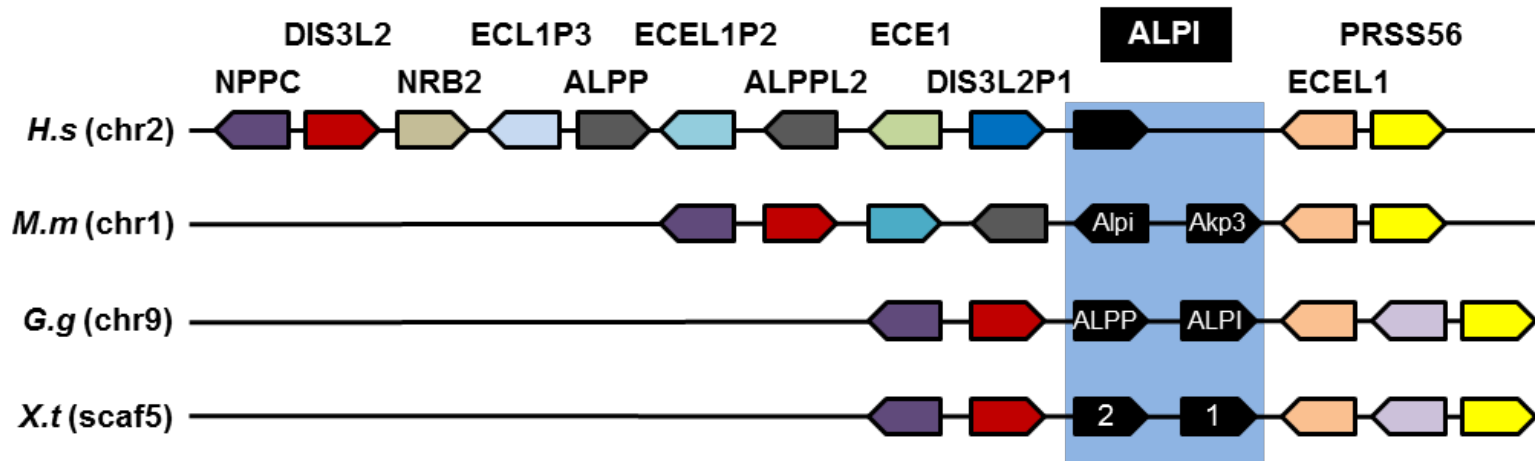


Fig S1. Synteny conservation of the *intestinal alkaline phosphatase (ALPI)* family genes in vertebrate genomes.



Tocco A.^{1,2}, Pinson B.^{3,4}, Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

¹University of Bordeaux, CIRID UMR 5164, F-33000, Bordeaux, France.

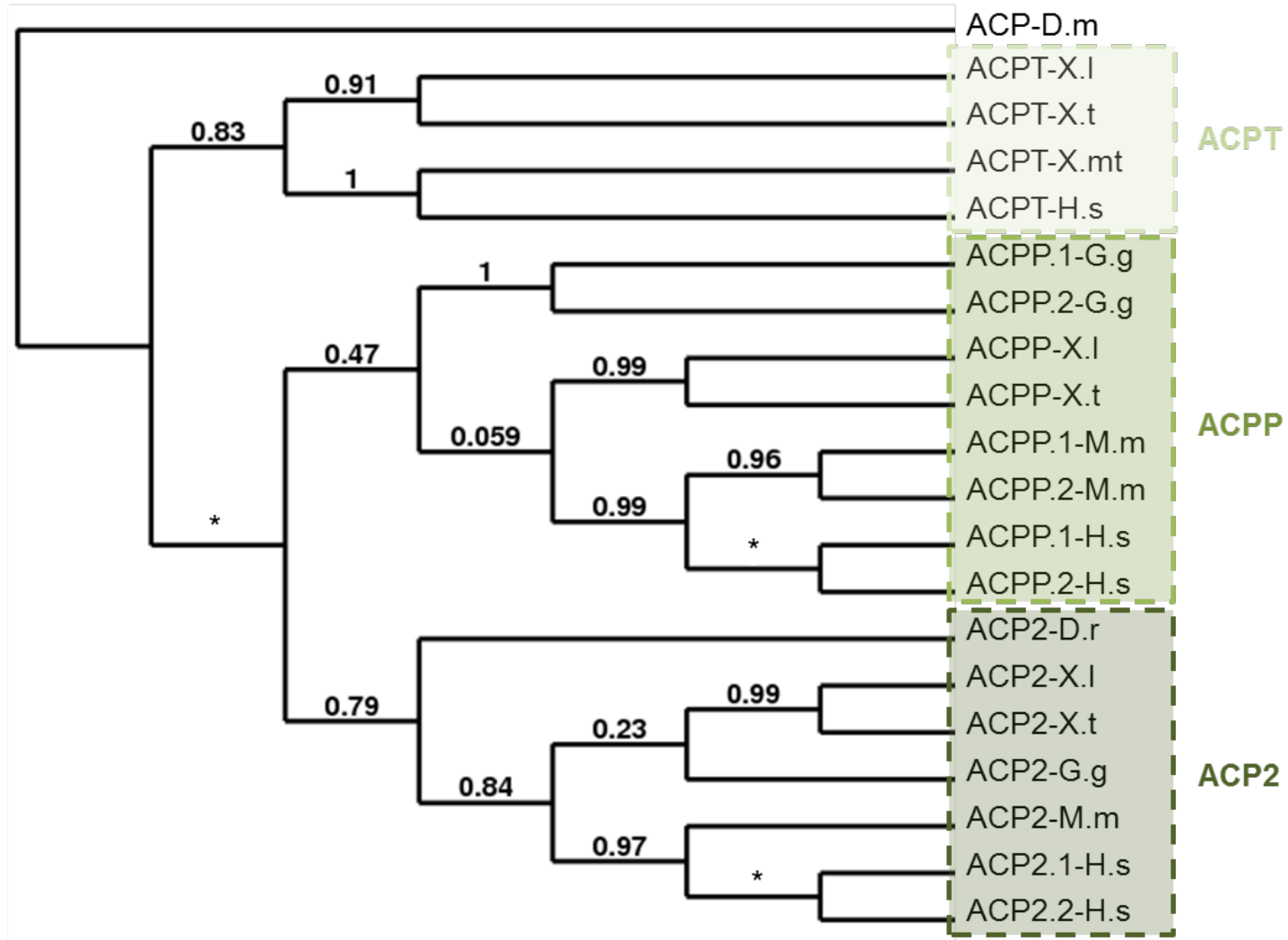
²CNRS, CIRID, UMR 5164, F-33000 Bordeaux, France

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Fig S2. Relatedness of the acid phosphatase (ACP) proteins.



Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*. Purinergic Signalling (2014)

¹University of Bordeaux, CIRID UMR 5164, F-33000, Bordeaux, France.

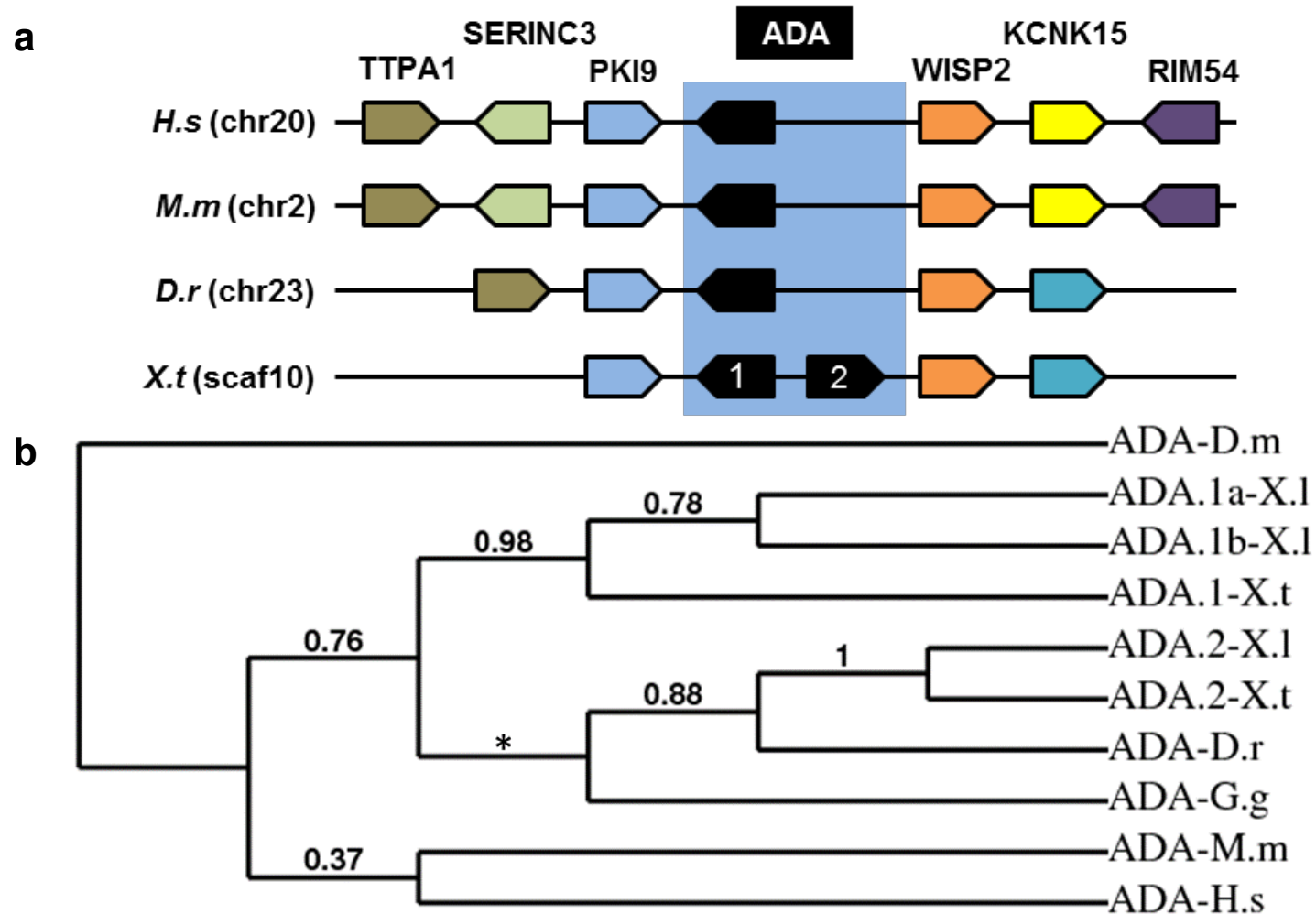
²CNRS, CIRID, UMR 5164, F-33000 Bordeaux, France

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⁴ CNRS, IBGC UMR 5095 1, F-33077 Bordeaux, France

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Fig S3. Conservative evolution of the *adenosine deaminase (ADA)* genes.



Tocco A.^{1,2}, Pinson B.^{3,4}, Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

¹University of Bordeaux, CIRID UMR 5164, F-33000, Bordeaux, France.

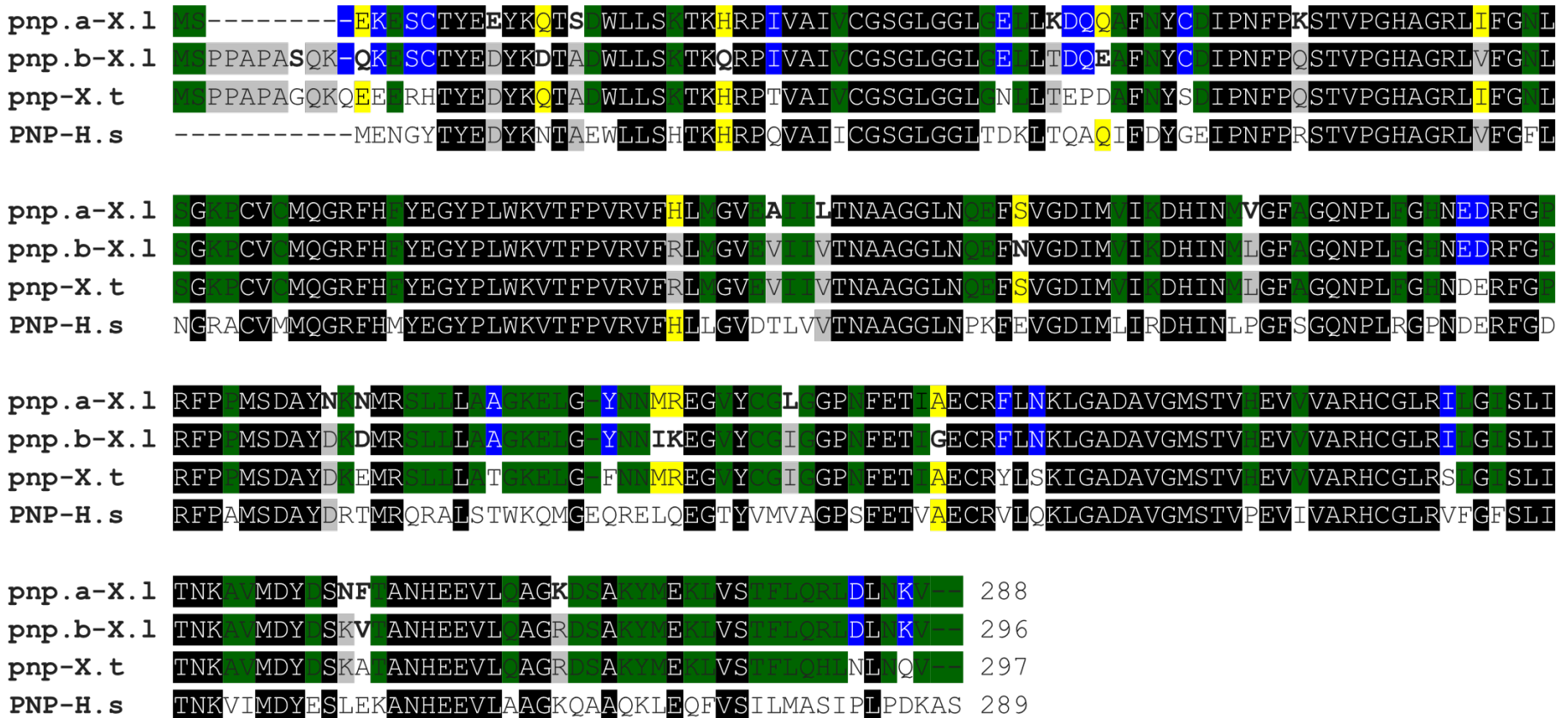
²CNRS, CIRID, UMR 5164, F-33000 Bordeaux, France

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Fig S4a. Conservative evolution of *purine nucleoside phosphorylase (PNP)* genes.



Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.**

Purinergic Signalling (2014)

¹University of Bordeaux, CIRID UMR 5164, F-33000, Bordeaux, France.

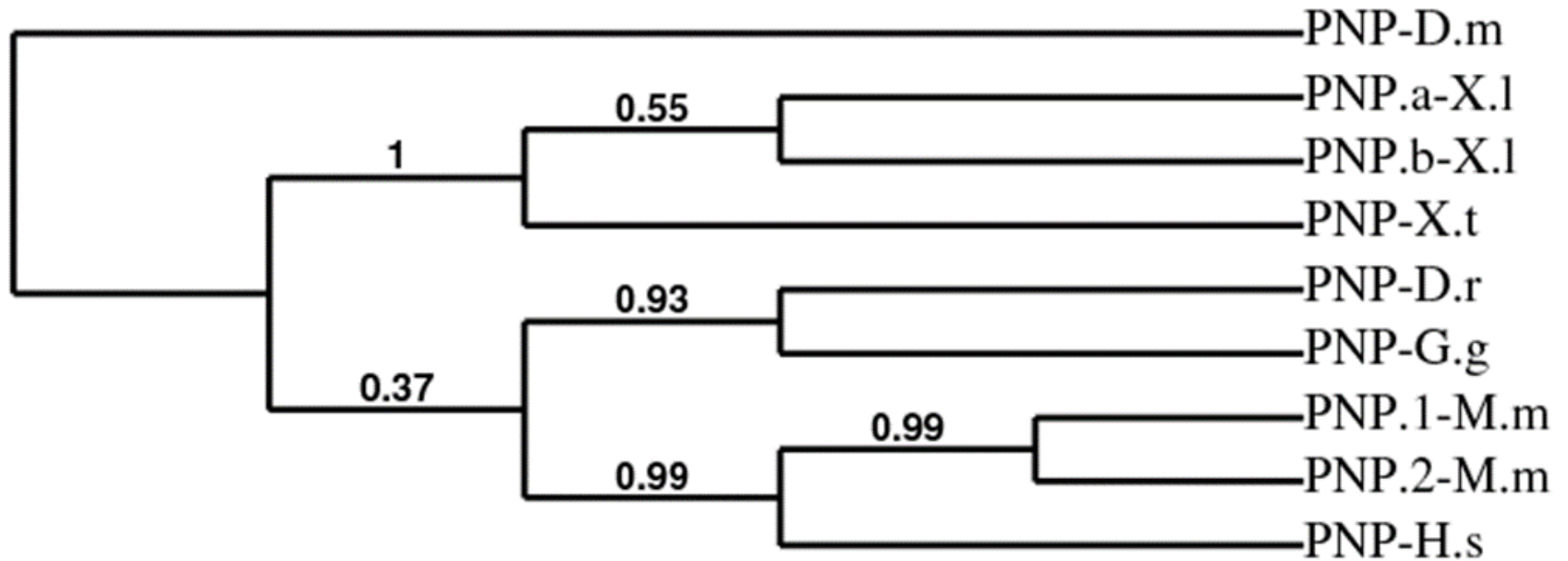
²CNRS, CIRID, UMR 5164, F-33000 Bordeaux, France

³Université de Bordeaux, IBGC UMR 5095 1, F-33077 Bordeaux, France

⁴CNRS, IBGC UMR 5095 1, F-33077 Bordeaux, France

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Fig S4b. Conservative evolution of *purine nucleoside phosphorylase (PNP)* genes.



Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

¹University of Bordeaux, CIRID UMR 5164, F-33000, Bordeaux, France.

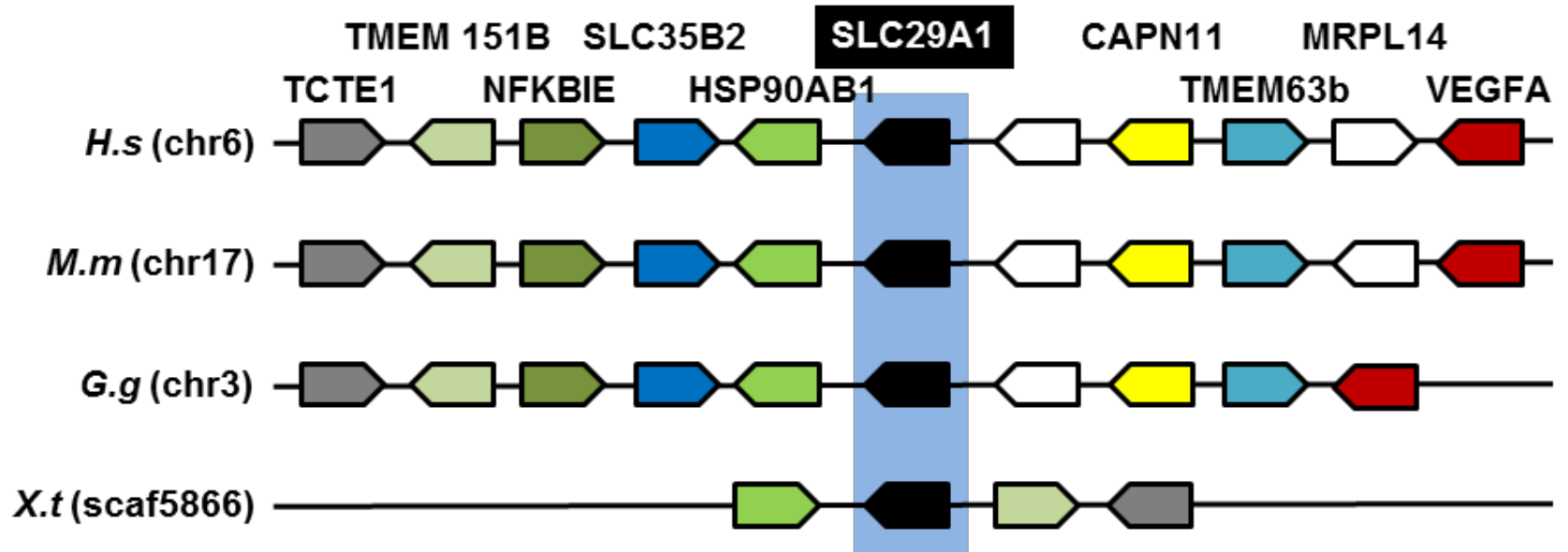
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Fig S5a. Conservative evolution of the *equilibrative nucleoside transporter* (*SLC29A*) genes.



Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

¹University of Bordeaux, CIRID UMR 5164, F-33000, Bordeaux, France.

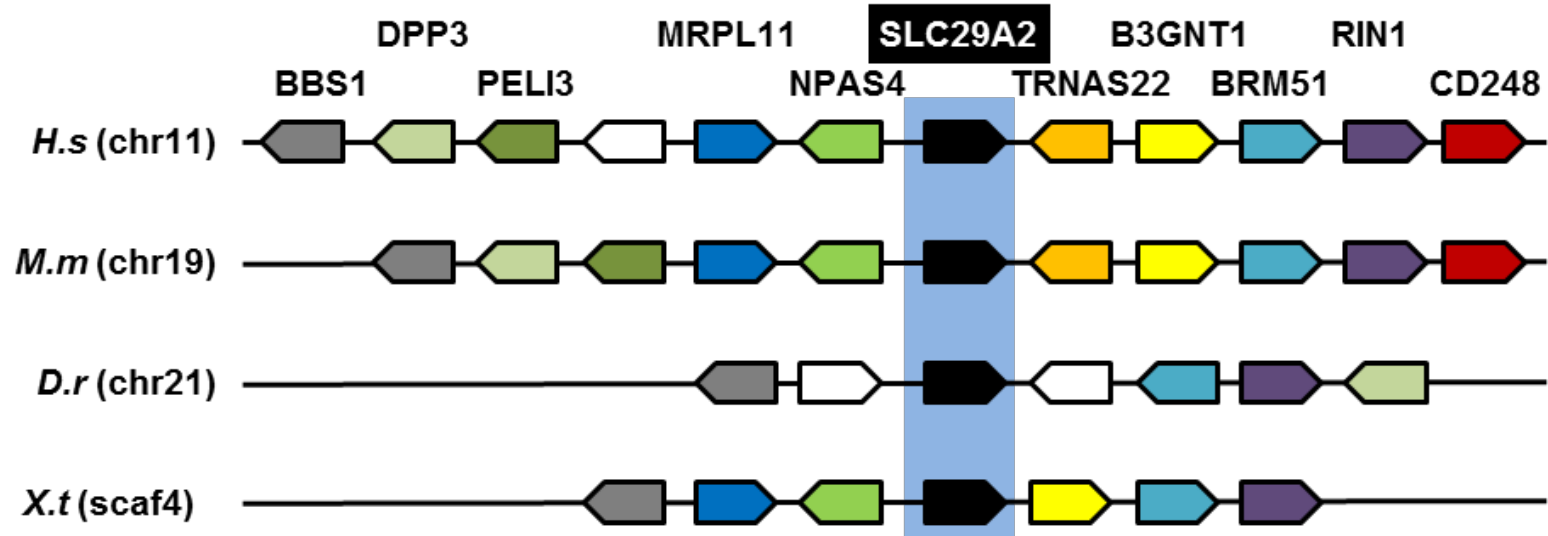
²CNRS, CIRID, UMR 5164, F-33000 Bordeaux, France

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Fig S5b. Conservative evolution of the *equilibrative nucleoside transporter* (*SLC29A*) genes.



Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

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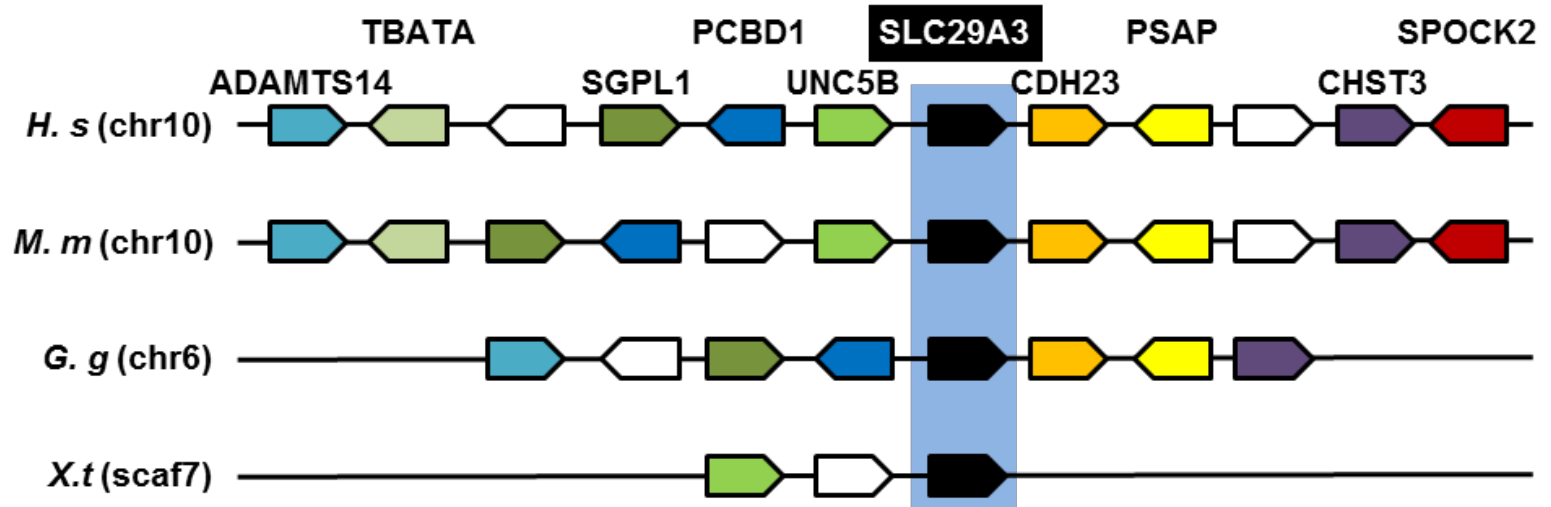
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Fig S5c. Conservative evolution of the *equilibrative nucleoside transporter* (*SLC29A*) genes.



Tocco A.^{1,2}, Pinson B.^{3,4}, Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

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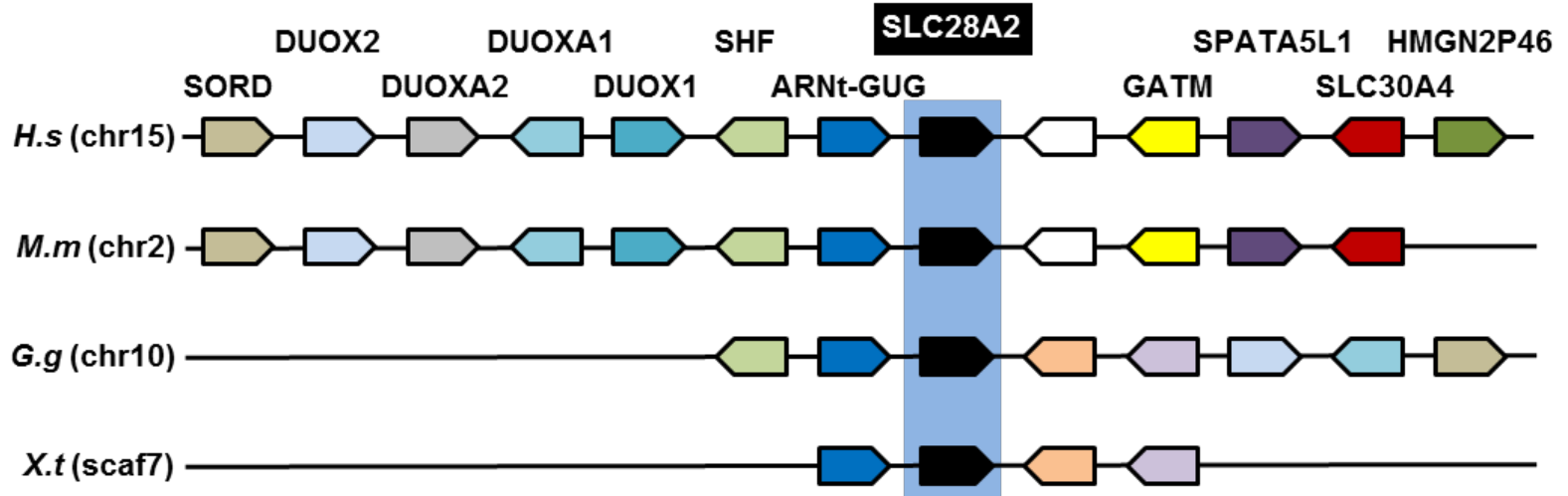
²CNRS, CIRID, UMR 5164, F-33000 Bordeaux, France

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Fig S6a. Conservative evolution of the *concentrative nucleoside transporter (SLC28A)* genes.



Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

¹University of Bordeaux, CIRID UMR 5164, F-33000, Bordeaux, France.

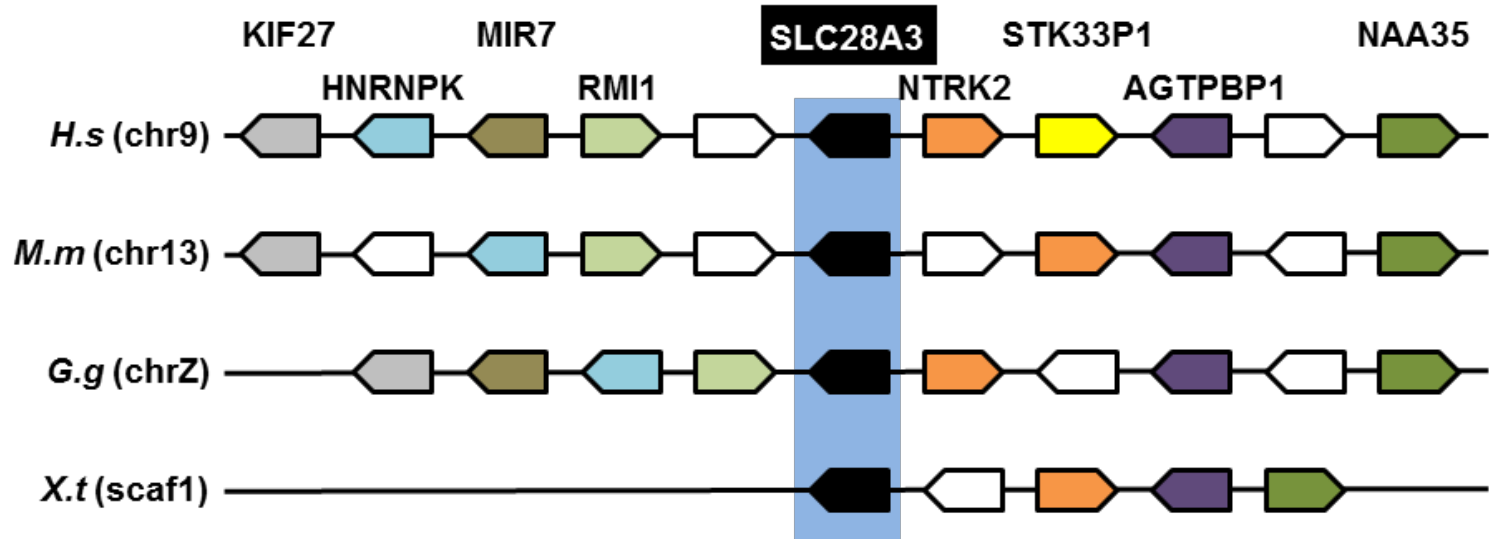
²CNRS, CIRID, UMR 5164, F-33000 Bordeaux, France

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Fig S6b. Conservative evolution of the *concentrative nucleoside transporter* (*SLC28A*) genes.



Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

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Table S1. Accession numbers of the different adenosine members clones used in this study.

Name		<i>X.laevis</i>				<i>X.tropicalis</i>		
Gene	Protein	Homeologue	GeneID	DNA	Protein	Gene ID	DNA	Protein
<i>nt5e</i>	<i>cd73</i>	N.d.	734513	NM_001095994	NP_001089463	100489347	XM_002933927	XP_002933973
<i>alpl</i>	<i>tnap</i>	N.d.	380589	NM_001087426	NP_001080895	100485467	XM_002943439	XP_002943485
<i>alpi.1</i>	<i>iap.1</i>	N.d.	100036885	NM_001097666	NP_001091135	548375	XM_002937341	XP_002937387
<i>alpi.2</i>	<i>iap.2</i>	N.d.	100127270	NM_001112847	NP_001106318	100144722	NM_001123474	NP_001116946
<i>acpt</i>	<i>tacp</i>	N.d.	446918	NM_001093611	NP_001087080	100494856	XM_002934647	XP_002934693
<i>acpp</i>	<i>pacp</i>	N.d.	N.d.	This work	This work	101735257	XM_004915370	XP_004915427
<i>adora1</i>	<i>a1</i>	<i>a</i>	378623	NM_001085844	NP_001079313	100127730	NM_001113069	NP_001106540
		<i>b</i>	N.d.	This work	This work			
<i>adora2a</i>	<i>a2a</i>	<i>a</i>	495175	NM_001094867	NP_001088336	100127551	XM_002938923	NP_001106398
		<i>b</i>	N.d.	This work	This work			
<i>adora2b</i>	<i>a2b</i>	<i>a</i>	N.d.	This work	This work	100496230	XM_002938923	XP_002938969
		<i>b</i>	N.d.	This work	This work			
<i>adora3.1</i>	<i>a3.1</i>	N.d.	N.d.	This work	This work	100496142	XM_002932802	XP_002932848
<i>adora3.2</i>	<i>a3.2</i>	N.d.	N.d.	This work	This work	100496301	XM_002932803	XP_002932849
<i>adora3.3</i>	<i>a3.3</i>	N.d.	N.d.	This work	This work	101734629	XM_004910728	XP_004910785
<i>adk</i>	<i>adk</i>	N.d.	444786	NM_001092888	NP_001086357	549452	NM_001016698	NP_001016698
<i>ada.1</i>	<i>ada.1</i>	<i>a</i>	444167	NM_001092271	NP_001085740	496434	NM_001011025	NP_001011025
		<i>b</i>	N.d.	This work	This work			
<i>ada.2</i>	<i>ada.2</i>	N.d.	447564	NM_001094271	NP_001087740	100135194	NM_001113897	NP_001107369
<i>pnp</i>	<i>pnp</i>	<i>a</i>	379499	NM_001086340	NP_001079809	448370	NM_001006719	NP_001006720
		<i>b</i>	N.d.	BC047264	This work			
<i>slc29a1</i>	<i>ent1</i>	<i>a</i>	496024	NM_001095291	NP_001088760	548435	NM_001015718	NP_001015718
		<i>b</i>	398868	NM_001089858	NP_001083327			
<i>slc29a2</i>	<i>ent2</i>	N.d.	444417	NM_001092519	NP_001085988	548864	NM_001016110	NP_001016110
<i>slc29a3</i>	<i>ent3</i>	<i>a</i>	445860	BC077451	AAH77451	100037858	NM_001097303	NP_001090772
		<i>b</i>	N.d.	This work	This work			
<i>slc28a2</i>	<i>cnt2</i>	N.d.	446617	NM_001093313	NP_001086782	100496776	XM_002934569	XP_002934615
<i>slc28a3</i>	<i>cnt3</i>	N.d.	N.d.	This work	This work	100492606	XM_002934977	XP_002935023

N.d.: not determined

Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.**

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Table S2. Primer sequences and PCR conditions for the required markers

	Primers (5'-3')	cDNA size (bp)	Genomic DNA size (bp)	Cycle s	Anneling temperature (°C)	References
<i>cd73</i>	U-GGCGTGAAGCTGCTTAT D-CAGTGCCCAACCTGTAGT	212	22 034	31	55	This work
<i>alpl</i>	U-TTGCCCACTAGCCCAAGCCC D-GAGGGTCCCCAGCAGGAGCA	169	10 750	29	61	This work
<i>alpi.1</i>	U-TCTCCTCCGCAACACATGT D-GGTCAGTTCTGTTGAACC	435	4 304	27	61	This work
<i>alpi.2</i>	U-CTATCCTCTCCCCGATGT D-CTGGATTTCCTCTGCATC	523	1 843	31	56	This work
<i>acpt</i>	U-ACAGCACCCCTCATAGCGTTA D-AGACAGAACAGCATCACGGT	354	1 828	31	61	This work
<i>adora1</i>	U-GCCTTGGTCATCCCACTCGCC D-GGACAGCACCAACATCCCGT	228 (a) / 232 (b)	24 478 (a) / 26 527 (b)	30	59	This work
<i>adora2a</i>	U-ATTGCAATTAGTACCGATTTTGT D-TTCTCCACATGTCACTTTTCATTTT	456 (a) / 453 (b)	4 970 (a) / 4 422 (b)	32	59	This work
<i>adora2b</i>	U-GGCCGTGGCCATTGACAGGTA D-AGCTGCTTACGGGCAACCATGA	327 (a) / ? (b)	48 274 (a) / >38 546 (b)	30	61	This work
<i>adora 3.1</i>	U-GGGTAATGAGACAGCCGAA D-CCTGCAGAAGATCCTGGTTG	355	5 829	33	60	This work
<i>adora3.3</i>	U-GATGAAGATTTTCATCTACA D-CTCCTCACGTTTTTTGAATT	321	11 427	34	55	This work
<i>adk</i>	U-CGGGGTTCTTCTCAGTC D-ACGTAGCAGCTTCCGTTTCA	186	15 826	24	63	This work
<i>ada.1</i>	U-CAAACCTCCCGCAGACACGGT D-GTGCCCGGGGTACGACTCAC	481 (a) / 481 (b)	6438 (a) / 8546 (b)	30	61	This work
<i>ada.2</i>	U-GTTGAGACGGAAGCCAAACAAG D-TCTTTGACCACTGAAGTGGCC	416	> 3000	31	61	This work
<i>pnp</i>	U-TAGCTGCTGGCAAGGAGCTGGGT D-TGTTGCCAACCCGCAGCTGTTCT	503 (a) / 510 (b)	1574 (a) / 2576 (b)	28	61	This work
<i>pnp.b</i>	U-TTCTGGGAGCTGTAGCCCGTCA D-GCTGGCGTCACATGGACACAAAA	510	510	30	61	This work
<i>slc29a1.a</i>	U-AATGCCCGACAGACCCGTACAA D-AGGTAAGTCCGAGGTGCTACCA	250	3817	28	61	This work
<i>scl29a2</i>	U-CAAGTACCGCTTGGTCGCTGTT D-TAGGTCTGAGGAAGGAGATCAG	485	4555	29	61	This work
<i>slc29a3</i>	U-GGGCTTCATTGCCCTGGAACCTT D-GACATGGCACCGATGGAACAGC	164 (a) / 168 (b)	2988 (a) / 1975 (b)	28	61	This work
<i>slc28a2</i>	U-CTATCCTGAGGTGGAAGAATCA D-ATTCCGATAATTGCCTGTAGGC	362	1434	30	61	This work
<i>slc28a3</i>	U-GCTAGCAGCAAGGTCTTAAG D-GCCTTCATATCTGTCCATGA	333	8043	29	61	This work
<i>odc</i>	U-GGAGCTGCAATTTGAGA D-TCAGTTGCCAGTGTGGTC	131	220	20	55	Bassez <i>et al.</i> , 1990
<i>ef1a</i>	U-CAGATTGGTGCTGGATATGC D-CACTGCCTTGATGACTCCTA	270	N. d.	20	55	Mohun <i>et al.</i> , 1989

N.d.: not determined

Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2},
Massé K. ^{1,2,*}. **Comparative genomic and
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Table S3. Cloning strategy used to identify *Xenopus* adenosine pathway genes.

Gene	<i>X.laevis</i>	<i>X.tropicalis</i>
<i>cd73</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>alpl</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>alpi.1</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>alpi.2</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>acpt</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>acp2</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>acpp</i>	BLAST search (genomic sequence)	Xenbase query (FL clone)
<i>adora 1.a</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>adora 1.b</i>	BLAST search (genomic sequence)	BLAST search (genomic sequence) Not found
<i>adora 2a.a</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>adora 2a.b</i>	BLAST search (genomic sequence)	BLAST search (genomic sequence) Not found
<i>adora 2b.a</i>	BLAST search (genomic sequence)	Xenbase query (FL clone)
<i>adora 2b.b</i>	BLAST search (genomic sequence)	BLAST search (genomic sequence) Not found
<i>adora 3.1</i>	BLAST search (genomic sequence)	Xenbase query (FL clone)
<i>adora 3.2</i>	BLAST search (genomic sequence)	Xenbase query (FL clone)
<i>adora 3.3</i>	BLAST search (genomic sequence)	Xenbase query (FL clone)
<i>adk</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>ada.1a</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>ada.1b</i>	BLAST search (genomic sequence)	BLAST search (genomic sequence) Not found
<i>ada.2</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>pnp.a</i>	BLAST search (genomic sequence)	Xenbase query (FL clone)
<i>pnp.b</i>	Xenbase query (FL clone)	BLAST search (genomic sequence) Not found
<i>slc29a1.a</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>slc29a1.b</i>	Xenbase query (FL clone)	BLAST search (genomic sequence) Not found
<i>slc29a2</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>slc29a3.a</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>slc29a3.b</i>	BLAST search (genomic sequence)	BLAST search (genomic sequence) Not found
<i>slc28a2</i>	Xenbase query (FL clone)	Xenbase query (FL clone)
<i>slc28a3</i>	BLAST search (genomic sequence)	Xenbase query (FL clone)

: Full Length

Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.

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Table S4. Identity conservation between *Xenopus* acid phosphatase proteins and their human orthologs.

		ACPT			ACPP				ACP2			
		X.l	X.t	H.s	X.l	X.t	.1 H.s	.2 H.s	X.l	X.t	.1 H.s	.2 H.s
ACPT	X.l	100										
	X.t	88.3	100									
	H.s	45.2	46.1	100								
ACPP	X.l	41.1	42.8	36.1	100							
	X.t	39.6	40.8	36.8	81.0	100						
	.1 H.s	42.1	41.4	39.0	51.0	48.1	100					
	.2 H.s	44.6	44.0	41.2	49.5	49.7	98.2	100				
ACP2	X.l	44.5	44.7	39.2	42.8	43.2	46.2	49.5	100			
	X.t	41.7	41.6	40.1	41.8	41.5	45.5	48.5	76.6	100		
	.1 H.s	43.8	45.1	41.4	46.3	45.1	45.5	47.4	58.6	58.9	100	
	.2 H.s	46.9	47.5	46.9	51.3	48.8	49.4	49.4	56.9	58.8	93.8	100

Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

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Table S5. Identity conservation between *Xenopus ada* proteins and their human orthologs.

		X.l			X.t		H.s
		ADA.1a	ADA.1b	ADA.2	ADA.1	ADA.2	
X.l	ADA.1a	100					
	ADA.1b	94.4	100				
	ADA.2	66.2	65.4	100			
X.t	ADA.1	95.8	94.1	67.9	100		
	ADA.2	67.7	68.0	91.0	68.3	100	
H.s		69.0	68.0	57.8	70.4	59.3	100

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Table S6. Identity conservation between *Xenopus* pnp proteins and their human orthologues.

	PNP.a X.l	PNP.b X.l	PNP X.t	PNP H.s
PNP.a X.l	100			
PNP.b X.l	89.9	100		
PNP X.t	86.8	89.9	100	
PNP H.s	65.5	63.3	64.7	100

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Table S7. Identity conservation between *Xenopus* SLC29A proteins and their human orthologs.

		X.l					X.t			H.s				
		SLC29A1.a	SLC29A1.b	SLC29A2	SLC29A3.a	SLC29A3.b	SLC29A1	SLC29A2	SLC29A3	SLC29A1	SLC29A2	SLC29A3a	SLC29A3b	SLC29A4
X.l	SLC29A1.a	100												
	SLC29A1.b	91.8	100											
	SLC29A2	45.5	44.4	100										
	SLC29A3.a	32.0	33.3	31.0	100									
	SLC29A3.b	31.2	32.2	30.3	89.7	100								
X.t	SLC29A1	88.4	90.2	46.6	33.6	32.8	100							
	SLC29A2	47.8	47.5	89.3	32.1	31.0	47.9	100						
	SLC29A3	24.5	24.5	27.9	85.1	83.6	25.0	26.4	100					
H.s	SLC29A1	61.2	61.4	44.9	34.9	34.4	61.1	46.9	29.3	100				
	SLC29A2	47.8	47.9	59.2	32.7	32.2	48.6	60.1	29.3	46.7	100			
	SLC29A3a	29.9	30.5	25.5	52.4	51.4	30.4	26.2	22.2	30.2	29.1	100		
	SLC29A3b	13.7	14.4	14.4	25.5	28.1	13.9	14.9	33.5	14.1	15.9	54.3	100	
	SLC29A4	21.4	21.3	21.2	20.5	19.2	22.9	22.9	15.4	21.1	23.3	23.1	11.9	100

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Table S8. Identity conservation between *Xenopus* SLC28A proteins and their human orthologs.

		X.l		X.t		H.s		
		SLC28A2	SLC28A3	SLC28A2	SLC28A3	SLC28A1	SLC28A2	SLC28A3
X.l	SLC28A2	100						
	SLC28A3	45.0	100					
X.t	SLC28A2	90.9	45.4	100				
	SLC28A3	48.7	91.1	49.8	100			
H.s	SLC28A1	58.0	40.5	56.1	42.7	100		
	SLC28A2	56.6	41.0	56.1	43.0	63.0	100	
	SLC28A3	46.4	62.0	44.8	63.4	42.1	40.9	100

Tocco A.^{1,2}, Pinson B.^{3,4} Thiébaud P.^{1,2}, Thézé N.^{1,2}, Massé K.^{1,2,*}. **Comparative genomic and expression analysis of the adenosine signalling pathway members in *Xenopus*.** Purinergic Signalling (2014)

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