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AD15_HUMAN	GGVNM	DHSTSILGVASSIA	HELGHSLGLD	HDLPGN	SCPCPGPAPAK	TCIM	EASTD	FLPGL	388
AD15_PANTR	GGVNM	DHSTSILGVASSIA	HELGHSLGLD	HDLPGN	SCPCPGPAPAK	TCIM	EASTD	FLPGL	405
AD15_CANFA	GGVNM	DHSTSILGVASSIA	HELGHSLGLD	HDLPGN	SCPCPGPAPAK	SCIM	EASTD	FLPGL	390
AD15_BOVIN	GGVNM	DHSTSILGVASSIA	HELGHSLGLD	HDSPGN	SCPCPGPAPAK	SCIM	QASTD	FLPGL	389
AD15_MOUSE	GGVNM	DHSTSILGVASSIA	HELGHSLGLD	HDSPGH	SCPCPGPAPAK	SCIM	EASTD	FLPGL	389
AD15_RAT	GGVNM	DHSTSILGVASSIA	HELGHSLGLD	HDSPGN	SCPCPGPAPAK	SCIM	EASTD	FLPGL	390
AD15_XENLA	GGVSM	DHSVTILGVASTLA	HQLGHN	LGLSHD	-DRKCGQPS	KGKK	--WIME	PSGGFLPGL	366
AD15_XENTR	GGVSM	DHSVTILGVASTLA	HQLGHN	LGLSHD	-DRKCGQPS	KGKK	--WIME	PSAGFLPGL	382
AD15a_DANRE	GGVNV	DHLVSVLGVASTVA	HELGHNL	GMSHD	TADRRCHCQNE	PLGGC	IMEP	STGFMPGQ	349
AD15b_DANRE	GGVNV	DHLVSVLGVASTVA	HELGHNL	GMSHD	TADRRCHCQNE	PLGGC	IMEP	STGFMPGQ	332

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AD15_HUMAN	NFSNCS	RRALEKALLD	GMGSC	LFERLP	SLPPMAA	-FCGNMF	VEPGE	QCDCG	FLDDC	VDP	447
AD15_PANTR	NFSNCS	RRALEKALLD	GMGSC	LFERLP	SLPTMAA	-FCGNMF	VEPGE	QCDCG	FLDDC	IDP	464
AD15_CANFA	NFSNCS	RQALEKALLD	GMGSC	LFERLP	SLPSMAT	-VCGNMF	VEPGE	QCDCG	FPDDCT	DP	449
AD15_BOVIN	NFSNCS	RQALEEALLG	MGSC	LFERLP	SLGPMAS	-VCGNMF	VEPGE	QCDCG	FPDECT	DP	448
AD15_MOUSE	NFSNCS	RQALEKALLD	GMGSC	LFERLP	SLAPMSS	-LCGNMF	VDPE	QCDCG	FPDECT	DP	448
AD15_RAT	NFSNCS	RWALEKALLD	GMGSC	LFEWPP	SLAPMSS	-LCGNMF	VDPE	QCDCG	FPDECT	DP	449
AD15_XENLA	EFSNCS	FDTLEFSLRR	GGGMC	LFNVPP	PKRLFGE	PQCGN	FLVEE	GEQCDC	GLSQE	CTDQC	426
AD15_XENTR	EFSNCS	LADLEFSLRR	GGGMC	LFNVPP	PKRLFGE	PQCGN	FLVEE	GEQCDC	GLTQD	CDP	442
AD15a_DANRE	LFSSC	SERDLSLSLL	HGGMC	LFNVQP	ESLLGG	PCGNLY	VEKGE	ECDCG	LLDECN	DP	409
AD15b_DANRE	LFSSC	SERDLSLSLL	HGGMC	LFNVQP	ESLLGG	PCGNLY	VEKGE	ECDCG	LLDECN	DP	392

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AD15_HUMAN	CDSL	TCQLRPGAQ	CASD	GPCCQNC	QLRPSGW	QCRPT	†	GD	CDLPE	FCP	GDSSQ	CPPDV	SLG	507	
AD15_PANTR	CDSST	CQLRPGAQ	CASD	GPCCQNC	QLRPSGW	QCRPT	†	GD	CDLPE	FCP	GDSSQ	CPPDV	SLG	524	
AD15_CANFA	CDYFT	CQLRPGAQ	CASN	GLCCQNC	QLRPAW	QCRPA	†	GD	CDLPE	FCP	GDSSH	CPPDV	SLG	509	
AD15_BOVIN	CDYFT	CQLRPGAQ	CASD	GLCCQNC	QLRPAW	QCRPT	†	GD	CDLPE	FCP	GDSSQ	CPPDV	SMG	508	
AD15_MOUSE	CDHFT	CQLRPGAQ	CASD	GPCCQNC	KLHPAG	WLCRPPT	†	DD	CDLPE	FCP	GDSSQ	CPD	IRLG	508	
AD15_RAT	CDYFT	CQLRPGAQ	CASD	GPCCQNC	KLQPAW	QCRPT	†	DD	CDLPE	FCP	GDSSQ	CPPD	IRLG	509	
AD15_XENLA	CESTL	CQFRGGA	ECSSG	DQCC	EGCKLV	SGSMCRE	PLG	VC	DLPE	YCNG	ESP	HCPPN	VYLQ	486	
AD15_XENTR	CDASL	CQLRSGA	QCSSG	DQCC	EGCKLV	SGSMCRE	PLG	AC	DLPE	YCNG	ESP	HCPPN	VYLQ	502	
AD15a_DANRE	CNAST	CKLVPGA	QCSSD	GIC	CENC	KLRVAG	SVCRE	PLG	EC	DLPE	HCTG	SSPY	CPPN	VFLQ	469
AD15b_DANRE	CNAST	CKLVPGA	QCSSD	GIC	CENC	KLRVAG	SVCRE	PLG	EC	DLPE	HCTG	SSPY	CPPN	VFLQ	452

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AD15_HUMAN	DGEPC	AGGQAVCMHGR	CASYA	QQCQ	SLWGP	GAQPAAP	LCLQTANT	†	RG	NAFG	SG	CRN	PSGS	567		
AD15_PANTR	DGEPC	AGGQAVCMHGR	CASYA	QQCQ	SLWGP	GAQPAAP	LCLQTANT	†	RG	NAFG	SG	CRN	PSGS	584		
AD15_CANFA	DGEPC	AGGQAVCVQGR	CASYA	QQCQ	ALWGP	AQPTAP	LCLIAANT	†	GD	AFG	SG	CRN	PSGS	569		
AD15_BOVIN	DGEPC	ASGQAVCMQGR	CASYA	QQCQ	ALWGP	GAQPAAP	LCLLTANT	†	GD	AFG	SG	CRN	PDGS	568		
AD15_MOUSE	DGEPC	ASGEAVCMHGR	CASYA	RQCQ	SLWGP	GAQPAAP	LCLQTANT	†	RG	NAFG	SG	CRN	PSGS	568		
AD15_RAT	DGEPC	ASGEAVCMHGR	CASYA	RQCQ	SLWGP	GAQPAAP	LCLQTANT	†	RG	NAFG	SG	CRN	PSGS	569		
AD15_XENLA	NGETC	DQG--YCYQ	GE	CRTI	QAQC	KDLWG	PGSS	PAPDP	CF	SKVNI	†	GD	KYGN	CRSL	NGT	544
AD15_XENTR	NGETC	DQG--YCYR	GE	CRTI	LAQC	KDLWG	PGS	APAPD	PCF	SKVNI	†	GD	KYGN	CRSP	PDG	560
AD15a_DANRE	NGEP	CKGGSSY	CYS	GV	CASL	DDQ	QMLWG	QNST	RAPP	ICF	SSVN	KQGN	KYGN	CGMP	NGS	529
AD15b_DANRE	NGEP	CKGGSSY	CYS	GV	CASL	DDQ	QMLWG	QNST	RAPP	ICF	SSVN	KQGN	KYGN	CGMP	NGS	512

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AD15_HUMAN	YV	SCTPR	DAICG	QLQC	QTGR	TQPL	LSIR	DL	LLWET	IDV	NGT--	EL	NC	SW	HLDL	GS	DVAQ	625								
AD15_PANTR	YV	SCTPR	DAICG	QLQC	QTGR	TQPL	LSIQ	DL	LLWET	IDV	NGT--	EL	NC	SW	HLDL	GS	DVAQ	642								
AD15_CANFA	YMSC	APKD	AMCG	QLQC	QGG	QAQ	PL	LS	ARDL	HWE	VLE	ANG	TQ	PL	NC	SW	HLDL	GD	DVAQ	629						
AD15_BOVIN	YV	SCAP	R	DAMCG	QLQC	QGG	RAQ	PL	LS	ARDL	RWE	MLE	ANG	TQL	RL	NC	SW	HLDL	GN	DVAQ	628					
AD15_MOUSE	YMP	CA	PRD	VMCG	QLQC	QWGR	RSQ	PL	LS	VQ	DL	SE	VLE	ANG	T--	QL	NC	SW	DL	DL	GN	DVAQ	626			
AD15_RAT	YMP	CN	LR	DAICG	QLQC	QWGR	NQ	PL	LS	VQ	DL	SE	VLE	ANG	T--	QL	NC	SW	DL	DL	GN	DVAQ	627			
AD15_XENLA	YLP	CA	ERD	VWCG	KIQ	CQGG	NS	SR	SLG	PAQ	T	VL	VS	VT	INGS--	EL	SC	RG	TH	FD	VG	DD	IWD	602		
AD15_XENTR	YLP	CA	ESD	VWCG	KIQ	CQGG	SARS	RLG	AGA	Q	T	VL	VS	VT	INGS--	EL	SC	RG	TH	FD	L	GD	IWD	618		
AD15a_DANRE	YIP	CL	KW	DVH	CGRI	QC	GGG	ER	PL	LS	NAE	I	L	T	T	VIL	NQ	S--	DFT	CR	GY	FNL	G	DD	VSD	587
AD15b_DANRE	YIP	CL	KW	DVH	CGRI	QC	GGG	ER	PL	LS	NAE	I	L	T	T	VIL	NQ	S--	DFT	CR	GY	FNL	G	DD	VFD	570

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AD15_HUMAN	P	L	L	T	L	P	-GT	ACG	P	G	L	V	C	I	D	H	R	C	Q	R	V	D	L	L	G	A	Q	E	C	R	S	K	C	H	G	H	V	C	D	S	N	R	H	C	Y	C	E	E	G	W	A	P	P	D	C	684					
AD15_PANTR	P	L	L	T	L	P	-GT	ACG	P	G	L	V	C	I	D	H	R	C	Q	R	V	D	L	L	G	A	Q	E	C	R	S	K	C	H	G	H	V	C	D	S	N	R	H	C	Y	C	E	E	G	W	A	P	P	D	C	701					
AD15_CANFA	P	L	L	A	L	P	-GT	ACG	P	D	L	V	C	I	D	H	Q	C	P	V	D	V	L	R	A	Q	E	C	R	S	K	C	H	G	H	V	C	D	S	K	G	H	C	H	C	E	E	G	W	A	P	P	D	C	688						
AD15_BOVIN	P	L	L	T	L	P	-GT	ACG	P	G	L	V	C	V	E	Q	Q	C	P	I	E	V	L	G	A	Q	E	C	R	R	C	H	A	H	G	V	C	D	S	N	R	R	C	H	C	E	E	G	W	A	P	P	D	C	687						
AD15_MOUSE	P	L	L	A	L	P	-GT	ACG	P	G	L	V	C	I	G	H	R	C	Q	P	V	D	L	L	G	A	Q	E	C	R	R	K	C	H	G	H	V	C	D	S	S	G	H	C	R	C	E	E	G	W	A	P	P	D	C	685					
AD15_RAT	P	L	L	A	L	P	-GT	ACG	P	G	L	V	C	I	G	H	R	C	Q	P	V	D	L	L	G	A	Q	E	C	R	S	K	C	H	G	H	V	C	D	S	S	G	H	C	D	E	G	W	A	P	P	D	C	686							
AD15_XENLA	S	A	I	L	V	A	T	G	T	P	C	G	A	G	K	V	C	V	G	H	K	C	E	D	V	S	K	L	K	V	Q	N	C	R	S	K	C	N	G	H	G	V	C	N	S	N	R	N	C	H	C	D	A	G	W	A	P	P	D	C	662
AD15_XENTR	S	A	V	L	V	A	T	G	T	P	C	G	T	G	K	V	C	I	G	K	C	E	D	V	S	R	L	K	V	Q	N	C	R	N	K	C	N	G	R	G	V	C	N	S	N	S	N	C	H	C	D	P	G	W	A	P	P	D	C	678	
AD15a_DANRE	P	A	M	V	L	Q	-GT	ACG	P	N	K	A	C	V	D	Q	K	C	R	D	V	S	M	F	G	V	D	E	C	R	S	K	C	H	G	H	V	C	N	S	N	K	N	C	H	C	D	E	G	W	A	P	P	D	C	646					
AD15b_DANRE	P	A	M	V	L	Q	-GT	ACG	P	N	K	A	C	V	D	Q	K	C	R	D	V	S	M	F	G	V	D	E	C	R	S	K	C	H	G	H	V	C	N	S	N	K	N	C	H	C	D	E	G	W	A	P	P	D	C	629					

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AD15_HUMAN      TTQLKATSS-----LTTGLLLSLLVLLVLMVGASYWYRARLHQRLCQLKG 730
AD15_PANTR      TTQLKATSS-----LTTGLLLSLLVLLVLMVGASYWYRARLHQRLCQLKG 747
AD15_CANFA      TSHVRATSS-----LTTGLPLSLLLVLVLLVGASYWHRARLHQRLCQLKG 734
AD15_BOVIN      TTHVRATSS-----LTTGLPLSLLLVLVLLVGASYWHRARLHQRLCQLKG 733
AD15_MOUSE      MTQLKATSS-----LTTGLLLSLLLLLVLLVGASYWHRARLHQRLCQLKG 731
AD15_RAT        MTQLRATSS-----LTTGLLLSLLLLLVLLVGASYWYRARLHQRLCQLKG 732
AD15_XENLA      AASGQGGSIDSGSVPLKNVGNSTALLMIFLLIVPLLILLSICYWKNSLQLRLGKLS 722
AD15_XENTR      VGSQGGSIDSGSLSGRPDSSVTALLLVFLLVPLLVLGICYIKRDTLQRLGKFST 738
AD15a_DANRE     RYSGNGLNT-----IQMRLIKLLVCFFCPCSLNAYFFFRKLYEVLGCMWFLM 695
AD15b_DANRE     RYSGNGG-----RYSNGG----- 636

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AD15_HUMAN      PT-CQYRAAQ---SGPSERPQPPQALLARGTK----- 759
AD15_PANTR      PT-CQYRAAQ---SGPPERPGPPQALLAQGTK----- 776
AD15_CANFA      PS-CQYRAAQ---SGPSECPGPPQVLLMPGAKPASC----- 768
AD15_BOVIN      PS-CQYRAAQ---SGPPERPGPPQALVMPGAK----- 762
AD15_MOUSE      SS-CQYRAPQ---SCPPERPGPPQRAQMTGTQKASVVSFPVPPSRPLPPNPVKKLQA 786
AD15_RAT        SS-CQYRAAQ---SGPPERPGPPQRAQMPGK----- 761
AD15_XENLA      SSKCQYRGAQTSDNQSRPQRPPPMRTQSTELQVMSTYN----- 761
AD15_XENTR      SSKCQYRVAQTGNDPSRPQRPPPNWAQGTLEQVMSTHS----- 777
AD15a_DANRE     PPSRSGTSGLTRVTSPSPRQASRYRTQQLAAHWPAPP----- 734
AD15b_DANRE     ---SVDSGP---AQEPRDSDPARVALLVIFLFLVPVSL----- 668

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AD15_HUMAN      -----SQGPAKPPPPRKPLPADPQGRCPSGDLPGPAGIPPL 796
AD15_PANTR      -----SQGPAKPPPPRKPLPADPQGRCPSGDLPGPAGIPPL 813
AD15_CANFA      -----LSHPQGPAPPPPPRKPLPANPQGRGPGDLPGPAGIPPL 808
AD15_BOVIN      -----SQGPTKPPPPRKPLPADPHGRRPSGDLPGPAGIPPL 799
AD15_MOUSE      ALADRGNPPTRPLPADPVVRRPKSQGPTKPPPPRKPLPANPQGQHPGDLPGPDGSLPL 846
AD15_RAT        -----PQGPTKPPPPRKPLPANPQGRPPLGDLPGPDGSLQL 798
AD15_XENLA      -----KPPVPRKPPPPKKPLPLDPSQAPL--LSVPAYPDHMI 797
AD15_XENTR      -----KPPVPGKPPPPKKPLPLDPLSQAPL--LTVPAYPDHMI 813
AD15a_DANRE     -----TKPLPPDPAPSESQMCKPTGARPAAPSKPLPPDPVL 771
AD15b_DANRE     -----LFVALR----- 674

AD15_HUMAN      VVPSRPAPPPPTVSS-LYL--- 814
AD15_PANTR      VVPSRPAPPPPTVSS-LYL--- 831
AD15_CANFA      VVPSRPAPPPPAASSSLYL--- 827
AD15_BOVIN      VVPSRPAPPPPAASS-PYL--- 817
AD15_MOUSE      VVPSRPAPPPPAASS-LYL--- 864
AD15_RAT        VVPSRPAPPPPAASS-LYL--- 816
AD15_XENLA      SAPSRPAPPPPHSQRAQQV--- 816
AD15_XENTR      AAPSRPAPPPPHSDRAQQV--- 832
AD15a_DANRE     SSRQNPVPPKPPVPKKPLPVD 793
AD15b_DANRE     -----

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Additional File 2. Complete sequence alignment of ADAM15 from representative vertebrate species. Sequences of human, chimpanzee (PANTR), canine (CANFA), bovine (BOVIN), mouse, rat, *X. laevis* (XENLA), *X. tropicalis* and zebrafish (partial without N-terminus) ADAM15 proteins were aligned using ClustalX. Amino acid residues with different properties are colored differently. Identical, conserved, and semi-conserved residues are indicated with “*”, “.”, and “:”, respectively. The highly conserved signal peptide in mammalian ADAM15 proteins, the zinc-binding motif (indicated with “Δ”; the Gln residues in *Xenopus* ADAM15 are underscored) and methionine-turn in the catalytic center, the two RGD integrin binding sites (indicated with “†” and “‡”), and the conserved cytoplasmic proline residues are highlighted in grey. Arrows point to signal peptide cleavage sites, and residues in the transmembrane region are indicated with “x”.