

Figure 4. Candidate novel member of the Ifi 200 family in mouse similar to the known mouse Ifi 205 IFN-induced protein. Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

		10	20	30	40	50	60	70	80	90	100
RI A430075K09											
	MENEYKRLVLLEGLECI	NKHQFNLFKSLMV	KDLNLEEDNQEKY	TTFQIANMMVKKFP	ADAGLDRLINFC	ERVPTLKKRAEIL	KKERSEVTEETS	SLEINRQ			
	*	+	*	*	*	*	*	*	*	*	*
SPTR Q08619											
	MVNEYKRIVLLRGL	ECINKHYFSLFKS	LLARDLNLERDN	QEQYTTIQIANM	MEEKFPADSG	LGKLI	EFCEEV	PALRKRAEIL	KKERSEVT	GETSLE	KNGQ
		110	120	130	140	150	160	170	180	190	200
RI A430075K09											
	EAS	PATPTSTTSHML	ASER	GKTSTTQEET	STAQ-----	-----	-----	-----	-----	-----	-----
	*	*	*	*	*	*	*	*	*	*	*
SPTR Q08619											
	EAG	PATPTSTTSHML	ASER	GETS	SATQEET	STAQAGT	STAQAGT	STAQAGT	STAQKR	KSMREEET	GVKKS
		210	220	230	240	250	260	270	280	290	300
RI A430075K09											
	SNIP	SAKNQKSQPQ	NQNI	PRGAVLH	SEPLTVMV	L	TATDPFEY	ESPEHEV	KNMFHAT	VATVSQY	FHV
	*										
SPTR Q08619											
	SNIL	SAKNQKSQPQ	NQNI	PRGAVLH	SEPLTVMV	L	TATDPFEY	ESPEHEV	KNMFHAT	VATVSQY	FHV
		310	320	330	340	350	360	370	380	390	400
RI A430075K09											
	SSV	LEAAPKQ	MIEVP	NCITR	NANASPK	ICDIQ	KGTS	GTVFY	GVFTLH	KKKVKT	QNTS
SPTR Q08619											
	SSV	LEAAPKQ	MIEVP	NCITR	NANASPK	ICDIQ	KGTS	GTVFY	GVFTLH	KKKVKT	QNTS
		410	420								
RI A430075K09											
	KL	VCGDHS	FKV	TKAG	KKKEA	STVQ					
SPTR Q08619											
	KL	VCGDHS	FKV	TKAG	KKKEA	STVQ					

Figure 5. Candidate novel mouse guanylate binding protein mGBP-5 (FANTOM2 clone E030025M22) similar to human IFN-induced guanylate binding protein 5 (Q96PP8). Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

	10	20	30	40	50	60	70	80	90	100															
RI E030025M22	MAPEIHMPEPLCLIGSTEGHLVTNQEALKILSAITQPVVVVAIVGLYRTGKSYLMNKL	AGKEKGF	SVGSTVQ	SHTKGIWMWCV	PHPK	QPDHTLV	L	L	D	T	E	G													
	*	+	+	*****	**	*	*	+	**	*															
SPTR Q96PP8	MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKL	AGKNGF	SVASTVQ	SHTKGIWIWCV	PHPNWP	NHNTLV	L	L	D	T	E	G													
	110	120	130	140	150	160	170	180	190	200															
RI E030025M22	LGDVEKDDK	KNDTQIF	ALAILLS	SSTFVYNT	MNKIDQ	GAIDLLH	NVTELT	DLLRTRN	SSDSNQ	TEGEG	PAD-	MSFFPDLVWTLR	DFFLDLQ	ANGHAITS	DE										
	*	*	*	+	+	+	*	*****	***	**			*	*	***	***	+	*							
SPTR Q96PP8	LGDVEKADN	KNDIQIF	ALALLS	SSTFVYNT	VNKIDQ	GAIDLLH	NVTELT	DLLKARN	SPDLDR	VED-	-	PADSASFFPDLVWTLR	DFCLGLE	IDGQLV	TPDE										
	210	220	230	240	250	260	270	280	290	300															
RI E030025M22	YLENSLKLK	QGS	DERTQT	FNLPRL	CIQKFF	VPKKCF	VFDAPALG	SKLSQ	LPTLS	NEELNS	DFVQDL	SEFC	SHIFTQ	SKTKT	LPGGI	QVNG	PRLES	LVLT	Y						
	+	*	*	*	*	+	*	***	*	*	***	+	***	+	*	+	*	*	*						
SPTR Q96PP8	YLENSLRPK	QGS	DQRVQ	NFNLPRL	CIQKFF	PKKKCF	I	FDLPAH	QKKLA	QLETLP	DDELE	PEFVQ	QVTE	FC	SYIF	SHSMT	KTLP	GGIMV	NGSRL	KNL	VLT	Y			
	310	320	330	340	350	360	370	380	390	400															
RI E030025M22	VDAINSGAL	PSIENT	VVT	LARRENS	AAVQKA	IGHYDQ	LMSEK	VQLPT	TETLQ	ELLDL	HRTC	CEREA	IEIFR	KHSF	KDEGE	FFQKE	LESLL	SAKQ	DEI	CKKNA					
	*	*	*	*	+	*	*	***	*	*	*	+	*	*	****	+	*	+	*	+	*				
SPTR Q96PP8	VNAISSG	DLPCI	ENAVL	ALALA	QRENS	AAVQKA	IAHYDQ	QMGQ	KVQLP	METLQ	ELLDL	HRTS	EREA	IEVFM	KN	SFKD	VDQ	SFQKE	LETLL	DAKQ	NDICK	RNL			
	410	420	430	440	450	460	470	480	490	500															
RI E030025M22	DASAALC	STLLG	SIFK	PLEQ	EVAQ	E	FYHK	PGGH	KLFLQ	RMEQL	KANYR	QQPG	KGTQ	AEEVL	QTYL	NAKET	VSRTI	LQTD	QVLT	DKEI	QSKAE	QERAE	EAAR		
	+	***	*	**	*	*	*	*	*	+	++	*	*	***	*	*	+	**	*	+	*	***	*	*	+
SPTR Q96PP8	EASSDYC	SALLK	DIFG	PLEE	AVKQ	GIYSK	PGGH	NLF	IQKTE	ELKAK	YYRE	PRKGI	QAEE	VLQ	KYLSK	ESV	SHAIL	QTDQ	AL	TET	EK	KKK	KEA	QVKA	EAAR
	510	520	530	540	550																				
RI E030025M22	LEAQRLE	AIRI	QEEQR	KAEMER	QHQE	LRQIA	LEKAR	V	AQEQ	QWIL	KQRA	Q													
	*	*	**	*	***	*	*	+	++	***	*	+	**	*	*	*	*	*	*	*	*	*	*	*	
SPTR Q96PP8	AEAQR	LAAI	Q	RNEQ	MMQ	ERER	LHQE	QVRQ	MEIA	KQNL	WLA	E	Q	Q	K	M	Q	E	Q	M	Q				

Figure 6. Hypothetical Toll/Interleukin receptor TIR domain structure containing protein (FANTOM2 clone B430113A10) similar to the hypothetical macaque protein (Q9bgz8). The TIR domain is shaded. Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

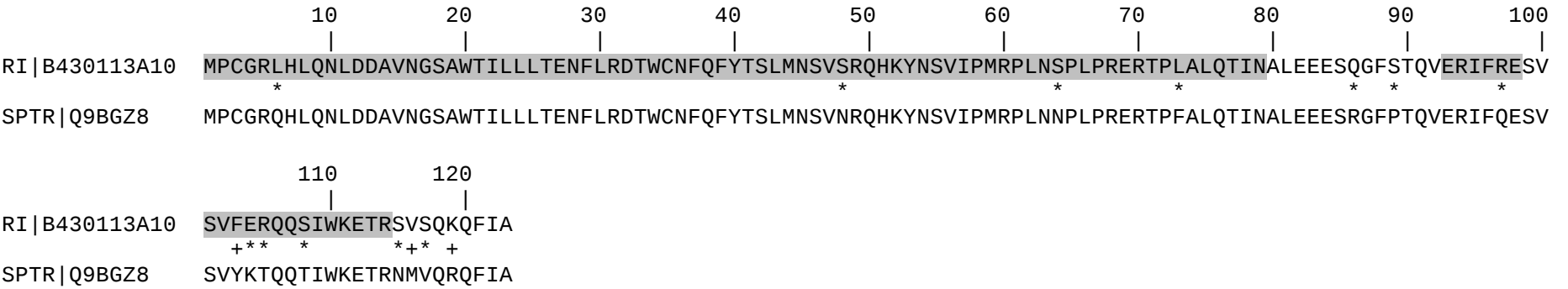


Figure 7. Candidate novel mouse interleukin-1 receptor associated kinase 2 – IRAK2 (FANTOM2 clone 4732448K15) showing similarity to human IRAK2 (O43187). Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

	10	20	30	40	50	60	70	80	90	100
RI 4732448K15	MACYIYQLPSWVLDL	CRNIDTLSEWDWMQF	ASYVITDLTQLRKIKSM	ERVQGV	SITRELLWWWSMRQATV	QQLVDLLCHLELYRAAQIVLSWKPV	PEST			
SPTR 043187	MACYIYQLPSWVLDL	CRNMDALSEWDWMEF	ASYVITDLTQLRKIKSM	ERVQGV	SITRELLWWWGM	RQATVQQLVDLLCRLELYRAAQIILNWKPAPEIR				
	110	120	130	140	150	160	170	180	190	200
RI 4732448K15	SPLPAFPEAVKPG- * + + + *	AVATSRRNLKDEQEKV *** + * * *	RPVKPRSLDTPIMAG	AQRQ - - -	RPC	EMDAPCSLKT	DAPDSPQSKYCST	STSAPKQERLLGLPGD	RLFW	
SPTR 043187	CPIPAFPDSVKPEKPLAASVRKA	EEQEQPVRMATFPGPGSSPARAHQ	PAFLQPPEEDAPHSLRSD	LP	TSSDSK - -	DF	STSIPKQEKLLSLAGD	SLFW		
	210	220	230	240	250	260	270	280	290	300
RI 4732448K15	RLFWEADVQATEDFDQSHRI	SEGT	FADIYQGQRNGVAF	AFKKLREVAGSSPGSMDR	FLQAEMQLCLRCCH	ANVLP	LLGFCTGRQFHSLIYP	MANGSL		
SPTR 043187	SLFWSEADVQATDDFNQNRKIS	QGT	FADVYRGHRHGKPFVFKKL	RETACSSPGS	IERFFQ	AELQICLR	CHPNVLPVLGFCAARQFHSFIYP	MANGSL		
	310	320	330	340	350	360	370	380	390	400
RI 4732448K15	SLHDRLWAQGN	SDMLPWPQR	SICSGLLLA	VEHLHSLDIIH	SNVKSANVLLDQHLNPKLAHPVAH	PHDPNKKTKY	VMRTHLFQASAAYLPEHFIRVGQL			
SPTR 043187	SLQDRLQGQGS	DPLPWPQ	RVSICSGLLCAVEYLHG	LEIIH	SNVKS	SNVLLDQNLTPKLAHPMAHLCPV	NKRSKYTMMKTHLLRTSAAYLPEDFIRVGQL			
	410	420	430	440	450	460	470	480	490	500
RI 4732448K15	TKQVDIFSCGIVLA	EVL	TGIPAMDKDRSPVYLKDLLLSEIPNSTSSVCSRK	TS	MGKAVVKEICQRHVEK	RAGLLPEACEEAWATAVSVCLRRRNASVEEA				
SPTR 043187	TKRVDIFSCGIVLA	EVL	TGIPAMDNNRSPVYLKDLLLSEIPSSTASLCSRK	TG	VENVMAKEICQKYLEKGAGRLPEDCAEALATAACLCLRRRN	TS	LVQEV			
	510	520	530	540	550	560	570	580	590	
RI 4732448K15	RVSLAGVEEQ	LRG-QLSLPWSRV	SEATGSSSNTPEETDDVDNSSLGVPSLVMMASCPGA	ASSPLFTGHGAAQPSTSGRQ	EADSSSEACTGPQTPQ	NAT				
SPTR 043187	CGSVA	AVEERLRGRETLLPWSGL	SEGTGSSSNTPEETDDVDNSSL	DASSMSVAPWAGAATPLLPTENGE	RLRVIVG	READSSSEACV	GLEPPQDVT			

Figure 8. Candidate novel mouse IL 20 receptor like gene (FANTOM2 clone E230031K19) showing similarity to human IL 20 receptor alpha (Q96SH8). Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

[illegible]

Figure 10. Candidate novel variant of the mouse gene (FANTOM2 clone 4921501K24) whose conceptual translation showed similarity to human TGF β induced factor 2 (TALE family homeobox) (Q9GZN2). Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

	10	20	30	40	50	60	70	80	90	100
RI 4921501K24	MSDSDLGEDEGLLSLTGKRKRRGNLPKESVKILRDWLYLHRYNAYPSEQEKLSSGQTNLVSVLQICNWFINARRRLLPDMLRKDGKDPNQFTISRRGGKA									
		*								
SPTR Q9GZN2	MSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLHRYNAYPSEQEKLSSGQTNLVSVLQICNWFINARRRLLPDMLRKDGKDPNQFTISRRGGKA									
	110	120	130	140	150	160	170	180	190	200
RI 4921501K24	SDVALPRGSSPSLLAVSVPAPTNMLSLSVCSMPLHSGQGGEKPAAPFPQVELESPKALVTPASTLTLLTRAEAGSPTGGLFNTPPPTPPEQDKDDFSSFQL									
		+		+		**	*	*		+
SPTR Q9GZN2	SDVALPRGSSPSVLAVSVPAPTNVLSLSVCSMPLHSGQGGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEAGSPTGGLFNTPPPTPPEQDKEDFSSFQL									
	210	220	230							
RI 4921501K24	LVEVALQRAAEMELKQKQEPAPPLLHTPLPFVSENAK									
			+	**		+	*		**	
SPTR Q9GZN2	LVEVALQRAAEMELKQKQDPSLPLLHTPIPLVSEN PQ									

Figure 11. Candidate novel variant mouse gene (FANTOM2 clone B930011D01) whose conceptual translation showed similarity to the mouse integrin β -like with EGF-like repeat domains (Q96QX7). Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

		10	20	30	40	50	60	70	80	90	100
RI B930011D01	RCECGRCTCYPPGDSRVY	GKTCECD	RRCEDLDGVVCGGHGM	CSCGRVC	EKGWFGKLCQH	L	RKCNMTEE	QSRSLCESADGT	LCSGKGSCHCGKCICS	GEE	
	+	+	*		*	+	*	+*		*	
SPTR Q96QX7	KCECGKCTCYPPGD	RRVYGKTCECD	RRCEDLDGVVCGGHG	TCS	CGRCVC	ERGWF	GKLCQHPRKCNMTEE	QSKNLCESADGI	LCSGKGSCHCGKCICSAE		
		110	120	130	140	150					
RI B930011D01	WYISGEFCDCDDR	DKHDGLICTGN	IGICSCGNCECW	DGWNGNACEIWL	GT EYP						
					+						
SPTR Q96QX7	WYISGEFCDCDDR	DKHDGLICTGN	IGICSCGNCECW	DGWNGNACEIWL	GSEYP						

Figure 12. Candidate novel mouse gene (FANTOM2 clone E330012C08) whose conceptual translation showed similarity to the human latent TGF- β binding protein 4S. Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved. Slash (/) and backslash (\) indicate potential frame shifts in cDNA sequences.

	10	20	30	40	50	60	70	80	90	100	
RI E330012C08	GPLAPAVPRPARPATPPAWTAARPAGRPRG/DPGFRAFLCPLICHNGGVCKPDRCLCPPDFAGKFCQLHSSGARPPAPAMPGLTRSVYTMPLANHRDDE										
	**		*		*			+			
SPTR 075412	GRPAPAVPRPARPATPPAWTAALPAGRPRG-DPGFRAFLCPLICHNGGVCKPDRCLCPPDFAGKFCQLHSSGARPPAPAIPGLTRSVYTMPLANHRDDE										
	110	120	130	140	150	160	170	180	190	200	
RI E330012C08	HGVASMVSVHVEHPQEASVVH QVERVSGPWEEANPEALARAEEAAARAEAAAPYTVLAQSAPREDGYSDASGFGYCFRELRGSECA SPLPGLRTQEVCCR										
				*	+			*			
SPTR 075412	HGVASMVSVHVEHPQEASVVH QVERVSGPWEEADAEAVARAEEAAARAEAAAPYTVLAQSAPREDGYSDASGFGYCFRELRGSECA SPLPGLRTQEVCCR										
	210	220	230	240	250	260	270	280	290	300	
RI E330012C08	GEG LAWGVHDCHPCA EHLRNSNQVSGPNGPCPPGFERVNGSCVDVDECATGGRCQHGE CANTRGGYTCVCPDGFLLDSSRSSCISQHVISEAKGPCYRVL										
	**	*	*	*	*	*	*	*		+	
SPTR 075412	GAG LAWGVHDCQLC SERLGN SERVSAPDGPCTGFERVNGSCEDVDECATGGRCQHGE CANTRGGYTCVCPDGFLLDSSRSSCISQHVISEAKGPCFRVL										
	310	320	330	340	350	360	370	380	390	400	
RI E330012C08	HDGGCSLPILRNITKQICCSRVGKAWGRGCQLCPPYGSEGFREICPAGPGYHYSASDLRYNTRPLNQDPPRVTFNQPRVPPATPRPPTGFLPTRRPEPR										
	*			+			*	+	***	**	
SPTR 075412	RDGGCSLPILRNITKQICCSRVGKAWGRGCQLCPPFGSEGFREICPAGPGYHYSASDLRYNTRPLGQEP RVSLSQPRTL PATSRPSAGFLP THRLEPR										
	410	420	430	440	450	460	470	480	490	500	
RI E330012C08	PDPGPQPEPRPRPEPRPRPESRPRPEPRPRPEPRPQESQRPESRPRPESQWPFEFLPSIPAWTGPEIPESGPSSSMCQRNPQVCGPGRCVPRPSGYT										
	+	*****									
SPTR 075412	PEP-----RPDPRPGPE-----FPLPSIPAWTGPEIPESGPSSSMCQRNPQVCGPGRCISRPSGYT										
	510	520	530	540	550	560	570	580	590	600	
RI E330012C08	CACDPGFRLGPQGTRCIDIDECRRVPTPCAPGRCENTPGSFRCVCGTGFGAGPRATECLDVDECRRVPPPCDRGRCENTPGSFLCVCPAGYQAAPHGASC										
	*	*	+	*	+	*	*	*	*		
SPTR 075412	CACDSGFRLSPQGTRCIDVDECRRVPPPCAPGRCENSPGSFRCVCGPGFRAGPRAAECLDVDECHRVPPPCDLGRCENTPGSFLCVCPAGYQAAPHGASC										

	610	620	630	640	650	660	670	680	690	700
RI E330012C08	QDVDECTQSPGLCGRGVCENLPGSFRCVCPAGFRGSACEEDVDECAQQPPPCGPGRC	NTAGSFHCAC	PAGFRSRGPGAPCQDVDECS	SRSPSPCAYGRCE						
		*	*							
SPTR 075412	QDVDECTQSPGLCGRGACKNLPGSFRCVCPAGFRGSACEEDVDECAQEPPPCGPGRC	NTAGSFHCAC	PAGFRSRGPGAPCQDVDECARSP	PPPCTYGRCE						
	710	720	730	740	750	760	770	780	790	800
RI E330012C08	NTEGSFKCVCPTGFQPNAAAGSECEDVDECENRLACPGQECVNSPGSFQCRAC	PAGHHLHRGRCTDVDECSSGT	-PCGLHGQCTNTKGSFHCSCSTGYRAP							
	*	*								
SPTR 075412	NTEGSFQCVCPMGFQPNAAAGSECEDVDECENHLACPGQECVNSPGSFQCRAC	PSGHHLHRGRCTDVDECSSGAPPCGPHGHCTNTEGSFRCSCAPGYRAP								
	810	820	830	840	850	860	770	780	790	900
RI E330012C08	SGQPGPCADINECLEGDFCFPHGECLNTDGSFTCTCAPGYRPGPRGASCLDVDEC	SEEDLCQSGICTNTDGSFECICPPGHRAGPDLASCLDIDE	CRERG							
	*	+								
SPTR 075412	SGRPGPCADVNECLEGDFCFPHGECLNTDGSFACTCAPGYRPGPRGASCLDVDEC	SEEDLCQSGICTNTDGSFECICPPGHRAGPDLASCLDVDEC	CRERG							
	910	920	930	940	950	960	670	980	990	1000
RI E330012C08	PALCGSQRCE	NSPGSYRCVRDCDPGYHPGPEGT	CDDIDE	CREYGSAICGAQR	CENTPGSYRCTPACDPGYQPTPGGGCQDVDEC	NRNSFCGAHAMCQNL	P			
		*	+	*	**					
SPTR 075412	PALCGSQRCE	NSPGSYRCVRDCDPGYHAGPEGT	CDDVDECQEY	GPEICGAQR	CENTPGSYRCTPACDPGYQPTPGGGCQDVDEC	NRNSFCGAHAVCQNL	P			
	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
RI E330012C08	GSFQCVCDQGYEGARDGRHCVDVNECETLQGVCGSALCENVEGSFLCVCPNS	PVEEFDPM	TGRCVPPRAPAGTFPGSQPQAPASPSLPARPPAPPPRRPS							
	+	*								
SPTR 075412	GSFQCLCDQGYEGARDGRHCVDVNECETLQGVCGAALCENVEGSFLCVCPNS	PVEEFDPM	TGRCVPPRTSAGMFPGSQPQAPASPVLPARPPPPPLRRPS							
	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
RI E330012C08	PPRQGPVSSGRRECYFDTAAPDACDNILARNVTWQECCTVGE	GWGSGCRIQQCPGTETA	AEYQSLCPHGRGYL	VPSGDLSARRDVDECQLFQDQVCKSGV						
	*	*								
SPTR 075412	TPRQGPVSGRRECYFDTAAPDACDNILARNVTWQECCTVGE	GWGSGCRIQQCPGTETA	AEYQSLCPHGRGYL	APSGDLSLRRDVDECQLFRDQVCKSGV						

Figure 13. Candidate novel mouse gene (FANTOM2 clone 9130025L13) whose conceptual translation showed similarity to the human FGF receptor 4B, the protein serine/threonine kinase. Asterisks (*) indicate difference between sequences, pluses (+) indicate conservative replacements, while other positions are conserved.

[illegible]