

**Supplementary Table S1.** Summary of ALG-2-interacting protein candidates analyzed in this article. Results of *in vitro* binding assays shown in Figure 1 are summarized. Fragments of proteins containing ABM-2 sequences were expressed and analyzed for binding with Nluc-ALG-2 by Far-western (FW) and pulldown assays.

Group	Protein name	UniProt ID	Expressed region	ABM-2		Intrinsically disordered <sup>c</sup>	Interaction <sup>d</sup>	
				Sequence <sup>a</sup>	PRR <sup>b</sup>		FW	Pulldown
A	Sec31A	O94979	790 - 1095	838- <b>PPPPGFI</b>	y	Y	++	+++
	SARAF	Q96BY9	195 - 339	223- <b>PPPPGFK</b>		Y	+++	++
	SHISA4	Q96DD7	122 - 197	153- <b>PPQPGFI</b>	y	Y	+	+
	cTAGE5	O15320	502 - 804	764- <b>PPRPGFF</b>	y	Y	++	+
B	FNDC3A	Q9Y2H6	59 - 250	117- <b>PPLPGFI</b>	y		+	+/-
	DIAPH3	Q9NSV4	550 - 636	613- <b>PPPLGFL</b>	y		+/-	-
C	SBF1	O95248	1119 - 1319	1313- <b>PPDPGFL</b>			-	-
	PIK3R4	Q99570	572 - 1034	974- <b>PPPPGWR</b>			-	-
	DMRTC2	Q8IXT2	150 - 271	206- <b>PPFPGFD</b>	y		-	-
	NR3C2	P08235	1 - 602	475- <b>PPVPGFD</b>			-	-
	CHRNA1	P02708	342 - 453	402- <b>PPPMGFH</b>			-	-
	STARD5	Q9NSY2	1 - 213	143- <b>PPKPGFV</b>			-	-
	CCER1	Q8TC90	1 - 406	94- <b>PPPPGFW</b>			-	-

<sup>a</sup> Residues identical with the ABM-2 sequence of Sec31A are shown in bold face.

<sup>b</sup> The letter y indicates that the ABM-2 sequence is contained in a Pro-rich region (PRR) annotated in the

<sup>c</sup> The letter Y indicates that the entire ABM-2 (7 a.a.) and its surrounding sequences on both sides (21 a.a.) are predicted to be located in an intrinsically disordered region (See Supplementary Figure S1).

<sup>d</sup> Relative binding abilities compared to Sec31A are scored and indicated by +++ (very strong), ++ (strong), + (moderate) +/- (weak), and - (negative) in the binding assays by Far Western (FW) and pulldown followed by Nluc-ALG-2 binding.

**Supplementary Table S2.**

Protein name	UniProt ID	Plasmid source	Nucleotide Sequence Acc. No.	clone ID	Expressed region	SGFP2-fusion (vector)	Full or partial	Forward primer	Reverse primer	Cloning site
CCER1	Q8TC90	RIKEN <sup>1)</sup>	BC024183	IRAK033D24	1-406	SGFP2-C1	FL	ctcaagcttcgaattccatgactcagaccctcgaca	ccgcggtaccgtcgacctaacagtgtaaagtcctgtgc	EcoRI/Sall
cTAGE5	O15320	RIKEN	BC064355	IRAK134N08	502-804	SGFP2-C1	P	ctcaagcttcgaattctccttatgcactcgatgttc	ccgcggtaccgtcgactgtcaggtttctgtgtgg	EcoRI/Sall
CHRNA1	P02708	NBRC	AK299445	FLJ58615	342-453	SGFP2-C1	P	ctcaagcttcgaattccaacacacaccaccgctca	ccgcggtaccgtcgacctagtccatcaccattgcaacgt	EcoRI/Sall
DIAPH3	Q9NSV4	NBRC <sup>2)</sup>	AK092024	FLJ34705	550-636	SGFP2-C1	P	ctcaagcttcgaattctcagtttggtccttgccag	ccgcggtaccgtcgacctatggtttcaacccaaatggc	EcoRI/Sall
DMRTC2	Q8IXT2	RIKEN	BC029202	IRAK051E15	150-271	SGFP2-C1	P	ctcaagcttcgaattcgaactcctgtgggcctctg	ccgcggtaccgtcgacctatggtctagctgaagagg	EcoRI/Sall
FNDC3A	Q9Y2H6	NBRC	AK302415	FLJ32842	59-250	SGFP2-C1	P	ctcaagcttcgaattctggtcctgctcaggttcaa	ccgcggtaccgtcgactatgtatcaactgtgtaccac	EcoRI/Sall
NR3C2	P08235	NBRC	AK304318	FLJ34705	1-481	SGFP2-C1	P	ctcaagcttcgaattcgatggagaccaaaggctac	ccgcggtaccgtcgacacaccaatcatatctttgaaggtc	EcoRI/Sall
PIK3R4	Q99570	OBS <sup>3)</sup>	BC110318	MHS6278-202758656	572-1034	SGFP2-C1	P	ctcaagcttcgaattcgaaagccaacgatgtttgttc	ccgcggtaccgtcgacatagatcaggtagtggtggtc	EcoRI/Sall
SBF1	O95248	RIKEN	BC009268	IRAL022F18	1119-1596	SGFP2-C1	P	ctcaagcttcgaattcgagcagcctgggtgaaagg	ccgcggtaccgtcgacctaagtgtagaagtcacac	EcoRI/Sall
STARD5	Q9NSY2	RIKEN	BC004365	IRAL013P20	1-213	SGFP2-C1	FL	ctcaagcttcgaattcaatggaccagcactggca	ccgcggtaccgtcgactagcattactcatggaattg	EcoRI/Sall
SARAF	Q96BY9	OBS	BC015012	MHS6278-202756988	195-339	SGG-SGFP2-N1	P	ctcaagcttcgaattgtcatgagtgacgggcagta	gcctccgcttgatctcgtctcctgtgtaccaccata	EcoRI/BamHI
SARAF	Q96BY9	OBS	BC015012	MHS6278-202756988	1-339	SGG-SGFP2-N1	FL	ctcaagcttcgaattccatctcatcgagcgccat	gcctccgcttgatctcgtctcctgtgtaccaccata	EcoRI/BamHI

<sup>1)</sup> Complete sequencing and characterization of 21,243 full-length human cDNAs. Ota T, Suzuki Y, Nishikawa T, Otsuki T, Sugiyama T, et al. Nat Genet. 2004 Jan;36(1):40-5. Epub 2003 Dec 21. PMID: 14702039

<sup>2)</sup> National Institute of Technology and Evaluation (NITE) Biological Resource Center. <https://www.nite.go.jp/nbrc/catalogue/NBRCDispSearchServlet?lang=en>

<sup>3)</sup> Open Biosystems. <https://horizondiscovery.com/en/about-us/about-open-biosystems>