Supplementary Information.

HDX-MS reveals dysregulated checkpoints that compromise discrimination against self RNA during RIG-I mediated autoimmunity

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[#]denotes equal contribution.



Supplementary Fig. 1a



Supplementary Fig. 1c

peptide sequence	charge	start	end	structur	e (i)	(ii)	(iii)	(iv)	(v)	(vi)	(vii)	(viii)	(ix)	(x)	(xi)
QDYIRKTLDPTYIL	3	13	26		36 (3)	65 (3)	15 (5)	21 (4)	9 (4)	17 (3)	4 (4)*	-1 (4)*	9 (5)	-1 (2)*	10 (4)
IRKTLDPTYIL	3	16	26		32 (2)	63 (5)	21 (2)	23 (5)	10 (5)	22 (3)	6 (4)	-1 (4)*	7 (3)	0 (2)*	13 (4)
SYMAPWFRE VMADWEDEEEVO	2	27	30		41 (3)	72 (5)	21 (4)	24 (4)	11 (3)	22 (3)	2 (4)*	-4 (4)* 2 (5)*	3 (3)*	0 (2)*	15 (3)
VQYIQA	2	38	43		25 (2)	70 (4) 56 (4)	20 (4)	18 (4)	3 (3)*	13 (4)	0 (2)*	-2 (3)	2 (4)	2 (3)*	7 (5)
YIQAEKNNKGPMEA	3	40	53		43 (4)	71 (5)	13 (5)	17 (3)	7 (4)	12 (7)	-2 (4)*	-2 (3)*	1 (4)*	-2 (4)*	1 (6)*
EKNNKGPMEAATL	2	44	56		39 (3)	55 (7)	15 (4)	15 (4)	5 (4)	16 (5)	2 (5)*	-3 (3)*	3 (5)*	-1 (3)*	8 (5)
LQEEGWFRGFL	2	64	74	CANDI	47 (4)	56 (8)	11 (5)	17 (4)	8 (4)	9 (4)	3 (4)*	2 (5)*	9 (4)	-3 (2)*	0 (4)*
ERGELDA	2	70	74		46 (2)	53 (4)	10 (3)	9 (6)	10 (5)	6 (6)	4 (7)* 1 (3)*	-2 (4)*	6 (3) 14 (5)	-1 (3)* 1 (2)*	4 (4)*
DALDHAGYSGL	2	75	85		27 (2)	54 (5)	16 (3)	20 (3)	9 (3)	21 (3)	2 (4)*	-1 (4)*	5 (3)	0 (2)*	7 (5)
LDHAGYSGL	2	77	85		32 (2)	50 (6)	11 (4)	11 (4)	5 (3)*	14 (4)	4 (5)*	-1 (5)*	5 (4)*	-1 (3)*	7 (3)
YEAIESW	1	86	92		22 (2)	66 (4)	29 (3)	32 (3)	19 (4)	30 (3)	2 (4)*	-2 (4)*	7 (3)	-1 (3)*	16 (4)
YEAIESWD	1	86	93		19 (2)	64 (6)	25 (4)	32 (3)	16 (3)	33 (3)	2 (4)*	1 (5)*	10 (6)	0 (3)*	17 (3)
	2	103	102		64 (3) 8 (1)	72 (5)	8 (4)	13 (3)	4 (2)* 7 (2)	6 (3) 28 (2)	-4 (5)* 3 (5)*	-2 (4)*	3 (4)*	-2 (2)* 1 (3)*	4 (4)*
YRLLLKRLQPEF	3	103	114		13 (1)	60 (4)	31 (3)	38 (4)	18 (5)	34 (3)	5 (4)*	2 (6)*	6 (3)	0 (3)*	13 (5)
LLKRLQPEF	2	106	114	Latch	17 (3)	66 (6)	30 (5)	37 (5)	21 (4)	37 (5)	6 (4)	-1 (5)*	7 (4)	0 (3)*	15 (5)
LLKRLQPEF	3	106	114	ragion	14 (3)	65 (6)	35 (3)	38 (6)	17 (7)	38 (4)	6 (4)	-3 (4)*	7 (3)	1 (4)*	19 (9)
KRLQPEF	2	108	114	region	21 (3)	76 (5)	31 (5)	34 (5)	18 (6)	34 (5)	6 (5)	-2 (6)*	4 (5)*	1 (4)*	13 (7)
KTRIPTDISDL	3	115	127		53 (3) 46 (2)	73 (5)	19 (4)	22 (3)	12 (3)	19 (3)	2 (4)*	-3 (4)*	3 (4)*	-2 (2)*	6 (4)
KTRIIPTDIISD	3	115	126		47 (2)	71 (4)	15 (5)	12 (4)	8 (4)	15 (4)	1 (4)*	2 (5)*	2 (5)*	-2 (3)*	7 (4)
ILQICSTKGMMAGAEKLVE	3	139	157		28 (1)	57 (4)	22 (2)	25 (2)	12 (2)	23 (2)	5 (3)	-1 (4)*	7 (2)	0 (2)*	13 (2)
LLRSDKENWPKTLKL	4	159	173	CARD2	36 (0)	75 (3)	12 (7)	29 (2)	14 (4)	12 (3)	-2 (3)*	-1 (5)*	-1 (2)*	0 (2)*	13 (5)
RSDKENWPKTLKL	3	161	1/3		34 (4)	65 (5)	16 (6)	18 (4)	10 (5)	20 (5)	3 (0)*	0 (4)*	4 (4)*	-2 (16)*	10 (5)
	3	174	175		28 (3)	59 (5)	23 (4)	20 (3)	10 (5)	21 (4)	-3 (4)* 0 (4)*	-3 (4)*	2 (4)* 4 (5)*	-3 (5)*	6 (5)
EKERNKFSEL	3	176	185		56 (2)	77 (5)	13 (4)	15 (4)	7 (3)	11 (4)	0 (3)*	-2 (4)*	4 (5)*	-2 (3)*	5 (4)
WIVEKGIKDVETEDLED	2	186	202		88 (2)	87 (6)	5 (2)	0 (4)*	-2 (5)*	-1 (5)*	-2 (3)*	-1 (2)*	-3 (2)*	0 (1)*	-2 (5)*
WIVEKGIKDVE	3	186	196		86 (4)	85 (6)	2 (3)*	2 (4)*	0 (4)*	-1 (7)*	-1 (3)*	-1 (3)*	0 (1)*	-2 (4)*	-2 (5)*
WIVEKGIKDVETEDL	3	186	200		86 (1)	84 (3)	4 (6)*	2 (6)*	-1 (6)*	-1 (6)*	-1 (6)*	-4 (5)*	-2 (6)*	-3 (5)*	-1 (5)*
EDKMETSDIQIE	2	201	200	linkor	64 (1) 70 (4)	61 (6) 75 (6)	5 (2)* 4 (5)*	3 (4)*	2 (4)*	-1 (4)* 1 (5)*	-2 (5)*	-4 (3)"	0 (6)*	-2 (4)*	1 (4)*
FYQEDPECQNL	2	212	222	IIIIKEI	73 (1)	63 (5)	3 (3)*	1 (3)*	-10 (5)	-4 (4)*	-1 (3)*	-1 (3)*	5 (5)*	-2 (5)*	1 (5)*
YQEDPECQNL	2	213	222		67 (3)	70 (5)	2 (5)*	-2 (5)*	-11 (6)	1 (5)*	1 (2)*	-3 (5)*	-1 (5)*	-2 (5)*	-3 (3)*
SENSCPPSEVSDTNL	2	223	237		71 (5)		5 (6)*	-2 (4)*	-9 (7)	-2 (5)*	-2 (6)*	-4 (5)*	-3 (5)*	-2 (6)*	-1 (5)*
VSDTNL	1	232	237		72 (5)		4 (6)*	-2 (3)*	-13 (7)	-2 (6)*	1 /E\\$	-3 (5)*	-2 (4)*	-2 (6)*	-1 (5)*
YSPEKPRNYOLE	3	238	249		79 (4) 62 (3)		1 (4)*	3 (4)*	-2 (4)*	-6 (4)	2 (5)*	-4 (5)*	-3 (4)*	-6 (3)	-3 (4)*
YSPFKPRN	3	238	245	HELI	62 (3)		4 (6)*	-1 (3)*	-2 (5)*	3 (6)*	-3 (2)*	-9 (6)	-10 (5)	-7 (5)	-11 (4)
LALPAMKGKNTIICAPTGCGKTFVSLL	3	250	276		46 (2)		0 (3)*	3 (2)*	4 (3)*	-4 (3)*	3 (3)*	-1 (4)*	-12 (3)	3 (7)*	-9 (4)
LALPAMKGKNTIICAPTGCGKTFVSLL	4	250	276		51 (1)		-5 (1)*	3 (1)*	-3 (3)*	2 (6)*	0 (5)*	-3 (4)*	-11 (3)	-4 (3)*	
	2	264	2/2		72 (3)		2 (4)*	0 (3)*	-3 (8)*	4 (5)*	-5 (3)*	4 /2\\$	-46 (6)	-10 (5)	-32 (5)
PQGQKGKVVF	3	286	295		54 (2) 63 (3)		-4 (4)*	-3 (3)*	-2 (3) 4 (5)*	4 (3)*	-2 (2)*	0 (4)*	-3 (2) 2 (4)*	-2 (4)*	-3 (3)
FANQIPVYEQQ	2	296	306		57 (2)		-12 (3)	-12 (4)	-10 (6)	-16 (4)	-4 (4)*	6 (5)	-9 (5)	-4 (5)*	-26 (6)
FANQIPVYEQQKSVF	2	296	310	motif la	56 (1)		-14 (3)	-12 (5)	-6 (4)	-18 (3)	-6 (3)	6 (5)	-10 (5)	-3 (4)*	-22 (6)
FANQIPVYEQQKSVFSKY	3	296	313	mouna	53 (1)		-13 (3)	-12 (5)	-14 (4)	-21 (4)	-6 (4)	6 (3)	-10 (5)	4 (5)*	-19 (6)
	4	318	341		59 (2)		-14 (2)	-3 (3)* 0 (2)*	-2 (4)*	-6 (3)	-1 (4)*	-2 (4)* 3 (2)*	0 (3)*	-1 (3)*	-1 (3)*
YRVTGISGATAENVPVEQIVE	3	319	339		72 (4)		3 (5)*	0 (6)*	-3 (4)*	-3 (6)*	-3 (3)*	-3 (4)*	-4 (4)*	-5 (5)	-1 (7)*
IIILTPQILVNNLKKGTIPSL	2	343	363		28 (2)		-6 (4)	-8 (3)	-3 (4)*	-10 (3)	-3 (3)*	-2 (4)*	-10 (3)	-4 (4)*	-16 (4)
IIILTPQILVN	2	343	353		41 (2)		-3 (3)*	-6 (4)	-3 (2)*	-9 (4)	3 (3)*	1 (3)*	-7 (2)	-4 (2)*	-13 (2)
	2	343	355		58 (2)		-8 (3)	-11 (3)	-5 (3)	-11 (3)	-1 (3)*	-1 (3)*	-10 (2)	-5 (3)	-20 (3)
III TPOILVNNEKKGTIPSE	3	343	365	motif lc	58 (2) 57 (2)		-6 (3)	-9 (3)	-3 (4)*	-11 (3)	-3 (3)*	-2 (4)*	-9(3)	-5 (4)	-16 (3)
IIILTPQILVNNLKKGTIPSLSIF	3	343	366		54 (2)		-5 (3)	-7 (2)	-1 (2)*	-8 (2)	-1 (3)*	-1 (4)*	-8 (3)	-5 (4)*	-14 (2)
LMIFDECHNTSKQHPYNM	3	368	385		29 (2)		-6 (2)	-4 (2)*	-2 (2)*	-10 (2)	3 (5)*	2 (3)*	-6 (3)	-1 (2)*	-10 (3)
IFDECHNTSKQHPYNMIM	2	370	387	motif Ila	30 (1)		-5 (2)	-4 (2)*	-1 (2)*	-10 (2)	2 (5)*	3 (7)*	-7 (2)	2 (7)*	-10 (3)
IFDECHNTSKQHPYNMIM	3	370	387		29 (2)		-6 (2)	-4 (2)*	-2 (2)*	-10 (2)	3 (5)*	2 (3)*	-6 (3)	-1 (2)*	-10 (3)
FNYLDQKLGGSSGPLPQVIG	2	388	407		33 (2) 33 (1)		2 (2)*	4 (3)* 3 (2)*	2 (4)*	-5 (2) -6 (4)	3 (3)" 4 (4)*	-1 (4)*	2 (2)*	-1 (3)*	3 (4)*
DQKLGGSSGPLPQVIGL	2	392	408		39 (2)		0 (2)*	4 (3)*	1 (4)*	-3 (2)*	1 (3)*	0 (3)*	2 (3)*	-1 (3)*	2 (4)*
TASVGVGDAKNTDEALD	2	409	425		61 (3)		-2 (4)*	-3 (4)*	-1 (4)*	-7 (4)	-3 (5)*	-1 (5)*	-8 (4)	-4 (4)*	-11 (4)
TASVGVGDAKNTDEAL	2	409	424		59 (3)		-3 (4)*	-3 (4)*	-2 (5)*	-6 (4)	-4 (2)*	-1 (5)*	-8 (4)	-5 (4)*	-10 (4)
DYICKL	2	425	430		1 (1) 3 (1)		-1 (1)*	1 (1)*	1 (1)* -3 (1)*	-3 (1)*	0 (2)*	0 (0)*	0 (2)*	0 (1)*	0 (0)*
CASLDASVIATVKHNLEEL	2	431	449		43 (2)		-5 (3)*	-1 (3)*	0 (3)*	-5 (2)*	3 (4)*	1 (4)*	2 (3)*	-3 (2)*	-2 (3)*
SVIATVKHNLEE	2	437	448		55 (3)		-2 (3)*	-1 (3)*	1 (3)*	-2 (3)*	-3 (4)*	-3 (3)*	-2 (3)*	-4 (3)*	1 (2)*
EQVVYKPQKF	3	450	459		55 (4)		3 (4)*	3 (4)*	2 (5)*	5 (5)*	4 (6)*	-8 (3)	-5 (3)*	-12 (4)	2 (6)*
VVYKPQKF	2	452	459		60 (3)		1 (4)*	4 (4)*	4 (4)*	2 (4)*	-1 (6)*	-3 (4)*	-3 (4)*	-6 (4)	-4 (4)*
FRKVESRISDKEKYILAOI	3	460	478		39 (3)		2 (4)*	-1 (3)*	-5 (4)	-2 (3)*	-1 (6)*	-4 (0)*	-4 (2)*	-0 (4)	-3 (4)
MRDTESL	2	479	485		5 (2)		-1 (2)*	-1 (2)*	-3 (2)*	-2 (2)*	-1 (2)*	0 (1)*	0 (4)*	0 (1)*	0 (1)*
AKRICKDLENL	3	486	496	HEL2i	69 (3)		-4 (5)*	-4 (4)*	-1 (4)*	-11 (4)	2 (6)*	-2 (5)*	-1 (5)*	-4 (3)*	-6 (4)
SQIQNREFGTQKYEQW	3	497	512		68 (2)		-1 (4)*	-1 (4)*	-1 (4)*	-7 (4)	0 (5)*	-2 (4)*	1 (3)*	-2 (4)*	0 (4)*
SQIQNREFGTQKYEQ	3	497	511		62 (3)		-1 (4)* 3 (2)*	-4 (3)* 2 (3)*	-1 (2)*	-13 (3)	-2 (5)* 5 (2)*	-3 (4)* 3 (5)*	-1 (3)*	-2 (4)*	-1 (4)*
IVTVQKACM	2	513	521		9 (2) 13 (2)		-4 (2)*	-2 (3)*	-2 (3)*	-9 (2)	5 (2)*	2 (4)*	3 (5)*	-1 (2)*	-2 (3) 1 (3)*
VFQMPDKDEESRICKA	3	522	537		60 (2)		-9 (3)	-12 (3)	-4 (4)*	-15 (3)	1 (6)*	-2 (4)*	-11 (3)	-8 (3)	-24 (3)
VFQMPDKDEESRICKALF	4	522	539	CTD·HFI 2i	51 (2)		-6 (3)	-10 (2)	-1 (2)*	-14 (3)	3 (5)*	-2 (4)*	-9 (3)	-7 (3)	-21 (2)
FQMPDKDEESRICKA	3	523	537		62 (3)		-7 (4)	-18 (3)	-4 (4)*	-19 (4)	2 (8)*	-2 (4)*	-11 (3)	-8 (3)	-24 (3)
	4	523 540	539		49 (2)		-6 (3)	-11 (3)	-3 (3)*	-20 (4)	2 (4)*	-2 (4)*	-10 (3)	-7 (2)	-24 (2)
	4	540	552		11 (2)		-1 (4)*	3 (5)*	2 (6)*	-5 (3)*	3 (2)* 4 (3)*	2 (4)*	2 (2)*	1 (4)*	-1 (5)*
YTSHLRKYNDAL	2	541	552		13 (2)		-1 (3)*	5 (5)*	1 (6)*	-1 (4)*	4 (2)*	2 (5)*	3 (4)*	0 (5)*	2 (7)*
ISEHARMKDALD	3	553	565		24 (2)		-2 (2)*	1 (3)*	-1 (3)*	-5 (3)	3 (4)*	1 (3)*	2 (3)*	0 (2)*	-1 (3)*
HARMKDALD	2	557	565		30 (2)		0 (3)*	0 (3)*	-2 (3)*	-4 (2)*	3 (3)*	0 (3)*	0 (3)*	1 (3)*	0 (2)*
	3	557	565		32 (2)		-1 (3)*	-1 (3)*	-2 (3)*	-5 (3)*	0 (3)*	0 (3)*	0 (3)*	-2 (2)*	-1 (2)*
YLKDFFSNV	2	566	579		34 (2)		14 (3)	12 (4)	9 (3) 10 (2)	9 (2)	2 (3)* 5 (4)*	0 (3)*	2 (2)*	-1 (4)*	2 (3)* 1 (2)*
YLKDFFSNVRAAGF	3	566	579	Gate motif	35 (2)		14 (4)	17 (3)	12 (3)	11 (3)	3 (4)*	-3 (3)*	1 (3)*	-4 (2)*	-1 (2)*
FFSNV	1	570	574					30 (2)	21 (3)	6 (3)	3 (3)*	0 (5)*	2 (3)*	-2 (2)*	3 (3)*
FFSNVRAAGFD	2	570	580		49 (1)		15 (5)	18 (4)	15 (5)	14 (4)	-1 (4)*	3 (6)*	2 (3)*		-2 (8)*
FFONVRAAGE	2	5/0	5/9		49 (2)		17 (3)	19 (3)	13 (3)	17 (3)	4 (4)*	-2 (4)*	0 (4)*	-1 (4)*	1 (5)*

WT RIG-I

peptide sequence	charge	start	end	structur	e (i)	(ii)	(iii)	(iv)	(v)	(vi)	(vii)	(viii)	(ix)	(x)	(xi)
DEIEQDLTQRFEEKLQE	3	580	596		25 (2)		3 (2)*	11 (3)	2 (3)*	2 (2)*	5 (3)*	0 (2)*	0 (2)*	-3 (2)*	-1 (2)*
DEIEQDLTQRFEEKLQEL	3	580	597		25 (1)		4 (2)*	8 (1)	3 (2)*	2 (3)*	3 (2)*	0 (3)*	0 (2)*	-1 (1)*	0 (2)*
DEIEQDLTQRFEEKLQELES	3	580	599	HFI 2i	27 (1)		4 (2)*	7 (1)	3 (2)*	1 (2)*	3 (3)*	0 (3)*	0 (3)*	-1 (2)*	-2 (2)*
QELESVSRDPSNENPKLED	3	595	613		47 (2)		2 (3)*	1 (2)*	1 (5)*	-3 (3)*	-1 (3)*	-1 (4)*	-7 (4)	-3 (4)*	-6 (5)
ESVSRDPSNENPKLEDLC	3	598	615		40 (1)		0 (1)*	3 (3)*	2 (3)*	0 (2)*	4 (6)*	-3 (3)*	-6 (7)	1 (3)*	-6 (3)
VSRDPSNENPKLED	2	600	613		58 (2)		3 (4)*	2 (4)*	1 (4)*	-1 (5)*	-2 (5)*	-3 (4)*	-7 (4)	-2 (4)*	-6 (4)
VSRDPSNENPKL	3	600	611		51 (3)		4 (4)*	3 (6)*	2 (5)*	1 (10)*	-2 (4)*	-5 (4)	-10 (4)	-3 (5)*	-6 (5)
	2	610	620		33 (3)		-4 (3)*	-1 (3)*	-2 (3)*	-3 (2)*	-1 (3)*	1 (4)*	-2 (3)*	0 (2)*	-4 (2)*
	2	620	637	HEL2	22 (1)		-1 (1)* 1 (2)*	1 (1)* 5 (3)*	1 (1)* 2 (5)*	-5 (1)*	2 (3)*	1 (2)*	-2 (3)*	-1 (2)* 0 (4)*	-3 (2)*
EVKTRALVDALKNWEGNPKI	3	633	653		31 (2)		-3 (3)*	-2 (2)*	-1 (3)*	-8 (3)	-2 (2)*	1 (3)*	-6 (3)	3 (3)*	-11 (2)
FVKTRALVDALKNWIEGNPKLSF	3	633	655		35 (2)		-3 (2)*	-3 (2)*	-2 (2)*	-10 (2)	- (-)	1 (3)*	-6 (2)	4 (4)*	-10 (2)
FVKTRALVDALKNWIEGNPKLSFLKPGIL	4	633	661		36 (2)		-3 (3)*	0 (2)*	5 (2)	-12 (2)	-3 (0)*	2 (5)*	-6 (3)		-12 (4)
SFLKPGIL	2	654	661	motifilv	40 (2)		1 (2)*	3 (3)*	1 (5)*	-2 (3)*	0 (2)*	-1 (5)*	-8 (2)	-5 (5)	-12 (5)
TGRGKTNQNTGMTLPAQKCIL	3	662	682		72 (4)		3 (5)*	0 (6)*	-4 (5)*	-3 (5)*	-4 (5)*	-3 (4)*	-4 (4)*	-6 (5)	-1 (7)*
TGRGKTNQNTGMTLPAQKCIL	4	662	682		67 (3)		4 (4)*	-3 (4)*	-5 (3)*	-1 (4)*	-2 (5)*	-4 (4)*	-3 (3)*	-6 (5)	0 (0)*
PAQKCIL	2	676	682		85 (3)		-1 (5)*	1 (3)*	0 (4)*	-3 (6)*	-2 (4)*	1 (2)*	-1 (3)*	-14 (6)	-4 (5)*
DAFKASGDHNIL	2	683	694		46 (3)		0 (3)*	2 (4)*	-2 (3)*	-2 (4)*	-1 (4)*	-2 (3)*	-1 (2)*	-4 (3)*	0 (4)*
DAFKASGDHNIL	3	683	694		47 (2)		0 (3)*	0 (4)*	-3 (3)*	-2 (5)*	0 (3)*	-2 (3)*	-2 (3)*	-4 (3)*	1 (4)*
FKASGDHNIL	3	685	594		39 (3)		-1 (3)*	0 (4)*	-3 (3)*	-3 (4)*	1 (5)*	-1 (3)*	0 (3)*	-2 (2)*	0 (4)*
	2	605	705		/1 (2)		0 (4)*	-4 (3)*	-5 (4)	-3 (6)*	0 (6)*	-2 (3)*	-49 (5)	-9 (4)	-39 (5)
	2	715	724		00 (2) 92 (4)		0.(6)*	-1 (3)* 5 (4)*	-3 (4)*	-2 (1)*	0 (2)* 2 (6)*	-3 (4)"	-30 (4)	-4 (4)*	-24 (3)
VVGNVIKM	2	717	724		72 (3)		2 (5)*	-1 (4)*	-2 (4) 2 (4)*	0 (3)*	-2 (0)	-4 (5)*	-34 (4)	-12 (4)	-40 (3)
IQTRGRGRARGSKC	4	725	738		74 (2)		3 (4)*	-3 (4)*	-3 (7)*	0 (5)*	3 (0)*	-7 (4)	-38 (5)	2 (7)*	-31 (6)
FLLTSNAGVIEKEQINM	2	739	755		44 (3)		-1 (4)*	2 (4)*	0 (5)*	-23 (3)	3 (5)*	2 (4)*	-9 (3)	-4 (3)*	-12 (4)
LTSNAGVIEKEQINM	2	741	755		55 (3)		-3 (5)*	-1 (4)*	-2 (4)*	-7 (3)	-1 (6)*	0 (1)*	-10 (4)	-5 (3)*	-15 (3)
AGVIEKE	2	745	751	Pincer	51 (3)		4 (4)*	2 (3)*	-3 (5)*		-3 (1)*	-2 (1)*	-7 (3)	-1 (5)*	-2 (5)*
KEQINM	2	750	755		41 (3)		2 (4)*	3 (4)*	2 (5)*	-3 (3)*	-5 (7)*	4 (5)*	-24 (2)	-10 (3)	-26 (6)
YKEKMMNDSIL	2	756	766		18 (2)		4 (3)*	10 (3)	3 (5)*	-1 (3)*	5 (5)	6 (4)	2 (3)*	-1 (3)*	1 (5)*
YKEKMMNDSIL	3	756	766		18 (3)		5 (4)*	6 (3)	3 (5)*	-1 (3)*	5 (4)	6 (4)	1 (3)*	-1 (3)*	1 (5)*
RLQTWDEAVF	2	767	776		52 (2)		-5 (4)*	-1 (3)*	-4 (3)*	1 (4)*	0 (3)*	0 (4)*	5 (2)	-1 (2)*	3 (2)*
WDEAVF	1	7/1	7/6		50 (3)		0 (4)*	-4 (2)*	4 (2)*	2 (2)*	1 (4)*	-2 (3)*	0 (4)*	-1 (7)*	1 (5)*
	4	770	789		19 (4)		-6 (4)	1 (4)*	0 (5)*	-/ (4)	-2 (0)*	2 (4)*	4 (5)*	1 (3)*	-4 (5)*
	2	791	803		22 (2)		-/ (4) 1 (4)*	0 (5)*	-2 (A)*	-6 (4)	0 (6)*	-11 (5)	-15 (3)		-0 (5)
VRVIEF	2	823	828		62 (3)		0 (4)*	4 (4)*	-2 (+) 0 (4)*	-13 (4)	-3 (4)*	0 (4)*	-3 (7)*	-1 (2)*	-2 (2)*
VRVIEECHY	2	823	831		41 (2)		-6 (4)	3 (3)*	4 (3)*	10(1)	-3 (4)*	1 (4)*	2 (5)*	-1 (3)*	-2 (3)*
VRVIEECHYTVLGDA	3	823	837		42 (4)		-1 (2)*	1 (2)*	-2 (4)*	-8 (4)	-2 (2)*	-1 (2)*	- (-/	0 (3)*	0 (5)*
VRVIEECHY	3	823	831		35 (2)		-7 (5)	-2 (4)*	0 (5)*	-9 (5)	-2 (6)*	-1 (4)*	3 (4)*	-2 (3)*	-2 (5)*
CHYTVLGDA	2	829	837		26 (1)		2 (2)*	3 (2)*	1 (2)*	0 (2)*	3 (3)*	-1 (3)*	0 (4)*	0 (2)*	-1 (2)*
TVLGDAFKECF	2	832	842		49 (2)		-3 (3)*	-1 (3)*	-1 (3)*	-6 (3)	-1 (3)*	0 (4)*	0 (3)*	1 (4)*	0 (4)*
FKECF	1	838	842		31 (3)		-8 (3)	-3 (4)*	-2 (5)*	-10 (4)	3 (7)*	1 (5)*	-1 (3)*	5 (3)*	-1 (5)*
FKECF	2	838	842		34 (2)		-9 (3)	-6 (4)	-9 (5)	-9 (4)	-2 (5)*	2 (6)*	0 (5)*	5 (4)*	0 (5)*
FVSRPHPKPKQFSS	4	842	855	Capping	77 (4)		-12 (5)	-13 (6)	-4 (4)*	-13 (6)	-21 (5)	1 (5)*	4 (3)*	-3 (6)*	-4 (5)*
VSRPHPKPKQFSSF	3	843	856	loop	74 (5)		-10 (6)	-15 (5)	-4 (5)*	-12 (6)	-24 (4)	0 (5)*	2 (6)*	-3 (6)*	-3 (6)*
EKDAKIE	2	857	863		(7 (4)		-12 (5)	-13 (0)	-2 (4)"	-13 (6)	-22 (0)	1 (5)*	4 (3)*	-3 (0)*	-4 (5)*
EKRAKIEC	2	857	864		40 (3)		-3 (3)*	-4 (5)*	-5 (5)	-9 (6)	-2 (4)	-1 (0)	-3 (3)	-1 (4)	-3 (5)*
EKRAKIEC	3	857	864		40 (3)		-6 (4)	-3 (5)*	-4 (6)*	-11 (5)	2 (4)*	0 (5)*	-1 (3)*	0 (4)*	0 (6)*
CARQNCSHDWGIHVKYKT	4	864	881		37 (3)		-1 (3)*	-3 (4)*	-3 (5)*	-7 (4)	- (.)	0 (5)*	-2 (2)*	2 (3)*	-1 (4)*
FEIPVIKIESF	2	882	892		11 (2)		-7 (2)	-5 (2)*	-4 (3)*	-10 (2)	-1 (4)*	1 (2)*	1 (2)*	-1 (2)*	-1 (3)*
FEIPVIKIES	2	882	891		16 (2)		-8 (2)	-3 (2)*	-2 (2)*	-6 (2)	-1 (5)*	3 (2)*	3 (2)*	-1 (2)*	1 (2)*
EIPVIKIESF	2	883	892		11 (2)		-8 (2)	-4 (2)*	-2 (2)*	-6 (2)		3 (2)*	3 (2)*	-1 (2)*	1 (2)*
VVEDIATGVQTL	1	893	904	RNA	65 (2)		-12 (4)	-9 (3)	-6 (3)	-14 (3)	-5 (3)	-1 (3)*	-3 (4)*	-5 (4)*	-10 (2)
VVEDIATGVQTL	2	893	904	binding	65 (3)		-10 (4)	-14 (3)	-11 (4)	-16 (4)	-6 (3)	3 (3)*	-1 (4)*	-5 (4)*	-10 (3)
IATGVQTL	2	897	904	ragion	66 (3)		-8 (5)	-20 (5)	-22 (5)	-18 (4)	-6 (3)	-1 (6)*	-6 (3)	-7 (5)	-6 (4)
YSKWKDFHFEKIPFDPAE	3	905	922		54 (3)		-9 (4)	-6 (3)	-3 (3)*	-5 (4)*	-1 (1)*	2 (4)*	1 (3)*	3 (4)*	-10 (4)
EKIPFDPAE	2	914	922		35 (3)		2 (3)*	1 (3)*	-1 (3)*	-3 (3)*	2 (5)*	0 (4)*	-1 (4)*	-1 (4)*	1 (3)*
EKIPFUPAEMSK	2	014	923		54 (3)		-2 (4)*	-1 (4)*	-3 (4)*	-5 (4)*	-5 (3)	-1 (3)*	-1 (Z)*	-2 (5)*	-1 (5)*
	2		725				0(4)	0(4)	-2 (4)	~ (4)	-5 (5)	-2 (3)	-2 (3)	-2 (4)	-2 (0)

HDX Dynamics Key

HDX Perturbation Key

H830A RIG-I

peptide sequence	charge	start	end	structure	(xii)	(xiii)	(xiv)
FQDYIRKTLDPTYILS	3	12	27		52 (3)	11 (3)	11 (3)
	3	13 16	26 26		78 (3)	11 (3)	10 (5)
SYMAPWFRE	2	27	35		40 (3) 53 (3)	17 (4)	14 (4)
YMAPWFREEEVQ	2	28	39	CARD1	55 (3)	14 (4)	14 (4)
	2	38 40	43 53		66 (4) 51 (3)	8 (5)	8 (5)
EKNNKGPMEAATL	2	44	56		45 (2)	11 (3)	11 (5)
LQEEGWFRGFL	2	64 65	74 74		48 (2)	9 (4)	6 (6)
FRGFLDA	2	70	76		52 (1)	9(3)	8 (4)
DALDHAGYSGL	2	75	85		34 (2)	13 (3)	13 (3)
LDHAGYSGL	2	77 86	85		36 (2)	10 (3)	9 (3)
YEAIESWD	1	86	93		29 (3)	23 (5)	22 (5)
YRLLL	2	103	107	Latch	12 (3)	24 (5)	23 (5)
YRLLLKRLQPEF	2	105	114	·	17 (3) 21 (4)	33 (5) 30 (5)	33 (5) 28 (6)
LLKRLQPEF	3	106	114	region	18 (4)	33 (5)	34 (6)
	4	106	126		7 (1)	10 (1)	8 (2)
KRLQPEF	3	108	114		21 (4)	34 (5) 33 (4)	33 (6)
KTRIIPTDIISD	3	115	126		62 (2)	12 (4)	11 (4)
KTRIPTDISDL	2	115	127	CARD2	59 (2)	14 (4)	13 (4)
KTRIIPTDIISDLSE	3	115	129		63 (2)	14 (4)	11 (4)
EEILQICSTKGMMAGAEKL	3	137	155		31 (1)	17 (3)	8 (5)
ILQICSTKGMMAGA	2	139	152		40 (2)	20 (2)	20 (3)
ILQICSTKGMMAGAEKLVE	3	139	157		29 (1)	19 (2)	18 (3)
LLRSDKENWPKTLKL	4	159	173		29 (2)	10 (3)	18 (3)
ALEKERNKFSEL	4	174	185		28 (2)	13 (4)	10 (6)
ALEKERNKFSEL	3	174	185		61 (3)	8 (3)	8 (4)
EKERNKFSEL	3	176	185		65 (2)	10 (4)	10 (6)
WIVEKGIKDVETEDL	3	186	200	linker	98 (2)	-2 (5)*	2 (3)*
WIVEKGIKDVETEDLED	2	186	202		97 (3)	0 (4)*	1 (5)*
WIVEKGIKDVETEDLEDKMETSD	3	186 187	208 200		95 (2)	0 (3)*	-1 (6)*
EDKMETSDIQIF	2	201	212		95 (5) 84 (3)	-2 (5)* 1 (4)*	1 (6)*
IQIFYQEDPECQNLSE	2	209	224		70 (2)	0 (3)*	-2 (6)*
YQEDPECQNL	2	212 213	222		81 (2)	-2 (3)*	-2 (6)*
SENSCPPSEVSDTNL	2	223	237		83 (4)	-2 (6)*	-1 (4)*
NSCPPSEVSDTNL	2	225	237		82 (4)	-1 (6)*	-1 (3)*
YSPFKPRN	3	232	237		92 (5)	-2 (6)* -2 (5)*	-2 (3)* -1 (7)*
YSPFKPRNYQLE	3	238	249	1 1	74 (3)	4 (4)*	3 (5)*
	2	238	249		73 (3)	3 (4)*	3 (5)*
LALPAMKGKNTICAPTGCGKTFVSLL	4	250	276		32 (3)	-1 (4)* 4 (3)*	1 (5)*
LALPAMKGKNTIICAPTGCGKTFVSLL	3	250	276	1 1	43 (2)	-1 (3)*	-5 (3)
	2	264 276	272	1 1	84 (3)	-1 (5)*	-1 (6)*
ICEHHLKKFPQGQKGKVVF	3	277	295	1 1	29 (1) 28 (2)	-3 (2)*	-3 (4)*
PQGQKGKVVF	3	286	295	L	79 (4)	-1 (4)*	-1 (7)*
FANQIPVYEQQ	2	296 296	306	motifia	74 (2)	-18 (3)	-15 (4)
FANQIPVYEQQKSVFSKY	3	296	313	mouria	56 (1)	-10 (2)	-11 (3)
FERHGYRVTGISGATAENVPVEQIVENND	4	314	342	[]	66 (3)	-4 (4)*	-3 (4)*
GYRVTGISGATAENVPVEQIVENND GYRVTGISGATAENVPVEQIVENN	3	314	342 341	1 1	65 (3) 71 (2)	-4 (4)*	0 (7)*
YRVTGISGATAENVPVEQIVE	3	319	339	1 1	84 (5)	-2 (7)*	-2 (8)*
IIILTPOIL	2	343	351	1 1	38 (1)	-5 (2)*	-4 (2)*
IIILTPQILVN	2	343	353	1 1	35 (1)	-4 (2)* -6 (2)	-3 (2)* -5 (2)*
IIILTPQILVNN	2	343	354		43 (2)	-8 (3)	-8 (4)
	2	343 343	355	1 1	52 (1)	-11 (2)	-10 (3)
IIILTPOILVNNLKKGTIPSL	2	343	363	motif Icl	68 (2)	-10 (3) -7 (4)	-6 (4) -6 (4)
IIILTPQILVNNLKKGTIPSLSI	3	343	365		68 (2)	-9 (3)	-7 (4)
IIILI POILVNNLKKGTIPSLSIF KGTIPSLSIFT	3	343 357	366 367	F4	65 (2)	-9 (3)	-7 (3)
KGTIPSLSIFT	3	357	367		61 (1)	4 (3)*	4 (3)*
LMIFDECHNTSKQHPYNM	3	368	385		36 (1)	-6 (2)	-6 (2)
IFDECHNTSKQHPYNMIM IFDECHNTSKQHPYNMIM	2	370	387	motif lla	36 (2)	-6 (2) -6 (2)	-6 (2) -6 (3)
FNYLDQKLGGSSGPLPQVIG	2	388	407		37 (1)	0 (2)*	0 (3)*
FNYLDQKLGGSSGPLPQVIGL	2	388	408 408	1 1	36 (1)	0 (2)*	0 (3)*
LTASVGVGDAKNTDEAL	2	408	424	1 1	43 (1) 70 (3)	-5 (4)	-5 (5)*
TASVGVGDAKNTDEAL	2	409	424	1 1	72 (3)	-5 (4)	-5 (5)*
	2	409 425	425 430	1 1	69 (3)	-5 (4)*	-4 (5)*
DYICKL	1	425	430	1 1	3(0)	0 (1)	1 (2)*
CASLDASVIATVKHNLEEL	2	431	449	1 1	37 (1)	0 (2)*	0 (3)*
EQVVYKPQKF	2	450	448 459		62 (2)	-1 (3)* 1 (4)*	-1 (3)* 1 (4)*
VVYKPQKF	2	452	459		83 (3)	-1 (5)*	-1 (5)*
VVYKPQKF	3	452	459		83 (3)	-1 (4)*	-1 (5)*
QLMRDTESL	з 2	477	485		<u>71 (2)</u> 9 (2)	0 (3)*	-3 (16)* -1 (5)*
MRDTESL	2	479	485		7 (0)	1 (1)*	1 (1)*
	3	486 497	496		76 (3)	-8 (3)	-6 (5)
SQIQNREFGTQKYEQW	3	497	512		76 (3)	-4 (5)* -3 (4)*	-4 (5)* -3 (5)*
WIVTVQKACM	2	512	521		11 (4)	0 (6)*	0 (5)*
IVTVQKACM	2	513 522	521		12 (1)	-2 (2)*	-1 (2)*
VFQMPDKDEESRICKALF	4	522	539	CTD:HEL2i	66 (2) 58 (2)	-11 (3) -10 (3)	-11 (4) -9 (3)
FQMPDKDEESRICKA	3	523	537		64 (2)	-11 (3)	-11 (4)
FQMPDKDEESRICKALF	4	523 540	539 552		53 (2)	-9 (2)	-9 (3)
LYTSHLRKYNDAL	3	540	552		8 (2)	2 (4)*	2 (4)*

H830A RIG-I							
peptide sequence	charge	start	end	structure	(xii)	(xiii)	(xiv)
LYTSHLRKYNDAL	4	540	552		8 (2)	2 (4)*	2 (4)*
LYTSHLRKYNDAL	3	540	552	HEL2i	8 (2)	2 (3)*	2 (4)*
IISEHARMKDALD	3	553	565		23 (2)	2 (3)*	2 (3)*
HARMKDALD	2	557	565		32 (2)	1 (2)*	1 (3)*
	3	565	579		31 (2)	1 (2)*	1 (3)*
VIKDEESNV	2	566	574		49 (2)	14 (4)	12 (4)
VIKDEESNVRAAGE	3	566	579	Gate motif	18 (1)	14 (2)	13 (2)
FESNV	1	570	574		46 (3)	27 (4)	25 (4)
FFSNVRAAGF	2	570	579		58 (2)	19 (5)	17 (5)
FFSNVRAAGFD	2	570	580		63 (5)	15 (6)	14 (6)
FSNVRAAGF	2	571	579		65 (2)	19 (4)	17 (5)
DEIEQDLTQRFEEKLQE	3	580	596		25 (0)	5 (2)	6 (2)
DEIEQDLTQRFEEKLQEL	3	580	597		25 (1)	6 (2)	6 (2)
DEIEQDLTQRFEEKLQELES	3	580	599		28 (1)	5 (2)	6 (2)
QELESVSRDPSNENPKLED	3	595	613		53 (2)	0 (3)*	0 (4)*
ESVSRDPSNENPKLEDLC	3	598	615		45 (1)	0 (2)*	0 (2)*
VSRDPSNENPKL	3	600	611		68 (4)	0 (6)*	-2 (6)*
VSRDPSNENPKLED	2	600	613		58 (3)	1 (4)*	0 (5)*
FILQEEYHLNPET	2	616	628	HFI 2	31 (1)	0 (2)*	0 (2)*
ILQEEYHLNPETITIL	2	617	632		26 (1)	0 (1)*	0 (2)*
EEYHLNPETITILFVKTR	2	620	637		40 (1)	0 (2)*	1 (3)*
FVKTRALVDALKNWIEGNPKL	3	633	653	motif IV/	30 (1)	-1 (2)*	-2 (3)*
FVKTRALVDALKNWIEGNPKLSF	3	633	655	mountv	32 (1)	-1 (3)*	-3 (4)*
FVKTRALVDALKNWIEGNPKLSFLKPGIL	4	633	661		33 (1)	0 (2)*	-2 (5)*
WIEGNPKL	2	646	653		42 (1)	0 (2)*	1 (3)*
WIEGNPKLSFLKPGIL	2	646	661		44 (2)	4 (2)*	1 (4)*
SFLKPGIL	2	654	661		43 (2)	1 (2)*	2 (4)*
KPGILIGRGKINQNIG	3	657	672		30 (4)	-4 (5)*	-1 (5)*
IGRGKINQNIGMILPAQKCIL	3	676	682		84 (3)	-3 (4)*	-3 (5)*
PAUNUL	2	692	604		77 (1)	-4 (2)*	3 (6)*
DAFKASODHNIL	2	683	694		55 (3)	-1 (4)*	-1 (4)*
EKASODHNIL EKASODHNII	2	685	694		52 (3)	0 (4)*	0 (5)*
	2	695	705		46 (3)	0 (4)*	-1 (4)*
	2	695	703		84 (3)	-5 (5)*	-3 (4)*
SVADEGIDIAGONE	2	698	708		85 (3)	-2 (0)*	0 (5)*
	4	709	721		38 (2)	4 (3)*	4 (4)*
VILYEYVGNVIKM	2	712	724		23 (2)	-2 (5)*	0 (4)*
YEYVGNVIKM	2	715	724		97 (2)	-2 (5)*	-5 (6)*
YVGNVIKM	2	717	724		91 (3)	-4 (5)*	-4 (6)*
IQTRGRGRARGSKC	4	725	738		66 (3)	-4 (4)*	-4 (5)*
FLLTSNAGVIE	2	739	749		65 (1)	-5 (2)*	-2 (3)*
FLLTSNAGVIEKEQINM	2	739	755	Pincer	46 (3)	4 (4)*	1 (4)*
LTSNAGVIEKEQINM	2	741	755		60 (2)	3 (5)*	0 (3)*
AGVIEKE	2	745	751		62 (2)	0 (4)*	0 (6)*
KEQINM	2	750	755		59 (2)	4 (3)*	3 (3)*
YKEKMMNDSIL	3	756	766		21 (2)	11 (3)	11 (4)
YKEKMMNDSIL	2	756	766		21 (2)	11 (3)	11 (4)
SILRLQT	2	764	770		26 (2)	1 (3)*	2 (4)*
RLQTWDEAVF	2	767	776		51 (1)	-2 (3)*	0 (3)*
WDEAVF	1	771	776		75 (2)	0 (3)*	-1 (3)*
FREKILHIQTHEKF	4	776	789		-18 (1)	-2 (2)*	-1 (3)*
REKILHIQTHEKF	3	///	/89		9 (2)	0 (4)*	-2 (3)*
	2	700	793		18 (1)	14 (2)	13 (2)
	2	701	203		63 (2)	10 (4)	4 (4)*
	2	823	878		98 (2)	0 (4)*	0 (5)*
TVI GDAFKECE	2	832	842		65 (2) 56 (2)	-4 (3)*	-4 (3)*
FKECE	1	838	842		36 (2) 46 (2)	-5(3)-	-10 (4)
FKECE	2	838	842		40 (2)	-14 (3)	-10 (4)
EVSRPHPKPKQESS	4	842	855		77 (2)	-19 (4)	-3 (4)*
VSRPHPKPKQESSE	4	843	856	Capping	78 (3)	-19 (4)	-3 (4)*
VSRPHPKPKQFSSF	3	843	856	loop	77 (2)	-22 (4)	-4 (4)*
EKRAKIF	2	857	863		49 (2)	-14 (2)	-9 (3)
EKRAKIFC	3	857	864		44 (3)	-13 (3)	-10 (3)
EKRAKIFC	2	857	864		43 (2)	-13 (4)	-8 (3)
CARQNCSHDWGIHVKYKT	4	864	881		15 (2)	-3 (2)*	-2 (2)*
DWGIHVKYKTFEIPVIKIESFVV	4	872	894		47 (2)	4 (3)*	3 (5)*
FEIPVIKIESF	2	882	892		14 (1)	-5 (3)	-5 (3)*
FVVEDIATGVQTL	2	892	904		64 (2)	-12 (4)	-11 (5)
VVEDIATGVQTL	2	893	904		74 (2)	-14 (3)	-12 (4)
VVEDIATGVQTL	1	893	904	KINA binding	72 (2)	-15 (3)	-12 (4)
YSKWKDFHFEKIPFDPAE	3	905	922	region	52 (2)	-4 (2)*	-4 (6)*
EKIPFDPAE	2	914	922		46 (3)	1 (3)*	1 (4)*
EKIPFDPAEMSK	2	914	925		65 (4)	-2 (5)*	-3 (6)*
EKIPFDPAEMSK	3	914	925		66 (4)	-1 (5)*	-2 (6)*

HDX Dynamics Key

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-10 0 HDX Perturbation Key

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E373A RIG-I

peptide sequence	charge	start	end	structure	(xv)	(xvi)	(xvii)	(xviii)	(xix)	(xx)	(xxi)	(xxii)
FQDYIRKTLDPTYIL	2	12	26		34 (2)	14 (3)	6 (3)	0 (3)*	2 (2)*	1 (2)*	7 (3)	13 (3)
FQDYIRKTLDPTYIL	3	12	26		33 (2)	14 (3)	6 (3)	0 (3)*	2 (2)*	1 (2)*	7 (3)	13 (3)
SYMAPWERFEEVO	2	27	39		49 (1)	10 (1)	3 (2)*	0 (1)*	3 (1)* 4 (3)*	2 (3)*	7 (4) 8 (2)	24 (4)
YMAPWFRE	2	28	35		52 (2)	12 (3)	5 (3)*	-1 (2)*	4 (3)*	-1 (3)*	8 (3)	10 (4)
YMAPWFREE	2	28	37	CARD1	51 (2)	13 (3)	6 (3)	1 (2)*	3 (4)*	1 (4)*	7 (3)	8 (4)
VQYIQA	1	38	43		47 (2) 48 (2)	15 (3)	6 (3)	-3 (3)*	4 (3)* 3 (2)*	1 (4)* 2 (3)*	8(2) 8(3)	11 (3)
YIQAEKNNKGPMEAATL	3	40	56		38 (2)	14 (3)	7 (3)	0 (3)*	4 (3)*	3 (3)*	8 (3)	13 (3)
LQEEGWFRGFL	2	64	74		38 (1)	17 (1)	13 (2)	1 (2)*	1 (4)*	-1 (3)*	1 (4)*	14 (3)
QEEGWERGEL QEEGWERGELDAL	2	65	74		47 (2)	8 (2)	4 (3)*	2 (2)*	3 (3)*	0 (3)*	4 (3)* 8 (3)	6 (3) 14 (4)
FRGFL	2	70	74		19 (1)	14 (2)	6 (2)	-2 (2)*	3 (1)*	0 (2)*	7 (2)	13 (2)
FRGFLDA	2	70	76		15 (1)	15 (2)	7 (2)	-2 (1)*	3 (1)*	1 (1)*	7 (2)	13 (2)
I DHAGYSGI	2	75	85		30 (2)	12 (2) 8 (2)	5 (2)	0 (3)*	3 (2)*	2 (3)* 5 (3)*	7 (2) 8 (3)	10 (3) 9 (3)
YEAIESWD	1	86	93		28 (2)	18 (2)	7 (2)	-3 (2)*	4 (3)*	2 (2)*	9 (3)	17 (2)
YEAIESWDFKKIEKLEE	3	86	102		52 (2)	7 (2)	0 (3)*	-3 (3)*	0 (2)*	-5 (5)*	0 (4)*	
DFKKIEKLEE	3	93	103		55 (3) 69 (2)	6 (3)	2 (3)*	2 (2)*	2 (3)*	-2 (6)*	4 (4)* 1 (4)*	3 (4)*
FKKIEKLEE	3	94	102		63 (2)	5 (3)	2 (3)*	1 (2)*	-2 (4)*	-3 (4)*	1 (3)*	3 (4)*
YRLLL	2	103	107		11 (4)	19 (4)	8 (5)	0 (4)*	2 (2)*	0 (2)*	8 (5)	15 (3)
LLKRLQPEF	2	105	114		19 (4)	26 (5)	13 (5)	3 (5)*	4 (2)*	7 (2)	15 (3)	22 (3)
KRLQPEF	2	108	114	Latch	19 (5)	31 (5)	15 (6)	5 (6)*	2 (2)*	7 (3)	23 (4)	24 (4)
KRLQPEF	3	108	114	ragion	15 (5)	31 (5)	16 (6) 8 (4)	0 (6)*	4 (2)* 1 (5)*	2 (3)*	13 (4)	22 (4)
KTRIPTDISD	3	115	126	region	53 (3)	13 (4)	8 (4)	-1 (3)*	3 (4)*	0 (5)*	5 (4)	o (5) 7 (4)
KTRIPTDISDL	2	115	127		52 (2)	14 (3)	8 (3)	2 (2)*	2 (4)*	1 (4)*	6 (3)	9 (4)
	3	115	127		51 (2)	14 (3)	8 (3)	1 (2)*	2 (4)*	1 (4)*	6 (3)	9 (4)
ILQICSTKGMMAGAEKL	3	139	155		34 (2)	16 (2)	8 (2)	-1 (2) ⁻ 3 (3)*	2 (3)* 3 (3)*	0 (2)*	5 (4)	12 (3)
ILQICSTKGMMAGAEKLVE	3	139	157	CANDZ	27 (2)	20 (3)	10 (2)	3 (2)*	4 (2)*	1 (2)*	8 (2)	14 (3)
	3	142	155		34 (2)	21 (3)	12 (3)	3 (3)*	4 (3)*	1 (3)*	8 (3)	13 (3) 11 (2)
LRSDKENWPKTLKLAL	4	160	175		29 (3) 26 (3)	20 (3)	8 (4)	2 (3)* 4 (3)*	-6 (3)*	-8 (3)	2 (4)* 3 (4)*	6 (2)
ALEKERNKFSEL	3	174	185		62 (2)	10 (4)	12 (4)	1 (2)*	1 (4)*	1 (4)*	-1 (6)*	4 (5)*
EKERNKFSEL	3	176	185		59 (1)	10 (4) 2 (4)*	6 (3) 3 (6)*	1 (2)*	-9 (4)	-3 (5)*	-2 (4)*	4 (4)* 1 (6)*
WIVEKGIKD	3	185	194		76 (3)	2 (4)* 3 (5)*	3 (6)* 4 (5)*	1 (4)*	4 (4)*	-1 (4) ⁻ 2 (3)*	3 (5)*	-1 (6)* 1 (5)*
WIVEKGIKDVE	2	186	196		89 (1)	2 (4)*	3 (5)*	2 (4)*	1 (3)*	-1 (3)*	1 (3)*	-1 (6)*
WIVEKGIKDVE	3	186	196		89 (1)	2 (4)*	4 (5)*	2 (4)*	1 (2)*	0 (9)*	2 (5)*	0 (6)*
EDKMETSD	2	201	202		75 (1)	2 (5)*	3 (6)* 1 (1)*	4 (3)* 0 (4)*	1 (1)*	-1 (5)*	0 (1)*	-2 (5)* -5 (1)*
IQIFYQEDPECQNL	2	209	222	linker	82 (2)	4 (5)*	5 (5)*	-7 (4)	1 (5)*	1 (5)*	2 (6)*	-2 (5)*
YQEDPECQNL YQEDPECQNL SE	2	213	222		77 (3)	1 (5)*	2 (6)*	-10 (5)	1 (4)*	0 (6)*	2 (6)*	-1 (7)*
SENSCPPSEVSDTNL	2	223	237		77 (3)	0 (5)*	2 (6)*	-9 (6)	1 (4)*	0 (5)*	2 (6)*	0 (3)
YSPFKPRN	2	238	245		89 (2)	2 (6)*	2 (6)*	1 (5)*	-5 (4)	-8 (4)	-5 (7)	-10 (6)
YSPEKPRN YSPEKPRNYOLE	3	238	245		89 (2)	2 (6)*	2 (6)*	1 (5)*	-3 (4)*	-8 (6)	-4 (5)* 3 (4)*	-8 (6)
LALPAMKGKN	3	250	259		45 (4)	3 (5)*	2 (6)*	3 (6)*	2 (4)*	0 (5)*	2 (5)*	2 (5)*
LALPAMKGKNTIIC	3	250	263		32 (4)	2 (5)*	1 (5)*	3 (5)*	-2 (4)*	-4 (5)*	0 (5)*	-2 (5)*
	3	250	264 271		67 (2) 52 (2)	4 (3)* -3 (4)*	4 (3)*	1 (4)*	-1 (4)*	-4 (5)*	0 (5)*	-5 (4)*
LALPAMKGKNTIICAPTGCGKTFVSL	3	250	275		46 (2)	3 (3)*	2 (4)*	-2 (4)*	-5 (3)	-12 (3)	-6 (4)	-17 (4)
LALPAMKGKNTIICAPTGCGKTFVSL	4	250	275	HEL1	43 (2)	2 (3)*	-1 (3)*	-6 (3)	-2 (3)*	-9 (3)	-5 (2)*	-11 (3)
LICEHHLKKFPQGQKGKVVF	4	276	295		32 (2)	1 (3)* 0 (3)*	-3 (3)* -6 (3)	-4 (2)* -10 (3)	-15 (3)	-23 (3)	-10 (5)	-23 (3) -25 (3)
FANQIPVYEQQKSVF	2	296	310		65 (2)	-16 (3)	-6 (4)	-10 (4)	2 (3)*	-5 (4)	-3 (4)*	-29 (4)
FANQIPVYEQQKSVFSKY	3	296	313		57 (2)	-14 (3)	-8 (3)	-3 (4)*	2 (3)*	-6 (3)	3 (3)*	-21 (4)
FERHGYRVTGISGATAENVPVEQ FERHGYRVTGISGATAENVPVEQ	3	314	336		66 (2) 71 (5)	0 (4)* 2 (5)*	0 (4)* 1 (5)*	-2 (3)* -3 (5)*	-2 (4)* 2 (3)*	-2 (3)* -7 (4)	-1 (5)* 1 (3)*	-3 (4)*
IILTPQIL	2	343	351		32 (2)	-2 (3)*	0 (3)*	-10 (2)	-1 (2)*	-3 (2)*	-1 (3)*	-13 (3)
	2	343	355		47 (2)	-8 (3)	-4 (3)*	-10 (3)	-2 (2)*	-6 (2)	1 (3)*	-23 (3)
	3	343	365		61 (2) 59 (2)	-6 (3)	-2 (3)* -2 (3)*	-6 (3) -11 (4)	-2 (4)* -2 (3)*	-5 (4)* -5 (3)*	-2 (3)* -2 (3)*	-16 (3)
VNNLKKGTIPSL	2	352	363	motif la	71 (2)	-7 (4)	-3 (4)*	-5 (4)*	-2 (5)*	-5 (5)	-3 (4)*	-11 (4)
VNNLKKGTIPSL	3	352	363		71 (2)	-7 (4)	-3 (4)*	-5 (4)	-2 (4)*	-5 (5)	-3 (4)*	-11 (4)
IFDACHNISKQHPYNM IFDACHNTSKQHPYNMM	3	370	387		40 (1)	-5 (2)* -4 (2)*	0 (3)*	-2 (2)*	0 (2)*	-2 (3)* -2 (2)*	-1 (3)* 0 (3)*	-15 (3)
IFDACHNTSKQHPYNMIM	4	370	387		34 (1)	-4 (2)*	1 (2)*	-1 (2)*	2 (2)*	-1 (2)*	0 (2)*	-13 (3)
FNYLDQKLGGSSGPLPQVIG	2	388	407		34 (2)	1 (3)*	1 (4)*	0 (3)*	1 (2)*	0 (3)*	3 (3)*	2 (3)*
DQKLGGSSGPLPQVIG	2	392	408		42 (2)	2 (3)*	1 (4)*	2 (2)*	2 (3)*	1 (4)* 0 (3)*	4 (3)* 3 (3)*	2 (3)*
TASVGVGDAKNTD	2	409	421		77 (3)	-1 (6)*	2 (12)*		-2 (7)*	-6 (8)	-3 (5)*	-15 (5)
TASVGVGDAKNTDEAL	2	409	424	motif Ic	64 (3)	1 (5)*	1 (4)*	-1 (4)*	-2 (5)*	-6 (6)	-2 (4)*	-12 (4)
DYICKL	2	425	430		3 (3)	1 (3)*	0 (4)*	-1 (3)*	0 (2)*	-1 (2)*	-2 (4) 1 (4)*	-1 (3)*
YICKL	2	426	430	motiflla	4 (3)	1 (4)*	1 (5)*	-1 (3)*	0 (2)*	-1 (2)*	1 (5)*	-1 (4)*
CASLDASVIATVKHNLEEL	2	431	449		39 (1)	4 (2)*	2 (2)*	1 (2)*	-3 (3)*	-11 (2)	-3 (2)*	3 (2)*
SVIATVKHNLEEL	2	437	449		54 (2)	5 (3)*	2 (3)*	2 (2)*	-6 (4)	-8 (3)	-2 (3)* -5 (3)*	-7 (3)
LEQVVYKPQKF	3	449	459		63 (2)	10 (4)	6 (3)	0 (4)*	-9 (4)	-16 (4)	-11 (3)	-17 (3)
EQVVYKPQKF	2	450	459		53 (2)	16 (4)	13 (4) 8 (3)	3 (2)*	-12 (5)	-10 (5)	-6 (3)	-10 (4)
LMRDTESLAKRICKDLEN	4	478	495		44 (2)	0 (2)*	1 (2)*	-1 (3)*	-7 (2)	-12 (1)	-16 (2)	-14 (4)
MRDTESLAKRICKDLENL	4	479	496		44 (2)	0 (2)*	1 (2)*	-1 (3)*	-6 (2)	-12 (1)	-16 (2)	-6 (2)
AKRICKDLENL	3	486	496 511	HEL2i	69 (3) 70 (2)	0 (4)*	1 (4)*	1 (3)*	-4 (5)* 0 (5)*	-4 (3)*	-3 (4)* 1 (4)*	-6 (4) -3 (5)*
SQIQNREFGTQKYEQW	3	497	512		64 (2)	0 (4)*	2 (4)*	0 (3)*	0 (4)*	-2 (5)*	1 (4)*	-4 (4)*
WIVTVQKACM	2	512	521		49 (4)	-4 (9)*	1 (6)*	3 (2)*	-2 (4)*	-1 (4)*	-1 (2)*	-4 (2)*
	2	522	531		70 (3)	-1 (6)*	0 (5)*	0 (4)*	-1 (5)*	-4 (5)*	-3 (5)*	-18 (5)
VFQMPDKDEESRICKA	4	522	537		61 (2)	-4 (4)*	-1 (3)*	0 (3)*	-2 (4)*	-6 (4)	-4 (3)*	-23 (3)
VFQMPDKDEESRICKALF	3	522	539		54 (1)	-4 (3)*	-1 (3)*	1 (2)*	-2 (3)*	-5 (3)	-3 (3)*	-19 (3)
SRICKALF YTSHLRKYNDALL	3	532 541	539 553		26 (2)	-5 (2)* 2 (4)*	-2 (2)* 2 (4)*	1 (2)*	-3 (2)* 0 (4)*	-5 (2)	-4 (3)*	-16 (3)
ISEHARMKDAL	3	553	564		25 (2)	3 (3)*	1 (4)*	1 (2)*	-2 (2)*	-5 (3)*	-1 (4)*	-3 (4)*
ISEHARMKDALD	3	553	565		22 (2)	2 (3)*	3 (3)*	1 (2)*	0 (3)*	-2 (3)*	0 (4)*	-2 (3)*
UYLKDFFSNVRAAGF YLKDFFSNV	3	565	579	Gate motif	44 (2)	11 (3)	12 (3)	-1 (3)* 3 (2)*	-3 (2)* 1 (2)*	-3 (3)* 0 (2)*	2 (3)*	-5 (4)* 2 (3)*
YLKDFFSNVRAAGF	3	566	579	Sate moul	43 (2)	15 (3)	13 (2)	-1 (4)*	1 (2)	3 (4)*	11 (3)	4 (3)*
FFSNVRAAGF	2	570	579	+4	55 (2)	17 (4)	12 (3)	3 (3)*	3 (6)*	0 (6)*	9 (3)	5 (5)*
FDEIEQDLTQRF	2	579 579	590 594		21 (2)	7 (2)	4 (3)* 2 (2)*	2 (2)*	0 (2)*	-3 (2)* 4 (3)*	-3 (3)* 5 (2)	-3 (2)* 1 (2)*
DEIEQDLTQRFEEKLQEL	3	580	597		24 (2)	5 (2)*	2 (2)*	2 (1)*	1 (2)*	-1 (2)*	0 (2)*	-1 (3)*
DEIEQDLTQRFEEKLQELES	3	580	599		26 (2)	4 (2)*	2 (2)*	4 (5)*	1 (2)*	-1 (2)*	0 (2)*	-2 (2)*

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	charge	start	end	structure	(xv)	(xvi)	(xvii)	(xviii)	(xix)	(xx)	(xxi)	(xxii)
ESVSRDPSNENPKLED	3	597	613		53 (2)	2 (4)*	1 (4)*	-2 (4)*	0 (4)*	-4 (5)*	-1 (4)*	-8 (4)
SVSRDPSNENPKLED	3	598	613		52 (2)	1 (4)*	1 (4)*	-3 (3)*	0 (4)*	-4 (5)*	-1 (3)*	-8 (4)
/SRDPSNENPKLED	3	600	613	HEL2	54 (3)	2 (5)*	1 (4)*	-2 (4)*	0 (5)*	-4 (5)*	-1 (4)*	-7 (4)
ILQEEYHLNPET	2	616	628		31 (2)	0 (2)*	0 (3)*	3 (2)*	-1 (2)*	-5 (2)*	-2 (3)*	-6 (2)
LQEEYHLNPET	2	617	628		32 (2)	1 (2)*	2 (3)*	0 (2)*	0 (2)*	-3 (2)*	-1 (3)*	-6 (3)
	2	61/	630		33 (1)	0 (1)*	-1 (2)*	0 (1)*	-2 (1)*	-3 (2)*	-3 (2)*	-7 (2)
	2	61/	632		24 (1)	0 (2)*	0 (3)*	-1 (2)*	0 (2)*	-3 (2)*	-1 (3)*	-5 (2)
THLNPET	2	621	628		53 (2)	0 (4)*	1 (3)*	0 (3)*	2 (3)*	-1 (3)*	1 (2)*	-4 (3)*
	2	622	620		61 (2)	0 (3)*	2 (3)*	-1 (3)*	-1 (3)*	-10 (4)	-2 (3)*	-15 (3)
VKTRALVDALKNWIEGNPKL	3	633	655		32 (1)	-1 (2)*	-1 (2)*	-5 (2)	-7 (2)	-19 (3)	-11 (4)	-19(2)
	4	633	653		32 (2)	-1 (2)*	-1 (2)*	-5 (2)	-5 (2)	-17 (3)	-10 (3)	-19 (2)
ALVDALKNWIEGNPRESFER	3	654	661	motiriv	32 (1)	-1 (2)*	-1 (2)*	-3 (7)*	-7 (2)	-19 (3)	-11 (4)	-19(2)
FLKPGIL	2	654	661		41 (3)	4 (4)*	2 (5)*	3 (5)*	-2 (4)*	-7 (4)	-4 (5)*	-15 (5)
	2	656	661		64 (2)	4 (4)*	2 (7)*	0 (3)*	-4 (6)*	-11 (4)	-/ (/)	-25 (7)
GRGKTNUNTGMTLPAU	3	662	676		78 (4)	3 (7)*	1 (5)*	-1 (5)*	-3 (7)*	-2 (7)*	0 (6)*	0 (7)*
JRGKINQNIGMILPAQK	4	662	679		78 (3)	1 (6)*	0 (6)*	-5 (4)	0 (4)*	-2 (6)*	0 (6)*	-2 (5)*
ILPAQK	2	6/3	6/9		85 (3)	4 (4)*	0 (6)*	-4 (7)*	-3 (5)*	-1 (7)*	0 (6)*	-2 (7)*
AFKASGDHNIL	2	683	694		47 (2)	2 (4)*	2 (3)*	1 (3)*	2 (4)*	-1 (4)*	1 (3)*	-1 (4)*
ATSVAUEGIDIAUCN	2	706	710		75 (2)	5 (4)*	2 (3)*	3 (4)*	-1 (6)*	-15 (5)	-5 (3)	-39 (3)
	1	705	/11		71 (2)	3 (4)*	1 (4)*	-2 (3)*	-1 (6)*	-11 (5)	-5 (4)*	-30 (3)
	2	/15	724		86 (3)	4 (5)*	3 (4)*	3 (4)*	-1 (/)*	-12 (5)	-7 (4)	-34 (4)
	2	741	/55		54 (2)	11 (4)	7 (3)	3 (3)*	-1 (5)*	-10(6)	-10 (4)	-23 (3)
EQINM	2	750	/55	Pincer	48 (2)	15 (4)	9 (3)	-2 (3)*	1 (4)*	-12 (4)	-8 (3)	-34 (3)
KEKMMNDSIL	2	/50	/00		17 (3)	20 (4)	13 (5)	5 (4)*	0 (2)*	-5 (3)	-1 (4)*	-8 (4)
KEKMMNDSIL	3	756	/00		17 (4)	20 (4)	13 (5)	4 (4)*	1 (2)*	-6 (3)	0 (4)*	-8 (4)
_RL	2	764	/68		11 (4)	1 (5)*	0 (5)*	1 (4)*	-1 (3)*	-2 (3)*	3 (6)*	0 (5)*
RLQT	2	/64	770		25 (3)	4 (3)*	2 (4)*	0 (4)*	2 (2)*	3 (2)*	7 (4)	8 (3)
QTWDEAV	2	/6/	775		53 (2)	3 (3)*	2 (3)*	1 (3)*	0 (4)*	-2 (6)*	5 (3)	5 (4)
QTWDEAVF	2	/6/	776		45 (2)	1 (2)*	2 (2)*	-4 (2)*	4 (2)*	5 (4)	5 (2)	7 (3)
AVF	1	772	//6		24 (2)	-4 (3)*	-2 (3)*	4 (3)*	2 (7)*	-1 (4)*	-2 (4)*	-11 (4)
SQEKPKPVPDK	2	791	803		78 (2)	12 (5)	10 (4)	5 (3)*	-9 (6)	-20 (5)	-14 (4)	-23 (4)
	3	814	827		45 (2)	-1 (4)*	-3 (4)*		-5 (6)*		-8 (5)	0 (2)*
RVIE	2	823	827		33 (2)	2 (3)*	1 (3)*	0 (3)*	-1 (3)*	-2 (3)*	1 (3)*	-2 (3)*
VIEE	2	823	828	CTD	62 (3)	1 (3)*	2 (4)*	-2 (4)*	-2 (2)*	-3 (3)*	-1 (4)*	-2 (3)*
RVIEECHY	3	823	831		40 (2)	-2 (2)*	2 (3)*	-6 (2)	0 (2)*	-3 (2)*	-1 (4)*	-3 (3)*
IYTVLGDA	2	829	837		31 (1)	1 (2)*	0 (2)*	-3 (2)*	0 (2)*	2 (4)*	2 (2)*	0 (2)*
'LGDA	1	832	837		52 (2)	1 (4)*	0 (3)*	-2 (3)*	0 (5)*	-1 (5)*	2 (3)*	0 (4)*
LGDAFKECF	2	832	842		51 (2)	-3 (3)*	-2 (3)*	-5 (3)*	1 (3)*	-1 (4)*	2 (3)*	1 (3)*
ECF	2	838	842	Capping	38 (2)	-9 (3)	-5 (4)	-10 (4)	0 (3)*	-2 (3)*	0 (5)*	-4 (4)*
RPHPKPKQFSSF	3	843	856	loon	77 (3)	-11 (5)	-1 (5)*	-13 (4)	-22 (6)	-7 (6)	-16 (5)	-3 (4)*
RPHPKPKQFSSF	4	843	856	loop	77 (3)	-11 (5)	-2 (5)*	-11 (5)	-22 (5)	-7 (6)	-17 (4)	-2 (3)*
KQFSSFEKRA	2	849	860		59 (2)	5 (3)	3 (3)*	2 (2)*	-6 (5)	-10 (4)	-5 (3)	-3 (5)*
IPVIKIES	2	882	891		16 (2)	-7 (2)	3 (4)*	1 (2)*	1 (2)*	0 (2)*	0 (4)*	-3 (3)*
IPVIKIESF	2	882	892		16 (2)	-7 (2)	-5 (3)*	-7 (2)	0 (1)*	0 (1)*	-1 (2)*	-3 (2)*
VED	1	892	896		17 (1)	-5 (2)	-3 (4)*	-9 (2)	0 (3)*	-1 (2)*	0 (4)*	-3 (4)*
EDIATGVQTL	2	893	904	KNA	69 (2)	-10 (3)	-6 (3)	-16 (3)	-1 (3)*	-5 (3)	-3 (4)*	-12 (3)
KWKUFHF	3	905	913	binding	66 (2)	-11 (3)	-9 (5)	-10 (2)	-23 (3)	-32 (5)	-17 (6)	-35 (7)
KWKUFHFEKIPFDPAE	4	905	922	and ing	55 (2)	-9 (3)	-10 (3)	-11 (3)	-24 (5)	-35 (4)	-25 (4)	-33 (9)
	2	914	922	region	43 (2)	-1 (3)*	0 (4)*	-5 (4)	-1 (3)*	-2 (4)*	1 (4)*	-1 (4)*
IPFDPAE	-	914	925		59 (3)	-1 (5)*	0 (4)*	-4 (5)*	1 (5)*	-1 (6)*	1 (4)*	-2 (5)*
IPFDPAE IPFDPAEMSK	2		005			the second se		C	1000	4 (0)*	0 / 4 \ 4	10.10

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end structure (xxiii) (xxiv) (xxv) (xxvi) (xxvii) (xxviii) (xxix) (xxx) charge peptide sequence start 27 26 35 23 (3) 27 (3) 21 (3) FQDYIRKTLDPTYILS 12 38 (2) 17 (3) 8 (2) 1 (1)* -5 (3)* 1 (2)* 1 (3)* 21 (3) 20 (3) IRKTLDPTYIL SYMAPWFRE 16 27 36 (2) 47 (2) 8 (3) 8 (2) 0 (2)* -6 (3) 0 (3)* 3 2 -4 (3)* -1 (3)* -2 (4)* -5 (4)* YMAPWFREEEVQ 2 39 43 53 74 76 85 85 92 93 45 (2) 34 (2) 24 (3) 20 (3) 10 (2) -3 (3)* -4 (4)* 0 (3)* -1 (3)* 28 38 40 64 70 75 77 VQYIQA 2 12 (3) 0 (4)* -5 (2)* 0 (4)* 0 (2)* -1 (2)* 12 (4) 19 (6) 23 (2) 19 (3) 14 (4) CARD1 YIQAEKNNKGPMEA LQEEGWFRGFL 47 (3) 52 (1) 3 10 (4) -3 (3)* -4 (4)* -2 (4)* -2 (6)* -4 (4)* 2 7 (3) 0 (2)* 2 (5)* -3 (5)* 1 (3)* 2 (3)* 15 (1) 28 (2) 21 (1) 15 (3) FRGFLDA 2 5 (3)* -1 (2)* 0 (2)* 0 (2)* -2 (1)* DALDHAGYSGL 2 -3 (3)* -3 (3)* 0 (4)* -1 (3)* 5 (2) -2 (4)* LDHAGYSGL 2 33 (3) 25 (2) 10 (4) -3 (4)* -4 (3)* 0 (5)* -1 (3)* YEAIESW 1 86 33 (3) 30 (3) 14 (4) 12 (3) -1 (3)* -2 (3)* 0 (2)* -1 (2)* 25 (2) 26 (3) 64 (1) 9 (1) 12 (4) YEAIESWD FKKIEKLEE 86 30 (3) 1 26 (3) -2 (3)* -4 (3)* -1 (2)* -1 (3)* 94 103 9 (4) 28 (2) 6 (4) 25 (3) 3 102 2 (2)* -3 (3)* -1 (4)* 0 (0)* -2 (4)* 107 8 (4) 23 (5) YRLLL 2 -2 (2)* -1 (2)* -2 (1)* -3 (4)* Latch YRLLLKRLQPEF 3 103 114 41 (4) 37 (5) -3 (3)* -1 (4)* -3 (4)* -6 (2) LLKR LLK KRL KRL KTR KTR ktr Ilqi ILQI ILQI LLR RSE ALE EKE WIV WIV IQIF FYC YQI SEN NSC VSE VSE VSE VSE LICE ICEH FAN FAN FAN FER

	2	100	114	region	12 (4)	35 (5)	30 (4)	23 (4)	-2 (2)	-4 (4)*	0 (3)	-1 (3)-
LLKRLQPEF	3	106	114	-	16 (4)	46 (5)	40 (5)	22 (5)	-3 (3)*	-6 (4)	0 (4)*	-1 (4)*
KRLQPEF	2	108	114		21 (5)	38 (6)	42 (6)	23 (5)	-1 (1)*	-4 (4)*	-4 (4)*	-9 (5)
KRLQPEF	3	108	114	CADDO	20 (5)	41 (6)	41 (6)	13 (6)	0 (1)*	-6 (3)	-2 (2)*	-6 (5)
KTRIIPTDIISDL	2	115	127	CARD2	51 (2)	22 (3)	17 (3)	8 (2)	2 (4)*	-6 (4)	-2 (2)*	1 (4)*
KTRIIPTDIISDL	3	115	127		51 (2)	22 (3)	17 (4)	7 (2)	-1 (4)*	-6 (4)	-5 (6)	1 (4)*
KTRIIPTDIISDLSE	3	115	129		58 (1)	21 (3)	13 (6)	4 (2)*	2 (4)*	-2 (4)*	2 (2)*	3 (4)*
II OICSTKGMMAGA	2	139	152		37 (2)	30 (3)	25 (4)	12 (2)	-2 (4)*	-3 (3)*	2 (3)*	0 (4)*
II OICSTKGMMAGAEKI	3	139	155		34 (4)	26 (4)	21 (4)	10 (4)	-2 (2)*	-2 (2)*	1 (1)*	0 (3)*
	2	130	157		26 (2)	20 (1)	26 (3)	13 (3)	2 (2)*	2 (2)*	1 (3)*	1 (3)*
LQCSTRGMMAGAERLVE	3	139	137		26 (2)	29(3)	20 (3)	13 (3)	-2 (2)*	-2 (3)*	1 (3)*	-1 (3)-
LLRSDKENWPKTLKL	4	159	1/3		28 (2)	32 (3)	26 (4)	14 (2)	-5 (4)*	-2 (4)*	-2 (3)*	0 (3)*
RSDKENWPKTLKLAL	4	161	175		26 (3)	24 (4)	14 (3)	18 (3)	2 (2)*	-3 (5)*	-1 (4)*	-3 (3)*
ALEKERNKFSEL	3	174	185		51 (2)	23 (4)	12 (3)	7 (3)	0 (1)*	-9 (4)	2 (2)*	1 (2)*
EKERNKFSEL	3	176	185		60 (2)	17 (3)	11 (4)	6 (2)	0 (3)*	-8 (4)	0 (1)*	0 (5)*
WIVEKGIKDVE	3	186	196		89 (3)	5 (5)*	-1 (6)*	-7 (5)	0 (5)*	-11 (5)	2 (6)*	3 (6)*
WIVEKGIKDVETEDI	3	186	200		92 (3)	3 (4)*	0 (5)*	-5 (5)	-1 (4)*	-8 (4)	-1 (6)*	2 (5)*
	2	196	200		96 (2)	A (A)*	0 (5)*	6 (4)	5 (2)*	11 (5)	1 (3)*	1 (6)*
WIVERGINDVETEDLED	2	100	202		00 (3)	4 (4)	0 (5)*	-0 (4)	5 (2)	-11(5)	1 (5)*	1 (0)
WIVEKGIKDVETEDLEDKMETSD	3	186	208	linker	87 (2)	3 (3)*	0 (5)*	-7 (3)	3 (4)*	-8 (6)	1 (5)*	1 (4)*
IVEKGIKDVETEDL	3	187	200		85 (3)	4 (4)*	0 (5)*	-5 (4)*	-3 (6)*	-5 (4)	2 (5)*	1 (5)*
EDKMETSDIQIF	2	201	212		79 (2)	4 (4)*	1 (4)*	-3 (2)*	-2 (5)*	-3 (2)*	1 (5)*	2 (5)*
IQIFYQEDPECQNLSE	2	209	224		87 (3)	2 (6)*	-3 (6)*	-11 (4)	-2 (4)*	-14 (6)	2 (6)*	3 (6)*
FYQEDPECQNL	2	212	222		72 (3)	4 (5)*	0 (6)*	-14 (5)	-2 (6)*	-18 (6)	1 (6)*	2 (6)*
YOEDPECONI	2	213	222		79 (4)	3 (5)*	0 (6)*	-17 (5)	-1 (6)*	-17 (6)	1 (7)*	1 (7)*
SENSODDEL/SDTNI	2	223	237		78 (3)	3 (5)*	0 (6)*	-16 (5)	0 (5)*	-17 (5)	1 (5)*	2 (6)*
	2	225	237		70(3)	3 (3)	4 (5)*	40 (5)	0 (3)	45 (5)	1 (5)*	2 (0)
NSCPPSEVSDINL	4	225	237		81 (4)	2 (4)-	-1 (5)*	-16 (5)	-2 (6)-	-15 (5)	1 (5)-	1 (6)-
VSDTNL	1	232	237		83 (3)	1 (5)*	0 (6)*	-13 (5)	0 (5)*	-9 (5)	1 (6)*	1 (6)*
YSPFKPRN	3	238	245		94 (3)	-3 (5)*	0 (7)*	-12 (5)	-4 (6)*	-6 (4)	-2 (6)*	
YSPFKPRNYQLE	3	238	249		65 (3)	0 (3)*	-3 (4)*	-5 (3)*	-3 (4)*	-8 (4)	1 (4)*	6 (4)
YSPFKPRNYQLE	2	238	249		65 (2)	0 (3)*	-6 (4)	-5 (3)	-4 (4)*	-8 (3)	-2 (0)*	8 (5)
LICENHI KKEPOGOKGKV//E	3	276	295		31 (3)	-14 (4)	1 (4)*	-3 (3)*	4 (1)*	-4 (3)*	-1 (2)*	-15 (5)
	3	277	295		28 (1)	-13 (4)	3 (2)*	-2 (2)*	3 (3)*	- (-)	-4 (3)*	-16 (3)
SANOPA/SOO	2	200	200		20(1)	42 (5)	32(4)	-2 (2)	A (A)*	7 (4)	4 (4)*	48 (4)
FANQIPVYEQQ	2	290	306	mont if In	74(3)	-42 (5)	-33 (4)	-29 (4)	-4 (4)-	-7 (4)	-1 (4)*	-10 (4)
FANQIPVYEQQKSVF	2	296	310	mouria	68 (3)	-37 (4)	-31 (4)	-21 (4)	-4 (4)*	-5 (4)*	0 (4)*	-15 (4)
FANQIPVYEQQKSVFSKY	3	296	313		62 (2)	-31 (3)	-27 (3)	-19 (3)	-3 (3)*		0 (3)*	-11 (3)
FERHGYRVTGISGATAENVPVEQIVENND	4	314	342		59 (1)	-1 (1)*	-5 (2)*	-9 (2)		-10 (4)	0 (4)*	
GYRVTGISGATAENVPVEQIVENN	4	318	341		60 (1)	0 (2)*	-2 (5)*	-9 (2)	-3 (2)*	-9 (3)	1 (4)*	-2 (2)*
VRVTGISGATAENVPVEOIVE	3	319	339		78 (3)	2 (4)*	-5 (2)	-9 (5)	-5 (4)	-10 (5)	1 (6)*	0 (6)*
III TPOI	2	343	351		32 (1)	-15 (2)	-12 (2)	-15 (1)	-2 (2)*	-5 (1)*	-1 (2)*	-5 (2)
	-	242	251		32 (1)	16 (2)	12 (2)	7 (4)	2 (2)*	-0 (1)	-1 (2)*	6 (2)
	1	343	351		32(1)	-10(2)	-13 (2)	-7 (1)	-2 (2)*	0 (2)-	-1 (2)*	-0 (2)
IILTPQILVN	2	343	353		34 (1)	-16(2)	-14 (2)	-22 (2)	-2 (2)*	-4 (2)*	0 (2)*	-5 (2)*
IIILTPQILVNNL	2	343	355		48 (2)	-26 (2)	-21 (3)	-13 (2)	-3 (3)*	-5 (3)	-2 (3)*	-10 (3)
IIILTPQILVNNLKKGTIPSL	3	343	363		64 (3)	-17 (3)	-16 (3)	-15 (3)	-4 (3)*	-11 (3)	-1 (3)*	-8 (3)
IIILTPQILVNNLKKGTIPSL	2	343	363	motif Ic	62 (3)	-18 (3)	-17 (4)	-15 (3)	-4 (3)*	-11 (3)	-1 (3)*	-8 (3)
III TPOL VNNLKKGTIPSLSI	3	343	365	mounte	61 (2)	-16 (3)	-14 (3)	-14 (3)	-4 (3)*	-12 (3)	-1 (3)*	-8 (3)
III TPOLI VNNI KKGTIPSI SIE	3	343	366		59 (2)	-15 (3)	-14 (3)	-13 (3)	-3 (3)*	-17 (3)	-1 (3)*	-7 (3)
	2	269	205	1	20 (2)	11 (2)	11 (3)	5 (2)	1 (4)*	2 (2)*	1 (2)*	1 (2)*
LMPDECHNISKQHPTNM	5	500	303	motifila	30(2)	-11(2)	-11(3)	-3 (2)	-1 (4)	-3 (3)	1 (3)	-1 (2)
IFDECHNTSKQHPYNMIM	3	370	387	mourna	33 (2)	-11 (2)	-11 (3)	-6 (2)	-1 (3)*	-3 (3)*	0 (2)*	-1 (Z)*
FNYLDQKLGGSSGPLPQVIG	2	388	407		36 (2)	1 (3)*	-1 (4)*	-2 (3)*	-2 (3)*	-5 (2)*	1 (3)*	3 (3)*
FNYLDQKLGGSSGPLPQVIGL	2	388	408		33 (3)	0 (3)*	-1 (4)*	-2 (3)*	-2 (3)*	-3 (3)*	1 (3)*	3 (3)*
DQKLGGSSGPLPQVIGL	2	392	408		37 (3)	1 (3)*	-2 (4)*	-3 (3)*	-2 (3)*	-3 (2)*	1 (3)*	3 (3)*
		400	42.4			17 101	47.00	0.703	0.0010		4 (0)0	
LTASVGVGDAKNTDEAL	2	400	424		63 (3)	-17(3)	-17(3)	-6(8)	-2 (5)*	-3 (3)*	1 (9)*	-3 (3)*
LTASVGVGDAKNTDEAL	2	409	424 424		63 (3) 64 (3)	-17 (3)	-17 (3)	-0 (8)	-2 (5)* -3 (3)*	-3 (3)* -7 (3)	1 (9)* 0 (4)*	-3 (3)* -3 (4)*
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEAL	2 2 2	409	424 424 425		63 (3) 64 (3)	-17 (3) -13 (4)	-17 (3) -14 (4) 14 (5)	-6 (8) -12 (4)	-2 (5)* -3 (3)*	-3 (3)* -7 (3)	1 (9)* 0 (4)*	-3 (3)* -3 (4)*
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD	2 2 2	408 409 409	424 424 425		63 (3) 64 (3) 61 (3)	-17 (3) -13 (4) -14 (4)	-17 (3) -14 (4) -14 (5)	-6 (8) -12 (4) -10 (4)	-2 (5)* -3 (3)* -4 (3)*	-3 (3)* -7 (3) -8 (3)	1 (9)* 0 (4)* 0 (4)*	-3 (3)* -3 (4)* -2 (4)*
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD DYICKL	2 2 2 2	409 409 425	424 424 425 430		63 (3) 64 (3) 61 (3) -23 (2)	-17 (3) -13 (4) -14 (4) 0 (2)*	-17 (3) -14 (4) -14 (5) 0 (3)*	-6 (8) -12 (4) -10 (4) -1 (2)*	-2 (5)* -3 (3)* -4 (3)* 0 (2)*	-3 (3)* -7 (3) -8 (3) 1 (1)*	1 (9) ^x 0 (4)* 0 (4)* 1 (3)*	-3 (3)* -3 (4)* -2 (4)* 0 (3)*
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD DYICKL	2 2 2 2 1	409 409 425 425	424 424 425 430 430		63 (3) 64 (3) 61 (3) -23 (2) -11 (2)	-17 (3) -13 (4) -14 (4) 0 (2)* -1 (2)*	-17 (3) -14 (4) -14 (5) 0 (3)* 0 (4)*	-6 (8) -12 (4) -10 (4) -1 (2)* -1 (2)*	-2 (5)* -3 (3)* -4 (3)* 0 (2)* 0 (3)*	-3 (3)* -7 (3) -8 (3) 1 (1)* 2 (1)*	1 (9)* 0 (4)* 0 (4)* 1 (3)* 0 (4)*	-3 (3)* -3 (4)* -2 (4)* 0 (3)* 0 (4)*
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD DYICKL DYICKL CASLDASVIATVKHNLEEL	2 2 2 1 2	409 409 425 425 431	424 424 425 430 430 449		63 (3) 64 (3) 61 (3) -23 (2) -11 (2) 35 (1)	-17 (3) -13 (4) -14 (4) 0 (2)* -1 (2)* -1 (1)*	-17 (3) -14 (4) -14 (5) 0 (3)* 0 (4)* -2 (2)*	-6 (8) -12 (4) -10 (4) -1 (2)* -1 (2)* -1 (2)*	-2 (5)* -3 (3)* -4 (3)* 0 (2)* 0 (3)* -1 (2)*	-3 (3)* -7 (3) -8 (3) 1 (1)* 2 (1)* -4 (1)*	1 (9)* 0 (4)* 0 (4)* 1 (3)* 0 (4)* 1 (2)*	-3 (3)* -3 (4)* -2 (4)* 0 (3)* 0 (4)* 12 (2)
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD DYICKL DYICKL CASLDASVIATVKHNLEEL SVIATVKHNLEE	2 2 2 1 2 2	408 409 425 425 431 437	424 424 425 430 430 449 448		63 (3) 64 (3) 61 (3) -23 (2) -11 (2) 35 (1) 60 (2)	-17 (3) -13 (4) -14 (4) 0 (2)* -1 (2)* -1 (1)* -5 (2)*	-17 (3) -14 (4) -14 (5) 0 (3)* 0 (4)* -2 (2)* -6 (3)	-6 (8) -12 (4) -10 (4) -1 (2)* -1 (2)* -1 (2)* -1 (1)* -7 (4)	-2 (5)* -3 (3)* -4 (3)* 0 (2)* 0 (3)* -1 (2)* -1 (3)*	-3 (3)* -7 (3) -8 (3) 1 (1)* 2 (1)* -4 (1)* -5 (3)*	1 (9)* 0 (4)* 1 (3)* 0 (4)* 1 (2)* -2 (12)*	-3 (3)* -3 (4)* -2 (4)* 0 (3)* 0 (4)* 12 (2) 10 (4)
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEAL DYICKL DYICKL CASLDASVIATVKHNLEEL SVIATVKHNLEE EQVVYKPQKF	2 2 2 1 2 2 3	409 409 425 425 431 437 450	424 424 425 430 430 449 448 459		63 (3) 64 (3) 61 (3) -23 (2) -11 (2) 35 (1) 60 (2) 69 (2)	-17 (3) -13 (4) -14 (4) 0 (2)* -1 (2)* -1 (1)* -5 (2)* -19 (3)	-17 (3) -14 (4) -14 (5) 0 (3)* 0 (4)* -2 (2)* -6 (3) -16 (4)	-6 (8) -12 (4) -10 (4) -1 (2)* -1 (2)* -1 (1)* -7 (4) -16 (3)	-2 (5)* -3 (3)* -4 (3)* 0 (2)* 0 (3)* -1 (2)* -1 (3)* -3 (3)*	-3 (3)* -7 (3) -8 (3) 1 (1)* 2 (1)* -4 (1)* -5 (3)* -1 (3)*	1 (9)* 0 (4)* 1 (3)* 0 (4)* 1 (2)* -2 (12)* 0 (3)*	-3 (3)* -3 (4)* -2 (4)* 0 (3)* 0 (4)* 12 (2) 10 (4) 21 (4)
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD DYICKL CASLDASVIATVKHNLEEL SVIATVKHNLEE EQVVYKPQKF V/VKPQKF	2 2 2 1 2 2 3 2	409 409 425 425 431 437 450 452	424 425 430 430 449 449 448 459 459		63 (3) 64 (3) 61 (3) -23 (2) -11 (2) 35 (1) 60 (2) 69 (2) 75 (3)	-17 (3) -13 (4) -14 (4) 0 (2)* -1 (2)* -1 (1)* -5 (2)* -19 (3) -14 (3)	-17 (3) -14 (4) -14 (5) 0 (3)* 0 (4)* -2 (2)* -6 (3) -16 (4) -12 (4)	-6 (8) -12 (4) -10 (4) -1 (2)* -1 (2)* -1 (2)* -1 (1)* -7 (4) -16 (3) -12 (4)	-2 (5)* -3 (3)* -4 (3)* 0 (2)* 0 (3)* -1 (2)* -1 (3)* -3 (3)* -4 (3)*	-3 (3)* -7 (3) -8 (3) 1 (1)* 2 (1)* -4 (1)* -5 (3)* -1 (3)* -3 (4)*	1 (9)* 0 (4)* 1 (3)* 0 (4)* 1 (2)* -2 (12)* 0 (3)* 1 (4)*	-3 (3)* -3 (4)* -2 (4)* 0 (3)* 0 (4)* 12 (2) 10 (4) 21 (4) 10 (4)
LTASVGVGDAKNTDEAL TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD DYICKL CASLDASVIATVKHNLEEL SVIATVKHNLEE EQVVYKPQKF VVYKPQKF VVYKPQKF	2 2 2 1 2 2 3 2 3 2 3	409 409 425 425 431 437 450 452 452	424 425 430 430 449 448 459 459 459		63 (3) 64 (3) -23 (2) -11 (2) 35 (1) 60 (2) 69 (2) 75 (3) 75 (3)	-17 (3) -13 (4) -14 (4) 0 (2)* -1 (2)* -1 (1)* -5 (2)* -19 (3) -14 (4)	-17 (3) -14 (4) -14 (5) 0 (3)* 0 (4)* -2 (2)* -6 (3) -16 (4) -12 (4) -10 (4)	-0 (8) -12 (4) -10 (4) -1 (2)* -1 (2)* -1 (2)* -1 (1)* -7 (4) -16 (3) -12 (4) -10 (4)	-2 (5)* -3 (3)* -4 (3)* 0 (2)* 0 (3)* -1 (2)* -1 (3)* -3 (3)* -4 (3)*	-3 (3)* -7 (3) -8 (3) 1 (1)* 2 (1)* -4 (1)* -5 (3)* -1 (3)* -3 (4)*	1 (9)* 0 (4)* 1 (3)* 0 (4)* 1 (2)* -2 (12)* 0 (3)* 1 (4)*	-3 (3)* -3 (4)* -2 (4)* 0 (3)* 0 (4)* 12 (2) 10 (4) 21 (4) 10 (4) 8 (5)
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-5 \ (3)^* \\ -5 \ (3)^* \\ -5 \ (3)^* \\ 1 \ (2)^* \\ 0 \ (5)^* \\ 3 \ (4)^* \\ 5 \ (5) \\ 1 \ (2)^* \\ 0 \ (2)^* \\ -7 \ (3) \\ -5 \ (3) \\ -5 \ (3) \\ 0 \ (3)^* \\ -5 \ (3) \\ 0 \ (3)^* \\ 1 \ (2)^* \\ 1 \ (2)^* \\ 1 \ (2)^* \\ 1 \ (2)^* \\ 0 \ (2)^* \\ 2 \ (4)^* \\ 1 \ (2)^* \\ 0 \ (2)^* \\ 2 \ (4)^* \end{array}$
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(2)^{*} \\ -2 \ (6)^{*}$	$\begin{array}{c} -3 \ (3)^*\\ -3 \ (4)^*\\ -2 \ (4)^*\\ -2 \ (4)^*\\ 0 \ (3)^*\\ 0 \ (4)^*\\ 12 \ (2)\\ 10 \ (4)\\ 21 \ (4)\\ 12 \ (2)\\ 10 \ (4)\\ 8 \ (5)\\ 12 \ (2)\\ 12 \ (2)\\ 12 \ (4)\\ 10 \ (4)\\ 8 \ (5)\\ 12 \ (2)\\ 12 \ (4)\\ 10 \ (4)\\ 8 \ (5)\\ 12 \ (2)^*\\ 2 \ (3)^*\\ 12 \ (2)^*\\ 2 \ (3)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 0 \ (2)^*\\ 12 \ (2)^*\\ 0 \ (2)^*\\ 12 \ (2)^*\\ 0 \ (2)^*\\ 12 \ (2)^*\\ 0 \ (2)^*\\ 12 \ (2)^*\\ 0 \ (2)^*\\ 12 \ (2)^*\\ 0 \ (2)^*\\ 12 \ (2)^*\\ 0 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 12 \ (2)^*\\ 22 \ (4)^*\\ 12 \ (2)^*\\ 22 \ (4)^*\\ 22 \ (2)^*\\ -2 \ (2)^*\ (2)^*\\ -2 \ (2)^*\ (2)^*\\ -2 \ (2)^*\ (2)^*\ (2)^*\\ -2 \ (2)^*\ (2)$
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(6)$	$\begin{array}{c} 1 \ (9)^{*} \\ 0 \ (4)^{*} \\ 0 \ (4)^{*} \\ 1 \ (3)^{*} \\ 0 \ (4)^{*} \\ 1 \ (2)^{*} \\ 2 \ (12)^{*} \\ 0 \ (4)^{*} \\ 1 \ (2)^{*} \\ 2 \ (12)^{*} \\ 0 \ (4)^{*} \\ 0 \ (4)^{*} \\ 0 \ (2)^{*} \\ 1 \ (4)^{*} \\ 2 \ (5)^{*} \\ 1 \ (4)^{*} \\ 2 \ (5)^{*} \\ 1 \ (4)^{*} \\ 2 \ (5)^{*} \\ 1 \ (4)^{*} \\ 2 \ (5)^{*} \\ 1 \ (4)^{*} \\ 2 \ (4)^{*} \\ 2 \ (4)^{*} \\ 0 \ (4)^{*} \\ 1 \ (2)^{*} \\ -1 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (3)^{*} \\ 0 \ (2)^{*} \\ -3 \ (13)^{*} \\ 0 \ (2)^{*} \\ -3 \ (13)^{*} \\ 0 \ (2)^{*} \\ -3 \ (13)^{*} \\ 1 \ (5)^{*} \\ 1 \ (5)^{*} \\ 1 \ (2)^{*} \\ 1 \ (3)^{*} \\ -1 \ (5)^{*} \\ 1 \ (3)^{*} \\ -1 \ (6)^{*} \\ -2 \ (6)^{*} $	-3 (3)* -3 (4)* -2 (4)* 0 (3)* 0 (3)* 12 (2) 10 (4) 21 (4) 10 (4) 8 (5)* 1 (2)* 2 (3)* -5 (3)* -1 (2)* 2 (3)* 5 (5)* 3 (4)* 5 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C268F RIG-I

IATSVADECID												-
AT3VADEGID	2	695	705		77 (2)	-6 (3)	-8 (5)	-20 (3)	-3 (4)*	-23 (3)	-3 (5)*	-38 (5)
IATSVADEGIDIAQCNL	2	695	711	Pincer	78 (2)	-5 (3)*	-5 (4)*	-12 (3)	-4 (4)*	-26 (4)	-3 (4)*	-40 (4)
IATSVADEGIDIAQCNLVILYEYVGNVIKM	3	695	724	Inteer	66 (2)	-8 (2)	-6 (3)	-12 (3)	-2 (3)*	-23 (2)	-2 (3)*	-45 (3)
VILYEYVGNVIKM	2	/12	724		68 (2)	-21 (2)	-18 (2)	-13 (3)	-3 (3)*	-19 (4)	-2 (2)*	-11 (2)
YEYVGNVIKM	2	/15	724		86 (2)	-27 (3)	-21 (3)	-12 (3)	-4 (3)*	-8 (3)	-3 (3)*	-17 (3)
YVGNVIKM	2	/1/	724		84 (2)	-28 (3)	-21 (3)	-12 (3)	-3 (3)*	-6 (3)	-4 (3)*	-17 (3)
IUTRORGRARGSKC	7	725	738		(7 (4)	-21 (4)	-15 (4)	-20 (5)	-5 (3)	-10 (4)	-2 (5)*	-20 (5)
	2	739	749		57 (2)	-21(2)	-14 (3)	-19(2)	3 (2)*	0 (1)*	2 (2)*	0 (2)*
	2	735	755		50(1)	-20 (2)	-20 (1)	-24 (4)	-2 (2)	-4 (3)	1 (2)*	0 (2)
KEOINM	2	750	755		57 (1)	38 (4)	-20 (2)	-22 (2)	-1 (3)	-3 (2)	-1 (3)	2 (5)*
	3	756	755		21 (2)	-30(4)*	-55 (5)	0 (4)*	-2 (4)	-3 (3)	-1 (4)*	-2 (J) 5 (J)
VKEKMMNDSI	2	756	766		21 (3)	-4 (4)*	-6 (4)	-2 (4)*	1 (3)*	-1 (4)*	0 (4)*	5 (4)*
SI DI OT	2	764	700		27 (3)	-4 (3)*	-3 (5)*	-4 (3)*	-1 (3)*	-3 (3)*	1 (4)*	10 (2)
RIOTWDEAVE	2	767	776		46 (1)	-6 (2)	-7 (2)	-4 (2)*	1 (2)*	2 (2)*	2 (3)*	7 (2)
WDEAVE	1	771	776		66 (3)	-1 (3)*	-2 (3)*	-6 (4)	-2 (4)*	-4 (2)*	2 (3)*	3 (3)*
RDSQEKPKPVPDK	2	791	803		90 (2)	-13 (3)	-18 (5)	-12 (2)	-3 (3)*	-7 (3)	1 (3)*	1 (2)*
VRVIEE	2	823	828		59(1)	1 (2)*	3 (2)*	-12 (2)	-1 (2)*	-7 (2)	-1 (2)*	-2 (2)*
VRVIEECHY	3	823	831		43 (1)	-1 (2)*	0 (3)*	-8 (1)	-2 (3)*	-10 (3)	1 (3)*	0 (3)*
VRVIEECHYTVLGDA	3	823	837	1 1	34 (1)	-1 (2)*	2 (0)*	-11 (1)	-1 (2)*	-9 (2)	-1 (2)*	-1 (2)*
CHYTVLGDA	2	829	837	1 1	30 (1)	1 (2)*	2 (2)*	-3 (2)*	-1 (2)*	-3 (1)*	0 (2)*	-2 (2)*
TVLGDAFKECF	2	832	842	1 1	52 (2)	-4 (3)*	-3 (3)*	-8 (3)	-3 (3)*	-14 (3)	0 (3)*	-1 (3)*
FKECF	1	838	842	1 1	42 (3)	-8 (4)	-7 (4)	-10 (3)	-3 (4)*	-9 (4)	-2 (5)*	-4 (4)*
FKECF	2	838	842	1 1	39 (3)	-8 (4)	-6 (4)	-12 (4)	-4 (4)*	-2 (4)*	-1 (4)*	-5 (4)*
FVSRPHPKPKQFSS	4	842	855		79 (3)	-6 (4)	-4 (5)*	-14 (4)	-4 (4)*	-10 (4)	0 (4)*	2 (5)*
VSRPHPKPKQFSSF	4	843	856	Capping	77 (3)	-6 (4)	-4 (5)*	-14 (4)	-4 (4)*	-10 (4)	2 (5)*	4 (6)*
VSRPHPKPKQFSSF	3	843	856	loon	75 (2)	-7 (4)	-4 (5)*	-18 (4)	-2 (4)*	-11 (5)	2 (4)*	3 (6)*
EKRAKIF	2	857	863	1000	49 (2)	-13 (3)	-13 (3)	-14 (3)	-3 (0)*	-4 (4)*	-1 (4)*	-3 (3)*
EKRAKIFC	3	857	864	1 1	26 (2)	-11 (3)	-12 (4)	-12 (3)	-2 (2)*	0 (5)*	-2 (0)*	-4 (4)*
EKRAKIFC	2	857	864	1 1	48 (3)	-10 (4)	-14 (3)	-19 (3)	-1 (2)*	-3 (2)*	0 (1)*	3 (4)*
CARQNCSHDWGIHVKYKT	4	864	881	1 1	35 (2)	-16 (3)	-2 (2)*	-8 (2)	-2 (3)*	2 (5)*	-3 (3)*	3 (4)*
FEIPVIKIES	2	882	891	1 1	14 (1)	-10 (2)	-6 (1)	-9 (1)	0 (1)*	1 (1)*	4 (6)*	1 (2)*
FEIPVIKIESF	2	882	892	1 1	18 (1)	-8 (2)	-8 (2)	-8 (1)	0 (1)*	1 (1)*	0 (1)*	0 (1)*
EIPVIKIESF	2	883	892	1 1	14 (1)	-6 (3)	-6 (1)	-9 (1)	0 (1)*	1 (1)*	4 (6)*	1 (2)*
FVVEDIATGVQTL	2	892	904	RNA	63 (2)	-16 (3)	-17 (2)	-23 (2)	-3 (3)*	-21 (4)	0 (3)*	-2 (3)*
VVEDIATGVQTL	2	893	904	hinding	72 (2)	-19 (3)	-17 (2)	-24 (2)	-3 (3)*	-11 (3)	-2 (2)*	-5 (3)
VVEDIATGVQTL	1	893	904	Dinung	71 (2)	-19 (3)	-20 (3)	-19 (2)	-3 (3)*	-9 (4)	-1 (3)*	-3 (3)*
EKIPFDPAE	2	914	922	region	51 (4)	-1 (4)*	-1 (5)*	-7 (4)	-3 (4)*	-9 (3)	0 (5)*	-3 (4)*
EKIPFDPAEMSK	2	914	925		61 (4)	-2 (4)*	-4 (6)*	-10 (4)	-3 (5)*	-9 (4)	0 (6)*	-1 (5)*
:KIPFDPAEMSK	3	914	925		62 (4)	-2 (4)*	-4 (6)*	-10 (4)	-3 (5)*	-6 (3)	0 (5)*	-1 (5)*
									*			
10 20 30 40	0 50 60	70 8	0 90	100	.50	-40 -30	-20	-10	0 10) 20	30	40

Supplementary Figure 1

A summary of all HDX experiments. (a) Schematic representations of all HDX characterizations performed in this study. (b) HDX consolidation view for all studied conformational states of WT/H830A/E373A/C268F RIG-I with the experimental order in **Supplementary Fig 1a**. (c) HDX Experimental view for all studied conformational states of WT/H830A/E373A/C268F RIG-I with the experimental order in **Supplementary Fig 1a**. In Supplementary Fig 1c, specific RIG-I domain/motifs are defined in Fig 1a (CARD2 latch region is the region that intra-molecularly interacts with HEL2i gate motif in the apo receptor state. In HEL2i, the CTD:HEL2i region is the HEL2i region that CTD clashes with upon RNA agonist binding).

The values listed under each HDX experiments demonstrate the averaged difference in percentage of deuterium incorporation of that corresponding peptide either derived from apo protein or between two different states across all exchange time points (i.e., 0s, 10s, 60s, 300s, 600s, 900s, 1500s and 3600s). Including time 0s there were 8 time points and each time point was replicated with two independent MS runs per conformational state of receptor or receptor complex. HDX analyses were performed duplicate or triplicate, with single preparations of each protein ligand complex. The intensity weighted mean m/z centroid value of each peptide envelope was calculated and subsequently converted into a percentage of deuterium incorporation. Corrections for back-exchange were made on the basis of an estimated 70% deuterium recovery, and accounting for the known 80% deuterium content of the deuterium exchange buffer. When comparing the two samples, the perturbation %D is determined by calculating the difference between the two samples. HDX Workbench colors each peptide according to the smooth color gradient HDX perturbation key (D%) shown in each indicated figure. Differences in %D between -5% to 5% are considered nonsignificant and are colored gray according to the HDX perturbation key ¹. In addition to the -5% to 5% test, Unpaired t-tests are calculated to detect statistically significant (p<0.05) differences between samples at each time point. At least one time point with a p value less than 0.05 was present in the data set further confirming that the difference is significant. A negative value represents decreased deuterium incorporation or

stabilization while a positive value represents increased deuterium incorporation or destabilization in the corresponding region of the receptor when a binding event takes place. Peptides exhibiting statistically insignificant or undetectable changes are colored gray. Blank region represents undetected peptide for corresponding experiment. The deuterium incorporation data from all overlapping peptides were consolidated to individual amino acid values using a residue averaging approach ². HDX Workbench was used to automate mapping of gradient colors to pymol structure model ³. For HDX experiments – i, ii, xii, xv and xxiii – measuring apo receptor dynamics, colors are coded according to HDX dynamics key. For the rest differential HDX experimental comparison views, colors are coded according to HDX perturbation key.





С

sequence	charge	start	end	structure	RIG-I ± 3p8l	sequence	charge	start	end	structure	RIG-I ± 3p8l
QDYIRKTLDPTYIL	3	13	26		1 (2)*	FKASGDHNIL	3	685	694		0 (5)*
SYMAPWFRE	2	27	35		3 (2)*	IATSVADEGID IATSVADEGIDIAOCNI	2	695 695	705		0 (5)* -5 (4)*
YMAPWFREEEVQ	2	28	39		3 (2)*	IATSVADEGIDIAQCNLVILYEYVGNVIKM	3	695	724		0 (6)*
VQYIQA YIQAEKNNKGPMEA	2	38 40	43 53		1 (2)* -1 (4)*		2	698 712	708		-1 (4)*
EKNNKGPMEAATL	2	44	56		-1 (3)*	YEYVGNVIKM	2	715	724		0 (4)*
LQEEGWFRGFL OFEGWFRGFI	2	64 65	74 74		1 (3)* 2 (3)*	YVGNVIKM	2	717	724		0 (4)*
FRGFLDA	2	70	76		3 (1)*	FLLTSNAGVIE	2	739	738		1 (3)*
DALDHAGYSGL	2	75 77	85		1 (4)* 0 (6)*	FLLTSNAGVIEKEQINM	2	739	755		1 (4)*
YEAIESW	1	86	92		-1 (1)*	LTSNAGVIEKEQINM AGVIEKE	2	741 745	755		0 (5)* -1 (5)*
YEAIESWD	1	86	93		-1 (2)*	KEQINM	2	750	755		0 (4)*
YRLLL	2	103	102		11 (4)	YKEKIMINDSIL	2	756 756	766 766		3 (2)*
YRLLLKRLQPEF	3	103	114	la tali	15 (4)	SILRLQT	2	764	770		3 (2)*
LLKRLQPEF LLKRLQPEF	2 3	106	114	latch	15 (5) 22 (6)	RLQTWDEAVF	2	767	776		-2 (2)*
KRLQPEF	2	108	114	region	21 (6)	FREKILHIQTHEKF	4	776	789		-3 (2) 1 (1)*
KRLQPEF	3	108	114		22 (5) 4 (3)*	THEKFIRDS	2	785	793	670	0 (0)*
KTRIIPTDIISDL	2	115	127		3 (3)*	VRVIEE	2	823	828	CID	-5 (2)*
KTRIPTDISDL	3	115	127		3 (3)*	VRVIEECHY	2	823	831	RNA binding	-6 (2)
EEILQICSTKGMMAGAEKL	3	137	155		8 (2)	VRVIEECHY VRVIEECHYTVI GDA	3	823	831 837	region	-8 (1) -3 (1)*
ILQICSTKGMMAGA	2	139	152	64000	7 (2)	CHYTVLGDA	2	829	837	- DNA binding	-1 (2)*
ILQICSTKGMMAGAEKL	3	139	155	CARD2	5 (2) 8 (2)	TVLGDAFKECF	2	832	842 842	rogion	-12 (5)
LLRSDKENWPKTLKL	4	159	173		1 (1)*	FKECF	2	838	842	region	-27 (5)
RSDKENWPKTLKLAL	4	161 174	1/5		5 (2) 3 (4)*	FVSRPHPKPKQFSS	4	842	855		1 (5)*
ALEKERNKFSEL	4	174	185		3 (3)*	VSRPHPKPKQFSSF VSRPHPKPKQFSSF	4	843	856		1 (5)*
EKERNKFSEL	3	176	185		2 (4)* 0 (5)*	EKRAKIF	2	857	863	RNA binding	-12 (4)
WIVEKGIKDVETEDL	3	186	200		0 (6)*	EKRAKIFC CARONCSHDWGIHVKYKT	4	864	881	region	-12 (2) -3 (1)*
WIVEKGIKDVETEDLEDKMETSD	3	186	208		-1 (5)*	DWGIHVKYKTFEIPVIKIESFVV	4	872	894	D	-2 (3)*
EDKMETSDIQIF	2	201	212		0 (4)*	FEIPVIKIES	2	882 882	891	RINA binding	-19 (3) -32 (1)
FYQEDPECQNL	2	212	222		-1 (3)*	EIPVIKIESF	2	883	892	region	-19 (3)
SENSCPPSEVSDTNL	2	213	222		0 (4)2	FVVEDIATGVQTL VVEDIATGVQTI	2	892 893	904		-3 (2)* -4 (4)*
NSCPPSEVSDTNL	2	225	237		-1 (6)*	VVEDIATGVQTL	2	893	904		-4 (3)*
VSDTNL VSPEKPRN	1	232	237		0 (5)*	ATGVQTL	2	897	904		3 (5)*
YSPFKPRNYQLE	2	238	249		4 (5)*	EKIPFDPAEMSK	2	914	922		-3 (4)*
	3	238	249 263		4 (5)*	EKIPFDPAEMSK	3	914	925		-4 (5)*
LALPAMKGKNTICAPTGCGKTFVSLL	3	250	276		1 (4)*						
LALPAMKGKNTIICAPTGCGKTFVSLL	4	250	276		-2 (2)*						
APIGCGKIF PQGQKGKVVF	3	286	295		-1 (3)*						
FANQIPVYEQQ	2	296	306		0 (4)*						
FANQIPVYEQQKSVF FANQIPVYEQQKSVFSKY	2	296 296	310 313		-3 (5)* 0 (2)*	50 40 20	20 40	0	10 20	20	40 50
FERHGYRVTGISGATAENVPVEQIVENND	4	314	342		-1 (2)*	UC- U+ UC	-20 -10	U	10 20	JU	40 JU
GYRVTGISGATAEN/PVEQIVENN	4	318	341		0 (3)*		HDX per	turbation k	(ev		
IILTPQIL	1	343	351		-3 (1)*		полереі	turbution			
IIILTPQIL	2	343	351		-3 (1)*						
IIILTPQILVN IIILTPQILVNN	2	343	355	motif lc	-6 (1) -6 (2)						
IIILTPQILVNNL	2	343	355		-5 (2)*						
	2	343	363		-3 (5)* -3 (5)*						
IIILTPOILVNNLKKGTIPSLSI	3	343	365		-3 (5)*						
IIILTPOILVINNLKKGTIPSLSIF	3	343 357	366 367		-3 (4)* 0 (2)*						
KGTIPSLSIFT	3	357	367		0 (2)*	Su	upplement	arv Figu	re 2		
LMIFDECHNTSKQHPYNM	3	368	385		-2 (2)*				-		
IFDECHNTSKQHPYNMIM	3	370	387		-2 (2)*						
FNYLDQKLGGSSGPLPQVIG	2	388	407		0 (1)*						
FNYLDQKLGGSSGPLPQVIGL DQKLGGSSGPLPQVIGL	2	392	408		0 (1)* 0 (2)*						
LTASVGVGDAKNTDEAL	2	408	424		0 (3)*						
TASVGVGDAKNTDEAL TASVGVGDAKNTDEALD	2	409 409	424 425		1 (4)* 0 (5)*						
TASVGVGDAKNTDEALDYICKL	3	409	430		3 (2)*						
DYICKL	1	425 425	430 430		0 (1)*						
CASLDASVIATVKHNLEE	2	431	448		1 (4)*						
CASLDASVIATVKHNLEEL	2	431 437	449 448		-1 (1)*						
EQVVYKPQKF	3	450	459		0 (3)*						
VVYKPQKF	2	452	459		2 (3)*						
MRDTESL	2	++∋∠ 479	459 485		2 (3)* 0 (1)*						
AKRICKDLENL	3	486	496		1 (3)*						
SUIUNREFGTU SUIUNREFGTUKYEU	2 3	497	507		0 (6)*						
SQIQNREFGTQKYEQW	3	497	512		0 (5)*						
WIVI VQKACM IVTVQKACM	2	512	521 521		0 (5)* 0 (1)*						
VFQMPDKDEESRICKA	3	522	537		0 (5)*						
VFQMPDKDEESRICKALF FQMPDKDEESRICKA	4 3	522 523	539 537		0 (4)* 1 (4)*						
FQMPDKDEESRICKALF	4	523	539		1 (4)*						
LYTSHLRKYNDAL	3	540 540	552		0 (4)*						
YTSHLRKYNDAL	2	541	552		0 (4)*						
IISEHARMKDALD	3	553	565		0 (1)*						
HARMKDALD HARMKDALD	2	557	565		-1 (2)* 0 (1)*						
DYLKDFFSNVRAAGF	3	565	579		2 (3)*						
YLKDFFSNV YLKDFFSNVRAAGE	2	566 566	574 579		0 (0)*						
FFSNV	1	570	574		1 (2)*						
FFSNVRAAGF	2	570 576	579 587		1 (2)*						
DEIEQDLTQRFEEKLQE	3	580	596		2 (1)*						
DEIEQDLTQRFEEKLQEL	3	580	597		2 (1)*						
DEIEQULTORFEEKLQELES QELESVSRDPSNENPKLED	3 3	580 595	599 613		2 (1)* -1 (5)*						
ESVSRDPSNENPKLEDLC	3	598	615		0 (6)*						
VSRDPSNENPKL VSRDPSNENPKLED	3	600 600	611 613		2 (3)*						
FILQEEYHLNPET	2	616	628		-1 (2)*						
	2	617 620	632 637		0 (1)*						
FVKTRALVDALKNWIEGNPKL	3	633	653		0 (3)*						
WEGNPKL	2	646 646	653		0 (4)*						
WIEGNPKLSFLKPGIL SFLKPGIL	2	654	661		1 (5)* 0 (6)*						
KPGILTGRGKTNQNTG	3	657	672		1 (3)*						
TGRGKTNQNTGMTLPAQKCIL TGRGKTNQNTGMTI PAQKCII	3	662 662	682 682		1 (4)* 1 (4)*						
PAQKCIL	2	676	682		1 (2)*						
DAFKASGDHNIL	2	683 683	694		0 (5)*						
UAI NAGURINIL	5	000	034		0 (5)						









Supplementary Figure 2

Supplementary Figure 2

Differential deuterium uptake plots of CTD capping loop peptide region (VSRPHPKPKQFSSF, +3) of WT (a) and H830A RIG-I (b) upon receptor perturbed by indicated RNAs. The data are plotted as percent deuterium uptake verse time on a logarithmic scale. The HDX plots of this CTD capping loop peptide between indicated groups were statistically analysis by HDX Workbench (Supplementary Fig. 1c)¹. (c) HDX perturbation view of RIG-I with and without 3p8I in longer HDX-MS time points (3 hr and 5 hr). This HDX perturbation view is presented as Supplementary Fig. 1c. (d) MS spectra of RIG-I CARD2 latch peptide Y103-114 derived from indicated complexes in indicated on-exchange time points. The quantity of each mass population was determined as Fig. 2a. (e) In each indicated state, the fraction of RIG-I CARDs molecules in the higher MS population (open conformation) to the total amount is plotted against the incubation HDX time points as Fig.2c. (f) Half-life $(t_{1/2})$ of respective partial unfolding event is determined by fitting an exponential curve as Fig. 2d. No halflife $(t_{1/2})$ of partial unfolding event is predicted I apo RIG-I in the indicated time points. (g) MS spectra of C268F RIG-I CARD2 latch peptide Y103-114 derived from indicated complexes in indicated on-exchange time points. The quantity of each mass population was determined as Fig. 2a.

ATPase based RNA titration_wt RIG-I_37 ⁰C 1 mM ATP / 10 nM wt RIG-I / RNA titration / 1X ATPase buffer



ATPase based RNA titration_wt RIG-I_37 ⁰C

1 mM ATP / 10 nM wt RIG-I / RNA titration / 1X ATPase buffer



Supplementary Figure 3

Supplementary Figure 3 (related to Table 1)

 K_d , ATPase hydrolysis activity of WT RIG-I for 3p8I and Cap0mA-10I. The data is derived from radiometric ATPase assay wherein a fixed concentration of protein is titrated with increasing concentration of RNA. The curves are fit to the quadratic equation to obtain the k_{atpase} and $k_{d, \text{app}}$ values. Error bars are from the time courses of the ATPase rate measurements at each RNA concentration.

Supplementary Table 1. Primers for generating RIG-I mutants

RIG-I mutants	Prime sequence
H830A	5'-GAGTGATAGAGGAATGCGCTTACACTGTGCTTGGAGATG-3'
	5'-CATCTCCAAGCACAGTGTAAGCGCATTCCTCTATCACTC-3'
E373A	5'-CTTTGATGATATTTGATGCGTGCCACAACACTAGTAAACAAC-3'
	5'-GTTGTTTACTAGTGTTGTGGCACGCATCAAATATCATCAAAG-3'
C268F	5'-ATATGTGCTCCTACAGGTTTTGGAAAAACCTTTGTTTCACTGC-3'
	5'-GCAGTGAAACAAAGGTTTTTCCAAAACCTGTAGGAGCACATAT-3'

References:

- 1. Pascal, B.D. et al. HDX workbench: software for the analysis of H/D exchange MS data. *J Am Soc Mass Spectrom* **23**, 1512-21 (2012).
- 2. Keppel, T.R. & Weis, D.D. Mapping residual structure in intrinsically disordered proteins at residue resolution using millisecond hydrogen/deuterium exchange and residue averaging. *J Am Soc Mass Spectrom* **26**, 547-54 (2015).
- 3. Zheng, J. et al. High-resolution HDX-MS reveals distinct mechanisms of RNA recognition and activation by RIG-I and MDA5. *Nucleic Acids Res* **43**, 1216-30 (2015).