

**Supplementary Fig. 1** | Vitamin K-dependent apoptotic reporter protein. (a) Schematic diagram of the domain structure of the VKD apoptotic reporter protein FIXgla-Fas. The signal peptide (SP), propeptide (PP), and Gla domain of factor IX (FIXgla) is fused to the extracellular N-terminus of Fas with a HPC4 tag between the two fusion parts for detection purpose. Residue Asp260 within the death domain (DD), important for Fas-FADD interaction, is indicated by a triangle. CRD, cysteine-rich domain; TM, transmembrane domain. Arrowheads indicate positions of the cleavage of signal peptide or propeptide before mature protein is secreted. (b) Effect of FIXgla-Fas reporter protein and its mutants on caspase-dependent apoptosis detected by immunoblotting. The Fas, FIXgla-Fas, the D260V mutant, or FIXgla-Fas with its death domain (DD) deleted ( $\Delta$ DD) constructs were transiently expressed in HEK293 cells. Transfected cells were incubated with 11  $\mu$ M vitamin K for 48 hours before harvesting the cells for immunoblotting. Control: HEK293 cells only. Top: Activation of caspase-8 was probed using anti-caspase-8 antibody. Full-length caspase-8 was indicated by an arrowhead, activated caspase-8 was indicated by asterisks. Bottom: total reporter protein expression probed by anti-HPC4 tag antibody. Similar results were observed at least twice as shown in Fig. 1b.

DAXX FADD FAE1	edicted Functional Partners:	Neighborhood Gene Fusion Cooccurence Coexpression Experiments Databases Textmining [Homology] <b>Score</b>
	FADD FAS-associated death domain protein; Apoptotic adaptor molecule that rec	· • • • 0.999
CASP8	CASP8 Caspase-8; Most upstream protease of the activation cascade of caspases	• • • • 0.999
FASLG	FASLG Tumor necrosis factor ligand superfamily member 6; Cytokine that binds to	• • • 0.999
	CASP10 Caspase-10; Involved in the activation cascade of caspases responsible for	0.997
CASP10 FAS	CFLAR CASP8 and FADD-like apoptosis regulator; Apoptosis regulator protein whic	0.996
RIPK1	DAXX Death domain-associated protein 6; Transcription corepressor known to rep	0.995
	<b>PTPN13</b> Tyrosine-protein phosphatase non-receptor type 13; Tyrosine phosphatase	••• 0.995
CFLAR	FAF1 FAS-associated factor 1; Potentiates but cannot initiate FAS-induced apopto	• • • 0.992
TRADD	BRIPK1 Receptor-interacting serine/threonine-protein kinase 1; Serine-threonine kin	• • • 0.985
	TRADD Tumor necrosis factor receptor type 1-associated DEATH domain protein; 7	

Supplementary Fig. 2 | Network analysis of Fas receptor using the STRING protein-protein interaction network database with default settings. Of the ten proteins that interact with Fas in this network, the sgRNA targeting eight of the proteins (CASP8, CASP10, CFLAR, FADD, FAF1, PTPN13, RIPK1, and TRADD) were enriched in the genome-wide CRISPR-Cas9 loss-of-function VKD screening. Detailed sgRNA enrichment of these genes can be found in Supplementary Table 1.



**Supplementary Fig. 3 | Genomic DNA sequence analysis of FSP1 knockout HEK293 cells.** The sgRNA of CCAGCGCTCACGGTTCATCG (FSP1-2) targeting exon 4 of *fsp1* was used to knock out the endogenous FSP1 in HEK293 cells. After single colonies were obtained, genomic DNA of the FSP1 knockout cells were extracted and used as a template for PCR amplification of the sgRNA targeted region. The sgRNA target sequence is indicated by blue arrows. Intron sequences are in lower case and exon sequences are in upper case. One of the single colonies has one allele has an 11-base deletion (top) while the other has a 1-base insertion (bottom) at the Cas9 cutting site.



**Supplementary Fig. 4 | Warfarin and vitamin K concentration titrations in HEK293 and TKO reporter cells. (a)** Immunoblotting of DKO cells and these cells with their fsp1 gene knocked out (TKO). Full-length FSP1 is indicated by an arrowhead. Similar results were observed at least twice. Top: anti-FSP1, bottom: anti-GAPDH. (b) Inhibition of VKD carboxylation in TKO reporter cells. The TKO reporter cells were seeded in a 96-well plate and incubated with increasing concentrations of warfarin in the cell culture medium containing 11  $\mu$ M vitamin K for the cell-based activity assay. The carboxylation activity of TKO cells without warfarin in the culture medium was normalized to 100%. Data are presented as mean ± SD of three independent experiments (n=3). (c) Vitamin K concentration titration of FIXgla-PC/HEK293 (HEK293) and TKO reporter cells. Reporter cells were seeded in 96-well plates and incubated with increasing concentrations of vitamin K for the cell-based activity assay. Carboxylated reporter protein FIXgla-PC in the cell culture medium were determined using ELISA without normalization. Data are presented as mean ± SD of three independent experiments (n=3).



**Supplementary Fig. 5 | Tissue specificity of FSP1 RNA from The Human Protein Atlas Database.** A low tissue specificity for the FSP1 gene was determined by The Human Protein Atlas Database (https://www.proteinatlas.org/ENSG00000042286-AIFM2/tissue). AIFM2 was the protein name in the database while searching this protein.



**Supplementary Fig. 6 | Rossmann fold structural motifs identified in FSP1.** Two Rossmann fold motifs were identified in FSP1 between residues 12 to 52 (top) and 143 to 183 (bottom). Rossmann fold motif structure typically contains an alpha helix flanked by two parallel beta strands. The loop connecting the first beta strand with the alpha helix contains the consensus sequence GxGxxG, which established direct interaction with the dinucleotide cofactor. Rossmann fold structures were obtain by Pymol using AlphaFold predicted model. Conserved glycine residues within the GxGxxG sequence that have been mutated in this study were indicated in the structure model.

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MG G Q V S V D E - S V H V V I V G G G F G G I A A Q H L K H Y G V P F M L I D V L D A F H H N V A A L R A S V Q T G F A R K T F I P Y K E T F M G S Q V S V D M G A V R V V I V G G G F G G I A A A S Q L Q T L N I P F M L V D M K D S F H H N V A A L R A S V Q S G F A K K T F I S Y S V T F M G G Q I S V D K - S V Q V V I V G G G F G G I E A A R L L Q D W G I P F I L V D M K D S F H H N V A A L R A S V Q S G F A K K T F I S Y S X T F M G G Q I S V D K - S V Q V V I V G G G F G G I E A A R K L K C W G V P Y L V D M R D S F H H N V A A L R A S V Q S G F A K T F I S Y S X T F M G S K L S I D E - N V H V V V G G G F G G I A A A I Q L K S L G V P Y T L I D M K D A F H H N V A A L R A S V Q S G F A K T F I S Y S X T F M G S K V S V E - S V R V V I V G G G F G G I A A A Y Q L K S F G I P Y L V D L K D A F H H N V A A L R A S V E S G F A K K T F I S Y S X T F M G S K V S V E - S V R V V I V G G G F G G I A A A Y Q L K S F G I P Y L V D L K D A F H H N V A A L R A S V E S G F A K K T F I S Y S X T F M G S Q V S V D T G A V H V V I V G G G F G G I A A A Y Q L K S F G I P Y L V D M K D S F H H N V A A L R A S V E S G F A K K T F I S Y S X T F M G S Q V S V D T G A V H V V I V G G G F G G I A A A Y Q L K S W A V P F V L V D M K D S F H H N V A A L R A S V E S G F A K K T F I S Y S Y T F M G S R L S V D - S V R V V I V G G G F G G I A A A Y Q L K S W A V P F V L V D M R D A F H H N V A A L R A S V E S G F A K K T F I S Y S Y T F M G S Q V S V D M G A V H V V V V G G G F G G I A A A Y Q L K S W G I P F V L V D M R D A F H H N V A A L R A S V E S G F A K K T F I S Y S Y T F M G S Q V S N D M G A V H V V V V G G G F G G I A A A Y Q L K S W G I P F V L V D M R D A F H H N V A A L R A S V E S G F A K K T F I S Y S Y T F M G S Q V S N D M G A V H V V V V G G G F G G I A A A Y Q L Q L N I P F T L V D M K D S F H H N V A A L R A S V E S G F A K K T F I S Y S Y T F M G S Q V S N D M G A V H V V I V G G G F G G I A A A Y Q L Q L N I P F T L V D M K D S F H H N V A A L R A S V E S G F A K K T F I S Y S Y F M G S Q V S N D M G A V H V V I	K D S <mark>F</mark> R	/ T <mark>F</mark> K	S١	SF	FI	к <mark>т</mark>	K۲	FΑ	i <mark>G</mark>	DS	V	S	A	. R	۱L	۸	<mark>Λ</mark>	V	N	н	H	F١	A <mark>f</mark>	) A	t D	I R	М	D	۷ <mark>۱</mark>	\	. L	L	F	ΡF	F	I	Е	W	S١	IS	н	LI	2 L	Q	_ (	L	L	A	A	Α.	A	E	Е	E	L	Ι	1	; ]	3	G	G	G	G	G	G	G	6	10	1	10	0	G	G	G	G	G	G	G	3	1	I	Ι	1	E	E	Ξ	ł	A	٩.	A	A	١	L	L	L	L	_		(	Q	Q	2	2	L	L		ł	ł	Н	Н	н	ł	ł	13	S	S
MG SQV SVDMG AV RVV I VG GG FG G I AAAS QL QTLNIPFML VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SK VS VDD - SV RVV I VG GG FG G I EAARLL QD WG I PFI L VD MR D S FHHNV AALRA SV QSG FAKKT FI SF SET F MG GQ I SVDK - SV QVV I VG GG FG G I EAARLL KC WG VPFV L VD MR D A FHHNV AALRA SV QSG FAKKT FI SF SKT F MG SK L SI DE - NV HVV VV GG GF GG I AAA I QL KSLG VPYT L I D I NR D A FHHNV AALRA SV QSG FAKKT FI SY SAT F MG GK L SVDE - NV HVV VV GG GF GG I AAA KQ LK CHG VPYT L I D I NR D A FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SK VS VEE - SV RVV I VG GG FG GI AAA XQ LK CHG VPYT L I D I NR D A FHHNV AALRA SV E SG FAKKT FI SY SAT F MG SQ VS VD TG AV HVV I VG GG FG GI AAAS QL QALNV PFML VD NK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS VD TG AV HVV I VG GG FG GI AAAS UL KSHG VPFML I D I L D A FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SR L S L DG - SV RVV I VG GG FG GI AAAS LLKSWA VPFVL VD MR D A FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SR L S VDD - SV RVV I VG GG FG GI AAAS L KSWA VPFVL VD MR D A FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SR L S VDD - SV RVV I VG GG FG GI AAAS L KSWA VPFVL VD MR D A FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS VDD - SV RVV I VG GG FG GI AAAS L L QS RG LAFT L I D L RD S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS VD MG AV HVV V VG GG FG GI AAAS QL QAL NI PFTL VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS VD MG AV HVV V VG GG FG GI AAAS QL QAL NI PFTL VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS MD AG AV HVV I VG GG FG GI AAAS QL QAL NI PFTL VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS MD AG AV HVV I VG GG FG GI AAAS QL QAL NI PFTL VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS MD AG AV HVV I VG GG FG GI AAAS QL QAL NI PFTL VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS MD AG AV HVV I VG GG FG GI AAAS QL QAL NI PFTL VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS MD AG AV HVV I VG GG FG GI EAA CQ L QU NI PFTL VD MK D S FHHNV AALRA SV E SG FAKKT FI SY SVT F MG SQ VS MD AG AV HVV I VG GG FG GI EAA CQ L QU NI PFTL VD	GLN <mark>F</mark> L	ET <mark>F</mark> C	/ K E	ΡY	FI	к <mark>т</mark>	R۲	FΑ	i <mark>G</mark> (	QТ	V (	S	A	. R	۱L	۸	Λ A	v	N	н	нı	F١	A <mark>f</mark>	) A	. D	Ĺ	v	D	I	. 1	1 L	Μ	F	ΡF	/ F	٧	G	Y	P	(H	к	LI	I L	н	21	Q	ς	A	A	Α.	A	٩,	A	A	I,	I	1	6	3	G	G	G	G	G	G	G	6	10	iC	10	0	G	G	G	G	G	G	G	3	1	I	Ι	1	A	A	Ą	ł	A	٩.	A	A	4	(	Q	Q	Q	Q	)	ł	Н	н	ł	I	L	L		ł	ŀ	ĸ	к	к	K	(	ł	ŀ	Н
MG SKV SVDD - SVR VV I VGGGFGG ME AA RL L QDWG I PF I L VDMR D S FHHNVAALRA SVQSGFAKK TF I SF SET F MG GQ I SVDK - SVQ VV I VGGGFGG I EAARK L KCWGVPFV L VDMR D A FHHNVAALRA AVQSGFAKK TF I SF SKT F MG SKL S I DE - NVH VV VGGGFGG I AAA QL KSLGVPYT L I DMKD A FHHNVGALRA SVQSGFAKK TF I SF SKT F MG SKV SVEE - SVR VVI VGGGFGG I AAA QL KSLGVPYT L I DIRD A FHHNVAALRA SVESGFAKK TF I SF SKT F MG SKV SVDE - NVH VV VGGGFGG I AAA QL KSFGI PFV L VD LK D A FHHNVAALRA SVESGFAKK TF I SF SKT F MG SKV SVDT GAVH VVI VGGGFGG I AAA SQL QAL NVPFM L VD KK D SFHHNVAALRA SVESGFAKK TF I SYSAT F MG SQV SVDT GAVH VVI VGGGFGG I AAA SQL QAL NVPFM L VD MK D SFHHNVAALRA SVESGFAKK TF I SYSAT F MG SRL SLDG - SVR VV VGGGFGG I AAA SQL KSWAVPFV L VD VRD A FHHNVAALRA SVESGFAKK TF I SYSVT F MG SRL S LDD - SVR VVI VGGGFGG I AAA SQL KSWAVPFV L VD MR D A FHHNVAALRA SVESGFAKK TF I SYSVT F MG SRL SVDD - SVR VVI VGGGFGG I AAA SQL KSWAVPFV L VD MR D A FHHNVAALRA SVESGFAKK TF I SYSVT F MG SRL SVDD - SVR VVI VGGGFGG I AAA SQL QAL NI PFT L VD MR D A FHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SVDM GAVH VVV VGGGFGG I AAA SQL QAL NI PFT L VD MK D SFHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SVDN GAVH VVV VGGGFGG I AAA SQL QAL NI PFT L VD MKD SFHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SVDN GAVH VVV VGGGFGG I AAA SQL QAL NI PFT L VD MKD SFHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SVDN GAVH VVV VGGGFGG I AAA SQL QAL NI PFT L VD MKD SFHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SMD KGAVH VVI VGGGFGG I AAA SQL QAL NI PFT L VD MKD SFHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SMD KGAVH VVI VGGGFGG I AAA SQL QAL NI PFT L VD MKD SFHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SMD KGAVH VVI VGGGFGG I AAA SQL QAL NI PFT L VD MKD SFHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SMD KGAVH VVI VGGGFGG I AAA SQL QAL NI PFT L VD MKD A FHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SMD KGAVH VVI VGGGFGG I AAA SQL QAL NI PFT L VD MKD A FHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SMD KGAVH VVI VGGGFGG I AAA SQL QAL NI PFT L VD MKD A FHHNVAALRA SVESGFAKK TF I SYSVT F MG SQV SMD KGAVH VVI VGGGFGG I AAA SQL QAL NI PFT L	KENFR	/ T <mark>F</mark> K	٢S١	SY	FI	к <mark>т</mark>	K۲	FΑ	i G (	ΕS	V	S	A	. R	۱L	A	A ۱	v	N	н	нł	F١	s <mark>f</mark>	) S	D	١ĸ	М	D	۷ <mark>۱</mark>	\	1 L	Μ	F	ΡF	F	I	Ν	L	ГΙ	T	Q	L	2 L	Q	5 (	s	S	A	A	Α.	A	٩,	A	A	E.	I	1	1	3	G	G	G	G	G	G	G	6	10	i	10	0	G	G	G	G	G	G	G	3	1	I	Ι	1	A	A	Ą	ł	A	٩.	A	A	١.	Ş	s	s	s	S	5	(	Q	Q	Ş	2	L	L		. (	. (	ç	Q	Q	ç	5	1	٦	Т
MG GQI SVDK - SVQ VV IVG GGFGG I E AARK L KCWG VPFV LVD MRD AFHHNVAALRAAVQS GFAKK TFI SFSKT MG SKL SIDE - NVH VV VVG GGFGG I AAAIQ L KSLGVPYT LID MKD AFHHNV AALRASVES GFAKK TFI SYSATF MG GKL SVDE - NVH VV VVG GGFGG I AAAIQ L KSLGVPYT LID IRD AFHHNVAALRASVES GFAKK TFI SYSATF MG SKV SVEE - SVRVV IVG GGFGG I AAAIQ L KSFGI PFV LVD LKD AFHHNVAALRASVES GFAKK TFI SYSATF MG SQV SVD TG AVHVV IVG GGFGG I AAAIQ L KSFGI PFV LVD LKD AFHHNVAALRASVES GFAKK TFI SYSATF MG SQV SVD TG AVHVV IVG GGFGG I AAAIQ L KSGI PFV LVD VND MKD SFHHNVAALRASVES GFAKK TFI SYSATF MG SRL SLD G - SVRVV IVG GGFGG I AAAIQ L KSWAVPFV LVD WRD AFHHNVAALRASVES GFAKK TFI SYSVTF MG SRL SVD D - SVRVV IVG GGFGG I AAAIQ L KSWAVPFV LVD WRD AFHHNVAALRASVES GFAKK TFI SYSVTF MG SRL SVD D - SVRVV IVG GGFGG I AAAIQ L KSWGI PFV LVD MRD AFHHNVAALRASVES GFAKK TFI SYSVTF MG SQV SVD MG AVHVV VG GGFGG I AAAIQ L KSWGI PFV LVD MRD AFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SVD D - SVRVV IVG GGFGG I AAAIQ L KSWGI PFV LVD MRD AFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SVDD - SVRVV VVG GGFGG I AAAIQ L KSWGI PFV LVD MRD AFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SVDD - SVRVV VVG GGFGG I AAAIQ L QALNI PFT LVD MKD SFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SVDD - SVRVV VVG GGFGG I AAASQL QALNI PFT LVD MKD SFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SVD AVHVV IVG GGFGG I AAASQL QALNI PFT LVD MKD SFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SVD AAHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SADVG AVHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHHNVAALRASVES GFAKK TFI SYSVTF MG SQL SADVG PVHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHNVAALRASVES GFAKK TFI SYSVTF MG SQL SADVG PVHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHNVAALRASVES GFAKK TFI SYSVTF MG SQL SADVG PVHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHNVAALRASVES GFAKK TFI SYSVTF MG SQL SADVG PVHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHNVAALRASVES GFAKK TFI SYSVTF MG SQL SADVG PVHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHNVAALRASVES GFAKK TFI SYSVTF MG SQL SADVG PVHVVI VG GGFGG I AAASQL QALNI PFT LVD MKD SFHNVAAL	k d s <mark>f</mark> q	E T <mark>F</mark> M	SE	SF	FI	к <mark>т</mark>	ĸ٢	FΑ	s <mark>G</mark> (	QS	V	S	A	. R	۱L	A	A ا	v	N	н	нı	FΙ	s <mark>F</mark>	<mark>)</mark> S	2 D	IR	М	D	۷I	\	L	Ι	F	ΡF	F	I	G	W	٥ı	0	Q	L	. L	L	۲I	R	F	A	A	Α.	A	٤,	Е	E	1	Μ	Ν	i N	3 1	3	G	G	G	G	G	G	6	10	1	10	¢	G	G	G	G	G	G	G	3 1	Ν	Μ	М	1 8	E	Е		ł	A	٩.	A	A	١	F	R	R	R	R	2	1	L	L	_		ι	L		. (	(	ç	Q	Q	ç	2	[	۵	D
MGSKLSIDE - NVH VV VVGGGFGGIAAAIQLKSLGVPYTLIDMKDAFHHNVGALRASVQSGFAKTTFISYSATF MGGKLSVDE - NVHVVVVGGGFGGIAAAKQLKCHGVPYTLIDIRDAFHHNVGALRASVESGFAKKTFISYKDTF MGSKVSVEE - SVRVVIVGGGFGGIAAASQLQALNVPFMLVDMKDSFHHNVAALRASVESGFAKKTFISYKDTF MGSQVSVDTGAVHVVIVGGGFGGIAAASQLQALNVPFMLIDILDAFHHNVAALRASVESGFAKKTFISYSATF MGGQVSIDE - TVHVVVVGGGFGGIAAASQLQALNVPFMLIDILDAFHHNVAALRASVQAGFAKQTFIPYKETF MGSRLSLDG - SVRVVVVGGGFGGIAAASLLKSWAVPFVLVDVRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD - SVRVVVGGGFGGIAAASQLKSWAVPFVLVDVRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD - SVRVVVGGGFGGIAAASQLKSWAVPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD - SVRVVVGGGFGGIAAASQLKSWGIPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD - SVRVVVGGGFGGIAAASQLKSWGIPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDVGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDVGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSADVGPVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSADVGPVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSADTGALHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMRDAFHNNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQLNIPFLLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMRDAFHNNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMRDAFHNNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMRDAFHNNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAASQLQALNIFFLVV	GGSFR	KT F (	s	SF	FI	к <mark>т</mark>	ĸ٢	ΕA	s <mark>G</mark> (	QS	V (	A	A	. R	۱L	A	<mark>ו</mark> A	v	N	н	н	F١	A F	<mark>)</mark> A	2 D	IR	М	D	v	\	Ľ	v	F	ΡF	F	٧	G	W	21	c	ĸ	LI	K L	ĸ	۲ł	R	F	A	A	Α.	A	E,	Е	Е	L	I	1	; ]	3	3	G	G	G	G	G	G	0	10	10	10	¢	G	G	G	G	G	G	G	3	1	I	Ι	1	E	E	Ξ	1	A	١.	A	A	١	F	R	R	R	२	ξ	1	ĸ	ĸ	¢	t,	ι	L		. 1	ŀ	ĸ	ĸ	ĸ	<	(	(	(	c
MGGKLSVDE-NVHVVVVGGGFGGIAAAKQLKCHGVPYTLIDIRDAFHHNPGALRASVESGFAKKTFISFRETF MGSKVSVEE-SVRVVIVGGGFAGIAAASQLQALNVPFMLVDKDAFHHNVAALRASVESGFAKKTFISYKDTF MGSQVSVDTGAVHVVIVGGGFGGIAAASQLQALNVPFMLVDMKDSFHHNVAALRASVESGFAKKTFISYSATF MGGQVSIDE-TVHVVIVGGGFGGIAAASQLQALNVPFMLVDVRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD-SVRVVVVGGGFGGIAAASQLKSWAVPFVLVDVRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD-SVRVVVVGGGFGGIAAASQLKSWAVPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD-SVRVVVVGGGFGGIAAASQLKSWAVPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD-SVRVVVVGGGFGGIAAASQLKSWAVPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVGGGFGGIAAASQLKSWAVPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVGGGFGGIAAASQLKSWGIPFVLVDMRDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDVGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDVGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMRDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF	NGN <mark>F</mark> K	AT <mark>F</mark> M	( S /	SΥ	FI	тт	ĸ٦	FΑ	i G i	Q S	V (	S	A	. R	۱L	βA	G	v	N	н	н	F١	A F	D A	D	١ĸ	М	D	I	1	Ľ	т	Y	P١	/ F	٧	G	L	5 1	S	ĸ	LI	L	Q	C (	I	1	A	A	Α.	А	٩,	A	A	I.	I	1	; ]	3	3	G	G	G	G	G	G	0	10	1	10	0	G	G	G	G	G	G	G	3	1	I	Ι		A	A	Ą	ł	A	١.	A	A	١	1	I	I	Ι	E	[	(	Q	Q	Q		L	L		. 1	ŀ	ĸ	ĸ	ĸ	k	(	5	ŝ	S
MG SKVS VEE - SVR VVI VGGGFAG IA AA TQLKSFGIPFVLVDLK DA FHHNVA ALRASVES GFARK TFISYKDTF MG SQVS VDTGAVHVVI VGGGFGG IA AA SQLQALNVPFMLVDMK DSFHHNVA ALRASVES GFAKK TFISYSATF MG GQVS IDE - TVHVVI VGGGFGG IA AA QHLKHHGVPFMLIDIL DA FHHNVA ALRASVES GFAKK TFISYSVTF MG SRLSLDG - SVR VVV VGGGFGG IA AA SLLKSWAVPFVLVDVR DA FHHNVA ALRASVES GFAKK TFISYSVTF MG SRLSVDD - SVR VVI VGGGFGG IA AA SQLKSWAVPFVLVDMR DA FHHNVA ALRASVES GFAKK TFISYSVTF MG SKLSVDD - SVC VVI VGGGFGG IA AA SQLKSWAVPFVLVDMR DA FHHNVA ALRASVES GFAKK TFISYSVTF MG SKLSVDD - SVC VVI VGGGFGG IA AA SQLKSWGIPFVLVDMR DA FHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSVDM GAVHVVVGG GFGG IA AA SQL KSWGIPFVLVDMR DA FHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSVDM GAVHVVVVG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSVDM GAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSVDVGAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSVDVGAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDA GAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDA GAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDA GAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDA GAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDA GAVHVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SKVSVDD - SVRVVI VG GGFGG IA AA SQLQALNIPFTLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SKVSVDD - SVRVVI VG GGFGG IA AA SQLQALNIPFLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDKGAVHVVI VG GGFGG IA AA SQLQALNIPFLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDKGAVHVVI VG GGFGG IA AA SQLQALNIPFLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDKGAVHVVI VG GGFGG IA AA SQLQALNIPFLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDKGAVHVVI VG GGFGG IA AA SQLQALNIPFLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQVSMDKGAVHVVI VG GGFGG IA AA SQLQALNIPFLVDMK DSFHHNVA ALRASVES GFAKK TFISYSVTF MG SQV	KEN <mark>F</mark> K	ET F P	RE	SF	FI	кт	ĸ٢	FΑ	i G (	ĒS	VE	S	A	. R	۱L	βA	G	Р	N	н	н	F١	A F	A (	D	R	Ι	D	I	. 1	Ľ	т	Y	P١	F	v	G	Н	C I	c	к	LI	L	Q	(	к	k	A	A	Α.	А	٩,	A	A	E,	I	1	; ]	3	3	G	G	G	G	G	G	0	10	10	10	0	G	G	G	G	G	G	G	3	1	I	Ι		A	A	Ą	ł	A	٩.	A	A	١	ł	K	к	ĸ	¢	(	. (	Q	Q	ç		L	L		ł	ŀ	ĸ	к	ĸ	k	(	(	0	С
MGSQVSVDTGAVH VVIVGGGFGGIAAASQLQALNVPFMLVDMKDSFHHNVAALRASVESGFAKKTFISYSATF MGGQVSIDE - TVH VVIVGGGFGGIAAAQHLKHHGVPFMLIDILDAFHHNVAALRASVQAGFAKQTFIPYKETF MGSRLSLDG - SVRVVVVGGGFGGIAAASLLKSWAVPFVLVDVRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSRLSVDD - SVRVVIVGGGFGGIAAASQLKSWAVPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDD - SVCVVIVGGGFGGIAAASQLKSWGIPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDD - SVRVVVVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFVLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSKLSVDD - SVRVVIGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSADJGALHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSKLSVDD - SVRVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSKLSVDD - SVRVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSKLSVDD - SVRVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF	Q D N <mark>F</mark> I	от <mark>г</mark> а	ĸ	SY	FI	к <mark>т</mark>	R	FΑ	i G (	ΕS	VE	s	A	. R	۱L	A	A N	v	N	нт	н	F١	A F	A (		. K	L	D	v	\	Ľ	v	F	Ρŀ	F	I	G	F	S F	s	к	LI	L	Q	Г (	т	ı,	A	A	Α.	А	۸,	A	A	I.	I	1	; 1	3	G	G	G	G	G	G	G	0	0	0	0	0	G	G	G	G	G	G	G	3	1	I	Ι	1	A	A	Ą	ł	A	٩.	A	A	١	1	Т	Т	Т	Г	Γ		Q	õ	Q		L	L		ł	ŀ	ĸ	к	к	k	Ċ	3	S	s
MGGQVSIDE - TVHVVIVGGGFGGIAAAQHLKHHGVPFMLIDILDAFHHNVAALRASVQAGFAKQTFIPYKETF MGSRLSUDG - SVRVVVVGGGFGGIAAASLLKSWAVPFVLVDVRDAFHHNVAALRAAVESGFAKKTFISYSVTF MGSRLSVDD - SVRVVIVGGGFGGIAAASQLKSWAVPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSTAD - VHVVVVGGGFGGIAAARQLKSWGIPFVLVDMRDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDMGAVHVVVVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSVDVGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFMLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSMDAGAVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSADVGPVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSADVGPVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHNVAALRASVESGFAKKTFISYSVTF MGSQVSADVGPVHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDAFHHNVAALRASVESGFAKKTFISYSVTF MGSQVSADTGALHVVIVGGGFGGIAAASQLQALNIPFTLVDMKDSFHNVAALRASVESGFAKKTFISYSVTF MGSQVSADTGALHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHNVAALRASVESGFAKKTFISYSVTF MGSQVSADTGALHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHNVAALRASVESGFAKKTFISYSVTF MGSQVSADTGALHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHNVAALRASVESGFAKKTFISYSVTF MGSQVSADTGALHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHNVAALRASVESGFAKKTFISYSVFF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHNVAALRASVESGFAKKTFISYSVFF MGSQVSMDKGAVHVVIVGGGFGGIAAASQLQALNIPFLVVDMKDSFHNVAALRASVESGFAKKTFISYSVFF	KDNFR	AT F P	(s/	SΥ	FI	к <mark>т</mark>	ĸ٢	FΑ	i G (	ES	VE	S	A	. R	۱L	A	A ا	v	N	н	н	F١	s <mark>F</mark>	) S		١ĸ	м	D	٧ <mark>۱</mark>	\	1 L	М	F	PI	/ F	v	N	L	۹ ۱	A (	Q	L	L	Q	5 (	s	s	A	A	Α.	A	٩,	A	A	Ε.	I	1	1	3	G	G	G	G	G	G	G	6	10	iC	10	0	G	G	G	G	G	G	G	3	1	I	I		A	A	Ą	1	A	٩.	A	A	1	ş	s	s	s	s	5	(	Q	õ	5		L	L		. (	. (	ç	Q	Q	0	),	ļ	ļ	A
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I	S	T	()	(P	s	K	E١	ד/	Ī	I	H	S	K	Ρ.	A	L	A D	A	E	LL	P	R	v	R	Q	E١	v	K	Εï	T I	- 1	C Q	) E	G	v	нI		- L	. N	н	ĸ	vs	S N	I L	D	к	Γ.	ΓL	N.	Q	FK	< E	N	II	V	VI	E		K	G	Т	E	۷	۷	Т	- [	DN	ľ
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I	ĸ	T	Ξ١	ΥP	A	K	E۱	ד /	L	1	H	S	K	I	A	L	A E	v	E	LL	H	IS	۷	R	Q	E١	v	ĸ	E I	I	L	. R	łΚ	G	۷	R	L	- L	S	E	R	V	S N	I L	E	Ν	F.	ΓP	N	Q	Fς	βK	N	I M	V	٧ľ	Ч	T E	K	G	Т	E	۷	I	A	- [	D١	
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I	K	T	ΞF	P	D	K	K١	/ 1	L	. I	H	S	R	N	V	L	A D	Р	E	LL	<b>-</b> P	S	v	R	Е	Q,	A	ĸ	E١	۷I	- L	. Q	ĮΚ	G	۷	E	L	- L	E.	Q	K	V	ΓN	L	. N	D	LE	ΞL	N.	٨.	ΤF	ĸκ	D	) I	۷	I	ĸ	T D	K	D	Т	Е	Ι	Т	А	- [	DL	

C - G	N S - A Y	FLASN (	AL-VNE-LQV	EGY-NIYA	IGDCADVKEPK	MAYHAGLHAN	VAVTNI-NSL	- Q K P L
	250	260	270	280	290	* * 300	310	:
I L <mark>C</mark> T <mark>G</mark> :	EKI <mark>NS</mark> S <mark>AY</mark>	RKA <mark>F</mark> ESR <mark>LAS</mark> S(	AL R V N E H L Q V	EGHS <mark>NIYA</mark>	<mark>I G D C A D V</mark> R T <mark>P K</mark>	MAYLAGLHAN	I <mark>AV</mark> A <mark>NI</mark> V <mark>NS</mark> V	K <mark>Q</mark> R P L
IL <mark>C</mark> N <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	S S A L G D Q M <mark>A</mark> D <mark>N (</mark>	AL M <mark>VN</mark> DH <mark>LQV</mark>	Q <mark>G</mark> F S <mark>N I Y A</mark>	I G D C A N V K E P K	MAYHAGLHAN	VVVTNIV <mark>NSL</mark>	KQKPL
IP <mark>C</mark> N <mark>G</mark> :	EKV <mark>NS</mark> S <mark>AY</mark>	CSA <mark>F</mark> ESR <mark>LASN(</mark>	ALQ <mark>VNEYLQV</mark>	EGYSNVYA	IGDCADVKEPK	MAYHAGLHAN	IVT <mark>TNI</mark> I <mark>NS</mark> M	K <mark>Q</mark> R P L
IL <mark>C</mark> T <mark>G</mark> :	[ K V <mark>N S</mark> S <mark>A Y</mark>	RSS <mark>F</mark> INK <mark>LASN(</mark>	ALK <mark>VNDHLQV</mark>	EGYDNIYA	IGDCADVKEPK	MAYHAGLHA <mark>D</mark>	VAVTNI <mark>NSL</mark>	TQKPL
IC <mark>C</mark> T <mark>G</mark> S	SKI <mark>NS</mark> E <mark>AY</mark>	RSSMSSC <mark>LA</mark> ENO	ALK <mark>VN</mark> KH <mark>LQV</mark>	EGFDNVYA	V <mark>G D C A</mark> N L S <mark>E P K</mark>	<mark>MAYHAGLHA</mark> G	VA <mark>ATNI</mark> I <mark>NSL</mark>	SGKAL
IV <mark>C</mark> NG	[ K V <mark>N S</mark> S <mark>A Y</mark>	H S A <mark>F</mark> D G H <mark>L A S N (</mark>	ALRVNEYLQV	EGYSHIYA	IGDCADVKEPK	<mark>MAYHAGLHA</mark> S	<mark>VAV</mark> ANI <mark>VNS</mark> R	KQRPL
IL <mark>C</mark> T <mark>G</mark> :	EKI <mark>NS</mark> S <mark>AY</mark>	SSA <mark>F</mark> RDQ <mark>LA</mark> NN(	ALK <mark>VN</mark> DY <mark>LQV</mark>	VGYDNIYA	IGDCSDVKEPK	MAYHAQLHAN	VVVTNIINSL	TEKPL
IL <mark>C</mark> T <mark>G</mark> :	EKV <mark>NS</mark> A <mark>AY</mark>	SGA <mark>F</mark> SDK <mark>LASN(</mark>	ALQVNEYLQV	K <mark>g y</mark> d <mark>n i y a</mark>	IGDCADVNEPK	MAYHAGLHAD	VAVTNIVNSL	TQKPL
IC <mark>C</mark> TG:	EKV <mark>NS</mark> S <mark>AY</mark>	SNALKLK <mark>LA</mark> DNO	ALRVNEHLQV	EGSENIYA	IGDCADVKEPK	MAYHAELHAK	<mark>vav</mark> knivnsl	TQKPL
IC <mark>C</mark> T <mark>G</mark> :	EKI <mark>NS</mark> S <mark>AY</mark>	ENS <mark>F</mark> KDAIVK <mark>N(</mark>	ALM <mark>VNKHLQV</mark>	EGMENIYA	IGDCADVKEPK	MAYHAGLH GA	VAVD <mark>NIINTL</mark>	KEKPL
LCCTG	KIS <mark>S</mark> SS <mark>Y</mark>	SSA <mark>F</mark> GDK <mark>LA</mark> ED(	ALI <mark>VN</mark> DY <mark>LQV</mark>	Q <mark>G</mark> H A <mark>N</mark> V Y A	V <mark>GDCA</mark> YIN <mark>EPK</mark>	MAYYAGIHAR	VAATNVRNSL	IGKSL
IV <mark>C</mark> NG:	[KI <mark>NS</mark> S <mark>AY</mark>	RSA <mark>F</mark> ESR <mark>LASN</mark>	ALKVNEFLQV	EGYSNIYA	IGDCADTKEPK	MAYHAGLHAN	<mark>VAV</mark> ANIV <mark>NS</mark> M	KQRPL
IC <mark>C</mark> TG	NKI <mark>NS</mark> E <mark>AY</mark>	RSSLTTCM <mark>A</mark> ES <mark>(</mark>	ALKVNQHLQV	EGFDNVYA	VGDCANLDEPK	LAYHAGLHAA	VAA <mark>TNI</mark> IS <mark>S</mark> L	TGKCL
V L <mark>C</mark> T <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	A A A <mark>F</mark> G D K M <mark>A S</mark> D (	ALK <mark>VN</mark> KHLQL	EGYENIYA	IGDCADLKEPK	MAYHAGLHAN	<mark>VV</mark> VTNIINSL	TQKPL
VL <mark>C</mark> T <mark>G</mark> :	IKI <mark>NS</mark> S <mark>AY</mark>	ATA <mark>F</mark> GDK <mark>LASN(</mark>	ALNVNKHLQL	EGYDNIYA	IGDCANL <mark>KEPK</mark>	MAYHAELHAN	IV <mark>V</mark> SNIINSL	THKPL
IL <mark>C</mark> T <mark>G</mark> :	IKI <mark>NS</mark> S <mark>AY</mark>	SSA <mark>F</mark> GEK <mark>LASN(</mark>	ALK <mark>VN</mark> QYLQV	EGYDNIYA	IGDCADVKEPK	MAYHAGLHAN	IV <mark>VTNI</mark> I <mark>NSL</mark>	TQKPL
FCCTGI	_ R V <mark>N S</mark> S <mark>A Y</mark>	KSS <mark>F</mark> SDHMTNS <mark>(</mark>	ALKVNEHLQV	EGFSNVFA	IGDCNNVNEAK	TAYNAELHAG	I <mark>A V G N I</mark> A <mark>N S</mark> V	NGKRL
IV <mark>C</mark> NG:	[ R I <mark>N S</mark> S <mark>A Y</mark>	RSA <mark>F</mark> ESH <mark>LA</mark> G <mark>N</mark>	ALR <mark>VNE</mark> YLQV	EGCSHVYA	IGDCADVKEPK	MAYHAGLHAS	<mark>VAV</mark> A <mark>NI</mark> V <mark>N</mark> AR	K Q R P L
IL <mark>C</mark> T <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	G S A <mark>F</mark> G D K M <mark>A S N (</mark>	ALR <mark>VNQHLQ</mark> L	EGYENIYA	I G D C A D L K E P K	MAYHAGLHAN	VVVTNIVNSL	KNKSL
IV <mark>C</mark> N <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	H S A <mark>F</mark> D S H <mark>L A S N (</mark>	ALRVNEHLQV	EGCSRVYA	IGDCADVKEPK	<mark>MAYHAGLHA</mark> G	I <mark>AV</mark> ANIVNSM	KQRPL
IV <mark>C</mark> N <mark>G</mark> :	[KI <mark>NS</mark> A <mark>AY</mark>	R S A <mark>F</mark> G D R <mark>L A S N (</mark>	ALR <mark>VNE</mark> YLQV	EGYSHIYA	I G D C A D V <mark>R E P K</mark>	MAYHASLHAN	<mark>VAV</mark> A <mark>NI</mark> V <mark>NS</mark> M	i k <mark>q</mark> r p l
IV <mark>C</mark> N <mark>G</mark> :	EKI <mark>NS</mark> S <mark>AY</mark>	R S A <mark>F</mark> D D G <mark>L A S N (</mark>	ALK <mark>VNE</mark> YLQV	EGCSHVYA	IGDCADVKEPK	MAYHAGLHAN	<mark>VAV</mark> A <mark>NI</mark> I <mark>NS</mark> M	i k <mark>q</mark> r p l
IV <mark>C</mark> N <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	CSA <mark>F</mark> ESR <mark>LASN</mark> S	ALRVNEYLQV	EGYSNIYA	IGDCADVKEPK	MAYHAGLHAN	IVT <mark>TNI</mark> V <mark>NS</mark> M	i k <mark>q</mark> r p l
IL <mark>C</mark> T <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	SSA <mark>F</mark> GDK <mark>LASN(</mark>	ALKVNQYLQV	EGYDNIYA	IGDCADVKEPK	MAYHAGLHAN	IV <mark>VTNI</mark> I <mark>NSL</mark>	TQKPL
IL <mark>C</mark> T <mark>G</mark> :	[ K V <mark>N S</mark> S <mark>A Y</mark>	R S A <mark>F</mark> S D K <mark>L A</mark> K N (	ALQ <mark>VNEHLQV</mark>	K <mark>g y</mark> k <mark>n i y a</mark>	I G D C A X <mark>V R E P K</mark>	MAYHASLHAD	VAV <mark>ANI</mark> VNSL	TNKPL
IL <mark>C</mark> NG	[KI <mark>NS</mark> S <mark>AY</mark>	SSA <mark>F</mark> ESR <mark>LASN(</mark>	ALRVNEFLQV	EGYSNIYA	IGDCADVKEPK	MAYHAGLHAN	<mark>vavtn</mark> lv <mark>ns</mark> m	KQRPL
IV <mark>C</mark> N <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	R S A <mark>F</mark> D D G <mark>L A S N (</mark>	ALK <mark>VNE</mark> YLQV	EGCSHVYA	IGDCADVKEPK	MAYHAGLHAN	<mark>VAVTNI</mark> I <mark>NS</mark> M	K <mark>Q</mark> R P L
IL <mark>C</mark> T <mark>G</mark> :	[KI <mark>NS</mark> S <mark>AY</mark>	ASA <mark>F</mark> ADK <mark>LASN(</mark>	ALK <mark>VN</mark> QH <mark>LQ</mark> L	EGYENIYA	IGDCADLKEPK	MAYHAGLHAN	IV <mark>VTNI</mark> I <mark>NS</mark> L	THKSL
IV <mark>C</mark> N <mark>G</mark> :	IKI <mark>NS</mark> F <mark>AY</mark>	RRA <mark>F</mark> ASQ <mark>LASN(</mark>	ALPVNEYLQV	EGCSHIYA	IGDCADVKEPK	MAYHAGLHAN	VAVANI INST	QQRPL
IC <mark>C</mark> TG	NKI <mark>NS</mark> TAY	SSSLSECLAED	SLNVNEHLOV	TGFQNVYA	VGDCANIKEPK	MAYHAGLHGG	VAATNIINNL	SGKPL

		- Y - PG - LTFLLSMGRNDGVGQISG - YVGRL - V AKSRDLFVSKSWKTM - Q P	
		* <sup>330</sup> 340 350 * 360 370	
1		A <mark>YKPGALTFLLSMGRNDGVGQISG</mark> F <mark>YVGRL</mark> M <mark>V</mark> RLT <mark>KSRDLFVS</mark> T <mark>SWKTM</mark> R <mark>Q</mark> SP <mark>P</mark> 373	
2		T <mark>YKPGALTFLLSMGRNDGVGQISGFYVGRL</mark> VVRF <mark>AKSRDLFVS</mark> T <mark>SWKTM</mark> RQTAPS- 373	
3		AYKPGALTFLLSMGRNDGVGQISGFYVGWLMVQLLKSRDLFVSTSWKTMKQSPP 373	
4		IYIPGSLIFLISMGSNDGVGQISGIYIGHFLVIVAKSKDLFVSKSWKKMGQHMPC- 373	
5		AYKPGALTELLAMGRNDGVGQTSGEYVGRLMVRLAKSRDLEVSSSWKTMROSPP 373	
7		IYKPGSLTFLISLGSNDGVGOISEYYVGHLLVTVLKSKDLFISKSWKKMHOHMPC - 373	
8		TYTPGSLTFLISLGRCDGVGQISDYYVGHLLVTVVKSRDLFVSQSWRKMGQCMPC- 373	
9		A <mark>YE</mark> PGRLTMLLSMGRNDGVGQIS <mark>NC</mark> YVGRILV <mark>VMAKSRGLLVW</mark> KSWWAMGQCVPS- 373	
10		V <mark>YNPGALTMLLSLGRDDGIGQLYG</mark> FHA <mark>GKFIV</mark> TL <mark>AKSKDLMVWKSWKEMDQ</mark> AI <mark>P</mark> K- 373	
11		TYKPGALSMLLSMGRNDGVGQFNGCYLGRFFVTMAKSRDIFVSKSWKEMGQTMPR- 374	
12		AYKPGALTELLSMGRNDGVGQISGEYVGRLMVRLAKSRDLLISISWKIMRQSPP 373	
14		TYERGSI TELLSMGRNDGVGQVNGYVGRLIVTTAKSRDLEVSKSWRTMGQKAPN- 373	
15		TYOPGSLTFLLSMGKNDGVGOVKGYVGHLLVTIAKSRDLFVSKSWKTMGOPMPS- 373	
16		T <mark>YQPGSLTFLLSMGRNDGVGQISGCYVGHLLV</mark> TI <mark>AKSRDLFVSKSWKTM</mark> GQTMPC- 373	
17		A <mark>Y</mark> RT <mark>GNVTMLLAMGRDDGVGQVNG</mark> FQLP <mark>R</mark> CL <mark>V</mark> ALLKSRDLLLW <mark>KSW</mark> REMK <mark>Q</mark> KQ <mark>P</mark> TP 373	
18		A <mark>YK</mark> PGALTFLLAMGRNDGVGQISGF <mark>YVGRL</mark> MVRLAKSRDLFVSSSWKTMRQSPP 373	
19	1	AYQPGSLTFLLSMGKNDGVGQINGYYVGRLVVTTAKSRDLFVYKSWKTMGQPMPN - 373	
20		AYKPGALTELLAMGRNDGVGQISGEYVGREMVRLAKSRDLEVSSSWKIMRQSPP 373	
21		AYRPGALTELLAMGRNDGVGQTSGEYVGRLMVRLAKSRDLETSSSWKTMRQSPP 373	
23		AYKPGALTFLLAMGRNDGVGQISGFYVGRLMVRLAKSRDLFVSTSWKTMRQSPP 373	
24		TYQ <mark>PGSLTFLLSMGRNDGVGQINGCYVGRL</mark> LVTIAKSRDLFVSKSWKTMGQTMPC- 373	
25		T <mark>YTPGSLTFLISLGRNDGVGQING</mark> Y <mark>YVGHLLV</mark> TAV <mark>KSKDLFVSKSWRKM</mark> H <mark>Q</mark> CM <mark>P</mark> C- 373	
26	•	AYK <mark>PGALTFLLSMGRNDGVGQISG</mark> FYVGRLMVRLAKSRDLFVSTSWKTMRQSPP 373	
27		AYRPGALTFLLAMGRNDGVGQISGFYVGRLMVRLAKSRDLFISSSWKTMRQSPP 373	
28			
30		SYRPGNVTMLLAMGRDDGVGQFNGYKLPRFLVTQGKSKGLLLWKSWRDMGQSAPS - 373	
1	+-	te U20210 U20210 DANTE Anostas is indus ing fastar mitashandria assas istad 2 0 S-Dan tradadutas OX-0508 CN-AU	
1. 2	tr	tr $\Delta 0.4X21$ CH5 $\Delta 0.4X21$ CH5 V/OMLB Apoptos is inducing factor mitochondria associated 2 O S=Van troglodytes OX=9598 Giv=An	-1VIZ PE=2 SV=1 20130 GN-AIEM2 DE-ASV-1
2. 3	tr	tr G3TEI2 G3TEI2 I OXAE Apontos is induc ing factor mitochondria associated 2 O S=1 oxodonta africana OX=9785 GN=A	IFM2 PF=4 SV=1
4.	tr	tr G1KUD7 G1KUD7 A NOC A L-amino-acid oxidase O S=A nolis carolinensis O X=28377 GN=aifm2 PE=3 SV=2	
5.	tr	tr E7FFC4 E7FFC4_DANRE A poptos is-induc ing factor mitochondria-assoc iated 2 OS=Danio rerio O X=7955 GN=aifm2 P	E=1 SV=1
6.	tr	tr E2RQW8 E2RQW8_CANLF Apoptos is induc ing factor mitochondria assoc iated 2 O S=Canis lupus familiaris O X=9615	GN=AIFM2 PE=4 SV=1
7.	tr	tr A 0A6J1UCF5 A 0A6J1UCF5_9SAUR L-amino-acid oxidase OS=Notechis scutatus OX=8663 GN=A IFM2 PE=3 SV=1	
8.	tr	tr A 0A670I7A9 A 0A670I7A9_PODMU L-amino-acid oxidase OS=Podarcis muralis OX=64176 GN=A IFM2 PE=3 SV=1	
9.	tr	tr M3XJX5 M3XJX5_LATCH P yr_redox_2 domain-containing protein O S=Latimeria chalumnae O X=7897 GN=A IFM2 P E	=4 SV=1
10.	tr	tr A 0A4W3HBP0 A 0A4W3HBP0_CALMI Pyr_redox_2 domain-containing protein OS=Callorhinchus milii OX=7868 GN=ai	fm2 PE=4 SV=1
11.	sp	sp B4F6I3 FSP1_XENTR Ferroptosis suppres sor protein 1 OS=Xenopus tropicalis O X=8364 GN=aifm2 P E=2 SV=1	
12.	sp	sp Q 8BUE4 FSP1_MOUSE Ferroptos is suppressor protein 1 OS=Mus musculus OX=10090 GN=Aifm2 PE=1 SV=1	
13.	tr	tr A UA672QUN3 AUA672QUN3_SINGR Apoptos is induc ing factor mitochondria associated 2 U S=Sinocyc iochelius grai	nami U X=75366 GN=alfm2P
1/	С: с	E=4 SV =1 s n RSEXES ESD 1. TA EGU Extrantos is sunnes sor protain 1.0 S-Taenionygia guttata 0.X-50720 GN=4 JEM2 D E=2 SV=1	
15	tr	tr F1BR24 F1BR24 CHICK P vr. redox 2 domain-containing protein O S=Gallus gallus O X=9031 GN=A IFM2 P E=4 SV=1	
16.	tr	tr K7G371 K7G371 PELSI Pvr redox 2 domain-containing protein OS=Pelodiscus s inensis OX=13735 GN=AIFM2 PE=4 SV	/=1
17.	tr	tr A0A3B5KF37 A0A3B5KF37_TAKRU Pyr_redox 2 domain-containing protein O S=Takifugu rubripes O X=31033 GN=aifn	12 PE=4 SV=1
18.	tr	tr A0A6G1AF34 A0A6G1AF34_CROCR A IFM2 factor (Fragment) O S=Crocuta crocuta OX=9678 GN=A ifm2 PE=4 SV=1	
19.	tr	tr A0A7K4LBN8 A 0A7K4LBN8_9AVES A IFM2 factor (Fragment) O S=Crypturellus undulatus O X=48396 GN=Aifm2 PE=4 S	SV=1
20.	tr	tr A 0A2U3ZUK2 A0A2U3ZUK2_ODORO apoptos is-induc ing factor 2 OS=Odobenus rosmarus divergens O X=9708 GN=A	IFM2 PE=4 SV=1
21.	tr	tr A0A6P5AS70 A0A6P5AS70_BOSIN apoptosis-inducing factor 2 O S=Bos indicus O X=9915 GN=AIFM2 PE=4 SV=1	
22.	tr	tr A0A6I9IIM4 A 0A6I9IIM4_VICPA apoptos is-induc ing factor 2 isoform X1 OS=Vicugna pacos OX=30538 GN=AIFM2 PE=	4 SV=1
23.	tr	tr A0A6I9J4K1 A 0A6I9J4K1_CHRAS apoptosis-inducing factor 2 O S=Chrysochloris asiatica OX=185453 GN=AIFM2 PE=4 S	V=1
24.	tr	tr A UA8C3ISU4 AUA8C3ISU4_CHRPI Apoptos is induc ing factor mitochondria assoc iated 2 O S=Chrysemys picta bellii O X	=8478 GN=AIFM2 PE=4SV=1

25. tr A 0A8D0DNU7 A0A8D0DNU7\_9SAUR Apoptos is induc ing factor mitochondria assoc iated 2 O S=Salvator merianae OX=96440 GN=AIFM2 PE=4SV=1

- 26. tr A 0A8C5Z5X0 A 0A8C5Z5X0\_MARMA Apoptos is induc ing factor mitochondria assoc iated 2 O S=Marmota marmota O X=9994 GN=AIFM2 P E=4 SV =1
- 27. tr A 0A8B7K828 A0A8B7K828\_CAMFR apoptosis-inducing factor 2 isoform X1 OS=Camelus ferus OX=419612 GN=A IFM2 PE=4 SV=1
- 28. tr A 0A8B7IJL1 A 0A8B7IJL1\_9AVES apoptosis-inducing factor 2 isoform X1 OS=Apteryx mantelli mantelli OX=202946 GN=AIFM2 PE=4 SV=1
- 29. tr A 0A671EWY5 A0A671EWY5\_RHIFE Apoptos is induc ing factor mitochondria assoc iated 2 O S=Rhinolophus ferrumequinum O X=59479 GN=AIFM2 P E=4 SV =1
- 30. tr A 0A6J2V437 A 0A6J2V437\_CHACN apoptosis-inducing factor 2 isoform X2 OS=Chanos chanos OX=29144 GN=aifm2 PE=4 SV=1

## Supplementary Fig. 7 | FSP1 sequence alignment from 30 diverse species using SnapGene.

Conserved sequences are highlighted in yellow. Consensus threshold was set as 95%. Residues mutated for functional study in this paper are indicated by asterisks. The GxGxxG conserved consensus sequences within the Rossmann fold are underlined.



**Supplementary Fig. 8 | Immunoblotting of FSP1 and its mutants with a His-tag at the C-terminus.** His-Tagged FSP1 and its mutants were transiently expressed in HEK293 cells. Forty-eight hours posttransfection, transfected cells were harvested and the cell lysates were used for SDS-PAGE electrophoresis. Protein bands were transferred to PVDF membrane and probed by anti-His antibody (left) or anti-GADPH antibody as described in the Methods. Similar results were observed at least twice times as shown in these blots.



**Supplementary Fig. 9 | Structure comparison of FSP1 and yeast Ndi1 and AIF.** (a) Superpositions of Ndi1 (pink, PDBcode 4G73) with a bound quinone (raspberry) and apoptosis inducing factor (AIF, PDBcode 4BUR, cornflower blue) onto the AlphaFold model of FSP1 (grey) display differences in the C-termini's surrounding the putative vitamin K (green) binding site. Red arrow denotes deviations between the kinked C-terminal helix of the FSP1 model and the equivalent penultimate helix of Ndi1. The C-terminus of AIF is located away from this position. Black arrow denotes the position of residue F360 located near the vitamin K quinone moiety in the FSP1 model. (b) Global superposition of Nid1 structure with Alphafold model of FSP1. (c) Global superposition of 4BUR with Alphafold model of FSP1.



Supplementary Fig. 10 | Synthetic route for VK-ASM (S11).



**Supplementary Fig. 11 | Activity-based fluorescence probe of vitamin K and ubiquinone for FSP1.** (a) Proposed activation mechanism of the activitybased fluorescent probe of ubiquinone (NIR-ASM) towards NQO1. The probe is inactive until the ubiquinone moiety is reduced to hydroquinone, and the rearrangement of the reduced intermediated releases the strong fluorescent tag ASM. (b) Fluorescence emission spectra of the fluorescence tag ASM (blue) and the activity-based probe of vitamin K before activation (orange) excited at 460 nm. Solution measurements were performed in 10×10 mm<sup>2</sup> quartz cuvettes. Photoluminescence spectra (PL) were measured using Edinburgh Instruments FS5 fluorescence spectrometer in steady-state mode with xenon lamp as the excitation source, exciting at 460 nm.



Supplementary Fig. 12 | Comparison of the effect of FSP1 mutations on activity-based fluorescence probes of NIR-ASM and VK-ASM. Wildtype FSP1 or its mutants were transiently expressed in TKO cells and the transfected cells were harvested 48 hours after transfection. Cell lysate was used for activity assays using the fluorescence probe NIR-ASM (**a**) and VK-ASM (**b**) for ubiquinone and vitamin K reduction, respectively, as described in the method section. Control: TKO cells without transfection. Data are presented as mean ± SD of three independent experiments (n=3).

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**Supplementary Fig. 13** <sup>1</sup>H and <sup>13</sup>C NMR spectra of synthetic intermediates (S4, S7, S9) and VK-ASM (S11)



Supplementary Fig. 13 (continued)



Supplementary Fig. 13 (continued)



Supplementary Fig. 13 (continued)



Supplementary Fig. 14 ESI MS Spectra of VK-ASM (S11)

558

m/z

556

550.6293 551.8956 553.8955 555.8901

554

552

558.7222 560.2551

560

562

566.2421

566

563.2336 565.9115

564

567.2455

568.2486

568

571.2198

570.<u>72</u>29

570

572.2225

572

573.2206

574

576.2500

576

D:\Williams\Liu\20220516\_YL-03-29

Relative Abundance 60-50

40

30-20-

10-

0-

540

545.2633

543.2524

544

541.2469

542

546.2663

546

547.2691

548

550

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