

	210	220	230	240	250	260	270	280	290	300	
									MYGSRPPP	RRDGLMSY	KQFI
PpSE											
SmSE											
OsSE3	KRPR	-----LDGR	--SP-----	PRGGR	FGFEHER	GRERSMNTSRRA	-----	PD	CLDSG	CDAPYNGQSNTRR	KGLMTYKQFI
AtSE	KRYR	RDDNGYDGR	--GSPRGGYGPP	DRRF	GYDHGGCYDREMGGRP	GYCDERPHGRFMGRY	-----	QD	WEGGRGGYGDASNS	CNPQRDGLMSY	KQFI
AtSE2	KRYR	RDDNGYDGR	--GSPRGGYGPP	DRRF	GYDHGGCYDREMGGRP	GYCDERPHGRFMGRY	-----	QD	WEGGRGGYGDASNS	CNPQRDGLMSY	KQFI
SISE	KRSRRD	-DYDGR	--GSPRGGFGHG	DRRY	GYDHQGCYDREMGGRP	GYPDERHHGRFAGRS	SSGGYRG-	G	DWG	PVRGGFADSFAGCN	QREGLKSYKQFI
SISE2	KRSRRD	-DYDGR	--GSPRGGFGHG	DRRY	GYDHQGCYDREMGGRP	GYPDERHHGRFAGRS	SSGGYRG-	G	DWG	PVRGGFADSFAGCN	QREGLKSYKQFI
CsSE	KRSRRDDGGYDGR	--GSPRGGFGPP	DRRF	GYDYGGCYEREMGR	PGYVDERPMGRFMGRS	SSGGYQ--	G	DWD	SNRGGHGDALNP	CGCQREGLMTY	KQFM
CsSE3	KRSRRDDGGYEP	RR--GSPRGGFGP	DRRF	GYDYTG	CYEREMGGRP	GYCDERPHGRFAGRS	SSGGYQSGP	S	EWD	SSRGGYGDASNT	GSTQREGLMSYKQFI
CsSE5	KRSRRDDGGYEP	RR--GSPRGGFGP	DRRF	GYDYTG	CYEREMGGRP	GYCDERPHGRFAGRS	SSGGYQSGP	S	EWD	SSRGGYGDASNT	GSTQREGLMSYKQFI
CsSE2	KRSRRDDGGYEP	RR--GSPRGGFGP	DRRF	GYDYTG	CYEREMGGRP	GYCDERPHGRFAGRS	SSGGYQSGP	S	EWD	SSRGGYGDASNT	GSTQREGLMSYKQFI
CsSE1	KRSRRDDGGYEP	RR--GSPRGGFGP	DRRF	GYDYTG	CYEREMGGRP	GYCDERPHGRFAGRS	SSGGYQSGP	S	EWD	SSRGGYGDASNT	GSTQREGLMSYKQFI
CsSE4											MSYKQFI
MiSE1	KRSRRDDGGYDGR	--GSPRGVFGPP	DRRF	GYDYAGCFEREMGGRP	GYCDERPHGRHISWP	FGGYS-GHS	DWD	SGRSGYNEVPNT	CTVQREGLMSY	KQFI	
MiSE2	KRSRRDDGGYDGR	--GSPRGGFGPP	DRRF	GYDYAGCYERE	IIGGRP	GYCDERPHGRYIGRPIGGYG-GPP	EWD	SGRGGYSDVPNT	CSAQREGLMSY	KQFI	
OsSE2	KRSRRDD	-GYDRR	GGRGSP-PRYGYD	DRRY	GYDHERC	-----GGRGGYD	DDRYHGRYQ	NRA	-----ADW	ADSGFGASND	--GPCITQREGLMTYKQFI
ZmSE	KRSRRDD	-GYDRR	GGRGSP-PRYGYD	DRRY	GYDHERC	-----GGRGGYD	DDRNQGRYL	NRA	-----PD	WDSGYGAAND	--GPCVTQREGLMTYKQFM
ZmSE2	KRSRRDD	-GYDRR	GGRGSP-PRYGYD	DRRY	GYDHERC	-----GGRGGYD	DDRNHGRYLN	RG	-----PD	WDSGYGAAND	--GPCVTQREGLMTYKQFM
OsSE1	-----	FD	RRRLGPGV-GYDNP	DRRY	CNDHGA	-----GGRGGYD	DERGCGRNF	NRA	-----PD	WDSGRGW	ND--GPANSRREGLMSYKQFM
ZmSE3	-----	FD	RRRLGPGVGGGHEQ	DRRY	CNGLGGI	-----GGRGC	-----	DSRYTNRA	-----PD	---SGRGGW	NE--GSCNSRREGLMSYKQFI
ZmSE4	-----	FD	RRRLGPGVGGGHEQ	DRRY	CNGLGGV	-----GGRGC	-----	DGOYTNRA	-----PD	WDSGRGGW	NE--GPCNSRREGLMSYKQFI

DUF3546 superfamily

	310	320	330	340	350	360	370	380	390	400										
PpSE	VELEDDI	LPGEA	ERYEYKSEY	ITTOKRAFFE	QHKKDDDWL	-----	REKYD	PARLE	IVLVR	RENENAKILSK	ELLAE	LQAGSL								
SmSE			YEEYK	AEYVSTOKR	AYFEQHKE	EDWL	REKYD	PSRL	DSL	MARRI	ETAKS	SARD	FILLE	LQAGSL						
OsSE3	QKLEDDV	SPICE	AEASRYQEYK	TSYITSQK	QDYFDH	HKNEDRL	KDMYH	PTNLL	SVIER	RNELCKAA	AKNL	ILDL	RS	SGTL						
AtSE	QLEDDI	LPSEAE	RRYQEYKSEY	ITTOKRAFF	NTHK	EDWL	KNKYH	PTNLL	SVIER	RNDLAQ	KVAK	DFLL	DL	QSGTL						
AtSE2	QLEDDI	LPSEAE	RRYQEYKSEY	ITTOKRAFF	NTHK	EDWL	KNKYH	PTNLL	SVIER	RNDLAQ	KVAK	DFLL	DL	QSGTL						
SISE	QLEDDI	LPAAEA	RRYQEYKACYIE	AQKRAY	FN	AHKDEEWL	KDKYH	PSNLI	SVIER	RNELARK	S	AK	DFLL	DL	QSGTL					
SISE2	QLEDDI	LPAAEA	RRYQEYKACYIE	AQKRAY	FN	AHKDEEWL	KDKYH	PSNLI	SVIER	RNELARK	S	AK	DFLL	DL	QSGTL					
CsSE	QLEDDI	LPAAEA	RRYQEYKSEY	ITTOKCA	FFD	SHKDEEWL	RDKYH	PTNL	LV	VIERR	NELAQ	RTAK	DFLL	DL	QSGTL					
CsSE3	QLEDDI	LPAAEA	RRYQEYKSEY	ISTOKR	VFF	DAHKDEEWL	KDKYH	PTNL	VAVI	ERRN	LARKV	AK	DFLL	DL	QSGTL					
CsSE5	QLEDDI	LPAAEA	RRYQEYKSEY	ISTOKR	VFF	DAHKDEEWL	KDKYH	PTNL	VAVI	ERRN	LARKV	AK	DFLL	DL	QSGTL					
CsSE2	QLEDDI	LPAAEA	RRYQEYKSEY	ISTOKR	VFF	DAHKDEEWY	SSFTL	FLL	CTLRCS	SYMCF	VCR	KDKYH	PTNL	VAVI	ERRN	LARKV	AK	DFLL	DL	QSGTL
CsSE1	QLEDDI	LPAAEA	RRYQEYKSEY	ISTOKR	VFF	DAHKDEEWL	KDKYH	PTNL	VAVI	ERRN	LARKV	AK	DFLL	DL	QSGTL					
CsSE4	QLEDDI	LPAAEA	RRYQEYKSEY	ISTOKR	VFF	DAHKDEEWL	KDKYH	PTNL	VAVI	ERRN	LARKV	AK	DFLL	DL	QSGTL					
MiSE1	QLEDDI	LPAAEA	RRYQEYKSEY	ISTOKR	VFF	DAHRDEEWL	KDKYH	PTNLL	SVIER	RNELARK	V	AK	DFLL	DL	QSGTV					
MiSE2	QLEDDI	LPAAEA	RRYQEYKSEY	ISTOKR	VFF	DAHKDEEWL	KDKYH	PTNLL	SVIER	RNELARK	V	AK	DFLL	DL	QSGTL					
OsSE2	QVLEDDI	SPAEAK	RYQEYRTEY	ITTOKR	AYFDL	HKNDDRL	KDKYH	PTNL	SSVI	DRR	NDSC	KAT	AK	DF	FD	LQ	NGTL			
ZmSE	QVLEDDI	SPAEAK	RYQEYRTEY	ITTOKR	AYFDL	HKNEDWL	KDKYH	PTNL	LSVI	ERRN	ERCKV	IA	AK	DF	FD	LQ	NGTL			
ZmSE2	L	VLEDDI	SPSEAE	RRYQEYRTEY	ITTOKR	AYFDL	HKNEDWL	KDKYH	PTNLL	SVIER	RNERCKV	IA	AK	DF	FD	LQ	NGTL			
OsSE1	QLEDDV	SPDEA	QRYEYKSEY	ITTOKK	AYFDL	HKNDDWL	KNKYH	PTNLE	IVM	ERRN	ELAR	TAN	Q	F	LQ	D	LONGSL			
ZmSE3	QLEDDV	SPVEA	QRYEYKSEY	ITTOKK	AYFAL	HKDEEWL	RNKYH	PTNLE	ENV	VIERR	NELAR	TT	AD	DF	FL	QL	QSGSL			
ZmSE4	QLEDDV	SPVEA	QRYEYKSEY	ITTOKK	AYFDL	HKNEDWL	RNKYH	PTNLE	ENV	VIERR	NELAR	TT	AN	DF	FL	KL	QSGDL			

DUF3546 superfamily

DUF3546 superfamily

	610	620	630	640	650	660	670	680	690	700	
PpSE	LGREKLD	TTANEAL	DPFVRK	IRDEKYGW	YGCCGAKG	GCTKLFH	GPEFVHKH	LKLNKHS	SDLVADV	VAKAREE	LYFQNYM
SmSE	L GKDKS	EASMS	EAL EPYVRK	IRDEKYGW	YGCLATG	CSKLFH	GPEFVHKH	LKLNKHP	ELVNE	SMAKLR	RELYFQNYM
OsSE3	TAKDKI	DASADK	VLESYMT	KVKDDNY	GWTYG	CCGAKGC	IKVFHAP	DFVLKHL	NLKH	PDLSK	LTSRVQED
AtSE	AAKEKID	AAAT	EALDPH	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVY	KHLKLNK	HTELV	TELTTKV
AtSE2	AAKEKID	AAAT	EALDPH	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVY	KHLKLNK	HTELV	TELTTKV
SISE	AAKEKID	AVAAE	EALDPY	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPDL	SVDLTTK
SISE2	AAKEKID	AVAAE	EALDPY	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPDL	SVDLTTK
CsSE	TAKDKI	EAAL	EAFDPY	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLN	LKHPEL	VMELTSK
CsSE3	TAKDKI	DAAAV	DALDPF	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPPEL	VIELTSK
CsSE5	TAKDKI	DAAAV	DALDPF	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPPEL	VIELTSK
CsSE2	TAKDKI	DAAAV	DALDPF	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPPEL	VIELTSK
CsSE1	TAKDKI	DAAAV	DALDPF	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPPEL	VIELTSK
CsSE4	TAKDKI	DAAAV	DALDPF	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPPEL	VIELTSK
MiSE1	TAKDKI	DAAAV	DALDPF	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPPEL	VMELTV
MiSE2	TAKDKI	DAAAV	DALDPF	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPPEL	VMELTV
OsSE2	AAKDKI	DAAAV	EVL	EPYVRK	IRDEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLRLK	HPPEL	VLELTSK
ZmSE	TAKDKI	DAAAA	EVL	EPLVRK	IRDEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLKLNK	HPDL	VLELTSK
ZmSE2	TAKDKI	DAAAA	EVL	EPLVRK	IRDEKYGW	YGCCGAKG	GCTKLFH	AAEFVH	KHLRLK	HPDL	VLELTSK
OsSE1	KAKDKI	DAAAV	EVL	DPHVRK	IRDEKYGW	YGCCGAKG	GCTKLFH	AAEFVQ	KHLKLNK	HADL	VRELTSK
ZmSE3	KAKEKID	GAAAT	EVLDPY	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVQ	KHLKLNK	HTDL	VDLTSK
ZmSE4	KGKEKID	GAAAT	EVLDPY	VRKIR	DEKYGW	YGCCGAKG	GCTKLFH	AAEFVQ	KHLKLNK	HADL	VDLTSK

ARS2 superfamily

	710	720	730	740	750	760	770	780	790	800	
PpSE	RGLRPGL	SGPI	GGPGNR	RAGPDW	PPSDH	PSRDR	GRFG	PRNCD	RYDQ	GPAREE	QRFER
SmSE	---	---	---	---	---	---	---	---	---	---	---
OsSE3	---	---	---	---	---	---	---	---	---	---	---
AtSE	---	---	---	---	---	---	---	---	---	---	---
AtSE2	---	---	---	---	---	---	---	---	---	---	---
SISE	---	---	---	---	---	---	---	---	---	---	---
SISE2	---	---	---	---	---	---	---	---	---	---	---
CsSE	---	---	---	---	---	---	---	---	---	---	---
CsSE3	---	---	---	---	---	---	---	---	---	---	---
CsSE5	---	---	---	---	---	---	---	---	---	---	---
CsSE2	---	---	---	---	---	---	---	---	---	---	---
CsSE1	---	---	---	---	---	---	---	---	---	---	---
CsSE4	---	---	---	---	---	---	---	---	---	---	---
MiSE1	---	---	---	---	---	---	---	---	---	---	---
MiSE2	---	---	---	---	---	---	---	---	---	---	---
OsSE2	---	---	---	---	---	---	---	---	---	---	---
ZmSE	---	---	---	---	---	---	---	---	---	---	---
ZmSE2	---	---	---	---	---	---	---	---	---	---	---
OsSE1	---	---	---	---	---	---	---	---	---	---	---
ZmSE3	---	---	---	---	---	---	---	---	---	---	---
ZmSE4	---	---	---	---	---	---	---	---	---	---	---

ARS2 superfamily

ARS2 superfamily

ARS2 superfamily

	810	820	830	840	850	860	870	880	890	900																																																			
PpSE	GPM	EPP	MFDH	FNG	PPVRGL	PGGL	FVP	DM	PGP	PQ	VLMPVPGAGPLGPFVPAPPEI	AMR	FLRE	GP	G	---	PFR	MCG	FDAGYQE	EENGG	PRG	GKR	GAP	GPM	MEGG																																				
SmSE	AS	EQP	MFD	PF	GGTNI	H---	GGAF	GS	ET	-P	PPVLMPVPGAGPLGPFVPAPPDV	IMR	MR	REH	GG	GPQ	PF	HPAP	FDP	S---	---	FDGGDR	GR	---	KGR																																				
OsSE3	PTP	SEL	TPGA	F	GGQGS	F---	---	VEM	PT	-	PPVLI	PVPGAGPLGPFVPAPPEV	VM	QMMR	PVMP	---	---	---	---	---	---	---	---	---	---	---																																			
AtSE	GNP	CE	VG	YDA	F	GGQGV	--	HVP	PFL	SD	INP	PPMLMPVPGAGPLGPFVPAPPEVAM	QMF	RD	PS	GNP	PF	EGS	GR	---	---	---	---	GG	---	-P																																			
AtSE2	GNP	CE	VG	YDA	F	GGQGV	--	HVP	PFL	SD	INP	PPMLMPVPGAGPLGPFVPAPPEVAM	QMF	RD	PS	GNP	PF	EGS	GR	---	---	---	---	GG	---	-P																																			
SISE	GNP	DE	EM	FDT	F	GGQGI	P--	VA-	SFP	SD	MAP	PPVLMPVPGAGPLGPFVPAPPEVAM	RMM	RE	QGG	P-	TP	FE	GG	-R	---	---	---	NGR	SGP	----	A																																		
SISE2	GNP	DE	EM	FDT	F	GGQGI	P--	VA-	SFP	SD	MAP	PPVLMPVPGAGPLGPFVPAPPEVAM	RMM	RE	QGG	P-	TP	FE	GG	-R	---	---	---	NGR	SGP	----	A																																		
CsSE	GN	IDDP	MFD	S	F	GGQGR	H--	VA-	PF	ASE	ET	-P	PPVLMPVPGAGPLGPFVPAPPEVAM	RML	RE	QGG	P-	PF	EG	GR	---	---	---	NGR	PGP	QL	GGS																																		
CsSE3	ANR	DES	MFD	T	F	GGQGI	R--	VAP	PF	PS	DI	PP	PPVLMPVPGAGPLGPFVPAPPEVAM	QMI	RD	QGG	P-	PF	EG	GR	---	---	---	HGR	PGP	QL	SGP																																		
CsSE5	ANR	DES	MFD	T	F	GGQGI	R--	VAP	PF	PS	DI	PP	PPVLMPVPGAGPLGPFVPAPPEVAM	QMI	RD	QGG	P-	PF	EG	GR	---	---	---	HGR	PGP	QL	SGP																																		
CsSE2	ANR	DES	MFD	T	F	GGQGI	R--	VAP	PF	PS	DI	PP	PPVLMPVPGAGPLGPFVPAPPEVAM	QMI	RD	QGG	P-	PF	EG	GR	---	---	---	HGR	PGP	QL	SGP																																		
CsSE1	ANR	DES	MFD	T	F	GGQGI	R--	VAP	PF	PS	DI	PP	PPVLMPVPGAGPLGPFVPAPPEVAM	QMI	RD	QGG	P-	PF	EG	GR	---	---	---	HGR	PGP	QL	SGP																																		
CsSE4	ANR	DES	MFD	T	F	GGQGI	R--	VAP	PF	PS	DI	PP	PPVLMPVPGAGPLGPFVPAPPEVAM	QMI	RD	QGG	P-	PF	EG	GR	---	---	---	HGR	PGP	QL	SGP																																		
MiSE1	ASH	DES	V	F	E	A	F	GG	-G	I	R--	VG	P	F	S	D	I	AP	PPVLMPVPGAGPLGPFVPAPPEVAM	QMF	RE	QGG	P-	PF	EG	GR	---	NGR	PGP	QL	SGP																														
MiSE2	VNH	DE	P	I	F	D	A	F	GG	-G	I	R--	VG	P	F	A	S	D	I	PP	PPVLMPVPGAGPLGPFVPAPPEVAM	R	F	RE	QGG	P-	PF	EG	GR	---	NGR	PGP	QL	GGP																											
OsSE2	DG	ADD	Q	M	F	D	A	F	R	G	R	P	N---	AP	F	V	A	E	L	PP	PPILMPVPGAGPLGPFVPAPPEI	AM	H	M	L	R	E	Q	G	P	P-	PF	EG	P	N	G	P	H	A	N	---	P	---	---	G	V	L	G	P	M	M	G	G	P							
ZmSE	DG	DD	Q	M	F	D	A	F	R	G	R	P	N---	AP	F	V	A	E	L	PP	PPILMPVPGAGPLGPFVPAPPEI	AM	H	M	L	R	E	Q	G	P	P-	PF	EG	P	N	G	P	H	A	N	---	P	---	---	G	M	L	G	P	M	M	G	G	P							
ZmSE2	DG	DD	Q	M	F	D	A	F	R	G	R	P	N---	AP	F	V	A	E	L	PP	PPILMPVPGAGPLGPFVPAPPEI	AM	H	M	L	R	E	Q	G	P	P-	PF	EG	P	N	G	P	H	A	N	---	P	---	---	G	M	L	G	P	M	L	G	G	S							
OsSE1	DN	P	DD	-	AY	D	S	Y	C	D	P	V	M	H---	GA	F	P	P	D	I	PP	PPVLMPVPGAGPLGPFIPAPPEVAM	RMM	RD	QGG	P-	PF	EG	P	T	G	P	R	P	R	---	---	---	RP	G	R	---	---	---	GG	L	P	M	G	G	P										
ZmSE3	EN	P	DD	P	V	Y	D	S	F	C	D	P	T	M	H---	GA	F	P	P	D	I	PP	PPVLMPVPGAGPLGPFIPAPPEVAM	H	M	L	R	D	Q	G	A	P-	PF	EG	P	S	G	P	H	P	R	---	---	---	K	A	G	R	G	S	GG	G	P	P	M	R	G	P			
ZmSE4	EN	P	DD	P	I	Y	D	S	F	C	D	P	A	M	H---	GA	F	P	P	D	I	PP	PPVLMPVPGAGPLGPFIPAPPEVAM	H	M	L	R	D	Q	G	A	P-	PF	EG	P	I	E	P	T	G	P	H	P	R	---	---	---	K	A	G	T	---	---	GG	G	P	S	M	R	G	P

ARS2 superfamily