DUF3546 superfamily

DUF3546 superfamily

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Sequence alignment, residues 610–700.

PpSE	LGREKLDTTANEALDPFVRKIRDEKYGWKYGCGAKGCTKLFHGPEFVHKHLKLKHSDLVADVVAKAREELYFQNYMSDPDAPGANQVTSSQPGQRDDDRGR
SmSE	LGKDKSEASMSEALEPYVRKIRDEKYGWKYGCLATGCSKLFHGPEFVHKHLKLKHPEIVNESMAKLRRELYYQNYMSDPNAPGVASVQANQR-DSRLHRRR
OsSE3	TAKDKIDASADKVLESYVTVKDDNYGWTYGCGAKGCIKVFHAPDFVLKHLNLKHPDLVSKLTSRVQEDIYFQNYMNDPNAPGGTPVMQQQSPEQQG----
AtSE	AAKEKIDAAATEALDPHVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVYKHLKLKHTELVTELTTKVREELYFQNYMNDPNAPGGQPATQQSGPRDRPIRRK
AtSE2	AAKEKIDAAATEALDPHVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVYKHLKLKHTELVTELTTKVREELYFQNYMNDPNAPGGQPATQQSGPRDRPIRRK
SlSE	AAKEKLDAVAAEALDPYVRKIRDEKYGWKYGCGAKGCTKLFHASEFVHKHLKLKHPDLSVDLTTKVREDLYFQNYMNDENSPGGTPVMLPSVPKEKPLRRR
SlSE2	AAKEKLDAVAAEALDPYVRKIRDEKYGWKYGCGAKGCTKLFHASEFVHKHLKLKHPDLSVDLTTKVREDLYFQNYMNDENSPGGTPVMLPSVPKEKPLRRR
CsSE	TAKDKIEAAALEAFDPYVRKIRDEKYGWKYGCGAKGCTKLFHAPEFVHKHLNLKHPELVMELTSKVREELYFQNYMNDTDAPGGTPVMQQSLPKDKPQRRR
CsSE3	TAKDKIDAAAVDALDPFVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVHKHLKLKHPELVIELTSKVREELYFQNYMNDPDAPGGTPVMQQPMPKDRPLRRK
CsSE5	TAKDKIDAAAVDALDPFVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVHKHLKLKHPELVIELTSKVREELYFQNYMNDPDAPGGTPVMQQPMPV
CsSE2	TAKDKIDAAAVDALDPFVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVHKHLKLKHPELVIELTSKVREELYFQNYMNDPDAPGGTPVMQQPMPKDRPLRRK
CsSE1	TAKDKIDAAAVDALDPFVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVHKHLKLKHPELVIELTSKVREELYFQNYMNDPDAPGGTPVMQQPMPKDRPLRRK
CsSE4	TAKDKIDAAAVDALDPFVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVHKHLKLKHPELVIELTSKVREELYFQNYMNDPDAPGGTPVMQQPMPKDRPLRRK
MiSE1	TAKDKIDAAAVDALDPFVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVHKHLKLKHPELVMELTVKVREELYFQNYMNDVDAPGGTPVIQQPLPKEKPLRRK
MiSE2	TAKDKIDAAAFDALDPFVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVHKHLKLKHPELVMELTVKVREELYFQNYMNDADAPGGTPVMQQPLPKEKPLRRK
OsSE2	AAKDKIDAAAVEVLEPYVRKIRDEKYGWKYGCGAKGCTKLFHAPEFVHKHLRLKHPELVLELTSKVREDLYFQNYMNDPNAPGGTPVMQQSAPD-KS-RQR
ZmSE	TAKDKIDAAAAEVLEPLVRKIRDEKYGWKYGCGAKGCTKLFHAPEFVHKHLKLKHPDLVLESTSKVREDLYFQNYMNDPNAPGGTPVMQQSAPD-RG-RRR
ZmSE2	TAKDKIDAAAAEVLEPLVRKIRDEKYGWKYGCGAKGCTKLFHAPEFVHKHLRLKHPDLVLESTSKVREDLYFQNYMKDPNAPGGTPVMQLSAPD-RG-RRR
OsSE1	KAKDKIDAAASEVLDPHVRKIRDEKYGWKYGCGAKGCTKLFHAPEFVQKHLKLKHADLVRELTSKVRENIYFDNYMSDPKAPGGMPIMQQPAPREKV-RQR
ZmSE3	KAKEKIDGAATEVLDPYVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVQKHIKLKHTDLVVDLTSKAREDIYFENYMNDPKAPGGTPIMQQPAPRGKG-RQR
ZmSE4	KGKEKIDGAATEVLDPYVRKIRDEKYGWKYGCGAKGCTKLFHAAEFVQKHLKLKHADLVVDLTSKVREDIYFENYMNDPKAPGGTPIMQQPAPRGKG-RQR

ARS2 superfamily

Sequence alignment, residues 710–800.

PpSE	RGLRPGLSGPIGGPGNRAGPDWPPSDHPSRDGRFGPRNGDRYDQGPGAREEQRFERGTRDEKGRFDRGGLELTPPFRDYPLGAGGPPFEGGGPAQGGPFEG
SmSE	--------------------------PGLLGNSDRSRGRGEDV--------------DKSPA----------------GDYPYEGAG-------------P--
OsSE3	---
AtSE	--------------------------PSMENRLRDDRGGRRERDGRANGNDRNDRSEDQQR----------GD------NDG
AtSE2	--------------------------PSMENRLRDDRGGRRERDGRANGNDRNDRSEDQQR----------GD------NDG
SlSE	--------------------------PGLDGRLKDDRGNRKDRDGRANGGERFDMSENPQS----------GDFQSNNDG----ASG
SlSE2	--------------------------PGLDGRLKDDRGNRKDRDGRANGGERFDMSENPQS----------GDFQSNNDG----ASG
CsSE	--------------------------MNLDGRLKDDRGNRRDRDNWANGGDRFDRSENPQS----------SDFPSANDG----TDG
CsSE3	--------------------------LGPDNRLKDERGNRRDRDYRANGSDRYDRSDNAQA----------SDFPSNDDV----PEG
CsSE5	--SDFPSNDDV----PEG
CsSE2	--------------------------LGPDNRLKDERGNRRDRDYRANGSDRYDRSDNAQA----------SDFPSNDDV----PEG
CsSE1	--------------------------LGPDNRLKDERGNRRDRDYRANGSDRYDRSDNAQA----------SDFPSNDDV----PEG
CsSE4	--------------------------LGPDNRLKDERGNRRDRDYRANGSDRYDRSDNAQA----------SDFPSNDDV----PEG
MiSE1	--------------------------LVPGNRLKDERGNRRERDYGANGSDRYDRPDSVQS----------SEFPLNNDG----PDG
MiSE2	--------------------------LGSDNRLKDERGNRRDRDYRANGSDRYDRSDNAQS----------SEFPSNNDG----PDG
OsSE2	--------------------------PGMDNRLRYDRANRREYDRAERDGSRYGRGDRS-----------------------PSL
ZmSE	--------------------------PSMDSRLKFDRGSNRDHDKADRDGVRYGRGDHS-----------------------PSR
ZmSE2	--------------------------PSMDSRLKFDRGSNKEHDKAERDGGRYGRDDHS-----------------------PSR
OsSE1	--------------------------PPIESRLRDERGNRRFDRN-DS--------PTHD---------------------GSS
ZmSE3	--------------------------PPIESRLRDERGNHRLD--------SD-------------------------GSG
ZmSE4	--------------------------PPIESRLRDERGNHRFDRNVDS-------PKRD---------------------GSG

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