

Q4FTU5_PSYA2	MKQLPLTKQQ	LIAAMISLSL	GSVAQAALTI	NGSASSESSA	RLSWGGA DSL	SEARSIMSKS	GSSSTIKKVD	NGSSTTNITN	TTSFGSNNS	YNNANSYNTT
A0A106BYZ8_SHEFR	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Q086W1_SHEFN	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Q8X665_ECO57	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Q3K9W6_PSEPF	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Q4FTU5_PSYA2	YRGSFGNSNM	IPISTDSRSV	AVIDAETGES	IYEKDA DIAR	PMA SITK VMT	AMV VLDAGLD	MREELTLDPE	DFVGPKRASS	NLKSGDRLNR	AEMLLMALMK
A0A106BYZ8_SHEFR	--AAQAVQNK	PQQELASGSA	MLVDLT TNEV	LYSSNP NQPV	PIASVTKLMA	AMVTLDAKL P	LDEKISVKIT	DSPVMRNIYS	RVRLDSVVTR	ETMLLLTLMS
Q086W1_SHEFN	--AAQAVQNK	PQQELASASA	MLVDLT TNEV	LYSSNP NQPV	PIASVTKLMA	AMVTLDAKLA	LDEKISVKIT	DSPVMRNIYS	RVRLGSVVTR	ETMLLLTLMS
Q8X665_ECO57	--KTAAATTA	SQPEIASGSA	MIVDLNTNKV	IYSNHPDLVR	PIASISK LMT	AMV VLDARLP	LDEKLKVDIS	QTP EMKGVYS	RVRLNSEISR	KDMLLLALMS
Q3K9W6_PSEPF	--TTAAPRDA	SQ LKIASGSA	LLMDLQT NKV	IYSSNP DVVV	PIASVSK LMT	GLV VVEAHQN	MDEWIDVDIS	HTPEMKG VFS	RVKLRS ELPR	REMLLIALMS

Q4FTU5_PSYA2	SENPAAKSLA	RNYPGGYS AF	MRAMNRKAQE	LGMSTAFFGD	PTGLDKRNIA	SSNDLVKMVR	AAGNYDVIRR	FSTTKSYDFF	VSNYASGNRT	YKANNTSSLV
A0A106BYZ8_SHEFR	SENRAATSLA	HNYPGGFKAF	VRAMNDKATA	LGMSQTRYVE	PTGLSPDNVS	SANDLILLLK	ASQTYPLL GK	LSSTTKKHV-	--NFESP RYA	LDFQNTNKL V
Q086W1_SHEFN	SENRAATSLA	HNYPGGFKAF	VRAMNDKATA	LGMSQTRYVE	PTGLSPDNVS	SANDLILLLK	ASQTYPLL GK	LSSTTKKHV-	--NFESP RYA	LDFQNTNKL V
Q8X665_ECO57	SENRAAASLA	HHYPGGYKAF	IKAMNAKAKS	LGMNNT RFVE	PTGLSVHNVS	TARDLT KLLI	ASKQYPLIGQ	LSTTR EDMA-	--TFSNPTYT	LPFRNTNHL V
Q3K9W6_PSEPF	SENRAAASLA	HHYPGGYAAF	IAAMNAKAKA	LGMTSTHFVE	PTGLSER NVS	TARDLSKLLV	AAHKQPLLIE	LT TTKEKTV-	--SFRKPNYT	LGFRNTDHL V

Q4FTU5_PSYA2	RDGSYP IGIS	KTGFINEAGR	CVVMETRVNN	RP AII VILGA	NSSATRWGDA	KNILNSLATR	RTV-----	-----	-----	-----
A0A106BYZ8_SHEFR	FKNNWNIALT	KTGF TNKAGH	CLVMLTE MNK	RK VAFVVLDS	FGKYTHMADA	NRLKNWLE TG	RTTPIPASAK	AYKKQRQA IL	NNSI-----	-----
Q086W1_SHEFN	FKNNWNIALT	KTGF TNKAGH	CLVMLTE MNK	RK VAFVVLDS	FGKYTHMADA	NRLKNWLE TG	RTTPIPASAK	AYKKQRQA IL	NNSI-----	-----
Q8X665_ECO57	YRDNWN IQLT	KTGF TNAAGH	CLVMRTVINN	KPVALVVM DA	FGKYTHFADA	SRLRTWIE TG	KVMPVPA AAL	SYKKQKAAQM	AAAGQTAQND	-----
Q3K9W6_PSEPF	NKADWDIRIT	KTGF TNPAGH	CLVLVTRMAN	RPVALVILDA	FGKYTHFADA	SRIRSWVETG	KSANVPAVAQ	QYKADKNLKS	RQSGVIEASK	-----

XX signal sequence     
 ↓ ↓ active Ser residue     
 ● conserved residue  
XX signal cleavage site     
 ↓ ↓ active Lys residue     
 \* substrate binding residue