

exon 15ext

canonical GEFPPPPPTPRKPPSSSSPVSA~~CLRRRRRRRL~~GTELPGPTESGDSRQMVH~~VE~~CQCAPITRFVARVIEFVLVDVGNM~~LE~~HPALYRFLAGT~~LR~~SLYELVD~~RP~~VGGRLGRFF~~FD~~GLRGLF

Z3-3772 GEFPPPPPTPRKPPSSSSPVSA~~CLRRRRRRRL~~GTELPGPTESGDSRQMVH~~VE~~CQCAPITRFVARVIEFVLVDVGNM~~LE~~HPALYRFLAGT~~LR~~SLYELVD~~RP~~VGGRLGRFF~~FD~~GLRGLF

Z3-1140 GEFPPPPPTPRKPPSSSSPVSA~~CLRRRRRRRL~~GTELPGPTESGDSRQMVH~~VE~~CQCAPITRFVARVIEFVLVDVGNM~~LE~~HPALYRFLAGT~~LR~~SLYELVD~~RP~~VGGRLGRFF~~FD~~GLRGLF

MW Z GEFPPPPPTPRKPPSSSSPVSA~~CLRRRRRRRL~~GTELPGPTESGDSRQMVH~~MS~~SWHG

Z3-1711 GEFPPPPPTPRKPPSSSSPVSA~~CLRRRRRRRL~~GTELPGPTESGDSRQMVH~~VE~~CQCAPITRFVARVIEFVLVDVGNM~~LE~~HPALYRFLAGT~~LR~~SLYELVD~~RP~~VGGRLGRFF~~FD~~GLRGLF

Tai255.1 GEFPPPPPTPRKPPSSSSPVSA~~CLRRRRRRRL~~GTELPGPTESGDSRQMVH~~VE~~CQCAPITRFVARVIEFVLVDVGNM~~LE~~HPALYRFLAGT~~LR~~SLYELVD~~RP~~VGGRLGRFF~~FD~~GLRGLF

B

Figure 1 displays a multiple sequence alignment of exon 15 and exon 15ext across 19 species. The alignment is presented in two columns, with exon 15 on the left and exon 15ext on the right. The species names are listed on the left side of the alignment. The alignment shows conserved regions in green and variable regions in yellow. The alignment is divided into two sections: exon 15 (positions 1-100) and exon 15ext (positions 101-200). The alignment is as follows:

Species	Exon 15 (1-100)	Exon 15ext (101-200)
Dmel	NEIINTCRDNI RCLEAVLRGPPGTVLSNH CAGQTK	1 GEFPPPPPTPRK-----PSSSSPVSA CLRRRRRR ---RLGT ELP -----
Dsim	NEIINTCRDNI RCLEAVLRGPPGTVLSNH CAGQTK	1 GEFPPPPPTPRK-----PSSSSPVSA GLRRRRRR ---RPGT ELP -----
Dsec	NEIINTCRDNI RCLEAVLRGPPGTVLSNH CAGQTK	1 GEFPPPPPTPRK-----PSSSSPVSA GLRRRRRR ---RPGAE LP -----
Dere	NEIINTCRDNI RCLEAVLRGPPGTVLSNH CAGQTK	1 GEFPPPPATPRK-----PSSSSPVSA AVRRRRRR ---RPGT ELP -----
Dyak	NEIINTCRDNI RCLEAVLRGPPGTVLSNH CAGQTK	1 GEFPPPPPTPRK-----PSSSSPVSA AGIRRRRR ---RPGT ELP -----
Dana	NEIINTCRDNI HCLEAVLRGPPGTVLSNH CADHTK	1 GEFQPPPP-----PSSSYAV DTGLRRRRRR ---TYR QAELELL -----
Dper	NEIINTCRDNI RCLEAVLRGPPGTVLSNQ CAGQTK	1 GESQQQPPSSSS-----TS SVRRRRRQHLAATPEGDADTAEPI IPG-----
Dpse	NEIINTCRDNI RCLEAVLRGPPGTVLSNQ CAGQTK	1 GESQQQPPSSSS-----TS SVRRRRRQHLAATPEGDADTAEPI IPG-----
Dwil	NEIINTCRDNI RCLEAVLRGPPGTVLSTH CAGQTK	1 GESA-----AR TKTSKNSVCNDD QOLIVOL-----
Dmoj	NEIINTCRDNI RCLEAVLRGPPGTVLSTQ CAGQTK	1 GESLPPGCR LIA -----TA T -----ATG QSAVTAAGAAAA TPMP-----
Dvir	NEIINTCRDNI RCLEAVLRGPPGTVLSTH CAGQTK	1 GESLPPAGCH LIP -----TA TGNLTAAPAAAAATAAAAA ATP-----
Dgri	NEIINTCRDNI RCLEAVLRGPPGTVLSSH CAGQTK	1 GESLPPAATCRRLM VRR -----ASTVA ATTALLNAAATASASAPAAQ PAALQOP-----
Ccap	TEIIKTCRDNI NCLSVLRGPPGTVVSAH CAGQTK	1 GELA-----VCII Q -----
Gmor	TEIIINTCRDNI CCLESVLR TLGSGSMFFNGGVGQ LK	1 GELA-----IYL H -----
Aaeg	DEIIKTCRENV RCLET VLLSQPGTVLTAACQD LRG	1 K-RKPS TTKRRTF CP PKS GGG TLRTLLNRKSR RVYF FG QDDDE F PQ TCDESIE FGG SGCS VDKT-----
Cpip	DEIIKTCRENV RCLET VLLSQPGTVLTAACQD LRG	1 KNRS PHNRKSPV SR-----RALL NRKSR RVYF HD NEGEE DDRSR PT TT ITDDR GDSD ND-----
Agam	SEIIITCRENV RCLESVLR CGPTVLTAACQD LRG	1 K-RM HP PPRAQ TTSG SS-----SAAE G EEND Y SG SS DEDD GG SS TT ICSD SS SS SS Y ST LG-----

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Dmel	35	-GPTESG--DSRQMVHMEVCQCAPITRFVARVIEFVLVDGNMLEHFALYRFLAGTLRSLEYELVDRPVGG--	101		101	-----RLGRFFDGLRGLF	114
Dsim	35	-GPTESG--DSRQMVOVECCQCAPITRFVARVIEFVLVDGNMLEHFALYRFLAGTLRSLEYELVDRPVGG--	101		101	-----RLGRFFVGLRGLF	114
Dsec	35	-GPTESG--DSRQMVOVECCQCAPITRFVARVIEFVLVDGNMLEHFALYRFLAGTLRSLEYELVDRPVGG--	101		101	-----RLGRFFVGLRGLF	114
Dere	35	-GPAEFS-GDSRQMAQVVECCQCAPITRFVARVIEFVLVDGNMLEHFALYRFLAGTLRSLEYELVDRPVGG--	102		102	-----RLGRFFVGLRGLF	115
Dyak	35	-GPTESSGDAROMMHVEVCQCAPITRFVARVIEFVLVDGNMLEHFALYRLFAGTLRSLEYELVDRPVGG--	103		103	-----RLGRFFVGLRGLF	116
Dana	40	ATPPESG--DCLAKSRMACQCAPISRFRLARVIEFVLNLGNMLEHFTIYRFLSRLRSLEYLVNRPVGG--	106		106	-----DLRRFFAAGLRGLL	119
Dper	43	-----GS LAIAECKCAPITRFVARLLEFVM DLGNLLEHFALYRFLAGTLRS LAYLVN RMPMG--	99		99	-----PLERLFGG LRGLL	112
Dpse	43	-----GS LAIAECKCAPITRFVARLLEFVM DLGNLLEHFALYRFLAGTLRS LAYLVN RMPMG--	99		99	-----PLERLFGG LRGLL	112
Dwil	32	-----APECKCAPITRFVARIIDFVT DVSNLLEHFTLYRFLMGLRSFYALVN RP LG--	84		84	-----RLERLFASFRGLL	97
Dmoj	37	-----IVECKCAPITRFVARIDFVLVDGNLLEHFTLYRFLAGTLRS LAYLVN RMPMG--	89		89	-----RLERLFAGVRGLL	102
Dvir	41	-----IAECKCAPITRFVARLIEFVMDLSNMLEHFTLYRFLAGTLRS LAYLVN RMPMG--	93		93	-----RLERLFAGVRGLL	106
Dgri	49	-----ILECKCAPITRFVIGRIIEFVLVDGNLLEHFALYRFLAGTLRS LAYLVN RMPMG--	101		101	-----RLERLFAGVRGLL	114
Ccap	8	-----LDCKCAPITRFIARIIDFSLDVSNMLMYFTLYRFFVNLKLSYLTINIRIP--	59		59	-----FFRRFF	65
Gmor	8	-----ESCOCAPINRFIARLLEFVLDMNNIFNNFTLYKKPFMK-----LY-VN-	49		49	-----FA	51
AaeG	91	VDDGGARRK----IVVVGHCECRCAKITRFIATLIEFLDVDGNLLRNFNLYKFPVGVLGFYRLVGFFGR--	155	...	166	-----GDDATFRALS VGIV	180
Cpib	83	VGAGKGRRK----VVVVSECCRCAKITRFVAVIDFLLDVGNLLRNFTLYRFPFGVLNGFYRLVGLFGR--	147	...	158	-----DDDDTLRKLAGVGV	172
Agam	134	RERRPRPKPKKVVVVRECCARITRFITAWLDIFLLDIGNVMNRNFTLYRFPFGVLNGFYRLVDFGGRDR	203	...	244	LARGADDLLKR LVTVII	260

C

