H.sapiens RUVBL1 ruvBlike 1 isoform X1	<mark>MKIEEVKSTTKTQRIAS</mark> HSHVKGLG	<mark>ILDESGLAKQA</mark> ASGLVGQE <mark>N</mark> ARE	E	<u>GVIVELIKSKK</u> MAGRAVLLAGI	<u>PPGTGKTALALA</u> IAQELG <mark>S</mark> KVPF	FCPMVGSEV YS <mark>T</mark> EIKKT	<u>TEVLMENFRRA</u> IGLRIKETKEV	<u>YEGEVTELTPCETENPMGGY</u>	<u>YGKT<mark>ISHV</mark>IIGLKT<mark>A</mark>F</u>	<u>KGTKQLKL</u> DPSI <mark>F</mark> ESLQ	<u>KERVEAG</u> DVIYIE <mark>A</mark> N	<u>SGAVKRQGR</u> CDT <mark>Y</mark> ATEFD	<mark>LEA</mark> EEYVPLPKGDVHKK	KE <mark>IIQDVTL</mark> HDLDV <mark>A</mark>	<u>NARPQĞ</u> GQ <mark>D</mark> ILS	<u>SMMGQLMKP</u> KKTEITDK	<u>LR<mark>GEINKV</mark>VNKYIDQG</u>	G <mark>IAELVPG</mark> VLF <mark>V</mark> DEVH	<u>HMLDIECFT</u> YLHRALES <mark>S</mark>	SI <mark>APIVIFA</mark> SNRGNC <mark>V</mark>	<u>IRGTED</u> ITSPHGI	PLDLLDRVMIIRTMLYT	<u>PQE<mark>MKQIIK</mark>IRAQ</u> TEGINI	ISEEALNHL
G.aculeatus ruvbl2 ruvBlike 2	MASTKVPEVRDITRIERIGAHSHIRGLG	LDDALEPRQVSQGMVGQLASRF	R	GVILEMIKDGHIAGRAVLIAG(QPGTGKTA <mark>I</mark> AMGIAQ <mark>S</mark> LGPDTPF	FTAMAGSEIFSLEMSKT	'EALSQAFRKAIGVRIKEETEI	II <mark>EGEV</mark> V <mark>E</mark> IQIDR <mark>P</mark> ATGS	SGAKVGKLTLKTTE	'EMETIYD <mark>L</mark> GNKMID <mark>SL</mark> S	KDKVQAGDVITIDKA	.T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>T</mark> RARDYD	AMGAQTQF <mark>V</mark> QC <mark>P</mark> EGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVCEWREEG	G <mark>K</mark> AEIIPGVLFIDEVH	HMLD <mark>M</mark> ECF <mark>SFL</mark> NRALESD	DLS <mark>PVL</mark> IMATNRGITR	IRGTN.YQSPHGI	:PIDLLDR <mark>LLIIAT</mark> SPYT	EKETRQILKIRCEEEDVEL	LSEEAHTVL
D.rerio ruvbl2 ruvBlike 2	MAAQVATTKVPEVRDITRIERIGAHSHIRGLG	LDDALEPR <mark>QVSQGMVGQL</mark> ASRF	R	G <mark>LILEM</mark> IKDGQIAGRAVLIAG(QPGTGKTA <mark>I</mark> AMGIAQ <mark>S</mark> LGPDTPF	FTALA <mark>GSE</mark> IFSLEMSKT	'EALSQAFRKAIGVRIKEETEI	[I <mark>EGEV</mark> V <mark>E</mark> IQIDR <mark>P</mark> ATG]	TGAKVGKLT <mark>LKT</mark> TF	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> S	KERVQAGDVITIDKA	.T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>TRA</mark> RDYD	AMGAQTQFVQCPEGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVSEWREEG	G <mark>K</mark> AEIIPGVLFIDEVH	HMLD I ECF <mark>SF</mark> L <mark>N</mark> RALESD	DLS <mark>PVL</mark> IMATNRGITR	IRGTN.YQSPHGI	:PIDMLDRLLIIATTPYT	EKETRQILKIRCEEEDVEL	LSEEAHTVL
D.rerio ruvbl2 ruvBlike 2 dupelabel1	MAAQVATTKVPEVRDITRIERIGAHSHIRGLG	LDDALEPR <mark>QVSQGMVGQL</mark> ASRF	R	GLILEMIKDGQIAGRAVLIAG(QPGTGKTA <mark>I</mark> AMGIAQ <mark>S</mark> LGPDTPF	FTALA <mark>GSE</mark> IF <mark>S</mark> L <mark>E</mark> MS <mark>KT</mark>	'EALSQAFRKAIGVRIKEETEI	[I <mark>EGEV</mark> V <mark>E</mark> IQIDR <mark>P</mark> AT <mark>G</mark>]	TGAKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> S	KERV <mark>Q</mark> AGDVI <mark>TI</mark> DKA	.T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>TRA</mark> RDY <mark>D</mark>	AMGAQTQFVQCPEGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVSEWREEG	G <mark>K</mark> AEIIPGVLFIDEVH	HMLDIECF <mark>SF</mark> L <mark>N</mark> RALES <mark>D</mark>	DLS <mark>PVLIMATNRG</mark> ITR	IRGT <mark>N.YQ</mark> SPHGI	PIDMLDRLLIIATTPYT	EKETRQILKIRCEEEDVEL	LSEEAHTVL
H.sapiens RUVBL2 ruvBlike 2 isoform 1	MATVTATTKVPEIRDVTRIERIGAHSHIRGLG	LDDALEPRQASQGMVGQLAARF	R	GVVLEMIREGKIAGRAVLIAG(QPGTGKTA <mark>I</mark> AMGMAQALGPDTPF	FTAIA <mark>GSE</mark> IF <mark>S</mark> L <mark>E</mark> MS <mark>KT</mark>	'EALTQAFRRSIGVRIKEETEI	[I <mark>EGEV</mark> VEIQIDRPAT <mark>G</mark>]	TGSKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> T	KDKVQAGDVITIDKA	T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>TRA</mark> RDY <mark>D</mark>	AMGSQTKFVQCPDGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVAEWREEG	G <mark>K</mark> AEIIPGVLFIDEVH	HMLDIE <mark>SFSFLN</mark> RALES <mark>D</mark>	DM <mark>APVL</mark> IMATNRGITR	IRGTS.YQSPHGI	PIDLLDRLLIVSTTPYS	EKDTKQILRIRCEEEDVEM	_MSEDAYTVL
E.caballus RUVBL2 ruvBlike 2 isoform X1	MATVAATTKVPEIRDVTRIERIGAHSHIRGLG	LDDALEPRQA <mark>SQGM</mark> VGQLAARF	R	GVVLEMIREGKIAGRAVLIAG(QPGTGKTA <mark>I</mark> AMGMAQALGPDTPF	FTAIA <mark>GSE</mark> IF <mark>SLE</mark> MS <mark>KT</mark>	'EALTQAFRRSIGVRIKEETEI	[I <mark>EGEV</mark> V <mark>E</mark> IQIDR <mark>P</mark> AT <mark>G</mark>]	T <mark>G</mark> SKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> T	KDKVQAGDVITIDKA	.T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>TRA</mark> RDYD	AMGSQTKFVQCPDGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAK <mark>V</mark> AEWREEG	G <mark>K</mark> AE <mark>II</mark> PGVLFIDEVH	HMLDIE <mark>S</mark> FSFL <mark>N</mark> RALES <mark>D</mark>	DM <mark>APVLIM</mark> ATNRGITR	IRGT <mark>S.YQ</mark> SPHGI	PIDLLDRLLIVSTSPYS	EKDT <mark>KQI</mark> LR <mark>IR</mark> CEE <mark>E</mark> DVEM	_MSEDAYTVL
F.catus RUVBL2 ruvBlike 2 isoform X1	MATVTATTKVPEIRDVTRIERIGAHSHIRGLG	LDDALEPRQASQGMVGQLAARF	R	GVVLEMIREGKIAGRAVLIAG(QPGTGKTA <mark>I</mark> AMGMAQALGPDTPF	FTAIA <mark>GSE</mark> IF <mark>SLE</mark> MSKT	EALTQAFRRSIGVRIKEETEI	[I <mark>EGEV</mark> VEIQIDRPATG]	TGSKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> T	KDKVQAGDVITIDKA	.T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>TRA</mark> RDYD	AMGSQTKFVQCPDGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVAEWREEG	G <mark>K</mark> AE <mark>II</mark> PGVLFIDEVH	HMLDIE <mark>S</mark> F <mark>SF</mark> LNRALES <mark>D</mark>	DMAPVLIMATNRGITR	IRGTS.YQSPHGI	PIDLLDRLLIVSTSPYS	EKDT <mark>KQI</mark> LR <mark>IR</mark> CEE <mark>E</mark> DVEM	_MSEDAYTVL
S.salar ruvbl2 ruvBlike 2	MAAQMATTKVPEVRDITRIERIGAHSHIRGLG	LDDALEPRQVSQGMVGQLASRF	R	GLTLEMIKDGHIAGRAVLIAG(QPGTGKTAIAMGIAQALGTDTPF	FTAMA <mark>GSEIFSLE</mark> MSKT	EALSQAFRKAIGVRIKEETEI	[I <mark>EGEV</mark> VEIQIDRPATG]	TGAKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GSKMI <mark>ESL</mark> S	KERVQAGDVITIDKA	.T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>TRA</mark> RDYD	AMGAQTQFVQCPEGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVSEWREEG	G <mark>K</mark> AE <mark>II</mark> PGVLFIDEVH	HMLD <mark>MECFSFLN</mark> RALESD	DLSPVLIMATNRGITR	IRGTN.YQSPHGI	PIDLLDRLLIIATSPYT	EKETRQILKIRCEEEDVEL	LSEEAHTVL
S.townsendi RUVBL2 ruvBlike 2	MATAP.ATKVPEVRDVTRIERIGAHSHIRGLG	LDDTLEPRQVSQGMVGQLAARF	R	G <mark>VILEMIKEGKI</mark> AGRAVLIAG(QPGTGKTAIAMGMSQALGLDTPF	FTA <mark>IAGSE</mark> IFSLEMSKT	EALTQSFRRSIGVRIKEETEI	[I <mark>EGEV</mark> VEIQIDRPATG]	TGAKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> T	KEKVQAGDVITIDKA	TGKITKLGRSFTRARDYD.	AMGSQTKFVQCPDGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVAEWREEG	G <mark>K</mark> AE <mark>VI</mark> PGVLFIDEVH	HMLD <mark>I</mark> ECF <mark>SF</mark> LNRALES <mark>D</mark>	DMAPVLIMATNRGITR	IRGTN.YQSPHGI	PIDLLDRLLIISTSPYS	DKETKQILKIRCEEEDVEM	_MNEDAYTVL
C.carcharias ruvbl2 ruvBlike 2	MATTT.ATKVPEVRDVTRIERIGAHSHIRGLG	LDDALEPRQVSQGMVGQLSARF	R	GVI <mark>LEMIKEGKI</mark> AGRAVLIAG(QPGTGKTAIAMGMAQTLGQDTPF	FTAIA <mark>GSE</mark> IF <mark>SLE</mark> MSKT	EALTQAFRRSIGVRIKEETEI	[I <mark>EGEV</mark> VEIQIDRPATG]	TGAKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GTKMI <mark>ECL</mark> T	KEKVQAGDVITIDKA	.T <mark>G</mark> KISKL <mark>GR</mark> SF <mark>TRA</mark> RDYD	AMGAQTKFVQCPDGELQKR	KEVVHTVTLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVAEWREEG	G <mark>K</mark> AE <mark>II</mark> PGVLFIDEVH	HMLDIECF <mark>SF</mark> LNR <mark>G</mark> LES <mark>D</mark>	DMAPVLIIATNRGITR	IRGTN.YKSPHGI	PIDLLDRLVIISTSPYN	EKETKQILKIRCEEEDVEM	_MSEDAYTVL
X.laevis ruvbl2.S RuvB like AAA ATPase 2 S homeolog	MATMA.ATKVPEVRDVTRIERIGAHSHIRGLG	LDDALEPRQVSQGMVGQLASRF	R	GVI <mark>LEMIKEGKI</mark> AGRAVLIAG(QPGTGKTA <mark>I</mark> AMGMAQALGSDTPF	FTAIA <mark>GSE</mark> IF <mark>SLE</mark> MSKT	EALTQAFRRSIGVRIKEETEI	[I <mark>EGEV</mark> VEVQIDRPATG]	TGAKVGKLT <mark>LKT</mark> TE	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> T	KEKVQAGDVITIDKA	.T <mark>G</mark> KITKL <mark>GR</mark> AF <mark>TR</mark> ARDYD	AMGSQTKFVQCPDGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVAEWREEG	G <mark>K</mark> AE <mark>II</mark> PGVLFIDEVH	HMLDIECF <mark>SF</mark> LNRALES <mark>D</mark>	DMAPVLIMATNRGITR	IRGTN.YQSPHGI	PIDLLDRLLIISTSPYN	EKETKQILKIRCEEEDVDM	MSEDACTVL
X.laevis ruvbl2.L ruvBlike 2	MATMA.ATKVPEVRDVTRIERIGAHSHIRGLG	LDDALEPRQVSQGMVGQLAARF	R	GVI <mark>LEMIKEGKI</mark> AGRAVLIAG(QPGTGKTAIAMGMAQALGSDTPF	FTAIA <mark>GSE</mark> IF <mark>SLE</mark> MSKT	EALTQAFRRSIGVRIKEETEI	[I <mark>EGEV</mark> VEVQIDRPATG]	TGAKVGKLTLKTTE	EMETIYD <mark>L</mark> GTKMI <mark>ESL</mark> T	KEKVQAGDVITIDKA	.T <mark>G</mark> KITKL <mark>GR</mark> AF <mark>TR</mark> ARDYD	AMGSQTKFVQCPDGELQKR	KEVVHTVSLHEIDVI	NSRTQGFLALF.	SGDTG <mark>EI</mark> KSE	VREQINAKVAEWREEG	G <mark>K</mark> AE <mark>II</mark> PGVLFIDEVH	HMLDIECF <mark>SF</mark> L <mark>N</mark> RALES <mark>D</mark>	DMAPVLIMATNRGITR	IRGTN.YQSPHGI	PIDLLDRLLIISTSPYN	EKETKQILKIRCEEEDVDM	MSEDAYTVL
S.townsendi RUVBL1 ruvBlike 1	MKIEEVKST <mark>S</mark> KTQRIAAHSHVKGLG	LDD <mark>SGAAKPAAAGLVGQEN</mark> ARE	E	G <mark>I</mark> IVELIKSKKMAGRAVLLAGI	PPGTGKTALALAIAQELG <mark>S</mark> KVPF	F <u>CPMV</u> GSE <u>VY</u> S <mark>T</mark> EIKKT	'EVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKTISHVIIGLKTAP	KGTKQLK	 				RPCGGIAIKN	I <mark>T</mark> SL		 		TINMSFSACL	CRGTEDIISPHGI	PLDLLDRVMIIRTMLYT	PQEMKQIIKLRAQTEGINI	ISEEALNHL
	MKIEEVKST <mark>S</mark> KTQRIAAHSHVKGLG	LD <mark>ES</mark> GTAK <mark>P</mark> AGAGLVGQE <mark>N</mark> ARE	EVSEGPCLALPRADGEPRGQARA <mark>A</mark> (CGVIVELIKSKKMAGRAVLLAGI	PPGTGKTALALAIAQELG <mark>S</mark> KVPF	FCPMVGSEVYS <mark>T</mark> EIKKT	EVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKT <mark>I</mark> SHVIIGLKT <mark>A</mark> F	KGTKQLK <mark>LDPSIF</mark> ESLQ	KERVE <mark>T</mark> GDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>Y</mark> ATEFD	LEA EEYVPLPKGDVHKK	KEIIQDVTLHDLDVA	NARPQGGQDILS	SMMGQLMKPKKTEITDK	LR <mark>G</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>I</mark> AELVPGVLF <mark>V</mark> DEVH	HMLDIECFTYLHRALES <mark>S</mark>	SISPIVIFASNRGNCV	IRGTED <mark>VV</mark> SPHG1	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIK <mark>L</mark> RAQTEGINI	ISEEALNHL
F.catus RUVBL1 ruvBlike 1 isoform X1	MKIEEVKSTTKTQRIA <mark>S</mark> HSHVKGLG	ILD <mark>ESGL</mark> AKQA <mark>AS</mark> GLVGQE <mark>N</mark> ARE	E	CGVIVELIKSKKMAGRAVLLAGI	PPGTGKTALALAIAQELG <mark>S</mark> KVPF	FCPMVGSEVYS <mark>T</mark> EIKKT	CEVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKTISHVIIGLKTA	KGTKQLKLDPSI <mark>F</mark> ESLQ	KERVEAGDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>Y</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>II</mark> QDVTLHDLDV <mark>A</mark>	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>G</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>I</mark> AELVPGVLF <mark>V</mark> DEVH	HMLDIECFTYLHRALES <mark>S</mark>	SI <mark>A</mark> PIVIFA <mark>S</mark> NRGNC <mark>V</mark>	IRGTED <mark>IT</mark> SPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIKĪRAQTEGINI	ISEEALNHL
	MKIEEVKST <mark>S</mark> KTQRIAAHSHVKGLG	LDESG <mark>a</mark> ak <mark>pagaglvgqen</mark> are	E	CGVIVELIKSKKMAGRAVLLAGI	PPGTGKTALALAIAQELG <mark>S</mark> KVPF	FCPMVGSEVYS <mark>T</mark> EIKKT	CEVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKTISHVIIGLKTA	KGTKQLKLDPSI <mark>F</mark> ESLQ	KERVEAGDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>Y</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>II</mark> QDVTLHDLDV <mark>A</mark>	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>G</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>I</mark> AELVPGVLF <mark>V</mark> DEVH	HMLDIECFTYLHRALES <mark>S</mark>	SIAPIVIFA <mark>S</mark> NRGNC <mark>I</mark>	IRGTED <mark>IV</mark> SPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIK <mark>L</mark> RAQ I EGINI	ISEEALNHL
X.laevis ruvbl1.L ruvBlike 1	MKIEEVKSTTKTQRIAAHSHVKGLG	LDEN <mark>GMAKQAAAGLVGQEN</mark> ARE	E	CGVIVELIKSKKMAGRAVLLAGI	PPGTGKTALALAIAQELG <mark>N</mark> KVPF	FCPMVGSEVYS <mark>T</mark> EIKKT	EVLMENFRRAIGLRI <mark>R</mark> ETKEV	YEGEVTELTPCETENPMGGY	YGKTISHVIIGLKTA	KGTKQLKLDPSI <mark>Y</mark> ESLQ	KERVE <mark>V</mark> GDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>Y</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>VI</mark> QDVTLHDLDV <mark>A</mark>	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>G</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>I</mark> AELVPGVLF <u>I</u> DEVH	HMLDIECFTYLHRALES <mark>S</mark>	SLAPIVIFATNRGNC <mark>I</mark>	IRGTED VASPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIKĪRAQTEGINI	ISEEALNHL
D.rerio ruvbl1 ruvBlike 1	MKIEEVKSTTKTQRIA <mark>S</mark> HSHVKGLG	LD <mark>EAGN</mark> AKQ <mark>SAS</mark> GLVGQE <mark>S</mark> ARE	E	G <mark>IIT</mark> ELI <mark>R</mark> SKKMAGRA <mark>I</mark> LLAGI	PPGTGKTALALA <mark>M</mark> AQELG <mark>N</mark> KVPF	FCPMVGSEVYS <mark>S</mark> EIKKT	CEVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKTISHVIIGLKTA	KGTKQLKLDPSI <mark>Y</mark> ESLQ	KERVE <mark>V</mark> GDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>F</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>II</mark> QDVTLHDLDV <mark>A</mark>	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>G</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>V</mark> AELVPGVLFIDEVH	HMLDIECFTYLHRALES <mark>S</mark>	SIAPIV <mark>V</mark> FASNRGNC <mark>L</mark>	IRGTED <mark>IS</mark> SPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIKIRAQTEG <mark>L</mark> NI	ISEEALSHL
E.caballus RUVBL1 ruvBlike 1	MKIEEVKSTTKTQRIA <mark>S</mark> HSHVKGLG	LD <mark>ESGL</mark> AKQ <mark>aas</mark> glvgqe <mark>n</mark> are	E	CGVIVELIKSKKMAGRAVLLAGI	PPGTGKTALALA <mark>T</mark> AQELG <mark>S</mark> KVPF	FCPMVGSEVYS <mark>T</mark> EIKKT	TEVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKT <mark>I</mark> SHVIIGLKT <mark>A</mark> F	KGTKQLKLDPSI <mark>F</mark> ESLQ	KERVE <mark>A</mark> GDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>Y</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>II</mark> QDVTLHDLDV <mark>A</mark>	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>G</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>I</mark> AELVPGVLF <mark>V</mark> DEVH	HMLDIECFTYLHRALES <mark>S</mark>	SIAPIV <mark>I</mark> FA <mark>S</mark> NRGNC <mark>V</mark>	IRGTED <mark>IT</mark> SPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIKIRAQTEG <u>I</u> NI	ISEEALNHL
X.laevis ruvbl1.S ruvBlike 1	MKIEEVKSTTKTQRIA <mark>T</mark> HSHVKGLG	LDENGIAKQA <mark>AA</mark> GLVGQE <mark>N</mark> ARE	E	CGVIVELIKSKKMAGRAVLLAGI	PPGTGKTALALAIAQELG <mark>N</mark> KVPF	FCPMVGSEVYS <mark>T</mark> EIKKT	EVLMENFRRAIGLRI <mark>R</mark> ETKEV	YEGEVTELTPCETENPMGGY	YGKTISHVIIGLKTA	KGTKQLKLDPSI <mark>Y</mark> ESLQ	KERVE <mark>V</mark> GDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>Y</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>VI</mark> QDVTLHDLDV <mark>A</mark>	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>A</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>I</mark> AELVPGVLF <u>I</u> DEVH	HMLDIECFTYLHRALES <mark>S</mark>	SLAPIVIFATNRGNC <mark>I</mark>	IRGTED VASPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIKIRAQTEGINI	ISEEALNHL
G.aculeatus ruvbl1 ruvBlike 1 isoform X1	MKIEEVKSTTKTQRIA <mark>T</mark> HSHVKGLG	LD <mark>EAGN</mark> AKQ <mark>SAC</mark> GLVGQEAARE	E	G <mark>I</mark> IVELI <mark>R</mark> SKKMAGRAVLLAGI	PPGTGKTALALA <mark>V</mark> AQELG <mark>N</mark> KVPF	FCPMVGSEVYS <mark>S</mark> EIKKT	CEVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKT <mark>I</mark> SHVIIGLKT <mark>G</mark> F	KGTKQLKLDPSI <mark>Y</mark> ESLQ	KERVE <mark>V</mark> GDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>F</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>IV</mark> QDVTLHDLDV <mark>S</mark>	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>A</mark> EINKVVN <mark>R</mark> YIDQG	G <mark>V</mark> AELVPGVLF <mark>V</mark> DEVH	HMLDIECFTYLHRALES <mark>T</mark>	TIAPIV <mark>V</mark> FASNRGNC <mark>L</mark>	IRGTED <mark>IS</mark> SPHGI	[PLDLLDRVMIIRTMLY <mark>K</mark>	<mark>S</mark> QE <mark>T</mark> KQIIKIRAQTEGINI	ISEDALTHL
S.salar ruvbl1 ruvBlike 1	MKIEEVKSTTKTQRIA <mark>S</mark> HSHVKGLG	LDDAG <mark>n</mark> akq <mark>nas</mark> glvgqe <mark>t</mark> are	E	G <mark>I</mark> IVELI <mark>R</mark> SKKM <mark>S</mark> GRAVLLAGI	PPGTGKTALALA <mark>M</mark> AQELG <mark>N</mark> KVPF	FCPMVGSEVYS <mark>S</mark> EIKKT	CEVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKT <mark>I</mark> SHVIIGLKT <mark>G</mark> F	KGTKQLKLDPSI <mark>Y</mark> ESLQ	KERVEAGDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>F</mark> ATEFD	LEAEEYVPLPKGDVHKK	KEIIQDVTLHDLDIA	NARPQGGQ <mark>D</mark> ILS	SMMGQLMKPKKTEITDK	LR <mark>A</mark> EINKVVN <mark>R</mark> YIDQG	G <mark>V</mark> AELVPGVLF <mark>V</mark> DEVH	HMLDIECFTYLHRALES <mark>T</mark>	TIAPIV <mark>V</mark> FASNRGNC <mark>L</mark>	IRGTED <mark>IS</mark> SPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIKIRAQTEGINI	ISEEALSHL
X.laevis ruvbl1.S ruvBlike 1 G.aculeatus ruvbl1 ruvBlike 1 isoform X1 S.salar ruvbl1 ruvBlike 1 C.carcharias ruvbl1 ruvBlike 1	MKIEEVKSTTKTQRIA <mark>S</mark> HSHVKGLG	LD <mark>ESGL</mark> AK <mark>V</mark> AAAGLVGQENARE	E	CG <mark>I</mark> IVELIKSKKM A GRAVLLAGI	PPGTGKTALALA <mark>I</mark> AQELG <mark>N</mark> KVPF	FCPMVGSEVYS <mark>S</mark> EIKKT	TEVLMENFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKT <mark>V</mark> SHVIIGLKT <mark>A</mark> F	KGTKQLKLDPSI <mark>Y</mark> ESLQ	KERVE <mark>V</mark> GDVIYIE <mark>A</mark> N	SGAVKRQGRCDT <mark>Y</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>IIQDVTLHDLDV</mark> A	NARPQGGQDILS	SMMGQLMKPKKTEITDK	LR <mark>G</mark> EINKVVN <mark>K</mark> YIDQG	G <mark>I</mark> AELVPGVLF <u>I</u> DEV <mark>F</mark>	PMLDIECFTYLHRALES <mark>S</mark>	SIAPIVIFATNRGNC <mark>V</mark>	VRGTEDIVSPHGI	PLDLLDRVMIIRTMLYT	P <mark>DEMM</mark> QIIKIRAQTEGI <mark>S</mark> I	ISEDALLHL
S.salar ruvb1 RuvBlike 1	MKIEEVKSTTKTQR <mark>V</mark> A <mark>S</mark> HSHVKGLG	LD <mark>eagnakQnas</mark> glvgQeaare	E	CG <mark>IIVELIR</mark> SKKM <mark>S</mark> GRAVLLAGI	PPGTGKTALALA <mark>M</mark> AQELG <mark>N</mark> KVPF	FCPMVGSEVYS <mark>S</mark> EIKKT	<u>TEVLME</u> NFRRAIGLRIKETKEV	YEGEVTELTPCETENPMGGY	YGKT <mark>I</mark> SHVIIGLKT <mark>G</mark> F	KGTKQLKLDPSI <mark>Y</mark> ESLQ	KERVEAGDVIYIE <mark>S</mark> N	SGAVKRQGRCDT <mark>F</mark> ATEFD	LEAEEYVPLPKGDVHKK	KE <mark>IIQDVTLHD</mark> LD <mark>I</mark> A	NARPQGGQDILS	MMGQLMKPKKTE ITDK	<u>LR<mark>AE</mark>INKVVN</u> RYIDQG	G <mark>v</mark> aelvpgvlf <mark>v</mark> devf	HMLDIECFTYLHRALES <mark>T</mark>	TIAPIV <mark>V</mark> FASNRGNC <mark>L</mark>	IRGTED IS SPHGI	PLDLLDRVMIIRTMLYT	PQE <mark>M</mark> KQIIKIRAQTEGINI	ISEEALSHL
consensus	*!**!******	<u> </u>	* !>	<u>: </u> ***!*!******!!!*!*!!	*!!!!!!!*!** <mark>*!</mark>	!****!!! * *!	!*!***!!** <mark>!!*!!*!</mark> *	<*!!!!*!********!**! >	*!** *****!!! >	*********	*******	******	*** ********	**********	**!**!** ***	*******	** ***** ****	* ** * *******	******	*******	*!!!** !!!!!	!*!*!!!**!**!*	*** *!!***!***!	**!*!***!

H.sapiens RUVBL1 ruvBlike 1 isoform X1	GEIGTKTTLRSHDSMNMLVQLIWKPAAFKYHLIVSTQYDDSAPHRV.GDCTQGILKLKSRPWKLPGVGSGHTWK	467
G.aculeatus ruvbl2 ruvBlike 2	TRIGMETSLRYAIQLISTAGLVCRKRKGTEVQVEDIKRVYSLFLDETRSSQYMKECQDSFLFNETQTPSMDTS TRIGQETSLRYAIQLISTAGLVCRKRRGTEVQVEDIKRVYSLFLDEARSSQYMKEYQDSFLFNETQTSQMDTS TRIGQETSLRYAIQLISTAGLVCRKRRGTEVQVEDIKRVYSLFLDEARSSQYMKEYQDSFLFNETQTSQMDTS	459
D.rerio ruvbl2 ruvBlike 2	TRIGQETSLRYAIQLISTAGLVCRKRRGTEVQVEDIKRVYSLFLDEARSSQYMKEYQDSELFNETQTSQMDTS	463
D.rerio ruvbl2 ruvBlike 2 dupelabel1	TRIGQETSLRYAIQLISTAGLVCRKRRGTEVQVEDIKRVYSLFLDEARSSQYMKEYQDSELFNETQTSQMDTS	463
H.sapiens RUVBL2 ruvBlike 2 isoform 1	TRIGLEDSIRYAIQLIDAASLVCRKRKGTEWQVDDLKRVYSLELDESRSTQYMKEYQDALLFNELKGETMDTS	463
E.caballus RUVBL2 ruvBlike 2 isoform X1	TRIGLETSLRYAIOLITAASLVCRKRKGTEVQVDDIKRVYSLFLDESRSTQYMKEYODAFLFNELKGETMDTS	463
F.catus RUVBL2 ruvBlike 2 isoform X1	TRIGLETSLRYAIQLITAASLVCRKRKGTEVQVDDIKRVYSLFLDESRSTQYMKEYQDAFLFNELKGETMDTS	463
S.salar ruvbl2 ruvBlike 2	TRIGOETSLRYAIOLISTAGLVCRKRRGTEVQVEDIKRVYSLFLDESRSSQYMKEYQDSELFNETTQPTMDTS	463
S.townsendi RUVBL2 ruvBlike 2	TRIGLETSLRYAIQLITAASLVCRKRKGTEVQVDDIKRVYSLFLDESRSTQYMKEYQDAFMFNELKGETMDTS TRIGLETSLRYSIQLITAANLVCKKRKGTEVQVDDIKRVYSLFLDESRSTQYMKEYQDAFMFNEMKGESMDTT	462
C.carcharias ruvbl2 ruvBlike 2	TR <mark>IGLETSLRYSIQLITAANL</mark> VCKKRKGTE <mark>V</mark> QVDDIKRVYSLFL <mark>D</mark> ESR <mark>STQYMKEYQDAFM</mark> FNEMKGESMDTT	462
X.laevis ruvbl2.S RuvB like AAA ATPase 2 S homeolog	TRIGLETSLRYSMQLITAASLVCRKRKGTEVQVDDIKRVYSLFLDESRSTQYMKEYQDAFMFN. EMKTDTMDTS TRIGLETSLRYSMQLITAASLVCRKRKGTEVQVDDIKRVYSLFLDESRSTQYMKEYQDAFMFN. EMKTDTMDTS GEIGTKTTLRYAVQLLTPANLLAKINGKDSIEKEHVEEINELFYDAKSSAKILADQQEKYMK. GDIGTKTTLRYAVQLLTPANLLAKINGKDSIEKEHIEEINELFYDAKSSAKILADQQEKYMK. GEIGTKTTLRYSVQLLTPANLLAKINGKDSIEKEHVEEISELFYDAKSSAKILADQQDKYMK. GEIGNKTTLRYSVQLLTPANLLAKINGKDSIEKEHVEEISELFYDAKSSAKILADQQDKYMK. GEIGNKTTLRYAVQLLTPANLLAKINGKDSIEKEHIEEINELFYDAKSSAKILADQQDKYMK. GEIGNKTTLRYAVQLLTPANLLAKINGKDSIEKEHIEEINELFYDAKSSAKILADQQEKYMK.	462
X.laevis ruvbl2.L ruvBlike 2	TR <mark>IGLETSLRYSMQLITAASL</mark> VCRKRKGTE <mark>V</mark> QVDDIKRVYSLFLDESR <mark>S</mark> TQYMKEYQDAFMFNEMKTDTMETS	462
S.townsendi RUVBL1 ruvBlike 1	GEIGTKTTLRYAVQLLTPANLLAKINGKDSIEKEHVEEINELFYDAKSSAKILADQQEKYMK	313
G.gallus RUVBL1 ruvBlike 1 isoform X1	GDIGTKTTLRYA <mark>V</mark> QLLTPA <mark>N</mark> LLAKINGKDSIE <mark>K</mark> EHIEEINELFYDAKSSAK <mark>IL</mark> ADQQEK <mark>Y</mark> MK	478
F.catus RUVBL1 ruvBlike 1 isoform X1	GEIGTKTTLRYSVQLLTPANLLAKINGKDSIEKEHVEEISELFYDAKSSAKILADQQDKYMK	456
C.mydas RUVBL1 ruvBlike 1 X.laevis ruvbl1.L ruvBlike 1	GEIGNKTTLRYA <mark>V</mark> QLLTPANLLAKINGKDSIE <mark>K</mark> EHIEEINELFYDAKSSAK <mark>IL</mark> ADQQEK <mark>Y</mark> MK	456
	GEIGTKTTLRYSVQLLTPANLLAKINGKDSIEKEHVEEISELFYDAKSSAKILAEQQEKFMK	456
D.rerio ruvbl1 ruvBlike 1	GEIGTKTTLRYSVQLLTPANLLAKINGKDSIEKEHVEEISELFYDAKSSAKILAEQQEKFMK GEIGTKTTLRYAVQLLTPASLLARVQGREVVEKEHVEEINELFYDAKSSAKILQDQHTKFMK	456
E.caballus RUVBL1 ruvBlike 1	GETGTKTTLRYSVOLLTPAHLLAKINGKDGIEKEHVEETSELFYDAKSSAKIDADQQDKYMK	456
X.laevis ruvbl1.S ruvBlike 1	GEIGTKTTLRYSVOLLTPANLLAKINGKDSIEKEHVEEINELFYDAKSSAKILAEQOEKFMKAEIGTKTTLRYAVOLLTPASLLGRVOGKENVEREQVEEINELFYDAKSSAKILODOHLKFMK	456
G.aculeatus ruvbl1 ruvBlike 1 isoform X1	<u>A</u> EIGTKTTLRYA <mark>V</mark> QLLTPA <mark>S</mark> LLGRVQGKENVER <mark>EQVEEINE</mark> LFYDAKSSAK I LQDQHLKFMK	456
S.salar ruvbl1 ruvBlike 1	GEIGTKTTLRYAAQLLTPASLLGRVQGKEVVEREQVEEINELFYDAKSSAKILQDQQHKFMK	456
C.carcharias ruvbl1 ruvBlike 1	GEIGTKTTLRYSVQLLTPANLL <mark>AKINGKDSIEK</mark> EHVEEINELFYDAKSSAKVL <mark>AEHQEKY</mark> MK	456
S.salar ruvb1 RuvBlike 1	GEIGTKTTLRYSVOLLTPANLLAKINGKDSIEKEHVEEINELFYDAKSSAKVLAEHQEKYMK GEIGTKTTLRYAAQLLTPASLLGRVQGKEGVEREQVEEINELFYDAKSSAKILQDQQHKYMK	456
consensus	**!!**!*!!** ***** !* * * * * * * * * *	

f X non-conserved f X $\geq 50\%$ conserved