

Trl

3L GAGA

DmelF	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
DmelA	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
DmelG	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
DmelD	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dsec	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
DmelC	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dyak	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dere	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dmell	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dsim	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
DmelB	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
DmelE	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
DmelH	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dana	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dpse	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dwil	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dvir	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dgri	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50
Dmoj	MSL PMNSLYSLTWGDYGTSLVSAI	QLLRCHGDLVDCTLAAGGRSFPAHKI	50



Trl

3L GAGA

DmelF	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
DmelA	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
DmelG	VLCAASPFLLDLLK-----	64
DmelD	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dsec	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
DmelC	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dyak	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dere	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dmell	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dsim	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
DmelB	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
DmelE	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
DmelH	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dana	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dpse	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dwil	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dvir	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dgri	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDHA	100
Dmoj	VLCAASPFLLDLLKNTPCCKHPVVMLAGVNANDLEALLEFVYRGEVSVDH	100

G

# Trl

3L GAGA

DmelF	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
DmelA	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
DmelG	- - - - - AAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	107
DmelD	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dsec	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
DmelC	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dyak	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dere	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dmell	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dsim	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
DmelB	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
DmelE	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
DmelH	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dana	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dpse	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dwil	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQL	L AT	150
Dvir	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150
Dgri	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHE	QDQLI AT	150
Dmoj	QLPSLLQAAQCLNI	QGLAPQTVTKDDYTTHSI	QLQHMI	PQHHDQDQLI	AT	150

# Trl

3L GAGA

DmelF	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
DmelA	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
DmelG	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	157
DmelD	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dsec	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
DmelC	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dyak	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dere	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dmell	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dsim	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
DmelB	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
DmelE	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
DmelH	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dana	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dpse	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dwil	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	T	G	Q	L	L	Q	A	T	T	Q	T	N	A	V	G	Q	Q	Q	T	I	V	T	T	D	A	A	K	H	D	Q	A	200
Dvir	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	H	Q	Q	T	I	V	T	A	D	A	S	K	H	D	Q	A	200
Dgri	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	H	Q	Q	T	I	V	T	A	D	T	S	K	H	D	Q	A	200
Dmoj	I	A	T	A	P	Q	Q	T	V	H	A	Q	V	V	E	D	I	H	H	Q	G	Q	I	L	Q	A	T	T	Q	T	N	A	A	G	H	Q	Q	T	I	V	T	A	D	T	S	K	H	D	Q	A	200

# Trl

3L GAGA

DmelF	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
DmelA	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
DmelG	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	205
DmelD	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
Dsec	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
DmelC	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
Dyak	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	E	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
Dere	VI	Q	S	F	L	P	A	R	K	R	K	P	R	A	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	E	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
Dmell	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
Dsim	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
DmelB	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
DmelE	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
DmelH	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	S	V	Q	-	-	248
Dana	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	N	K	K	S	P	T	A	S	K	I	S	K	V	D	G	M	D	T	I	M	G	T	P	T	S	S	H	G	S	G	-	-	-	-	245	
Dpse	VI	Q	A	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	V	E	G	M	D	T	I	I	G	T	P	T	S	S	H	G	G	G	V	V	Q	Q	250	
Dwil	VI	Q	A	F	L	P	A	R	K	R	K	P	R	G	K	K	M	S	P	T	A	P	K	I	S	K	V	D	G	M	D	T	I	M	G	T	P	T	S	S	H	S	A	A	G	G	Q	Q	V	250
Dvir	VI	Q	S	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	S	A	P	K	V	P	K	I	E	G	M	D	T	I	M	G	T	P	T	S	S	Q	L	A	A	Q	Q	Q	Q	250	
Dgri	VI	Q	S	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	S	K	I	E	G	M	D	T	I	M	G	T	P	T	S	S	H	A	A	A	Q	Q	Q	Q	250	
Dmoj	VI	Q	S	F	L	P	A	R	K	R	K	P	R	V	K	K	M	S	P	T	A	P	K	I	T	K	I	E	G	M	G	T	I	M	D	T	P	T	S	H	L	T	G	-	-	Q	Q	Q	248	

# Trl

3L GAGA

DmelF	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
DmelA	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
DmelG	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	250		
DmelD	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
Dsec	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
DmelC	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
Dyak	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
Dere	-	-	-	-	-	QVL	G	ENGAE	G	QLL	T	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
Dmell	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
Dsim	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
DmelB	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
DmelE	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
DmelH	-	-	-	-	-	QVL	G	ENGAE	G	QLL	S	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	293		
Dana	-	-	-	-	-	QVL	G	ENGAE	G	QLL	T	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	290		
Dpse	-	-	-	Q	-	QVL	G	ENGSE	G	QML	T	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	296		
Dwil	Q	V	Q	Q	-	QVL	S	ENGAE	S	QL	I	TSTPI	I	KSEGQK	A	ETI	VTMDPNNMI	PVTSANA	299
Dvir	V	V	Q	Q	Q	QVL	D	ENGAET	Q	LL	T	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	300		
Dgri	V	V	Q	Q	Q	QVL	D	ENGAET	Q	LL	S	TPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	300		
Dmoj	V	V	Q	Q	Q	QVL	D	ENGAET	Q	LL	T	STPI	I	KSEGQKVETI	VTMDPNNMI	PVTSANA	298		

3L GAGA

DmelF	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
DmelA	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
DmelG	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	299
DmelD	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
Dsec	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
DmelC	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
Dyak	ATGEITTAQGA	TGSSGGNTTSGLS	TPKAKRAKHPPGSEKPRSRSQSEQP	342
Dere	ATGEITTAQGA	TGSSGGNTTGGLS	TPKAKRAKHPPGSDKPRSRSQSEQP	342
Dmell	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
Dsim	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
DmelB	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
DmelE	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
DmelH	ATGEITPAQGA	TGSSGGNTSGVLS	TPKAKRAKHPPGTEKPRSRSQSEQP	342
Dana	ATGEITTAQGST	SSGGNTSGVSS	TPKAKRTKHPPGTDKPRSRSQSEQP	338
Dpse	ATGEITTAATGTT	GTSSGGNTSGTTS	TPKTKRTKHPPGTEKPRSRSQSEQP	345
Dwil	T	TGEITTAAGTTVTP	SAGSGTTS	349
Dvir	ATGEITTAASGTTVTP	GASGTTATP	- - - KAKRTKHPPGTEKPRSRSQSEQP	347
Dgri	ATGEITTAASGTTVTP	SASGTTATP	- - - KAKRTKHPPGTEKPRSRSQSEQP	347
Dmoj	ATGEITTAASGATVT	TGTGTTATP	- - - KAKRTKHPPGTEKPRSRSQSEQP	345

# Trl

3L GAGA

DmelF	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGVKKEKK	T	T	SGKK	S	S	SG	S	S	GS	G	392
DmelA	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGVKKEKK	T	T	SGKK	S	S	SG	S	S	GS	G	392
DmelG	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	329
DmelD	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	372
Dsec	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGVKKEKK	T	T	SGKK	S	S	SG	S	S	GS	G	392
DmelC	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	372
Dyak	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGVKKEKK	T	I	SGKK	S	S	SG	S	S	GS	G	392
Dere	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGVKKEKK	I	I	SGKK	S	S	SG	S	S	GS	G	392
Dmell	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGVKKEKK	T	T	SGKK	S	S	SG	S	S	GS	G	392
Dsim	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	372
DmelB	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	372
DmelE	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	372
DmelH	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	372
Dana	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	368
Dpse	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGVKKEKK	T	S	SGKK	S	G	SG	T	S	GS	G	395
Dwil	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	379
Dvir	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGI	K	K	KEKK	T	P	SGKK	P	G	GS	T	397
Dgri	ATCPI	CYAVI	RQSRNL	RRHLEL	RHF	AKPGV	-	-	-	-	-	-	-	-	-	-	377
Dmoj	ATCPI	CYAI	I	RQSRNL	RRHLEL	RHF	AKPGI	-	-	-	-	-	-	-	-	-	375





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Species	Sequence	Length
DmelF	QQQQQQQ <span style="border: 1px solid black;">QQQQQQ</span> QQQQQAMT V S GAT GGQVQQQVQ <span style="border: 1px solid black;">QVQQQ</span> V <span style="border: 1px solid black;">QQ</span> <span style="border: 1px solid black;">Q</span> QQQQQQQQ	477
DmelA	QQQQQQQ <span style="border: 1px solid black;">QQQQQQ</span> QQQQQAMT V S GAT GGQVQQQVQ <span style="border: 1px solid black;">QVQQQ</span> V <span style="border: 1px solid black;">QQ</span> <span style="border: 1px solid black;">Q</span> QQQQQQQQ	477
DmelG	- - - - -	329
DmelD	- - - - -	372
Dsec	QQQQQQQ <span style="border: 1px solid black;">QQQQQQ</span> QQAMT V S G- - AT V GGQVQQQVQ <span style="border: 1px solid black;">QVQQQ</span> V <span style="border: 1px solid black;">QQ</span> <span style="border: 1px solid black;">Q</span> QQQQQQQQ	475
DmelC	- - - - -	372
Dyak	QQQQQQQ <span style="border: 1px solid black;">QQQQQQ</span> Q- - - AMT V S GAT GGQVQQQVQ <span style="border: 1px solid black;">QVQQQ</span> V <span style="border: 1px solid black;">QQ</span> <span style="border: 1px solid black;">Q</span> QQ- - - -	469
Dere	QQQQQQQ <span style="border: 1px solid black;">QQQQQQ</span> - - - - AMT V S GAA GGQVQQQVQ <span style="border: 1px solid black;">QVQQQ</span> V <span style="border: 1px solid black;">QQ</span> <span style="border: 1px solid black;">Q</span> QQ- - - -	467
Dmell	QQQQQQQ <span style="border: 1px solid black;">QQQQQQ</span> QQQQQAMT V S GAT GGQVQQQVQ <span style="border: 1px solid black;">QVQQQ</span> V <span style="border: 1px solid black;">QQ</span> <span style="border: 1px solid black;">Q</span> QQQQQQQQ	477
Dsim	- - - - -	372
DmelB	- - - - -	372
DmelE	- - - - -	372
DmelH	- - - - -	372
Dana	- - - - -	368
Dpse	QQQQQQQ <span style="border: 1px solid black;">QQQQQQ</span> QQQQQQQQQQPT MT V T T T S SGG <span style="border: 1px solid black;">QVQQQ</span> QQ <span style="border: 1px solid black;">QQ</span> <span style="border: 1px solid black;">Q</span> QQVQVQQ	495
Dwil	- - - - -	379
Dvir	- - - - - <span style="border: 1px solid black;">QQQQQQ</span> QQQQQQQQQQQQT MT V T T T A GGG <span style="border: 1px solid black;">QVQQQ</span> QV <span style="border: 1px solid black;">QQ</span> V <span style="border: 1px solid black;">Q</span> VQQQQPL	480
Dgri	- - - - -	377
Dmoj	- - - - -	375

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Species	Sequence	Length
DmelF	QL QHHQI I DS SGNIT TAT TTS A QAAAAAQQ QAAG QQQQL V AQ SDGSESGA P	527
DmelA	QL QHHQI I DS SGNIT TAT TTS A QAAAAAQQ QAAG QQQQL V AQ SDGSESGA P	527
DmelG	- - - - -	329
DmelD	- - - - -	372
Dsec	QL QHHQI I DS SGNIT TAT TTS A QAAAAAQQ QAAG QQQQL V AQ SDGSESGA P	525
DmelC	- - - - -	372
Dyak	- L QHHQI I DS SGNIT TAT TTS A QAAAAAQQ QAAG QQQQL V AQ SDGSESGA P	518
Dere	- L QHHQI I DS SGNIT TAT TTS A QAAAAAQQ QAAG QQQQL V AQ SDGSESGA P	516
Dmell	QL QHHQI I DS SGNIT TAT TTS A QAAAAAQQ QAAG QQQQL V AQ SDGSESGA P	527
Dsim	- - - - -	372
DmelB	- - - - -	372
DmelE	- - - - -	372
DmelH	- - - - -	372
Dana	- - - - -	368
Dpse	QL QHHQI I DS SGNIT TAT TS - A QAAA V QQ QAAG QQQQL V AQA ADGSESGA P	544
Dwil	- - - - -	379
Dvir	QHHQI I DSSGN MTT P T T S A QAAA QQQA NN QQQQ QQQQL V AQ SDGSESGT P	530
Dgri	- - - - -	377
Dmoj	- - - - -	375

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Species	Sequence	Position
DmelF	L S I A Q V Q T L Q G H Q I I G N L N Q V N I T D F	553
DmelA	L S I A Q V Q T L Q G H Q I I G N L N Q V N I T D F	553
DmelG	- - - - -	329
DmelD	- - - - -	372
Dsec	L S I A Q V Q T L Q G H Q I I G N L N Q G N - - -	547
DmelC	- - - - -	372
Dyak	L S I A Q V Q T L Q G H Q I I G N L N Q G N - - -	540
Dere	L S I A Q V Q T L Q G H Q I I G N L N Q G N - - -	538
Dmell	L S I A Q V Q T L Q G H Q I I G N L N Q G N - - -	549
Dsim	- - - - -	372
DmelB	- - - - -	372
DmelE	- - - - -	372
DmelH	- - - - -	372
Dana	- - - - -	368
Dpse	M S I A Q V Q T L Q G H Q I I G N L N Q G N - - -	566
Dwil	- - - - -	379
Dvir	L S I A Q V Q T L Q G H Q I I G N L N Q G N - - -	552
Dgri	- - - - -	377
Dmoj	- - - - -	375