

	1	10	20
Prupe.2G167000.1MDRRD.....PMA	LSG.SASYFTSRG.....	LTQSGLHGS
Prupe.5G037000.1MDSREVPQQQQPPP	PPQQQSMVGPSPSYQT...	SMPSNLPNSGPMGGP
Prupe.5G098800.1MDGRE.....AMG	LSG.SAQYYIHRGGVGGSM	PGS...QAGGLHTP
Prupe.5G005600.1	MSGSETGVMTSRB.....	PFSVGLQKSLQSQAA...	AIQNMRLLNFSPDGSAA

	30	40	50	60	70	
Prupe.2G167000.1	QGL...IHP	LSNPNTAFQSN	LGGGNI	GSALP...IE	PSSGITP...H	GVNVGVP
Prupe.5G037000.1	NPARFPFNAV	PPQPPQQQPTTSKP	QMDSLSP...	SPYDGS	LRFCGSGG	CFSIDSS...
Prupe.5G098800.1	PG...FRH	MSNTVLQPPQSN	VRVSV	VGSTFS...VE	PS...REN	FPHHGLSMNV
Prupe.5G005600.1	AALYKPVAAT	TSPTYQSAA	AGGSA	VPFLAAGEGSP	GAAVMA	APAAAGLNMNM...

	80	90	100	110
Prupe.2G167000.1	GEVVKRKRGRPRKY	GP	PDGTVSL	LS
Prupe.5G037000.1	ASAAKKKRGRPRKY	SP	PDGNIAL	LGLAP
Prupe.5G098800.1	GEVVKRKRGRPRKY	GP	PDGTVSL	LS
Prupe.5G005600.1	SEPMKRKRGRPRKY	GP	PDGTVSL	LS

	120	130	140	150	160	170
Prupe.2G167000.1	.KRG	RGRPPSGKKQL	ASLG	ELLSG	SAGMGFTPHIITIA	MGEDIA
Prupe.5G037000.1	.KKN	RGRPPSGKKQL	DALG...	AGGVGFTPHVIMVQ	AGEDIA	AAKVMFS
Prupe.5G098800.1	.KRS	RGRPPSGRKQL	ATLG	DWMNT	SAGLAFAPHVITIG	AGEDIA
Prupe.5G005600.1	IKA	RGRPPSGTKKQL	DALG...	SVGF	GFSPHVITVK	AGEDVSAKIMFS

	180	190	200	210	220	230
Prupe.2G167000.1	CILSANGAVSTVTLRQP	STSG	GTVTYEGRFEI	ILCLSGSYLLTES	SGSRNR	TGGLSVSLAS
Prupe.5G037000.1	CILSANGAICNVTLRQP	AMSG	GTVTYEGRFEI	ILCLSGSYLLTES	SGSRNR	TGGLSVSLAG
Prupe.5G098800.1	CILSGSGTASSVTLRQP	PASTG	SVTEGRFQIL	CLSGSYLLVAED	GGPRNR	TGGISVSLSS
Prupe.5G005600.1	CILSANGAISNVTLRQP	ATSG	GTVTYEGRFEI	ILCLSGSYLLTES	SGSRNR	TGGLSVSLSG

	240	250	260	270	280	290
Prupe.2G167000.1	PDGRVIGGGVGGMLIAAS	PPVQVIVGSFI	WSSSKTK	SKKREAVEGATDLDH	QTV	DNSVALN
Prupe.5G037000.1	SDGQVLGGGVAGMLVAAS	PPVQVIVGSFI	ADGKKNS	NFLKS..GPSSPPPS	QMLN	FGAPM
Prupe.5G098800.1	PDGRVIGGAVA.MLIAAT	PPVQVIVGSFI	YGGSKTK	NKQVAGPNSDENSEP	QH.NEKL	LALP
Prupe.5G005600.1	PDGRVIGGGVAGMLIAAS	PPVQVIVGSFI	ADGRKEPK	TTNQL..EPVAP...	KLAPSS	GPT

	300	310	320	330
Prupe.2G167000.1	SISQDQSLSDSA	SLAAWQAS	RPLD....IR	NTH.VDIDL
Prupe.5G037000.1	TAASPSSQGASS	ESSDENSGS	PLNRGPVLYNNAS.	QPIHNM
Prupe.5G098800.1	SNTPPTQNYNPS	GAGIWPGR	QVD....LR	NPH.TGIDL
Prupe.5G005600.1	GASSPQSRGTL	LESSGGP	GSPLNQSTGGCN	NSNPQGMSSM