```
                   1         10         20         30         40         50
Prupe.2G146200.1   MEAKEGM.SSGV.RVGGVEAPSAYHGAPNAENPTRVAGMPVADVSAMNVGVDGARVVRAE
Prupe.2G282300.1   MEEKDNL.VSGV.AVSGEEAPDTYR..................................
Prupe.6G347600.1   MEPNENQ.LSSY.....FQHPTTTTG..................TGTAATVT....ATNT
Prupe.6G117900.1   MEENNMV.TTSQPPQ..TESKPNNEVE................T...............
Prupe.5G081500.1   MEGREGVNSSGV.TVVASDAPSDYH..................................
Prupe.7G119600.1   MEEKEST.FSGSPGNSGTESPPVTQM..................VNIPMGMD....VNMS

                   60         70         80         90        100        110
Prupe.2G146200.1   APSAYHGAPKTEDPTQVAGMPPAKVAETNV..GDDGATVKRKRGRPRKY...GPGGTVTM
Prupe.2G282300.1   ...IAPRNENPSPSGGPTMAAAATASPMSL..ALTGTEVKKKRGRPRKY...GPDKTVSS
Prupe.6G347600.1   ASPTNGLLPNTHSTDGSHMVYSHSVPSSAV..TSPLEPAKRKRGRPRKY...GTPEQALA
Prupe.6G117900.1   ..FMEPVQMNIEPNQD...LDQSGAPIGRVELTGTDVLVKRKRGRPRKYEMVGEEGNVVG
Prupe.5G081500.1   ...VAPRSENTTHNAGSTPPAPVAPPPAAALPAAASLPMKKKRGRPRKY...GPDGSVTM
Prupe.7G119600.1   SEIINNNSNNPVSTTTTTEIAEIAAAAATV..GSGDLSGKKKRGRPRKY...DADGNLRL

                                     120        130        140        150
Prupe.2G146200.1   A..........MSQMP.....GSPPASGTGGNLSSGVRGRGRGRGSGRGRGRGRGR
Prupe.2G282300.1   A..........LSPMP.....ISSSI.PLTGEFSAWKRGRGRPV...............
Prupe.6G347600.1   A..........KKAAT.....TSSHS..SSSKEKKDHHGSASPSY..............
Prupe.6G117900.1   L..........VSASP.....SSTYS..GSYSESLPKRGRGRPK...............
Prupe.5G081500.1   A..........LSPKP.....ISSSAPPPVIDFSAEKRGKVKPT...............
Prupe.7G119600.1   GYNSNINKGGGVAPPPPPGFYLSSPA.SEFSSSSSSKRGRGRPP...............

                  160        170        180        190        200        210
Prupe.2G146200.1   GWSDGSNAKQHEAPAMESGGDWSVVVTPSTDYTPHVITAEPGEDLTFKIISVAEQGPRAI
Prupe.2G282300.1   ....DSVKKSHKYDVFESSGEK.IAYSVGANFTPHVLTVHAGEDVTMKIMSFSQQGSRAI
Prupe.6G347600.1   ...SGSTKKSQQF.......SLGNAGQGFTPHVLTVAAGEDVGQKIMFFMQQSKREI
Prupe.6G117900.1   ....G....SGKLQLLSPRGGL.SVDPAGGGFYTQVLTAETGEDIVHKILSLSETNPRSL
Prupe.5G081500.1   ....SSVSKT.KYEV.ENLGEW.VACSVGANFTPHIITVNSGEDVMMKIISFSQQGPRAI
Prupe.7G119600.1   ....G....SGNWQVLASLGEL.FANTAGGDFTPHVVTVSTGEDVAGKILSFSQKGPRGI

                  220        230        240        250        260        270
Prupe.2G146200.1   WIISANGAVSNVRLRRPDTDEGSITLEGVFEIAHLSGSFMFYDNRGT..MSGGLSVSLSG
Prupe.2G282300.1   CILSANGTISNVTLRQPSSSGGTLTYEGRFEILSLSGSYIAIENAGTKSRSGGMSVALAG
Prupe.6G347600.1   CILSASGTISNASLRQPATSGGNITYEGRFEIISLSGSYVRTDLGG...RAGGLSVCLSS
Prupe.6G117900.1   CILTATGVVCSAVIRQPSSYTGILRFKGRFQILTLSGSFVYDATQNRRGKNGMLSVALCH
Prupe.5G081500.1   CVLSANGVISSVTLRQPDSSGGTLTYEGRFEILSLSGSFMPNETGGTRSRSGGMSVSLAS
Prupe.7G119600.1   CVLSANGAVSNVTIRQPGSSGGILTYEGRFELLSLSGSFTVTEIGGVRNRTGGLSVSLAG

                   280        290        300        310        320
Prupe.2G146200.1   PNGSCIGGAVCGSLIAAGHVQVVVGSFAPGKPDVLPKEVTNQNSGEPQ...........
Prupe.2G282300.1   PDGRVVGGGLAGMLIAAGPVQVVVGSFLPGHQQEQKPKKQRLEPVSSSI.........VP
Prupe.6G347600.1   TDGQIIGGGVGGPLKAAGPVQVIVGTFMVDAKKDVTAGVKGDASATK...........LP
Prupe.6G117900.1   PDGNIFGGAVAGALIAAEPVQIIATSFLQETSSNTSKELKRRHSAESSTSTSMLGN.SSC
Prupe.5G081500.1   PDGRVVGGGVAGLLVAASPVQVVVGSFLSGNQHEQKPKKQKHDYISNA..........TP
Prupe.7G119600.1   PDGRVIGGGIAGLLTAASPIQIVVGSFTPNGYKAHKRKHYRENNVASPIS....GSLDTV

                                     330                                340
Prupe.2G146200.1   .................PNLGSSPPG....................QSENRAPAS.....
Prupe.2G282300.1   IVVNAVSGEEMKVCGGVKPILTSPSF....HGNNSTSVNP....MHSFKNSAPESKS.LS
Prupe.6G347600.1   TAGEMMN......VSFRSAVDSSGRTL..VRGNDDQQAIGGSHFMIQGMHVAPSRPTDWR
Prupe.6G117900.1   LAMVPLLMPPPTIVHDESCISPTSALLEFPSHSGAGNVIA....ANRNMNPATLPGFDQN
Prupe.5G081500.1   TMAVPISSVDPK.....PNFSSSTSF....RGDNWSSL...........PSDPKTKT...
Prupe.7G119600.1   TVATPISQAQPESESRLTTISPLPAQ....SHGEADKIMI....QMQTSNAISTSAV.WN

Prupe.2G146200.1   ..................................................
Prupe.2G282300.1   E......................EESKGPGQ..PNCEVSY........
Prupe.6G347600.1   GGPDARGTGAYELTGRAGRAAHQSPENGDYDQIPD.............
Prupe.6G117900.1   A......................LQPMPDPTTSPHIDTFIP.......
Prupe.5G081500.1   ..................................DINVSLPGGVI...
Prupe.7G119600.1   G......................TELKSEHRPSPDINVSVPGVSVTGE
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