

|                |                                |                                                                                   |    |
|----------------|--------------------------------|-----------------------------------------------------------------------------------|----|
| NTDB id 1029   | TT RS02230 WP 011228203.1      | .....MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKPEPKGLQAEVRIPALERGPGLK           | 65 |
| NTDB id 1402   | DSB67 RS12670 WP 010643257.1   | .MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSI SFI.....TKISHRVKKGK | 67 |
| NTDB id 1169   | A1552VC RS11075 WP 000648511.1 | MKAT.....QTLPLKNYRWKGINSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLL.....ARLTHRVKSK    | 68 |
| NTDB id 1112   | NGFG RS09215 WP 003689811.1    | .MAKNGGFSFLFAKKEKRFIFEGRHASDCLKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE   | 70 |
| NTDB id 1113   | AAA85695.1 219..1451( )        | .MAKNGGFSFLFAKKEKRFIFEGRHASDCLKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE   | 70 |
| NTDB id 1252   | GC085 RS07730 WP 011213805.1   | .MDK.....NSPPLLTFHYQGINKAGQK.MEGDIQARSLATAKADLRKQGI VTNKVVKKKRKLFD.....RKNKKITQA  | 67 |
| NTDB id 132448 | XFPR RS10910 WP 010894959.1    | .....MTSFLWEGTDRKGVK.IKGEQTARTANLLRAELRRQGITPLVVKPRPKPLF.....GQAGKRITPK           | 60 |
| NTDB id 1198   | PSJM300 03950 AFN76868.1       | .MAQ.....KAIKNSVFTWEGLD RQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS.....AGKKIKPM   | 66 |
| NTDB id 1016   | ACIAD RS01680 WP 004920476.1   | MAAK.....KTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITTIRIREKRKNIFE....GLLKKKKVKPL  | 69 |
| NTDB id 1059   | ABD1 RS01610 WP 000279215.1    | MAVK.....KAQMMPFTFAYEGVDRKGIVK.IKGEPLAKNMALAKVTLRKQGVTVRNIREKRKNILE....GLFKKKVTTL | 69 |
| consensus      |                                | *** * * **** * * * * * ! * * * * * **** * *                                       |    |

[illegible]

|                |                                |                                                                                    |     |
|----------------|--------------------------------|------------------------------------------------------------------------------------|-----|
| NTDB id 1029   | TT RS02230 WP 011228203.1      | DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQLITDGLSELPLLTRFLIAVSDLLRAATL  | 224 |
| NTDB id 1402   | DSB67 RS12670 WP 010643257.1   | SQVFERLATYREKSEQLRAKVIKALIYPAMVVVLVALGVSYLMLTRVIEPEFEKMFTFGADLPAPTQMVLNLSAWTQNWGP  | 227 |
| NTDB id 1169   | A1552VC RS11075 WP 000648511.1 | PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTRVIEPEFESMFKGFGAELPWFTQQVKLSHWVQAYS    | 228 |
| NTDB id 1112   | NGFG RS09215 WP 003689811.1    | ESLIDKLAIYKEKTQAIRKKVKTKALTYPVSIVAIAIGLVFMVMIFVLPAFKFEVYANMGALPALTQTVMDSDFVSYGW    | 230 |
| NTDB id 1113   | AAA85695.1 219..1451( )        | ESLIDKLAIYKEKTQAIRKKVKTKALTYPVSIVAIAIGLVFMVMIFVLPAFKFEVYANMGALPALTQTVMDSDFVSYGW    | 230 |
| NTDB id 1252   | GCO85 RS07730 WP 011213805.1   | DIMLDKVATYKEKIEIKKKIKKALTYPVAVMVVALLVTAGLLIYVVPQFESLFKGFADLPAMTRAVITMSEFMQAYWY     | 227 |
| NTDB id 132448 | XFPR RS10910 WP 010894959.1    | ETVLDTIASYKENIEALKGKIRKALFYPPVAIVAAVALIVSSILLIYVVPQFEDVFKGFGAELPAPTQMIVNFSNFMQRWWW | 220 |
| NTDB id 1198   | PSJM300 03950 AFN76868.1       | ETILDRVATYKEKTEALKAKIKKAMNYPVAVVLVAVIVTAILLIKVVPQFQDVVFANFGAELPAPFTLMVIGLSEALQAWWY | 226 |
| NTDB id 1016   | ACIAD RS01680 WP 004920476.1   | EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVVPVFKDLFTSFGADLPAPTQLVNVNSNMWDYWF   | 229 |
| NTDB id 1059   | ABD1 RS01610 WP 000279215.1    | ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVVPVFKDLFTSFGADLPAPTQMNVNMSKNMQEYWF  | 229 |
| consensus      |                                | *****!****!*!!*!!!!!!!*!!!!*!!!!!!!!!!!!!!*!!!!*!!!!*!!!!*!!!!*!!!!*!!!!*!!!!*     |     |

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consensus

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