




Consensus


- 1. MAT1-1-10 *Verpa bohemica* strain No. 20020 Gene05695
- 2. MAT1-1-10 *Verpa bohemica* strain No. 20124 Gene05694
- 3. MAT1-1-10 *Verpa bohemica* strain No. 21108 Gene05692
- 4. MAT1-1-10 *Verpa conica* strain No. 21110 Gene05312
- 5. MAT1-1-10 *Morchella sp. Mes-20* NC AV161143
- 6. MAT1-1-10 *Morchella rufobrunnea* NC QQL94651

		
	M×E×YL×YHDNR-RDD×RRE×LLRLGHALIKVKNDLAFFPSTRLD××IRKVLVFCIATLKEFEVK×L×××FLD××QD×YP	
1	MTE-YLAYHDNR-RDDPRRESLLRLGHALIKVKNDLAFFPSTRLDPNIRKVLVFCIATLKEFEVKKLNLKFLDKVQDVYP	78
2	MTE-YLAYHDNR-RDDPRRESLLRLGHALIKVKNDLAFFPSTRLDPNIRKVLVFCIATLKEFEVKKLNLKFLDKVQDVYP	78
3	MTE-YLAYHDNR-RDDPRRESLLRLGHALIKVKNDLAFFPSTRLDPNIRKVLVFCIATLKEFEVKKLNLKFLDKVQDVYP	78
4	MAEAYLVCHDNR-RDDSRREALLRLGHALIKVKNDLAFFPSKRLDSQIRDLVLVFCIAILKEFEVKTLRQEFLEGGQDIYP	79
5	MPQPYLSYKDHFILNDQRREAILRLGRVLIQTKNDLTFFPRTPYFSKIRKAIIFCTDTLKEFKIKNLHPALLDRHKDIYP	80
6	MPQTYLSYKDHFILNNERREAVLRLGRILIQTKNELAFFPRTPYNSKIRRVMIFCTETLKEFKIKNLHPALLDRRKDIYP	80

		
	LANLYNLGIQI×AL×EIQ××L×T×L×QWK×DV×AVQ×SFP×GS×DIG×VLA×VHEFLVF×TLTNRIHPFHTLTE×SIK×A	
1	LANLYNLGIQIMALLEIQDVLTYQLCQWKQDVGVAVQASFPDGS-DIGIVLADVHEFLVFSTLTNRHPFHTLTTESSIKRA	157
2	LANLYNLGIQIMALLEIQDVLTYQLCQWKQDVGVAVQASFPDGS-DIGIVLADVHEFLVFSTLTNRHPFHTLTTESSIKRA	157
3	LANLYNLGIQIMALLEIQNVLYTYQLCQWKQDVGVVQTSFPDGS-DIGIVLADVHEFLVFSTLTNRHPFHTLTTESSIKRA	157
4	LANLYNLGIQILALQEIQRFFTELDQWKYDVEAVQASSPGGSDDIGTVLAEVHEFLVFATLTNRHPFHILTEFSIKHA	159
5	LANLYNLGVQILALREVNIIRLERDIEKWNCGKTLQGSPLPEDCDVRLILVEVHEFLAFATIANQIHFPHTLTPYSIRCA	160
6	LTHLYNLGVQILALREVNIIRLERDIKRWNCRLKALQDSFPENSSDVGVLVAEVHEFLVFATIANQVHTSHTLTYYISIRLA	160

		
	VQ×AKHSEFL×ASHT×SIL×AAFSIQ××L××××TS×TK××YVVSDAV×L××T×I×IA×DWYK××××S×S××EK×××××	
1	VQIAKHSEFLADASHSVSILQAAFSIQSGLEALGTSNTKDKYVVSDAVTLSTTTIFIARDWYKNHELSSMSAEK×××××	231
2	VQIAKHSEFLADASHSVSILQAAFSIQSGLEALGTSNTKDKYVVSDAVTLSTTTIFIARDWYKNHELSSMSAEK×××××	231
3	VQIAKHSEFLADASHTVSILQAAFSIQSGLEALGASNTKDKYVVSDAVTLSTTTIFIARDWYKNHELSSMSAEK×××××	231
4	VQVAKHSEFLTEASNTISILAAALSIGNELDS--ASGPKNNRVSSAIIPPQTVIHIADWYKSYKSSISVAEKACCHSN	237
5	AKAAQNSRLLTEAAHTLSILRAAFSIQNELQIRRTSKTTRSRIISNAVSLPKVALNICSDWYNRYGSHA×××××××	229
6	AEAAKGSIFTTEATHTISILRAAFVQNEIQIRTL-MRRNYIISDPVSLPQIVLTLCSDWYNHRKDHAS×××××××	229

		
	×××××IRQEA×LP×IPF××L×TWFINARRRI××GQTI×P×LK××V×××××S×K×P××××××-×××PMD×××××	
1	×××××IRQEARLPVIPFDHLLTWFINARRRILVAGQTISPALKVVVHNLITSDKKPPP×××××SYVPMDDSNY	295
2	×××××IRQEARLPVIPFDHLLTWFINARRRILVAGQTISPALKVVVHNLITSDKKPPP×××××SYVPMDDSNY	295
3	×××××IRQEARLPVIPFDHLLTWFINARRRILVAGQTISPALKVVVHNLITSDKKPPP×××××SHVPMDDSNY	295
4	KFHVKTANYQEFRREAQLPMIPFNRLFTWFIN××	294
5	×××××LYTKIRRNEISTPIPFEKLVTFWFTNARRRIKHNQAIRPGLKAIIVDEALSS-KRSFKTDIH-IQTRGSNGDD	299
6	×××××RIFNDFHQNDKSTQIPFENLMTWFCNGRRRIITCGQTINFDLKAIIDGAVSS-KIPSKIETRGDDTDGNDGDG	301

		
	E×HY×IPLT×LIAEFLDELGE×PK×LLPLKHL×VDPPLP×SRSPI×F×FLV×××AD××TQ××Q×LL××IY×LFN×××××C	
1	EFHYNIPLTQLIAEFLDELGEVPSKLLPLKHLAVDPPLPESRSPISFDFLVDLEADRSTQIAQSLLQKIYRLFNTTIYRC	375
2	EFHYNIPLTQLIAEFLDELGEVPSKLLPLKHLAVDPPLPESRSPISFDFLVDLEADRSTQIAQSLLQKIYRLFNTTIYRC	375
3	EFHYNIPLTQLIAEFLDELGEVPSKLLPLKHLAVDPPLPESRSPISFDFLVNTEAD×××××××××××××××××××	351
4	EPHYDIPLTELILELLGELGEMPKLIL-LKHSTVDPPLPRNRSPIFFNLFVNMGADGVQTETQNLKKIYNLFNMTAYRC	373
5	DPEWEIPLSRMIAEFLDELGDAPHELDPPSNLVIN--NFGSGPPIPLPTLLVDNNMDKVTQGCQQLKSIYSLFNEISCAC	377
6	EPEWEIPLSRMIAEFLDELGDAPHELDSPSHPITN--ISSRDIPLV--FPVNNSMDKFAQGCQYLLKSIYNLFNEVSSAC	377

		
	L×××Q×AHLW×××××Y×Y×××A×××××N×LRA×G×ALATRRLN××YF×E××VC×××L××××N×NP×RSDLLEAVFEICN	
1	LQVTQGAHLWSMREQYEVAVRATREIEKNYLRAVGTALATRRLNPAYFGEKIVCNRLGAPTNNNPIRSDLLEAVFEICN	455
2	LQVTQGAHLWSMREQYEVAVRATREIEKNYLRAVGTALATRRLNPAYFGEKIVCNRLGAPTNNNPIRSDLLEAVFEICN	455
3	×××	400
4	LEVIQRAHWVNMEKQYEVAVRAKKEIDKNYLRAAGIALATRRLNTVHFEEIIVCRKSLVEQNNRNPFLKVLDAVFEICN	453
5	LDIFQRAYWLDERNRYSYTLGAKRDMYDNCRAISVLLGTRESNETYFEWQ×××××××××××××××××××××××	444
6	LDILQRAHWLDAKNKQYHTSKAKIDMDRSLCRAINVLATKKPKNTYLECQ×××××××××××××××××××××××	444

