

Bacterial ORF Alignment

Accession	Sequence	Alignment	Score
N.a. I2MPPIGGRM.....PGIDGKTFEDFGE.....	28
N.a. I1	-----MLPDTIERAVRSLPTVIRSRKVNGLYRLKLSPL-LWEHAVQRIAPNKGGAM-----	-----PGVDGQTE-DGFSPE-----	70
L.1. I1	-----MKPTMAILERISKNSQENIDVFTRLYRLLRPD-ITVYVQNYLSYKNGAS-KGILDQ-----	-----ADDFG-----	69
B.ct. I2	-----MRPNVFNLSLKHSS-NLNIYFKERGLYVLFNPEE-MFVAVQNYLSKTYGNM-----	-----AGADGR-----	70
QYF. I1	-----MINMSTTVSDTELKSRLLKILKLYCSTNYNKRELOQMNFMML-MAVAKTAARNGAG-----	-----PGIDGNTI-DSI-----	79
D.h. I1	-----MRSEIIVLKSLTEKSK---DESVKFORLYNLYNPEFWLALYNYIYKNGSM-----	-----PMDGTLI-SGI-----	69
D.h. I2	-----MRSPOIVLENLQROSQK---QDYRFERLYNLYNDFYLLAYOKLYANGAM-----	-----PGVDRTLI-DGI-----	69
S.me. I2	-----MTDHRDKVWVLGQIRKLYQMSKANPDQWRDMGWLLDLR-VLRHAWQRVASKNGGE-----	-----AGVDGTVL-GRIRNR-----	82
E.c. I4	-----MORKLATWAADTFLRIQRLRLRLITQFE-WLAEAAIRILLSSKGAAH-----	-----PGVDGVNK-TMLQAR-----	67
S.f. I1	-----MORKLATWAADTFLRIQRLRLRLITQFE-WLAEAAIRILLSSKGAAH-----	-----PGVDGVNK-TMLQAR-----	67
C.sp. I1	-----MSNTSLKTTAEWNTIPIWRKLSRVYKIQRYQAQRDTPKAVRKLQKTMRSWSG-KALAVRQVQDNQOKKA-----	-----AGIDGVKS-LKFSAR-----	92
G.v. I1	-----MYEWNLSNWQIQRVFKLQTRIFKASQGRDFKAVRKLQKLLIRSWSA-RCLAVRQVQDNQOKKA-----	-----AGVDGVKS-LTKPKAR-----	84
T.sp. I1	-----LVNKKASIKLRLLGNPKFPLSVAWDITDDMLDQCUNLWIKRSDLWKKRVFYKIQELIYKASRGRKTRMRFKQKLLKMSYDA-NLLAVRQVQDNQOKKA-----	-----VGLDKRNI-LYMQAR-----	121
N.sp. I4	-----MIVVEQVAMYSKTSFKTYVYKMRVFLQKRYKASGRDFKAVRKLQKLLIRSWSA-KCLAVRQVQDNQOKKA-----	-----AGVDGRKN-LSEKAR-----	104
B.a. I1	-----MNTVMNMSKAVSQVQVQWNSIQWKIENVVKLQRQRYRQEPKRRVVKRLQRLMRKSKAN-LLLSIKRVQIQNKKRR-----	-----AGIDGTLI-NTPEDR-----	98
B.c. I1	-----MNTSERASAHVSYTNKAVQMVTYLQRQRYRABEQOQKRVKRLQRLMRSEAN-LLLSIKRVQIQNKKRR-----	-----AGVDEHTA-LRSRRR-----	92
E.c. I5	-----MTEQATTCCKGASLLNGDWSHSINWQCYREVRRILQARIYKATREKKGKVKLSQWLLTHSFSGRRAVAVRVTNSGKRR-----	-----PGVDGTVL-SSPEVK-----	96
A.v. I1	-----MSASEKEVPASSLASWHTIDWATSHRRVRGLQVRIAKAAKRNQRVKTLQRLMRVFSFAKALAVRVTNSGRR-----	-----PGVDGVTL-STPEVK-----	95
B.t. I1	-----MNEIKTSCASTDRKWTSEIDWNKCVIAVNLQARIVKAKAKHGRVKVLSQWLLTHSFFYA-KALAVRVTNSGSD-----	-----AGVDKVKV-STPNAR-----	96
B.me. I2	-----MNTSLRA5AHVSHDKWYSIDWSIQKYVAKLQRQRYRABEQOQKRVKRLQRLMRSEAN-LLLSIKRVQIQNKKRR-----	-----PGVDGTVL-SKPNER-----	97
A.v. I3	-----MPEFARHQAATPSSSASPHAKSNWPSWCWRESVDRQLQVRLAKATBERGWVQAOQLLRISYSGLMVAWRVTNSGKK-----	-----PGIDGKIM-STPVAK-----	102
B.f. I1	-----MSMQAMQAMQPVTQTRAVYVTEEAAPFVSDIACGRHESDASALLAALTRMLKCAKRVRAKKA-----	-----AGVDGLDI-DQARH-----	91
B.f. I2	-----MSMQAMQAMQAGAGVARGEAARVFSDEACGRRPEPTNSALLQALTRMLKCAKRVRAKKA-----	-----AGVDGLDI-DQARH-----	102
Ma.sp. I1	-----MQIKEARQDNRSLSCSPGFKNWNSIEMKVRHVSRLQARIVKAEKGRIGKVKALQIILTKLSLAARALAVRVTNSGK-----	-----PGVDGSLM-KTPEVK-----	93
R.m. I1	-----MQIRIAKATQRDWRVKALQRLSRTFSFAKASAVRVTNSGKRR-----	-----AGVDRELM-DSPEVR-----	69
Tr.e. I8	-----AEVKDRFNSIEGAKPEKLEKWDLWIKTKKCVNLRRIYRKAQMSQWVKVSLMKLRLSYSNLLSVRRVQENQKIR-----	-----MGRDAQTA-KTSVEK-----	99
P.p. I2	-----MIVIGSAAKTDAIGTAPSHAERMWLQANWGLIKEDVKRLQARIAKATBERGWVQAOQLLRISYSGLMVAWRVTNSGKK-----	-----PGVDGKIM-ATPAK-----	102
M.a. I1-1	-----MPTCHWSRKQGLLIMNVNKKPEITSVTDLTKDELTKQWKSIDWKRKVEVNNLQSRISAASAENQKVIYVKNLSRLLRSFYAKLLSIRKVVTKGSSR-----	-----PGIDGTVL-SSSADK-----	115
M.a. I1-2	-----MPTCHWSRKQGLLIMNVNKKPEITSVTDLTKDELTKQWKSIDWKRKVEVNNLQSRISAASAENQKVIYVKNLSRLLRSFYAKLLSIRKVVTKGSSR-----	-----PGIDGTVL-SSSADK-----	114
M.a. I1-3	-----MPTCHWSRKQGLLIMNVNKKPEITSVTDLTKDELTKQWKSIDWKRKVEVNNLQSRISAASAENQKVIYVKNLSRLLRSFYAKLLSIRKVVTKGSSR-----	-----PGIDGTVL-SSSADK-----	115
M.m. I1-1	-----MNVREPEITSVTDLTKDELTKQWKSIDWKRKVEVNNLQSRISAASAENQKVIYVKNLSRLLRSFYAKLLSIRKVVTKGSSR-----	-----PGIDGTVL-SSSADK-----	100
M.m. I1-2	-----MNVREPEITSVTDLTKDELTKQWKSIDWKRKVEVNNLQSRISAASAENQKVIYVKNLSRLLRSFYAKLLSIRKVVTKGSSR-----	-----PGIDGTVL-SSSADK-----	100
X.f. I1	-----BERKMTQAACAGALSDSGWHCIDWANCHEVRRILQTRIVKATQERGWKVKALQWLLTHSFSGRKALAVRVTNSGK-----	-----PGVDKVVV-ETPEKK-----	99
R.r. I1	-----MTAIGKAAANAGASSHGQIQDQTDWGIQTAVKRLQVRIAKATRECWRKVKALQRLSRTFSFAKASAVRVTNSGKRR-----	-----PGVDGEIM-TTPVAR-----	98
P.p. I1	-----MPPVGVTVSLVAVMQKFTAETIILSPQKPRMPSDAKVSMSVAWTSAKSGTLMERVLAFA-NLRRAVRRVNSKGA-----	-----PGADGTVL-ADLAGH-----	100
S.me. I3	-----MQEARMHQVPAARASGGRQEALESPGSEATPCRCDAQSGTGPGLLEALALARE-NLORAWRVRKANKGA-----	-----AGADGSLI-EAFAAH-----	90
S.p. I1	-----MSKLDKLSRE-NMELANQVNSKGS-----	-----AGIDGTVL-EEEDNY-----	69
S.ag. I1	-----MQTKKERTHMSLELKDSSRN-NMELANQVNSKGS-----	-----AGIDGTVL-EQDDY-----	49
A.v. I2	-----MLETMSSEMHQTCACERHARQGEAEPAKVSREBAEPHEMSESALLEALTE-NLORAWRVRKANKGA-----	-----AGVDGLDI-DQARH-----	91
A.v. I4	-----MSRAMHQVETGRVMQCRGEASQSPSDEAHLFQSGEDAGRLRQVYAKE-NMORAWRVRKANKGA-----	-----AGVDGLDI-DQARH-----	91
D.h. I3	-----MPLKMIETDNTNNEEELFEQLSSE-NINQAVRQVKKKGA-----	-----GGIDGMQV-DELLPY-----	65
N.e. I1	-----HRAALNQDDHNDQDQLLEAVLARD-NLAWRVRKNSRGA-----	-----PGIDGTVL-AEWFPH-----	62
N.e. I2	-----MLARD-NLAWRVRKNSRGA-----	-----PGIDGTVL-AEWFPH-----	62
G.s. I1	-----MPVERVIDRPTPEEHLERILATENMMLAKWRVANKGA-----	-----PGVDGTVL-DAPFER-----	67
O.i. I1	-----MLMNQLSRD-NLILAKRVERNKGS-----	-----HGIDEMSV-KFLRRH-----	41
P.p. I3	-----MPPVGVAVSLVTVMQKFTAETVIPSQKPRVTPDSAKVSTASVTWNAEPDPTLMEVLAFA-NLRRAVRRVNSKGA-----	-----PGADGTVL-ADLAGY-----	100
B.h. I1	-----MKERMQKTSQAQAHDFQQRARTSEBWEYEQVTFMWMTEDNIEVDFPKHEKLELLRTE-NLORAWRVRKANKGA-----	-----PGVDGMDV-KSIRLH-----	46
E.t. I3	-----MKERMQKTSQAQAHDFQQRARTSEBWEYEQVTFMWMTEDNIEVDFPKHEKLELLRTE-NLORAWRVRKANKGA-----	-----PGVDGMDV-KSIRLH-----	46
A.g. I1	-----MKFMPSNDLFEHLQED-NLSAAWKRVRANKGA-----	-----AGIDGNTI-DEFPAN-----	99
S.ma. I2	-----MNLNSHRSQCDSDEBQSTVNNSTSEYNOIDHDLMAKVLNSH-NLSAAWKRVRANKGA-----	-----AGIDNMSI-BEENDF-----	55
M.sp. I1	-----MSLLEWERDLSVFKTDFPCKRTKVGHQWLSACEERALTRGLMYKVCDSL-NLILAKRVERNKGS-----	-----PGVDGMQV-KELRYW-----	99
C.a. I1	-----MKNSEKMQKLTYSYKEWSCIBRELQNSTRAHSISTAFDRKDDGKLYETNLLERLDRQ-NMNLAKRVRANKGA-----	-----HGVDGMKV-DELLQY-----	90
P.a. I1	-----MPPVGVAVSLVTVMQKFTAETVIPSQKPRVTPDSAKVSTASVTWNAEPDPTLMEVLAFA-NLRRAVRRVNSKGA-----	-----PGADGTVL-ADLAGY-----	100
P.a. I2	-----MPCRTAEASPGQKAVPRHGGRRPMPADSATPMASVTWKAEPNLTMERVLAFA-NLRRAVRRVNSKGA-----	-----PGADGLSV-DELAGY-----	92
S.t. I1	-----MPCRTAEASPGQKAVPRHGGRRPMPADSATPMASVTWKAEPNLTMERVLAFA-NLRRAVRRVNSKGA-----	-----PGADGLSV-DELAGY-----	92
B.me. I1	-----MLKRRKLHNEYDMQYFNPDSLVAQSANQJFDELDMDSDD-NLORAWRVRKANKGA-----	-----AGVDGLDI-EDNMR-----	86
C.d. I1	-----MTVIVSNKKALREFNEDYDKIQIDELYGLDSAFVFRDLRSLAQEIE-NLILAKRVERNKGS-----	-----AGDKRITL-IDVGE-----	55
B.a. I2	-----MNGNSKAPKPKKLLHNEYIYQVFLDNLQYKATKNSFNKMSIISDE-NILAYRNKIKKSGS-----	-----AACDNWNI-KNIEG-----	85
E.f. I1	-----SLMKKNETLVLEDLRAHYEYMQNTFDDLYAKSKNGD-IFTHLMDILSRE-NILAYRNKIKKSGS-----	-----AGIDGTLI-KDIGL-----	98
E.f. I3	-----MFLVLTSGQEKRSKQKIRNSHEYDMEGTFDRLYAESKDKTFNHLMIEIESE-NIKLAYRTIKKTSGD-----	-----SGVDKRLI-ADLAKL-----	92
E.f. I4	-----MEVRLNTRKIRWYEDLQETFDQLFTQSKNKKFYLYLELISEN-NILAYRTIKKTSGD-----	-----PGTDSFTI-DNKXEM-----	84
E.f. I5	-----MERDKTMTNFKISLKNKQLRHAEYDMTTFDELMHSAVSFNKMLMPTIDDN-NILAYRNKIKKSGS-----	-----AGVDGTVL-KDIEKL-----	84
E.f. I2	-----MNQNLKETPKNNKRLRYAYYQIETIYDELPNKSNKG-IFPKNLGMLISTD-NILAYRTIKKTSGD-----	-----AGIDGTVL-KDIEKL-----	89
N.p. I1	-----MIRHSYLITSEWKNFVWKILQKRVFKLQRIYKAKESNLVAKSLQKLLIKSTSARLALRVLQNLGKR-----	-----AGIDGKRI-TQERM-----	92
Th.e. I1	-----MTVQDTTSAVNTQIETSIWLNWAKANREKLVKQVRIKAVKESBWKVQALQ-MLTHSFFKALAVRVTNSGKRR-----	-----PGVDGTVL-STQEQK-----	93
Tr.e. I2	-----MNKAKILKRRCLGNPKFPLSVAWDITDIPNCSVNPFKKRWLDNWKVYVFLKQKLIYRASRSRGIIRKRKYQKLLKSHDALLAVRQVQDNQOKKA-----	-----AGIDGKNI-LPQMOR-----	117
Tr.e. I3	-----MTKTRKPNVVVTYVNRKRLKRVVYVFLKQKLIYQAAQRQDVKAVRKLQKLLIKSHSARLAVRQVQDNQOKKA-----	-----AGIDGKNI-LPQMOR-----	117
Tr.e. I4	-----MEKAKILKRRMCKPESFPLSVAWDITDIPDKICVNPFLKWRDLDWKKVFNKQKLIYRASRSRGIIRKRKYQKLLKSHDALLAVRQVQDNQOKKA-----	-----AGIDGKNI-LPQMOR-----	89
Tr.e. I5	-----MNTRETTTVEWVKHWKAVNRAIFRLQKRIYKASHGDTKAVKQLLKVKSARLAVRQVQDNQOKKA-----	-----PGIDGVGE-LAPLQK-----	91
Tr.e. I6	-----MNVQVSNINLTKWRDLDWKKVFNKQKLIYRASRSRGIIRKRKYQKLLKSHDALLAVRQVQDNQOKKA-----	-----MVDVGLKN-LPQMOR-----	117
Tr.e. I7	-----MSNTSLKTEWKEWREINWTVERRVFKLQKRIYRASRQDVIYVRLQKMLKMSYGRILLAVRQVQDNQOKKA-----	-----IPVGGVLLSIP-DKCFA-----	91
S.me. I1	-----MKNKAIILKRLDNPFSFVAVDAYDIPSGACVNPFLKWRDLDWKKVFNKQKLIYRASRSRGIIRKRKYQKLLKSHDALLAVRQVQDNQOKKA-----	-----BEIRKMKRKQKILLTK-----	82
B. j. I1	-----MKSQDPLRITKR-MVWEAKLKKGGK-A-----	-----AGVDGLDI-EDFAD-----	53
R.e. I1	-----SSCNGNBAKGRRYFADEEGQAPASGKVSAKPWNIAFG-TWEAYQVKANRGA-----	-----AGIDDEAL-AEPEQN-----	78
E.c. I1	-----MNVERRRNQVSASQENCKQJEAAGROKPFQVSKL-HVVEAVRVRKANKGA-----	-----AGVDNGLI-KDFERD-----	73
E.c. I3	-----MORKSFEIKALVWASLDVRRNKGA-----	-----PGCDGQTL-KMFDQO-----	48
E.c. I2	-----MTKIKAFNIDKS-LVSAVRRVTSAGA-----	-----AGIDGQSL-ADDFKR-----	49
P.1. I2	-----MSARVPMRGTAEQAVVAKDRNGSAGKGLPHCADGTTATTQKAGGRTAVKSAKPPVSKRQVDAKRVKANKGA-----	-----AGIDGQSL-ADDFKR-----	49
M.a. I5-1	-----MDETTPPEISKDIVQAEFRVKAANKGA-----	-----AGVDNENI-AAFESD-----	49
M.a. I5-2	-----MDETTPPEISKDIVQAEFRVKAANKGA-----	-----AGVDNENI-AAFESD-----	49
M.a. I5-3	-----MDETTPPEISKDIVQAEFRVKAANKGA-----	-----AGVDNENI-AAFESD-----	49
UMB	-----MSW-RENEED-LHQVVKL-----	-----MSW-RENEED-LHQVVKL-----	22
A.v. I5	-----MHDTEKSDSQIVAEKPANKAGLLAEWAEPRPQTKGNAEQRMHRTO@RAMTQSLDRVTAARLRKDKRF@TALFHHIN-VDLRAAF@FALRRAA-----	-----PGVDGTVL-QDEED-----	117
B.j. I2	-----MEGRFPTKNSQCARI@TQSRGNTLRL@L@AVKAA@RR@DR@QF@L@FHHISE@LL@C@SF@QL@K@R@SA-----	-----PGCE@GI@W@EN@EN-----	89
P.1. I1	-----QRES@DLV@P@MK@SKKTR@RA@GD@P@ERT@P@Q@E@AR@IT@RT@SR@V@L@M@N@ER@V@NA@AQ@V@Q@RT@T@SL@H@LD@-Q@AL@R@AF@R@Q@K@Q@AS-----	-----AGVDGTVL-AKVEP-----	109
S.me. I4	-----MMV@E@E@K@S@D@L@I@V@A@Q@AN@PK@G@A@S@V@E@R@S@K@G@A@N@Q@H@M@R@T@N@R@S@V@R@E@A@K@Q@V@T@T@P@H@L@L@-V@E@A@F@L@S@E@K@A-----	-----AGVDGIRW-MDVA@N-----	116
S.p. I1	-----MRFV@Q@I@PK@VEN@MT@TEL@N@P@V@DK@W@S@I@P@K@R@L@K@I@V@R@L@Q@K@I@G@K@N@T@R@L@V@K@L@L@L@S@K@A@K@L@A-----I@R@V@T@Q@-L@N@T@-GR@K@-----	-----AGVDGKKA-L@P@SQ@R-----	105
N.sp. I2	-----M@S@I@P@H@V@G@V@H@G@N@L@S@S@W@G@S@V@I@A@A@R@Y@E@K@L@A@E@K@S@I@H@R@S@V@K@E@S@W@K@L@P@K@F@R@D@L@F@R@L@Q@R@V@F@A@Q@N@K@R@K@A@R@F@L@Q@L@L@S@K@A@G@F@L@A-----I@R@I@S@Q@-L@N@A@-GR@K@-----	-----AGVDGKNI-L@P@SQ@R-----	130
N.sp. I3	-----M@V@R@H@S@A@S@E@L@W@K@L@P@K@F@R@D@L@F@R@L@Q@R@V@F@A@Q@N@K@R@K@A@R@F@L@Q@L@L@S@K@A@G@F@L@A-----I@R@I@S@Q@-L@N@A@-GR@K@-----	-----AGVDGKNI-L@P@SQ@R-----	90
Ma.sp. I2	-----M@I@K@S@I@R@I@Q@D@L@R@K@I@Y@K@A@I@D@S@W@R@V@L@Y@H@V@E@P@T@N@E@A@M@A@R@K@K@V@A-----	-----PGIDGTVL-EAIEES-----	81
S.ag. I2	-----M@I@Q@A@N@I@F@E@V@Y@F@Q@K@I@Y@L@S@T@K@D@N@K@K@F@G@V@L@Y@V@K@D@I@L@K@V@N@F@V@Y@K@R@K@S@-----	-----AGIDDFLI-E@E@I@E@Y@-----	78
ruler 1	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150		

N.a.e.12	TASVATGAKKPKPVRVVFKPG	-KG-KRRPLGLP	RRDLRLVQEVARQQLERIVYFSKA	HGFGRFRRCHTALHESKRAVV	-TQVKWLVDDVAGFFDNID	H-DILLKLRKR	-IDDERFDLRLDMLKAGVME	157	
N.a.e.11	TERLANGTTRQOPRRVVTPKA	-NG-QKRRPLGVP	EDKLVOEVRTILQIVSEPLFRSH	HGFGRFRRCHTALHESKRAVV	-TQVKWLVDDVAGFFDNID	H-DVLSLLKRR	-IADRFRVRLIRGLKAGVVE	159	
L.1.1	IQSLDKDTYVPPVRRMYIAK	-NSKMRPLGTP	FTDKLQOEAIRLILSEVYFPEDV	HGFGRFRRCHTALKTRKEFR	-GGARVWFVEDGDKGFNDI	H-VLLIGLNLK	-IKDKMKSOLTYFKLKAGVLE	200	
B.c.t.12	IGSLKNETPPNPSKRRVTPK	-NG-KRRPLGTP	FDKLVVEVMRMILAEYSSGFHT	HGFGRFRRCHTALDIKQFT	-TAVKWFVEDGDKGFNDI	H-DVLLNLKRR	-IADRFRVRLIRGLKAGVVE	198	
QVY11	HKEVFNKRNPKFVAVRQPK	-ND-KRRPLGTP	IKDRIVKLSQLLTFEVEFSEH	HGFGRFRRCHTALKTRKEFR	-QGLTIKIKEDLKEKFDVI	H-DLMMKTRM	-IKDKMKSOLTYFKLKAGVME	208	
D.h.11	TASLKDQSVOPHARRVYIEK	-NSQKRRPLGIS	LANDLKVOEVVRMLLESIFEP	TSFKHGFGRFRRCHTALIQGDF	-TGVNWVVEDGIEACQFSDI	H-HVLELLQRR	-IDBASPISLMMFKLKAGVLE	199	
D.h.12	IQSLKRRVOPARRRVTPK	-SGKRRPLGI	QOANDLKVOEVVRMLLESIFEP	TSFKHGFGRFRRCHTALIQGDF	-TGVNWVVEDGIEACQFSDI	H-HMLVNLRR	-IQDENFISLWKFLKAGVLE	199	
S.me.12	QADRLSARVPARRKLIPKAG	QFPRLGTP	IRDRVVOGAAKILLSPTRAO	HVHWYVGFGRFRRCHTALYVRAAL	P KRRDDE	RRNRLLPVVWVVEDGDKGFNDI	H-HLLE-RMRKR	-IGDRFRVRLVGLFLKAGVIT	226
E.c.14	RDDELSGHVQPLPARVYVPEK	-NG-KLRRPLGIP	LRDRIVRAMLAMEPWTSEDFHT	HGFGRFRRCHTALVTKLQL	DCGETRGRVWVEGDLSSVFDI	VH-HRLLMKAVRR	-ISDARFMTLLKTKAGHID	200	
S.f.11	RDDELSGHVQPLPARVYVPEK	-NG-KLRRPLGIP	LRDRIVRAMLAMEPWTSEDFHT	HGFGRFRRCHTALVTKLQL	DCGETRGRVWVEGDLSSVFDI	VH-HRLLMKAVRR	-ISDARFMTLLKTKAGHID	201	
C.sp.11	N-MKLNH-KVKARVVRTVPGNV	-NG-KRRPLGIP	MDRAGQSLVKLALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	RYSNKRVLLDADISCKFDI	H-ERKLLTKINT	-PMTRRQIKAWLKAGVLD	217	
G.v.11	N-LRISSE-KAKPVRVVIARPTG	-EKRRPLGTP	PMTRARALITLALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	RQSQSKVLDLADISCKFDI	H-QALLKMKNTS	-SARTRQIRAWLKAGVME	209	
T.sp.11	M-LKRSYFKASVRFVWVPEKE	-EKRRPLGTP	PMTRARALITLALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	RQSQSKVLDLADISCKFDI	H-NTKESR	-EADLRRVRLIRGLKAGVVE	245	
N.sp.14	G-MKLDG-KASVRFVWVPEKE	-EKRRPLGTP	PMTRARALITLALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	RQSQSKVLDLADISCKFDI	H-NTKESR	-EADLRRVRLIRGLKAGVVE	243	
N.a.e.11	KKLVSVRNKAQPKVRAVYVPEK	-NG-KRRPLGIP	PVKDRIPNMVKNALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	SRGTNRMVPEGDLQCFDNI	H-EMILSCLTF	-BY-SNAINVMKAGCID	226	
B.c.e.11	IKLNTLQHRPKKARVYVPEK	-NG-KLRRPLGIP	IKDRIVRAMLAMEPWTSEDFHT	HGFGRFRRCHTALVTKLQL	NTNSKRVWVEGDLQCFDNI	H-ENILKQSYF	-PG-RKLLKRWLMKAGVLE	220	
E.c.e.15	INFLKRRGKVVOPKRRVYVPEK	-NG-KSRRPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	AQKTSAEVWVEGDLQCFDNI	H-QWLDNI	-STDRQLTKWKLKAGVLE	222	
A.v.11	ITLRLQRTGVRPPLRRVYVPEK	-NG-QRRPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	GRKHSQVWVEGDLQCFDNI	H-DWLIANV	-LDKAVLRKWLKAGVLE	221	
B.t.11	ITLRLKRRGKVVOPKRRVYVPEK	-NG-KLRRPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	AKASAEVWVEGDLQCFDNI	H-EWLLNNI	SMD-KVMLRKLWKLKAGVLE	221	
B.me.12	LVKCNVFRHRPKKAPVYVPEK	-NG-KLRRPLGIP	MRDRVONVKNALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	NTNSKRVWVEGDLQCFDNI	H-NWMEQ	SDF-PGN-TLTKRWLMKAGVLE	225	
A.v.13	ASALQKRGVRRPKVRRVYVPEK	-DG-KERPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	AKRSAEVWVEGDLQCFDNI	H-DWLLITN	-PMDKTLRWLMKAGVLE	228	
B.f.11	REOLLKTRVPRVRRVYVPEK	-DG-BERPLGIP	IQALLVQLIPDLFSEH	HGFGRFRRCHTALVTKLQL	QSRRLVVVDEKFDVI	H-DLDRKRIDD	-AVDIRVRLIRGLKAGVVE	222	
B.f.12	REHLLRTVRRVRRVYVPEK	-DG-BERPLGIP	VTRDLIQALLVQLIPDLFSEH	HGFGRFRRCHTALVTKLQL	QSRRVVVVDEKFDVI	H-DLDRLQKRIDD	-AVDIRVRLIRGLKAGVVE	222	
Ma.sp.11	VOHLRRKVKASALRRVYVPEK	-NG-KRRPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SRKLAGRVWVEGDLQCFDNI	H-QWLDNI	-PDKMLNWLKAGVVE	225	
R.m.11	VOHLRRKVKASALRRVYVPEK	-NG-KRRPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SRKLAGRVWVEGDLQCFDNI	H-QWLDNI	-PDKMLNWLKAGVVE	225	
R.m.11	VOHLRRKVKASALRRVYVPEK	-NG-KRRPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SRKLAGRVWVEGDLQCFDNI	H-QWLDNI	-PDKMLNWLKAGVVE	225	
Tr.e.18	KEMLYTLRQVAKPVRVYVPEK	-NR-QQPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	QKQKDTWVDEKFDVI	H-EXYLKAIE	-IPQRELRKWLKAGVLE	226	
P.p.12	MEMSHRSRALPRVYVPEK	-NG-QKRRPLGIP	PMLCRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	AKRTSPVWVEGDLQCFDNI	H-EWMLKN	-PMDKTLRWLMKAGVLE	228	
M.a.11-1	ALQLTNGVRVRAKPKTRVYVPEK	-NG-KLRRPLGIP	PMYDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SKKIAPVWVEGDLQCFDNI	H-TWLLDNI	-PMDKTLRWLMKAGVVE	241	
M.a.11-2	ALQLTNGVRVRAKPKTRVYVPEK	-NG-KLRRPLGIP	PMYDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SKKIAPVWVEGDLQCFDNI	H-TWLLDNI	-PMDKTLRWLMKAGVVE	241	
M.a.11-3	ALQLTNGVRVRAKPKTRVYVPEK	-NG-KLRRPLGIP	PMYDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SKKIAPVWVEGDLQCFDNI	H-TWLLDNI	-PMDKTLRWLMKAGVVE	241	
M.a.11-4	ALQLTNGVRVRAKPKTRVYVPEK	-NG-KLRRPLGIP	PMYDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SKKIAPVWVEGDLQCFDNI	H-TWLLDNI	-PMDKTLRWLMKAGVVE	241	
M.a.11-5	ALQLTNGVRVRAKPKTRVYVPEK	-NG-KLRRPLGIP	PMYDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	SKKIAPVWVEGDLQCFDNI	H-TWLLDNI	-PMDKTLRWLMKAGVVE	241	
X.f.11	VDELRRHGHKARPRVYVPEK	-NG-KLRRPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	NGHSAQVWVEGDLQCFDNI	H-DWLLGNV	-PMDKRMLEMMKAGVME	225	
R.r.11	VMSLRHHVTRMPRRVYVPEK	-NG-KRRPLGIP	PMLCRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	ARRKATWVWVEGDLQCFDNI	H-DWLEHM	-PMDKTLRWLMKAGVVE	224	
P.p.11	KARLMAGEVHPQVRAVVEIPK	-QG-GTRQPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	ASGRVWVEGDLQCFDNI	H-DLMACIERR	-EDKRALRLRREYLAGVMS	230	
S.me.13	REVRLAGTVRRMVRVYVPEK	-DG-BERPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	QSGRRVVVDEKFDVI	H-DLDRLSKR	-ISDRVRLIRGLKAGVVE	220	
S.p.11	KELIKQRKKVQPVLEVEIPK	-DG-GIROLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	NDGVEVVVDEKFDVI	H-DRLMSLVHNT	-LEDGVEESLRKYLHSSVVI	179	
S.ag.11	KELIKERSRVRVLEVEIPK	-NG-GVNRPLGIP	PMDRAGQSLVKLALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	NDGVEVVVDEKFDVI	H-DRLMSLVHNT	-LEDGVEESLRKYLHSSVVI	190	
A.v.12	REOLLRTRVPRVRRVYVPEK	-DG-SORPLGIP	IQALLVQLIPDLFSEH	HGFGRFRRCHTALVTKLQL	QSRRLVVVDEKFDVI	H-DLDRKRIDD	-AVDIRVRLIRGLKAGVVE	222	
A.v.14	QOQLMRRQVQLSRRVYVPEK	-DG-BERPLGIP	VTRDLIQALLVQLIPDLFSEH	HGFGRFRRCHTALVTKLQL	QSGRRVVVDEKFDVI	H-DLDRKRIDD	-AVDIRVRLIRGLKAGVVE	222	
D.h.13	IESELEGTTRVTPVRRVYVPEK	-NG-KTRPLGIP	VTRDLIQALLVQLIPDLFSEH	HGFGRFRRCHTALVTKLQL	TAGKVVVDEKFDVI	H-QSLQILSER	-IKDRVRLIRGLKAGVVE	195	
N.e.e.11	REIEAGRVRRPQVRRVYVPEK	-DG-GORPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	KAGRVWVEGDLQCFDNI	H-DLMSLLRS	-IADRLLALGRYLRAGVIV	192	
N.e.e.12	REIEAGRVRRPQVRRVYVPEK	-DG-GORPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	KAGRVWVEGDLQCFDNI	H-DLMSLLRS	-IADRLLALGRYLRAGVIV	192	
G.s.11	RASLTAQTQPQVRRVYVPEK	-TG-GTRPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	ROGVRVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	191	
O.i.11	RELRKKTTPSPVRRVYVPEK	-SG-GVRRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	KGVVVVDEKFDVI	H-DKLMVLAKR	-IKDRVRLIRGLYLRAGVME	177	
P.p.13	KARLMAGEVHPQVRAVVEIPK	-QG-GTRQPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	TAGHRVWVEGDLQCFDNI	H-DLMACIERR	-EDKRALRLRREYLAGVMS	230	
B.h.11	KNEILBSHPVRRVYVPEK	-NG-GVRRPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	KGVVVVDEKFDVI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	176	
E.c.12	IEELOGQENRTPVRRVYVPEK	-NG-KRRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	SENLVVVDEKFDVI	H-OKVRRV	-IKDRVRLIRGLYLRAGVME	219	
A.g.11	KQVLTQCVQVRRVYVPEK	-DG-GTRQPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	KEGRVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	185	
S.ma.12	QOQLMRRQVQLSRRVYVPEK	-DG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	QSGRRVVVDEKFDVI	H-DLDRLSKR	-ISDRVRLIRGLKAGVVE	220	
M.sp.11	IEQLEGNRTRMPTKQVRRVYVPEK	-GG-GVRRPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	KEGNNVWVEGDLQCFDNI	H-DRMLWLR	-ISDRVRLIRGLKAGVVE	220	
C.a.11	IASIFNKKCPKAVRREVEIPK	-DG-GIRPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	BEGRVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	229	
P.a.11	KARLMAGEVHPQVRAVVEIPK	-QG-GTRQPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	TAGHRVWVEGDLQCFDNI	H-DLMACIERR	-EDKRALRLRREYLAGVMS	230	
P.a.12	RELRQTEGEVQVRAVVEIPK	-DG-GVRRPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	AAGRVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	222	
S.t.11	KSOLERQEPVRRVYVPEK	-DG-SKRPLGIP	VVDRLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	KQKRVVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	185	
B.me.11	IEQLEGNRTRMPTKQVRRVYVPEK	-NG-KRRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	NTKESR	-EADLRRVRLIRGLKAGVVE	213		
C.f.11	VQNRFRNQPQSVRRVYVPEK	-NG-KTRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	QKVVVDEKFDVI	H-DLDRKRIDD	-AVDIRVRLIRGLKAGVVE	221	
B.a.12	IVRRRFQNVQPKVRREVEIPK	-NG-OTRPLGIP	PMWDRILIQCIQVMEPCEAKFEN	HGFGRFRRCHTALVTKLQL	NKQNLTVVWVEGDLQCFDNI	H-VKLMQVW	-IADRLLALGRYLRAGVIV	220	
E.f.11	EVVSPHGVRRPKVRRVYVPEK	-NG-KTRPLGIP	PMWDRILIQCIQVMEPCEAKFEN	HGFGRFRRCHTALVTKLQL	QISQVWVEGDLQCFDNI	H-SKLKQ	-IADRLLALGRYLRAGVIV	228	
E.f.13	LIRKQENRTRMPTKQVRRVYVPEK	-NG-KTRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	QVCHLVVWVEGDLQCFDNI	H-TKLRQ	-IADRLLALGRYLRAGVIV	224	
E.f.14	LILSOLNEMKPKVRRVYVPEK	-NG-EKRPLGIP	PMWDRILIQCIQVMEPCEAKFEN	HGFGRFRRCHTALVTKLQL	NTSKMVAWVWVEGDLQCFDNI	H-RLLKQ	-IADRLLALGRYLRAGVIV	215	
E.f.15	IKRRFDKVRPKVRRVYVPEK	-NG-KLRRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	NQSKMNVVWVEGDLQCFDNI	H-TKLMQ	-IADRLLALGRYLRAGVIV	226	
E.f.12	KVRRNFMKPKVRRVYVPEK	-NG-KTRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	LKVIVVWVEGDLQCFDNI	H-NADKFR	-IADRLLALGRYLRAGVIV	225	
N.p.11	VLLKSAFVWVRRVYVPEK	-NG-KVRLGIP	ISDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	RSSCNKDKRVWVEGDLQCFDNI	H-KATMDR	-IADRLLALGRYLRAGVIV	220	
Th.e.11	IKLRRRQPKVRRVYVPEK	-NG-KORPLGIP	PMKDRAMQALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	ARAKSREVVWVEGDLQCFDNI	H-EWLLANV	-LDKAVLRKWLKAGVLE	221	
Tr.e.12	VLLKSKSHKALNPRVYVPEK	-GKDEKPLGIS	MYDRALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	NKPKVWVEGDLQCFDNI	H-DALKRT	-IADRLLALGRYLRAGVIV	244	
Tr.e.13	LVNMLMHSKASCRVYVPEK	-GKTEKPLGIS	MYDRALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	KOKSKVWVEGDLQCFDNI	H-EKLDKI	-IADRLLALGRYLRAGVIV	217	
Tr.e.14	YANLKRDLKASPKVRRVYVPEK	-GRNQKRRGIL	HLYDGLQIIVKMEPEWAEHFE	NVSYGFGRFRRCHTALVTKLQL	NDEPKVWVEGDLQCFDNI	H-HALLK	-IADRLLALGRYLRAGVIV	245	
Tr.e.15	LANNLKNKAKVRRVYVPEK	-GKRKRRKRL	GPVDRALAKLALSEPWEAKFEP	NVSYGFGRFRRCHTALVTKLQL	NQSSYVWVEGDLQCFDNI	H-RKLNK	-IADRLLALGRYLRAGVIV	219	
Tr.e.16	VYLLKSHSKALNPRVYVPEK	-GLNAKFSLIS	PMYDRALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	KKYFLD	VLDLQIIVKMEPEWAEHFE	NVSYGFGRFRRCHTALVTKLQL	263	
Tr.e.17								219	
Tr.e.18	KMRRSHKASPVRRVYVPEK	-GRRKPLGIP	PMYDRALVLLALEPVAE	VADQRFGRFRSTADAIACQFVNL	KPKKVVWVEGDLQCFDNI	H-BQLK	-IADRLLALGRYLRAGVIV	202	
S.me.11	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	HKPKVWVEGDLQCFDNI	H-DALLK	-IADRLLALGRYLRAGVIV	208	
B.j.11	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	177	
R.e.e.11	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	177	
E.c.c.11	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	177	
E.c.c.12	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	178	
P.1.12	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	178	
M.a.15-1	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	179	
M.a.15-2	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	179	
U.VB	WNRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	152	
A.v.15	WRVRSVFPVRRVYVPEK	-NG-BERPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	WQVWVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	148	
B.j.12	HGVRRQRTVRRPQVRRVYVPEK	-DG-KORPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	ETRQVNVVWVEGDLQCFDNI	H-QWVLR	-IADRLLALGRYLRAGVIV	248	
P.1.11	HGVRRQRTVRRPQVRRVYVPEK	-DG-KORPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	MERKVNWVEGDLQCFDNI	H-DLDRFR	-IADRLLALGRYLRAGVIV	220	
S.me.14	CDRVHTGSPVRRVYVPEK	-DG-KRRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	MSQVNVWVEGDLQCFDNI	H-EWLLQ	-IADRLLALGRYLRAGVIV	240	
S.m.a.11	HRRHGSRVRRPQVRRVYVPEK	-DG-KORPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	VRTNVWVEGDLQCFDNI	H-EWLLR	-IADRLLALGRYLRAGVIV	247	
N.sp.11	VLVKQVRRPQVRRVYVPEK	-DG-TRRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	NGQVWVEGDLQCFDNI	H-KFLMQ	-IADRLLALGRYLRAGVIV	236	
N.sp.12	IKQSSQNHQVRRVYVPEK	-DG-TRMPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	SKAKRNVWVEGDLQCFDNI	H-SIMEN	-IADRLLALGRYLRAGVIV	260	
N.sp.13	VLVKQVRRPQVRRVYVPEK	-DG-TRRPLGIP	VTRDLIQALLVQLIPDLFSDY	HGFGRFRRCHTALVTKLQL	ASSGQVWVEGDLQCFDNI	H-DLMMVGR	-VDRKVLIRGLYLRAGVME	179	
Ma.sp.12	K								

N.a.i.12 ---GRAHTQYSSTPOGGVSPILLANIVLH-ELDEFMAGRITAFKQKTRATINPEYRRLAGRIAKRRERLRKLEASDNADQVTVKAILAEINTLSKQMRSLPSRDAMDAGFRRLRVCRAADDFLIGVIGSKDDARGV-FAEVRTFLTEV 301
N.a.i.11 ---DWFVHKYSSTPOGGVSPILLANIVLH-ELDMFMQAKMAGFDKQQRSPSPDARRIRNRLSVVRRITVDQLRAKRRDDPVRVTSFLEEGIRLKAERLAVPASDAPDNYRRLRVCRAADDFLIGVIGSKSEARQI-MEEVRTLSDH 343
L.l.1.1 ---NWOVHKYSSTPOGGVSPILLANIVLH-ELDKFVLQKLM-----KFDRESPERITIPVYRELHNEIKRISHRLKLLKGGEEKAKVLLVEYQKRRKRLFTLCTSQTNKVLKVVYRADDPLIVSIVKSGKEDCWI-KEQCLKPFIHNE 335
B.t.c.12 ---DWFVHKYSSTPOGGVSPILLANIVLH-KFKRKLKEYIN-----FNKGVTRKSDARVYLYVEKRYLAKLKLNEKDVYKRVQMTAEIKLREERNYFARNEMDSIKRLKVVYRADDPLIVSIVKSGKEDCWI-KEDIKNLKLEA 337
C.YT.I1 ---QIKYELSSSTPOGGVSPILLANIVLH-YTIDKMELEIK-----ESTFRKAKNPEYKAYQ@MHKIKLIDQRLNLEKTKVYRADDPLIVSIVKSGKEDCWI-KQVITWMLBQD 318
D.h.1.1 ---QWENYNDVGVPOGGVSPILLANIVLH-ELDTFMSKEYAFPIHKTTHRRSSSNYCHARVNAKRYKSRATVGNLTPSEKKSMMKEQRALSQKQRETAHDVDDTFKIIQYARVADGPIVGVIGSKTDABRV-KTDKQPLAGE 343
D.h.1.2 ---DQVONALYSSTPOGGVSPILLANIVLH-ELDLVMEYEQ-RFDKGNRROAKDYGRAARTQYRKKVYDRLMLWITLTDSEKKAQRETRALRKLRECFANDPMDTYRRIQVYRCDFFVLVIGIGSKTDAEKV-KADICRFLSD 341
S.me.12 ---EDQFLRDAGTPOGGVSPILLANIALSIAEIRVERWYTH-----RKKYQARRKNSVAAASARDSRIAQRVCLVYRADDFFVVLVIGSGLEEMAE-KSALADWLK 330
E.c.14 ---VGLFRAASEGVPOGGVSPILLANIMLN-EFDQVLYHERYL-----SGKARKDRWYNNISIQRGSRSTAVRENWQWKPAVAYCRVADDFVVLVIGSKQAQAEI-REECRQVLEGS 305
S.f.1.1 ---VGLFRAASEGVPOGGVSPILLANIMLN-EFDQVLYHERYL-----SGKARKDRWYNNISIQRGSRSTAVRENWQWKPAVAYCRVADDFVVLVIGSKQAQAEI-REECRQVLEGS 306
C.sp.11 ---NGHFSSTTEGTPGGVSPILLANIALH-GLKLVKEFAA-----SQRGGKVKVQNQNSISLIRVADDFVILAP-NKQIIVL-KEIVKTLALAE- 300
G.v.1.1 ---GSELPFPTGTPGGVSPILLANIALH-GMEERKQVSK-----MAGLIRVADDFVCIHT-DQQIVVSG-QTVLEEWLAG- 281
T.sp.11 ---NKHFSSTTEGTPGGVSPILLANIALH-GMEERKQVSK-----MAGLIRVADDFVCIHT-DQQIVVSG-QTVLEEWLAG- 328
N.sp.14 YALREKSDHTSMGVPOGGVSPILLANIALH-GMNRKQVLA-----TLPGVKARNKQALIVYRADDVFLIK-DIVLLOA-KAVYQWMLG- 320
B.a.1.1 ---NKTfYKTEGTPGGVSPILLANIALH-GMEKELVRYH-----FKPRDQAMLYPDSIGVYRADDVVICN-KKEAESM-YAKLQVLDK- 310
B.c.1.1 ---QSFAEQEOTPOGGVSPILLANIALH-GMEELGITYK-----KNYKANDSYMNPACTFLIRVADDFVILAP-KEQALSV-YMRLRPLKD- 307
E.c.1.5 ---KQQLFVNSGTPGGVSPILLANIALD-GLBALLASEFK-----KRTVKGRLVNKNVYRADDVFIIGE-SKELLESOVLVYRFFMAE- 306
A.v.1.1 ---SGQLNPGAGTPOGGVSPILLANIALD-GLKALSERFG-----QRNTKASYTKVNVYRADDVFIIGI-SKELLVNEKVPVAAVFAE- 304
B.t.1.1 ---NKELFPEEGTPGGVSPILLANIMLD-GLQTMALAKYH-----KKFVTRKTTTYYPVHLVYRADDVFIIGR-NKEALEI-KPLVDFLKE- 306
B.me.12 ---QDMLHTTEGTPGGVSPILLANIALC-GMEETGITVYK-----KTYKSNGGYKIDPKCKIGRVLVADDFVIVLE-KKEQAESM-YQMLVPLRK- 312
A.v.1.3 ---GTLFAEAGTPOGGVSPILLANIMLD-GLBQAALTSVA-----STERRRPFKVVAVYRADDVFIIGA-KSLLEHQRVPAEAFLEK- 310
B.f.1.1 ---DGVVQERQCTPOGGVSPILLANVLLD-EVDKALERGH-----CFVYVADDCNVYVR-RRAGRVYRALLRRLKRL- 293
B.f.1.2 ---DGVVQERQCTPOGGVSPILLANVLLD-EVDKALERGH-----CFVYVADDCNVYVR-RRAGRVYRALLRRLKRL- 293
Ma.sp.11 ---KGAFAHAEAGTPOGGVSPILLANMALLD-GLDALQARFG-----SKISPRKACRNLVYRADDVFIIGS-PELLENEKVPVONFLSE- 308
R.m.1.1 ---OGQFQAEAGTPOGGVSPILLANVALN-GLQQARFLE-----TTLGVNQTRKLVNVYRADDVFIIGS-PEVLEHEKVPVWEQFLAI- 273
Tr.e.18 ---AEVPHKEGTSSRGISPLLANIAFD-GMERLLARYKT-----VKTYQCTPTDDEYTKKKLKDQVYRADDVFIIGS-SEEDIKAIPIETEK-WLSE- 321
P.p.1.2 ---EGLTFAOAGTPOGGVSPILLANMALLD-GLAAVHASVG-----PTKRAREKSNVYRADDVFIIGI-SKEILHSLVPAVQFMAI- 310
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N.a.I2  ---HRDQATRKA-----TARARKKVL-CVPCFKATHGGFLPEQR-----
N.a.I1  ---HAGFSRHMA-----AARQQRKRVL-CGRCHNDVHAGCPTRDRRTARSRGEFNALKGARSVRRGA
L.l.I1  ---GKERWEMAM-----TARQRKLVV-CFCHHRHVIHKHK-----
B.t.I2  ---GKSDWEKMK-----LARRRKLAV-CSCCHAKIDPDRRLRLN-----
G.Y.T1  ---RKSVMNKST-----KVLCLDCHEMTDQQMHDRLNKKKKKKRINS
D.h.I1  ---GSRWVERVM-----TERRRKLVV-CPCYQOIH-----
D.h.I2  ---GSHFWVERVM-----LKMRRKLVV-CNECHRALHSVDSE-----
S.me.I2 -----
E.c.I4 -----
S.f.I1 -----
C.sp.I1 -----KDVVDNLQALRRHCHDVKTAADNSYNQPKSDTEINVMW-----
G.v.I1 -----RNISSNKQLLRRHCHQKTAARIRIQQLSQSRITAEERLQLOAKRQALLEDYQPYKSKKRITDAEWMGQW
T.sp.I1 -----DMSIKNKQLLRRHCHQKTAALDNKTYKILDLDEYEWVNDMLLKKQCTYTVKGRSSEEDPEVKVSR
N.sp.I4 -----KDSYDNLQALRRHCHQKTAEDKCAVTVEDEEDYVNLNRF-----
B.a.I1  -----KDEYDNLLELHCSCHKQEHALLEWYSGKGLPKVQAMLRKSQKIFINSKKAVRTMLNFTFKFKK
B.c.I1  -----SNLNLKLVHLPCLY-----
E.c.I5 -----SNCLSNLMLHPM-CHTLVHAKGIHVVKPAHESGRKA-----
A.v.I1  -----GDELDNLVLLHPN-CHRLVHSAAPALSIEKGLTKA-----
B.t.I1  LLDHSCRRKVIQTNMK-----
B.me.I2 LVHVPCK-----
A.v.I3 -----
B.f.I1 -----
B.f.I2 -----
Ma.sp.I1 -----
R.m.I1 -----SDALGNRVLLHPNCHVQVHEHGRTVVKFVLEMSL
Tr.e.I8 -----
P.p.I2 -----
M.a.I1-1 -----
M.a.I1-2 -----
M.a.I1-3 -----
M.m.I1-1 -----
M.m.I1-2 -----
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R.r.I1 -----
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M.sp.I1 -----
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P.a.I1 -----
P.a.I2 -----
S.t.I1 -----
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C.d.I1  EVHHIKPLSLGSDNNKLVIVTKETHLHAHKRETIVHMLPVLKKERSLEKLNKLRALAGNSETEMNY-----
B.a.I2  HCHHKRWSETKDSSKLLILKPSVHRLIHAHKTEETINQLNLELKFNEEGLKLNKLRKLVKNEECI-----
E.f.I1  HCHHIVPTAGSGNDKLLVKEAVHRLIHAHKTEETIQKYLALLNKLVQILRLNKRVLVLAGNPELNLI-----
E.f.I3  HCHHVPVNSGSDSEVAVNLVSKAVHLLIHASSEPTIEKYLKSLNDNKOIEKLNKLRKLVKNEECPIL-----
E.f.I4  HCHHYLPKSLGGDDKFDLRIIHKDIHLLIHTNKMIIIDHVNLKLLPEQIAKINLYRKMKNLQNIQ-----
E.f.I5  ECHHINPYHLSKDDSKLVLIISREIHLIHAHTEETILKLLRLLKLNHYQIRKLNLYRKKANFPISLKMN-----
E.f.I2  HCHHKLWSEKDDSKNLLLSKEMHKLVHCTDEVKIREVLYWNKLSDSVNVKVKLRKLVNKTITLPLCEQMPKYEGLTLF-----
N.p.I1  NHDNWKNNLVAIHMCCHQIHS@TAQAENIQEPVAKATRPVLKERCGR-----
Th.e.I1 QVHSDRQHSRSLKEGL-----
Tr.e.I2 KI-----
Tr.e.I3 -----
Tr.e.I4 RSEKGNSTSKNKELLRHCHDTKTALEREISQSED-----
Tr.e.I5 -----
Tr.e.I6 GNSQDLPECYLWVNDMLTLKQCTLELGLLEEPDEAKVSCPVLKTSRVG-----
Tr.e.I7 RSEGGDNTTKNKQLLRRHCHDTKTA-----
S.me.I1 -----
B.j.I1 -----
R.e.I1 -----
E.c.I1 -----
E.c.I3 -----
E.c.I2 -----
P.l.I2 -----
M.a.I5-1 -----
M.a.I5-2 -----
M.a.I5-3 -----
UMB -----
A.v.I5 -----
B.j.I2 -----
P.l.I1 -----
S.me.I4 -----
S.ma.I1 -----
N.sp.I1 -----
N.sp.I2 -----
N.sp.I3 -----
Ma.sp.I2 -----
S.ag.I2 -----
ruler .....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870...

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