CLUSTAL O (1.2.4) multiple sequence alignment

*Bg*FREP3.3 AEO50747.1 --MLLSLELIRKFPTDTRSSHELVIDAQPEVISLELTPQLVVNCSITDSHVPGLDTINSL 58

*Bg*FREP3.3 AAO59915.1 MARLFLLFILC-VFVVSLAGSELVIDVQPNVISPEITPQLVINCSITNNEVQQLDLIKSL 59

*Bg*FREP3.2 AEO50746.1 MERLFLLLVLC-VFVVSLAGSELVIDVQPNVISPEITPQLVINCSITNNKVQQLDLIKSL 59

*Bg*FREP3.2 AAK28656.1 MARLFLLFILC-VFVVSLAGSELVIDVQPNVISPEITPQLVINCSITNNEVQTLDLIKSL 59

*Bg*FREP3.1 AEO50745.1 MARLFPRLVLC-VFIVPLAGSELVIDVQPNVISPEITPQLVINCSVTNNQVQHLEVIKSL 59

*Bg*MFREP3 AAK13548.1 ---LFLLFILC-VFVVSLAGSELVIDVQPNVISPEITPQLVINCSITNNEVQTLDLIKSL 56

*Bg*FREP3.3 \*: :: . :. \*\*\*\*\*.\*\*:\*\*\* \*:\*\*\*\*\*:\*\*\*:\*:..\* \*: \*:\*\*

*Bg*FREP3.3 AEO50747.1 SLSRYNETKKEFDVLLSLDTHTLSLQQLVQFRHAQISFGNLYVTLTLRNPTQSDAKVYRC 118

*Bg*FREP3.3 AAO59915.1 TLSRYNETIREFDDLIALDSLTLNLKQFVRFKYSQISFGNLYITLTLPNPTQFDARIYKC 119

*Bg*FREP3.2 AEO50746.1 TLSRYNETIRDFDELIALDSLTLNLKQFVRFKYSQISFGNRYITLILHNPTQFDARIYKC 119

*Bg*FREP3.2 AAK28656.1 TLSRYNETIREFDELIALDSLTLNLKQFVRFKYSQISFGNRYITLILHNPTQFDARIYKC 119

*Bg*FREP3.1 AEO50745.1 TLSRYNEIIREFDELIALDSLTQNLKQFVRFKYSQISFGNLYITLTLPNPTQFDARIYRC 119

*Bg*MFREP3 AAK13548.1 TLSRYNETIREFDELIALDSLTLNLKQFVRFKYSQISFGNRYITLILHNPTQFDARIYKC 116

*Bg*FREP3.3 :\*\*\*\*\*\* ::\*\* \*::\*\*: \* .\*:\*:\*:\*:::\*\*\*\*\*\* \*:\*\* \* \*\*\*\* \*\*::\*:\*

*Bg*FREP3.3 AEO50747.1 NVSGDDSLWKNITRVFKKEIKYETNLTVLLEEIRRLREEKDRDQLSCQKEKLN----DSK 174

*Bg*FREP3.3 AAO59915.1 NATGANSDGTNISLFAKKAVEYETNSTALIEEIRRIKKDENY--CSFKKDDLADIKQRSR 177

*Bg*FREP3.2 AEO50746.1 NATGDNSEGANISLFAKKGVEYETNSTALIEEIRRIKKDENY--CSFKKDDLSDSKQRSR 177

*Bg*FREP3.2 AAK28656.1 NATGTNSEGANISLFAKKAVEYETNSTALIEEIRRIKKDENY--CSFKKDDLSDSKQRSR 177

*Bg*FREP3.1 AEO50745.1 NADGANSEGTNISLFTKKAVEYETNSTALIEEIRRIKKDENK--CSLKKDDLSDIKQRWR 177

*Bg*MFREP3 AAK13548.1 NATGTNSEGANISLFAKKAVEYETNSTALIEEIRRIKKDENY--CSFKKDDLSDXKQRSR 174

*Bg*FREP3.3 \*. \* :\* \*\*: . \*\* ::\*\*\*\* \*.\*:\*\*\*\*\*:::::: \* :\*:.\* :

*Bg*FREP3.3 AEO50747.1 LHFVGNSKVVKELFDPLTLTCSIQDLMNDRNETSTVQSIYILHEANGIIATISKDQPVVT 234

*Bg*FREP3.3 AAO59915.1 VYFSGSSDIIKERIEPLTLKCTFQVLKTDQNDTSRLQSLYILHESKGVIAYVNKDQPVVT 237

*Bg*FREP3.2 AEO50746.1 VYFSGSSDIIKERIEPLTLKCTFQVLKTDQNEISRLQSLYILHETKGVIAYVNKDQPVVT 237

*Bg*FREP3.2 AAK28656.1 VYFSGSSDIIKERIEPLTLKCTFQVLKTDQNETSRLQSLYILHESKGVIAYVNKDQPVVT 237

*Bg*FREP3.1 AEO50745.1 VYFSESSKIIKERIEPLTLKCTFQILTPDENETSRLQSLYILHESNGVVANINKDQAVIT 237

*Bg*MFREP3 AAK13548.1 VYFSGSSDIIKERIEPLTLKCTFQVLKTDQNETSRLQSLYILHESKGVIAYVNKDQPVVT 234

*Bg*FREP3.3 ::\* .\*.::\*\* ::\*\*\*\*.\*::\* \* \*.\*: \* :\*\*:\*\*\*\*\*::\*::\* :.\*\*\* \*:\*

*Bg*FREP3.3 AEO50747.1 TNQDVNLLAVIGKLHDDSSKNSYLQVTWSNPKFSESGKYFCGAHANNAQGRNEHWNEMLT 294

*Bg*FREP3.3 AAO59915.1 SLQGSNIQDVEGEIYDNAIKDSYLQVTWSNLKHSESGKYFCEAHNKYSEGRIDKSSNMLT 297

*Bg*FREP3.2 AEO50746.1 SLQGSHIQDVEGEIYDNAIKDSYLQVTWSNLKHTESGKYFCEAHNQYSEGRIDKTSNMLT 297

*Bg*FREP3.2 AAK28656.1 SLQGSNIQDVEGEIYDNAIKDSYLQVTWSNLKHSESGKYFCEAHNKYSEGRIDKSSNMLT 297

*Bg*FREP3.1 AEO50745.1 TIQGGNFENAQGEISGDQSKESYLQVTWSNLKHSDSGKYFCEAHVKHSKGKAERLNEMLT 297

*Bg*MFREP3 AAK13548.1 SLQGSNIQDVEGEIYDNAIKDSYLQVTWSNLKHSESGKYFCEAHNXYSEGRIDXSSNMLT 294

*Bg*FREP3.3 : \*. :: . \*:: .: \*:\*\*\*\*\*\*\*\*\* \*.::\*\*\*\*\*\* \*\* ::\*: : .:\*\*\*

*Bg*FREP3.3 AEO50747.1 ITVERLQFDDIVKVMYDIQRQVDEDKKRLQTFHENLTNNFIILNTNLQSIENVRRDVRTN 354

*Bg*FREP3.3 AAO59915.1 ITVERPTFDDLVEAMHKLFTQVDGAKESLKAINQNIKN---------------------- 335

*Bg*FREP3.2 AEO50746.1 ITVERPTFDDLVEAMHKLFTQVDGAKESLKAINQNIKN---------------------- 335

*Bg*FREP3.2 AAK28656.1 ITVERPTFDDLVEAMHKLFTQVDGAKESLKAINQNIKN---------------------- 335

*Bg*FREP3.1 AEO50745.1 IEVISPTIDDLMEVIQKLVTQVDGDKESLQDVKQNIMN---------------------- 335

*Bg*MFREP3 AAK13548.1 ITVERPTFDDLVEAXXKLFTQVDGAKESLKAINQNIKN---------------------- 332

*Bg*FREP3.3 \* \* :\*\*:::. .: \*\*\* \*: \*: .::\*: \*

*Bg*FREP3.3 AEO50747.1 QESINGIKDELLSNKQNIVNNKKDINTAKESINVIKEELLSNKQNIVNNKRDIDTMEESI 414

*Bg*FREP3.3 AAO59915.1 --------------------INKDLDFKEQNITSIKQEVIRNQNNIQILSEDLNIKE--- 372

*Bg*FREP3.2 AEO50746.1 --------------------INKDLDFKEQNITSIKEEVIRNQNNIQILSEDSNIKE--- 372

*Bg*FREP3.2 AAK28656.1 --------------------INKDLDFKEQNITSIKQEVIRNQNNIQILSEDLNIKE--- 372

*Bg*FREP3.1 AEO50745.1 --------------------IKEDLNTKEQNIISIKEDLNTKQQSIISIKEEFKTKQ--- 372

*Bg*MFREP3 AAK13548.1 --------------------INKDLDFKEQNITSIKQEVIRNQNNIQILSEDLNIKE--- 369

*Bg*FREP3.3 ::\*:: ::.\* \*\*::: :::.\* ..: . :

*Bg*FREP3.3 AEO50747.1 NVIRHELLSNKQNIVNNKKDIHTTQESIIGILEELLRNQQNIVNNKKDINTTQDSIREIQ 474

*Bg*FREP3.3 AAO59915.1 ---------------------------------------QNLTSIKADLSTKQQTFLNIK 393

*Bg*FREP3.2 AEO50746.1 ---------------------------------------QNMTSIREDLSTKQQTFLNIK 393

*Bg*FREP3.2 AAK28656.1 ---------------------------------------QNLTSIKADLSTKQQTFLNIK 393

*Bg*FREP3.1 AEO50745.1 ---------------------------------------EN---IQKDVTINQQNIQKIK 390

*Bg*MFREP3 AAK13548.1 ---------------------------------------QNLTSIKADLSTKQQTFLNIK 390

*Bg*FREP3.3 :\* : \*:. .\*:.: :\*:

*Bg*FREP3.3 AEO50747.1 EELLRNQQNIENAKEELKSKQDSMKSIQDELLSNLHNMNISSIWKVLSNFSTAVMDMKDD 534

*Bg*FREP3.3 AAO59915.1 EDVILNQQIIHKIKQDLNTYRHNMSNIEE------------HLEVILANLSTASIKVKNQ 441

*Bg*FREP3.2 AEO50746.1 EDVILNQQNIDKIKQDLNTYRHNMSYIEE------------HLEVILANLSSASMKVKNQ 441

*Bg*FREP3.2 AAK28656.1 EDVILNQQIIHKIKQDLNTYRHNMSNIEE------------HLEVILTNLSTASIKVKNQ 441

*Bg*FREP3.1 AEO50745.1 EELDSKEQSMIIIREDFSACQQNISAFKE------------NIEIMFANLSTSFMQVKTQ 438

*Bg*MFREP3 AAK13548.1 EDVILNQQIIHKIKQDLNTYRHNMSNIEE------------HLEVILTNLSTASIKVKNQ 438

*Bg*FREP3.3 \*:: ::\* : ::::.: :..:. ::: : :::\*:\*:: :.:\* :

*Bg*FREP3.3 AEO50747.1 IDKGKTEIKQNKSSITKLHPRSCRDVNSTDDRVVVTLASGLKVMCDTKTDGGGWIIFQRR 594

*Bg*FREP3.3 AAO59915.1 TDEGSK--------MSYPHRKSCRDVNSTEERVVVTLTSGLKVMCDTKTDGGGWIIFQRR 493

*Bg*FREP3.2 AEO50746.1 TDEGST--------LSYPPRKSCRDVNSTDERVVVTLTSGLKVMCDTKTDGGGWIIFQRR 493

*Bg*FREP3.2 AAK28656.1 TDEGSK--------MSYPPRKSCRDVNSTDERVVVTLTSGLKVMCDTKTDGGGWIIFQRR 493

*Bg*FREP3.1 AEO50745.1 INKGNQE------DQHLIPKIICRDVNSTDERVVVTLTSGLKVMCDTKTDGGGWIIFQRR 492

*Bg*MFREP3 AAK13548.1 TDEGSK--------MSYPPRKSCRXVNSTDDRVVVTLASGLKVMCDTKTDGGGWIIFQRR 490

*Bg*FREP3.3 ::\*. \*\* \*\*\*\*::\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

*Bg*FREP3.3 AEO50747.1 INGSVDFYRGWQEYRDGFGDYNIGEFYLGNENIYMLTSTGQYDLRIDLKYKNNSFFAQYS 654

*Bg*FREP3.3 AAO59915.1 INGSVDFYRDWKEYRDGFGDYNIGEFYLGNENIFNLTSNGQYNLRIDLKYKNNAFFAQYS 553

*Bg*FREP3.2 AEO50746.1 ISGNVDFYRGWKEYRDGFGDYNIGEFYLGNENIYMLTSTGQYDLRIDLKYKNNAFFAQYS 553

*Bg*FREP3.2 AAK28656.1 INGNVDFYRGWKEYRDGFGDYNIGEFYLGNENIYMLTSTGQYNLRIDLKYKNKAFFAQYS 553

*Bg*FREP3.1 AEO50745.1 INGKVDFYRGWKEYRDGFGDYTIGEFYLGNEYISKLTSTRNFDLRIDFKYNHKTYFVEYS 552

*Bg*MFREP3 AAK13548.1 INGSVDFYRGWKEYRDGFGDYNIGEFYLGNENIYMLTSTGQYNLRIDLKYKNKAFFAQYS 550

*Bg*FREP3.3 \*.\*.\*\*\*\*\*.\*:\*\*\*\*\*\*\*\*\*.\*\*\*\*\*\*\*\*\* \* \*\*\*. :::\*\*\*\*:\*\*:::::\*.:\*\*

*Bg*FREP3.3 AEO50747.1 SFKILSEKEKYKLNIGVYSGNAGDSFSRHNNSFFTTFDRDNDENSSNCAVVYTGAWWYKR 714

*Bg*FREP3.3 AAO59915.1 SFKILSEKEKYKLNIGAYSGNAGDSFSYHNNAFFTTFDRDNDEHSSNCAVEFRGGWWYHS 613

*Bg*FREP3.2 AEO50746.1 GFKILSEKEKYKLNIGVYSGNAGDSFSIHNNSFFTTFDRDNDENSSNCAVDYTGAWWYQS 613

*Bg*FREP3.2 AAK28656.1 GFKILSEKEKYKLNIGAYSGNSGDNFSSHNNAFFTTFDRDNDEYSYNCAVDYTGAWWYHS 613

*Bg*FREP3.1 AEO50745.1 DFRILNETNNYQLKIGKYKGNASDEFSYHNNMQFSTFDRDNDVDKRNCALQFTGAWWYH- 611

*Bg*MFREP3 AAK13548.1 GFKILSEKEKYKLNIGAYSGNSGDNFSSHNNAFFTTFDRDNDEYSYNCAVDYTGAWWYHS 610

*Bg*FREP3.3 .\*:\*\*.\*.::\*:\*:\*\* \*.\*\*:.\*.\*\* \*\*\* \*:\*\*\*\*\*\*\* . \*\*\*: : \*.\*\*\*:

*Bg*FREP3.3 AEO50747.1 GCHHSNLNGKWGSSDHGKGVNWHVVSNFDSSVSFTEIKIREI 756

*Bg*FREP3.3 AAO59915.1 GCLHCNLNGQWGSTDHGKGVNWYDLSKYDSSLSFTEMKIREI 655

*Bg*FREP3.2 AEO50746.1 GCHSCNLNGKWGSTDYGKGVNWYTLSTFYSSLSFTEMKIREI 655

*Bg*FREP3.2 AAK28656.1 SCLNCNLNGKWGSSDFAKGVNWYDLSRFDSSVSFTEMKIREI 655

*Bg*FREP3.1 AEO50745.1 SCHYSNLNGQWGSKEYSKGANWESITGYEASVSFVEMKIRER 653

*Bg*MFREP3 AAK13548.1 SCLNCNLNGKWGSSDFAKGVNWYDLSRFDSSVSFTEMKIREI 652

*Bg*FREP3.3 .\* .\*\*\*\*:\*\*\*.:..\*\*.\*\* :: : :\*:\*\*.\*:\*\*\*\*

**Figure 1—figure supplement 6. Alignment of multiple *Bg*FREP3 amino acid sequences and distribution of identified peptides.**