

Supplementary Figure S4

IMC1

Identity 72.1%; Similarity: 83.7%

| | | |
|--------|--|-----|
| TgIMC1 | MFKDCADPCSDCCQPAEQQRGQATLPSHVLPQTS DSPAIHVTAEASQRLS-SPRALQQL | 59 |
| SnIMC1 | MFQECCEKASNCQPSDEAALRENVARSSAIGEGRVAGAA-PAGTSQEQTNMAESSSS *: | 59 |
| TgIMC1 | HGTQESVRSVTLEERADRSRTVPIGEETERQWVAITAYQPIDTVTKTVEVPVVRTVETYY | 119 |
| SnIMC1 | TQVQDAYQSVTLEERADRSRTAPVTEQTERQWVAITAYQPIDTVTKTVEVPVVRTVETYY *: | 119 |
| TgIMC1 | PKVVVEEKIVEVPKYIPEYVEKVVVEPEVQYVDKIVEVPEYQYQYKYPKVIETKENIIQR | 179 |
| SnIMC1 | PKVVVEEKIIQVPKYVPEYVEKVVVEPEVKYVDKLEIPDYQFQYKYPKVIETKENVIQR *: | 179 |
| TgIMC1 | PKYETKYIEKVVEVAQVKEVVRVYQDVEEVEEIIIRYVPKDSVPEEWKRIQEEQDKRAEAL | 239 |
| SnIMC1 | PKYETKYTEKVVEVSQVKEVVRVYQEVVEEIIIRYVPKGHAIPEEWKRAQEEQQRREEEK *: | 239 |
| TgIMC1 | KEKEAKEEEEELKGLLEERKLHEERVREQIKVQQQIIQQQLSARAEQERLLKERREAEMV | 299 |
| SnIMC1 | KEKEAQEKQALEGLLAEKELQDKRMTDQQRIQQEIVQRQ---RAEHERIIKERKEAERL *: | 296 |
| TgIMC1 | HFPVAVGAPPLPTIPKVEQVFKPKVIKQVEIQKHVPIISVDVPPYMPKPVVVSQVQVPL | 359 |
| SnIMC1 | QYGLPEGAPPMPFIPKVEQVFKPKVVKQVEIQKHVPIISVDVPPYMPKPVVVPVQVQVPL *: | 356 |
| TgIMC1 | KFRDHFVVPVRRRVPRIRWTNEVYEVECIKEKPFQVQDVIKPVPCDVEIRVHEFVER | 419 |
| SnIMC1 | KFRDHFVVPVRRRVIPRIRWTNEVYEVECIKEKPFQVQDVIKPVPCDVEIKVHEFVER *: | 416 |
| TgIMC1 | AAPINPAELSQADIHAMWVRNADLAEKRKQELGDKYPYVKHPAGTVFGEPGCSEEEGEV | 479 |
| SnIMC1 | AAPINPAELSQADIHAMWVRNADLAEKRKAEELGDKYPYVKHPAGTVFGEPGCSEGEV *: | 476 |
| TgIMC1 | ESAQAEEGGQPAGAEPALALHPGHPLNMTYLQNEWIKKSTVTTHEMYTPEWFEAHQKALFN | 539 |
| SnIMC1 | G-GEAQEGEAREGVEPLALHPGHPLNMTYLQNEWIKKETTATHEMYTPEWFEAHQKALHN *: | 535 |
| TgIMC1 | LTMQPTQVQLSAEQAAKLQQEAQFGDAPWIEEAHAGVPMKPAAPEPEAAQCCVMCAV- | 598 |
| SnIMC1 | LTMQHPTQVQLSAEQASQLQQEQPQFGAPWLDEGVTTQKKGRARDVADSQCCPVCNSV *: | 595 |
| TgIMC1 | -CGGDGVCRCQC | 609 |
| SnIMC1 | CGGDGVCCKCEC *:*:*:*:*:*: | 607 |

IMC3

Full length protein identity 56.0%; Similarity: 66.8%

Fragment for antiserum generation identity 33.5%; Similarity: 43.7%

| | | |
|--------|---|-----|
| TgIMC3 | -----MSDAGT-----PPAVQGELSQPQERVEVVVQPISESPDAS | 35 |
| SnIMC3 | MASPEADASSASPAGPGGATDTEVEQTPGIAAERRTGVLTEGGQQVQITIQIPAL---T | 57 |
| | * | |
| TgIMC3 | SEAEQAGVAAGAFHAEVYPYPPVSTGMPAPEQPAEMHLLPA-----NGQLPEI | 83 |
| SnIMC3 | GGPGSVQIEERTFHSEVYPYHPVVSATLPSQEGPKYGGSPAESAETAEAGRAVGVPVAV | 117 |
| | . . . : : * | |
| TgIMC3 | -AEGAETEGLLAPVARPPPQVMTALGPMPLPPEVRQKIPEKRVAKPIVEEREIYVSKKEVR | 142 |
| SnIMC3 | YDADEVAGGAGPVARPPPQVMTALGPMPLPAEIRKKIPEKRVAKPIVEEREIVAKKEVQ | 177 |
| | . : * . * | |
| TgIMC3 | ERTIEVPHVHYEHKFAEVARSLKIKKLVPRVREVVEIPREVIKPIVEEKVIEVPQGVKY | 202 |
| SnIMC3 | ERTVEVPHVHYEHKFAEVATKLIKKLVPRVTEVIKEVPREVIKPIVEEKVIEVPQGVKY | 237 |
| | * | |
| TgIMC3 | VEVPEVPCLYPKIVPKPKVQVIERIVETIKPVVKEKIVEVPTVVQIPKIKTVEVPY | 262 |
| SnIMC3 | VEVPEVPCMYPKIVAKPKIQVVERVETIKPVVKEKIVEVPTVVQIPKIKTVEVPY | 297 |
| | * | |
| TgIMC3 | YVPRYVEKVIPIPYQPPDAATLPLMVGGLPSRVSATMPTPFQVGPAGHANEVNLNPF | 322 |
| SnIMC3 | YVPRYVEKVIPIPYQPPDTATLPMVMGGLPSRITATMPTPFQVGPVAGQVSEFNLNPF | 357 |
| | * | |
| TgIMC3 | ARVDVTVSQSPAGPHSPLSASPQTGTAASLK----LGRPATLVNPDRSAPAIIDLPEGFT | 378 |
| SnIMC3 | AKVDIKVSHGPTGLSATFPA--PGLLPPQSVGGTDSGAATRMSPGSPGPAIELPEGFQ | 415 |
| | * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : | |
| TgIMC3 | WGPPPNAPPGTFPA-----PAMPGPGAAGLPV | 406 |
| SnIMC3 | WGPPPNAPPLTPLCQPVAGSIFSGTPGGGARAREGSVSLTGLPPSAVPGFPA--SGPAG | 474 |
| | * | |
| TgIMC3 | GAADGLNMPPMITCPPEVGNVVFAGFLADPDILTRRGVMAYQGFKEGTFQMLFPPLAP | 466 |
| SnIMC3 | GGPNVMNMPMITCPPEVGNVQVFSGLSDPDILTRSGVMAYQSFKRKGTQMLFPPLAP | 534 |
| | * . : : * | |
| TgIMC3 | QFGIPLDQGTGAPDVNTIVSVNEQMAQSRHHLIEDLQQQVESEFDQK-----VNASAMS | 520 |
| SnIMC3 | QPGVPMNPPGTPDVRTLDQVASQAAGQGRHDVLEAIQKAEEHEHERASKAGLASVLSACAP | 594 |
| | * * * * * * * : * * * * * * . * . * * * * . * * * : * * * * * * * * * * * | |
| TgIMC3 | CTPWASPAVQEREVVEEQ | 538 |
| SnIMC3 | CESCAPEVTPQREIVVEEQ | 612 |
| | * * . . : * * * * * * | |

IMC7

Full length protein identity 24.5%; Similarity: 39.0%

Fragment for antiserum generation identity 23.6%; Similarity: 40.9%

| | | |
|--------|---|-----|
| TgIMC7 | -----MEFT-----ADNA | 8 |
| SnIMC7 | MKGFTPQAYEGWCQPVAIPIIPNPGEYTMRSCTRWGACCGTWKRMYPYQTFPLITTYVRGA | 60 |
| | * : . . * | |
| TgIMC7 | APLTEQNAPQDV--EAVKPDVIENAAETANEESAAPTLKRLVSKTTHIKTVTESLSRKQT | 66 |
| SnIMC7 | LPYIEHEKLMSTNGLAVAPQRAAVKVRVSGSKTSPMVGNGTQITMVGSGTQITIPVVG | 120 |
| | * * : . . * * : : * : . . . * : : * : : * | |
| TgIMC7 | KEI-----TTNTLHMGWKETKEAFLAPRSTITHADGSESEIARFVPSVQVVDLPLDLVYT | 121 |
| SnIMC7 | QTIPVVGSGTQITIPVREVTEENTCMK-----PRVLTQVIECEDTKY | 161 |
| | : * * : * : * : : : * * . : : . | |
| TgIMC7 | VPEVKTRMVNYIFECFARGHSRLVPREFPVDTPFVVPQYQDVSVPVVMSQTFVPELQETS | 181 |
| SnIMC7 | IPKVEVRTVQRTIEVASKTEKRFVPREVPVDTPFIVPRFEDRDVPVVVSNTISPEIBETE | 221 |
| | : * : . * * : * : . . : * * * * * : * : * * * * * : * * : * * : | |
| TgIMC7 | RVVQVPVARYVPKLVPVDVFPVPRVAIPIKAGEVTQVSKNTVISDDLMRQLSVEMNPHLE | 241 |
| SnIMC7 | AVVEVPVARYVPHLVPINVYVPRVAIPVVLDESQEAAPALPTESLQQLIKELNPHLE | 281 |
| | * * : * * * * * : * * : * * * * * : : : . : : : : * * * * * : | |
| TgIMC7 | ALNQFNAQQAQVMNNVVARAQELATQMDCPVPSREKIEVNASAGSGAGATIVDEQGNKQL | 301 |
| SnIMC7 | EIDKFNAGQNVKFQELLEKSQKAANFAKCPVPEPQSTPILKITEIEPEGE-ESDHLVKQI | 340 |
| | : : * * * * : : : : : * : * . * * * * . : : : : . : : * * : | |
| TgIMC7 | QLDMGGKELRSVEMVFKRLHDDINTSKCVEENMQITEDIILCVHRDLNGGRLESFPGNA | 361 |
| SnIMC7 | CFSTGGYQAAEVESLFTALTATSTTDSEAD-----TSAHKGMSGEQTDPDPT---- | 387 |
| | : . * * : . * * : * . * . * . . : : . . * : : * : : | |
| TgIMC7 | GIPMIFRAPDQKPSVANGLPERVPLRSLTNDLSHAAAQNESATTTGEASLPTALNAEQ | 421 |
| SnIMC7 | -----HDDMLSAATGASDSQRCTSV---MSGKDATEGVAAVASGKASATTEERKSDA | 436 |
| | * : * * . * : * : * * * : * : * * * * * * . . : | |
| TgIMC7 | TTAVPIAA | 429 |
| SnIMC7 | SKA----A | 440 |
| | : . * * | |

IMC15

Full length protein identity 25.5%; Similarity: 34.7%

Fragment for antiserum generation identity 15.8%; Similarity: 23.8%

| | | |
|---------|---|-----|
| TgIMC15 | ----- | 0 |
| SnIMC15 | MAFDLPKVPRLPEPGSAAVPLPSLPSFAAAAATHRPLRCLGTFIVEATPASAGAQTKR | 60 |
| TgIMC15 | ----- | 0 |
| SnIMC15 | RATRSSSCCHSRFCFRSSSCRRYSMTSTSGNRDTSSSSVTASNTANSSQPAGLRDNSKGS | 120 |
| TgIMC15 | ----- MRICLPPVPQGREAVPDASANVRRQAFSERFRQCEHER | 38 |
| SnIMC15 | FASLCCNGEAAAAASFQGYSDVHGCYPPPAAGARGDDGSRNGMPKHVVDQK-----NVA :: * ** * .. .: .: ::::: : : | 175 |
| TgIMC15 | LPSGVPRPQTTPRCSGTILIEPAPTGTNNRQQAPTGRCDMSGSCASV-----A-E | 87 |
| SnIMC15 | AAAAVDDCLVPACRSRINGS CFL--RNCCPEEGAAASVAPSCAPAAAHVLRPEEAKA :. * . * ** : * . . * . . : : *** . * | 232 |
| TgIMC15 | SAAACLWQTSPRRWRPTPREPKMCFEEPSQSL-----RFRTSPRPFSCAETTR--M | 139 |
| SnIMC15 | GSSCCCFARRSR-ASSSPSTASPCVPNGLIPRPRVLTAGTAVTPRRFSFTDLRSATVL .:::** : * : * . * . : ** *** :: : : | 291 |
| TgIMC15 | CTTPCSSTD-----DR-----CTSRRSIYGTPQIQT-----FSASS- | 170 |
| SnIMC15 | PSPPARTTAAAPPQEKHQMLQQQLQQQQQLQQQQQLQQQQQLQQQQQLQQQQQLQQQQQL : * . : * : : . : : : * : * : : . . | 351 |
| TgIMC15 | -AGTQAYIRPLGQSSRSVSPWQSALAPASSAVSSTETH---GIGI-----Y | 213 |
| SnIMC15 | QLQQQQQLQQQQQRPFTTFWWEPS TDSASSCCRAGQAKEQRQLLLHAATAPLPLSSSL * : : * : . * : : * * . : : : : : | 411 |
| TgIMC15 | ATQSQQASHVRVTGGVDSILGPSAPA-----P--TVSSP-----SHIP | 249 |
| SnIMC15 | HAPHPLAVHIYGGLESLVAVALSLLGNSNIGLLGNLFLPATAKKKSTTPQLNRAP : . : * : : * * : : : . * : : * : . . : : * | 471 |
| TgIMC15 | AFSQSSCGSTNSAPGNGQS-----TWCQTSPTVTVGGQANA | 284 |
| SnIMC15 | ALKEAA---FSSPGKERRKSRDAGPPCLSGTTSRMTTASSMSPFCSSPPCNSSGSSTP * : : : : * : * : : : * . : * . * . : . | 527 |
| TgIMC15 | SA-QVKI--AQAPAAASSQPNYSRAKT TQAVVEQKMVPEGYDRVEHMPRLRPVSVVENR | 341 |
| SnIMC15 | PSFHHRQASSWSPRRGLGAP-VAATGQSGVVENQLLRNEGYEKHEVIVPLLRPVKIVEKQ : : : : : * . . * : : : . * : * : * * : : * * * * . : * * : * | 586 |
| TgIMC15 | IEIPVVKVVD TIVHKQKIEERIRFVDKPVQVEVEKFVEVPEVIYSDVIVEVPEIVEVIKH | 401 |
| SnIMC15 | VEVPLIKRVDTVVPAARIEEKITFIDKPIVQQVERFVEVPEVHYTDVIVEVPEVIHVEKR : * : * : * * * : * : * * : * * * : * * : * * * * * * * * * * * : * * : | 646 |
| TgIMC15 | VPKEEIRENITYVPRFETKIIPKYVDVPIIKIVDRYEEVHEIHEVLKPVAKVKVVDVPKE | 461 |
| SnIMC15 | VPKEKIVENVIVPRFEELIPKYVEVPVKIVDRYEEVQTEEV LKLVKPVKVVVEVPRE * * * * : * * : : * * * * : * * * * : * * : * * * * * * : : * * * * : * * : | 706 |
| TgIMC15 | FTRIVPKYSVHKTKSKVSVPDIQYKEVPRYRMRYEPKILRDTVINHIPQYLDIEVPYVEVP | 521 |
| SnIMC15 | VLRVVPKYVVHKTKEIPVVLQHKVPVRYKMRYPKIIQGVKVIPQIKDVEIPYPVP . * : * * * * * * . : : * * : * * * * : * * * * * * : : * : * * * * * * * * | 766 |
| TgIMC15 | KVTVDVQPFVTTYRDHQYVVPVSHSVTPVLLPGDHTQVVDVPEKPYVVVHDKFTPR-P | 580 |
| SnIMC15 | VVKEVPAPYFVEKYRDRPVAVPVSHLVLPVFKEGSHAQQVDVAVPTVLLVHDQLQPMAR * . * * * : * * . * * : * * * * * * * : * . * : * * * * * . * : * * * : * | 826 |
| TgIMC15 | PIPELIPGQAVLRGVTHLTKERLTAEQEQQLARQTTPSRPASPDHRFWEREREAE LRAPL | 640 |
| SnIMC15 | PVPQLLAGAAAATA-QPLDRCLNPEQRGS-----PATPM--LF----- * : * : * * . . * * . * . * * : . * * : * * : : : | 862 |
| TgIMC15 | SPVHIRPPRQRKFFAGMPRQSCGPMPSVDAQCQSPWQHVOQTNTLSYPN | 692 |
| SnIMC15 | ----- | 862 |