

The core region of BALiBASE 2

For BALiBASE 2, authors did not publish the XML file allowing automated use of these blocks. The location of the block is only available in HTML file, the uppercase of character (i.e., http://bips.u-strasbg.fr/en/Products/Databases/BALiBASE2/ref7/test/msl_ref7.html). We have generated the XML following the original BALiBASE annotation (<column-score>) and are now providing these files as the following.

.....

7tm_core-block.xml

.....

```
<?xml version="1.0"?>
```

```
<!DOCTYPE macsim SYSTEM "http://www-bio3d-igbmc.u-strasbg.fr/macsim.dtd">
```

```
<macsim>
```

```
<alignment>
```

```
<aln-name>1</aln-name>
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```
<seq-name>grhr_claga</seq-name>
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```
<seq-data>-----MSG
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```
NTTLLSNPTNVLDNSSVLNVSVPVVKWETPTF---TTAARFRVAATLVLFVFRAASNLSVLLSVTRGRGRRLAS-HLRPLIA
```

```
SLASADLVMTFVVMPLDAVWNVTV--QWYAGDA-----MCKLMCFLKLFAMHSAAFILVVVSLDRHHAILHPLDTL---DA
```

```
GRRNRRLMLLTAWILSLLASPQLFIFRAIKAKGVD-----FVQCATHGSF-----
```

```
-----QQH
```

```
WQETAYNMFHFVTLVYFPLLVMISLCYTRILVEINRQMHRSKDKAGEP-----
```

```
-----
```

```
-----CLRRSGTDMIPKARMKT-LKMTIIIVASFVICWTPYLLGIWYWFQ-----PQMLHVIPDYVHHVFFVFG
```

```
NLNTCCDPVIYGFPTPSFRADLSRCFCWRNQNASAKSLPHFSGHRREVSGEAESDLGSG---DQPSGQ-----
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```
-----</seq-data>
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</sequence>
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RSVGNSSPWVPLTTEGSNGSQEAARLGEG-DSPLGDVRN---EELAKLEIAVLAVIFVAVLGNSSVLLALHRTPRKTS---R
```

```
MHLFIRHLSLADLAVAFFQVLPQLCWDITS--SFRGPDW-----LCRVVKHLQVFAMFASAYMLVVMTADRYIAVCHPLKTL-
```

```
--QQPARRSRLMIATSWVLSFILSTPQYFIFSVIEIEVNGTK-----TQDCWATFIQ-----
```

```
-----
```

```
---PWGTRAYVTWMTSGVFPVAVVVLGTCYGFICYHIWRNIRGKTASSRHSKGDKGSGEAVGPFH-----
```

```
-----
```

```
-----KGLLVTPCVSSVKSISRAKIRT-VKMTFVIVSAYILCWAPFFIVQMWSVWD-----ENFIWTDS
```

```
ENPSITITALLASLNCCNPWIYMFSGHLLQDCVQSFPCCHSMAQKFAKDDSDSMSRRQTSYSNNRSPTNSTGMWKDS
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PKSSKSIRFIPVST-----</seq-data>
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HLSIADLVVAVFQVLPQLLWDITF--RFYGPLD-----LCRLVKYLQVVGMPFASTYLLLLMSLDRCLAICQPLRSL-----RRRTDRL
AVLATWLGCLVASVPQVHIFSLREVADG-----VFDCWAVFIQ-----
-----PWGPKA
YVTWITLAVYIVPVIVLAACYGLISFKIWQNLRLKTAASAAAAAEGSDAAGG-----
-----
-----AGRAALARVSSVKLISKAKIRT-VKMTFIIVLAFIVCWTPFFVQMWSVWD-----VNAPKEASAFIIMLLASL
NSCCNPWIYMLFTGHLFHELQRFLLCCSARYLKGSRPGETSISKKSNSSTFVLSRCSQQSSQRSCSQPSSA-----
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LIASLAVTDLLVSILVMPISTMYVTG--RWTLGQV-----VCDFWLSSDITCCTASILHLCVIALDRYWAITDAVEYS--AKRTPK
RAAVMIALVWVFSISLPPFF--WRQAKA-----EEEVSECVNTDH-----
-----ILY
TVYSTVGAFYFPTLLLIYALYGRIVVEARSRLKQTPNRTGKRLTRAQLITDSPGSTSSVTSINSRVPDVPSES-----GSPVYVNQ
VKVRVS-----
-----DALLEKKKLMAARERKA-TKTLGILGAFIVCWLPFFIISLVMPIC-----KDAC--WFHLAIFD
FFTWLGYNLSLINPIIYMSNEDFKQAFHKLIRFKCTS-----
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LIASLAVTDLLVSILVMPISTMYVTG--RWTLGQV-----VCDLWLSSDITCCTASIMHLCVIALDRYWAITDAVEYS--AKRTP
KRAAIMIRLVWVFSICISLPPFF--WRQAKA-----EEEVSECLVNTDH-----
-----VL
YTVYSTVGAFYLPPTLLLIYALYGRIVVEARSRLKQTPNRTGKRLTRAQLITDSPGSTTSSVTSINSRAPDVPSES-----GSPVYVN
QVKVRVS-----
-----DALLEKKKLMAARERKA-TKTLGILGVFIVCWLPFFIISLVMPIC-----KDAC--WFHQAI
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SLAVTDLLVSILVMPISTMYVTG--RWTLGQV-----VCDFWLSSDITCCTASIMHLCVIALDRYWAITDAVEYS--AKRTPKR
AAIMIVLVWVFSISLPPFF--WRQAKA-----EEEMLD CFVNTDH-----
-----VLYT
VYSTVGAFYLPTLLLIALLYGRIYVEARSRIKQTPNKTGKRLTRAQLITDSPGSTSSVTSINSRAPDVPSES-----GSPVYVNQV
KVRVS-----
-----DALLEKKKLMAARERKA-TKTLGILGAFIVCWLPFFIISLVMPIC-----KDAC--WFHMAIFDF
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SLAVTDLLVSILVMPISTMYVTG--RWTLGQV-----VCDFWLSSDITCCTASIMHLCVIALDRYWAITDAVEYS--AKRTPRR
AAVMIALVWVFSISLPRFF--WRQAKA-----EEEVLDC LVNTDH-----
-----VLYT
VYSTVGAFYLPTLLLIALLYGRIYVEARSRIKQTPNKTGKRLSRAQLISDSPGSTSSVTSINSRVPDVPSES-----GSPVYVNQV
KVRVS-----
-----DALLEKKKLMAARERKA-TKTLGILGAFIVCWLPFFIISLVMPIC-----KDAC--WFHMAIFDF
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IASLAFTDLLVSILVMPISTMYVTG--RWTLGQA-----LCDFWLSSDITCCTASIMHLCVIALDRYWAITDAVGYS--AKRTPR
RAAGMIALVWVFSICISLPPFF--WRQAKA-----EEEVLDC LVNTDH-----
-----VL
YTVYSTGGAFYLPTLLLIALLYGRIYVEARSRIKQTPNKTGKRLTRAQLITDSPGSTSSVTSINSRAPEVPCDS-----GSPVYVN
QVKVRVS-----
-----DALLEKKKLMAARERKA-TKTLGVILGAFIVCWLPFFIISLVMPIC-----KDAC--WFHMAI
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ASLAVTDLLVSILVMPISTMYTVTG--RWTLGQV-----V CDFWLSSDITCCTASILHLCVIALDRYWAITDAVEYS--AKRTPKR
AAGMIIMVWVFSVSISMPPLF--WRQAKA-----E EVADCSVNTDH-----
-----IL
YTVYSTVGAFYFPTLLLIALLYGRIYVEARSILKQTPNRTGKRLTRAQLITDSPGSSSSGTSINSRAPEGPSES-----GSPVYVN
QVKVKVS-----
-----DALLEKKKLMAARERKA-TRTLG IILGAFIVCWLPFFIISLALPIC-----DDAC--WFHLAIFD
FFNWLGYLNSLINPIIYTKSNDDFKQAFQKLMRFRRTS-----
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TDLLVSILVMPISIA YTITH--TWNFGQI-----L CDIWLSSDITCCTASILHLCVIALDRYWAITDALEYS--KRRTAGHAATMIAIV
WAISICISIPPLF--WRQAKA-----QEEMSDCLVNTSQ-----
-----ISYTIYSTCGAFY
IPSVLLIILYGRIYRAARNRILNP-PSLYGKRFTTAHLITGSAG--SSLCSLNSSLHEGHSHA-----GSPLFFNHVKIKLA-----
-----
-----DSALERKRISAARERKA-TKILG IILGAFIICWLPFFVSVLVPIC-----RDSC--WIHPALFDFFTWLGYLNSLINPII
YTVFNEEFRQAFQKIVPFRKAS-----
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MTDLLVSILVMPISIPYTITQ--TWSFGQL-----L CDIWLSSDITCCTASILHLCVIALDRYWAITDALEYS--KRRTAGHAAAMI
AIVWAISICISIPPLF--WRQARA-----HEEISDCLVNTSQ-----
-----ISYTIYSTCGAF
YIPSLLLIILYGRIYRAARNRILNP-PSLYGKRFTTAHLITGSAG--SSLCSLNPSLHEEHAHSA-----GSPLFFNHVKIKLA-----
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-----DSVLERKRISAARERKA-TKTLG IILGAFIICWLPFFVASLVPIC-----RDSC--WIHPALFDFFTWLGYLNSLINP
IITYVFNEEFRQAFQKVVFHFRKAS-----
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LLVSILVMPISIAYTTR--TWNFGQI-----LCDIWVSSDITCCTASILHLCVIALDRYWAITDALEYS--KRRTAGHAAAMIAAV
WAISICISIPPLF--WRQATA-----HEEMSDCLVNTSQ-----
-----ISYTIYSTCGAFYI
PSILLIILYGRIYVAARSILNP-PSLYGKRFTTAQLITGSAG--SSLCSLNPSLHESHTHTV-----GSPLFFNQVKIKLA-----
-----
-----DSILERKRISAARERKA-TKTLGILGAFIICWLPFFVSVLVPIC-----RDSC--WIHPALFDFFTWLGYLNSLINPVYI
TVFNEDFRQAFQRVVHFRKAS-----
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TTDLLVSILVMPISIAYTTR--TWNFGQI-----LCDIWVSSDITCCTASILHLCVIALDRYWAITDALEYS--KRRTAGHAGAMI
AAVWVISICISIPPLF--WRQAQA-----QEEMSDCLVNTSQ-----
-----ISYTIYSTC
GAFYIPSVLLIILYSRIYRAARSILNP-PSLSGKRFTTAHLITGSAG--SSLCSLNPSLHEGHMHP-----GSPLFFNHVRIKLA-----
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-----DSVLERKRISAARERKA-TKTLGILGAFIVCWLPFFVSVLVPIC-----RDSC--WIHPALFDFFTWLGYLNS
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<seq-info><length>1066</length></seq-info>
<seq-data>-----MSPS
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TDLLVSILVMPISIAYTITH--TWNFGQV-----LCDIWVSSDITCCTASILHLCVIALDRYWAITDALEYS--KRRTAGHAAAMIA
VWVAISICISIPPLF--WRQAKA-----HEEVSDCLVNTSQ-----
-----ISYTIYSTCGAF
YIPSVLLIVLYGRIYMAARNRILNP-PSLYGKRFTTAHLITGSAG--SSLCSLSPSLGEGHSHA-----GSPLFFNPVRIKLA-----
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-----DSVLERKRISAARERKA-TKTLGILGAFIGCWLPFFVASLVPIC-----RDSC--WMPPGLFDFFTWLGYLNS
LINPIIYTVFNEDFRQAFQRVHFRKAF-----
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MTDLLVSILVMPISIAAYTTTR--TWSFGQI-----LCDIWLSSDITCCTASILHLCVIALDRYWAITDALEYS--KRRTAGRAAVMIA
TVWVISICISIPPLF--WRQAKA-----QEDMSDCQVNTSQ-----
-----ISYTIYSTCG
AFYIPSVLLIILYGRIYVAARNRILNP-PSLYGKRFTTAQLITGSAG--SSLCSLSPSLQEERSHAA-----GPPLFFNHVQVKLA---
-----
-----EGVLERKRISAARERKA-TKTLGIILGAFIVCWLPFFVASLVLPIC-----RASC--WLHPALFDFFTWLGYLN
SLINPIIYTVFNEEFRQAFQRVVHVRKAS-----
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TDMLVSILVMPISIVYTVSK--TWSLGQI-----VCDIWLSSDITFCTASILHLCVIALDRYWAITDALEYS--KRRTMRRRAAVMV
AVVWVISISIMPPLF--WRQAKA-----HEELKECMVNTDQ-----
-----ISYTYLSTF
GAFYVPTVLLIILYGRIYVAARSRIKFT-PSYSGKRFTTAQLIQTSAG--SSLCSLNSASNQEAHLHSGAGGEGGGSPFLVNSVK
VKLA-----
-----DNVLERKRLCAARERKA-TKTLGIILGAFIICWLPFFVVTLVWAIC-----KEC--SFDPLLFDVFT
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LVMPLSIYIVMD--RWKLGYP-----LCEVWLSVDMTCCTCSILHLCVIALDRYWAITNAIEYA--RKRTAKRAALMILTVWTISI
FISMPPLF--WRSHRR-----LSPPPSQCTIQHDH-----
-----VIYTIYSTLGAFYIPLTI
LILYYRIYHAAKSLYQKRGSSRHLSNRSTDSQNSFAS---CKLTQTFCVSDFSTSDP-----TTEFEKPHASIRIPFDNDL-----
-----
-----DHPGERQQISSTRERKA-ARILGLILGAFILSWLPFFIKELIVGLS-----IY--TVSSEVADFLTWLGYNLSLINPLLYTS
FNEDFKLAFKKLIRCREHT-----
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LVMPFSIVYIVRE--SWIMGQV-----VCDIWLSVDITCCTCSILHLSAIALDRYRAITDAVEYA--RKRTPKHAGIMITIVWIISVF
ISMPPPLF--WRHQG-----TSRDDECIKHDH-----
-----IVSTIYSTFGAFYIPLALILIL
YKIIYRAAKTLYHKRQASRIAKEEVNGQVLESSEKSTKSVSTSYVLEKSLSDP-----STDFDKIHSTVRSRSEFKH-----
-----
-----EKSRRQKISGTRERKA-ATTLGLILGAFVICWLPFFVKELVVNVC-----DKC--KISEEMSNFLAWLGYLNSLINPLIY
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LVMPFSIVYIVRE--SWIMGQV-----LCDIWLSVDIICCTCSILHLSAIALDRYRAITDAVEYA--RKRTPKQAGIMITIVWIISVFI
SMPPPLF--WRHQG-----TSRDDECIKHDH-----
-----IVSTIYSTFGAFYIPLVLILIL
YKIIYKAAKTLYHKRQASRIAKEELNGQVLESSEKSIKVMSTTYVPEKSLSDP-----STDFDKIHNTVKSPRCKLRH-----
-----
-----EKSRRQKISGTRERKA-ATTLGLILGAFVICWLPFFVKELVVNVC-----EKC--KISEEMANFLAWLGYLNSLINPLI
YTIFNEDFKKAFQKLVRCQY-----
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LVMPFSIVYIVRE--SWIMGQV-----LCDIWLSVDIICCTCSILHLSAIALDRYRAITDAVEYA--RKRTPRHAGIMITIVWVISVFI
SMPPPLF--WRHQG-----TSRDDECVIKHDH-----
-----IVSTIYSTFGAFYIPLVLILIL
YKIIYRAARTLYHKRQASRMIIKEELNGQVFLESSEKSIKLVSTSYMLEKSLSDP-----STDFDRIHSTVKSPRSELKH-----
-----
-----EKSRRQKISGTRERKA-ATTLGLILGAFVICWLPFFVKELVVNVC-----EKC--KISEEMSNFLAWLGYLNSLINPLI
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GSLAVTDLMVSVLVLPMAALYQVLN--KWTLGQD-----ICDLFIALDVLCTSSILHLCAIALDRYWAITDPIDYV--NKRTPRR
AAVLISVTWLGFSISIPPML-GWRS-----AEDRANPDACIISQDP-----
-----GYTI
YSTFGAFYIPLILMLVLYGRIFKAARFRIRKTVKKTEKAKASDMCLTSPAVFHKRANGDAVSAEWKRGYKFKPS-SPCANGA
VRHGEEMESLEIIEVN--SNSKTHLPNTP-QSSSHE-----
-----NINEKTTGTRRKIALARERKT-VKTLGIIMGTFIFCWLPFFIVALVLPFC-----
-AENC--YMPEWLGAVINWLGYSNSLLNPIIYAYFNKDFQSAFKKILRCKFHRH-----
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DLMVSVLVLPMAALYQVLN--RWTLGQI-----PCDIFISLDMLCCTSSILHLCVIALDRYWAITEPIDYM--KKRTPRRAVLIS
VTWLVGFSISIPPML-IMRSQPSSM-----AEDRANSKQCKITQDP-----
-----WYTIYS
TFGAFYIPLTLMLVLYGRIFKAARFRIRRTVRKTEKKKVS DTCALSPAMFHRKTPGDAHGKSWKRSVEPRP--LPNVNGAVK
HAGEGESLDIIEVQ--SNSRCNLPLNTPGTVPLE-----
-----NRHEKATETKRKIALARERKT-VKTLGIIMGTFILCWLPFFIVALVMPFC-----
QESC--FMPHWLKDVINWLGYSNSLLNPIIYAYFNKDFQSAFKKIIKCHFCRA-----
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VTDLMVSVLVLPMAALYQVLN--KWTLGQV-----TCDLFIALDVLCTSSILHLCAIALDRYWAITDPIDYV--NKRTPRRAAA
LISLTWLGFLISIPPML-GWRT-----PEDRSDPDACTISKDH-----
-----GYTIYSTF
GAFYIPLLLMLVLYGRIFRAARFRIRKTVRKVEKKGAGTSLGTSSAPPPKSLNGQP GSGDWRRCAENRAVGTPCTNGAVR
QGDDEATLEVIEVHRVGN SKEHLPLPSESGSNSYAPACLE-----
-----RKNERNAEAKRKMALARERKT-VKTLGIIMGTFILCWLPFFIVALVLPFC
-----ESSC--HMPALLGAIINWLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCKFCRR-----
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ALISLTLWIGFLISIPPML-GWRA-----PEDRSNPNECTISKDH-----
-----GYTIYST
FGAFYIPLLLMLVLYGRIFRAARFRIRKTVKKVEKKGAGTSFGTSSAPPPKKS LNGQPGSGDCRRAENRAVGTPCANGAVR
QGEDDATLEVIEVHRVGNSKGDLPSESGATSYVPACLE-----
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-----DLWVVVFQFQHI
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SLTPALCATLLRPIDAD-----HHEKR-GFFGWFNRAFLRLTG
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GFFSG---KRFVPIITSV-SSLVIGVIFSFVWPLIQNGINAASSL-----IADSTVGLFFYATIYRLLIPFGLHHIFYTPFYFMMGEYTD
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HIWN
VPSQMQIGEYTNA-----GQVFHGDIPRYMAGDP-----
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MAGL-FALVAGALSGVIWPSIQGGLDALAHAV----STSGALGQFVYGTNLRALIPVGLHHVLNSYFWFGMGTCQEILVSG
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-----TAGMFMMSGFFPIMMFGL-PGAALAMYFAAPKERRPMVGG
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VA-----KGTRFFSGEFVVMIF
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-----ATRFLSQGKMPAFLGGL-
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