A

N- | 4 - 148 | 256-294 | 319-360 | 365-385 | 428-509 | 513 - 631 | 666-696 | 729-777 | 791-818 | 823-850 | 1115 - 1218 | -C

- ATP binding cassette domain
- Coiled - coiled domain
- SMC flexible hinge domain
- Coiled - coiled domain
- ATP binding cassette domain

B

Smc1b protein Domains	% identical sequence between zebrafish and:	
	Human	Mouse
Whole protein	53.04	52.11
N-terminal ATP binding domain	62.75	64.13
Coiled-coiled domain 1	56.41	48.72
Coiled-coiled domain 2	28.57	35.71
Coiled-coiled domain 3	57.14	57.14
Coiled-coiled domain 4	52.44	50.00
Flexible hinge domain	66.95	64.41
Coiled-coiled domain 5	35.48	35.48
Coiled-coiled domain 6	30.61	26.53
Coiled-coiled domain 7	53.57	53.57
Coiled-coiled domain 8	32.14	35.71
C-terminal ATP binding domain	75.96	75.96

C N-terminal ABC domain

```
                                       Walker A                        Amino acid #
zSmc1b  MGFLKQLDVENFKSWRGKQTIGPFKRFNCIIGTNGSGKSNVMDALGFVMGERAANLRVKH     60
mSmc1b  MGHLELLLVENFKSWRGRQVIGPFKRFTCIIGPNGSGKSNVMDALSFVMGEKTTNLRVKN     60
hSMC1B  MAHLELLLVENFKSWRGRQVIGPFRRFTCIIGPNGSGKSNVMDALSFVMGEKIANLRVKN     60
            *..*: * *********:.*****:** .**** ********************.*****: :*****:

zSmc1b  TRDLIHGAHIGNPVSTFASVTMIYCGDNDEEMTFSRRISGESSEYLVNGKHVTLAKYTGE     120
mSmc1b  IQELIHGAHTGKPVSSSASVTIIYIEDSGEEKTFTRIIRGGCSEYHFGDKPVSRSVYVAQ     120
hSMC1B  IQELIHGAHIGKPISSSASVKIIYVEESGEEKTFARIIRGGCSEFRFNDNLVSRSVYIAE     120
            ::******* *:*:*:. ***.:**  :..** **:* * .**: ...: *: : * .:

zSmc1b  LQKIGIVVKAKNCLVYQGAVESIAMMNAKERTKMFERISGSGDLNIEYFTKLAVLQKAKE     180
mSmc1b  LENIGIIVKAQNCLVFQGTVESISMKKPKERTQFFEEISTSGEFIGEYEAKKKKLQKAEE     180
hSMC1B  LEKIGIIVKAQNCLVFQGTVESISVKKPKERTQFFEEISTSGELIGEYEEKKRKLQKAEE     180
            *:::****:***:****:*:****:: : ****::**.** **:: ** * .****:*
```

D Flexible hinge domain

```
                                                          Amino acid #
zSmc1b  LTKLQNARLDSQENRRQQKRDEVLESLRRLYPDTVYGRLVELCQPIHKKYQLAVTKVFGK     540
mSmc1b  RNELQNAGIDNHEGKRQQKRAEVLEHLKRLYPDSVFGRLLDLCHPIHKKYQLAVTKLFGR     540
hSMC1B  RSELQNAGIDTHEGKRQQKRAEVLEHLKRLYPDSVFGRLFDLCHPIHKKYQLAVTKVFGR     540
            .:**** :*.::*.:****** ****:*.*****:*:****::**:.**************:**:

zSmc1b  NMNAIVVTSAYVAHDCIRYLKEERAEPETFLPIDYIDVPILNERLREVQGAKMVVDVVQC     600
mSmc1b  YMVAIVVASEKIAKDCIRFLKAERAEPETFLALDYLDIKPINERLREIKGCKMMIDVIKT     600
hSMC1B  FITAIVVASEKVAKDCIRFLKEERAEPETFLALDYLDIKPINERLRELKGCKMVIDVIKT     600
            : ****:* :*:****:** *********** :**:*:  :*****::*.**::**::**::

zSmc1b  SQNAPQLKRVIQYVCGNSLVCETLKDARRIAFDGPERLQTVALDGTLFRKSGVISGGSSD     660
mSmc1b  --QFPQLKKVIQFVCGNGLVCETVEEARHIAFGGPERRKAVALDGTLFLKSGVISGGSSD     658
hSMC1B  --QFPQLKKVIQFVCGNGLVCETMEEARHIALSGPERQKTVALDGTLFLKSGVISGGSSD     658
            : ****:***.****.*****:::**:** ***  ::*********:.*************
```

E C-terminal ABC domain

```
                                      Signature motif          Amino acid #
zSmc1b  QIYKKLCRNASAQAILSAENPNEPYLDGINYNCVAPGKRFMAMDNLSGGEKAIAALALVF     1140
mSmc1b  QIYKKLCRNNSAQAFLSPENPEEPYLDGISYNCVAPGKRFMPMDNLSGGEKCVAALALLF     1137
hSMC1B  QIYKKLCRNNSAQAFLSPENPEEPYLEGISYNCVAPGKRFMPMDNLSGGEKCVAALALLF     1138
            ********* ****:** ***:**** ** :** *.*********** ****:********:*****:*

                Walker B   D Loop
zSmc1b  AIHSFRPAPFFVLDEVDAALDNTNIGKVTGFFRMMSRESCQIIVISLKEEFYSRADALLG     1200
mSmc1b  AVHSFRPAPFFVLDEVDAALDNTNIGKVSSYIKEQSQEQFQMIIISLKEEFYSKADALIG     1197
hSMC1B  AVHSFRPAPFFVLDEVDAALDNTNIGKVSSYIKEQTQDQFQMIVISLKEEFYSRADALIG     1198
            *:************************.:::  :::. *:*:*********:*****:*

zSmc1b  VYSMFDECMFSRLLTLDLTPYPLKDENATDREKDK---------------     1235
mSmc1b  VYPEHNECMFSHVLTLDLSKYPDTEDQEGSRSHRKPRVPRVSMSPKSPQSR     1248
hSMC1B  IYPEYDDCMFSRVLTLDLSQYPDTEGQESSKRHGESR-------------     1235
            :*  .::****::*****: **  .: : .: : :
```