Supplementary Materials

STAT5A and STAT5B—Twins with Different Personalities in Hematopoiesis and Leukemia

Barbara Maurer, Sebastian Kollmann, Judith Pickem, Andrea Hoelbl-Kovacic and Veronika Sexl

Figure S1

Human

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Length: 804
Identity:     732/804 (91.0%)
Similarity:   748/804 (93.0%)
Gaps:          27/804 ( 3.4%)
Score: 3787.0

':' for a similarity which scores more than 1.0
'.' for any small positive score
'|' for an identity where both sequences have the same residue regardless
of its score
space for a mismatch or a gap
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Oligomerisation domain
Coiled-coil domain
DNA binding domain
Linker domain
SH2 domain
Transactivation domain
Phosphorlyation
Acetylation
Methylation
O-GlcNAc

```
STA5A_HUMAN        1 MAGWIQAQQLQGDALRQMQVLYGQHFPIEVRHYLAQWIESQPWDAIDLDN
50
                     ||.|||||||||:||.|||.|||||||||||||||:||||||.||::||||
STA5B_HUMAN        1 MAVWIQAQQLQGEALHQMQALYGQHFPIEVRHYLSQWIESQAWDSVDLDN
50

STA5A_HUMAN       51 PQDRAQATQLLEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQKTYDR
100
                     ||:..:||||||||||||||||||||||||||||||||||||||||.||||
STA5B_HUMAN       51 PQENIKATQLLEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQNTYDR
100

STA5A_HUMAN      101 CPLELVRCIRHILYNEQRLVREANNCSSPAGILVDAMSQKHLQINQTFEE
150
                     ||:||||||||||||||||||||||.|||||.|.||||||||||||||||
STA5B_HUMAN      101 CPMELVRCIRHILYNEQRLVREANNGSSPAGSLADAMSQKHLQINQTFEE
150

STA5A_HUMAN      151 LRLVTQDTENELKKLQQTQEYFIIQYQESLRIQAQFAQLAQLSPQERLSR
200
                     |||||||||||||||||||||||||||||||||||||..||||||||||||
STA5B_HUMAN      151 LRLVTQDTENELKKLQQTQEYFIIQYQESLRIQAQFGPLAQLSPQERLSR
200
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STA5A_HUMAN      201 ETALQQKQVSLEAWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDD
250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_HUMAN      201 ETALQQKQVSLEAWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDD
250

STA5A_HUMAN      251 ELIQWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLC
300
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_HUMAN      251 ELIQWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLC
300

STA5A_HUMAN      301 QQLPIPGPVEEMLAEVNATITDIISALVTSTFIIEKQPPQVLKTQTKFAA
350
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_HUMAN      301 QQLPIPGPVEEMLAEVNATITDIISALVTSTFIIEKQPPQVLKTQTKFAA
350

STA5A_HUMAN      351 TVRLLVGGKLNVHMNPPQVKATIISEQQAKSLLKNENTRNECSGEILNNC
400
                     ||||||||||||||||||||||||||||||||||||||||:.||||||||
STA5B_HUMAN      351 TVRLLVGGKLNVHMNPPQVKATIISEQQAKSLLKNENTRNDYSGEILNNC
400

STA5A_HUMAN      401 CVMEYHQATGTLSAHFRNMSLKRIKRADRRGAESVTEEKFTVLFESQFSV
450
                     ||||||||||||||||||||||||||:||||||||||||||:||||||||
STA5B_HUMAN      401 CVMEYHQATGTLSAHFRNMSLKRIKRSDRRGAESVTEEKFTILFESQFSV
450

STA5A_HUMAN      451 GSNELVFQVKTLSLPVVVIVHGSQDHNATATVLWDNAFAEPGRVPFAVPD
500
                     |.||||||||||||||||||||||||:||||||||||||||||||||||||
STA5B_HUMAN      451 GGNELVFQVKTLSLPVVVIVHGSQDNNATATVLWDNAFAEPGRVPFAVPD
500

STA5A_HUMAN      501 KVLWPQLCEALNMKFKAEVQSNRGLTKENLVFLAQKLFNNSSSHLEDYSG
550
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_HUMAN      501 KVLWPQLCEALNMKFKAEVQSNRGLTKENLVFLAQKLFNNSSSHLEDYSG
550

STA5A_HUMAN      551 LSVSWSQFNRENLPGWNYTFWQWFDGVMEVLKKHHKPHWNDGAILGFVNK
600
                     ||||||||||||||||.||||||||||||||||||.||||||||||||||||
STA5B_HUMAN      551 LSVSWSQFNRENLPGRNYTFWQWFDGVMEVLKKHLKPHWNDGAILGFVNK
600

STA5A_HUMAN      601 QQAHDLLINKPDGTFLLRFSDSEIGGITIAWKFDSPERNLWNLKPFTTRD
650
                     ||||||||||||||||||||||||||||||||||||.||..|||.||||||
STA5B_HUMAN      601 QQAHDLLINKPDGTFLLRFSDSEIGGITIAWKFDSQERMFWNLMPFTTRD
650

STA5A_HUMAN      651 FSIRSLADRLGDLSYLIYVFPDRPKDEVFSKYYTPV-----LAKAVDGYV
695
                     ||||||||||||||:||||||||||||||:|||||||     .||||||||
STA5B_HUMAN      651 FSIRSLADRLGDLNYLIYVFPDRPKDEVYSKYYTPVPCESATAKAVDGYV
700

STA5A_HUMAN      696 KPQIKQVVPEFVNASADAGGSSATYMDQAPSPAVCPQAPYNMYPQNPDHV
745
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                     |||||||||||||||||||.||||||||||||||||.|||||||||.|
STA5B_HUMAN      701
KPQIKQVVPEFVNASADAGGGSATYMDQAPSPAVCPQAHYNMYPQNPDSV750

STA5A_HUMAN      746 LDQDGEFDLDETMDVARHVEELLRRPMDS-----LDSRLSPPAGLFTSAR
790
                     ||.||:|||::||||||.|||||.|||||     ..|
STA5B_HUMAN      751 LDTDGDFDLEDTMDVARRVEELLGRPMDSQWIPHAQS-------------
787

STA5A_HUMAN      791 GSLS    794

STA5B_HUMAN      788 ----    787
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Murine

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# Length: 798
# Identity:     730/798 (91.5%)
# Similarity:   749/798 (93.9%)
# Gaps:          17/798 ( 2.1%)
# Score: 3787.0

':' for a similarity which scores more than 1.0
'.' for any small positive score
'|' for an identity where both sequences have the same residue regardless
of its score
space for a mismatch or a gap
```

Oligomerisation domain
Coiled-coil domain
DNA binding domain
Linker domain
SH2 domain
Transactivation domain
Phosphorlyation
Acetylation
Methylation
O-GlcNAc

```
STA5A_MOUSE        1 MAGWIQAQQLQGDALRQMQVLYGQHFPIEVRHYLAQWIESQPWDAIDLDN
50
                     ||.||||||||||||.|||.|||||||||||||||:||||||.||:|||||
STA5B_MOUSE        1 MAMWIQAQQLQGDALHQMQALYGQHFPIEVRHYLSQWIESQAWDSIDLDN
50

STA5A_MOUSE       51 PQDRGQATQLLEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQNTYDR
100
                     ||:..:||||||||||||||||||||||||||||||||||||||||:||||
STA5B_MOUSE       51 PQENIKATQLLEGLVQELQKKAEHQVGEDGFLLKIKLGHYATQLQSTYDR
100

STA5A_MOUSE      101 CPMELVRCIRHILYNEQRLVREANNCSSPAGVLVDAMSQKHLQINQRFEE
150
                     |||||||||||||||||||||||||.|||||.|.||||||||||||.|||
STA5B_MOUSE      101 CPMELVRCIRHILYNEQRLVREANNGSSPAGSLADAMSQKHLQINQTFEE
150
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STA5A_MOUSE      151 LRLITQDTENELKKLQQTQEYFIIQYQESLRIQAQFAQLGQLNPQERMSR
200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_MOUSE      151 LRLITQDTENELKKLQQTQEYFIIQYQESLRIQAQFAQLGQLNPQERMSR
200

STA5A_MOUSE      201 ETALQQKQVSLETWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDD
250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_MOUSE      201 ETALQQKQVSLETWLQREAQTLQQYRVELAEKHQKTLQLLRKQQTIILDD
250

STA5A_MOUSE      251 ELIQWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLC
300
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_MOUSE      251 ELIQWKRRQQLAGNGGPPEGSLDVLQSWCEKLAEIIWQNRQQIRRAEHLC
300

STA5A_MOUSE      301 QQLPIPGPVEEMLAEVNATITDIISALVTSTFIIEKQPPQVLKTQTKFAA
350
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_MOUSE      301 QQLPIPGPVEEMLAEVNATITDIISALVTSTFIIEKQPPQVLKTQTKFAA
350

STA5A_MOUSE      351 TVRLLVGGKLNVHMNPPQVKATIISEQQAKSLLKNENTRNECSGEILNNC
400
                     ||||||||||||||||||||||||||||||||||||||||:.||||||||
STA5B_MOUSE      351 TVRLLVGGKLNVHMNPPQVKATIISEQQAKSLLKNENTRNDYSGEILNNC
400

STA5A_MOUSE      401 CVMEYHQATGTLSAHFRNMSLKRIKRADRRGAESVTEEKFTVLFESQFSV
450
                     ||||||||||||||||||||||||||:||||||||||||||:||:||||||
STA5B_MOUSE      401 CVMEYHQATGTLSAHFRNMSLKRIKRSDRRGAESVTEEKFTILFDSQFSV
450

STA5A_MOUSE      451 GSNELVFQVKTLSLPVVVIVHGSQDHNATATVLWDNAFAEPGRVPFAVPD
500
                     |.||||||||||||||||||||||||:||||||||||||||||||||||||
STA5B_MOUSE      451 GGNELVFQVKTLSLPVVVIVHGSQDNNATATVLWDNAFAEPGRVPFAVPD
500

STA5A_MOUSE      501 KVLWPQLCEALNMKFKAEVQSNRGLTKENLVFLAQKLFNISSNHLEDYNS
550
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
STA5B_MOUSE      501 KVLWPQLCEALNMKFKAEVQSNRGLTKENLVFLAQKLFNISSNHLEDYNS
550

STA5A_MOUSE      551 MSVSWSQFNRENLPGWNYTFWQWFDGVMEVLKKHHKPHWNDGAILGFVNK
600
                     ||||||||||||||||.||||||||||||||||||.||||||||||||||||
STA5B_MOUSE      551 MSVSWSQFNRENLPGRNYTFWQWFDGVMEVLKKHLKPHWNDGAILGFVNK
600

STA5A_MOUSE      601 QQAHDLLINKPDGTFLLRFSDSEIGGITIAWKFDSPDRNLWNLKPFTTRD
650
                     |||||||||||||||||||||||||||||||||||.:|..|||.||||||
STA5B_MOUSE      601 QQAHDLLINKPDGTFLLRFSDSEIGGITIAWKFDSQERMFWNLMPFTTRD
650

STA5A_MOUSE      651 FSIRSLADRLGDLNYLIYVFPDRPKDEVFAKYYTPV-----LAKAVDGYV
695
                     ||||||||||||||||||||||||||||||::||||||     .|||.||||
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```
STA5B_MOUSE       651 FSIRSLADRLGDLNYLIYVFPDRPKDEVYSKYYTPVPCEPATAKAADGYV
700

STA5A_MOUSE       696 KPQIKQVVPEFVNASTDAGASATYMDQAPSPVVCPQPHYNMYPPNPDPVL
745
                      ||||||||||.|||||||:.|||||||||||||||.||||||||||.||
STA5B_MOUSE       701 KPQIKQVVPEFANASTDAGSGATYMDQAPSPVVCPQAHYNMYPPNPDSVL
750

STA5A_MOUSE       746 DQDGEFDLDESMDVARHVEELLRRPMDSLDARLSPPAGLFTSARSSLS
793
                      |.||:|||:::|||||.|||||.|||||   :..|.|..
STA5B_MOUSE       751 DTDGDFDLEDTMDVARRVEELLGRPMDS---QWIPHAQS---------
786
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Figure S1. Protein alignment of human or murine STAT5A and STAT5B. Alignment and visualization were done using EMBL-EBI search and sequence analysis tools [1].

References

1. Madeira, F.; Park, Y.m.; Lee, J.; Buso, N.; Gur, T.; Madhusoodanan, N.; Basutkar, P.; Tivey, A.R.N.; Potter, S.C.; Finn, R.D., et al. The EMBL-EBI search and sequence analysis tools APIs in 2019. *Nucleic Acids Res.* **2019**, *47*, W636–W641, doi:10.1093/nar/gkz268.