Sequences and residue numbering schemes for Src and Abl1

Kinase catalytic domains ares highlighted in red, and the conserved residues analyzed in the main text (Fig. 5) are highlighted with yellow background.

Human Abl1 sequence:

```
1      MLEICLKLVG CKSKKGLSSS SSCYLEEALQ RPVASDFEPQ GLSEAARWNS KENLLAGPSE     60
61     NDPNLFVALY DFVASGDNTL SITKGEKLRV LGYNHNGEWC EAQTKNGQGW VPSNYITPVN    120
121    SLEKHSWYHG PVSRNAAEYL LSSGINGSFL VRESESSPGQ RSISLRYEGR VYHYRINTAS    180
181    DGKLYVSSES RFNTLAELVH HHSTVADGLI TTLHYPAPKR NKPTVYGVSP NYDKWEMERT    240
241    DITMKHKLGG GQYGEVYEGV WKKYSLTVAV KTLKEDTMEV EEFLKEAAVM KEIKHPNLVQ    300
301    LLGVCTREPP FYIITEFMTY GNLLDYLREC NRQEVNAVVL LYMATQISSA MEYLEKKNFI    360
361    HRDLAARNCL VGENHLVKVA DFGLSRLMTG DTYTAHAGAK FPIKWTAPES LAYNKFSIKS    420
421    DVWAFGVLLW EIATYGMSPY PGIDLSQVYE LLEKDYRMER PEGCPEKVYE LMRACWQWNP    480
481    SDRPSFAEIH QAFETMFQES SISDEVEKEL GKQGVRGAVS TLLQAPELPT KTRTSRRAAE    540
541    HRDTTDVPEM PHSKGQGESD PLDHEPAVSP LLPRKERGPP EGGLNEDERL LPKDKKTNLF    600
601    SALIKKKKKT APTPPKRSSS FREMDGQPER RGAGEEEGRD ISNGALAFTP LDTADPAKSP    660
661    KPSNGAGVPN GALRESGGSG FRSPHLWKKS STLTSSRLAT GEEEGGGSSS KRFLRSCSAS    720
721    CVPHGAKDTE WRSVTLPRDL QSTGRQFDSS TFGGHKSEKP ALPRKRAGEN RSDQVTRGTV    780
781    TPPPRLVKKN EEAADEVFKD IMESSPGSSP PNLTPKPLRR QVTVAPASGL PHKEEAGKGS    840
841    ALGTPAAAEP VTPTSKAGSG APGGTSKGPA EESRVRRHKH SSESPGRDKG KLSRLKPAPP    900
901    PPPAASAGKA GGKPSQSPSQ EAAGEAVLGA KTKATSLVDA VNSDAAKPSQ PGEGLKKPVL    960
961    PATPKPQSAK PSGTPISPAP VPSTLPSASS ALAGDQPSST AFIPLISTRV SLRKTRQPPE   1020
1021   RIASGAITKG VVLDSTEALC LAISRNSEQM ASHSAVLEAG KNLYTFCVSY VDSIQQMRNK   1080
1081   FAFREAINKL ENNLRELQIC PATAGSGPAA TQDFSKLLSS VKEISDIVQR             1130
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Sequences for human and chicken Src, aligned using Clustal Omega:

```
SRC_HUMAN   1     MGSNKSKPKD ASQRRRSLEP AENVHGAGGG AFPASQTPSK PASADGHRGP SAAFAPAAAE    60
SRC_CHICK   1     MGSSKSKPKD PSQRRRSLEP PDSTH---HG GFPASQTPNK TAAPDTHRTP SRSFGTVATE    57
                  ***.******  *********  :..*     *  .*******.*  *: * ** * * :*.  .*:*

SRC_HUMAN   61    PKLFGGFNSS DTVTSPQRAG PLAGGVTTFV ALYDYESRTE TDLSFKKGER LQIVNNTEGD   120
SRC_CHICK   58    PKLFGGFNTS DTVTSPQRAG ALAGGVTTFV ALYDYESRTE TDLSFKKGER LQIVNNTEGD   117
                  ********.*  **********  *********  **********  **********  **********

SRC_HUMAN   121   WWLAHSLSTG QTGYIPSNYV APSDSIQAEE WYFGKITRRE SERLLLNAEN PRGTFLVRES   180
SRC_CHICK   118   WWLAHSLTTG QTGYIPSNYV APSDSIQAEE WYFGKITRRE SERLLLNPEN PRGTFLVRES   177
                  *******:**  **********  **********  **********  *******  **  **********

SRC_HUMAN   181   ETTKGAYCLS VSDFDNAKGL NVKHYKIRKL DSGGFYITSR TQFNSLQQLV AYYSKHADGL   240
SRC_CHICK   178   ETTKGAYCLS VSDFDNAKGL NVKHYKIRKL DSGGFYITSR TQFSSLQQLV AYYSKHADGL   237
                  **********  **********  **********  **********  ***.******  **********

SRC_HUMAN   241   CHRLTTVCPT SKPQTQGLAK DAWEIPRESL RLEVKLGQGC FGEVWMGTWN GTTRVAIKTL   300
SRC_CHICK   238   CHRLTNVCPT SKPQTQGLAK DAWEIPRESL RLEVKLGQGC FGEVWMGTWN GTTRVAIKTL   297
                  *****.****  **********  **********  **********  **********  **********

SRC_HUMAN   301   KPGTMSPEAF LQEAQVMKKL RHEKLVQLYA VVSEEPIYIV TEYMSKGSLL DFLKGETGKY   360
SRC_CHICK   298   KPGTMSPEAF LQEAQVMKKL RHEKLVQLYA VVSEEPIYIV TEYMSKGSLL DFLKGEMGKY   357
                  **********  **********  **********  **********  **********  ****** ***

SRC_HUMAN   361   LRLPQLVDMA AQIASGMAYV ERMNYVHRDL RAANILVGEN LVCKVADFGL ARLIEDNEYT   420
SRC_CHICK   358   LRLPQLVDMA AQIASGMAYV ERMNYVHRDL RAANILVGEN LVCKVADFGL ARLIEDNEYT   417
                  **********  **********  **********  **********  **********  **********

SRC_HUMAN   421   ARQGAKFPIK WTAPEAALYG RFTIKSDVWS FGILLTELTT KGRVPYPGMV NREVLDQVER   480
SRC_CHICK   418   ARQGAKFPIK WTAPEAALYG RFTIKSDVWS FGILLTELTT KGRVPYPGMV NREVLDQVER   477
                  **********  **********  **********  **********  **********  **********

SRC_HUMAN   481   GYRMPCPPEC PESLHDLMCQ CWRKEPEERP TFEYLQAFLE DYFTSTEPQY QPGENL        536
SRC_CHICK   478   GYRMPCPPEC PESLHDLMCQ CWRKDPEERP TFEYLQAFLE DYFTSTEPQY QPGENL        533
                  **********  **********  ****:*****  **********  **********  ******
```