

Sequences and residue numbering schemes for Src and Abl1

Kinase catalytic domains are highlighted in red, and the conserved residues analyzed in the main text (Figs. 5 and 6) are highlighted with yellow background.

Human Abl1 sequence:

1	MLEICLKLVG	CKSKKGLSSS	SSCYLEEALQ	RPVASFEPQ	GLSEAAWNS	KENLLAGPSE	60
61	NDPNLFVALY	DFVASGDNTL	SITKGEKLRV	LGYNHNGEWC	EAQTKNGQGW	VPSNYITPVN	120
121	SLEKHSWYHG	PVSRNAAEYL	LSSGINGSFL	VRESESPGQ	RSISLRYEGR	VYHYRINTAS	180
181	DGKLYVSSSE	RFNTLAEVLH	HHSTVADGLI	TTLHYPAKPR	NKPTVYGVSP	NYDKWEMERT	240
241	DITMKHKLGG	GQYGEVYEGV	WKYSLTVAV	KTLEDTMEV	EEFLKAAVM	KEIKHPNLVQ	300
301	LLGVCTREPP	FYIITEFMTY	GNLLDYLREC	NRQEVNAVVL	LYMATQISSA	MEYLEKKNFI	360
361	HRDLAARNCL	VGENHLVKVA	DFGLSLMTG	DTYAHAGAK	FPIKWTAPES	LAYNKFSIKS	420
421	DVWAFGVLLW	EIATYGMSPY	PGIDLSQVYE	LLEKDYRMER	PEGCPEKVYE	LMRACQWNP	480
481	SDRPSFAEIH	QAFETMFQES	SISDEVEKEL	GKQGVRGAVS	TLLQAPELPT	KTRTSRRAAE	540
541	HRDTTDVPDM	PHSKGQGESD	PLDHEPAVSP	LLPRKERGPP	EGGLNEDERL	LPKDKKTNLF	600
601	SALIKKKKKT	APTPPKRSSS	FREMDGQPER	RGAGEEEGRD	ISNGALAFPT	LDTADPAKSP	660
661	KPSNGAGVPN	GALRESGGSG	FRSPHLWKKS	STLTSSRLAT	GEEEGGGSSS	KRFLRSCSAS	720
721	CVPHGAKDTE	WRSVTLPRLD	QSTGRQFDSS	TFGGHKSEKP	ALPRKRAGEN	RSDQVTRGTV	780
781	TPPPRLVKKN	EEAADEVFKD	IMESSPGSSP	PNLTPKPLRR	QVTVAPASGL	PHKEEAGKGS	840
841	ALGTPAAAEF	VTPTS KAGSG	APGGTSKGPA	EESRVRRHKH	SSESPGRDKG	KLSRLKPAPP	900
901	PPPAASAGKA	GGKPSQSPSQ	EAAGEAVLGA	KTATSLVDA	VNSDAAKPSQ	PGEGLKKPVL	960
961	PATPKPQSAK	PSGTPISPAP	VPSTLPSASS	ALAGDQPSST	AFIPLISTRV	SLRKTRQPPE	1020
1021	RIASGAITKG	VVLDSTEALC	LAISRNSEQM	ASHSAVLEAG	KNLYTFCVSY	VDSIQQMRNK	1080
1081	FAFREAIKLN	ENNLRELQIC	PATAGSGPAA	TQDFSKLLSS	VKEISDIVQR		1130

Sequences for human and chicken Src, aligned using Clustal Omega:

SRC_HUMAN	1	MGSNKS PKD	ASQRRRSLEP	AENVHAGGG	AFPASQTPSK	PASADGHRGP	SAAFAPAAAE	60
SRC_CHICK	1	MGSSKSKPKD	PSQRRRSLEP	PDSTH--HG	GFPASQTPNK	TAAPDTHRTP	SRSFGTVATE	57
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SRC_HUMAN	61	PKLFGGFNSS	DTVTSPQRAG	PLAGGVTTFV	ALYDYESRTE	TDLSFKKGER	LQIVNNTGED	120
SRC_CHICK	58	PKLFGGFNTS	DTVTSPQRAG	ALAGGVTTFV	ALYDYESRTE	TDLSFKKGER	LQIVNNTGED	117
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SRC_HUMAN	121	WWLAHSLSTG	QTGYIPSNYV	APSDSIQAE	WYFGKITRRE	SERLLLNAEN	PRGTFLVRES	180
SRC_CHICK	118	WWLAHSLTTG	QTGYIPSNYV	APSDSIQAE	WYFGKITRRE	SERLLNPEN	PRGTFLVRES	177
		*****.*	*****	*****	*****	*****	*****	
SRC_HUMAN	181	ETTKGAYCLS	VSDFDNAKGL	NVKHYKIRKL	DSGGFYITSR	TQFNSLQQLV	AYYSKHADGL	240
SRC_CHICK	178	ETTKGAYCLS	VSDFDNAKGL	NVKHYKIRKL	DSGGFYITSR	TQFSSLQQLV	AYYSKHADGL	237
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SRC_HUMAN	241	CHRLTTVCPT	SKPQTQGLAK	DAWEIPRESL	RLEVKLGGQC	FGEVWMGTWN	GTTRVAIKTL	300
SRC_CHICK	238	CHRLTNVCPT	SKPQTQGLAK	DAWEIPRESL	RLEVKLGGQC	FGEVWMGTWN	GTTRVAIKTL	297
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SRC_HUMAN	301	KPGTMSPEAF	LQEAQVMKKL	RHEKLVQLYA	VVSEPIYIV	TEYMSKGSLL	DFLKGETGKY	360
SRC_CHICK	298	KPGTMSPEAF	LQEAQVMKKL	RHEKLVQLYA	VVSEPIYIV	TEYMSKGSLL	DFLKGEEMKY	357
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SRC_HUMAN	361	LRLPQLVDMA	AQIASGMAYV	ERMNVVHRDL	RAANILVGEN	LVCKVADFGL	ARLIEDNEYT	420
SRC_CHICK	358	LRLPQLVDMA	AQIASGMAYV	ERMNVVHRDL	RAANILVGEN	LVCKVADFGL	ARLIEDNEYT	417
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SRC_HUMAN	421	ARQGAKFPIK	WTAPEAALYG	RFTIKSDVWS	FGILLTELTT	KGRVPYPGMV	NREVLQOVER	480
SRC_CHICK	418	ARQGAKFPIK	WTAPEAALYG	RFTIKSDVWS	FGILLTELTT	KGRVPYPGMV	NREVLQOVER	477
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SRC_HUMAN	481	GYRMPCPPEC	PESLHDLMCQ	CWRKEPEERP	TFEYLQAFLE	DYFTSTEPQY	QPGENL	536
SRC_CHICK	478	GYRMPCPPEC	PESLHDLMCQ	CWRKDPEERP	TFEYLQAFLE	DYFTSTEPQY	QPGENL	533
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