

S100 fused-type proteins (SFTPs) in chicken and quail

A) Accession numbers and amino acid sequences of chicken SFTPs

>NP_001165847.1 Chicken_cornulin (CRNN)

MAQLQENINGIITVFYTYARSDGDSSTLSRGELRQLIEQEFQDVITDARDPRTVDEVLFFLDEDDSSGKIDFGEFLSLIFRVAKACHR
QLQQYLEPEYDQELTVQEEADGEQQHNQVLEQGVSEQVQEGGTPQQDQDTQQHQESEEPPKNHQTQQKQEGGTPKYQDTQKIEKSEI
PKVQDTQKTQEVETPKNNSTQQKKSETPKDNQDTHQDDRAKTPQSPKRGENVVTKSPPEEDRNTQEAETPKHDPKPHQDKVTETP
KLGQDHHQRHELKPAEQSHTSPTKTPGGTTDKTKDHVAHWQDPSPKGTQELPPPVRGTSPHPDPRPSGTQHDPAPHLNPNTVIVREGS
GAEAHVPGQQQHGAGHGKGVHVAEQEHLQPQWPPRK

>NP_001338424.2 Chicken_scaffoldin (SCFN)

MSHFLDSVSTIITVFYQHAKEDGQSKLNRRKMKEFIEKEFADAIVNPHDPQTIEKILQFLEWDGDGEIDFNEFLLLVFRVAKACYW
YLQKGQCLLTQRTKLITSSKTIQFEPIKNRGSQQQLQEEEPQTLERNRHPPCIPFPQPDTRVQDLETHEETGSHRQQHNTQSRADARQ
STRPSEIIPQEYEEQTQEPDQSRQRQPPPELDRLGDLQSHKHGSLKAAQNDERQNEKPPQREQLADVRSCSHSCEPQLLPDRSD
RQPREPALPAYDQRNHRPQDQEAHAVHRSSRRPHEPEEADRGRHNQPRNPPELLKDESRNHLRKLEQKELERSSRPCKPECLDSER
LHQSYLEPLVISHKYNNTRELEEDYEQGKTQKDRKSCSMEERTQEDSVAEAEATVKIRRETQKREEREEAKRPRESARYQRTQ
ENTVAEAEADVEIHRVSRGRERELEDRRPHESVRHVKTQENI VAEAEADVEIRRVSREREREQEDRRPRDSEYDRDTREDIVAEAEA
NVEIRRVSRGREREEDRRPDELVRVYVKTQEDIVAEAEADVQIPCVSRKREREGELRRPRESVRYERTREDIAAEAEADVEIRHVVTQK
SETGQEDRKPRESQRYDKTREDIVAEAEADVEIRRVSRGREREQEDRRPRESQRYERTREDIAAEAEADVEIRRVSRERKREEEARR
PRELLRSGQRWEDIVAEAEADVEIHRVSREREREERARRPRDSVRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPRDSVRYER
TREDIVAEAEADVEIRHVSRRGREREQEAARRPRDSVRYERTREDIVAEAEADVEIRRVSRGREREERARRPHELVRVYVKTQEDIVAEAE
ANVEIHRVSREREREERARRPRDSVRYERTREDIAAEAEADVEIRRVSRGREREERARRPNELVRVYVKTQEDTVAEAEADVEIHHVSR
EREREERARRPRDSVRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPRESQRYERTREDIAAEAEANVEIRRVSRERKREEEARR
RPRDSVRYERTREDTVAEAEADVEIRRVSRGREREERARRPCELVRVYVKTQEDIVAEAEADVEIHRVSRGREREQDNRRPRESQRYER
TREDIVAEAEAEVEIHRASRRGREREERARRPDDSVRYVKTREDIVAEAEAEVEIRRVSREREREERARRPRDSVRYERTREDIVAEAE
ADVEIRRVSRGREREQEDRRPRESQRYERTREDIVAEAEADVEIRHVSRREREREERARRPRESVRYERTREDIVAEADLEIRRVSR
RKREEEARRPRESQRYERTREDIVAEAEADVEIRRVSRGREREERARRPRESVRYVKTQEDIVAEAEADVEIYRVSREREREERARRP
DSVRYDRDTREDIAAEAEADVEIRRVSRGREREERARRPNELVRVYVKTQEDTVAEAEADVEIHRVSREREREERARRPRDSVRYERTRE
DIVAEAEADVEIRRVSRGREREQEDRRPRESQRYERTQEDIVAEAEADVEIRRVSRGREREQEDRRPHKSQRYERTREDIAAEAEAD
VEIRRVSRGREREQEDRRPRESQRYERTREDIVAEAEADVEIRRVSRGREREERARRPRELVRVYVKTQEDIVAEAEADVEIHRVSRER
EREREERARRPRDSVRYERTREDIVAEAEADVEIRRVSQGREREQEDRRPCESQRYERTREDIVAEAEADVEIRRVSRGREREQEDRRP
CESQRYERTREDIVAEAEAEVEIHRASRRGREREERARRPDDSVTYVKTREDIVAEAEAEVEIRRVSREREREERARRPRDSVRYERT
EDIVAEAEAEVEIHRASRRGREREERARRPDDSVRYVKTREDIVAEAEAEVEIRRVSREREREERARRPRDSVRYERTREDIVAEAEAD
VEIRRVSQGREREQEDRRPCESQRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPCESQRYERTREDIVAEAEAEVEIHRASRG
REREERARRPDDSVRYVKTREDIVAEAEAEVEIRRVSREREREERARRPRDSVRYERTREDIVAEAEAEVEIHRASRRGREREERARRP
DSVRYVKTREDIVAEAEAEVEIRRVSREREREERARRPRDSVRYERTREDIVAEADLEIRRVSRERKREEEARRPRESQRYERTRED
IVAEAEADVEIRRVSRGREREERARRPRESVRYVKTQEDIVAEAEADVEIYRVSREREREERARRPRDSVRYDRDTREDIAAEAEADVEI
RRVSRGREREERARRPNELVRVYVKTQEDTVAEAEADVEIHRVSREREREERARRPRDSVRYERTREDIVAEAEADVEIHRVSRGRERE
QEDRRPRESQRYERTQEDIVAEAEADVEIRRVSRGREREQEDRRPHKSQRYERTREDIAAEAEADVEIRRVSRGREREQEDRRPRES
QRYERTREDIVAEAEADVEIRRVSRGREREERARRPRELVRVYVKTQEDIVAEAEADVEIHRVSREREREERARRPRDSVRYERTREDI
VAEAEADVEIHRVSREREREERARRPRDSVRYERTREDIVAEAEAEVEIRRVSQGREREQEDRRPCESQRYERTREDIVAEAEADVE
NRRVSRGREREQEDRRPRESQRYERTREDIVAEAEAEVEIHRASRRGREREERARRPDDSVRYVKTREDIVAEAEAEVEIRRVSRERER
EEEARRPRDSVRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPRESQRYERTREDIVAEAEADVEIHRVSREREREERARRPRD
SVRYERTREDIVAEADLEIRRVSRERKREEEARRPRESQRYERTREDIVAEAEADVEIRRVSRGREREERARRPRESVRYVKTQEDIV
AEAEADVEIYRVSREREREERARRPRDSVRYDRDTREDIAAEAEADVEIRRVSRGREREERARRPNELVRVYVKTQEDTVAEAEADVEIHR
VSREREREERARRPRDSVRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPRESQRYERTQEDIVAEAEADVEIRRVSRGREREQ
EDRRPHKSQRYERTREDIAAEAEADVEIRRVSRGREREQEDRRPRESQRYERTREDIVAEAEADVEIRRVSRGREREERARRPRELVR
YVKTQEDIVAEAEADVEIHRVSREREREERARRPRDSVRYERTREDIVAEAEADVEIHRVSREREREERARRPRDSVRYERTREDIV
AEAEADVEIRRVSQGREREQEDRRPCESQRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPRESQRYERTREDIVAEAEAEVEI
HRASRRGREREERARRPDDSVRYVKTREDIVAEAEAEVEIRRVSREREREERARRPRDSVRYERTREDIVAEAEADVEIRRVSRGRERE
QEDRRPRESQRYERTREDIVAEAEADVEIHRVSREREREERARRPRDSVRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPRES
QRYERTQEDIVAEAEADVEIRRVSRGREREQEDRRPHKSQRYERTREDIAAEAEADVEIRRVSRGREREQEDRRPRESQRCERTRED
IVAEAEADVEIRRVSRGREREERARRPRELVRVYVKTQEDIVAEAEADVEIHRVSREREREERARRPRDSVRYDRDTREDIVAEAEADVE
IRRVSQGREREQEDRRPRDSVRYDRDTREDIVAEAEADVEIRHVTKREREQEDRRPRKSQRYERTREDIVAEAEAEVEIRRVSRGRERE
ERARRPNDVRYVKTREDIVAEAEAEVEIRRVSREREREERARRPRDSVRYERTREDIVAEAEADVEIRRVSRGREREQEDRRPHE
SQRYERTREDIVAEAEADVQIHRVSRGREREQEAARRPRESVRYEKTQEDILAEAEADVEIHRVSREREREERARRPRESLYERTQED
IVTDAEAEVCREEVERADSLHEYEEAVKERRAVRARAREEAPVRERRLDRQRDLEVERNRFPGHDDQGERQERSLYQTVDVDSRDLV
PPGEVPSVTDVVRVYIPSPDPVPEVQAVPEPCFPQSIAYLIHVIQNLNDPKATTYEICQQSNDSGQPVYVRKCYVSPQPPVGPCK
ESSVLEPELQHLPLSSSSQENARELEEPRKGEIRERSATGVKEGASAPELDSLEDDTSQAETREDRRDHQSPSVHDVEEKNHQPEGDG
PKATEEEVSEQAESQGNKDREAKSRSPAARAPELQEAHKQGGQAAEPCHPVQRDEAGCCHEDAELPSPDRSRQAREEENSKRSSQ
QENNTQPQREEERSPMAPQALSHPMKDEAKAP

Antibody binding sites are shaded yellow. Additional putative binding sites with around 90% sequence conservation are present but not highlighted.

B) Amino acid sequences of SFTPs and accession numbers of the coding sequences in the genome of the Japanese quail

>Quail_cornulin (CRNN)

MAQLQENINGIITAFYTYARSDGDCSTLSRGELRQLIEQEFEDVIVDARDPRTVEKVLLFLDEDSSGKVDFGEFLSLVFRVAKACHR
QFQQYLEPEDDQELTVQEEADGEQHHNQVQEQGVSEEVQESGTTQQHQEGEEKNHQDTQQKQEGETPKNQDTQNIKTETPKVQDT
QQTQEVETPNNQGTQEKKIEIPKDIQDTHQDDRATAPEEGPKRGENVVTETPEKDRNTPEAEKTPKHDPKLHQDKVTETPELGQNNH
HREELPAEQSHTSPTVTPTGRITDNTKNPSPKETQELPPPVRGTDPHDPQPSGTRRDPAPHPDLTVTVREGSVAAEAEVPGHQHGH
AHGKGKHVVEKENLQPPPRK

Coding sequence (GenBank accession number NC_029540.1, nucleotide numbers 891426-891563, 890345-891316, reverse complement)

>Quail_scaffoldin (SCFN) preliminary*

MSHFLDSVSTIITVFYQHAKEDGDQSKLNRRKMKEFIQKEFADAIANPHDPQTIDKILQFLEWDGDGEIDFNEFLLLVFRVAKACYW
YLQRGQCILQRTKLITSSKTIREFEIKNRGSRQQLQEEEPQTHPPYIPEPQQDTRVQDLEIREETGSHRQQRNTESRADARQSSRPR
EMIPQEEYEQSQEPDQGSRRRQPPELDRLGLQYHKGSLKAAQORDERQNLREQLADVRSCHSCEPQLLPDRSGRQPREPTLP
AYDQRNHRPQDQEAQAARGSRPHEPEEADRGRRNQPRKPELLKDERSRNHLRELEQKELESSRQPCCKPECLDSEWQHQSYLEP
LVIDHRYNKTREMEDYYEQGKIQRDRRPRESMTYERTEEDIVVEAEADVEIRRETQKRERGLEARRPHESVKYVKTREDIEAEAEAD
VEIHRVSRVREREAEARRPGESVRRERTREDIVAELEGDVEIRRVTVQERKRVVEARRPDASA**RYERTREDIVAEAE**VDVDIRRVTRT
REREDTRRPRESV**RYERTREDIVAEAE**ADVEIHRVSRVREREAEARRPGESVRRERTREDIVAELEGDVEIRRVTVQERKRKEEARRP
GEPDRYRRTRREDIVAEAEADVEIHHVTRKREREDARRPHESV**RYERTREDIVAEAE**ADVEISRVSREREAEARRPGESVRRERTR
EDIVAEVEGDVKIHRVTQECKRVVEARRPDASA**RYERTREDIVAEAE**VDVDIRRVSRVREREAEARRPGESVRRERTQEDIVAEVEG
DVEIHRVTRKTGERGCQETQRESVRYERRWRHCG

Antibody binding sites are shaded yellow.

Coding sequence of SCFN gene

NC_029540.1, nucleotides 885529-885666, 882990-885305 (reverse complement)

* Because of possible sequence assembly errors in the repetitive sequence region, the sequence is considered preliminary. The coding sequence may actually be longer and include sequences up to position NC_029540.1, nucleotide 878530 (reverse complement).

C) Alignment of binding sites of the anti-scaffoldin antiserum

Chicken	RYERTREDIAAEAE
Quail	RYERTREDIVAEAE

Supplementary Figure S1. Sequences of S100 fused-type proteins (SFTPs) in chicken and quail. The amino acid sequences of chicken cornulin (CRNN) and scaffoldin (SCFN) were downloaded using the indicated accession numbers from GenBank (A). Sequences of quail CRNN and SCFN were predicted on the basis of the current genome sequence of the Japanese quail (B). Binding sites of the anti-scaffoldin antiserum (Mlitz et al. 2014) are highlighted by yellow shading in SCFN sequences and compared between chicken and quail (C).