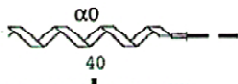
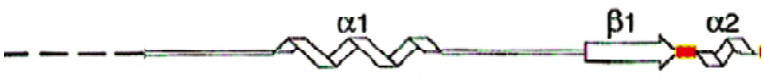



SUPPLEMENT: ALIGNMENT OF ALL KNOWN SIRT2 OPEN READING FRAMES WITH AN INDICATION OF THE TERTIARY STRUCTURE AND KEY PHOSPHORYLATION AND CATALYTIC SITES

Alignment done at the Genomatix server (<http://www.genomatix.de>). Indicated above the top line describing the Drosophila isoform 1 open reading frame (ORF) is the known folding of human SIRT2 based on the crystal structure described by Finnin et al., Nature Structural Biol. 8, 621-625 (2001); small numbers beneath these folding data correspond to the numbering of the human isoform 1 SIRT2 ORF. Indicated with double underlining in the N-terminal extension of 31-37 residues (i.e., 1-31 in Drosophila) are proposed sites for phosphorylation by casein kinase II (CKII) on SER residues. Indicated as single underlining in the L-1 loop are the proposed PRO-directed kinase sites suggested by analysis of human, mouse, and Drosophila ORFs using a neural net algorithm described by Nikolai Blom at the Technical University of Denmark (Kreegipuu et al., Nucleic Acids Res. 27, 237-239 (1999)).

							
		< ----- not in 1J8F crystal ----- >					
drosophila_SIRT2_lon	1	mgd-----IE VK---KEEQP TTPSNSSSSD DDEEAPDDTM DKVRRFFANT					
bovine_SIRT2_long	1	MADPDPSPDE ETQAGKVQ-- EAQDS ³¹ SD ³² TE AGATGGEAEM DFLRNFFSQT					
trypanosoma_bruc AAC	1	m-----					
silurana_SIRT2	1	-----					
pig_SIRT2	1	MAEPDPSPDV ETQTGKVQEA QDS ³¹ SD ³² TE EGAAGGEAEM DFLRNFFSQT					
dictyostelium_SIRT2	1	-----					
chicken_SIRT2	1	-----					-M ELLRNLLART
human_SIRT2_long	1	MAEPDP SHPL ETQAGKVQ-- EAQDS ³¹ SD ³² SE GGAAGGEADM DFLRNLF SQT					
anopheles_SIRT2_long	1	- <u>SE</u> DDAEDPY HSE S I S I E-- RIRQYLS ³¹ DKL GFHTGDGFEN Eng-----					
onchorhynchus_SIRT2	1	-----					-M DFLRNLF SKT
fugu_rubripes_SIRT2	1	-----					-M EFLRNLF SKN
leishmania_SIRT2	1	mtasprap--					
cryptococcus_neof_T1	1	-----					
danio_rerio_SIRT2	1	MSEEVSKRVE EE--ADTPG LEGQ ³¹ SD ³² SD EGDASGDTEM DFLRSLFSRT					
mouse_SIRT2_long	1	MAEPDPSPDPL ETQAGKVQ-- EAQDS ³¹ SD ³² TE GGATGGEAEM DFLRNLF TQT					
rat_SIRT2_long	1	MAEPDP SHPL ETQAGKVQ-- EAQDS ³¹ SD ³² SE GGAAGGEADM DFLRNLF SQT					
neurospora_crassa	1	MGQEV Savpe					
bee_apis_SIRT2	1	-----					
oryzias_latipes_meda	1	MAEEe----- -Q---EEVTP DLQDL ³¹ SD ³² SS DDEAAAGAEM DFLRNLF SST					
danio_rerio_SIRT2	1	MSEEVSKRVE EE--ADTPG LEGQ ³¹ SD ³² SD EGDASGDTEM DFLRSLFSRT					

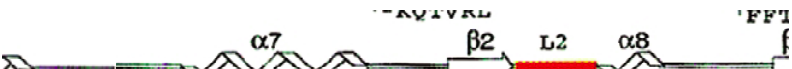
D (D33A)
Double underlined S and T residues in CK2 motifs

							
drosophila_SIRT2_lon	43	LHLG--GSSD AKEEVKVEKV IPDLSFDGFA EHWRVHGF RK IVTMVGAGIS					
bovine_SIRT2_long	49	LGLG--TQKE -----RL LDEL TLEGVS RYMQSERCR R VICLVGAGIS					
trypanosoma_bruc AAC	2	----- TEPK LAT THV VGEPTFEGLA RFIERN NITK IFVMVGAGIS					
silurana_SIRT2	1	-----					IIVMAGAGIS
pig_SIRT2	51	LGLG--TQKE -----RL LDEL TLEGVS RYMQSERCR R VICLVGAGIS					
dictyostelium_SIRT2	1	-----					---MTGAGIS
chicken_SIRT2	12	LGLGtePP-E -----RV LDEL SLAGIA RFMQSERCR R VVCMVGAGIS					
human_SIRT2_long	49	LSLG--SQKE -----RL LDEL TLEGVA RYMQSERCR R VICLVGAGIS					
anopheles_SIRT2_long	41	-SGG--AARR -----RV LETVDIDGVL KHWSGGFKK IVTMVGAGIS					
onchorhynchus_SIRT2	12	LGI---SG-E -----KV LDEL TLEGVA SYIQSGKCKN IICMVGAGIS					
fugu_rubripes_SIRT2	12	LGIG--TP-D -----KV LDEL TLEGVA QYIKSGKCKN IICMVGAGIS					
leishmania_SIRT2	9	-----HQE -----HV LGEPTLEGLA HYIREKNVRR IILVLV GAGAS					
cryptococcus_neof_T1	1	-----					VIFLLGAGIS
danio_rerio_SIRT2	48	LGLS--PG-D -----KV LDEL TLDSVA RYILSGXCKN IICMVGAGIS					
mouse_SIRT2_long	49	LGLG--SQKE -----RL LDEL TLEGVT RYMQSERCR K VICLVGAGIS					
rat_SIRT2_long	49	LSLG--SQKE -----RL LDEL TLEGVA RYMQSERCR R VICLVGAGIS					
neurospora_crassa	11	-----TTKP -----EN LSERSLPAVA DYIKSGKARK VVVL T GAGIS					
bee_apis_SIRT2	1	-----					---ELSIDGII DYIKEKENCK IITMAGAGIS
oryzias_latipes_meda	42	LGLG--SA-E -----KV LDAL TLEGVA QYIKSGKCKN IICMVGAGIS					
danio_rerio_SIRT2	48	LGLS--PG-D -----KV LDEL TLDSVA RYILSGKCKN IICMVGAGIS					

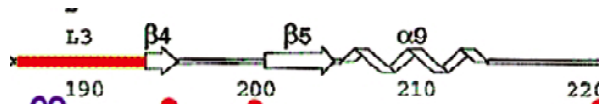


Species	Residue	90	100	110	120	130
drosophila_SIRT2_lon	91	TSAGIPDFRS	PGSGLY ^u SNLK	KYELPHPTAI	F ^u DLDYFEKNP	APFFALAK--
bovine_SIRT2_long	89	TSAGIPDFRS	PNTGLYANLE	KYRLPYPEAI	FEISYFKKHP	EPFFALAK--
trypanosoma_bruc_AAC	42	VAAGIPDFRS	PHTGLYAKLS	RYNLNSPEDA	FSLPLLRQQP	SVFYNILMdm
silurana_SIRT2	11	TASGIPDFRT	PGSGLYDNLQ	KYDIPYPEAI	FDINYFVCNP	NPF ^u FHLAK--
pig_SIRT2	91	TSAGIPDFRS	PSTGLYANLE	KYRLPYPEA-	FEIGYFKKHP	EPFFALAK--
dictyostelium_SIRT2	8	VAAGIPDFRS	PKTGLYEKLD	KYDLPYREAI	FDIEYFKKNP	KPFYVLSK--
chicken_SIRT2	53	TAAGIPDFRS	PGTGLYANLG	RYELPYPEAI	FDISYFKQHP	EPFFALAK--
human_SIRT2_long	89	TSAGIPDFRS	PSTGLYDNLE	KYHLPYPEAI	FEISYFKKHP	EPFFALAK--
anopheles_SIRT2_long	80	TSAGIPDFRS	PNTGLYNNLM	KYNLPYQAI	FELEYLHQNP	KPFFTLAK--
onchorhynchus_SIRT2	50	TSAGIPDFRS	PDTGLYANLQ	KYNLPYPEAI	FQIDYFKKHP	EPFFALAR--
fugu_rubripes_SIRT2	51	TSAGIPDFRS	PGTGLYANLQ	KYNLPYPEAI	FQIDYFKKHP	EPFFALAR--
leishmania_SIRT2	44	VAAGIPDFRS	PDTGIYANLG	KYNLEDPDA	FSLTLLREKP	EIFYSIAR--
cryptococcus_neof_TI	11	TSAGIPDFRS	PSTGLYHNLQ	ALELPFEAV	FELGFFQRRP	EPFWTLAK--
danio_rerio_SIRT2	87	TSAGIPDFRS	PGTGLYANLQ	KYNLPYPEAI	FQIDYFKKHP	EPFFALAR--
mouse_SIRT2_long	89	TSAGIPDFRS	PSTGLYANLE	KYHLPYPEAI	FEISYFKKHP	EPFFALAK--
rat_SIRT2_long	89	TSAGIPDFRS	PSTGLYDNLE	KYHLPYPEAI	FEISYFKKHP	EPFFALAK--
neurospora_crassa	47	TAAGIPDFRS	PETGLYANLA	ALELEPEDV	FSLPFFKENP	KPFYVLAK--
bee_apis_SIRT2	29	TSAGIPDFRS	PTSGLYHNLE	KYNLPHQAI	FELDFEMENP	EPFFMLAK--
oryzias_latipes_medea	81	TSAGIPDFRS	PETGLYANLQ	KYNLPYPEAI	FQIDYFKKHP	EPFFTLAK--
danio_rerio_SIRT2	87	TSAGIPDFHS	PGTGLYANLQ	KYNLPYPEAI	FQIDYFKKHP	EPFFALAR--

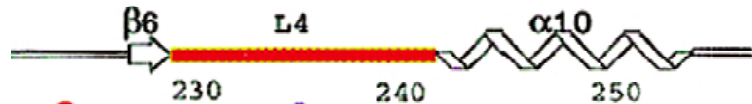
single underlined S residues in SP motif in L-1 loop
 curly underlined S or T residues in L-1 loop



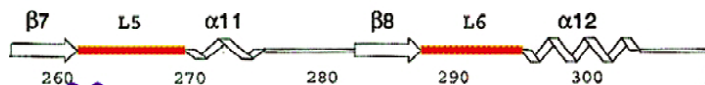
Species	Residue	140	150	160	170	180
drosophila_SIRT2_lon	139	E--LYPGS-F	IPTPAHYFIR	LLNDKGLIQR	HYTQ ^u NIDTLD	RLTGLPEDKI
bovine_SIRT2_long	137	E--LYPGQ-F	KPTICHYFIR	LLKEKGLLIR	CYTQ ^u NIDTLE	RVAGLEPEDL
trypanosoma_bruc_AAC	92	D--LWPGK-Y	CPTTVHHFIS	LLAKKMLLC	CCTQ ^u NIDGLE	RACGIPESLL
silurana_SIRT2	59	E--LFPGK-Y	KPNLVHYFIK	LLHDKGLLIR	CYTQ ^u NIDGLE	RIAGIPVEKI
pig_SIRT2	138	E--LYPGQ-F	KPTICHYFIR	LLKEKGLLIR	CYTQ ^u NIDTLE	RVAGLEQEDL
dictyostelium_SIRT2	56	E--LFPGS-F	NPTTVHYFIK	LLSDKGLLIR	NFTQ ^u NIDTLE	RIAGIPANKL
chicken_SIRT2	101	E--LLPGQ-L	KPTVCHYFMR	LLKEKGLLIR	CYTQ ^u NIDTLE	RVAGLQPEEL
human_SIRT2_long	137	E--LYPGQ-F	KPTVCHYFMR	LLKDKGLLIR	CYTQ ^u NIDTLE	RIAGLEQEDL
anopheles_SIRT2_long	128	E--LYPGT-F	KPTPSHYFVR	LLEQKGLLVR	HYTQ ^u NIDTLE	RIAGIPEDKI
onchorhynchus_SIRT2	98	E--LYPGQ-F	KPTVCHYFIK	LLKDKGLIKR	CYSQ ^u NIDTLE	RVAGLEGEDL
fugu_rubripes_SIRT2	99	E--LYPGQ-F	KPTVCHYFMK	LLKDKGLLRR	CYSQ ^u NIDTLE	RVAGLEGDDL
leishmania_SIRT2	92	ElnLWPGH-F	QPTAVHHFIR	LLQDEGRLLR	CCTQ ^u NIDGLE	KAAGVSPPELL
cryptococcus_neof_TI	59	E--IYPGR-X	XPTPTHYLLQ	LFNRHNLKRR	VFTQ ^u NIDTLE	TLAGLPPHLI
danio_rerio_SIRT2	135	E--LYPGQ-F	KPTVYHYFIK	MLKDKGLLRR	CYSQ ^u NIDTLE	RVAGLEGEDL
mouse_SIRT2_long	137	E--LYPGQ-F	KPTICHYFIR	LLKEKGLLIR	CYTQ ^u NIDTLE	RVAGLEPQDL
rat_SIRT2_long	137	E--LYPGQ-F	KPTICHYFMR	LLKDKGLLIR	CYTQ ^u NIDTLE	RIAGLEQEDL
neurospora_crassa	95	D--LYPGK-F	HPTISHVFIS	LLATKGLLYQ	LFTQ ^u NIDCLE	RAAGVPADLI
bee_apis_SIRT2	77	E--LLPddgF	KPTPSHYFIR	LLWEKGLLIR	HYTQ ^u NIDTLE	RIAGLPSEKL
oryzias_latipes_medea	129	E--LYPGQ-F	KPTICHYFIK	LLKNKGLLRR	CYTQ ^u NIDTLE	RVAGLEKEDL
danio_rerio_SIRT2	135	E--LYPGQ-F	KPTVCHYFIK	MLKDKGLLRR	CYSQ ^u NIDTLE	RVAGLEGEDL



drosophila_SIRT2_lon	186	IEAHGSFHTN	HCIK--CRKE	YD-MDWMKAE	-IFADRLP--	-----	KC
bovine_SIRT2_long	184	VEAHGTFYTS	HCISSGCRQE	YS-LSWMKEK	-IFSEVTP--	-----	KC
trypanosoma_bruc_AAC	139	VEAHGSFSSA	SCVDCHAKYD	i---NIARAE	-TRAGKVP--	-----	HC
silurana_SIRT2	106	VEVHGTFSSA	SCSL--CYTP	FP-ANEAKEL	-IFDGNPP--	-----	CC
pig_SIRT2	185	VEAHGTFYTS	HCVSASCRHE	HA-CGWMKEK	-IFSEVTP--	-----	KC
dictyostelium_SIRT2	103	VEAHGSFATS	HCVS--CKKE	YS-TEYVKER	-IFKDELP--	-----	EC
chicken_SIRT2	148	VEAHGTFQTA	HCLRSSCRHQ	YD-LSWVKEK	-IFSLSVP--	-----	KC
human_SIRT2_long	184	VEAHGTFYTS	HCVSASCRHE	YP-LSWMKEK	-IFSEVTP--	-----	KC
anopheles_SIRT2_long	175	VEAHGTFYTN	HCLE--CKIA	YS-LEFVKKE	kIFADEVP--	-----	TC
onchorhynchus_SIRT2	145	IVAHTGTFYTS	HCVSFMCRKE	YD-LDWMKEK	-IFSDDIP--	-----	KC
fugu_rubripes_SIRT2	146	IEAHGTFYTS	HCVSFCCRKE	YS-LGWMEEK	-IFSDDVP--	-----	RC
leishmania_SIRT2	141	VEAHGSFAAA	ACIE--CHTP	FS-IEQNYLE	-AMSGTVS--	-----	RC
cryptococcus_neof_TI	106	VEAHGSFATA	HCLK--CRRE	VDrEEVLKAG	-VRKGEVvrc	datlkamg	KG
danio_rerio_SIRT2	182	IEAHGTFHTS	HCVSxlxs--	-----	-----	-----	-----
mouse_SIRT2_long	184	VEAHGTFYTS	HCVNTSCRKE	YT-MGWMKEK	-IFSEATP--	-----	RC
rat_SIRT2_long	184	VEAHGTFYTS	HCVSASCRHE	YP-LSWMKEK	-IFSEVTP--	-----	KC
neurospora_crassa	142	VEAHGSFASQ	RCID--CKTP	YP-DDKMRH	-VSRAEVP--	-----	HC
bee_apis_SIRT2	125	VEAHGTFHTG	RCLK--CRAP	YT-LPWMKEQ	-IFKNVIP--	-----	K-
oryzias_latipes_meda	176	IEAHGTFYTT	-----	-----	-----	-----	-----
danio_rerio_SIRT2	182	IEAHGTFHTS	HCVSFLCRKE	YS-MDWMKNQ	-IFSEEIP--	-----	KC



drosophila_SIRT2_lon	222	---QKCQGVV	KPDIVFFGEN	LPKRFYSSPE	EDFQDCDLLI	IMGTSLEVQP	
bovine_SIRT2_long	222	---EKCQSVV	KPDIVFFGEN	LPARFFSCMQ	SDFLKVDLLI	IMGTSLQVQP	
trypanosoma_bruc_AAC	175	---NQCGGIV	KPDVVFVGEN	LPEAFFNvag	li-EETEELL	ILGTSLQVHP	
silurana_SIRT2	142	---KFCAGPV	KPDIVFFGED	LPQTFQAYQ	-DFPKADLLI	IMGTSLKIEP	
zebrafish_SIRT2	220	---DSCGSLV	KPDIVFFW--	-----	-----	-----	
tetdictyostelium_SIRT2	139	tetSGCKGIV	KPDIVFFGES	LPSRFNDCAR	EDFTKCDLLL	VIGTSLKVHP	
chicken_SIRT2	186	---DKCQSVV	KPDIVFFGEN	LPSRFFQS--	-DFQKVDLLI	IMGHFTARSQ	
human_SIRT2_long	222	---EDCQSLV	KPDIVFFGES	LPARFFSCMQ	SDFLKVDLLL	VMGTSLQVQP	
anopheles_SIRT2_long	212	p---CGGVI	KPDIVFFGEG	LPERFHMLPH	QDFAECDLLI	IMGTSLTVQP	
onchorhynchus_SIRT2	183	---DKCSN--	-----	-----	-----	-----	
fugu_rubripes_SIRT2	184	---EKCSS--	-----	-----	-----	-----	
leishmania_SIRT2	177	---STCGGIV	KPNVVFVGEN	LPDAFFDALH	HDAPIAELVI	IIGTSMQVHP	
cryptococcus_neof_TI	153	---KKCGGLV	KPDIVFFGEG	LPDRFFKC--	-----	DLLI	VIGTSLQVQP
danio_rerio_SIRT2	200	-----	-----	-----	-----	-----	
mouse_SIRT2_long	222	---EQCQSVV	KPDIVFFGEN	LPSRFFSCMQ	SDFSKVDLLI	IMGTSLQVQP	
rat_SIRT2_long	222	---EDCQSLV	KPDIVFFGES	LPARFFSCMQ	SDFLKVDLLL	VMGTSLQVQP	
neurospora_crassa	178	---EKCNGLV	KPDIVFFHEN	LPSLFFDRRH	ma-EEADLIL	VLGTSLTVHP	
bee_apis_SIRT2	160	-----	-----	-----	-----	-----	
oryzias_latipes_meda	185	-----	-----	-----	-----	-----	
danio_rerio_SIRT2	220	---DSCGSLV	KPDIVFFW--	-----	-----	-----	

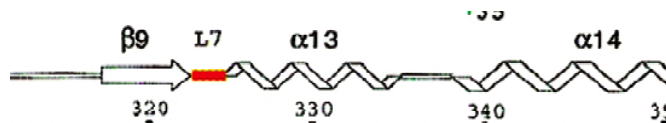


drosophila_SIRT2_lon	269	FASLVWRP	RCIRLLINRD	AVGQASCV--	---LFMdpnt	r-SLLF----	
bovine_SIRT2_long	269	FASLIGKAPL	STPRLLINKE	KTGQTDPF--	---LGMMMAL	GGGMDF----	
trypanosoma_bruc_AAC	221	FADLALMVP	DVPRVLFNLE	RVGGRMFRFP	tdtrtpnfras	syrlstgngn	
silurana_SIRT2	188	FASLVNTVKP	SIPRLLI--	-----	-----	-----	
pig_SIRT2	270	FASLISKAPL	STPRLLINKE	KTGQTDPF--	---LGMMMGL	GGGMDF----	
dictyostelium_SIRT2	189	FASLINFa-K	GCPRVLINFE	EVGTNPY--	-----	-GGFKF----	
chicken_SIRT2	230	PFASLVSVPA	STPRLLITKE	KTGQSDVF--	---MS-LMGF	GCGMDF----	

human_SIRT2_long	269	FASLISKAPL	STPRLLINKE	KAGQSDPF--	---LGMIMGL	GGGMDF----
anopheles_SIRT2_long	258	FASLVEYVND	DCVRLINRD	KVGCNSFgf-	---LR-SMVF	GEGLCF----
onchorhynchus_SIRT2_	188	-----	-----	-----	-----	-----
fugu_rubripes_SIRT2_	189	-----	-----	-----	-----	-----
leishmania_SIRT2	224	FALLPCVVPK	SVPRVVMNRE	RVGGLLFRFP	DDPLN-TVhe	davakegrss
cryptococcus_neof_TI	192	FASLVDYVPS	TCPRLLINRE	AVG--PFSDL	ESTFS-SLPP	SISKLL----
danio_rerio_SIRT2	200	-----	-----	-----	-----	-----
mouse_SIRT2_long	269	FASLISKAPL	ATPRLLINKE	KTGQTFDPF--	---LGMIMGL	GGGMDF----
rat_SIRT2_long	269	FASLISKAPL	STPRLLINKE	KAGQSDPF--	---LGMIMGL	GGGMDF----
neurospora_crassa	224	FAGLPDLAPF	EVPRVLFNME	RVGSLgsqpd	-----	-----
bee_apis_SIRT2	160	-----	-----	-----	-----	-----
oryzias_latipes_meda	185	-----	-----	-----	-----	-----
danio_rerio_SIRT2	235	-----	-----	-GKS AFP--IFHFN	ESGLS-SMXP	fxsxmng----

drosophila_SIRT2_lon	309	-----	-----	-----	-----	-----D
bovine_SIRT2_long	310	-----	-----	-----	-----	-----D
trypanosoma_bruc_AAC	271	gskissg--	-----	-----	DSSSSSSVDG	YDQFtlaenD
silurana_SIRT2	205	-----	-----	-----	-----	-----D
pig_SIRT2	311	-----	-----	-----	-----	-----D
dictyostelium_SIRT2	220	-----	-----	-----	-----	-----N
chicken_SIRT2	270	-----	-----	-----	-----	-----D
human_SIRT2_long	310	-----	-----	-----	-----	-----D
anopheles_SIRT2_long	299	-----	-----	-----	-----	-----D
onchorhynchus_SIRT2_	188	-----	-----	-----	-----	-----
fugu_rubripes_SIRT2_	189	-----	-----	-----	-----	-----
leishmania_SIRT2	273	ssqsrpsas	prreegtd	spsspneev	EASTSSSSDG	YGQYgdyha-
cryptococcus_neof_TI	235	-----	-----	-----	-----	-----N
danio_rerio_SIRT2	200	-----	-----	-----	-----	-----
mouse_SIRT2_long	310	-----	-----	-----	-----	-----D
rat_SIRT2_long	310	-----	-----	-----	-----	-----D
neurospora_crassa	254	-----	-----	-----	-----	-----
bee_apis_SIRT2	160	-----	-----	-----	-----	-----
oryzias_latipes_meda	185	-----	-----	-----	-----	-----
danio_rerio_SIRT2	261	-----	-----	-----	-----	-----

*



drosophila_SIRT2_lon	310	KPNNTRDVAF	LGDCDAGVMA	LAKALGWDQE	LQQLITSERk	kl-----
bovine_SIRT2_long	311	SKKAYRDVAW	LGDCDQGCLA	LADLLGWKKE	LEDLVRKEH-	-----
trypanosoma_bruc_AAC	298	ETGVLRDIFV	PGDCQVSVRS	FAQALGFGEQ	LDASVREGRE	IFE-----
silurana_SIRT2	205	-----	-----	-----	-----	-----
pig_SIRT2	312	SKKAYRDVAW	LGDCDQGCLA	LADLLGW--	-----	-----
dictyostelium_SIRT2	221	QPSNKLDVKC	IGDCQTLVID	LIKLLGWENE	FNQIVK----	-----
chicken_SIRT2	271	SDKAYRDVAW	LGDCDEGCLA	LAELLGWKKE	LQELVRKEHA	-----
human_SIRT2_long	311	SKKAYRDVAW	LGECDAQCLA	LAELLGWKKE	LEDLVRREHA	-----
anopheles_SIRT2_long	300	LPGNRRDVAW	TGNCDGCFE	LADQLGW--	-----	-----
onchorhynchus_SIRT2_	188	-----	-----	-----	-----	-----
fugu_rubripes_SIRT2_	189	-----	-----	-----	-----	-----
leishmania_SIRT2	322	HPDVCRDVLV	RGDCQENVVT	LAEYLGISEA	LAKRMLSDA	-----
cryptococcus_neof_TI	236	GPSPSRDMFY	EGDADLGAWK	LAELLGWKDE	LEEMVKKGRE	ELE-----
danio_rerio_SIRT2	200	-----	-----	-----	-----	-----
mouse_SIRT2_long	311	SKKAYRDVAW	LGDCDQGCLA	LADLLGWKKE	LEDLVRREHA	-----
rat_SIRT2_long	311	SKKAYRDVAW	LGECDAQCLA	LAELLGWKKE	LEDLVRREHA	-----
neurospora_crassa	254	-----	DVLV LGDCDTGVRQ	LASALGWREE	LEAEWRKlvg	deeadrqlg
bee_apis_SIRT2	160	-----	-----	-----	-----	-----
oryzias_latipes_meda	185	-----	-----	-----	-----	-----
danio_rerio_SIRT2	261	-----	-----	-----	-----	-----



no more xray data >

drosophila_SIRT2_lon	352	-----	-----	-----	SGSQNSEELQ	QGKEKPQSDP
bovine_SIRT2_long	350	-----	-----	-----	-----	-----
trypanosoma_bruc_AAC	341	-----	-----	-----	-----	-----
silurana_SIRT2	205	-----	-----	-----	-----	-----
zebrafish_SIRT2	266	-----	-----	-----	-----	-----
pig_SIRT2	339	-----	-----	-----	-----	-----
dictyostelium_SIRT2	257	-----	-----	-----	-----	-----
chicken_SIRT2	311	-----	-----	---	AIDA-	-----
human_SIRT2_long	351	-----	-----	---	SIDAQSG	AGVNPSTSA SPKKSPPPAK
anopheles_SIRT2_long	327	-----	-----	-----	-----	-----
onchorhynchus_SIRT2_	188	-----	-----	-----	-----	-----
fugu_rubripes_SIRT2	189	-----	-----	-----	-----	-----
leishmania_SIRT2	362	-----	-----	---	Apa--TA	QRAPNet---
cryptococcus_neof_TI	279	-----	-----	-----	-----	-----
danio_rerio_SIRT2	200	-----	-----	-----	-----	-----
mouse_SIRT2_long	351	-----	-----	---	NIDAQSG	SQAPNPSTTI SPKKSPPPAK
rat_SIRT2_long	351	-----	-----	---	SIDAQSG	AGVNPSTSA SPKKSPPPAK
neurospora_crassa	298	sskrqvelhd	evsqlvhvdvd	kvl	HVHDVSS	SGSSSPSPEA VAEKEPIAAT
bee_apis_SIRT2	160	-----	-----	-----	-----	-----
oryzias_latipes_meda	185	-----	-----	-----	-----	-----
danio_rerio_SIRT2	261	-----	-----	-----	-----	-----

drosophila_SIRT2_lon	372	DKMTSGDRDK	kdasl	-----	-----	-----
bovine_SIRT2_long	350	-----	-----	-----	-----	-----
trypanosoma_bruc_AAC	341	---	RTRRREK	vveg	-----	-----
silurana_SIRT2	205	-----	-----	-----	-----	-----
zebrafish_SIRT2	266	-----	-----	-----	-----	-----
pig_SIRT2	339	-----	-----	-----	-----	-----
dictyostelium_SIRT2	257	-----	-----	-----	-----	-----
chicken_SIRT2	315	-----	-----	-----	-----	-----
human_SIRT2_long	378	DEARTTEREK	PQ	-----	-----	-----
anopheles_SIRT2_long	327	-----	-----	-----	-----	-----
onchorhynchus_SIRT2_	188	-----	-----	-----	-----	-----
fugu_rubripes_SIRT2	189	-----	-----	-----	-----	-----
leishmania_SIRT2	374	-----	-----	-----	-----	-----
cryptococcus_neof_TI	279	---	Re	-----	-----	-----
danio_rerio_SIRT2	200	-----	-----	-----	-----	-----
mouse_SIRT2_long	378	EAARTKEKEE	QQ	-----	-----	-----
rat_SIRT2_long	378	DEARTTEREK	P	-----	-----	-----
neurospora_crassa	348	QQevqqsesa	svkesvett	lteevkvsga	-----	-----
bee_apis_SIRT2	160	-----	-----	-----	-----	-----
oryzias_latipes_meda	185	-----	-----	-----	-----	-----
danio_rerio_SIRT2	261	-----	-----	-----	-----	-----



ANTON SCOTT GOUSTIN, Ph.D.

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http://www.genomatix.de/cgi-bin/dialign/dialign.pl?SHOW=antonsirt2.seq_66042.html&TASK=dialign