

Figure 1 - figure supplement 1

		SH2-like	
Ce-COMP-1	-MTLVESKHDFEMTEKSMENDDDIKDAI---	FNNVPITFIEAVFLKNPGDFSMSKSLDG--AYYLSIVPGNNKMKKETS	73
C. briggsae	-MTLVESKSNEVITEKRSMSDDEEIKDAL---	FVNVSIPFIENFVLKNPGDFCVSTNLEG--ILYLSIVAHPNKTKEGP	73
C. sinica	-MTLVESKSDFOITKKSLLEDNEEEVEDAL---	FLNVLPFIESFVFKNPQGDFCVSRTLDD--IAYLSIVAHPKKNKKGTP	73
C. tropicalis	-MTLVESKHEFETTKKLIENDRDTESM---	FSNVNTIPFIETFVLKNPGDGYCVYKTIDG--VTYLSIVAKPNKNKKGTP	73
C. remanei	MMTLLVESKAEFEITKRSMEDESEIKDAV---	FYNVTVPFVETFVLKNPGDFCISRTIDG--AYYLSIAANK-KDKKGEV	73
C. japonica	-MTSLFASTQNSLETTVPRPDMFDDFHENATIFDVTTIFIETFVLQKPGDFCVSQTLKG--QLFLSMLAES--AKDGD	74	
C. angaria	-MASVKNSAEIDEKQMIYIDVPLNCTQI---	FVLQKPGEYCITQSCKTDKMLFLTIMLESEHGEILIT	64
H. contortus	-MAAEVCRVTE-RNAELDAADLLTMNINRVSLGNIPEDFI-SFLKPKPGDFCISTNSFA--SYVLSIQSDK-----D	68	
N. americanus	MNTICKESNVDRFQMDVNKVCLGEVPSDFI-SFLDKCGDFCISTNALN--SYVFSIKSDG-----Q	59	
A. ceylanicum	MLATVASEVAEKRRADAELDAADLLTMNVNKVCLGEIPSDFV-SFLERPGDFCISTNALN--SYVFSIKSDE-----H	70	
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Ce-COMP-1	R-AIHLRIDHSENEAYIQGMLFARSOTLEQLVYHLNDFTDILGGVLDENISMNRLLGLSSTNVHNICKTGKRIKDKKIQ	152	
C. briggsae	R-VINLRIEQSGKVEVIPGLIFARASSMRKLQLQNENIDILCGVLDENLSMDCLLGQSSVMHNILHTDKLITNQKSL	152	
C. sinica	R-IIINLVIEATGKDVGVPGLIFARAETVGKLIYQLKNENTDILSGVLEEKLSLNRLLLGQSSVMHNIPHTGKLVSNQKML	152	
C. tropicalis	Q-MVHLPIETSKKEVEIKGMLFASAKSIGOLIYQLRHEHIDILSGVLDLMIKSMNHFLDTNSTVMHNIIHWKONIVVKDKMH	152	
C. remanei	R-VVNLRLVDLLEKEVIGPMMFARADTLPOLIYQLHENMDILSGVLEEKLTMRLLGPOVTAHMNIQFTGKSVKVQRKL	152	
C. japonica	R-IVHLQVRAYDDGYGFRGMLFARGKTLQGLIFQL-HENIDILCGVLEKQLRFAHMMTASSIEVHNIIHEFKVEKVVI	151	
C. angaria	RLNQKILENDMKLIVIEQGIIIFSKSSTIHGMINKTSIDSNLNGEONIELNKLIINTSLAQNNIYENIEIRNKIII	144	
H. contortus	K-IFHLLTLENTEDGFRIRSMLFATGTTIGELIYNIRDSSLVLSGVVLGCPVYPRRMIIKDVLGQFRIFEAEHIIS-KKLV	146	
N. americanus	K-TFHLLTLETLGRGFRIRGMLFATGATIGELIYNIRDSSLVLSGVVLGCRVYPRRLITKRLPSFQIYGEDCIVS-KRLT	137	
A. ceylanicum	K-TFHLLTLEKLRKGYRIRGMLFATGATIGELIYNIRDSSLVLSGVVLRCRAYPRRLITKEVLPFCRITYSDECIS-KRLS	148	
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	gk1149 deletion	kinase-like	
Ce-COMP-1	SODFFHLYVTGEMKFADGKIKKKALFEELHNPT--ISDLKVFYENLVEGKALAARNLPIRLPIGAIL--NPPTLIYEHQEN	228	
C. briggsae	YRDIQTMITYTGEKMFKADGKIKEAIFEQILHCRPGSTDHKVFFEKIVNGKALSNKNLPIRLPIGAIL--TPPTLIYEN-KV	229	
C. sinica	SVDIDLTIYTGEKMFKADGKIKEALFBEQITHPDMSISERKVLFEKLVNGKNLANKNLPIRLPIGAIL--SPPTLIYENNKV	230	
C. tropicalis	FQDVEITIYTGEKMFKADGKIKEVLFEEITSPD--KTKYKVFFEKLVNGKALSTKLNPIRLPIGAI--NPPTLIYEQNGT	228	
C. remanei	SDQTASPIYIIGEMKFSDFGKIKEGVFEEFPGGQQNPTELKTFEKLVNSKSLRGKNLPIRIPIGAIM--NPPTLIYENNKL	230	
C. japonica	DRLSHFTKYTGEMKFADGVRKVEAMFEEAKNVD--NEYMEKFSKMWTVAALEKHLVPLVRLPIAAFI--SPPTLIYDLOKE	227	
C. angaria	ANDHKTMTYKGEITLFDGTQKQEVEIVEPSPAM---DSDDFRKKIEEFRRFKMQLPVRLPIAAV--STALMFPAG--	216	
H. contortus	NEDSRFKYYESQVLM-NDTYTNVLLKGSSRRMS-PAEWREQMYDELRSVFARELHLPMTVHGILRA-ENGYVIYDNK--	221	
N. americanus	HEDLDFFRYSHANIII-DQKFINVILKENKRLN-ETNWQMHMYDELRSVSYLAKELHLPVRIILGLIRARNEQYIYDNN--	213	
A. ceylanicum	YEDVDFRYFRGNIFI-NQEFDTDVILKENKRLT-DANWKMHMDELRSVSYLAKELHLPVRIILGLIR--NNGYIIYDSN--	223	
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Ce-COMP-1	QVGCSLKDFLKNFDTHLDAQRIKLCASAARVILSELHRFDIYHGASKVDNFYV--LGYNKEKTMNYELVFNGASGLLYEG	306	
C. briggsae	ELGSLLESFLKTRQSELDLTQRIKFCSSAVRILSELHQCDIYHGASQMENFYVEFAGFKPKTMKNYELVFSANGLLIQG	309	
C. sinica	ELGNTLEKFLKNREQLDLTQRIKFCSSAVRILSELHQCDIYHGASQMENFYVEFAGFKPKTMKNYELVFSANGLLVOG	310	
C. tropicalis	EIGCSLEHFKNYIDLDSLQRIKLCSSVVRILSELHHMDIYHGASRIENFYVEQNGKNSKTKNFEIWFNGANGLIFEQ	308	
C. remanei	EVGCNLEDFLFFFHQNRLDTQRIKICSSAVRVLSELHHADIYHGASQLEHFYVDFVGKNEBDIKNYELVFNQASGLIREG	310	
C. japonica	NSGFSLSYILKHHDNLLDLTQRVKLCSSAVRVMSELHQADIFHGALIAKNNFLNFI-NDGVKEYELVFNQPSGLLFLG	306	
C. angaria	-KGYNLCYILCNYQHSLDFVQRIKICSSICRVSFSEVLADDFYHGQILAEHFYCCQIDESETGVKTMELMFASADGLVDS-	294	
H. contortus	-PGCEFSRFLLEYYDDKLDLGTRIKLCLRALSVMGSLYNADIYCGAVKLDNFYAYVVGALPY--RIQLVFTGADLTPL-	297	
N. americanus	-PGCDFSRFMEENADRFDGCVKIKICRALASVMSELFNADIYCGTVKMENFFVYYDAPCG--QIQIVFAEGRDLTPV-	289	
A. ceylanicum	-PGCDFARFMEENGDRMDCGLKIKLCRALASVMGSLFNADIYCGAVKMFENHVYYVAQRLR--KRLKSSLFIFPEQL-	299	
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Ce-COMP-1	KSDNTVTMVVDYDSNAPEVAFTRKLSKESGVFTLGRLFQILESEILKSYSEPPQEEPRVLNDMRRLIGRATRANPSQRPT	386	
C. briggsae	KSDNTVHVVDYDSTAPEVAFTRKLTKESGVFNGLRLFQILKPDLIQSYKES--EEPRALNEMRHLISRTHPNPTRRPT	388	
C. sinica	KSDNTVRVHVVDYDSTAPEVAFTRKLTKESGVFNGLRLFQILKPDLIQSYKDC-QEEPRSLNEMRHLVARATHPNPTRRPT	389	
C. tropicalis	ITDNTVSVIVDYDSNAPEVAFTRKLTKESGVFNMGRLFQILKPDLIKAYKDQP--EPRALEEMRHLIARATHPNPTRRPT	386	
C. remanei	KSDNSVSVIDYDSTAPEVAFTRKLTKESGVFNGLRLFQILKPDLFKSYSESNEGSPESLTEMRRLISRATHPNPTRRPT	390	
C. japonica	KSDCSVSLIDYDLNAPELAFTRKLTKEGSVFNIGRLFQILKTEILKTYQKNAPEDPALREMROQIARATRPNPYHRPT	386	
C. angaria	RIEKRTNMIDYDQYAPEVSFTRILNRPGVFNTGKLFARIQPDLVKEEKS---WPGALKAMKVLIDKSVRPNPYDRPT	370	
H. contortus	EKTKPIDSGDFSQMAPEVSWTRLITPAGVHSMGLVRLRVLGHPPELPSQDPN--ASILPRINALISKLHPPRPSERPS	374	
N. americanus	DQLRPVDSGDFTRMAPEVTWTRILTPAGVFSMGLLREVLEFGPRLSSKDPN--FELVTRVEALIRKCMHSRPSERPS	366	
A. ceylanicum	SQLRPVESGDFTRMAPEVTWTRILTPAGVYSMGLVLRRAVLESGVRPSSKDPN--FEMLTTRVEALIYQKCTHSKP SERPS	376	
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	me69: G389R		
Ce-COMP-1	MNGIVMLIRELLMALPKSTSPINV--VHYDQFQRK	419	
C. briggsae	MHGVVMMIRDIQKNTQSTSPINI--VHFQFTKN	421	
C. sinica	MHGVVIMVRDILQKAPQSTSPINV--VHFQFTKN	422	
C. tropicalis	MHGIIIMIRDVLLTPDSSSVNI--VHFQFSTE	419	
C. remanei	MHGIVMMIRDVLLKAPKNSHICM--VHFQFTN	422	
C. japonica	TNGIVMMIRETLKILPPSSAPVN--VHYDQFAI	418	
C. angaria	IDGMVIMCRHILTLLELSPKSDCKFNFVHYNQYD	404	
H. contortus	MNGIFLELDNAAGS-----VRHTRQPRWTPI	400	
N. americanus	VHGIFIELDSIASFIK-----QTRHFFWQPV	392	
A. ceylanicum	VHGIFIELDAITKH--QTKYQFWQPL	402	