Query	27	NPFAAL-AQPALEYALDAWQRTVLLLDILRQRGNESAEHELEGMPPVLVFEHELLADGRQ NP A +	85
Sbjct	49		108
Query	86	LPEPANYALLRIVPPADSPTDPALRPFVVIDPRAGHGPGIGGFKADSEIGIALRTGHPCY P NYALL+I+PP D + RP+V+IDPRAGHGPGIGGFK DS++G+A+R GHP Y	145
Sbjct	109	FERPVNYALLKIIPPDGVTIDDSRRPYVIIDPRAGHGPGIGGFKDDSQVGVAMRAGHPVY	168
Query	146	FITFFYEPCPGQTIESVARAEAAFLQIVGERHPDAPGKPFIIGNCQAGWALMMLAAVAPE F+ FF +P PGQT+ V AE F++ V E HP + KP IIGNCQ GWA MML A P	205
Sbjct	169	FVIFFRDPEPGQTLLDVCEAEQQFIKRVRELHPHS-AKPAIIGNCQGGWAAMMLGASDPG	227
Query	206	RTGPLLLAGAPLAYWSGVRGRNPMRYSGGLLGGSWLASLIADLGNGRFDGAWLVEN TGP+++ GAP++YWSG G NPMRYSGGLLGG+WLAS ADLGNG+FDGAWLV+N	261
Sbjct	228	TGPTTT GAPTTINGG G NPARISGGLIGGTWLAS ADLGAGTPGAWLVTN TGPTVINGAPMSYWSGAWSEGEGDNPMRYSGGLLGGTWLASYTADLGNGKFDGAWLVQN	287
Query	262	FEQLNPANTLWEKLYDVYAKADTEGPRFLDFERWWGGHFLMNRAEIDWIVQKLFVGNRLT FE LNP+N+LW+K Y++Y KADTE PRFL+FERWWGG++LMNR EI+WI + LFVGN+L	321
Sbjct	288	FENLNPSNSLWDKYYNLYKKADTEPPRFLEFERWWGGYYLMNREEIEWITRNLFVGNKLW	347
Query	322	AGEVRSTDGKTVVDLRNVRSPVIIFASWGDNITPPQQALNWIPDLYASDEELVANDQVIV GEV++ GK DLR +RSP+++FAS GDNITPPOQA NW+ D+Y S EE+ A OVIV	381
Sbjct	348	GEV++ GK DLR +RSP+++FAS GDNITPPQQA NW+ D+Y S EE+ A QVIV GGEVKNAGGKA-FDLREIRSPIVLFASMGDNITPPQQAFNWVVDIYGSTEEIKARGQVIV	406
Query	382	YCLHPTVGHLGIFVSAGVANREHSELFCALDLIDVLPPGLYEAKIEDVAPDLRHRDLVEG	441
Sbjct	407	+H +VGHLGIFVS VA +EH+++ L I++LPPGLY I + + D V+ GMMHRSVGHLGIFVSGKVAQKEHAQIVSVLKSIELLPPGLYGMVIHERKGSDGVD-	461
Query	442	RYLMRFERRGIADILALDDGRDDERAFEVVRRVAEVNOHIYDTFASPWVRAMSNELSA	499
Sbjct	462	Y ++FE + +I + + R DE+ FE V +++ Q Y+ FA P+V+A+SNE++A -YEVQFEEHSLEEIASRLNRFERADEKPFETVANLSDFTQRAYELFAQPYVQAVSNEMTA	520
Query	500	OWLRALRPARLERELATDVNPWMAWIGALAPLVREHRAPVSADNPLLTLEHAASAQIVSA	559
Sbjct	521	+ LR P R++ L +D+NPWMAW+ A VR R + D+PL E + "+ + RVLREFHPLRMQNWLFSDLNPWMAWLKPAADAVRASRQTLEPDHPLRQQEQVGAEMLSAG	580
Query	560	LDOFRDLRDAWYERAFEAIYASPAMAALVGLRAPAPVNLESPVTVALRKELAARRLHD	617
Sbjct	581	LD +R +RDA E F +YA+ P S T A AA HD LDAYRAVRDAMTEYTFFNVYANLFPFQPRSEPT-ARAGTPAATDPHDLP	628
Query	618	AEAAIGOGGTLEAFVRVLAYVADRPSAIEERPFNLLRRIAREOOOATGOSGGOADL	673
Sbjct	629	A AA+GQGG EA R+ ++ R + L R+ ++ T + +L EVKAALAAVGQGGYAEAIARLACLLSRRGEPLPLSRLELRKELVTDYADLLPEL	682
Query	674	AAFKTAVROOSFIVELDPORAIRALPALVPDRETERKLMVAAHEV 718	
Sbjct	683	A++ +Q I R P++A+ LPAL+ + R++L A ++ EPDAWREIRGRQELITRYAPEQALATLPALLRYQADRQRLQALAEKL 729	

Fig. S1: Alignment of the A0671 protein (query) with the B1632 protein (subject).

The image was taken from blastP analysis of the A0671 protein. Identical or similar (+) amino acids present in both proteins are indicated in the respective middle lines.