

Figure 1 displays the multiple sequence alignment of the JAZ1 protein from various species, including *Gibberella zeae* (Gb), *Psidium cattleianum* (Ps), *Phytophthora infestans* (Ph), *Phytophthora sojae* (Pso), *Phytophthora blight* (Pb), *Phytophthora capsici* (Pca), *Phytophthora ramblensis* (Pra), *Phytophthora sojae* (Pso), *Phytophthora blight* (Pb), *Phytophthora capsici* (Pca), *Phytophthora ramblensis* (Pra), *Phytophthora sojae* (Pso), *Phytophthora blight* (Pb), *Phytophthora capsici* (Pca), and *Phytophthora ramblensis* (Pra). The alignment is shown in three blocks, with the first block (1-120) and the second block (121-240) highlighted in red. The third block (241-360) is shown in black. The consensus sequence is provided at the bottom of each block. The alignment shows high conservation of the JAZ1 protein across the species, with the first block (1-120) and the second block (121-240) being highly conserved. The third block (241-360) shows more variation, particularly in the C-terminal region.

1 120 240 360 424

GbJAZ05	(1)	MSRDQAVAMDFLGVKSSGKNEGETDPNSVISQTKQECLANEETVKSSSETATGSEATKTSSAPGQTMKSDFSQAFSLFSKYFREKGNANAVMGAQENFNLGKPLEQQTNEDV	K	GSKPAKD
GbJAZ10	(1)	-----		
PsJAZ01	(1)	MSQDQAVAMDFLGVKSGVKKESQTDENPVTAQSKQE-----PVATEQMTSPAASAPSEGSTMNFSQAFSLFSKHFNEKGNGNAAIGRGENVYLGN-----GKEDV	K	GSKPVNE
TcJAZ01	(1)	-----		MTHMNQEKSGIMQMF
TcJAZ02	(1)	-----		MTKERSDIMQMF
PsJAZ11	(1)	-----		MGLVVSTKL
PsJAZ07	(1)	-----		
PsJAZ13	(1)	-----MVKVVAAMDFLGLSEKEKSELTKGNSNSEGIQKDQTEMNAVVTASTDKAQWNNNNAMRSDGSFKNRFCE	K	GSFTSQL
Consensus	(1)			K
		121		240
GbJAZ05	(121)	D-VSTQLGLFPQQTGFGSHLRPLILGTDHKIVAPTASQPWPFRLQA-----S-----N-SPAMRSIVTSTTTQTVKPPTAQLTIFYAGMVSVYDDM		
GbJAZ10	(1)	--MPPPERVIVSAGFGSPLRPLILGTDHKIVAPTASQPWPFRLQA-----S-----N-SPAMRSIVTSATTQTVKPPTAQLTIFYAGMVNVYDDM		
PsJAZ01	(105)	ENVSTQLGLFSQSGFGS-LRPFPGAQKGFASSTTAQWLFRLGILP-----P-----N-SPAMRPAVTS-TPPIKPPTAQLTIFYAGMVNVYDDV		
TcJAZ01	(16)	GQQCAMDQDSSQKSGFGSVPLPVAAGFQHRKPHLQGLFPMFR-----P-----AGKEARG--AQLTIFYGGMNVYDDI		
TcJAZ02	(13)	VQQCAMDQDSTQKSGFGS-PVAATAEVQHRNLHLHPLFRSAG-----C-----AVAQKSGSAQLTIFYGGMNVYDDI		
PsJAZ11	(10)	KLGTAFEEQCDEETGLPSWITSVNGGAKRAVADCISR-----LA-----PS-MIPEKPSSAKLSIFYGGTVYIYDDI		
PsJAZ07	(1)	-MASAFEHCNQEKGLPSWIKTVNGGAKRAAADFIPR-LDLSVVGSCFNSIHLFPNQSGFGSPIAVLPDSEHRTSSDDHQDGCSGFVTSFRPAASTIPSKQSCAQLTIFYGGVNVYDDI		
PsJAZ13	(80)	RDGLAFEHCDEEKSPSWIRTVNGVAKRSVADCIPRLDLNVGSSSNLINLFPDQSGFGSPIAVKGGFDHRTS-DNDGDGCSGFVTSFRPTASMSISGKQSCAQLTIFYGGTVNVYDDI		
Consensus	(121)	SAEEQSGFGSIRPVGGKVASPFRLLA	SMSASTKPTAQLTIFYGGMNVYDDI	
		241		360
GbJAZ05	(205)	PADKAQAIMLLADSGNPSNHKFVKAANFGQQTTPATTPPSTPLGSVTRTPVSLQITGTDDVPVPAMPSPGGPNQQTVRKLQADLPIARKNSLQRFLEKR--KDRLITKAPYATTSLANK		
GbJAZ10	(84)	PADKAQAIMLLADSGNPSNHKFVKAANFGQQTTPATPLSTPLGSVTRTPVSLQISTGTDDVPVPAMPSSLGGPNQQTVRKLQADLPIARKNSLQCFLEKR--KDRLITKAPYATTSLANK		
PsJAZ01	(187)	PADKAQAIMLLADSGNPLNASFIKANFAQQTPCVSPVSSPLSSIPTSLSLQTSQVTTTEVATPTMP--LAPNHHQPIRKQLADLPIARKHSLQRFLEKR--KDRLMTKAPYPASPAPMK		
TcJAZ01	(83)	SADKAQALMLTASTG-----KPMQKNSS-YASEPQPTKSVKLSLVNSTELE-----LTVDLPIARKNSLQRFLEKR--NHRLNAKAPYTISQENPK		
TcJAZ02	(81)	SADKAQAIMLLASSG-----KPIQKNSSGGYASQPQPTK-----PDLPIARKNSLQRFLEKR--NHRLNAKAPYTISQENPK		
PsJAZ11	(76)	PTDKAQAIMLLASSGNYS-----SYPHTKVHNGW-SQTEQKLS-VPVIKLSNGSGIHPQ----TSSPKLRTGSSDPIARKHSLQRFLEKRRDRVNAKAPYKTAEAERS		
PsJAZ07	(119)	PADKAQAIMLLASSENYS-----GYPHTKVQNSTCRSQTELKTS-LPVMKFSGES-----DLPIGRKHSLSQRFLEKRNKERVIANAKSPYTAADAANT		
PsJAZ13	(199)	PADKAQAIMLLADSGNHS-----SYPTQLQKDCRSQITEVKISPLPLVLKQEGSRIHHQ----PAS--YKMYTDLPIARKYSLQRFLEKRNRLNAKSPYSTAAEADN		
Consensus	(241)	PADKAQAIMLLASSGN S	P TK SS SSIT TKLS L VV TTEVS	VRKL ADLPIARKNSLQRFLEKR K RLNAKAPYTTA A K
		361		424
GbJAZ05	(323)	KPDVDKLPISTKSPEN--NCLSRSTSPLPPSSRPFGCCN-----ENSTSQEASPSPIAHMA		
GbJAZ10	(202)	KPDVSSVDSVPVPIEPKKDRCAQVGLVLVAIRPVQDLNSKLWMIGSWWLPMGADGCPLDELRL		
PsJAZ01	(303)	SEMEESVSASPLLLSCQ-----SPSSLTSRPLSGVCCN-----ENSVTQEPSPPPVSAIYS		
TcJAZ01	(166)	PSPCL-----		
TcJAZ02	(150)	PSPCL-----		
PsJAZ11	(177)	SIVQSECKRKVSI-----		
PsJAZ07	(205)	PKGLRS--NS--PP--ESHPPP-----		
PsJAZ13	(299)	TKPRRYPSSSAIPLHSNCPR-----		
Consensus	(361)	S P		

Figure 1. Multiple sequence alignment of the deduced protein sequences of GbJAZ9, PsJAZ4, TcJAZ5, TcJAZ7, TcJAZ6, and TcJAZ9. The alignment is shown in two parts, with the first part covering residues 1 to 120 and the second part covering residues 121 to 240. The consensus sequence is provided at the bottom of each part. The alignment is color-coded to highlight conserved regions and specific motifs. A red box highlights a conserved region in the first part of the alignment, specifically residues 100-110, which correspond to the LSLPPFDSIMRS motif. The second part of the alignment shows a conserved region around residue 230, which corresponds to the STALCPTPSTC TS motif. The consensus sequence for the first part is: (1) A A K D D DL AEEN SD K TLK GSTI GK VEVEK MRSSK GTAASM TV VR QLPNLD LSLPPFETLEL AP. The consensus sequence for the second part is: (121) QKSPF VSPS NAF FRSP K QQE QLTIFY GTV VYNVSPDLAKAIMMAAN STALCPTPSTC TS IQ LTPK.

### AVPQARK-motif

[illegible]

V(E/A)RDF(L/M)GL-motifs

		1		120
GbJAZ04	(1)	MEREKIV	ERDFMGLTNAN	
PsJAZ12	(1)	MQRVKIV	ERDFMGLINSE	
TcJAZ03	(1)	MDREKIV	ERDFMGLINSD	
PsJAZ03	(1)	--MESMER	DFMGLGRRNGNEMESEKTSNNEQPHGE-----R-EKIMSLSLFQEA EKSTKLQLSSGSFCGLSEAIGKAGIANGSGKVSVPNTSMQWTYWTKAAALQQFMSFKNYQEER	
GbJAZ11	(1)	MERNSLV	ARDFLGLSNRVPEKSGRDLSGLKEGELNCPTNGMQLGSA SVTKECMFGGKAGNNNNNAQVQTEADVQQREELKRYFKDK-VCLANMALQWPYSNKAAALQQFMSFKNFQEER	
PsJAZ02	(1)	MERDSV	VARDFLGLSGGK-DISRGSNGSESK-----SSTSAAQVQAQSQAAQREEMKPYLKDN GVC LANISLQWPYSNKPAALEQFISFK---QEG	
TcJAZ08	(1)	MERESV	VARDFLGLNHAR--NNLSGDS-----QTQTESQRDGP IKG YFKDN-VSLANMSLQWPYSNKAAALQQFISFKNL-QEG	
Consensus	(1)	MERESTV	ERDFMGLNA	V L N SLQW Y K AAL QFISFK E
		121		240
GbJAZ04	(19)	-----GGIEE	ADKDE---K---ATKDFNTDSTAQAGNNYP-VASGVPCRQYGVSSLVYSAGSIDGSSSSAHPIEEARGFPSSNLSLSMPNFR EHGSPAF LKGQPT	
PsJAZ12	(19)	-----VVAEK	DNELGSDS---ANKAPCQHFGVSSVAHSTG SIDGLSSSAHHIDEAGGFPPSSLSLSMSNFR EHLGFNAISKGLQA	
TcJAZ03	(19)	-----EIADK	KEDDS-----VTKDSCTDAPVDDGSHNSLPNNDVPCQHLGTS PMAYPAGSMEGLSSSVHPVVEYGVFPSSNISLPMQNYGQHL SALAILKGQQA	
PsJAZ03	(111)	PEKRKF	NQLVSSGLQPVATVDTFKSNHRSTSASQKSCNFSPISKDNAEFRNGYS-GTNCVPNQHF EVPPANFSVKAFDDQSF CNSSIEQAGAF LREKASHSPPNFR EHFSSPASFKGQDS	
GbJAZ11	(120)	PKKNLCDQLANS	GFHP ISTADAFDISKRSTAGTQKNFNLDPSARNTAELGN YYS-GQHSP LNRHFGVSHIAYPAQALDDRGSSAYNIQEIGTYP CSNHSPSISNLGS---PAFFKGQ--	
PsJAZ02	(88)	PKKSSFDQLSNS	GFRP ISTADAFDLINKSAPGMQKNFNHDPMARNTIESGN YYS-GQGALSRHFGLSHITYSAHPFDEQGSSGYNMQKVGTFP CSNHSLSVSNLGS---PAYFKGE--	
TcJAZ08	(76)	SKKSSFDQLSNS	GVHP ISTADVFDVNNRNTTGSQAFNL DPAARNATESGN YHF-GQNGSVSRPFSVSRIMYSAKTVDDRASQGYNNQEGRAFPPSSNYSHPVSNSSSI---PAYFN GH--	
Consensus	(121)	K QL SG PISTAD F R G QK N DP TR E GNYYS GQN P RHF	GVSI YSA SIDD SSSAH I EAGAFPPSSN SLSMSNF HI PAFFKGQ	
		241		360
GbJAZ04	(115)	-YAATCITPPVVKPFASLPLSGQHSFFPAASTIYGGSTP-ARATDLP	GPASAQLTIFYAGTVN VYDDVPADKAQGLMLLAGSAR--SPKVTNLPPRSSAISTTTAVGSHSMPTTPPFCS	
PsJAZ12	(109)	-TSTSCVTTSMVNP	SAIQK---NSFFPAAAGVYPPSSTATSNATAVPGKQPCTQLTMFYAGTVN VYDNPVPEKAQVLMLLAASAR--SKKMTNLSPRSSAMPTSIATAVHAMPITSPFSS	
TcJAZ03	(113)	-VSSACGASSMANPFPIQ---HSFFPDCAGVYPTTRATSKSATIPGNP--AQLTIFYAGTVN VYDDVPADKAQGLMLLAASAR--LSKTINLPPRSSLSMMPMATGCHT PSIASPFTS		
PsJAZ03	(230)	-----TAALGGKLLSSIPFTRQAPVLCGAAASTVGTTPMRADSNLPGKLASAQLTIFYAGTVN VYDNI PPDKAHAIMLSAENGSSMSTKMTDLS PQNFVMSTPVPTNSHSRPATPTICS		
GbJAZ11	(233)	QAMAI	ISCVTPMVKPLLGT PFAQGHSFLPVVGASTSTTIP-GATPIIPGKPANAQLTIFYAGTVN VYDEV PADKAQAIMFLAGSGNSWSGKIDNPPPQTP--AMSMPTGGHIKPAPPVC-S	
PsJAZ02	(201)	--QAAGTTAPLMRQFQG	MPLAGQHSFLPVVGASASTTIP-GAVASVSEKPAGAQLTIFYAGSVN VYDDVPADKAQAIMFLAGNGNFWSGKTATPPSQSPAMPISVATNGHARQATPIG-P	
TcJAZ08	(191)	--QATATSSLMAQQFQGIPLTGQHSFLPILGASASTSIL-GCGPSVPEKPAGAQLTIFYAGSVN VYDDIPADKAQAIMFMAGNGNPSSGKTATPPPQS--STISLSAIGHVKKATSVG-P		
Consensus	(241)	A TS MVKPF IP GQHSFLP AAS TT P G VPGKPA AQLTIFYAGTVN VYDDVPADKAQAIMLLAGSG S KM NLPPQS MSISMATG HAKPATP S		
		361		480
GbJAZ04	(231)	NRQNRVFPITPQAPPQKA-----QPSIQHSEPAAVTSSSGDSQVNTIIVTPSNQQEASKSSPAGITPARIIPR-VPQARKASLARFLEKRKERVHTQVPPAAKKSPDCSSQRE		
PsJAZ12	(222)	KQPNRVFPMTSQAPLQKA-----QASIQPNPYSAVTLNADDSQIIQSIATSSNQQEASKSSDAGITPAPLISR AVPQARKASLARFLEKR RERIITKAPYPTKKSPDCSPQRE		
TcJAZ03	(223)	SLPNQACNTTPQAPLQKP-----QENNQPNSSSTAVSLNAGDSQKNQCIVTSIGQQEASISSAMVITPVVPVPRAVPQARKASLARFLEKRKERISIKAPYPTKKSPDASPQRE		
PsJAZ03	(344)	SRPNALTSMIPQGPQKSHMPIPQVHPQKSQICSKPGQSTGVSSSN GELKSNQNNGAGSNQQEGAKQMVSASTPNGVIPRALPQARKASLARFLEKRN GRVTPNLSSPTEKSPHHSSLQQ		
GbJAZ11	(349)	SMSNPLPPI NVHVHPQKS-----QASIQTSQSTTVSSSAGDLQTTQMNGTPTNQQEAPKLSAAGSTPNPI MPRAVPQARKASLARFLEKRKERVCTKVYPYSKKSPEHSSHRE		
PsJAZ02	(317)	RLSNALSPTNPQVHSQNS-----HATVQTSQSITAISSAGDSQTNQNNGASSNLHETPKVNAAVSTPAPIMPRAVPQARKASLARFLEKRKERVCTKAPYQTKKSFDDSSHGE		
TcJAZ08	(305)	SPLNALPATNPQVDSQKSET-----TVQSQTSQSITAI FPSTGDPDANQSNVTLSNPQETP-LNASGSTPTSI MSRAVPQARKASLARFLEKRKERVITKAPYPTKKSPEDSSLSD		
Consensus	(361)	S N L PI PQAP QKS Q SIQ SQSTAVSSSAGDSQ NQ NGT SNQQEASK SAAGSTP PIIPRAVPQARKASLARFLEKRKERV TKAPYPTKKSPD SS RE		
		481		554
GbJAZ04	(338)	NSQSPKRCSTSPPLDGRPSKQHKLMNG-DEKFPINSECMTSFPDRHEEEKSCFLEDEMNEREECETTVEVRS A		
PsJAZ12	(330)	ESPSSK--HIPPLDGCLTKQNQLISKGLDEKFPIDSESMGSFLDKDQKEHSCSLKVSCKEMGECETTVEASIL		
TcJAZ03	(331)	QSPSSK--HASSPLDECLTKNHQVASTGLEEKISFDS ESIG---SFQKDHSCLQKAPKIEGEDCEITV-----		
PsJAZ03	(464)	E---KSFSSMSSFDGCS SPQHDTVSDALHMKKLSRSDSMAHANHLTLQKAGFMLEERKIAFGTRNC-----		
GbJAZ11	(457)	KSLSPKHSSSLPLEDGCKSQ---QQDGS DGFVVPKSEDMADCVNKDRHEKAWSLKA EKNDIRDCEMQMT----		
PsJAZ02	(425)	VPLSPTRSS-TPLVDGYKSQ-----RNEFMPRSEEKASCLGKEQHEQPWPPKVEKNEIKECQLQLT----		
TcJAZ08	(414)	KSLSPKCSS-TPPMDGCKS-----QHESMTNSEEKGSQLWQ-----		
Consensus	(481)	S SPK S SPPLDGC S Q L G D KFM SE MAS L K E S LK K E ECE V		



### MERDFLG-motif

Figure 1 displays the multiple sequence alignment of the JAZ3 protein from Arabidopsis thaliana (AtJAZ3) and its orthologs from other plant species. The alignment is shown in a color-coded format, with conserved regions highlighted in yellow and variable regions in green. The alignment is divided into four segments, each starting with a position number (1, 121, 241, 361) and ending with a position number (120, 240, 360, 480). The sequences are aligned from top to bottom, with AtJAZ3 at the top and the consensus sequence at the bottom. The consensus sequence is shown in a black box. The alignment shows high conservation across the sequences, particularly in the regions highlighted in yellow.

### ELDFLGL-motif

Species	Accession	Residue	Sequence
AtJAZ10	(1)	1	MSKATIELDFLGL
AtJAZ10.3	(1)	1	MSKATIELDFLGL
AtJAZ10.4	(1)	1	MSKATIELDFLGL
OsJAZ07	(1)	1	MSTRAPV
Consensus	(1)	1	MSKATIELDFLGL
AtJAZ10	(117)	121	QVSRNKAGEIMKVANEAA
AtJAZ10.3	(117)	121	QVSRNKAGEIMKVANEAA
AtJAZ10.4	(117)	121	QVSRNKAGEIMKVANEAA
OsJAZ07	(99)	121	DVSHDKAEAIMRMATEAT
Consensus	(121)	121	QVSRNKAGEIMKVANEAA