

Computational study of SnRK2 in Arabidopsis thaliana: An *in silico* approach for homology modeling and functional characterization of SRK2G/SnRK2.1

Mst. Saleha Sultana*, Ravi Kant Ojha, Mohammad Majharul Islam, Md. Anik Ashfaq Khan, Kaniz Fatema and Pijush Sutradhar

Department of Genetic Engineering and Biotechnology, Shahjalal University of Science and Technology, Sylhet-3114, Bangladesh

Supplementary Data



Figure 1. Multiple Sequence Alignment of five sequences where domain of all is marked by red color.

Table 3. Prediction of antigenic peptides in selected *Arabidopsis* SRK proteins

Entry	Number	Start Position	Sequence	End Position
P43291	1	25	NSKELVAM	32
	2	62	RFKEVVLTPTHLAIAM	77
	3	86	FERICSA	92
	4	101	RYFFQQLISGVSYCHAMQICHRD	123
	5	135	PAPRLKICDF	144
	6	146	YSKSSLHS	154
	7	156	PKSTVGTPAYIAPEVLS	172
	8	182	DVWSCGVTLYVMLVGA	197
	9	214	QKIMAVQYKIPDYVHISQDCKNLLSRIFVANS	245
	10	256	KHSWFLK	262
	11	291	EIMKIVAD	298
	12	301	TPPPVSR	307
	13	348	DKTVKEVHASGE	359
P43292	1	16	GVARLLR	22
	2	26	TKELVAM	32
	3	51	NHRSLKHPNI	60
	4	62	RFKEVILTPTHLAIVME	78
	5	86	FDRICTA	92
	6	100	ARYFFQQLICGVYCHSLQICHRD	123
	7	131	LDGSPAPLLKICDF	144
	8	146	YSKSSILHS	154
	9	156	PKSTVGTPAYIAPEVLS	172
	10	179	KHADVWSCGVTLYVMLVGA	197
	11	215	RIMAVQYKIPDYVHISQECKHLLSRIFVT	243
	12	256	NHPWYLKLNPKELLESAQAAY	276
	13	281	TSFSLQSVEDIMKIV	295
	14	303	PSTSAVKS	310
	15	337	YEKHVKEAQSCQE	349
Q940H6	1	20	RYELVKD	26
	2	43	SNELVAVKY	51
	3	73	RHPNIVRFKEVILTPTHLAIVME	95
	4	103	FERICNA	109
	5	118	RFFFQQLISGVSYCHAMQVCHRD	140
	6	152	PAPRLKICDF	161
	7	163	YSKSSVLHSQPKSTVGTPAYIAPEVLLK	190
	8	194	DGKVADVWSCGVTLYVMLVGA	214
	9	230	IHRILNVQYAIIPDYVHISPECRHLISRIFVADP	262
	10	277	FLKNLPA	283
	11	309	MQIIAEATVPP	319
	12	325	LNHYLTG	331
Q39193	1	8	PIMPIDLPI	16
	2	22	RYDFVKD	28
	3	44	VTKELVAVKY	53
	4	75	RHPNIVRFKEVILTPSHLAIVME	97
	5	104	LYERICNA	111
	6	120	RFFFQQLISGVSYCHAMQICHRD	142
	7	154	PAPRLKICDF	163
	8	165	YSKSSVLHSQPKSTVGTPAYIAPEILLR	192
	9	197	GKLADVWSCGVTLYVMLVGA	216
	10	232	IQRILSVTYSIPEDLHLSPECRHLISRIFVAD	263
	11	306	SLDTIMQIISE	316
	12	318	TIPTVRN	324
Q39192	1	21	RYDFVKD	27
	2	44	TKELVAVKY	52
	3	74	RHPNIVRFKEVILTPTHLAIIM	95
	4	103	LYERICNA	110
	5	119	RFFFQQLSGVSYCHSMQICHRD	141
	6	153	PAPRLKICDF	162
	7	164	YSKSSVLHSQPKSTVGTPAYIAPEVLLR	191
	8	197	KIADVWSCGVTLYVMLVGA	215
	9	231	IQRILSVKYSI	241
	10	247	ISPECCHLISRIFVAD	262
	11	265	TRISPEI	272
	12	274	THSWFLKNLPA	284
	13	305	SLDTIMQIISEATIPAVRN	323

Table 7. 3D2GO server predicted functions of SRK2G

GO Term	Description	Confidence
GO:0032559	adenyl ribonucleotide binding	0.99
GO:0030554	adenyl nucleotide binding	0.99
GO:0032555	purine ribonucleotide binding	0.99
GO:0032553	ribonucleotide binding	0.99
GO:0017076	purine nucleotide binding	0.99
GO:0016773	phosphotransferase activity, alcohol group as acceptor	0.99
GO:0005524	99ATP binding	0.99
GO:0006468	protein amino acid phosphorylation	0.99
GO:0004672	protein kinase activity	0.99
GO:0016772	transferase activity, transferring phosphorus-containing groups	0.99
GO:0016301	kinase activity	0.99
GO:0000166	nucleotide binding	0.99
GO:0016740	transferase activity	0.98
GO:0004674	protein serine/threonine kinase activity	0.98
GO:0005515	protein binding	0.96
GO:0003824	catalytic activity	0.95
GO:0007049	cell cycle	0.62
GO:0007067	Mitosis	0.57
GO:0003674	Molecular function	0.49
GO:0048015	phosphoinositide-mediated signaling	0.49
GO:0005813	Centrosome	0.45
GO:0007165	signal transduction	0.43
GO:0019899	enzyme binding	0.43