

COVID-19 Information

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Job Title OsProt ...
RID [3GPNN2J9016](#) Search expires on 03-22 19:00 pm
Program BLASTP
Database swissprot
Query ID lcl|Query_673604
Description OsProt ...
Molecule type amino acid
Query Length 1183

Descriptions

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2; AltName: Full=Protein FLAGELLIN-SENSING 2 homolog; Short=OsFLS2; AltName: Full=Protein FLAGELLIN-SENSITIVE 2 homolog; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	2138	2138	100%	0.0	100.00%	1183	Q0JA29.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2; AltName: Full=Protein FLAGELLIN-SENSING 2; AltName: Full=Protein FLAGELLIN-SENSITIVE 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	947	947	95%	0.0	45.14%	1173	Q9FL28.1
RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At2g33170; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	519	519	94%	1e-163	32.18%	1124	O49318.1
RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At5g63930; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	514	514	91%	5e-162	32.88%	1102	Q9LVP0.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI1; AltName: Full=Protein RECEPTOR OF RGF1 4; AltName: Full=Protein RGF1 INSENSITIVE 1; AltName: Full=Protein ROOT CLAVATA-HOMOLOG 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	502	502	91%	3e-157	32.94%	1141	Q9LHP4.1
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase At1g17230; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	482	482	94%	5e-150	31.14%	1101	Q9SHI2.2
RecName: Full=Receptor-like protein kinase; Flags: Precursor [Ipomoea nil]	Ipomoea nil	464	464	91%	2e-143	31.94%	1109	P93194.2
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase RGI4; AltName: Full=Protein RECEPTOR OF RGF1 2; AltName: Full=Protein RGF1 INSENSITIVE 4; AltName: Full=Protein STERILITY-REGULATING KINASE MEMBER 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	460	460	91%	7e-142	31.65%	1090	F4K6B8.1
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1; AltName: Full=Protein BARELY ANY MERISTEM 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	435	729	95%	2e-133	33.51%	1003	O49545.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At3g47570; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	431	724	94%	9e-132	35.12%	1010	C0LGP4.1
RecName: Full=Leucine-rich repeat receptor-like protein kinase PEPR2; AltName: Full=Elicitor peptide 1 receptor 2; Short=PEP1 receptor 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	431	431	94%	3e-131	29.36%	1088	Q9FZ59.1
RecName: Full=MDIS1-interacting receptor like kinase 2; Short=AtMIK2; AltName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g08850; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	428	781	91%	1e-130	32.68%	1045	Q8VZG8.3
RecName: Full=LRR receptor-like serine/threonine-protein kinase EFR; AltName: Full=Elongation factor Tu receptor; Short=EF-Tu receptor; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	404	686	94%	1e-121	33.26%	1031	C0LGT6.1
RecName: Full=Brassinosteroid LRR receptor kinase BRL3; AltName: Full=BRI1-like receptor kinase 3; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	408	408	94%	1e-121	32.38%	1214	Q6ZCZ2.1
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM2; AltName: Full=Protein BARELY ANY MERISTEM 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	402	849	95%	3e-121	31.37%	1002	Q9M2Z1.1
RecName: Full=Leucine-rich repeat receptor-like kinase protein CLV1a; AltName: Full=CLAVATA1-like protein 1A; Short=GmCLV1A; Flags: Precursor [Glycine max]	Glycine max	400	669	95%	6e-121	31.78%	981	A0A0R0HPY5.1
RecName: Full=MDIS1-interacting receptor like kinase 1; Short=AtMIK1; AltName: Full=Leucine-rich repeat receptor-like protein kinase PXL2; AltName: Full=Protein PHLOEM INTERCALATED WITH XYLEM-LIKE 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	399	701	95%	5e-120	31.93%	1013	Q9M0G7.1
RecName: Full=Leucine-rich repeat receptor-like kinase protein SUNN; AltName: Full=Protein SUPER NUMERIC NODULES; Flags: Precursor [Medicago truncatula]	Medicago truncatula	394	875	94%	1e-118	31.94%	974	G7JIK2.2
RecName: Full=Leucine-rich repeat receptor-like kinase protein CLV1B; AltName: Full=CLAVATA1-like protein 1B; Short=GmCLV1B; AltName: Full=Nodule autoregulation receptor protein kinase; Short=GmNARK; AltName: Full=Protein NITRATE-TOLERANT SUPERNODULATING 1; Flags: Precursor [Glycine max]	Glycine max	394	667	95%	3e-118	31.01%	987	Q9M6A7.1
RecName: Full=Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g24130; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	392	835	91%	8e-118	33.55%	980	Q9ZUI0.1
RecName: Full=Receptor-like protein kinase HSL1; AltName: Full=Protein HAESA-LIKE1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	392	910	93%	8e-118	31.48%	996	Q9SGP2.1
RecName: Full=Serine/threonine-protein kinase BRI1-like 1; AltName: Full=BRASSINOSTEROID INSENSITIVE 1-like protein 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	393	393	94%	2e-116	29.96%	1166	Q9ZWC8.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase ER2; AltName: Full=ERECTA homolog 2; Short=ER homolog 2; Short=OsER2; AltName: Full=Receptor-like cytoplasmic kinase 85; Short=OsRLCK85; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	385	1170	94%	4e-115	32.86%	986	I1Z695.2
RecName: Full=LRR receptor-like serine/threonine-protein kinase ER1; AltName: Full=ERECTA homolog 1; Short=ER homolog 1; Short=OsER1; AltName: Full=Receptor-like cytoplasmic kinase 204; Short=OsRLCK204; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	379	826	92%	4e-113	31.97%	978	Q69SP5.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase GSO2; AltName: Full=Protein EMBRYO SAC DEVELOPMENT ARREST 23; AltName: Full=Protein GASSHO 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	385	1389	87%	4e-113	35.64%	1252	Q9FIZ3.2
RecName: Full=LRR receptor-like serine/threonine-protein kinase GSO1; AltName: Full=Protein GASSHO 1; AltName: Full=Protein SCHENGEN 3; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	383	1393	82%	3e-112	35.97%	1249	C0LQG5.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase ERECTA; AltName: Full=Protein QUANTITATIVE RESISTANCE TO PLECTOSPHAERELLA 1; AltName:	Arabidopsis thaliana	376	663	94%	5e-112	32.65%	976	Q42371.1

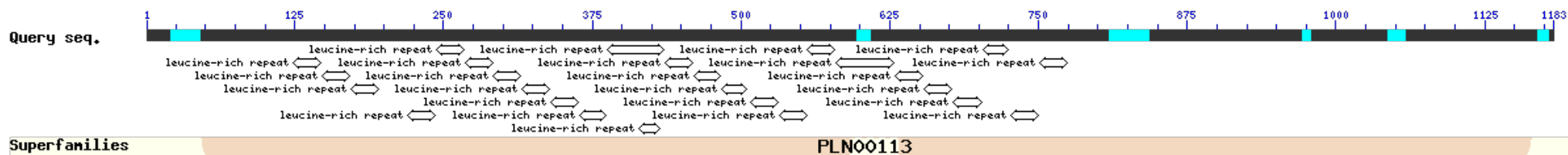
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Full=Protein QUANTITATIVE RESISTANCE TO RALSTONIA SOLANACEARUM 1; AltName: Full=Protein TRANSPIRATION EFFICIENCY 1; Flags: Precursor [Arabidopsis thaliana]								
RecName: Full=Brassinosteroid LRR receptor kinase; AltName: Full=Altered brassinolide sensitivity 1; AltName: Full=Systemin receptor SR160; AltName: Full=tBRI1; Flags: Precursor [Solanum lycopersicum]	Solanum lycopersicum	379	379	85%	2e-111	31.02%	1207	Q8GUQ5.1
RecName: Full=Systemin receptor SR160; AltName: Full=Brassinosteroid LRR receptor kinase; Flags: Precursor [Solanum peruvianum]	Solanum peruvianum	379	379	85%	2e-111	31.02%	1207	Q8L899.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase ERL2; AltName: Full=Protein ERECTA-like kinase 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	373	1450	92%	5e-111	31.95%	967	Q6XAT2.1
RecName: Full=Putative receptor-like protein kinase At3g47110; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	373	647	94%	3e-110	33.50%	1025	Q9SD62.1
RecName: Full=Leucine-rich repeat receptor-like protein kinase PEPR1; AltName: Full=Elicitor peptide 1 receptor 1; Short=PEP1 receptor 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	374	506	86%	6e-110	34.80%	1123	Q9SSL9.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase SIK1; AltName: Full=ERECTA homolog 2; Short=ER homolog 2; Short=OsER2; AltName: Full=Stress-induced protein kinase 1; Short=OsSIK1; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	370	927	93%	7e-110	32.17%	980	Q658G7.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI2; AltName: Full=Protein RECEPTOR OF RGF1 3; AltName: Full=Protein RGF1 INSENSITIVE 2; AltName: Full=Protein ROOT CLAVATA-HOMOLOG1 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	374	513	87%	8e-110	33.51%	1135	C0LGV1.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase ERL1; AltName: Full=Protein ERECTA-like kinase 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	366	937	92%	2e-108	32.02%	966	C0LGW6.1
RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At1g35710; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	369	519	86%	5e-108	34.50%	1120	Q9LP24.1
RecName: Full=Receptor-like protein kinase BRI1-like 3; AltName: Full=BRASSINOSTEROID INSENSITIVE 1-like protein 3; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	367	367	94%	2e-107	30.10%	1164	Q9LJF3.1
RecName: Full=Probable inactive leucine-rich repeat receptor kinase XIAO; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	365	800	88%	2e-106	35.78%	1157	G9LZD7.1
RecName: Full=Leucine-rich repeat receptor-like kinase protein THICK TASSEL DWARF1; AltName: Full=CLAVATA1-like protein; AltName: Full=CLV1 related kinase 5; Short=ZmKIN5; Flags: Precursor [Zea mays]	Zea mays	353	629	91%	3e-103	31.67%	996	P0DL10.1
RecName: Full=Receptor protein-tyrosine kinase CEPR1; AltName: Full=Protein C-TERMINALLY ENCODED PEPTIDE RECEPTOR 1; AltName: Full=Protein XYLEM INTERMIXED WITH PHLOEM 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	351	655	91%	7e-103	30.99%	966	Q9FGL5.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI5; AltName: Full=Protein RECEPTOR OF RGF1 5; AltName: Full=Protein RGF1 INSENSITIVE 5; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	352	1227	91%	1e-102	30.40%	1072	C0LGF5.2
RecName: Full=Leucine-rich repeat receptor protein kinase EMS1; AltName: Full=Protein EXCESS MICROSPOROCTES 1; AltName: Full=Protein EXTRA SPOROGENOUS CELLS; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	353	519	85%	3e-102	34.94%	1192	Q9LYN8.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI3; AltName: Full=Protein RECEPTOR OF RGF1 1; AltName: Full=Protein RGF1 INSENSITIVE 3; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	348	1076	83%	8e-101	36.85%	1091	C0LGR3.1
RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g36180; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	347	480	90%	3e-100	34.10%	1136	C0LGS2.1
RecName: Full=Receptor-like protein kinase HAIKU2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	344	575	91%	3e-100	31.04%	991	Q9LJM4.1

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RecName: Full=Leucine-rich repeat receptor-like protein kinase PXL1; AltName: Full=Protein PHLOEM INTERCALATED WITH XYLEM-LIKE 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	345	1167	94%	4e-100	29.00%	1029	Q9FRS6.1
RecName: Full=Receptor protein-tyrosine kinase CEPR2; AltName: Full=Protein C-TERMINALLY ENCODED PEPTIDE RECEPTOR 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	341	893	95%	3e-99	31.35%	977	Q9C7T7.1
RecName: Full=Leucine-rich repeat receptor protein kinase MSL1; AltName: Full=MSP1 protein homolog 1; AltName: Full=MSP1-like protein 1; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	347	1483	86%	9e-99	34.03%	1413	Q7F8Q9.1
RecName: Full=Leucine-rich repeat receptor-like tyrosine-protein kinase PXC3; AltName: Full=Protein PXY/TDR-CORRELATED 3; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	332	992	91%	7e-97	31.67%	890	Q22938.1
RecName: Full=Phytosulfokine receptor 1; Short=DcPSKR1; AltName: Full=Phytosulfokine LRR receptor kinase 1; Flags: Precursor [Daucus carota]	Daucus carota	332	555	94%	1e-95	30.54%	1021	Q8LPB4.1
RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g12460; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	319	936	95%	3e-92	29.94%	882	C0LGE4.1
RecName: Full=Leucine-rich repeat receptor protein kinase MSP1; AltName: Full=Protein MULTIPLE SPOROCYTE 1; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	323	770	85%	3e-91	31.65%	1294	Q8RZV7.1
RecName: Full=Receptor-like protein kinase 7; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	317	568	95%	9e-91	29.82%	977	F4I2N7.1
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM3; AltName: Full=Protein BARELY ANY MERISTEM 3; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	308	734	84%	2e-87	35.47%	992	O65440.3
RecName: Full=Receptor-like protein 52; Short=AtRLP52; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	300	300	59%	5e-86	32.11%	811	Q7FZR1.1
RecName: Full=Receptor-like protein 19; Short=AtRLP19; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	295	295	60%	7e-83	28.34%	983	Q9ZUK3.1
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase SKM1; AltName: Full=Protein STERILITY-REGULATING KINASE MEMBER 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	295	578	94%	7e-83	32.82%	960	O82318.1
RecName: Full=Brassinosteroid LRR receptor kinase BRL2; AltName: Full=BRI1-like receptor kinase 2; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	297	464	88%	7e-83	32.24%	1110	Q7G768.1
RecName: Full=Receptor-like protein 50; Short=AtRLP50; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	288	288	63%	5e-81	30.94%	891	Q93YT3.1
RecName: Full=Receptor-like protein 12; Short=AtRLP12; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	286	723	46%	9e-81	33.33%	847	Q9C9H7.2
RecName: Full=Serine/threonine-protein kinase BRI1-like 2; AltName: Full=BRASSINOSTEROID INSENSITIVE 1-like protein 2; AltName: Full=Protein VASCULAR HIGHWAY 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	287	433	89%	2e-79	32.04%	1143	Q9ZPS9.1
RecName: Full=Receptor-like protein 33; Short=AtRLP33; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	277	277	62%	2e-77	30.50%	875	F4J8G2.1
RecName: Full=Receptor-like protein 31; Short=AtRLP31; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	274	1085	62%	1e-76	29.83%	860	Q8RX63.1
RecName: Full=Receptor protein kinase CLAVATA1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	274	892	87%	1e-75	32.91%	980	Q9SYQ8.3
RecName: Full=Leucine-rich repeat receptor-like kinase protein HAR1; AltName: Full=Protein HYPERNODULATION ABERRANT ROOT FORMATION 1; Flags: Precursor [Lotus japonicus]	Lotus japonicus	271	685	87%	2e-74	32.28%	986	Q8GRU6.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
RecName: Full=Receptor-like protein 9DC3; Flags: Precursor [Solanum pimpinellifolium]	Solanum pimpinellifolium	267	267	63%	4e-74	30.38%	863	Q5MR23.1
RecName: Full=Receptor-like protein 9DC1; Flags: Precursor [Solanum pimpinellifolium]	Solanum pimpinellifolium	266	266	63%	7e-74	30.63%	863	P0DO05.1
RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	267	630	87%	3e-73	37.28%	1016	Q9LRT1.1
RecName: Full=Receptor-like protein 35; Short=AtRLP35; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	265	265	59%	1e-72	30.81%	943	Q9SRL7.1
RecName: Full=Receptor-like protein EIX1; AltName: Full=EIX receptor 1; Flags: Precursor [Solanum lycopersicum]	Solanum lycopersicum	265	457	63%	2e-72	32.02%	1031	Q6JN47.2
RecName: Full=Receptor kinase-like protein Xa21; Contains: RecName: Full=Receptor kinase-like protein Xa21, processed; Flags: Precursor [Oryza sativa Indica Group]	Oryza sativa Indica Group	265	1115	88%	3e-72	37.34%	1025	Q1MX30.1
RecName: Full=Receptor-like protein kinase 5; AltName: Full=Protein HAESA; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	264	1256	85%	4e-72	32.28%	999	P47735.1
RecName: Full=Receptor-like protein 38; Short=AtRLP38; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	260	578	58%	4e-72	32.49%	784	Q9LS79.1
RecName: Full=Receptor-like protein 53; Short=AtRLP53; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	263	263	64%	6e-72	29.10%	957	Q9S9U3.1
RecName: Full=Protein BRASSINOSTEROID INSENSITIVE 1; Short=AtBRI1; AltName: Full=Brassinosteroid LRR receptor kinase; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	265	665	88%	7e-72	30.81%	1196	O22476.1
RecName: Full=Receptor-like protein 32; Short=AtRLP32; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	260	260	59%	1e-71	30.08%	868	Q9M9X0.1
RecName: Full=Receptor-like protein 34; Short=AtRLP34; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	262	464	60%	1e-71	30.53%	957	Q9SRL2.1
RecName: Full=LRR receptor-like serine/threonine-protein kinase HSL2; AltName: Full=Protein HAESA-LIKE2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	262	897	88%	1e-71	34.73%	993	C0LGX3.1
RecName: Full=Receptor-like protein 37; Short=AtRLP37; AltName: Full=Protein EMBRYO DEFECTIVE 2800; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	258	590	58%	3e-71	31.34%	835	Q9LS80.1
RecName: Full=Receptor like protein 23; Short=AtRLP23; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	257	257	60%	2e-70	30.67%	890	O48849.1
RecName: Full=Leucine-rich repeat receptor-like protein kinase TDR; AltName: Full=Protein PHLOEM INTERCALATED WITH XYLEM; AltName: Full=Tracheary element differentiation inhibitory factor receptor; Short=AtTDR; Short=TDIF receptor; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	259	897	86%	2e-70	33.53%	1041	Q9FII5.1
RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase IRK; AltName: Full=Inflorescence and root apices receptor-like kinase; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	257	857	84%	5e-70	37.08%	964	Q9LY03.1
RecName: Full=Receptor kinase-like protein Xa21; Contains: RecName: Full=Receptor kinase-like protein Xa21, processed; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	258	1208	88%	5e-70	37.02%	1037	Q2R2D5.1
RecName: Full=Leucine-rich repeat receptor-like kinase protein FLORAL ORGAN NUMBER1; Short=OsFON1; AltName: Full=CLV1-like LRR receptor kinase; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	257	715	84%	5e-70	35.38%	994	Q5Z9N5.1
RecName: Full=Leucine-rich repeat receptor-like protein kinase PXC2; AltName: Full=Protein PXY/TDR-CORRELATED 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	257	1022	87%	7e-70	35.25%	967	Q9LZV7.1
RecName: Full=Receptor-like protein 18; Short=AtRLP18 [Arabidopsis thaliana]	Arabidopsis thaliana	254	608	59%	1e-69	30.43%	826	Q9ZUK7.3
RecName: Full=Receptor-like protein 46; Short=AtRLP46; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	253	1123	60%	2e-69	32.96%	811	F4JGB6.1

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RecName: Full=Receptor-like protein 11; Short=AtRLP11; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	251	251	59%	5e-69	30.34%	784	Q9C9H6.1
RecName: Full=Receptor-like protein 42; Short=AtRLP42; AltName: Full=Protein RESPONSIVENESS TO BOTRYTIS POLYGALACTURONASES 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	253	253	60%	6e-69	29.99%	890	Q9LJS0.1
RecName: Full=Receptor-like protein 40; Short=AtRLP40; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	253	253	60%	6e-69	29.71%	883	Q9LRW9.1
RecName: Full=Receptor-like protein Cf-9; Flags: Precursor [Solanum pimpinellifolium]	Solanum pimpinellifolium	252	252	63%	8e-69	30.31%	863	Q40235.1
RecName: Full=Tyrosine-sulfated glycopeptide receptor 1; AltName: Full=PSY1 receptor [Arabidopsis thaliana]	Arabidopsis thaliana	253	827	85%	4e-68	33.04%	1095	Q9C7S5.1
RecName: Full=Receptor-like protein 41; Short=AtRLP41; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	250	250	60%	5e-68	30.16%	881	Q9LJS2.1
RecName: Full=Receptor-like protein 7; Short=AtRLP7; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	251	436	58%	6e-68	32.33%	974	Q9C699.2
RecName: Full=Receptor-like protein 36; Short=AtRLP36; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	244	887	60%	2e-67	30.34%	718	Q1PEN0.2
RecName: Full=Receptor-like protein 15; Short=AtRLP15; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	245	928	61%	5e-66	30.17%	965	Q9C6A8.1
RecName: Full=Brassinosteroid LRR receptor kinase BRL1; AltName: Full=BRI1-like receptor kinase 1; Flags: Precursor [Oryza sativa Japonica Group]	Oryza sativa Japonica Group	245	689	90%	3e-65	31.17%	1214	Q69JN6.1
RecName: Full=Receptor-like protein 13; Short=AtRLP13; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	244	575	60%	3e-65	28.87%	1068	Q9C6A6.1
RecName: Full=Receptor-like protein 43; Short=AtRLP43; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	238	668	63%	4e-65	32.75%	711	Q9LJW7.1
RecName: Full=Receptor-like protein 49; Short=AtRLP49; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thaliana	240	240	60%	6e-65	28.72%	844	Q9SVM3.2

»
Graphic Summary



Distribution of the top 271 Blast Hits on 100 subject sequences



Alignments

Alignment view Pairwise CDS feature Restore defaults

RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2; AltName: Full=Protein FLAGELLIN-SENSING 2 homolog;
Short=OsFLS2; AltName: Full=Protein FLAGELLIN-SENSITIVE 2 homolog; Flags: Precursor [Oryza sativa Japonica Group]
Sequence ID: **Q0JA29.1** Length: 1183 Number of Matches: 1
Range 1: 1 to 1183

Score	Expect	Method	Identities	Positives	Gaps	Frame
2138 bits(5539)	0.0()	Compositional matrix adjust.	1183/1183(100%)	1183/1183(100%)	0/1183(0%)	
Query 1		MERNKFASKMSQHYTKTICIAvvlvavlfslssaaaagsgaavsvQLEALLEFKNGVADD				60
Sbjct 1		MERNKFASKMSQHYTKTICIAVVLVAVLFSLSAAAAGSGAAVSVQLEALLEFKNGVADD				60
Query 61		PLGVLAVGWRVKGSGDGA VRGGALPRHCNWTGVACDGAGQVTSIQLPESKLRGALSPFLGN				120
Sbjct 61		PLGVLAVGWRVKGSGDGA VRGGALPRHCNWTGVACDGAGQVTSIQLPESKLRGALSPFLGN				120
Query 121		ISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVVSSNYFAGGIPSSLCNCSAMWALALNVN				180
Sbjct 121		ISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVVSSNYFAGGIPSSLCNCSAMWALALNVN				180
Query 181		NLTGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLKGIMVVDLSCNQLSGSIPPEIGD				240
Sbjct 181		NLTGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLKGIMVVDLSCNQLSGSIPPEIGD				240
Query 241		LSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFSNFTGEIPGELGELTNLEVMRLYKN				300
Sbjct 241		LSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFSNFTGEIPGELGELTNLEVMRLYKN				300
Query 301		ALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELPSLQRLSLHANRLAGTVPASLTN				360
Sbjct 301		ALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELPSLQRLSLHANRLAGTVPASLTN				360
Query 361		LVNLTILELSENHLSGPLPASIGSLRNLRLRRLIVQNNLSLGGQIPASISNCTQLANASMSFN				420
Sbjct 361		LVNLTILELSENHLSGPLPASIGSLRNLRLRRLIVQNNLSLGGQIPASISNCTQLANASMSFN				420
Query 421		LFSGPLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFDGQQLKLDLSENSFTGGLSRLVGQ				480
Sbjct 421		LFSGPLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFDGQQLKLDLSENSFTGGLSRLVGQ				480
Query 481		LGNLTVLQQLGNALSGEIPPEEIGNMTKLSLKLGRNRFAGHVPASISNMSSLQLLDLGHN				540
Sbjct 481		LGNLTVLQQLGNALSGEIPPEEIGNMTKLSLKLGRNRFAGHVPASISNMSSLQLLDLGHN				540
Query 541		RLDGVFPAEVFELRQLTILGAGSNRFAGPIPDVANLRSLSFLDLSSNMLNGTVPAAIgr				600
Sbjct 541		RLDGVFPAEVFELRQLTILGAGSNRFAGPIPDVANLRSLSFLDLSSNMLNGTVPAAIgr				600
Query 601		ldqlltldlshnrlagAIPGAVIASMSNVQMYLNLNSNAFTGAIPAEIGGLVMVQTIDLS				660
Sbjct 601		LDQLLTLDLshnrlagAIPGAVIASMSNVQMYLNLNSNAFTGAIPAEIGGLVMVQTIDLS				660
Query 661		NNQLSGGVPATLAGCKNLYSLDLSGNSLTGELPANLFPQLDLLTTLNISGNDLDGEIPAD				720
Sbjct 661		NNQLSGGVPATLAGCKNLYSLDLSGNSLTGELPANLFPQLDLLTTLNISGNDLDGEIPAD				720
Query 721		IAALKHIQTLDVSRNAFAGAIPPALANLTALRSLNLSNFTFEGVPPDGGVFRNLTMSLQ				780
Sbjct 721		IAALKHIQTLDVSRNAFAGAIPPALANLTALRSLNLSNFTFEGVPPDGGVFRNLTMSLQ				780
Query 781		GNAGLCGGKLLAPCHGHAAGKRVFSRTGLvllvllalstllllmvatillvsyrryrr				840

Sbjct 781 GNAGLCGGKLLAPCHGHAAGKRVFSRGTGLVILVVLIALSTLLLLMVATILLVSYRRYRR 840
 Query 841 krrAADIAGDSPEAAVVPELRRFSYGQAAATNSFDQGNVIGSSNLSTVYKGVLAGDAD 900
 Sbjct 841 KRRRAADIAGDSPEAAVVPELRRFSYGQAAATNSFDQGNVIGSSNLSTVYKGVLAGDAD 900
 Query 901 GGMVVAVKRLNLEQFPSKSDKCFLTELATLSRLRHKNLARVVGAWAEGKIKALVLDYMV 960
 Sbjct 901 GGMVVAVKRLNLEQFPSKSDKCFLTELATLSRLRHKNLARVVGAWAEGKIKALVLDYMV 960
 Query 961 NGDLDGAIHGGaaappapSRWTVRERLRVCVSAHGLVYLHSGYDFPVVHCDVKPSNVL 1020
 Sbjct 961 NGDLDGAIHGGAAAPPAPSRWTVRERLRVCVSAHGLVYLHSGYDFPVVHCDVKPSNVL 1020
 Query 1021 LDGDWEARVSDFGTARMLGVHLPaaanaaaqstatssaFRGTVGYMAPEFAYMRTVSTKV 1080
 Sbjct 1021 LDGDWEARVSDFGTARMLGVHLPAAANAAAQSTATSSAFRGTGYMAPEFAYMRTVSTKV 1080
 Query 1081 DVFSFGVLAMELFTGRRPTGTIEEDGVPLTLQQLVDNAVSRGLDGVHAVLDPRMKVATEA 1140
 Sbjct 1081 DVFSFGVLAMELFTGRRPTGTIEEDGVPLTLQQLVDNAVSRGLDGVHAVLDPRMKVATEA 1140
 Query 1141 DLSTAADVLAVALSCAAFEPADRPDMGAVLSSLLKMSKLVGED 1183
 Sbjct 1141 DLSTAADVLAVALSCAAFEPADRPDMGAVLSSLLKMSKLVGED 1183

RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2; AltName: Full=Protein FLAGELLIN-SENSING 2; AltName:
 Full=Protein FLAGELLIN-SENSITIVE 2; Flags: Precursor [Arabidopsis thaliana]
 Sequence ID: **Q9FL28.1** Length: 1173 Number of Matches: 1
 Range 1: 30 to 1149

Score	Expect	Method	Identities	Positives	Gaps	Frame
947 bits(2449)	0.0()	Compositional matrix adjust.	520/1152(45%)	737/1152(63%)	60/1152(5%)	
Query 46	QLEALLEFKNGVADDPLGVLAGWRVVGKSGDGA VRGGALPRHCNWTGVACDGAGQVTSIQL					105
Sbjct 30	++EAL FKNG+++DPLGVL+ W + G+L RHCNWTG+ CD G V S+ L EIEALKSFKNGISNDPLGVLSDWITII - - - - -GSL-RHCNWTGITCDSTGHVVSVSL					79
Query 106	PESKLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVSSNYFAGGIPS-					164
Sbjct 80	E +L G LSP + N++ LQV+DLTSN+F G IP ++G+L EL QL++ NYF+G IPS LEKQLEGLVLSPIANLTYLQVLDLTSNFTGKIPAEIGKLTENLQLILYLNYFSGSIPSG					139
Query 165	-----SLCNCSAMWALALNVNNTGAIPSCIGDLSNLEIFEA					201
Sbjct 140	+C S++ + + NNLTG IP C+GDL +L++F A IWELKNIFYLDLRNLLSGDVPEEICKTSSLVLIGFDYNNLTGKIPECLGDLVHLQMFVA					199
Query 202	YLNLDGELPPSMAKLKGIMVVDLSCNQLSGSIPEIGDLSNLQILQLYENRFSGHIPRE					261
Sbjct 200	N+L G +P S+ L + +DLS NQL+G IP + G+L NLQ L L EN G IP E AGNHLTGSIPVSIPTLANLTDLDLSGNQLTGKIPRDFGNLLNLQSLVLTENLLEGDIPAE					259
Query 262	LGRCKNLTLLNIFSGNFTGEIPGELGELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDL					321
Sbjct 260	+G C +L L ++ N TG+IP ELG L L+ +R+YKN LTS IP SL R L +L L IGNCSSLVQLELYDNQLTGKIPAEELGNLVLQALRIYKNKLTSSIPSSLFRLTQLTHLGL					319
Query 322	SMNQLAGPIPELGPSELQRLSLHANRLAGTVPASLTNLVNLTILELSENHLSGPLPAS					381
Sbjct 320	S N L GPI E+G L SL+ L+LH+N G P S+TNL NLT+L + N++SG LPA SENHLVGPISSEIGFLESLEVLTLHSNFTGEFPQSITNLRNLTVLTVGFNNISGELPAD					379
Query 382	IGSLRNLRLIVQNNSLSGQIPASISNCTQLANASMSFNLFSGPLPAGLGRLOSLMFLSL					441
Sbjct 380	+G L NLR L +N L+G IP+SISNCT L +S N +G +P G GR+ +L F+S+ LGLLTNLRNLSAHDNLLTGPSSISNCTGLKLLDLSHNQMTGEIPRGFGRM-NLTFISI					438
Query 442	GQNSLAGDIPDDLFDCCQLQKLDLSENSFTGGLSRLVQGLGNLTVLQLOGNALSGEIPEE					501
Sbjct 439	G+N G+IPDD+F+C L+ L +++N+ TG L L+G+L L +LQ+ N+L+G IP E GRNHFTGEIPDDIFNCSNLETLSVADNNTGTLPKPLIGKQLRILQVSYNSLTGPPIRE					498
Query 502	IGNMTKLISLKLGRNRFAGHVPASISNMSSLQLLDLGHNRLDGVFPFAEVEFELRQLTILGA					561
	IGN+ L L L N F G +P +SN++ LQ L + N L+G P E+F+++ L++L					

Sbjct 499 IGNLKDNLTYLHNSNGFTGRIPREMSNLTLLQGLRMYSDLEGIPIPEEMFDMKLLSVLDL 558

Query 562 GSNRFAGPIPDVANLRSLSFDLSSNMLNGTVPAAIgrldqlltldlSHNRLAGAIPGA 621
 +N+F+G IP + L SL++L L N NG++PA+L L L T D+S N L G IPG

Sbjct 559 SNNKFSGQIPALFSKLESLTYLSLQGNKFNFSIPASLKSLSLLNTFDISDNLLTGTIPGE 618

Query 622 VIASMSNVQMYLNLNSNAFTGAIPAEIGGLVMVQTIIDLSNNQLSGGVPATLAGCKNLYSL 681
 ++AS+ N+Q+YLN SNN TG IP E+G L MVQ IDLSNN SG +P +L CKN+++L

Sbjct 619 LLASLKNMQLYLNFNSNNLLTGTIPKELGKLEMVQEIDLSNNLFSGSI PRSLQACKNVFTL 678

Query 682 DLSGNSLTGELPANLFPQLDLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAI 741
 D S N+L+G +P +F +D++ +LN+S N GEIP + H+ +LD+S N G I

Sbjct 679 DFSQNNLSGHIPDEVFQGMDMIISLNSRNSFSGEIPQSFNGMTHLVSLDLSSNNLTGEI 738

Query 742 PPALANLTALRSLNLSSNTFEGVPVDPGGVFRNLTMSLQGNAGLCGGKL-LAPCHGHAAG 800
 P +LANL+ L+ L L+SN +G VP+ GVF+N+ S L GN LCG K L PC

Sbjct 739 PESLANLSTLKHKLKLANNLKGHVPESGVFKNINASDLMGNTDLCGSKKPLKPC--TIKQ 796

Query 801 KKRVSF-RTGlvilvvlialstllllmvatillvsyrryrrkrrAADIAGDSPEAAVVVP 859
 K FS RT +++++ A + LL+L++ IL ++ ++ +++ + ++A+

Sbjct 797 KSSHFSKRTRVILIIILGSAALLLVLLVLIILTCCCKKEKKIENSSESLPDLDSAL--- 853

Query 860 ELRRFSYGLAAATNSFDQGNVIGSSNLSVYKGVLAGDADGGMVVAVKRLNLEQFPSKS 919
 +L+RF +L AT+SF+ N+IGSS+LSTVYKG L + G V+AVK LNL++F ++S

Sbjct 854 KLKRFEPKELEQATDSFNANSANIIGSSSLSTVYKGQL---EDGTVIIVKVLNLFKEFSAES 909

Query 920 DKCFLTELATLSRLRHKNLARVVGYAWEAGKIKALVLDYMVNGDLGAIHG Gaaappap 979
 DK F TE TLS+L+H+NL +++G+AWE+GK KALVL +M NG+L+ IHG AA

Sbjct 910 DKWIFYTEAKTSQLKHRNLVKILGFAWESGKTALVLPFMENGNLEDTIHGSAAPIG--- 966

Query 980 SRWTVRERLRVCSVAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARMLG 1039
 ++ E++ +CV +A G+ YLHSGY FP+VHCD+KP+N+LLD D A VSDFGTAR+LG

Sbjct 967 ---SLLEKIDL CVHIASGIDY LHSYGFPIVHCDLK PANILLSDRVAHVSDFGTARILG 1023

Query 1040 VHL PaaanaaaqstatssaFRGTVGYMAPEFAYMRTVSTKVDVFSFGVLAMELFTGRRPT 1099
 +TA++SAF GT+GY+APEFAYMR V+TK DVFSFG++ MEL T +RPT

Sbjct 1024 FR-----EDGSTTASTSAFEGTIGYLAPEFAYMRKVTTKADVFSFGIIMMELMTKQRPT 1077

Query 1100 GTIEEDGVPLTLQQLVDNAVSRGLDGVHAVLDPRM--KVATEADLSTAADVLAVALSCAA 1157
 +ED +TL+QLV+ ++ G G+ VLD + + + D L + L C +

Sbjct 1078 SLNDEDSQDMTLRQLVEKSIGNRKGMRVRLDMELGDSIVSLKQEEAIEDFLKLCFCTS 1137

Query 1158 FEPADRPDMGAV 1169
 P DRPDM +

Sbjct 1138 SRPEDRPDMNEI 1149

RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At2g33170; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **O49318.1** Length: 1124 Number of Matches: 1

Range 1: 38 to 1095

Score	Expect	Method	Identities	Positives	Gaps	Frame
519 bits(1336)	1e-163()	Compositional matrix adjust.	371/1153(32%)	568/1153(49%)	126/1153(10%)	
Query 48	EALLEFKN	GVADPLGLV	LAGVRGKSGD	GAVRGGALPRHCN	WTGVACDGAGQ	----- 99
Sbjct 38	+ LLE KN	D L L W	G	CNW GV C	G	
Query 100	VTSIQLPESK	LRGALSPFLGN	ISTLQVIDLTS	NAFAGGIPPQLGR	LGELEQLVVSSNYFA	159
Sbjct 87	VTS+ L	L G +SP +G + L	++L NA G IP ++G			130
Query 160	GGIPSSLNCS	AMWALALNVN	NLTGAIPSCIGD	LSNLEIFEAYL	NNLDGELPPSMAK	LKG 219
Sbjct 131	-----NCS	KLEVMFLN	NNQFGGSIPVE	INKLSQLRSF	NICNNKLSGPLPEE	IGDLYN 182
Query 220	IMVVDLSCN	QLSGSIPPEIGD	LSNLQILQYENR	FSGHIPRELGRCK	NLTLLNIFSN	GFT 279
Sbjct 183	+ + N L+G	+P +G+L+ L +	+ +N FSG+IP E+G+C	NL LL + N +		242
Query 280	GEIPGELGEL	TNLEVMRLYK	NALTSEIPRSLR	RCVSLNLDLSMN	QLAGPIPEL	GELPS 339

Sbjct	243	GE+P E+G L L+ + L++N +IP+ + SL L L N L GPIIP E+G + S GELPKIEIGMLVKLQEVILWQNKFSGFIPKDIGNLTSLETALALYGNLSLVGPIPISEIGNMKS	302
Query	340	LQRSLHANRLAGTVPASLTNLVNLITILELSENHLSGPLPASIGSLRNLRLIVQNNSLS	399
Sbjct	303	L++L L+ N+L GT+P L L + ++ SEN LSG +P + + LR L + N L+ LKKLYLYQNQLNGTIPKELGKLSKVMIEDFSENLLSGEIPVELSKISELRLLYLFQNKLT	362
Query	400	GQIPASISNCTQLANASMSFNLFSGPLPAGLGRQLMFLSLGQNSLAGDIPDDLFDGCGQ	459
Sbjct	363	G I P +S LA +S N +GP+P G L S+ L L NSL+G I P L GIIPNELSKLRNLAKLDLSINSLTGIPIPPGFQNL TSMRQLQLFHNSLSGVIPQGLGLYSP	422
Query	460	LQKLDLSENSFTGGLSRLVGLGNLTVLQLQGNALSGEIPEEIGNMTKLISLKLGRNRFA	519
Sbjct	423	L +D SEN LSG+IP I + LI L LG NR LWVVD FSENQ-----LSGKIPPFICQSNLILLNLGSRIF	458
Query	520	GHPASISNMSSLQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRFAGPIPDVANLRS	579
Sbjct	459	G++P + SL L+ NRL G FP E+ +L L+ + NRF+GP+P + + GNIPPGVLRCKSLLQLRVVGNRLTGQFPTELCKLVNLSAIELDQNRFSGPLPPEIGTCQK	518
Query	580	LSFLDLSSNMLNGTVPAAalgrldqlltldlSHNRLAGAIPGAVIASMSNVQMY--LNLSN	637
Sbjct	519	L L L++N + +P + +L L+T ++S N L G I P + ++N +M L+LS LQRHLAANQFSSNLPNEISKLSNLVTFNVSSNSLTGPIP----SEIANCKMLQRDLRSR	574
Query	638	NAFTGAIPAEIGGLVMVQTIDLSNNQLSGGVPATLAGCKNLYSLDLSGNSLTGELPANLF	697
Sbjct	575	N+F G++P E+G L ++ + LS N+ SG +P T+ +L L + GN +G +P NSFIGSLPPELGSLLHQLEILRLSENRFSGNIPFTIGNLTHLTELQMGGNLFSGSIP----	630
Query	698	PQLDLLTTL----NISGNLDGEIPADIAALKHIQTLDVSRNAFAGAIPPALANLTALRS	753
Sbjct	631	PQL LL++L N+S ND GEIP +I L + L ++ N +G I P NL++L PQLGLLSSLQIAMNLSYNDFSGEIPPEIGNLHLLMYLSLNNHLSGEIPTTFENLSSLLG	690
Query	754	LNLSSNTFEGPVPDGGVFRNLTMSSLQGNAGLCGGKLLA--PCHG---HAAGKRVFSRT	808
Sbjct	691	N S N G +P +F+N+T++S GN GLCGG L + P H H + K +R CNFSYNLTLGQLPHTQIFQNMTLTSFLGNKGLCGGHLRSCDPSHSSWPHISSLKAGSARR	750
Query	809	GlvilvvlialstlllvmvatillvsyrryrrkrAAADIAGDSP--EAAVVVPELRRFS	865
Sbjct	751	G +++++ + ++ ++V + R + A + P E+ + RF+ G--RIIIIVSSVIGGISLLLIAIVVHFLRNPVEPTAPYVHDKEPFFQESDIYFVPKERFT	808
Query	866	YGQLAAATNSFDQGNVIGSSNLSLTVYKGVLAGDADGGMVVAVKRLN-----LEQFPSKSD	920
Sbjct	809	+ AT F ++G TVYK V+ G +AVK+L + +D VKDILEATKGFHDSYIVGRGACGTVYKAVMP----SGKTIAVKKLESNREGNNNSNNTD	864
Query	921	KCFTELATLSRLRHKNLARVVGYAWEAGKIKALVL-DYMVNGDLGAIHGGaaappap	979
Sbjct	865	F E+ TL ++RH+N+ R+ + + G L+L +YM G L +HGG + NSFRAEILTLGKIRHRNIVRLYSFCYHQGSNSNLLLYEYMSRGSGLGELLHGGKSHSMDWP	924
Query	980	SRWTVRERLRVCVSAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARMLG	1039
Sbjct	925	+R+ + + A GL YLH ++H D+K +N+L+D ++EA V DFG A+++ TRFA-----IALGAAEGLAYLHHDCKPRIIHRDIKSNLILIDENFEAHVDFGLAKVID	978
Query	1040	VHLPaaanaaaqstatssaFRGTVGYMAPEFAYMRTVSTKVDVFSFGVLAMELFTGRRPT	1099
Sbjct	979	+ L + + SA G+ GY+APE+AY V+ K D++SFGV+ +EL TG+ P MPL-----SKSVSAVAGSYGYIAPEYAYTMKVTEKCDIYSFGVVLELLTGKAPV	1028
Query	1100	GTIEEDG--VPLTLQQLVDNAVSRGLDGVHAVLDPRM-KVATEADLSTAADVLAVALSCA	1156
Sbjct	1029	+E+ G T + D++++ +LDP + KV + L+ V +A+ C QPLEQGGDLATWTRNHIRDHSLTS-----EILDOPYLTKVEDDVILNHMITVTKIAVLCT	1082
Query	1157	AFEPADRPDMGAV 1169	
Sbjct	1083	P+DRP M V KSSPSDRPTMREV 1095	

RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At5g63930; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **Q9LVP0.1** Length: 1102 Number of Matches: 1

Range 1: 59 to 1074

Score	Expect	Method	Identities	Positives	Gaps	Frame
514 bits(1323)	5e-162()	Compositional matrix adjust.	361/1098(33%)	538/1098(48%)	97/1098(8%)	

Query	87	CNWTGVACDGDAGQVTSIQLPESKLRGALSPFLGNISTLQVIDTSNAFAGGIPQLGRGL	206
Sbjct	59	C WTGV C PE LS ++L+S +G + P +G L CGWTGVMCSNYSSD-----PE-----VLS-----LNLSSMVLSGKLSPSIGGLV	97
Query	147	ELEQLVSSNYFAGGIPSSLCNCSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNNL	206
Sbjct	98	L+QL +S N +G IP + NCS++ L LN N G IP IG L +LE Y N + HLKQLDLSYNGLSGKIPKEIGNCSSLETLKLNNNQFDGEIPVEIGKLVLENLIYNNRI	157
Query	207	DGELPPSMALKGIMVVDLSCNQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRCK	266
Sbjct	158	G LP + L + S + N +SG +P IG+L L + +N SG +P E+G C+ SGSLPVEIGNLSSLSQLVTYSNNISGQLPRSIGNLKRLTSFRAGQNMISGSLPSEIGGC	217
Query	267	NLTLNIFSNFGTGEIPGELGELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQL	326
Sbjct	218	+L +L + N +GE+P E+G L L + L++N + IPR + C SL L L NQL SLVMLGLAQNLQSGELPKEIGMLKLSQVILWENEFSGFIPREISNCTSLETLALYKNQL	277
Query	327	AGPIPPELGELPSLQRLSLHANRLAGTVPASLTNLVNLTIELSENHLSGPLPASIGSLR	386
Sbjct	278	GPIP ELG+L SL+ L L+ N L GT+P + NL ++ SEN L+G +P +G++ VGPIPKELGDLQSLLEFLYLYRNGLTIPREIGNLSYAIEIDFSENALTGEIPELEGNIE	337
Query	387	NLRRLIVQNNLSGQIPASINCTQLANASMSFNLFSGPLPAGLGRQLSMLFSLGQNSL	446
Sbjct	338	L L + N L+G IP +S L+ +S N +GP+P G L+ L L L QNSL GLELLYL FENQLTGTIPVELSTLKNLSKLDLSINALTGPIPLGFQYLRGLFMLQLFQNSL	397
Query	447	AGDIPDDLFDGQQLKLDLSENSFTGGLSRLVGLGNLTVLQLQGNALSGEIPEEIGNMT	506
Sbjct	398	+G IP L L LD+S+N +G + + N+ +L L N LSG IP I SGTIPPKLGWYSDLWVLDMSDNHLSGRIPSYLCLHSNMIIILNLGTNNLSGNIPTGITTC	457
Query	507	KLISLKLGRNRFAGHVPASISNMSSLQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRF	566
Sbjct	458	L+ L+L RN G P+++ ++ ++LG NR G P EV L L N F TLVQLRLARNNLVGRFPSNLCKQVNVTAIELGQNRFRGSIPREVGNCALQRLQLADNGF	517
Query	567	AGPIPDVANLRSLSFLLDLSSNMLNGTVPAAIgrldqlltldlSHNRLAGAIPGAVIASM	626
Sbjct	518	G +P + L L L++SSN L G VP+ TGELPREIGMLSQGLTNISSNKLTGEVPS-----EI	549
Query	627	SNVQMY--LNLSSNAFTGAIPAIEIGGLVMVQTIDLSNNQLSGGVPATLAGCKNLYSLDLS	684
Sbjct	550	N +M L++ N F+G +P+E+G L ++ + LSNN LSG +P L L L + FNCKMLQRLDMCCNNSFGTLPEVGSLYQLELLKLSNNNSGTIPVALGNLSRLELQMG	609
Query	685	GNSLTGELPANLFPQLDLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPA	744
Sbjct	610	GN G +P L L LN+S N L GEIP +++ L ++ L ++ N +G IP + GNLFNGSIPRELGSLTGLQIALNLSYNKLTGEIPELSNLVMEFLLLNNNNSGEIPSS	669
Query	745	LANLTALRSLNLSSTNTEGFPVDPGGVFRNLTMSLQGNAGLCGGKL-----LAPCHG	796
Sbjct	670	ANL++L N S N+ GP+P + RN++MSS GN GLCG L AP FANLSSLLGYNFYSNLTGPIP---LLRNISMSSFIGNEGLCGPPLNQCITQPFAP--S	724
Query	797	HAAGKRVFSRTGlvilvvliaIstllllmvatillvsyrryrkrAAADIAGDSPEAAV	856
Sbjct	725	+ GK + ++ + + L+L+ + L+ A D + QSTGKPGGMRSSKIIAITA AVIGGVSLMLIALIVYLMRRPVRTVASSAQDGPSEMSLDI	784
Query	857	VVPELRRFSYGQLAAATNSFDQGNVIGSSNLSTVYKGVLAGDADGGMVAVKRL--NLEQ	914
Sbjct	785	P F++ L AAT++FD+ V+G TVYK VL G +AVK+L N E YFPPKEGFTFQDLVAATDNFDES FVVGACGTVYKAVLP---AGYTLAVKKLASNHEG	840
Query	915	FPSKS-DKCFLELATLSRLRHKNLARVVGAWAEGKIKALVLDYVMVNGDLDAIHGGaa	973
Sbjct	841	+ + D F E+ TL +RH+N+ ++ G+ G L+ +YM G L +H + GNNNNVDNSFRAEILTGNIRHRNIVKLHGFCNHQGS-NLLLYEYMPKGS LG EILHDPSC	899
Query	974	appapSRWTVRERLRVCVSAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFG	1033
Sbjct	900	W+ +R ++ + A GL YLH + H D+K +N+LLD +EA V DFG NLD-----WS--KRFKIALGAAQGLAYLHHDCKPRIFHRDIKSNNILDDKFEAHVGDG	952
Query	1034	TARMLGVHLPaaanaaaqstatssaFRGTVGYMAPEFAYMRTVSTKVDVFSFGVLAMELF	1093
Sbjct	953	A++ + +P + + SA G+ GY+APE+AY V+ K D++S+GV+ +EL LAKV--IDMP-----HSKSMIAAGSYGIAPEYAYTMKVTEKSDIYSYGVVLELL	1002
Query	1094	TGRRPTGTIEEDG--VPLTLQQLVDNAVSRGLDGVHAVLDPRMKVATEADLSTAADVLA	1151
Sbjct	1003	TG+ P I++ G V + +A+S G VLD R+ + E +S VL + TGKAPVQPIDQGGDVNWVRSYIRRDALSSG-----VLDARLTLEDERIVSHMLTVLKI	1056
Query	1152	ALSCAAFEPADRPDMGAV 1169	
Sbjct	1057	AL C + P RP M V 1074 ALLCTSVSPVARPSMRQV	

RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI1; AltName: Full=Protein RECEPTOR OF RGF1 4; AltName: Full=Protein RGF1 INSENSITIVE 1; AltName: Full=Protein ROOT CLAVATA-HOMOLOG1 2; Flags: Precursor [Arabidopsis thaliana]
 Sequence ID: **Q9LHP4.1** Length: 1141 Number of Matches: 1
 Range 1: 71 to 1059

Score	Expect	Method	Identities	Positives	Gaps	Frame
502 bits(1293)	3e-157()	Compositional matrix adjust.	361/1096(33%)	541/1096(49%)	121/1096(11%)	
Query 88		NWTGVACDGAGQVTSIQLPESKLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGE				147
Sbjct 71		NWTFITCSSQGFITDI-----DIESVPLQLSLPKNLPAFRS				106
Query 148		LEQLVSSNYFAGGIPSSLCNCSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNNLD				207
Sbjct 107		LQKLTISGANLTGTLPELGDCLGLKVLDLSSNGLVGDIPWLSKLRNLETILNSNQLT				166
Query 208		GELPPSMAKLKGIMVVDLSCNQLSGSIPPEIGDLSNLQILQLYENR-FSGHIPRELGRCK				266
Sbjct 167		GKIPPDISKCSKLSLILFDNLLTGSIPTELKLSGLEVIRIGGNKEISGQIPSEIGDCS				226
Query 267		NLTLNIFSNFTGEIPGELGELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQL				326
Sbjct 227		NLTVLGLAETSVSGNLPSSLGKLLKLETLSTIYTTMISGEIPSDLGNCSELVDLFLYENSL				286
Query 327		AGPIPPPELPSLQRLSLHANRLAGTVPASLTNLVNLTIELSENHLSGPLPASIGSLR				386
Sbjct 287		SGSIPREIQGLTKLEQLFLWQNSLVGGIPEEIGNCSNLKMDLSLNLSSGIPSSIGRLS				346
Query 387		NLRRILVQNSLSGQIPASISNCTQLANASMSFNLFSGPLPAGLGRQLSMLFSLGQNSL				446
Sbjct 347		FLEEFMISDNKFSGSIPTTISNCSLVLQQLDKNQISGLIPSELGTLTKLTLFFAWSNQL				406
Query 447		AGDIPDDLFDGQQLKLDLSENSFTGGLSRLVQGLGNLTVLQQLQGNALSGEIPEEIGNMT				506
Sbjct 407		EGSIPPLADCTDLQALDLRSNLTGTIPSGLFMLRNLTKLLISNSLSGFIPEIGNCS				466
Query 507		KLISLKLGRNRFAGHVPASISNMSSLQLLDLGHNRLDGVPFAEVFELRQLTILGAGSNRF				566
Sbjct 467		SLVRLRLGFNRITGEIPSGIGSLKKNIFLDFSSNRLHGKVPDEIGSCSELQ MIDLSNNSL				526
Query 567		AGPIPDVANLRSLSFLDLSSNMLNGTVPAAlgrldqlltldLSHNRLAGAIPGAVIASM				626
Sbjct 527		EGSLPNPVSSLSGLQVLDVSNQFSGKIPAS-----LGRLVSLNKL I-----				568
Query 627		SNVQMYLNLNSNAFTGAIPAEIGGLVMVQITDLSNNQLSGGVPATLAGCKNL-YSLDLSG				685
Sbjct 569		-----LSKNLFSGSIPTSLGMCSTGLQLDLGNSNELSGEIPSELGDIENLEIALNLS				620
Query 686		NSLTGELPANLFPQLDLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPAL				745
Sbjct 621		NRLTGKIPSKI-ASLNKLSILDLSHNMLEG---DLAPLANIE-----				658
Query 746		ANLTALRSLNLSNFTFEGPVPDGGVFRNLTMSSLQGNAGLCGGK----LLAPCHGHAAGK				801
Sbjct 659		-NLVSL---NISYNSFSGYLPDNKLFRLSPQDLEGNKCLCSSTQDSCFLT YRKGNGLD				714
Query 802		KRVFSRTGLvivilvialstlllvmatilvsvrryrkrAADIAGDSPEAAVVVPEL				861
Sbjct 715		DGDASRTRKRLRLTALLITLVVLMILGAVAVIRARRNIDNERDSELGETYKWQFTPFQK				774
Query 862		RRFSYQGLAAATNSFDQGNVIGSSNLSTVYKGVLAGDADGGMVAVKRL-----NLE				913
Sbjct 775		LNFSVDQIIRC---LVEPNVIGKGCSTGVVYR---ADVNGEVIIVKKLWPAMVNGGHDE				827
Query 914		QFPSKSDKCFTELATLSRLRHKNLARVVGVAWEAGKIKALVLDYVMVNGDLGAIHGaa				973
Sbjct 828		KTKNVRDS-FSAEVKTLGTIRHKNIVRFLGCCWNR-NTRLLMYDYPNGSLGSLHERRG				885
Query 974		apppapSRWTVRERLRVCVSAHGLVYLHSGYDFPVPVHCDVKPSNVLLDGDWEARVSDFG				1033
Sbjct 886		SSLD---WDL--RYRILLGAAQGLAYLHHDCLPPIVHRDIKANNILIGLDFEPIADFG				939

Query 1034 TARMGLVHLPaaanaaaqstatssaFRGTVGYMAPEFAYMRTVSTKVDVFSFGVLAMELF 1093
 A+++ S+ G+ GY+APE+ Y ++ K DV+S+GV+ +E+
 Sbjct 940 LAKLVD-----EGDIGRCSNTVAGSYGYIAPEYGYSMKITEKSDVYSYGVVLEVL 990

Query 1094 TGRRPTGTIEEDGVPLTLQQLVDNAVSRGLDGVHAVLDPRMKVATEADLSTAADVLAVAL 1153
 TG++P +G+ LVD R G VLD ++ TEA+ VL AL
 Sbjct 991 TGKQPIDPTVPEGI-----HLVDWV--RQNRGSLEVLDSTLRSRTEAEADEMMQVLGTAL 1043

Query 1154 SCAAFEPADRPDMGAV 1169
 C P +RP M V
 Sbjct 1044 LCVNSSPDERPTMKDV 1059

RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase At1g17230; Flags: Precursor [Arabidopsis thaliana]
 Sequence ID: **Q9SHI2.2** Length: 1101 Number of Matches: 1
 Range 1: 29 to 1068

Score	Expect	Method	Identities	Positives	Gaps	Frame
482 bits(1240)	5e-150()	Compositional matrix adjust.	351/1127(31%)	542/1127(48%)	92/1127(8%)	
Query 48	EALLEFKNGVADDPLGVLAGWRVKGSGDGAVRGGALPRHCNWTGVACDGAGQVTSIQLP					107
Sbjct 29	RVLLEFK-AFLNDSNGYLASWNQLDSNP-----CNWTG+AC VTS+ L					76
Query 108	SKLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVSSNYFAGGIPSSLC					167
Sbjct 77	MNLSGTLSP-----ICLHGLRKLNVSTNF-----+L L +L VS+N+					102
Query 168	NCSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLKGIMVVDLSC					227
Sbjct 103	-----ISGPIQDLSLCSRLEVLDLCTNRFHGVIPQIQLTMIITLKKLYLCE					148
Query 228	NQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFSNFTGEIPGELG					287
Sbjct 149	NLGSIP +IG+LS+LQ L +Y N +G IP + + + L ++ NGF+G IP E+ NYLFGSIPRQIGNLSSLQELVIYSNNLTGVIPPSMAKLRQLRIIRAGRNFGSGVIPSEIS					208
Query 288	ELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELGEPLSLQRLSLHA					347
Sbjct 209	GCESLKVGLAENLLEGLPKQLEKLQNLTDLILWQNRLSGEIPPSVGNISRLEVLALHE					268
Query 348	NRLAGTVPASLTNLVNLTIELSENHLSGPLPASIGSLRNLRLRRLIVQNNLSGQIPASIS					407
Sbjct 269	NYFTGSIPREIGKLTMKRLYLYTNQLTGEIPREIGNLIDAAEIDFSENQLTGFIPKEFG					328
Query 408	NCTQLANASMSFNLFSGLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFDGQQLKLDLSE					467
Sbjct 329	HILNLKLLHLFENILLGPIPRELGELELLEKLDLSINRLNGTIPQELQFLPYLVDLQFLD					388
Query 468	NSFTGGLSRLVGQLGNLTVLQLOGNALSIGEIPPEIGNMTKLI SLKLGSRNFAGHVPASIS					527
Sbjct 389	NQLEGKIPPLIGFYNSFVLDMSANLSGPIPAHF CRFQTLILLSLGSNKLSGNIPRDLK					448
Query 528	NMSSLQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRFAGPIPDVANLRSLSFLDLSS					587
Sbjct 449	TCKSLTKMLGDNQLTGSPLIELFNQLNTALELHQNWLSGNISADLGLKNLERLRAN					508
Query 588	NMLNGTVPAAIgrldqlltldlSHNRLAGAI PGAVIASMSNVQMYLNL SNNAFTGAIPAE					647
Sbjct 509	NNFTGEIPPEIGNLTKIVGFNISSNQLTGHIPKE-LGSCVTIQR-LDLSGNKFSGYIAQE					566
Query 648	IGGLVMVQTIDLSNNQLSGGVPATLAGCKNLYSLDLSGNSLTGELPANLFPQLDLLTTLN					707
Sbjct 567	LGQLVYLEILRLSDNRLTGEIPHSFGDLTRLMELQLGGNLLSENIPVELGKLTSLQISLN					626
Query 708	ISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAI PPALANLTALRSLNLSNTFEGPVPD					767
Sbjct 627	ISHNNLSGTIPDSLGNLQMLEILYLNNDKLSGEIPASIGNLMSLLICNISNNNLVGTVPD					686
Query 768	GGVFRNLTMSLQGNAGLGGKLL--LAPCHGHAAGKRVF---SRTGlvilvvlialstl					822
	VF+ + S+ GN GLC + P H+ K S+ ++ + I + ++					

Sbjct 687 TAVFQRMDSSNFAGNHLGLNLSRSHQPLVPHSDSKLNWLLINGSQRKILTTICIVIGSV 746

Query 823 lllmvatillvsyrryrrkrAAADIAGDSPEAAVVVPELRRFSYGQLAAATNSFDQGNVI 882
L+ + RR D + P+ + F+Y L AT +F + V+

Sbjct 747 FLITFLGLCWTIKRREPAFVALEDQTKPDVMDSYYPFK-KGFTYQGLVDATRFSEDVVL 805

Query 883 GSSNLSTVYKGVLAGDADGGMVAVKRLNLEQFPSKSDKCFLELATLSRLRHKNLARVV 942
G TVYK + GG V+AVK+LN + SD F E++TL ++RH+N+ ++

Sbjct 806 GRGACGTVYK---AEMSGGEVIKVKLNRSRGEASDNSFRAEISTLGKIRHRNIVKLY 861

Query 943 GYAWEAGKIKALVLDYMVNGDLDGAIHGaaapppapSRWTVRERLRVCSVAHGLVYLH 1002
G+ + L+ +YM G L + G W R R+ + A GL YLH

Sbjct 862 GFCYHQNS-NLLLYEYMSKGSLSGEQLQRGEKNCLLD--WNA--RYRIALGAAEGLCYLH 915

Query 1003 SGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARMLGVHLPaaanaaaqstatssaFRGT 1062
+VH D+K +N+LLD ++A V DFG A+++ + + +A A G+

Sbjct 916 HDCRPQIVHRDIKSNILLDERFQAHVGDVFLAKLIDLSSYSKMSAVA-----GS 965

Query 1063 VGYMAPEFAYMRTVSTKVDVFSFGVLAMELFTGRRPTGTIEEDGVPLTLQQLVDNAVSRG 1122
GY+APE+AY V+ K D++SFGV+ +EL TG+ P +E+ G L V ++ R

Sbjct 966 YGYIAPEYAYTMKVTEKCDIYSFGVVLELITGKPPVQPLEQGG--DLVNWVRRSI-RN 1021

Query 1123 LDGVHAVLDPRMKVATEADLSTAADVLAVALSCAAFEPADRPDMGAV 1169
+ + D R+ + + + VL +AL C + PA RP M V

Sbjct 1022 MIPTIEMFDARLDTNDKRTVHEMSLVKIALFCTSNPASRPTMREV 1068

RecName: Full=Receptor-like protein kinase; Flags: Precursor [Ipomoea nil]

Sequence ID: **P93194.2** Length: 1109 Number of Matches: 1

Range 1: 57 to 1088

Score	Expect	Method	Identities	Positives	Gaps	Frame
464 bits(1194)	2e-143()	Compositional matrix adjust.	352/1102(32%)	540/1102(49%)	89/1102(8%)	
Query 87		CNWTGVACDGAGQVTSIQLPESKLRGALS PFLGNISTLQVIDLTSNAFAGGIPPQLGRLG				146
Sbjct 57		C+W GV CD V ++ +L+S +G P++ L CSWLGVECDRRQFVDTL-----NLSSYGISGEFGPEISHLK				92
Query 147		ELEQLVVSNSNYFAGGIPSSLCNCSAMWALALNVNNTGAI PSCIGDLSNLEIFEAYLNNL				206
Sbjct 93		L+++V+S N F G IPS L NCS + + L+ N+ TG IP +G L NL + N+L HLKKVVLSGNGFFGSI PSQLGNCSLLEHIDLSSNSFTGNIPDTLGALQNLRLNSLFFNSL				152
Query 207		DGELPPSMAKLKGIMVVDLSCNQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRCK				266
Sbjct 153		G P S+ + + V + N L+GSIP IG++S L L L +N+FSG +P LG IGFPPELLSIPHLETYFTGNGLNGSIPSNIGNMSELTTLWLDNDFSGPVPSSLGNIT				212
Query 267		NLTLNIFNSNGFTGEIPGELGELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQL				326
Sbjct 213		L L + N G +P L L NL + + N+L IP C + + LS NQ TLQELYLNDNNLVGTLPVTLNLENLVYLDVRNNSLVGAIPLDFVSCQIDTISLSNNQF				272
Query 327		AGPIPPPELGELPSLQRLSLHANRLAGTVPASLTNLVNLTI ELSENHLSGPLPASIGSLR				386
Sbjct 273		G +PP LG SL+ + L+G +P+ L L L L+ NH SG +P +G + TGGLPPGLGNCTSLREFGAFSCALSGPI PSCFGQLTKLDTLYLAGNHFSGRIPPELGKCK				332
Query 387		NLRRILIVQNNLSGQIPASISNCTQLANASMSFNLFSGPLPAGLGRLQSLMFLSLGQNSL				446
Sbjct 333		++ L +0 N L G+IP + +0L + N SG +P + ++0SL L L ON+L SMIDLQLQQNQLEGEIPGELGMLSQQLYLHLYTNLNSGEVPLSIWKIQSLQSLQLYQNNL				392
Query 447		AGDIPDDLFDGQQLKLDLSENSFTGGLSRLVQGQGNLTVLQQLQGNALS GEIPEEIGNMT				506
Sbjct 393		+G++P D+ + QL L L EN FTG + + +G +L VL L N +G IP + + SGELPVDMTTELKQLVSLALYENHFTGVIPODLGANSSEVLDLTRNMFTHIPPNLCSQK				452
Query 507		KLISLKLGRNRFAGHVPASISNMSSLQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRF				566
Sbjct 453		KL L LG N G VP+ + S+L+ L L N L G P + E + L N F KLKRLLLGYNYLEGSVPSDLGGCSTLERLILEENLRGGLP-DFVEKQNLFFDLSGNNF				511
Query 567		AGPIPDVANLRSLSFLDLSSNMLNGTVPAALgrldqlltldlSHNRLAGAIPGAVIASM				626
Sbjct 512		GPIP ++ NL++++ + LSSN L+G++P LG L +L L+LSHN L G +P + + TGPIPPSLGNLKNVTAIYLSNQLSGSIPPELGSVVKLEHLNLSHNILKGIPL- - - -SEL				567
Query 627		SNVQMY - -LNLSNAFTGAIPAEIGGLVMVQTIDLSNNQLSGGVPATLAGCKNLYSLDLS				684

Sbjct 568 SNCHKLSELDASHNLLNGSIPSTLGSLELTCLKLSLGENSFSGGIPTSLFQSNKLLNLQLG 627

Query 685 GNSLTGELPANLFPQLDLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPA 744
GN L G++P L L +LN+S N L+G++P D+ LK ++ LDVS N +G +

Sbjct 628 GNLLAGDIPP- -VGALQALRSLNLSNKLNGQLPIDLGKLMLEELDVSNNLSGTL- RV 684

Query 745 LANLTALRSLNLSNNTFEGVPVDPG- GVFRNLTMSLQGNAGLC-----GGKLLA 792
L+ + +L +N+S N F GPVP F N + +S GN+ LC +L

Sbjct 685 LSTIQSLTFINISHNLFSGVPVPSLTKFLNNSPSTFSGNSDLCINCPADGLACPESSILR 744

Query 793 PCHGHAAGKRVFSRTGLvlvllialstllllmvatillvsyrryrrkrAAIAGDSP 852
PC+ + K S G +++++ +L +

Sbjct 745 PCNMQSN TGKGLSTLG-----IAMI VLGALLFIICLFLFSAFLFLHCKKSVQ 792

Query 853 EAAVVVPELRRFSYQGLAAATNSFDQGNVIGSSNLSTVYKGVLAGDADGGMVVAVKRLNL 912
E A+ E ++ AT + + VIG T+YK L+ D V AVK+L

Sbjct 793 EIAISAQEGDGSLLNKVLEATENLNDKYVIGKGAHGTIYKATLSPDK----VYAVKCLVF 848

Query 913 EQFPSKSDKCFLELATLSRLRHKNLARVVGYAWEAGKIKALVLDYMVNGDLGAIHGGa 972
+ S + E+ T+ ++RH+NL ++ + W + ++ YM NG L +H

Sbjct 849 TGIKNGS- VSMVREIETIGKVRHRNLIKLEEF- WLRKEYGLIITYTMENGLHDILH--- 903

Query 973 aapppapSRWTVRERLRVCVSAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDF 1032
PP P W+ R + V AHGL YLH D +VH D+KP N+LLD D E +SDF

Sbjct 904 ETNPPKPLDWSTRH--NIAVGTAHGLAYLHFDCDPAIVHRDIKPMNILLSDLEPHISDF 961

Query 1033 GTARMLGVHLPaaanaaaqstatssaFRGTGYMAPEFAYMRTVSTKVDVFSFGVLAMEL 1092
G A++L + ++ S+ +GT+GYMAPE A+ S + DV+S+GV+ +EL

Sbjct 962 GIAKLLD-----QSATSIPSNTVQGTIGYMAPENAFITVKSRESDEVYSYGVVLEL 1012

Query 1093 FTGRR---PTGTIEEDGVPLTLQQLVDNAVSRGLDGVHAVLDPRM--KVATEADLSTAAD 1147
T ++ P+ E D V +V + ++DP + ++ + +

Sbjct 1013 ITRKKALDPSFNGETDIVGWV-----RSVWTQTGEIQKIVDPSLLELIDSSVMEQVTE 1066

Query 1148 VLAVALSCAAFEPADRPDMGAV 1169
L++AL CA E RP M V

Sbjct 1067 ALSLALRCAEKEVDKRPTMRDV 1088

RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase RGI4; AltName: Full=Protein RECEPTOR OF RGF1

2; AltName: Full=Protein RGF1 INSENSITIVE 4; AltName: Full=Protein STERILITY-REGULATING KINASE MEMBER 2; Flags:

Precursor [Arabidopsis thaliana]

Sequence ID: **F4K6B8.1** Length: 1090 Number of Matches: 1

Range 1: 60 to 1033

Score	Expect	Method	Identities	Positives	Gaps	Frame
460 bits(1183)	7e-142()	Compositional matrix adjust.	344/1087(32%)	533/1087(49%)	117/1087(10%)	
Query 87		CNWTGVACDGAGQVTSIQLPESKLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLG				146
Sbjct 60		C W G+ C+ GOV+ IQL QV+D F G +P CQWVGIKCNERGQVSEIQL-----QVMD-----FQGPLPA-----				89
Query 147		ELEQLVVSNSYFAGGIPSSLCNCSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNLL				206
Sbjct 90		-----++L ++ L+L NLTG+IP +GDLS LE-----TNLRQIKSLTLLSLSVNLTSVNLTSIPKELGDLSLE-----				123
Query 207		DGELPPSMALKKIMVVDLSCNQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRCK				266
Sbjct 124		-----V+DL+ N LSG IP +I L L+IL L N G IP ELG-----VLDLADNLSLGEIPVDIFKLLKLLKILSLNTNNLEGVIPSELGNLV				168
Query 267		NLTLNIFSNFTGEIPGELGELTNLEVMRLYKNA-LTSEIPRSLRRCVSLNLDLSMNQ				325
Sbjct 169		NL L +F N GEIP +GEL NLE+ R N L E+P + C SL+ L L+ NLIETLTFDNKLAGIERTIGELKNLEIFRAGGNKLRGELPWEIGNCESLVTLGLAETS				228
Query 326		LAGPIPELGEPLSLQRLSLHANRAGTVPASLTNLVNLITILELSENHLSGPLPASIGSL				385
Sbjct 229		L+G +P +G L +Q ++L+ + L+G +P + N L L L +N +SG +P S+G L LSGRPLASIGNLKKVQTIALYTSLLSGPIPDEIGNCTELQONLYLYQNSISGSIPVSMGRL				288
Query 386		RNLRRLLIVQNNLSLGGQIPASISNCTQLANASMSFNLFSGPLPAGLGRQLQSLMFLSLGQNS				445

Sbjct	289	+ L+ L++ N+L G+IP + C+ +S NL +G +P G L +L L L N KKLQSLLLWQNNLVGKIPTELGTCPFLVDLSENLLTGNIPRSFGNLPNLQELQLSVNQ	348
Query	446	LAGDIPDDLDFCGQLQKLDLSENSFTGGLSRLVQGGLNLTVLQQLGNALSGEIPEEIGNM L+G IP++L +C +L L++ N +G + L+G+L +LT+ N L+G IPE +	505
Sbjct	349	LSGTIPEELANCTKLTHLEIDNNQISGEIPLIGKLTSLTMFFAWQNQLTGIIPELSQC	408
Query	506	TKLISLKLGRNRFAGHVPASISNMSSLQLLDLGHNRDGVFPAEVFELRQLTILGAGSNR +L ++ L N +G +P I + +L L L N L G P ++ L L NR	565
Sbjct	409	QELQAIDLSYNNLSGSGIPNGIFEIRNLTKLLLLSNYLSGFIPPDIGNCTNLYRLRLNGNR	468
Query	566	FAGPIPDVANLRSLFSLDLSNMLNGTVPAAalgrldqlltldlSHNRLAGAIPGAVIAS AG IP + NL++L+F+D+S N L G +P + L +DL N L G +PG + S	625
Sbjct	469	LAGNIPAEIGNLKNLNFIDISENRLIGNIPPEISGCTSLEFVDLHNSGLTGGLPGTLPKS	528
Query	626	MSNVQMYLNLSNNAFTGAIPAEIGGLVMVQITIDLSNNQLSGGVPATLAGCKNLYSLDLSG + +++LS+N+ TG++P IG L + ++L+ N+ SG +P ++ C++L L+L	685
Sbjct	529	LQ----FIDLSDNSLTGSLPTGIGSLTELTKLNLAKNRFSGEIPREISSCRSLQLLNLGD	584
Query	686	NSLTGELPANLFPQLDLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPAL N TGE+P L L +LN+S N GEIP+ ++L ++ TLDVS N AG + L	745
Sbjct	585	NGFTGEIPNELGRIPSLAISLNLSCNHFTGEIPSRFSSLNLGTLDVSHNKLGNLN-VL	643
Query	746	ANLTALRSLNLSNTFEGPVPDGGVFRNLTMSSLQGNAGLCGGKLLAPCHGHAAGKKRVF A+L L SLN+S N F G +P+ FR L +S L+ N GL P +G +	805
Sbjct	644	ADLQNLVSLNISFNFEFSGELPNTLFFRKLPLSVLESNKGLFIST--RPENGIQTRHRSAV	701
Query	806	SRTGlvilvvlialstllllmvatillvsyrryrrkrrAADIAGDSPE---AAVVPELR T + ++VA +++ +A I G E V + +	862
Sbjct	702	KVT-----MSILVAASVVLVMAVYTLVKAQRITGKQEELDSWEVTLYQKL	747
Query	863	RFSYGLAAATNSFDQGNVIGSSNLSTVYKGVLAGDADGGMVAVKRLNLEQFPSKSDKC FS + +DLS S NVIG+ + VY+ + G +AVK++ + + ++	922
Sbjct	748	DFSIDDIVKNLTS---ANVIGTGSSGVVYRVVTIPS---GETLAVKKM---WSKEENRA	796
Query	923	FLTELATLSRLRHKNLARVVGYAWEAGKIKALVLDYMVNGDLGAIHGaaapppapSRW F +E+ TL +RH+N+ R++G+ +K L DY+ NG L +HG + W	982
Sbjct	797	FNSEINTLGSIRHRNIIRLLGWC-SNRNLKLLFYDYLPNGSLSSLLHGAGKGGSG--ADW	853
Query	983	TVRERLRVCVSAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARMLGVHL R V + VAH L YLH P++H DVK NVLL +E+ ++DFG A++ V	1042
Sbjct	854	EAR--YDVLGVAHALAYLHHDCLPPIHLHGDVKAMNVLLGSRFESYLADFGLAKI--VSG	909
Query	1043	PaaanaaaqstatssaFRGTGYMAPEFAYMRTVSTKVDVFSFGVLAMELFTGRRPTGTI + + + G+ GYMAPE A M+ ++ K DV+S+GV+ +E+ TG+ P	1102
Sbjct	910	EGVTDGDSKLSNRPLAGSYGYMAPEHASMQHITKSDVYSYGVVLEVLTKHPLDPD	969
Query	1103	EEDGVPLTLQQLVDNAVSRGLDGVHAVLDPRMKVATEADLSTAADVLAVALSCAAFEPAD G L Q V + ++ G +LDPR++ + + LAV+ C + + +D	1162
Sbjct	970	LPGGAHLV--QWVRDHLA-GKKDPREILDPRLRGRADPIMHEMLQTLAVSFLCVSNKASD	1026
Query	1163	RPDMGAV 1169 RP M +	
Sbjct	1027	RPMMKDI 1033	

RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1; AltName: Full=Protein BARELY ANY

MERISTEM 1; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **O49545.1** Length: 1003 Number of Matches: 2

Range 1: 69 to 961

Score	Expect	Method	Identities	Positives	Gaps	Frame
435 bits(1118) 2e-133() Compositional matrix adjust. 320/955(34%) 470/955(49%) 65/955(6%)						
Query	218	KGIMVVDLSCNQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFSNG + + +DLS LSG++ P++ L LQ L L EN SG IP E+ L LN+ +N	277			
Sbjct	69	RHVTSLDLSGLNLSGTLSPDVSHLRLLQNLSLAENLISGPPEISSLSGLRHLNLSNNV	128			
Query	278	FTGEIPGELGE-LTNLEVMRLYKNALITSEIPRSLRRCVSLNLDLSMNQLAGPIPELGE F G P E+ L NL V+ +Y N LT ++P S+ L +L L N AG IPP G	336			
Sbjct	129	FNGSFPDEISSGLVNLRVLDVYNNLTDGLPVSVTNTLQLRHLHLGGNYFAGKIPPSYGS	188			

Query 337 LPSLQRLSLHANLAGTVPASLNLVNLITILESE-NHLSGPLPASIGSLRNLRLIVQN 395
 P ++ L++ N L G +P + NL L L + N LP IG+L L R N
 Sbjct 189 WPVIEYLAVSGNELVGVKIPPEIGNLTTLRELYIGYYNAFEDGLPEIGNLSELVRFDGAN 248

Query 396 NSLSGQIPASISNCTQLANASMSFNL FSGPLPAGLGRQLSMLFSLGQNSLAGDIPDDL 455
 L+G+IP I +L + N+FSGPL LG L SL
 Sbjct 249 CGLTGEIPPEIGKQLDRTLFLQVNVFSGPLTWELGTLSL----- 289

Query 456 DCGQLQKLDLSENSFTGGLSRLVGLGNLTVLQLOGNALSGEIPEEIGNMTKLISLKLGR 515
 + +DLS N FTG + +L NLT+L L N L GEIPE IG++ +L L+L
 Sbjct 290 -----KSMDLNMMFTGEIPASFAELKNLTLNLFNRNKLHGEIPEFIGDLPELEVLQWE 344

Query 516 NRFAGHVPASISNMSSLQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRFAGPIPDAVA 575
 N F G +P + L L+DL N+L G P + +L L N G IPD++
 Sbjct 345 NNFTGSIPQKLGENGKLNLDLSSNKLGTLPNMCNKGKLETITLGNFLFGSIPDSL 404

Query 576 NLRSLFSLDLSSNMLNGTVPAAIgrldqlltldLSHNRLAGAIPIGAVIASMSNVQMYLNL 635
 SL+ + + N LNG++P L L +L ++L N L+G +P A S++ Q ++L
 Sbjct 405 KCESLTRIRMGENFLNGSIPKGLFGLPKLTQVELQDNYLSGELPVAGGVSVNLGQ--ISL 462

Query 636 SNNFTGAIPAEIGGLVMVQITDLSNNQSGVVPATLAGCKNLYSLDLSGNSLTGELPAN 695
 SNN +G +P IG VQ + L N+ G +P+ + + L +D S N +G +
 Sbjct 463 SNNQLSGPLPPAIGNFTGVQKLLLDGNKFGQPIPSEVQKQLQSKIDFSHNLFSGRIAPE 522

Query 696 LFPQLDLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPALANLTLRSLN 755
 + + LLT +++S N+L GEIP +I A+K + L++SRN G+IP +++++ +L SL+
 Sbjct 523 I-SRCKLLTFVDLSRNEISGEIPNEITAMKILNYLNLNRNHLVGSIPGSISSMQSLTSLD 581

Query 756 LSSNTFEGPVPDGGVFRNLTMSSLQGNAGLCGGKLLAPCH-GHAAGKKRVFSRTGlvilv 814
 S N G VP G F +S GN LC G L PC G A G + S+
 Sbjct 582 FSYNNLSGLVPGTGQFSYFNYSFLGNPDLG-GPYLGPCKDGVAKGGHSHSK----- 633

Query 815 vliaIstllllmvatillvsyrryrrrrrAADIAGDSPEAAVVPELRRFSYGLAAATN 874
 ++ S LLL++ ++ +A + S A + +R + +
 Sbjct 634 GPLSASMKLLLVLGLLVCISIAFAVVAIKARSLKKASESRAWRLTAFQRLDF-TCDDVLD 692

Query 875 SFDQGNVIGSSNLSTVYKGVLAGDADGGMVAVKRLNLEQFPSKSDKFLTELATLSRLR 934
 S + N+IG VYKGV+ G +VAVKRL S D F E+ TL R+R
 Sbjct 693 SLKEDNIIIGKGGAGIVYKGVMP----NGDLVAVKRLAAMSRGSSHDHGFNAEIQTLGRIR 748

Query 935 HKNLARVVGYAWEAGKIKALVLDYVMVNGDLGAIHGaaapppapSRWTVRERLRVCSV 994
 H+++ R++G+ + LV +YM NG L +HG +R+ ++ +
 Sbjct 749 HRHIVRLLGFC-SNHETNLLVYEMPNGSLGEVLHGKGGHLDWTRY-----KIALEA 801

Query 995 AHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARMLGVHLPaaanaaaqsta 1054
 A GL YLH +VH DVK +N+LLD ++EA V+DFG A+ L + ++
 Sbjct 802 AKGLCYLHHDCSPLIVHRDVKSNNILDLSNFEAHVADFLAKFL-----QDSGTSE 852

Query 1055 tssaFRGTVGYMAPEFAYMRTVSTKVDVFSFGVLAMELFTGRRPTGTIEEDGVPLTLQQL 1114
 SA G+ GY+APE+AY V K DV+SFGV+ +EL TGR+P G DGV + Q
 Sbjct 853 CMSAIAAGSYGYIAPEYAYTLKVDEKSDVYSFGVLLLELVTGRKPVGEF-GDGVDIV--QW 909

Query 1115 VDNVAVSRGLDGVHAVLDPRMKVATEADLSTAADVLAVALSCAAFEADRPDMGAV 1169
 V D V VLDPR+ + + V VA+ C + +RP M V
 Sbjct 910 VRKMTDSNKDSVLKVLDPRL---SSIPHEVTHVFYVAMLCVEEQAVERTMREV 961

Range 2: 25 to 606

Score	Expect	Method	Identities	Positives	Gaps	Frame
293 bits(751) 3e-82() Compositional matrix adjust. 194/594(33%) 299/594(50%) 18/594(3%)						
Query	46	QLEALLEFKN-- -GVADDPLGVLGWRVKGSGDGAVRGGALPRHCNWTGVACD-GAGQVT				101
Sbjct	25	+ ALL K G DD L+ W+V S C W GV CD VT				72
Query	102	SIQLPESKLRGALS PFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVSSNYFAGG				161
Sbjct	73	S+ L L G LSP + ++ LQ + L N +G IPP++ L L L +S+N F G				132
Query	162	SLDLSGLNLSGTLSPDVSHLRLQLNLSLAENLISGPPIPEISSLSGLRHLNLSNNVFNGS				
Query	162	IPSSLCN-CSAMWALALNVNNTGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLGKI				220
Sbjct	133	P + + + L + NNLTG +P + +L+ L N G++PPS I				192
Sbjct	133	FPDEISSGLVNLRLVLDVYNNNTGDLPVSVTNLTQLRHLHLGGNYFAGKIPPSYGSWPVI				

Query 221 MVVDLSCNQLSGSIPPEIGDLSNLQILQL-YENRFSGHIPRELGRCKNLTLLNIFSNGT 279
 + +S N+L G IPPEIG+L+ L+ L+ Y N F +P E+G L + + G T
 Sbjct 193 EYLAVSGNELVGVKIPPEIGNLTTLRELYIGYNAFEDGLPPEIGNLSELVRFDGANCGLT 252

Query 280 GEIPGELGELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELGEPS 339
 GEIP E+G+L L+ + L N + + L SL ++DLS N G IP EL +
 Sbjct 253 GEIPPEIGKQLKLDLTLFLQVNVFSGPLTWELGTLSSLKSMDSLNNMFTGEIPASFAELKN 312

Query 340 LQRSLHANRLAGTVPASLTNLVNLILELSENHLSGPLPASIGSLRNLRLRRLIVQNNSLS 399
 L L+L N+L G +P + +L L +L+L EN+ +G +P +G L + + +N L+
 Sbjct 313 LTLNLFNRNKLHGEIPEFIGDLPELEVLQWENNFTGSIPQKLGENGKLNLDLSSNKLT 372

Query 400 GQIPASISNCTQLANASMSFNLFSGPLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFDGCG 459
 G +P ++ + +L N G +P LG+ +SL + +G+N L G IP LF +
 Sbjct 373 GTLPPNMCSGNKLETITLGNFLFGSIPDSL GKCESLTRIRMGENFLNGSIPKGLFGLPK 432

Query 460 LQKLDLSENSFTGGLSRLVQGLGNLTVLQQLGNALSGEIPEEIGNMTKLISLKLGRNRFA 519
 L +++L +N +G L G NL + L N LSG +P IGN T + L L N+
 Sbjct 433 LTQVELQDNVLSGELPVAGGVSVNLGQISLNNQLSGPLPPAIGNFTGVQKLLLDGNKFQ 492

Query 520 GHVPASISNMSSLQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRFAGPIPDVANLRS 579
 G +P+ + + L +D HN G E+ + LT + N +G IP+ + ++
 Sbjct 493 GPIPSEVGLKQLSKIDFSHNLFSGRIAPEISRCKLLTFVDLSRNELSGEIPNEITAMKI 552

Query 580 LSFLLDSSNMLNGTVPAAIgrldqlltldLSHNRLAGAIPGAVIASMSNVQMYL 633
 L++L+LS N L G++P ++ + L +LD S+N L+G +PG S N +L
 Sbjct 553 LNYLNLNRNHLVGSIPGSISSMQSLTSLDFSYNNLSGLVPGTGQFSYFNYSFL 606

RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At3g47570; Flags: Precursor [Arabidopsis thaliana]
 Sequence ID: COLGP4.1 Length: 1010 Number of Matches: 2
 Range 1: 64 to 984

Score	Expect	Method	Identities	Positives	Gaps	Frame
431 bits(1107) 9e-132() Compositional matrix adjust. 340/968(35%) 499/968(51%) 67/968(6%)						
Query 216		KLKGMVVDLSCNQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFS	275			
Sbjct 64		K K + ++L QL G I P IG+LS L L LYEN F G KNKRVTHELELGRQLGGVISPSIGNLSFLVSLDYENFFGG-----	104			
Query 276		NGFTGEIPGELGELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELGE	335			
Sbjct 105		IP E+G+L+ LE + + N L IP L C LLNL L N+L G +P ELG -----TIPQEVGQLSRLEYLDMGINYLRGPIPLGLYNCSRLNLRRLDSNRLGGSVPSSELG	159			
Query 336		ELPSLQRSLHANRLAGTVPASLTNLVNLILELSENHLSGPLPASIGSLRNLRLRRLIVQN	395			
Sbjct 160		L +L +L+L+ N + G +P SL NL L L LS N+L G +P+ + L + L + SLTNLVQLNLYGNMRGKLPSTSLGNLTLLLEQLALSHNNLEGEIPSDVAQLTQIWSLQLVA	219			
Query 396		NLSGQIPASISNCTQLANASMSFNLFSGPLPAGLG-RLQSLMFLSLGQNSLAGDIPDDL	454			
Sbjct 220		N+ SG P ++ N + L + +N FSG L LG L +L+ ++G N G IP L NNFSGVFPALYNLSSLKLLGIGYNHFSGRLRPDLGILLPNLLSFNMGGNYFTGSIPTTL	279			
Query 455		FDCGQLQKLDLSENSFTGGLSRLVQGLGNLTVLQQLGNALS-----EIPPEEIGNMTKL	508			
Sbjct 280		+ L++L ++EN+ TG + G + NL +L L N+L E + N T+L SNISTLERLGMNENLGTGSIPTF -GNVPNLKLFLHTNSLGSDDRDLFLTSLTNCTQL	338			
Query 509		ISLKLGRNRFAGHVPASISNMSS-LQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRFA	567			
Sbjct 339		+L +GRNR G +P SI+N+S+ L LDLG + G P ++ L L L N + ETLGIGRNRLLGGDLPISIANLSAKLVTLDLGGTLISGSIPYDIGNLQKILIDQNMLS	398			
Query 568		GPIPDVANLRSLSFLDSSNMLNGTVPAAIgrldqlltldLSHNRLAGAIPGAVIASMS	627			
Sbjct 399		GP+P ++ L +L +L L SN L+G +PA +G + L TLDLS+N G +P S+ GPLPTSLGKLLNLRVLSLFSNRLSGGIPAFIGNMTMLETLDLSNNGFEGIVP----TSLG	454			
Query 628		NVQMYLNL--SNAFTGAIPAEIGGLVMVQITIDLSNNQLSGGVPATLAGCKNLYSLDLSG	685			
Sbjct 455		N L L +N G IP EI + + +D+S N L G +P + +NL +L L NCSHLLLELWIGDNKLNLTIPLEIMKIQLLRDMSGNSLIGSLPQDIGALQNLGTLTSLGD	514			
Query 686		NSLTGELPANLFPQLDLLLLNISGNDLGEIPADIAALKHIQTLDVSRNAFAGAIPPAL	745			
Sbjct 515		N L+G+LP L N L + +L + GN G+IP D+ L ++ +D+S N +G+IP NKLSGKLPQTLGNCLTM-ESLFLEGNLFYGDIP-DLKGLVGVKEVDLSNNDLSGSIPPEYF	572			

Query 746 ANLTALRSLNLSNSTFEGPVPDGGVFRNLTMSLQGNAGLCGGK ---LAPCHGHAAGKK 802
 A+ + L LNL N EG VP G+F N T S+ GN LCGG + L PC A
 Sbjct 573 ASFSKLEYLNLSFNLEGGKVPVKGIFENATTVSIVGNNDLCGGIMGFQPKCLSQAQPSV- 631

Query 803 RVFSRTGLvilvvlialstllllmvatillvsyrryrrrAAADIAGDSPEAAVVPELR 862
 V + + VV+ + LL++ + V+ R++++ + +P V+ E
 Sbjct 632 -VKKHSSRLKKVIGVSVGITLLLLFMASVTLIWLRKRKKNKETNNPTPSTLEVLHE-- 688

Query 863 RFSYGLAAATNSFDQGNVIGSSNLSTVYKGVLAGDADGGMVAVKRLNLEQFPSKSDKC 922
 + SYG L ATN F N++GS + TVYK +L + VVAVK LN+++ + K
 Sbjct 689 KISYGLRNATNGFSSNMVSGSGFVYKALLL TEKK - - VVAVKVLNMQR - -RGAMKS 743

Query 923 FLTELATLSRLRHKNLARVV - - -GYAWEAGKIKALVLDYMVNGDLGAIHGAAapppa 978
 F+ E +L +RH+NL +++ ++ + +AL+ ++M NG LD +H
 Sbjct 744 FMAECESLKDHRNLVKKLTACSSIDFQGNFRALYEFMPNGSLDMWHLHPEEVEEIH 803

Query 979 pSR-WTVRERLRVCSVAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARM 1037
 PSR T+ ERL + + VA L YLH P+ HCD+KPSNVLLD D A VSDFG AR+
 Sbjct 804 PSRTLTLERLNIADVASVLDYLHVHCHEPIAHCDLKPSNVLLDDDLTAHVSDFLARL 863

Query 1038 LGVHLPaaanaaaqstatssaFRGTGYMAPEFAYMRTVSTKVDFVFSFGLAMELFTGRR 1097
 L + + +S+ RGT+GY APE+ S DV+SFG+L +E+FTG+R
 Sbjct 864 - - -LLKFDEESFFNQLSSAGVVRTIGYAAPEYGVGGQPSINGDVYSFGILLLEMFTGKR 919

Query 1098 PTGTIEEDGVPLTLQQLVDNAV - SRGLDGV - HAVLDPKMKVATEADLSTAADVLAVALSC 1155
 PT E G TL +A+ R LD V ++L ++V + V V L C
 Sbjct 920 PTN - -ELFGNFTLNSYTKSALPERILDIVDESILHIGLRVGFVP - VECLTMVFEVGLRC 976

Query 1156 AAFEPADR 1163
 P +R
 Sbjct 977 CEESPMNR 984

Range 2: 27 to 616

Score	Expect	Method	Identities	Positives	Gaps	Frame
293 bits(751) 3e-82() Compositional matrix adjust. 224/631(35%) 315/631(49%) 51/631(8%)						
Query 48	EALLEFKNGVADDPLGVLGWRVKGSGDGAVRGGALPRHCNWTGVACDGAGQ-VTSIQLP					106
Sbjct 27	+ALL+FK+ V++D VL+ W + P CNW GV C + VT ++L QALLQFKSQVSEDKRVVLSWN - - - - -HSFPL - CNWKGVTCGRKNKRVTHLELG					74
Query 107	ESKLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVSSNYFAGGIPSSL					166
Sbjct 75	+L G +SP +GN+S L +DL N F G IP ++G+L LE L + NY G IP L RLQLGGVISPSIGNLSFLVSLDLYENFFGGTIPQEVGQLSRLEYLDMGINYL RGP I PLGL					134
Query 167	CNCSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLKGIMVVDLS					226
Sbjct 135	NCS + L L+ N L G++PS +G L+NL Y NN+ G+LP S+ L + + LS YNCSRLLNLRDLSNRLLGGSVPSELGSLTNLVLQNLNLYGNMNRGKLP TSLGNLTLLEQLALS					194
Query 227	CNQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFSNFTGEIPGEL					286
Sbjct 195	N L G IP ++ L+ + LQL N FSG P L +L LL I N F+G + +L HNNLEGEIPSDVAQLTQIWSLQLVANNFSGVFPALYNLSSLKLLGIGYNHFSGRLRPDL					254
Query 287	GELT-NLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELGEPLSLQRLSL					345
Sbjct 255	G L NL + N T IP +L +L L ++ N L G IP G +P+L+ L L GILLPNLLSFMGGNYFTGSIPTTLSNISTLERLGMNENL TGSIP - TFGNVPNLKLLFL					313
Query 346	HANRLAG - - - - -TVPASLTNLVNL TLELSENHLSGPLPASIGSLR-NLRLIVQNNSL					398
Sbjct 314	H N L SLTN L L + N L G LP SI +L L L + + HTNSLGSDDRDLFLTSLTNTCTQLETLGIGRNLGGDLPISIANLSAKLVTLDLGGTLI					373
Query 399	SGQIPASISNCTQLANASMSFNLFSGPLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFCG					458
Sbjct 374	SG IP I N L + N+ SGPLP LG+L +L +LSL N L+G IP + + SGSIPYDIGNLINLQKILIQNMLSGPLPTSLGKLLNLRYSLSFNRSLSGGIPAFIGNMT					433
Query 459	QLQKLDLSENSFTGGLSRLVGLGNLTVLQQLGNALSGEIPEEIGNMTKLISLKLGRNRF					518
Sbjct 434	L+ LDLS N F G +P +GN + L+ L +G N+ MLETLDLSNNGF - - - - -EGIVPTSLGNCSHLELWIGDNKL					469
Query 519	AGHVPASISNMSSLQLLDLGHNRDGVFPAEVFELRQLTILGAGSNRFAGPIPDVANLR					578
Sbjct 470	G +P I + L LD+ N L G P ++ L+ L L G N+ +G +P + N NGTIPLEIMKIQLLRDMSGNSLIGSLPQDIGALQNLGTL SLGDNKLSGKLPQTLGNCL					529

Query 579 SLSFLDLSSNMLNGTVPAAAlgrldqlltldlSHNRLAGAIIPGAVIASMSNVQMYLNLSSN 638
 ++ L L N+ G +P L L + +DLS+N L+G+IP AS S ++ YLNLS N
 Sbjct 530 TMESLFLEGNLFYGDIP-DLKGVLGVKEVDLSNNDLSGSIP-EYFASFASKLE-YLNLSFN 586

Query 639 AFTGAIPAEIGGLVMVQTIDL-SNNQLSGGV 668
 G +P + G T+ + NN L GG+
 Sbjct 587 NLEGKVPVK-GIFENATTVSIVGNNDLCCGI 616

RecName: Full=Leucine-rich repeat receptor-like protein kinase PEPR2; AltName: Full=Elicitor peptide 1 receptor 2; Short=PEP1
 receptor 2; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **Q9FZ59.1** Length: 1088 Number of Matches: 1
 Range 1: 33 to 1069

Score	Expect	Method	Identities	Positives	Gaps	Frame
431 bits(1109)	3e-131()	Compositional matrix adjust.	330/1124(29%)	540/1124(48%)	90/1124(8%)	
Query 49	ALLEFKNGVADDPLGVLAGWRVKGSGDGAVRGGALPRHCNWTGVACDGAGQVTSIQLPES					108
Sbjct 33	ALLSLLKHFDKVPLEAVASTWKENTSE-----TTPCNNWFGVICDLSGNV-----					77
Query 109	KLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVVSSNYFAGGIPSSLCN					168
Sbjct 78	-----VETLNLASGLSGQLGSEIGELKSLVTLDSLNSFSGLLPSTLGN					122
Query 169	CSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNNDGELPPSMALKKGIMVVDLSCN					228
Sbjct 123	CTSLEYLDLSNNDFSGEVDPDIFGSLQNLTF--YLDR-----N					158
Query 229	QLSGSIPPEIGDLSNLQILQLYENRFGSHIPRELGRCKNLTLLNIFSNFTGEIPGELGE					288
Sbjct 159	NLSGLIPASVGGELIELVDLRMSYNNLSGTIPELLGNCCKLEYLALNNKLNGLSPASLYL					218
Query 289	LTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELDELPSLQRLSLHAN					348
Sbjct 219	LENLGEFVSNNSLGGRLHFGSSNCKKLVSLDLSFNDFQGGVPPPEIGNCSSLHSLVMVKC					278
Query 349	RLAGTVPASLTNLVNLITILELSENHLSGPLASIGSLRNLRLRRLIVQNNSLSGQIPASISN					408
Sbjct 279	NLTGTIPSSMGMLRKVSVIDLSDNRLSGNIPQELGNCSSLETLKLNDNQLQGEIPPALSK					338
Query 409	CTQLANASMSFNLFSGPLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFDGQQLKLDLSEN					468
Sbjct 339	LKKLQSLLELFFNKLSGEIPIGIWKIQSLTQMLVYNNLTGELPVEVTQLKHLKKTTFN					398
Query 469	SFTGGLSRLVQGLNLTVLQQLGNALSGEIPEEIGNMTKLISLKLGRNRFAGHVPASISN					528
Sbjct 399	GFYGDIPMSLGNRSLEEVDLLGNRFTGEIPPHLCHGQKLRFLILGSNQLHGKIPASIRQ					458
Query 529	MSSLQLLDLGHNRDLGVFPAEVEFELRQLTILGAGSNRFAGPIPDVANLRSLSFLDLSSN					588
Sbjct 459	CKTLERVRLLEDNKLSGVLP-EFPESLSLSYVNLGNSFEGSIPRSLGSCKNLLTIDLSQN					517
Query 589	MLNGTVPAAAlgrldqlltldlSHNRLAGAIIPGAVIASMSNVQMYLNLSSNAFTGAIPAEI					648
Sbjct 518	KLTGLIPPELGNLQSLGLLNLSHNYLEGPLPSQL--SGCARLLYFDVGSNSLNGSIPSSF					575
Query 649	GGLVMVQTIDLSSNQLSGGVPATLAGCKNLYSLDLSGNSLTGELPANLFPQLDLLTTLNI					708
Sbjct 576	RSWKSLSLTVLSDNNFLGAIPOFLAELDRISDLRIARNAFGGKIPSSVGLLKSRLRYGLDL					635
Query 709	SGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPALANLTALRSLNLSNNTFEGVPVDPG					768
Sbjct 636	SANVFTGEIPTTLGALINLERLNISSNKLTPGL-SVLQSLKSLNQVDVSYNQFTGPIPVN					694
Query 769	GVFRNLTMSSLQGNAGLCCGKLLAPCHGHAAGKRVFSRTGlvilvvlialstllllmva					828
Sbjct 695	LLSNS---SKFSGNPDLG---IQASYSVSAIRKEF-KSCKGQVKLSTWKIALIAAGSS					746

Query 829 tillvsyrryrrkrAAADIAGDSPEAAVVVPELRRFSYQGLAAATNSFDQGNVIGSSNLS 888
 +L +L +A ++ E ++ AAT++ D +IG
 Sbjct 747 LSVLALLFALFLVLCRCKRGTKEDANTLAEGLSLLLKNVLAATDNLDDKYIIRGAHG 806

Query 889 TVYKGVLAGDADGGMVAVKRLNLEQFPSKSDKCFTELATLSRLRHKNLARVVGAWEA 948
 VY+ L G AVK+L + +++++ E+ T+ +RH+NL R+ + W
 Sbjct 807 VVYRASLG----SGEEYAVKKLIFAEH-IRANQNMKREIETIGLVRHRNLIRLERF-WMR 860

Query 949 GKIKALVLDYMVNGDLGAIHGaaappapSRWTVRERLRVCVSAHGLVYLHSGYDFP 1008
 + ++ YM NG L +H G W+ R + + ++HGL YLH P
 Sbjct 861 KEDGLMLYQYMPNGSLHDVLRHGNQGEAVLD--WSA--RFNIALGISHGLAYLHHDCHPP 916

Query 1009 VVHCDVKPSNVLLDGDWEARVSDFGTARMLGVHLPaaanaaaqstatssaFRGTVGYMAP 1068
 ++H D+KP N+L+D D E + DFG AR+L ST +++ GT GY+AP
 Sbjct 917 IHRDIKIPENILMDSMEPHIGDFGLARILD-----DSTVSTATVTGTGYIAP 965

Query 1069 EFAYMRTVSTKVDVFSFGVLAMELFTGRRPTG-TIEEDGVPLTLQQLVDNAVSRGLDGVH 1127
 E AY S + DV+S+GV+ +EL TG+R + ED ++ + V ++ D
 Sbjct 966 ENAYKTVRSKESDVYSYGVVLELVTGKRALDRSFPEDINIVSWVRSLSSYEDEDDTAG 1025

Query 1128 AVLDPRM--KVATEADLSTAADVLAVALSCAAFEPADRPDMGAV 1169
 ++DP++ ++ A V +AL C P +RP M V
 Sbjct 1026 PIVDPKLVDELDTKLRQAIQVTDLALRCTDKRPENRPSMRDV 1069

RecName: Full=MDIS1-interacting receptor like kinase 2; Short=AtMIK2; AltName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g08850; Flags: Precursor [Arabidopsis thaliana]
 Sequence ID: **Q8VZG8.3** Length: 1045 Number of Matches: 2
 Range 1: 117 to 1040

Score	Expect	Method	Identities	Positives	Gaps	Frame
428 bits(1101) 1e-130() Compositional matrix adjust. 315/964(33%) 483/964(50%) 75/964(7%)						
Query 241		LSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFSNFGTGEIPGELGELTNLEVMRLYKN				300
Sbjct 117		L NL + L NRFSG I GR L ++ N GEIP ELG+L+NL+ + L +N LPNLTFVDLSMNRFSGTISPLWGRFSKLEYFDLSINQLVGEIPPELGDSLNLDTLHLVEN				176
Query 301		ALTSEIPRSLRRCVSLNLDLSMNLQLAGPIPELPSLQRLSLHANRLAGTVPASLTN				360
Sbjct 177		L IP + R + + + N L GPIP G L L L L N L+G++P+ + N KLNLSIPSEIGRLTKVTEIAIYDNLTLTGPISSFGNLTCLVNLVLFINSLSGSIPSEIGN				236
Query 361		LVNLTILELSENHLSGPLPASIGSLRNLRLIVQNNLSLGGIPASISNCTQLANASMSFN				420
Sbjct 237		L NL L L N+L+G +P+S G+L+N+ L + N LSG+IP I N T L S+ N LPNLRELCLDRNNTLTKIPSSFGNLTLLNMVFENQLSGEIPPEIGNMTALDTLSLHTN				296
Query 421		LFSGPLPAGLGRQLSLMFLSLGQNSLAGDIPDDLFDGQQLKLDLSENSFTGGLSRLVGQ				480
Sbjct 297		+GP+P+ LG +++L L L N L G IP +L + + L++SEN TG + G+ KLTGPIPSTLGNIKTLAVLHLYLNQLNGSIPPELGEMESMIDLEISENKLTPVDPDSFGK				356
Query 481		LGNLTVLQLQGNALSGEIPEEIGNMTKLISLKLGRNRFAGHVPASISNSSLQLLDLGHN				540
Sbjct 357		L L L L+ N LSG IP I N T +L L+L N F G +P +I L+ L L N LTALEWFLRDNQLSGPIPPGIANSTELTVLQLDTNNTGFLPDTICRGGKLENLTLDDN				416
Query 541		RLDGVFPAEVFELRQLTILGAGSNRFAGPIPDVANLRSLSFLDLSSNMLNGTVPAAIgr				600
Sbjct 417		+G P + + + L + N F+G I +A +L+F+DLS+N +G + A + HFEGVPVKSLRDCKSLIRVRFKGNFSFGDISEAFGVYPTLNFIDLSSNNFHHGQLSANWEQ				476
Query 601		ldqlltldLSHNRLAGAIP-----GAVIASMSNVQMY--LNLSNN				638
Sbjct 477		+L+ LS+N + GAIP G + S+SN+ L L+ N SQKLVAFILSNNSITGAIPPEIWNMTQLSQLDLSSNRITGELPESISNINRISKLQLNGN				536
Query 639		AFTGAIPAEIGGLVMVQTIDLSNNQLSGGVPATLAGCKNLYSLDLSGNLSTGELPANLFP				698
Sbjct 537		+G IP+ I L ++ +DLS+N+ S +P TL LY ++LS N L +P L RLSGKIPSGIRLLTNLEYLDLSSNRFSEIPPTLNNLPRLYYMNLSRNDLQDTIPEGL-T				595
Query 699		QLDLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPALANLTALRSLNLSS				758
Sbjct 596		+L L L++S N LDGEI + +L++++ LD+S N +G IPP+ ++ AL +++S KLSQLQMLDLSYNQLDGEISSQFRSLQNLERLDLSHNNLSGQIPPSFKDMLALTHVDVSH				655
Query 759		NTFEGVPDGGVFRNLTMSLQGNAGLCGG---KLLAPCHGHAAGKKRVFSRTGlvilv				814
Sbjct		N +GP+PD FRN + +GN LCG + L PC + KK R ++ ++				

Sbjct 656 NNLQGPIDNAAFRAPPDAFEAGNKGKCLCGSVNTTQGLKPC-SITSSKKSHKDRNLIYYL 714

Query 815 vliaIstllllmvatillvsyrryrrkrAADIAGDSPEAAVVPELRRFSYGQLAAATN 874
V I + ++L + A I + +R ++ D + E + + Y ++ AT

Sbjct 715 VPIIGAIILSVCAGIFICFRKRTKQIEEHTD-SESGGETLSIFSGDKVRYQEIKATG 773

Query 875 SFDQGNVIGSSNLSTVYKGVLAGDADGGMVVAVKRLNLEQFPKSD----KCFLTELATL 930
FD +IG+ VYK L ++AVK+LN S S+ + FL E+ L

Sbjct 774 EFDPKYLIGTGGHGKVKAKLPN-----AIMAVKKNLNETTDSISNPSTKQEFLEIRAL 828

Query 931 SRLRHKNLARVVGVAWEAGKIKALVLDYMVNGDLGAIHGaaappapSRWTVRERLRV 990
+ +RH+N+ ++ G+ + LV +YM G L + A + R+ V

Sbjct 829 TEIRHRNVVKLFGFC-SHRRNTFLVYEYMERGSLRKVLENDDEAKKLDWKG-----RINV 882

Query 991 CVSVAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARMLGVHLPaaanaa 1050
VAH L Y+H +VH D+ N+LL D+EA++SDFGTA++L

Sbjct 883 VKGVAHALSYMHDRSPAIVHRDISSGNILLGEDYEAKISDFGTAKL-----K 931

Query 1051 qstatssaFRGTVGYMAPEFAYMRTVSTKVDFVFSFGLAMELFTGRRP-----TGTEIED 1105
++ SA GT GY+APE AY V+ K DV+SFGVL +E+ G P T +

Sbjct 932 PDSSNWSAVAGTYGYVAPELAYAMKVTEKCDVYSFGVLTLEVIKGEHPGDLVSTLSSSP 991

Query 1106 GVPLTLQQLVDNAVSRGLDGVHAVLDPKMKVATEADLSTAADVLAVALSCAAFEPADRPD 1165
L+L+ + D H + +P ++ E ++L VAL C +P RP

Sbjct 992 DATLSLKSISD-----HRLPEPTPEIKEE-----VLEILKVALLCLHSDPQARPT 1036

Query 1166 MGAV 1169
M ++

Sbjct 1037 MLSI 1040

Range 2: 85 to 665

Score	Expect	Method	Identities	Positives	Gaps	Frame
352 bits(904) 1e-102() Compositional matrix adjust. 227/608(37%) 317/608(52%) 28/608(4%)						
Query 89	WTGVACD	GAGQVTSIQLPESKLRGALS	PF-LGNI	STLQVIDL	TSNAFAGGIPPQLGRLGE	147
Sbjct 85	WGVAC	G + + L + + G F ++ L +DL+ N F+G I P GR +	WYGVAC-SLGS	IIRLNLTNTGIEGTFEDFPFSSLPNLT	FVDLSMNRFSGTISPLWGRFSK	143
Query 148	LEQLVSSNYFAGGIPSSLCNCSAMWALALNVN	LTGAIPSCIGDLSNLEIFEAYLNNLD				207
Sbjct 144	LEYFDLSINQLVGEIPELGLSNLDTLHLVENKLN	GSIPSEIGRLTKVTEIAIYDNL				203
Query 208	GELPPSMAKLKGIMVVDLSCNQLSGSIPPEIGDLSN	LQILQLYENRFSGHIPRELGRCKN				267
Sbjct 204	GPISPSFGNLT	TKLVNLYLFINSLSGSIPSEIGNLPNRELCLDRN	NLTGKIPSSFGNLKN			263
Query 268	LTLNIFSNFTGEIPGELGELTNLEVMRLYKNAL	TSEIPRSLRRCVSLNLDLSMNOLA				327
Sbjct 264	VTLNMFENQLSGEIPPEIGNMTALDTLSLHTNKL	TGPIPSTLGNIKTLAVLHLYLNQLN				323
Query 328	GPIPELGEPSLQRLSLHANRLAGTVPASLTNLV	NLTILELSENHLSGPLPASIGSLRN				387
Sbjct 324	GSIPPELGEMESMIDLEISENKLTPVPDSFGKLT	ALEWFLFRDNQLSGPIPPGIANSTE				383
Query 388	LRLIVQNNLSGQIPASISNCTQLANASMSFNL	FSGPLPAGLGRQLQSLMFLSLGQNSLA				447
Sbjct 384	LTVLQLDTNFTGFLPDTICRGGKLENLTLDDNH	FEGVPKSLRDKSLIRVRFKGNFS				443
Query 448	GDIPDDLFDGQQLKLDLSENSFTGGLSRLVGL	GNLTVLQLOGNALSGEIPEEIGNMTK				507
Sbjct 444	GDI + L +DLS N+F G LS Q L L N+++G IP EI NMT+	GDISEAFGVYPTLNFIDLSNNNFHGQLSANWEQSQKLVAFILSNNSITGAIPEIWNMTQ				503
Query 508	LISLKLGRNRFAGHVPASISNSSLQLLDLGHNR	LDGVFPAEVFELRQLTILGAGSNRFA				567
Sbjct 504	LSQLDLSSNRITGELPESISNIRISKLQLNGNR	LSGKIPSGIRLLTNLEYLDLSSNRFS				563
Query 568	GPIPDVANLRSLSFLDLSSNMLNGTVPAAI	grldqlltldLSHNRLAGAIPGAIVASMS				627
Sbjct 564	SEIPPTLNNLPRLYMNL	SRNDLQTIPEG-----LTKLS				598
Query 628	NVQMYLNL	SNAFTGAIPAEIGGLVMVQITDLSNNQLSGGVPATLAGCKNLYSLDLSGNS				687
	+QM L+LS N G I ++ L ++ +DLS+N LSG +P + L +D+S N+					

Sbjct 599 QLQM-LDLSYNQLDGEISSQFRSLQNLERLDLSHNNLSGQIPPSFKDMLALTHVDVSHNN 657
 Query 688 LTGELPAN 695
 L G +P N
 Sbjct 658 LQGPIPDN 665

RecName: Full=LRR receptor-like serine/threonine-protein kinase EFR; AltName: Full=Elongation factor Tu receptor; Short=EF-Tu receptor; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **COLGT6.1** Length: 1031 Number of Matches: 2
 Range 1: 84 to 983

Score	Expect	Method	Identities	Positives	Gaps	Frame
404 bits(1037)	1e-121()	Compositional matrix adjust.	318/956(33%)	460/956(48%)	101/956(10%)	
Query 253	RFSGHIPRELGRCKNLTLLNIFSNQFTGEIPGELGELTNLEVMRLYKNAITSEIPRSLRR					312
Sbjct 84	+ +G I +G L LLN+ N F IP ++G L L+ + + N L IP SL KLTGVISPSIGNLSFLRLLNLADNSFGSTIPQKVGRLFRLQYLNMSYNLLEGRIPSSLSN					143
Query 313	CVSLLNLDLSMNQLAGPIPELQELPSLQRLSLHANRLAGTVPASLTNLVNLITILELSEN					372
Sbjct 144	C L +DLS N L +P ELG L L L L N L G PASL NL +L L+ + N CSRLSTVDLSSNHLGHGVPSLGLSLSKLAIDLKSKNLTGNFPASLGNLTSLQKLDFAYN					203
Query 373	HLSGPLPASIGSLRNLRLRLIVQNSLSGQIPASISNCTQLANASMSFNLFSGPLPAGLGR					432
Sbjct 204	+ G +P + L + + NS SG P ++ N + L + S++ N FSG L A G QMRGEIPDEVARLTQMVFFQIALNSFSFGGFPALYNISSLESLSLADNSFSGNLRADFGY					263
Query 433	LQSLMFLSL-GQNSLAGDIPDDLFDGQQLQKLDLSENSFTGGLSRLVQGQGNLTVLQLQG					491
Sbjct 264	L + L G N G IP L + L++ D+S N +G + G+L NL L ++ LLPNLRRLLLGTNQFTGAIPKTLANISSLERFDISSNYLSGSIPLSFGKLRNLWWLGIRN					323
Query 492	-----NALSGEIPEEIGNM-TKLISLKLGRNRFAG					520
Sbjct 324	N L GE+P I N+ T L SL LG+N +G NSLGNNSSSGLEFIGAVANCTQLEYLDVGYNRLGGELPASIANLSTTLTSLFLGQNLISG					383
Query 521	HVPASISNMSSLQQLDLGHNRLDGVFPAEVFEQRILGAGSNRFAGPIPAVANLRSL					580
Sbjct 384	+P I N+ SLO L L N L G P +L L ++ SN +G IP N+ L TIPHDIGNLVSLQELSLETNMLSGELPVSFGKLLNLQVVDLYSNAISGEIPSYFGNMTRL					443
Query 581	SFLDLSSNMLNGTVPAAIgrldqlltldLSHNRLAGAIPIGAVIASMSNVQMYLNLNSNAF					640
Sbjct 444	L L+SN +G +P +LGR LL L + NRL G IP ++ S Y++LSNN QKLHLNSNSFHGRIPQSLGRCRYLLDLWMDTNRLNGTIPQEILQIPS--LAYIDLNNFL					501
Query 641	TGAIPAEIGGLVMVQITDLSNNQLSGGVPATLAGCKNLYSLDLSGNSLTGELPANLFPQL					700
Sbjct 502	TG P E+G L ++ + S N+LSG +P + GC ++ L + GNS G +P TGHFPEEVGKLELLVGLGASYNKLSGKMPQAIGGCLSMEFLLFMQGNISFDGAIP-----					554
Query 701	DLLTTLNISGNDLDGEIPADIAALKHIQTLDVSRNAFAGAIPPALANLTALRSLNLSNT					760
Sbjct 555	DI+ L ++ +D S N +G IP LA+L +LR+LNLS N -----DISRLVSLKNVDFSNNNLSGRIPRYLASLPSLRNLNLSMKN					595
Query 761	FEQVVPDGGVFRNLTMSLQGNAGLCGG---KLLAPCHGHAAGKRVFSRTGLvllvlli					817
Sbjct 596	FEG VP GVFRN T S+ GN +CGG L PC A+ +KR ++ + FEGRVPTTGVFRNATAVSFVGNNTNICGGVREMQLKPCIVQASPRKRKPLSVRKKVVSIGIC					655
Query 818	alstllllmvatillvsyrryrkrAAADIAGDSPEAAVVPELRRFSYGQLAAATNSFD					877
Sbjct 656	LLL++ L + + ++K A+D G+ ++ + + SY +L +AT+ F IGIASLLLIIIVASLCWFMKRKKKNNASD--GNPSDSTTLGMFHEKVSYEELHSATSRFS					713
Query 878	QGNVIGSSNLSTVYKGVLAGDADGGMVAVKRLNLEQFPSKSDKCFLTELATLSRLRHKN					937
Sbjct 714	N+IGS N V+KG+L + +VAVK LNL + K F+ E T +RH+N STNLIGSGNFGNVFKGLLGP---NKLVAVKVLNL--LKHGATKSFMAECETFKGIRHRN					768
Query 938	LARVVGYA---WEAGKIKALVLDYMVNGDLGAIHGaaappapSR-WTVRERLRVCV					992
Sbjct 769	L+++ E +ALV ++M G LD + SR T E+L + + LVKLITVCSLSDSEGNDFRALVYEFMPKGSMDMWLQLEDLERVNDHSRSLTPAEKLNIAI					828
Query 993	SVAHGLVYLHSGYDFPVVHCDVKPSNVLLDGDWEARVSDFGTARMLGVHLPaaanaaaqs					1052
Sbjct 829	VA L YLH PV HCD+KPSN+LLD D A VSDFG A++L + + + DVASALEYLVHCHDPVAHCDIKPSNILLDDDLTAHVSDFGLAQLLYKY----DRESFLN					884

Query 1053 tatssaFRGTVGYMAPEFAYMRTVSTKVDVFSFGVLAMELFTGRRPTGTIEEDGVPLTLQ 1112
 +S+ RGT+GY APE+ S + DV+SFG+L +E+F+G++PT
 Sbjct 885 QFSSAGVRGTIGYAAPEYGMGGQPSIQGDVYSFGILLLEMFSGKKPT----- 931

Query 1113 QLVDNAVSRGLDGVHAVLDPRMKVATEADLSTAAD-----VLAVALSCAAFEPADR 1163
 D + + G +H+ + T + S A D VL V + C+ P DR
 Sbjct 932 ---DESFA-GDYNLHSYTKSILSGCTSSGGSNAIDEGLRLVLQVGIKCSEEYPRDR 983

Range 2: 32 to 601

Score	Expect	Method	Identities	Positives	Gaps	Frame
282 bits(721) 4e-78() Compositional matrix adjust. 202/583(35%) 294/583(50%) 23/583(3%)						
Query 47	LEALLEFKNGVADD-PLGVLGWRVVGKSGDGAVRGGALPRHCNWTGVACDGAGQ-VTSIQ	104				
Sbjct 32	MQALLEFKSQVSENNKREVLASWNHSSP-----FCNWIGVTCGRRRERVISLN	79				
Query 105	LPESKLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVSSNYFAGGIPS	164				
Sbjct 80	LGGFKLTGVISPSIGNLSFLRLLNLADNSFGSTIPQKVGRLFRLQYLNMSYNLLEGRIPS	139				
Query 165	SLCNCSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLKGIMVVD	224				
Sbjct 140	SLSNCSRLSTVDLSSNHLGHGVPSELGSLSKLAILDLSKNNLTGNFPASLGNLTSLQKLD	199				
Query 225	LSCNQLSGSIPEIGDLSNLQILQLYENRFSGHIPRELGRCKNLTLLNIFSNFTGEIPG	284				
Sbjct 200	FAYNQMRGEIPDEVARLTQMVFQIALNSFSGGFPPALYNISSLESLSLADNSFSGNLRA	259				
Query 285	ELGELTNLEVMRLY-KNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELGELPSLQRL	343				
Sbjct 260	DFGYLLPNLRRLLLTGNQFTGAIPKTLANISSLERFDISSNYLSGSIPLSFGKLRNLWWL	319				
Query 344	SLHANRLAGTVP-----ASLTNLVNLTIELSENLHSGPLPASIGSLR-NLRRILVQNN	396				
Sbjct 320	GIRNNSLGNSSSGLEFIGAVANCTQLEYLDVGYNRLGGELPASIANLSTTLTSLFLGQN	379				
Query 397	SLSGQIPASISNCTQLANASMSFNLFSGPLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFD	456				
Sbjct 380	LISGTIPHDIGNLVSQELSLETNMLSGELPVSFGLKLLNLQVVDLYSNAISGEIPSYFGN	439				
Query 457	CGQLQKLDLSENSFTGGLSRLVQQLGNLTVLQLOGNALSGEIPEEIGNMTKLISLKLGRN	516				
Sbjct 440	MTRLQKHLHNSNSFHGRIPQSLGRCRYLLDLWMDTNRLNGTIPQEILQIPSLAYIDLSNN	499				
Query 517	RFAGHVPAISNMSSLQLLDLGHNRDGVFPAEVFELRQLTILGAGSNRFAGPIPDAVAN	576				
Sbjct 500	FLTGHFPEEVGKLELLVGLGASYNKLSGKMPQAIGGCLSMEFLLFMQGNISFDGAIPD-ISR	558				
Query 577	LRSLSFLDLSSNMLNGTVPAAlgrldqlltldlSHNRLAGAIP 619					
Sbjct 559	LVSLKNVDFSNMNSGRIPRYLASLPSLRNLNLSMKNKFEGRVP 601					

RecName: Full=Brassinosteroid LRR receptor kinase BRL3; AltName: Full=BRI1-like receptor kinase 3; Flags: Precursor [Oryza sativa Japonica Group]

Sequence ID: **Q6ZCZ2.1** Length: 1214 Number of Matches: 1

Range 1: 43 to 1177

Score	Expect	Method	Identities	Positives	Gaps	Frame
408 bits(1048) 1e-121() Compositional matrix adjust. 383/1183(32%) 553/1183(46%) 117/1183(9%)						
Query 53	FKNG-VADDPLGVLGWRVVGKSGDGAVRGGALPRHCNWTGVACDGAGQVTSIQLPESKLR	111				
Sbjct 43	FKDASVAADPGGALAGW-----ANSTTPGSP----CAWAGVSC-AAGRVRALDLSGMSLS	92				

Query	112	GALSPFLGNISTLQVI-DLTSNAFAGGIP- - - -PQLGRLEGEQLVSSNYFAGGIPSS- G L + DL NAF G + P+ L ++ +SSN F G +P +	165
Sbjct	93	GRLRLDALLALSALRRDLRGNAFHGDLRHSPPRAAPCALVEVDISSNTFNGTLPRAF	152
Query	166	LCNCSAMWALALNVNNTLGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLGIMVVDL L +C + L L+ N+LTG L L++ L++ G L S+ GI ++L	225
Sbjct	153	LASCGGLQTLNLSRNSLTGGGYPFPPSLRRLDMSRNQLSD-AGLLNYSLTGCHGIQYLN	211
Query	226	SCNQLSGSIPPEIGDLSNQLIQLYENRFSGHIPRELGRCK- -NLTLNIFSNNGFTGEIP S NQ +GS+P + + + +L L N SG +P NLT L+I N F+ +I	283
Sbjct	212	SANQFTGSLP-GLAPCTEVSVDLDSWNLMMSGVLPFRFVAMAPANLTYLSIAGNNFSMDIS	270
Query	284	G-ELGELTNLEVMRLYKNALTSE-IPRSLRRCVSLNLDLSMNQL-AGPIPELGELPSL E G NL ++ N L S +PRSL C L LD+S N+L +GPIP L EL +L	340
Sbjct	271	DYEFGGCANLTLDDWSYNRLRSTGLPRSLVDCRRLEALDMSGNKLKLSGPIPTFLVELQAL	330
Query	341	QRLSLHANRLAGTVPASLTNLVN-LTILELSENHLSGPLPASIGSLRNLRLIVQNNLS +RLSL NR G + L+ L L L+LS N L G LPAS G R L+ L + NN LS	399
Sbjct	331	RRLSLAGNRFTGEISDKLSILCKTLVELDLSSNQLIGSLPASFGQCRFLQVLDLGNQLS	390
Query	400	GQ-IPASISNCTQLANASMSFNLFSG- -PLPAGLGRQLQSLMFLSLGQNSLAGDI -PDDL G + I+N + L + FN +G PLPA R L + LG N G+I PD	455
Sbjct	391	GDFVETVITNISSLRVLRPFNNITGANPLPALASRCPLLEVIDLGSNEFDGEIMPDLCS	450
Query	456	DCGQLQKLDLSENSFTGGLSRLVGLGNLTVLQQLQGNALSGEIPEEIGNMTKLISLKLGR L+KL L N G + + NL + L N L G+IP EI + KL+ L L	515
Sbjct	451	SLPSLRKLLLPNNYINGTVSSLSNVCNLESIDLFSNLLVGQIPPEILFLLKLVLDLVA	510
Query	516	NRFAGHVPASIS-NMSSLQLLDLGHNRDLGVFPAEVFELRQLTILGAGSNRFAGPIPD N +G +P N ++L+ L + +N G P + L L N G IP	574
Sbjct	511	NNLSGEIPDKFCFNSTALETLVISYNSFTGNIPESITRCVNIWLSLAGNNLTSIPSGF	570
Query	575	ANLRSLSFLDLSSNMLNGTVPAALgrldqlltldlSHNRLAGAIP- - - - -GAVIASMS NL++L+ L L+ N L+G VPA LG L+ LDL+ N L G IP G + ++	627
Sbjct	571	GNLQNLAILQLNKNSLSGKVPaelGSCSNLIWLDLNSNELTGTIPPQLAAQAGLITGAIV	630
Query	628	NVQMYLNLNSNAFTGAI PAEIGGLVMVQTTIDLSNNQLSGGVPATLAGCKNLYS- - - - - + + + L N A G I G V+ + +D+ ++L+ L +Y+	680
Sbjct	631	SGKQFAFLRNEA- -GNICPGAG- -VLFEFLDIRPDRLANFPAVHLCSSSTRIYTGTTVYTF	686
Query	681	- - - - -LDLSGNSLTGELPANLFPQLDLLTTLNISGNDLDGEIPADIAALKHIQTLDV LDLS NSLTG +PA+ F + L LN+ N+L G IP LK I LD+	732
Sbjct	687	RNNGSMIFLDLSYNSLTGTIPAS- FGNMTYLEVLNLGHNELTGAIPDAFTGLKIGALDL	745
Query	733	SRNAFAGAIPPALANLTALRSLNLSNNTFEGVPVDPGGVFRNLTMSLQGNAGLCCGKLLA S N G IPP L L ++S+N G +P G S + N+GLCG L	792
Sbjct	746	SHNHLTGVIIPPGFGLHFLADFVDSNNLTGEIPTSGQLITFPASRYENNSGLCGIPLN	805
Query	793	PCHGHAAGK- - - - -KRVFSRTglvilvvlialstllllmvatillvsyrryrrkrAA H AG R F+R + + V L L LL++ L ++ ++ +A	845
Sbjct	806	CVHNSGAGGLPQTSYGHNRNFARQSVFLAVTLSVLILFSLIIHYKWLKFKHKNKTKEIQAG	865
Query	846	- - -DIAGDSPEA- - - - -AVVPELRRFSYGQLAAATNSFDQGNVIGSSNLS + G S + A+ LR+ ++ L ATN F +IGS	888
Sbjct	866	CSESLPGSSKSSWKLSGIGEPSLNMAIFENPLRKLTFSDLHQATNGFCAETLIGSGGFG	925
Query	889	TVYKGVLAGDADGGMVAVKRLNLEQFPSKSDKCFTELATLSRLRHKNLARVVGAWEA VYK L G +VAVK+L F + D+ F E+ T+ +++H+NL ++GY +	948
Sbjct	926	EVYKAKL- - - -KDGNI VAVKKL- -MHFTGQGDREFTAEMETIGKIKHRNLVPLLGYC-KI	978
Query	949	GKIKALVLDYMVNGDLGAIHGaaappapSRWTVRERLRVCSVAHGLVYLHSGYDFP G + LV +YM NG LD +H A W R++ + + A GL +LH	1008
Sbjct	979	GDERLLVYEYMKNGSLDFVLHDKGEANMDL- -NWATRKK- -IAIGSARGLAFLHHSVPH	1034
Query	1009	VVHCDVKPSNVLLDGDWEARVSDFGTARMLGV- -HLPaaanaaaqstatssaFRGTVGY ++H D+k SNVLLDG+++A VSDFG AR++ HL T S GT GY	1065
Sbjct	1035	IIHRDMKSSNVLLDGNFDAYVSDFGMARLMNALDSHL- - - - -TVSMLSGTPGY	1082
Query	1066	MAPEFAYMRTVSTKVDVFSFVGLAMELFTGRRPTGTIEEDGVPLT- -LQQLVDNAVSRGL + PE+ +TK DV+S+GV+ +EL TG++P E L ++Q+V++ S	1123
Sbjct	1083	VPPEYQDFRCTTKGDVYSYGVVLELLTGKKPIDPTEFGDSNLVGVWVKQMVEDRCSE- -	1140
Query	1124	DGVHAVLDPKMKVATEADLSTAADVLAVALSCAAFEPADRPDM 1166 + DP + T ++L L +A C +P RP M	
Sbjct	1141	- - - - -IYDPTLMATTSSLELEL-YQYLKIAICRCLDDQPNRRPTM 1177	

RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM2; AltName: Full=Protein BARELY ANY

MERISTEM 2; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **Q9M2Z1.1** Length: 1002 Number of Matches: 3

Range 1: 50 to 957

Score	Expect	Method	Identities	Positives	Gaps	Frame
402 bits(1033)	3e-121()	Compositional matrix adjust.	314/1001(31%)	483/1001(48%)	97/1001(9%)	
Query 173		WALALNVNNTGAI PSCIGDLSNLEIFEAYLNNDGELPPSMAKLKGMVVDLSCNQLSG				232
Sbjct 50		WNLSTTFCSWTGV--TCDVSLRHVTSLDLSGLNLSGTLSSDVAHLPLLQNLSLAANQISG				107
Query 233		SIPPEIGDLSNLQILQLYENRFSGHIPRELGR-CKNLTLLNIFSNFTGEIPGELGELTN				291
Sbjct 108		PIPPQISNLYELRHLNLSNNVFNFSFPDELSSGLVNLRLVLDLYNNLTGDLPVSLTNLTQ				167
Query 292		LEV MRLYKNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPEL GELPSLQRLSL-HANRL				350
Sbjct 168		LRHLHLGGNYFSGKIPATYGTWPVLEYLAVSGNELTGKIPPEIGNLTTLRELYIGYYNAF				227
Query 351		AGTVPASLTNLVNL TIELESENHLSGPLPASIGSLRNLRRLLVQNNSLSGQIPASISNCT				410
Sbjct 228		ENGLPPEIGNLSELVRFDAANCGLTGEIPPEIGKQLKLDLTLFQVNAFTGTITQELGLIS				287
Query 411		QLANASMSFNLFSGPLPAGLGRQLSMLFSLGQNSLAGDIPDDLDFCGQLQKLDLSENF				470
Sbjct 288		SLKSMDLNMMFTGEIPTSFSQLKNLTLLNLFNRKLYGAIPEFIGEMPELEVLQWENNF				347
Query 471		TGGLSRLVGQLGNLTVLQQLGNALSGEIPEEIGNMTKLISLKLGRNRFAGHVPASISNMS				530
Sbjct 348		TGSI PQKLGENGRVLIDLSSNKLGTLPNMCSGNRLMTLITLGNFLFGSIPDSL GKCE				407
Query 531		SLQLLDLGHNRDLGVFPAEVEFELRQLTILGAGSNRFAGPIPDVANLR-SLSFLDLSSNM				589
Sbjct 408		SLTRIRMGENFLNGSIPKELFGLPKLSQVELQDNYLTGELPISGGGVSGDLGQISLSNNQ				467
Query 590		LNGTVPAAlgrldqlltldlSHNRLAGAI P GAVIASMSNVQMYLNLNNAFTGAIPAEIG				649
Sbjct 468		LSGSLPAA-----IGNLSGVQKLL-LDGNKFSGSIPEIG				501
Query 650		GLVMVQTIDLSNNQLSGGVPATLAGCKNLYSLDLSGNSLTGELPANLFPQLDLLTTLNIS				709
Sbjct 502		RLQQLSKLDFSHNLSFGRIAPEISRCKLLTFVDLSRNELSGDIP-NELTGMKILNYLNLS				560
Query 710		GNDLDGEIPADIAALKHIQTLDVSRNAFAGAI P PALANLTALRSLNLSNTFEGPVPDGG				769
Sbjct 561		RNHLVGSIPVTIASMQSLTSVDFSYN-----NLS-----GLVPSTG				596
Query 770		VFRNLTMSLQGNAGLCGGKLLAPC-HGHAAGKRVFSRTGlvilvvlialstllllmva				828
Sbjct 597		QFSYFNYTSFVGNSHLC-GPYLGPCKGKTHQSHVKPLSAT-----TKLLLLVLG				643
Query 829		tillvsyrryrrkrAADIAGDSPEAAVVPELRRFSYQLAAATNSFDQGNVIGSSNLS				888
Sbjct 644		LLFCSMVFAIVAIKARSLRNASEAKAWRLTAFQRLDF-TCDDVLDLSEKEDIIGKGGAG				702
Query 889		TVYKGVLAGDADGGMVAVKRLNLEQFPKSDKCFLELATSRLRHKNLARVVGAWEA				948
Sbjct 703		IVYKGTMP----KGDLVAVKRLATMSHGSSHDHGFNAEIQTLGRIRHRHIVRLLGFC-SN				757
Query 949		GKIKALVLDYMVNGDLGAIHG GaaappapSRWTVRERLRVCSVAHGLVYLHSGYDFP				1008
Sbjct 758		HETNLLVYEYMPNGSLGEVLHGKGGH----HWNT--RYKIALEAAKGLCYLHHDCSPL				811
Query 1009		VVHCDVKPSNVLLDGDWEARVDFGTARMLGVHLPaaanaaaqstatssaFRGTVGYMAP				1068
Sbjct 812		IVHRDVKSNNILLDSNFEAHVADFLAKFL-----QDSGTSECMSAIAGSYGYIAP				862
Query 1069		EFAYMRTVSTKVDVFSFGVLAMELFTGRRPTGTIEEDGVPLTLQQLVDNAVSRGLDGVHA				1128

E+AY V K DV+SFGV+ +EL TG++P G DGV + Q V + D V
 Sbjct 863 EYAYTLKVKDEKSDVYSFGVLLLELITGKPKVGEF-GDGVDIV--QWVRSMTDSNKDCVLK 919
 Query 1129 VLDPRMKVATEADLSTAADVLAVALSCAAFEAPDRPDMGAV 1169
 V+D R+ + + + V VAL C + +RP M V
 Sbjct 920 VIDLRL---SSVPVHEVTHVFYVALLCVEEQAVERTMREV 957

Range 2: 27 to 607

Score	Expect	Method	Identities	Positives	Gaps	Frame
290 bits(743) 4e-81() Compositional matrix adjust. 193/593(33%) 306/593(51%) 17/593(2%)						
Query	46	QLEALLEFKNGVA-DDPLGVLGWRVVGKSGDGA VRGGALPRHCNWTGVACDGA-GQVTSI				103
Sbjct	27	+L ALL K+ D+ +L W + + C+WTGV CD + VTS+ ELHALLSLKSSFTIDEHSPLLTWNLSST-----FCSWTGVTCDVSLRHVTSL				74
Query	104	QLPESKLRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVSSNYFAGGIP				163
Sbjct	75	L L G LS + ++ LQ + L +N +G IPPQ+ L EL L +S+N F G P DLSGLNLSGTLSSDVAHLPLLQNLSLAANQISGPIPPQISNLYELRHLNLSNNVFNFSFP				134
Query	164	SSLCN-CSAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNNLDGELPPSMAKLGIMV				222
Sbjct	135	L + + L L NNLTG +P + +L+ L N G++P + + DELSGGLVNLRLVLDLYNNLTGDLPVSLNLTQLRHLHLGGNYFSGKIPATYGTWPVLEY				194
Query	223	VDLSCNQLSGSIPPEIGDLSNLQILQL-YENRFSGHIPRELGRCKNLTLLNIFSNFTGE				281
Sbjct	195	+ +S N+L+G IPPEIG+L+ L+ L+ Y N F +P E+G L + + G TGE LAVSGNELTGKIPPEIGNLTTRELYIGYNAFENGLPPEIGNLSELVRFDAANCGLTGE				254
Query	282	IPGELGELTNLEVMRLYKNALTSEIPRSLRRCVSLNLDLSMNQLAGPIPELGEPLSLQ				341
Sbjct	255	IP E+G+L L+ + L NA T I + L SL ++DLS N G IP +L +L IPPEIGKLQKLDLTLFQVNAFTGTITQELGLISSLKSMDLSNNMFTGEIPTSFSQLKNLT				314
Query	342	RLSLHANRLAGTVPASLTNLVNLTIELSENHLSGPLPASIGSLRNLRLIVQNNLSLQ				401
Sbjct	315	L+L N+L G +P + + L +L+L EN+ +G +P +G L L + +N L+G LLNLFNRNKLYGAIPEFIGEMPELEVLQWENNFTGSIPQKLGENGRLVILDLSNKLGT				374
Query	402	IPASISNCTQLANASMSFNLSFGPLPAGLGRQLQSLMFLSLGQNSLAGDIPDDLFCGQLQ				461
Sbjct	375	+P +++ + +L N G +P LG+ +SL + +G+N L G IP +LF +L LPPNMCSGNRLMTLITLGNFLFGSIPDSLKCESLTRIRMGENFLNGSIPKELFGLPKLS				434
Query	462	KLDLSENSFTGGLSRLVGQL-GNLTVLQIQGNALSGEIPEEIGNMTKLISLKLGRNRFAG				520
Sbjct	435	+++L +N TG L G + G+L + L N LSG +P IGN+++ + L L N+F+G QVELQDNYLTGELPISGGGVSGDLGQISLSNQLSGSLPAAIGNLSGVQKLLLDGNKFSG				494
Query	521	HVPASISNMSSLQLLDLGHNRLDGVFPAEVFELRQLTILGAGSNRFAGPIPAVANLRSL				580
Sbjct	495	+P I + L LD HN G E+ + LT + N +G IP+ + ++ L SIPPEIGRLQQLSKLDFSHNLFSGRIAPEISRCKLLTFVDLSRNELSGDIPNELTGMKIL				554
Query	581	SFLDLSSNMLNGTVPAAIgrldqlltldlSHNRLAGAI PGAVIASMSNVQMYL 633				
Sbjct	555	++L+LS N L G++P + + L ++D S+N L+G +P S N ++ NYLNLNRNHLVGSIPVTIASMQSLTSVDFSYNNLSGLVPSTGQFSYFNYSFV 607				

Range 3: 251 to 610

Score	Expect	Method	Identities	Positives	Gaps	Frame
155 bits(393) 3e-37() Compositional matrix adjust. 111/367(30%) 175/367(47%) 38/367(10%)						
Query	110	LRGALSPFLGNISTLQVIDLTSNAFAGGIPPQLGRLGELEQLVSSNYFAGGIPSSLCNC				169
Sbjct	251	L G + P +G + L + L NAF G I +LG + L+ + +S+N F G IP+S LTGEIPPEIGKLQKLDLTLFQVNAFTGTITQELGLISSLKSMDLSNNMFTGEIPTSFSQL				310
Query	170	SAMWALALNVNLTGAIPSCIGDLSNLEIFEAYLNN-----				205
Sbjct	311	+ L L N L GAIP IG++ LE+ + + NN KNLTLNLFNRNKLYGAIPEFIGEMPELEVLQWENNFTGSIPQKLGENGRLVILDLSNKL				370
Query	206	LDGELPPSMAKLGIMVVDLSCNQLSGSIPPEIGDLSNLQILQLYENRFSGHIPRELGRG				265
Sbjct	371	L G LPP+M +M + N L GSIP +G +L +++ EN +G IP+EL LTGTLPPNMCSGNRLMTLITLGNFLFGSIPDSLKCESLTRIRMGENFLNGSIPKELFGL				430

Query 266 KNLTLNIFSNFTGEIP-----GELGELTNLEVMRLYKNALTSEIPRSLRRCVSLLN 318
 L+ + + N TGE+P G+LG+++ L N L+ +P ++ +
 Sbjct 431 PKLSQVELQDNYLTGELPIISGGGVSGDLGQIS-----LSNNQLSGSLPAAIGNLSGVQK 484

Query 319 LDLSMNQLAGPIPPLEGELPSLQRLSLHANRLAGTVPASLTNLVNLTIELSEHLSGPL 378
 L L N+ +G IPPE+G L L +L N +G + ++ LT ++LS N LSG +
 Sbjct 485 LLLDGNKFGSIPPEIGRLQQLSKLDFSHNLFSGRIAPEISRCKLLTFVDLSRNELSGDI 544

Query 379 PASIGSLRNLRLIVQNNSLSGQIPASISNCTQLANASMSFNLFSGPLPAGLGRLOSLMF 438
 P + ++ L L + N L G IP +I++ L + S+N SG +P+ G+ +
 Sbjct 545 PNELTGMKILNLYLNLSRNHLVGSIPVTIASMQSLTSVDFSYNNLSGLVPS-TGQFSYFNY 603

Query 439 LSLGQNS 445
 S NS
 Sbjct 604 TSFVGNS 610

Taxonomy

Reports

Lineage

Organism	Blast Name	Score	Number of Hits	Description
Mesangiospermae	flowering plants		101	
.Poaceae	monocots		14	
..Oryza sativa	monocots		13	
...Oryza sativa Japonica Group	monocots	2138	12	Oryza sativa Japonica Group hits
...Oryza sativa Indica Group	monocots	265	1	Oryza sativa Indica Group hits
..Zea mays	monocots	353	1	Zea mays hits
.Arabidopsis thaliana	eudicots	947	74	Arabidopsis thaliana hits
.Ipomoea nil	eudicots	464	1	Ipomoea nil hits
.Glycine max	eudicots	400	2	Glycine max hits
.Medicago truncatula	eudicots	394	1	Medicago truncatula hits
.Solanum lycopersicum	eudicots	379	2	Solanum lycopersicum hits
.Solanum peruvianum	eudicots	379	1	Solanum peruvianum hits
.Daucus carota	eudicots	332	1	Daucus carota hits
.Lotus japonicus	eudicots	271	1	Lotus japonicus hits
.Solanum pimpinellifolium	eudicots	267	4	Solanum pimpinellifolium hits

Organism

Description	Score	E value	Accession
Oryza sativa Japonica Group (Japanese rice) [monocots]			
RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2; AltName: Full=Protein FLAGELLIN-SENSING 2 homolog; Short=OsFLS2; AltName: Full=Protein FLAGELLIN-SENSITIVE 2 homolog; Flags: Precursor [Oryza sativa Japonica Group]	2138	0.0	Q0JA29

Description	Score	E value	Accession
RecName: Full=Brassinosteroid LRR receptor kinase BRL3; AltName: Full=BR11-like receptor kinase 3; Flags: Precursor [Oryza sativa Japonica Group]	408	1e-121	Q6ZCZ2
RecName: Full=LRR receptor-like serine/threonine-protein kinase ER2; AltName: Full=ERECTA homolog 2; Short=ER homolog 2; Short=OsER2; AltName: Full=Receptor-like cytoplasmic kinase 85; Short=OsRLCK85; Flags: Precursor [Oryza sativa Japonica Group]	385	4e-115	I1Z695
RecName: Full=LRR receptor-like serine/threonine-protein kinase ER1; AltName: Full=ERECTA homolog 1; Short=ER homolog 1; Short=OsER1; AltName: Full=Receptor-like cytoplasmic kinase 204; Short=OsRLCK204; Flags: Precursor [Oryza sativa Japonica Group]	379	4e-113	Q69SP5
RecName: Full=LRR receptor-like serine/threonine-protein kinase SIK1; AltName: Full=ERECTA homolog 2; Short=ER homolog 2; Short=OsER2; AltName: Full=Stress-induced protein kinase 1; Short=OsSIK1; Flags: Precursor [Oryza sativa Japonica Group]	370	7e-110	Q658G7
RecName: Full=Probable inactive leucine-rich repeat receptor kinase XIAO; Flags: Precursor [Oryza sativa Japonica Group]	365	2e-106	G9LZD7
RecName: Full=Leucine-rich repeat receptor protein kinase MSL1; AltName: Full=MSP1 protein homolog 1; AltName: Full=MSP1-like protein 1; Flags: Precursor [Oryza sativa Japonica Group]	347	9e-99	Q7F8Q9
RecName: Full=Leucine-rich repeat receptor protein kinase MSP1; AltName: Full=Protein MULTIPLE SPOROCTE 1; Flags: Precursor [Oryza sativa Japonica Group]	323	3e-91	Q8RZV7
RecName: Full=Brassinosteroid LRR receptor kinase BRL2; AltName: Full=BR11-like receptor kinase 2; Flags: Precursor [Oryza sativa Japonica Group]	297	7e-83	Q7G768
RecName: Full=Receptor kinase-like protein Xa21; Contains: RecName: Full=Receptor kinase-like protein Xa21, processed; Flags: Precursor [Oryza sativa Japonica Group]	258	5e-70	Q2R2D5
RecName: Full=Leucine-rich repeat receptor-like kinase protein FLORAL ORGAN NUMBER1; Short=OsFON1; AltName: Full=CLV1-like LRR receptor kinase; Flags: Precursor [Oryza sativa Japonica Group]	257	5e-70	Q5Z9N5
RecName: Full=Brassinosteroid LRR receptor kinase BRL1; AltName: Full=BR11-like receptor kinase 1; Flags: Precursor [Oryza sativa Japonica Group]	245	3e-65	Q69JN6
Arabidopsis thaliana (thale cress) [eudicots]			
RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2; AltName: Full=Protein FLAGELLIN-SENSING 2; AltName: Full=Protein FLAGELLIN-SENSITIVE 2; Flags: Precursor [Arabidopsis thaliana]	947	0.0	Q9FL28
RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At2g33170; Flags: Precursor [Arabidopsis thaliana]	519	1e-163	O49318
RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At5g63930; Flags: Precursor [Arabidopsis thaliana]	514	5e-162	Q9LVP0
RecName: Full=LRR receptor-like serine/threonine-protein kinase RG1; AltName: Full=Protein RECEPTOR OF RGF1 4; AltName: Full=Protein RGF1 INSENSITIVE 1; AltName: Full=Protein ROOT CLAVATA-HOMOLOG1 2; Flags: Precursor [Arabidopsis thaliana]	502	3e-157	Q9LHP4
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase At1g17230; Flags: Precursor [Arabidopsis thaliana]	482	5e-150	Q9SHI2
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase RGI4; AltName: Full=Protein RECEPTOR OF RGF1 2; AltName: Full=Protein RGF1 INSENSITIVE 4; AltName: Full=Protein STERILITY-REGULATING KINASE MEMBER 2; Flags: Precursor [Arabidopsis thaliana]	460	7e-142	F4K6B8
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1; AltName: Full=Protein BARELY ANY MERISTEM 1; Flags: Precursor [Arabidopsis thaliana]	435	2e-133	O49545
RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At3g47570; Flags: Precursor [Arabidopsis thaliana]	431	9e-132	C0LGP4
RecName: Full=Leucine-rich repeat receptor-like protein kinase PEPR2; AltName: Full=Elicitor peptide 1 receptor 2; Short=PEP1 receptor 2; Flags: Precursor [Arabidopsis thaliana]	431	3e-131	Q9FZ59
RecName: Full=MDIS1-interacting receptor like kinase 2; Short=AtMIK2; AltName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g08850; Flags: Precursor [Arabidopsis thaliana]	428	1e-130	Q8VZG8
RecName: Full=LRR receptor-like serine/threonine-protein kinase EFR; AltName: Full=Elongation factor Tu receptor; Short=EF-Tu receptor; Flags: Precursor [Arabidopsis thaliana]	404	1e-121	C0LGT6
RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM2; AltName: Full=Protein BARELY ANY MERISTEM 2; Flags: Precursor [Arabidopsis thaliana]	402	3e-121	Q9M2Z1
RecName: Full=MDIS1-interacting receptor like kinase 1; Short=AtMIK1; AltName: Full=Leucine-rich repeat receptor-like protein kinase PXL2; AltName: Full=Protein PHLOEM INTERCALATED WITH XYLEM-LIKE 2; Flags: Precursor [Arabidopsis thaliana]	399	5e-120	Q9M0G7
RecName: Full=Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g24130; Flags: Precursor [Arabidopsis thaliana]	392	8e-118	Q9ZUI0
RecName: Full=Receptor-like protein kinase HSL1; AltName: Full=Protein HAESA-LIKE1; Flags: Precursor [Arabidopsis thaliana]	392	8e-118	Q9SGP2

Description	Score	E value	Accession
<u>RecName: Full=Serine/threonine-protein kinase BRI1-like 1; AltName: Full=BRASSINOSTEROID INSENSITIVE 1-like protein 1; Flags: Precursor [Arabidopsis thaliana]</u>	393	2e-116	Q9ZWC8
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase GSO2; AltName: Full=Protein EMBRYO SAC DEVELOPMENT ARREST 23; AltName: Full=Protein GASSHO 2; Flags: Precursor [Arabidopsis thaliana]</u>	385	4e-113	Q9FIZ3
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase GSO1; AltName: Full=Protein GASSHO 1; AltName: Full=Protein SCHENGEN 3; Flags: Precursor [Arabidopsis thaliana]</u>	383	3e-112	C0LQG5
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase ERECTA; AltName: Full=Protein QUANTITATIVE RESISTANCE TO PLECTOSPHERELLA 1; AltName: Full=Protein QUANTITATIVE RESISTANCE TO RALSTONIA SOLANACEARUM 1; AltName: Full=Protein TRANSPIRATION EFFICIENCY 1; Flags: Precursor [Arabidopsis thaliana]</u>	376	5e-112	Q42371
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase ERL2; AltName: Full=Protein ERECTA-like kinase 2; Flags: Precursor [Arabidopsis thaliana]</u>	373	5e-111	Q6XAT2
<u>RecName: Full=Putative receptor-like protein kinase At3g47110; Flags: Precursor [Arabidopsis thaliana]</u>	373	3e-110	Q9SD62
<u>RecName: Full=Leucine-rich repeat receptor-like protein kinase PEPR1; AltName: Full=Elicitor peptide 1 receptor 1; Short=PEP1 receptor 1; Flags: Precursor [Arabidopsis thaliana]</u>	374	6e-110	Q9SSL9
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI2; AltName: Full=Protein RECEPTOR OF RGF1 3; AltName: Full=Protein RGF1 INSENSITIVE 2; AltName: Full=Protein ROOT CLAVATA-HOMOLOG1 1; Flags: Precursor [Arabidopsis thaliana]</u>	374	8e-110	C0LGV1
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase ERL1; AltName: Full=Protein ERECTA-like kinase 1; Flags: Precursor [Arabidopsis thaliana]</u>	366	2e-108	C0LGW6
<u>RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At1g35710; Flags: Precursor [Arabidopsis thaliana]</u>	369	5e-108	Q9LP24
<u>RecName: Full=Receptor-like protein kinase BRI1-like 3; AltName: Full=BRASSINOSTEROID INSENSITIVE 1-like protein 3; Flags: Precursor [Arabidopsis thaliana]</u>	367	2e-107	Q9LJF3
<u>RecName: Full=Receptor protein-tyrosine kinase CEPR1; AltName: Full=Protein C-TERMINALLY ENCODED PEPTIDE RECEPTOR 1; AltName: Full=Protein XYLEM INTERMIXED WITH PHLOEM 1; Flags: Precursor [Arabidopsis thaliana]</u>	351	7e-103	Q9FGL5
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI5; AltName: Full=Protein RECEPTOR OF RGF1 5; AltName: Full=Protein RGF1 INSENSITIVE 5; Flags: Precursor [Arabidopsis thaliana]</u>	352	1e-102	C0LGF5
<u>RecName: Full=Leucine-rich repeat receptor protein kinase EMS1; AltName: Full=Protein EXCESS MICROSPOROCTES 1; AltName: Full=Protein EXTRA SPOROGENOUS CELLS; Flags: Precursor [Arabidopsis thaliana]</u>	353	3e-102	Q9LYN8
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase RGI3; AltName: Full=Protein RECEPTOR OF RGF1 1; AltName: Full=Protein RGF1 INSENSITIVE 3; Flags: Precursor [Arabidopsis thaliana]</u>	348	8e-101	C0LGR3
<u>RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g36180; Flags: Precursor [Arabidopsis thaliana]</u>	347	3e-100	C0LGS2
<u>RecName: Full=Receptor-like protein kinase HAIKU2; Flags: Precursor [Arabidopsis thaliana]</u>	344	3e-100	Q9LJM4
<u>RecName: Full=Leucine-rich repeat receptor-like protein kinase PXL1; AltName: Full=Protein PHLOEM INTERCALATED WITH XYLEM-LIKE 1; Flags: Precursor [Arabidopsis thaliana]</u>	345	4e-100	Q9FRS6
<u>RecName: Full=Receptor protein-tyrosine kinase CEPR2; AltName: Full=Protein C-TERMINALLY ENCODED PEPTIDE RECEPTOR 2; Flags: Precursor [Arabidopsis thaliana]</u>	341	3e-99	Q9C7T7
<u>RecName: Full=Leucine-rich repeat receptor-like tyrosine-protein kinase PXC3; AltName: Full=Protein PXY/TDR-CORRELATED 3; Flags: Precursor [Arabidopsis thaliana]</u>	332	7e-97	Q22938
<u>RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g12460; Flags: Precursor [Arabidopsis thaliana]</u>	319	3e-92	C0LGE4
<u>RecName: Full=Receptor-like protein kinase 7; Flags: Precursor [Arabidopsis thaliana]</u>	317	9e-91	F4I2N7
<u>RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM3; AltName: Full=Protein BARELY ANY MERISTEM 3; Flags: Precursor [Arabidopsis thaliana]</u>	308	2e-87	O65440
<u>RecName: Full=Receptor-like protein 52; Short=AtRLP52; Flags: Precursor [Arabidopsis thaliana]</u>	300	5e-86	Q7FZR1
<u>RecName: Full=Receptor-like protein 19; Short=AtRLP19; Flags: Precursor [Arabidopsis thaliana]</u>	295	7e-83	Q9ZUK3
<u>RecName: Full=Leucine-rich repeat receptor-like serine/threonine-protein kinase SKM1; AltName: Full=Protein STERILITY-REGULATING KINASE MEMBER 1; Flags: Precursor [Arabidopsis thaliana]</u>	295	7e-83	Q82318
<u>RecName: Full=Receptor-like protein 50; Short=AtRLP50; Flags: Precursor [Arabidopsis thaliana]</u>	288	5e-81	Q93YT3
<u>RecName: Full=Receptor-like protein 12; Short=AtRLP12; Flags: Precursor [Arabidopsis thaliana]</u>	286	9e-81	Q9C9H7

Description	Score	E value	Accession
<u>RecName: Full=Serine/threonine-protein kinase BRI1-like 2; AltName: Full=BRASSINOSTEROID INSENSITIVE 1-like protein 2; AltName: Full=Protein VASCULAR HIGHWAY 1; Flags: Precursor [Arabidopsis thaliana]</u>	287	2e-79	Q9ZPS9
<u>RecName: Full=Receptor-like protein 33; Short=AtRLP33; Flags: Precursor [Arabidopsis thaliana]</u>	277	2e-77	F4J8G2
<u>RecName: Full=Receptor-like protein 31; Short=AtRLP31; Flags: Precursor [Arabidopsis thaliana]</u>	274	1e-76	Q8RX63
<u>RecName: Full=Receptor protein kinase CLAVATA1; Flags: Precursor [Arabidopsis thaliana]</u>	274	1e-75	Q9SYQ8
<u>RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040; Flags: Precursor [Arabidopsis thaliana]</u>	267	3e-73	Q9LRT1
<u>RecName: Full=Receptor-like protein 35; Short=AtRLP35; Flags: Precursor [Arabidopsis thaliana]</u>	265	1e-72	Q9SRL7
<u>RecName: Full=Receptor-like protein kinase 5; AltName: Full=Protein HAESA; Flags: Precursor [Arabidopsis thaliana]</u>	264	4e-72	P47735
<u>RecName: Full=Receptor-like protein 38; Short=AtRLP38; Flags: Precursor [Arabidopsis thaliana]</u>	260	4e-72	Q9LS79
<u>RecName: Full=Receptor-like protein 53; Short=AtRLP53; Flags: Precursor [Arabidopsis thaliana]</u>	263	6e-72	Q9S9U3
<u>RecName: Full=Protein BRASSINOSTEROID INSENSITIVE 1; Short=AtBRI1; AltName: Full=Brassinosteroid LRR receptor kinase; Flags: Precursor [Arabidopsis thaliana]</u>	265	7e-72	Q22476
<u>RecName: Full=Receptor-like protein 32; Short=AtRLP32; Flags: Precursor [Arabidopsis thaliana]</u>	260	1e-71	Q9M9X0
<u>RecName: Full=Receptor-like protein 34; Short=AtRLP34; Flags: Precursor [Arabidopsis thaliana]</u>	262	1e-71	Q9SRL2
<u>RecName: Full=LRR receptor-like serine/threonine-protein kinase HSL2; AltName: Full=Protein HAESA-LIKE2; Flags: Precursor [Arabidopsis thaliana]</u>	262	1e-71	C0LGX3
<u>RecName: Full=Receptor-like protein 37; Short=AtRLP37; AltName: Full=Protein EMBRYO DEFECTIVE 2800; Flags: Precursor [Arabidopsis thaliana]</u>	258	3e-71	Q9LS80
<u>RecName: Full=Receptor like protein 23; Short=AtRLP23; Flags: Precursor [Arabidopsis thaliana]</u>	257	2e-70	O48849
<u>RecName: Full=Leucine-rich repeat receptor-like protein kinase TDR; AltName: Full=Protein PHLOEM INTERCALATED WITH XYLEM; AltName: Full=Tracheary element differentiation inhibitory factor receptor; Short=AtTDR; Short=TDIF receptor; Flags: Precursor [Arabidopsis thaliana]</u>	259	2e-70	Q9FII5
<u>RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase IRK; AltName: Full=Inflorescence and root apices receptor-like kinase; Flags: Precursor [Arabidopsis thaliana]</u>	257	5e-70	Q9LY03
<u>RecName: Full=Leucine-rich repeat receptor-like protein kinase PXC2; AltName: Full=Protein PXY/TDR-CORRELATED 2; Flags: Precursor [Arabidopsis thaliana]</u>	257	7e-70	Q9LZV7
<u>RecName: Full=Receptor-like protein 18; Short=AtRLP18 [Arabidopsis thaliana]</u>	254	1e-69	Q9ZUK7
<u>RecName: Full=Receptor-like protein 46; Short=AtRLP46; Flags: Precursor [Arabidopsis thaliana]</u>	253	2e-69	F4JGB6
<u>RecName: Full=Receptor-like protein 11; Short=AtRLP11; Flags: Precursor [Arabidopsis thaliana]</u>	251	5e-69	Q9C9H6
<u>RecName: Full=Receptor-like protein 42; Short=AtRLP42; AltName: Full=Protein RESPONSIVENESS TO BOTRYTIS POLYGALACTURONASES 1; Flags: Precursor [Arabidopsis thaliana]</u>	253	6e-69	Q9LJS0
<u>RecName: Full=Receptor-like protein 40; Short=AtRLP40; Flags: Precursor [Arabidopsis thaliana]</u>	253	6e-69	Q9LRW9
<u>RecName: Full=Tyrosine-sulfated glycopeptide receptor 1; AltName: Full=PSY1 receptor [Arabidopsis thaliana]</u>	253	4e-68	Q9C7S5
<u>RecName: Full=Receptor-like protein 41; Short=AtRLP41; Flags: Precursor [Arabidopsis thaliana]</u>	250	5e-68	Q9LJS2
<u>RecName: Full=Receptor-like protein 7; Short=AtRLP7; Flags: Precursor [Arabidopsis thaliana]</u>	251	6e-68	Q9C699
<u>RecName: Full=Receptor-like protein 36; Short=AtRLP36; Flags: Precursor [Arabidopsis thaliana]</u>	244	2e-67	Q1PEN0
<u>RecName: Full=Receptor-like protein 15; Short=AtRLP15; Flags: Precursor [Arabidopsis thaliana]</u>	245	5e-66	Q9C6A8
<u>RecName: Full=Receptor-like protein 13; Short=AtRLP13; Flags: Precursor [Arabidopsis thaliana]</u>	244	3e-65	Q9C6A6
<u>RecName: Full=Receptor-like protein 43; Short=AtRLP43; Flags: Precursor [Arabidopsis thaliana]</u>	238	4e-65	Q9LJW7
<u>RecName: Full=Receptor-like protein 49; Short=AtRLP49; Flags: Precursor [Arabidopsis thaliana]</u>	240	6e-65	Q9SVM3
<u>Ipomoea nil (Japanese morning glory) [eudicots]</u>			
<u>RecName: Full=Receptor-like protein kinase; Flags: Precursor [Ipomoea nil]</u>	464	2e-143	P93194

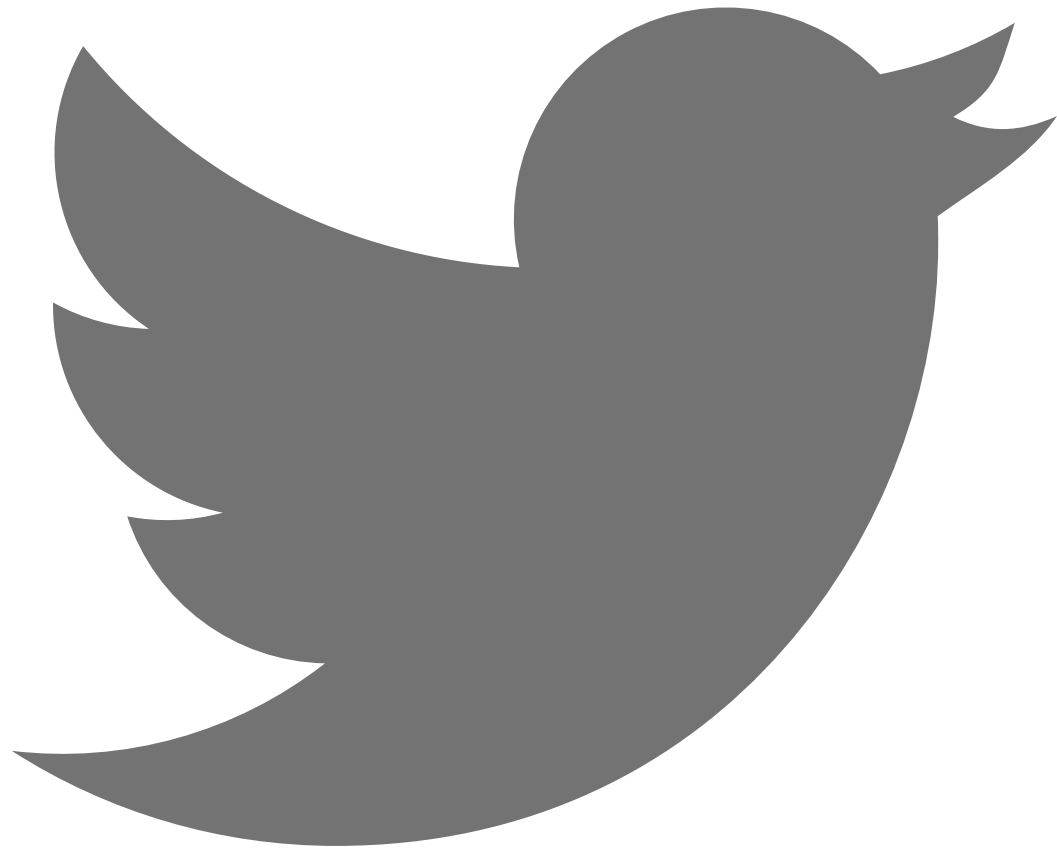
Description	Score	E value	Accession
Glycine max (soybean) [eudicots]			
RecName: Full=Leucine-rich repeat receptor-like kinase protein CLV1a; AltName: Full=CLAVATA1-like protein 1A; Short=GmCLV1A; Flags: Precursor [Glycine max]	400	6e-121	A0A0R0HPY5
RecName: Full=Leucine-rich repeat receptor-like kinase protein CLV1B; AltName: Full=CLAVATA1-like protein 1B; Short=GmCLV1B; AltName: Full=Nodule autoregulation receptor protein kinase; Short=GmNARK; AltName: Full=Protein NITRATE-TOLERANT SUPERNODULATING 1; Flags: Precursor [Glycine max]	394	3e-118	Q9M6A7
Medicago truncatula (barrel medic) [eudicots]			
RecName: Full=Leucine-rich repeat receptor-like kinase protein SUNN; AltName: Full=Protein SUPER NUMERIC NODULES; Flags: Precursor [Medicago truncatula]	394	1e-118	G7JIK2
Solanum lycopersicum (tomato) [eudicots]			
RecName: Full=Brassinosteroid LRR receptor kinase; AltName: Full=Altered brassinolide sensitivity 1; AltName: Full=Systemin receptor SR160; AltName: Full=tBRI1; Flags: Precursor [Solanum lycopersicum]	379	2e-111	Q8GUQ5
RecName: Full=Receptor-like protein EIX1; AltName: Full=EIX receptor 1; Flags: Precursor [Solanum lycopersicum]	265	2e-72	Q6JN47
Solanum peruvianum [eudicots]			
RecName: Full=Systemin receptor SR160; AltName: Full=Brassinosteroid LRR receptor kinase; Flags: Precursor [Solanum peruvianum]	379	2e-111	Q8L899
Zea mays [monocots]			
RecName: Full=Leucine-rich repeat receptor-like kinase protein THICK TASSEL DWARF1; AltName: Full=CLAVATA1-like protein; AltName: Full=CLV1 related kinase 5; Short=ZmKIN5; Flags: Precursor [Zea mays]	353	3e-103	P0DL10
Daucus carota (carrot) [eudicots]			
RecName: Full=Phytosulfokine receptor 1; Short=DcPSKR1; AltName: Full=Phytosulfokine LRR receptor kinase 1; Flags: Precursor [Daucus carota]	332	1e-95	Q8LPB4
Lotus japonicus [eudicots]			
RecName: Full=Leucine-rich repeat receptor-like kinase protein HAR1; AltName: Full=Protein HYPERNODULATION ABERRANT ROOT FORMATION 1; Flags: Precursor [Lotus japonicus]	271	2e-74	Q8GRU6
Solanum pimpinellifolium [eudicots]			
RecName: Full=Receptor-like protein 9DC3; Flags: Precursor [Solanum pimpinellifolium]	267	4e-74	Q5MR23
RecName: Full=Receptor-like protein 9DC1; Flags: Precursor [Solanum pimpinellifolium]	266	7e-74	P0DO05
RecName: Full=Receptor-like protein 9DC2; Flags: Precursor [Solanum pimpinellifolium]	266	7e-74	P0DO06
RecName: Full=Receptor-like protein Cf-9; Flags: Precursor [Solanum pimpinellifolium]	252	8e-69	Q40235
Oryza sativa Indica Group (long-grained rice) [monocots]			
RecName: Full=Receptor kinase-like protein Xa21; Contains: RecName: Full=Receptor kinase-like protein Xa21, processed; Flags: Precursor [Oryza sativa Indica Group]	265	3e-72	Q1MX30

Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
Mesangiospermae	101	12	
. Poaceae	14	3	
.. Oryza sativa	13	2	
... Oryza sativa Japonica Group	12	1	Oryza sativa Japonica Group hits
... Oryza sativa Indica Group	1	1	Oryza sativa Indica Group hits
.. Zea mays	1	1	Zea mays hits

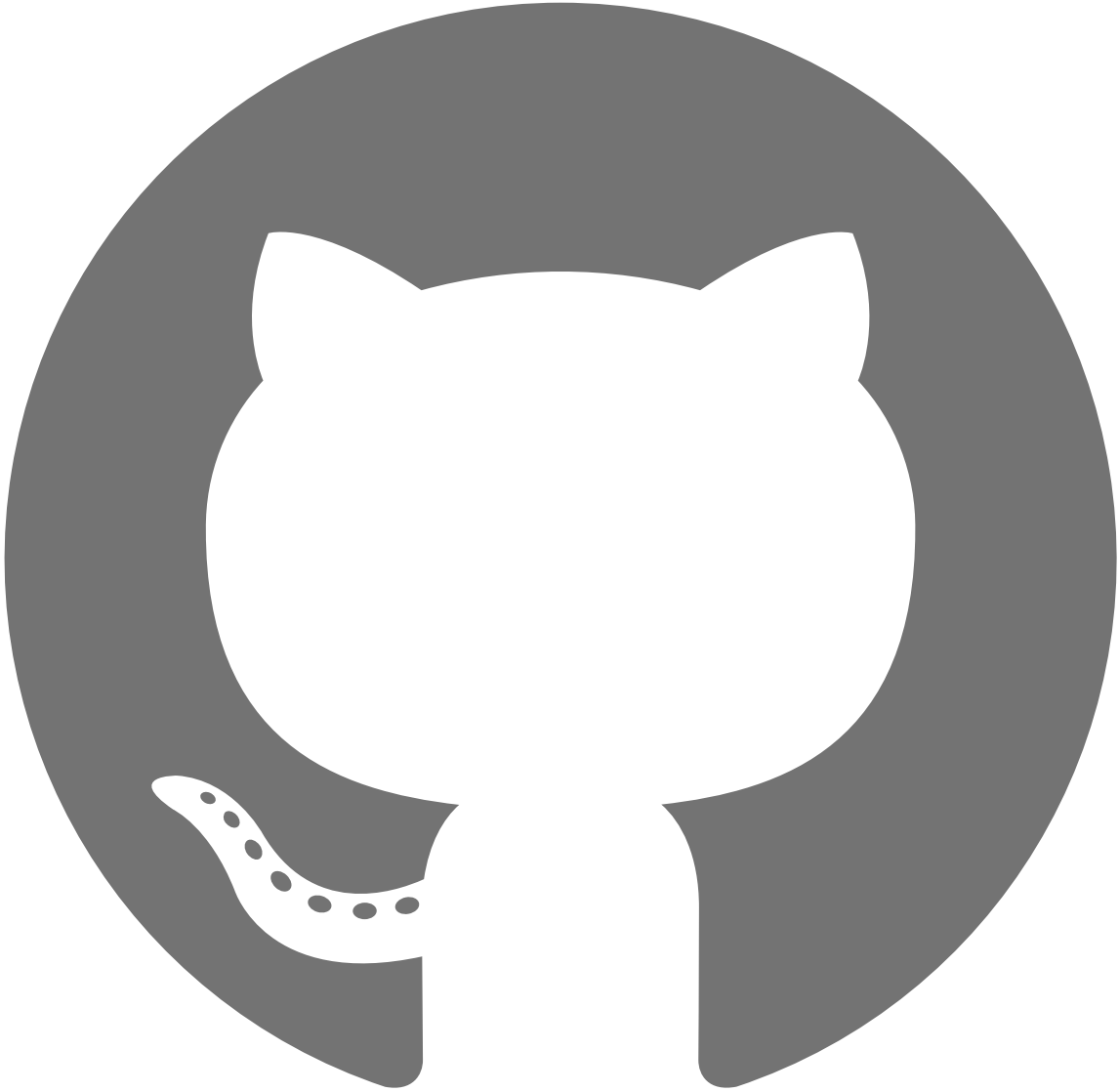
. Pentapetalae	<u>87</u>	9	
.. rosids	<u>78</u>	4	
... Arabidopsis thaliana	<u>74</u>	1	<u>Arabidopsis thaliana hits</u>
... NPAAA clade	<u>4</u>	3	
.... Glycine max	<u>2</u>	1	<u>Glycine max hits</u>
.... Hologalegina	<u>2</u>	2	
..... Medicago truncatula	<u>1</u>	1	<u>Medicago truncatula hits</u>
..... Lotus japonicus	<u>1</u>	1	<u>Lotus japonicus hits</u>
.. asterids	<u>9</u>	5	
... Solanales	<u>8</u>	4	
.... Ipomoea nil	<u>1</u>	1	<u>Ipomoea nil hits</u>
.... Solanum subgen. Lycopersicon	<u>7</u>	3	
..... Solanum lycopersicum	<u>2</u>	1	<u>Solanum lycopersicum hits</u>
..... Solanum peruvianum	<u>1</u>	1	<u>Solanum peruvianum hits</u>
..... Solanum pimpinellifolium	<u>4</u>	1	<u>Solanum pimpinellifolium hits</u>
... Daucus carota	<u>1</u>	1	<u>Daucus carota hits</u>

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