

Supplementary Table 3.

Comparison between LRR Nod1 and Nod2 mutants

Nod2		Nod1		Structure
Mutation	Pos#	Mutation	Pos#	
	698	A611V	611	
	707	L620Q	620	
S714N	714		627	
S714C	714		627	
R716H	716		629	
F719I	719		632	
P723S	723		636	
A725T	725		638	
A726T	726		639	
K731R	731		644	
	732	Q645E	645	
H734L	734		647	
G738R	738		651	β
	746	I659M	659	T1
	749	T662I	662	T1
E751K	751		664	α
	752	Q665N	665	α
	754	V667M	667	α
K757M	757		670	α
A759V	759		672	α
G761S	761		674	α
L762M	762		675	β
L769V	769		682	β
G775D	775		688	T1
E778K	778	D691V	691	α
C779Y	779		692	α
A783T	783		696	α
V785M	785		698	α
R790Q	790		703	T2
V793M	793		706	T2
A794T	794		707	β
	802	L715I	715	T1
I805N	805		718	α
P812T	812		725	α
V816L	816	R729H	729	T2
D824N	824		737	T1
	825	N738I	738	T1
D829Y	829		742	T1
R830Q	830		743	α
G831D	831		744	α
C833S	833		746	α
K834M	834		747	α
I836V	836		749	α
I836F	836		749	α
L840M	840		753	α
	854	Q767H	767	T1
A860G	860		773	α
	868	D781N	781	α
	870	C783S	783	T2
L876I	876		789	β
	877	K790E	790	β
G879R	879		792	β
Y882H	882	K795E	795	T1
T884I	884		797	T1
Q889P	889		802	α
V890A	890		803	α
L891M	891		804	α
A892V	892		805	α
	898	S811N	811	T2
T899A	899		812	T2
L904M	904		817	β
W907L	907		820	β
	910	Q823E	823	T1
V911M	911		824	T1
D913V	913		926	T1
D913E	913		826	T1
G915E	915		828	α
	916	A829T	829	α
A920T	920		833	α
	934	L847I	847	β
V935M	935		848	β
A944V	944	G857R	857	α
A946S	946	S859R	859	α
L947M	947		860	α
L949V	949		862	α
L949M	949		862	α
	952	Q865L	865	α
	953	Q866H	866	α
V955F	955		868	T2
M956T	956		869	T2
E959K	959		872	β
L960V	960		873	β
C961Y	961		874	β
Q968H	968		881	T1

G978E	978		891	α
	979	L892M	892	α
S984T	984		897	T2
K986I	986	K899R	899	β
K989E	989	W902G	902	β
S991F	991		904	β
	996	T909P	909	T1
G999R	999		912	α
A1000T	1000		913	α
A1002S	1002	Q915H	915	α
N1010S	1010		923	α
	1011	T924N	924	T2
T1012I	1012		925	T2
T1012S	1012		925	T2
G1032C	1032		945	α
	1037	I950F	950	α
L1038F	1038		951	α

Abbreviations and Colour Code

Pos# Position in the corresponding protein
Structure Predicted secondary structure in LRR

coloured high lights

ability to respond to synthetic ligand is retained
ability to respond to ligand is lost or partially lost (less than 25% of the wild-type response) but mutant can activate NF- κ B in overexpression studies
constitutive NF- κ B activation

coloured letters

bold mutant with single amino acid substitution
blue deletional, insertional or nonsense mutation

Structure

α α helix
 β β strand
T1 turn following an α helix
T2 turn following a β strand
