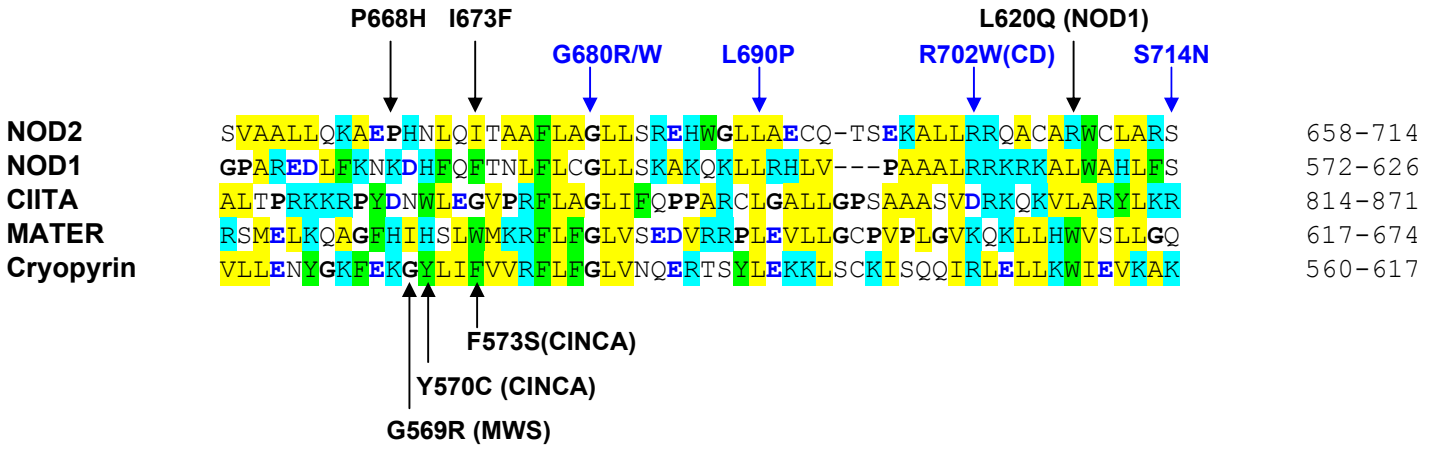
**Supplementary Fig. 1**
**Alignment of NOD2 (aa 658-714) with corresponding sequence of related NOD family members**




The amino acid sequence of NOD2 (aa 658-714; GenBank NP_006083) was aligned with that of representative NOD family members including human NOD1(GenBank NP_071445), CIITA (GenBank AAB92362 and NP_000237), MATER (GenBank NP_703148), cryopyrin (GenBank NP_899632) using the BLAST program. Homologous amino acid residues are highlighted with same colors; black bold for P and G (alpha/beta breaker), blue bold for D and E (acidic residues), blue highlight for R, K, and H (positively charged residues), green highlight for W, F, and Y (aromatic residues), and yellow highlight for I, L, V, A, and M (hydrophobic residues). The constitutively active mutants of NOD1 and NOD2 (this study) and naturally occurring Cryopyrin point mutants causing the autoinflammatory disorders CINCA and MWS are indicated by black arrows. Notice that constitutively active NOD2 mutant I673F is at the same position that the Cryopyrin mutant F573S causing the disease CINCA. Loss-of-function NOD2 mutants of NOD2 are indicated by blue arrows.