

## [LRR conservation mapping to predict functional sites within protein leucine-rich repeat domains.](#)

**Authors:** [Helft, Laura](#) / [Reddy, Vignyan](#) / [Chen, Xiyang](#) / [Koller, Teresa](#) / [Federici, Luca](#) / [Fernández-Recio, Juan](#) / [Gupta, Rishabh](#) / [Bent, Andrew](#)

**Publication:** PloS one

**Volume / Pagination:** 6 / e21614

**Palabras clave:** [Amino Acid Sequence](#), [Arabidopsis](#), [Arabidopsis Proteins](#), [Conserved Sequence](#), [Crystallography](#), [X-Ray](#), [Ligands](#), [Models](#), [Molecular](#), [Molecular Sequence Data](#), [Mutagenesis](#), [Site-Directed](#), [Mutation](#), [Plant Proteins](#), [Protein Interaction Mapping](#), [Protein Kinases](#), [Protein Structure](#), [Secondary](#), [Protein Structure](#), [Tertiary](#), [Proteins](#), [Receptors](#), [Pattern Recognition](#), [Repetitive Sequences](#), [Amino Acid](#), [Reproducibility of Results](#), [Sequence Homology](#), [Amino Acid](#)

Barcelona Supercomputing Center - Centro Nacional de Supercomputación

---

**Source URL (retrieved on 13 Dic 2024 - 23:36):** <https://www.bsc.es/es/research-and-development/publications/lrr-conservation-mapping-predict-functional-sites-within>