

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

ISOLDE

RRID:SCR_025577

Type: Tool

Proper Citation

ISOLDE (RRID:SCR_025577)

Resource Information

URL: <https://tristanic.github.io/isolde/>

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Description: Software environment to ease task of building macromolecular models into low to medium resolution experimental maps. Physically realistic environment for model building into low-resolution electron-density maps. Can generate maps directly from crystallographic F/sigF data in MTZ format and automatically re-calculate them when model changes, and/or generate "static" maps from pre-calculated F/phi data.

Resource Type: software application, software resource

Defining Citation: [PMID:29872003](#)

Keywords: software environment, model building, building macromolecular models, low resolution electron density maps, experimental maps,

Funding: Wellcome Trust

Availability: Free, Freely available

Resource Name: ISOLDE

Resource ID: SCR_025577

License URLs: <https://tristanic.github.io/isolde/licensing/index.html>

Record Creation Time: 20240803T053302+0000

Record Last Update: 20260829T183412+0000

Ratings and Alerts

No rating or validation information has been found for ISOLDE.

No alerts have been found for ISOLDE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Courbon GM, et al. (2026) Structural basis for EtfD-mediated coupling of β -oxidation and the respiratory chain in mycobacteria. The EMBO journal, 45(8), 2785.

Avery NG, et al. (2026) Computational design of an ultrapotent deltacoronavirus miniprotein inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 123(18), e2533456123.

Lupton CJ, et al. (2026) Structure of the lysosomal KICSTOR-GATOR1-SAMTOR nutrient-sensing supercomplex. Cell.

Liao Z, et al. (2026) Faf1 accelerates p97-mediated protein unfolding by promoting ubiquitin engagement. Cell reports, 45(6), 117393.

Lövestam S, et al. (2025) Cryo-EM structure of the vault from human brain reveals symmetry mismatch at its caps. Structure (London, England : 1993), 33(10), 1643.

Du B, et al. (2025) Molecular basis of human taurine transporter uptake and inhibition. Nature communications, 16(1), 7394.

Chen S, et al. (2025) Cryo-electron tomography reveals the microtubule-bound form of inactive LRRK2. eLife, 13.

Rose K, et al. (2025) In situ cryo-ET visualization of mitochondrial depolarization and mitophagic engulfment. Proceedings of the National Academy of Sciences of the United States of America, 122(31), e2511890122.

Houser A, et al. (2025) Structural insights into subunit-dependent functional regulation in epithelial sodium channels. Structure (London, England : 1993), 33(2), 349.

Voss WN, et al. (2024) Hybrid immunity to SARS-CoV-2 arises from serological recall of IgG antibodies distinctly imprinted by infection or vaccination. Cell reports. Medicine, 5(8), 101668.

Chen S, et al. (2024) Cryo-electron tomography reveals the microtubule-bound form of inactive LRRK2. bioRxiv : the preprint server for biology.

Senn KA, et al. (2024) Control of 3' splice site selection by the yeast splicing factor Fyv6. *eLife*, 13.

Pandey A, et al. (2024) Therapeutic Targeting and Structural Characterization of a Sotorasib-Modified KRAS G12C-MHC I complex Demonstrates the Antitumor Efficacy of Hapten-Based Strategies. *Cancer research*.