

Resource Summary Report

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HKL-2000

RRID:SCR_015547

Type: Tool

Proper Citation

HKL-2000 (RRID:SCR_015547)

Resource Information

URL: <http://www.hkl-xray.com/hkl-2000>

Proper Citation: HKL-2000 (RRID:SCR_015547)

Description: Software package for structural determination and other functions in the field of structural biology. Its programs can perform strategy and simulation, 3-D processing, mosaicity refinement during processing, variable spot size, easy change of the space group, report generation, and other functions.

Resource Type: software application, 3-d visualization software, software resource, data processing software

Defining Citation: [PMID:27754618](#)

Keywords: structural biology, structure determination process, simulation, 3d processing, mosaicity, strategy,

Availability: Commercially available, License required, Runs on Linux, Runs on Mac OS

Resource Name: HKL-2000

Resource ID: SCR_015547

Alternate URLs: www.hkl-xray.com

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260728T043459+0000

Ratings and Alerts

No rating or validation information has been found for HKL-2000.

No alerts have been found for HKL-2000.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 205 mentions in open access literature.

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

Lin X, et al. (2025) Structural insights into VRC01-class bnAb precursors with diverse light chains elicited in the IAVI G001 human vaccine trial. *bioRxiv : the preprint server for biology*.

Matsuzaki C, et al. (2025) A thermostable and highly active fungal GH3 ??-glucosidase generated by random and saturation mutagenesis. *Proceedings of the Japan Academy. Series B, Physical and biological sciences*, 101(3), 177.

Yan L, et al. (2025) A broadly neutralizing antibody recognizes a unique epitope with a signature motif common across coronaviruses. *Nature communications*, 16(1), 7580.

Guo Y, et al. (2025) ASFV pE146L-induced ER remodeling is essential for viral replication. *Journal of virology*, 99(9), e0083425.

Lin X, et al. (2025) Structural insights into VRC01-class bnAb precursors with diverse light chains elicited in the IAVI G001 human vaccine trial. *Proceedings of the National Academy of Sciences of the United States of America*, 122(33), e2510163122.

Huang X, et al. (2025) Crystal Structure of an Aldo-keto Reductase MGG_00097 from *Magnaporthe grisea*. *The plant pathology journal*, 41(2), 167.

Wang K, et al. (2025) Structural basis for antibiotic resistance by chloramphenicol acetyltransferase type A in *Staphylococcus aureus*. *Scientific reports*, 15(1), 37020.

Kim JH, et al. (2025) A putative membrane-associated YdjB-like protein from *Salmonella enterica* exhibits a non-canonical ACT-like fold. *PloS one*, 20(12), e0336436.

Schleich FA, et al. (2025) Vaccination of nonhuman primates elicits a broadly neutralizing antibody lineage targeting a quaternary epitope on the HIV-1 Env trimer. *Immunity*, 58(6), 1598.

Kimura-Someya T, et al. (2024) Structural analyses of the GI.4 norovirus by cryo-electron microscopy and X-ray crystallography revealing binding sites for human monoclonal antibodies. *Journal of virology*, 98(5), e0019724.

Chen L, et al. (2024) Structural basis of the activation of MARTX cysteine protease domain from *Vibrio vulnificus*. *PloS one*, 19(8), e0307512.

Baca CF, et al. (2024) The CRISPR-associated adenosine deaminase Cad1 converts ATP to ITP to provide antiviral immunity. *Cell*, 187(25), 7183.

Song X, et al. (2024) The structure of TRAF7 coiled-coil trimer provides insight into its function in zebrafish embryonic development. *Journal of molecular cell biology*, 16(1).

Chiang WT, et al. (2024) Structural basis and synergism of ATP and Na⁺ activation in bacterial K⁺ uptake system KtrAB. *Nature communications*, 15(1), 3850.

Lin SM, et al. (2024) Structural basis of water-mediated cis Watson-Crick/Hoogsteen base-pair formation in non-CpG methylation. *Nucleic acids research*, 52(14), 8566.

Zhang Y, et al. (2024) Structural mechanisms for binding and activation of a contact-quenched fluorophore by RhoBAST. *Nature communications*, 15(1), 4206.

Chen CC, et al. (2024) A distinct dimer configuration of a diatom Get3 forming a tetrameric complex with its tail-anchored membrane cargo. *BMC biology*, 22(1), 136.

Lin MG, et al. (2024) Unraveling the structure and function of a novel SegC protein interacting with the SegAB chromosome segregation complex in Archaea. *Nucleic acids research*, 52(16), 9966.

Tang S, et al. (2024) Dual dimeric interactions in the nucleic acid-binding protein Sac10b lead to multiple bridging of double-stranded DNA. *Heliyon*, 10(11), e31630.

Fu J, et al. (2024) Legionella maintains host cell ubiquitin homeostasis by effectors with unique catalytic mechanisms. *Nature communications*, 15(1), 5953.