

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

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

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: 20260905T133300+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 215 mentions in open access literature.

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

Jain M, et al. (2026) Structural basis for conserved and distinct antigen recognition by a lineage of malaria-protective antibodies. PLoS pathogens, 22(6), e1014243.

Chen J, et al. (2026) Structures of clinical antibodies bound to IL-33 uncover two distinct epitopes underlying differential efficacy. mAbs, 18(1), 2639673.

Zhang Y, et al. (2026) MORC2 mediates transcriptional regulation through liquid-liquid phase separation. eLife, 14.

Wang SC, et al. (2026) Structural basis for asymmetric bis-intercalator targeting of DNA triplex junctions enabling dual inhibition of topoisomerase I and oncogene transcription. Nucleic acids research, 54(10).

Jang H, et al. (2026) Structural Insights into MltC from Acinetobacter baumannii: Conservation of the Catalytic Residue and Flexibility in Substrate Recognition. Journal of microbiology and biotechnology, 36, e2511019.

Siroy A, et al. (2026) Oligomerization is required for channel formation of MctB and for copper resistance of Mycobacterium tuberculosis. The Journal of biological chemistry, 302(2), 111037.

Wang H-Q, et al. (2026) Structural and functional insights into Uly1040, an ulvan lyase from polysaccharide lyase family 40. Applied and environmental microbiology, 92(2), e0210125.

Li SH, et al. (2026) Childhood immunological imprinting of cross-subtype antibodies targeting the hemagglutinin head domain of influenza viruses. Cell host & microbe, 34(5), 873.

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.

Ko IT, et al. (2025) Structural insights into substrate binding, residue contributions, and catalytic mechanism of phosphopantetheine adenylyltransferase from *Helicobacter pylori*. *Bioscience reports*(8), 19.

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.

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).