

Resource Summary Report

Generated by [NIF](#) on Sep 2, 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: 20260829T183110+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 [NIF](#).

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.

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).

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

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*.

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.

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

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.

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