

Resource Summary Report

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Pointless

RRID:SCR_014218

Type: Tool

Proper Citation

Pointless (RRID:SCR_014218)

Resource Information

URL: <http://www.ccp4.ac.uk/html/pointless.html>

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Description: Pointless scores all the possible Laue groups consistent with the crystal class, which is based on cell dimension restraints, by matching potential symmetry equivalent reflections. For chiral systems, the Laue group uniquely implies the point group then checks sets of reflections which may be systematically absent to suggest a possible spacegroup. There is also a check for lattice centering, i.e., a check for whole classes of reflections having essentially zero intensity, including a check for obverse/inverse twinning in rhombohedral systems. Pointless is also capable of converting XDS, Scalepack, SHELX or SAINT formats to MTZ.

Resource Type: software resource, software application

Defining Citation: [DOI:10.1107/S090744491003982X](https://doi.org/10.1107/S090744491003982X)

Keywords: laue group, space group, crystal structure, data reduction

Resource Name: Pointless

Resource ID: SCR_014218

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260801T191056+0000

Ratings and Alerts

No rating or validation information has been found for Pointless.

No alerts have been found for Pointless.

Data and Source Information

Usage and Citation Metrics

We found 129 mentions in open access literature.

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

Lourenço FM, et al. (2026) Interaction of Staphylococcus aureus di-iron Repair of Iron Centers protein with the iron-sulfur cluster assembly SUF system. Protein science : a publication of the Protein Society, 35(1), e70406.

Nesa ML, et al. (2025) Crystal structure of ferric recombinant horseradish peroxidase. Journal of biological inorganic chemistry : JBIC : a publication of the Society of Biological Inorganic Chemistry, 30(3), 221.

Neißner K, et al. (2025) The structural basis for high-affinity c-di-GMP binding to the GSPII-B domain of the traffic ATPase PilF from Thermus thermophilus. The Journal of biological chemistry, 301(1), 108041.

Liu M, et al. (2025) Enzymatic combinatorial synthesis of E-64 and related cysteine protease inhibitors. Nature chemical biology, 21(11), 1783.

Das T, et al. (2025) Efficient coordination between the winged helix domain and the aromatic-rich loop restructures the ATPase domain and facilitates DNA unwinding by human RECQ1. Nucleic acids research, 53(11).

Froes TQ, et al. (2025) Barbituric Acid Derivatives as Covalent Inhibitors of Leishmania braziliensis Dihydroorotate Dehydrogenase. Journal of medicinal chemistry, 68(18), 18869.

Rettie SA, et al. (2025) Accurate de novo design of high-affinity protein-binding macrocycles using deep learning. Nature chemical biology, 21(12), 1948.

Dumina MV, et al. (2025) Hyperthermophilic L-Asparaginase from Thermococcus sibiricus and Its Double Mutant with Increased Activity: Insights into Substrate Specificity and Structure. International journal of molecular sciences, 26(12).

Zakharova K, et al. (2025) Crystal structures of Salmonella enterica FraB deglycase reveal a conformational heterodimer with remarkable structural plasticity at the active site. Protein science : a publication of the Protein Society, 34(9), e70260.

Youle RL, et al. (2025) KHNYN is a manganese-dependent endoribonuclease required for ZAP-mediated antiviral restriction. Nucleic acids research, 53(22).

Feldman D, et al. (2025) Massively parallel assessment of designed protein solution properties using mass spectrometry and peptide barcoding. bioRxiv : the preprint server for biology.

Tangpeerachaikul A, et al. (2025) Zidesamtinib Selective Targeting of Diverse ROS1 Drug-Resistant Mutations. Molecular cancer therapeutics, 24(7), 1005.

Broerman AJ, et al. (2025) Design of facilitated dissociation enables timing of cytokine signalling. *Nature*, 647(8089), 528.

Juodeikis R, et al. (2025) Extracellular vesicle-linked vitamin B12 acquisition via novel binding proteins in *Bacteroides thetaiotaomicron*. *The Biochemical journal*, 482(23), 1793.

Basanta B, et al. (2024) The conformational landscape of human transthyretin revealed by cryo-EM. *bioRxiv : the preprint server for biology*.

Nam K, et al. (2024) Elucidating Dynamics of Adenylate Kinase from Enzyme Opening to Ligand Release. *Journal of chemical information and modeling*, 64(1), 150.

Mpakali A, et al. (2024) Stabilization of the open conformation of insulin-regulated aminopeptidase by a novel substrate-selective small-molecule inhibitor. *Protein science : a publication of the Protein Society*, 33(9), e5151.

Penning S, et al. (2024) Unveiling the versatility of the thioredoxin framework: Insights from the structural examination of *Francisella tularensis* DsbA1. *Computational and structural biotechnology journal*, 23, 4324.

Mahana Y, et al. (2024) Structural evidence for protein-protein interaction between the non-canonical methyl-CpG-binding domain of SETDB proteins and C11orf46. *Structure (London, England : 1993)*, 32(3), 304.

McMinimy R, et al. (2024) Reactive oxygen species control protein degradation at the mitochondrial import gate. *Molecular cell*, 84(23), 4612.