

Resource Summary Report

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

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 application, software resource

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: 20260905T133257+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 134 mentions in open access literature.

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

Ma C, et al. (2026) Zinc-finger transcription factor Fzf1 binds to its target DNA in a non-canonical manner. *Nucleic acids research*, 54(3).

Somiya M, et al. (2026) Computational design of membrane fusion proteins. *bioRxiv : the preprint server for biology*.

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.

Veselkova B, et al. (2026) Structural basis of porcine reproductive and respiratory syndrome virus 2 neutralization by a GP4-targeting monoclonal antibody. *The Journal of general virology*, 107(6).

Orkwis JA, et al. (2026) Helminth proteins recapitulate key structural motifs of MIF to facilitate immunomodulation of host receptors. *iScience*, 29(7), 116513.

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.

Neiβner 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.

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

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).

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

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).

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

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

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.

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*.

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

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

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.