

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 application, software resource

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

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

Funding:

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Ratings and Alerts

No rating or validation information has been found for Pointless.

No alerts have been found for Pointless.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 114 mentions in open access literature.

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

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.

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.

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

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.

Teixeira Nunes M, et al. (2023) Functional and structural insights into the multi-step activation and catalytic mechanism of bacterial ExoY nucleotidyl cyclase toxins bound to actin-profilin. *PLoS pathogens*, 19(9), e1011654.

Gres AT, et al. (2023) Multidisciplinary studies with mutated HIV-1 capsid proteins reveal structural mechanisms of lattice stabilization. *Nature communications*, 14(1), 5614.

Haataja T, et al. (2023) Enzyme kinetics by GH7 cellobiohydrolases on chromogenic substrates is dictated by non-productive binding: insights from crystal structures and MD simulation. *The FEBS journal*, 290(2), 379.

An L, et al. (2023) Hallucination of closed repeat proteins containing central pockets. *Nature structural & molecular biology*, 30(11), 1755.

Ogbu CP, et al. (2023) Structural Basis of *Clostridium perfringens* Enterotoxin Activation and Oligomerization by Trypsin. *Toxins*, 15(11).

Rouet R, et al. (2023) Broadly neutralizing SARS-CoV-2 antibodies through epitope-based selection from convalescent patients. *Nature communications*, 14(1), 687.

Paloyan A, et al. (2023) Structural and biochemical characterisation of the N-carbamoyl-L-alanine amidohydrolase from *Rhizobium radiobacter* MDC 8606. *The FEBS journal*, 290(23), 5566.

Abellon-Ruiz J, et al. (2023) BtuB TonB-dependent transporters and BtuG surface lipoproteins form stable complexes for vitamin B12 uptake in gut *Bacteroides*. *Nature communications*, 14(1), 4714.

Lee J, et al. (2023) Important Structural Features of Thiolate-Rich Four-Helix Bundles for Cu(I) Uptake and Removal. *Inorganic chemistry*, 62(17), 6617.

Bajaj T, et al. (2023) Crystal structure of the kinase domain of a receptor tyrosine kinase from a choanoflagellate, *Monosiga brevicollis*. *PloS one*, 18(6), e0276413.

Abdullayev S, et al. (2023) Selectively Modified Lactose and N-Acetyllactosamine Analogs at Three Key Positions to Afford Effective Galectin-3 Ligands. *International journal of molecular sciences*, 24(4).

Martynowycz MW, et al. (2023) A robust approach for MicroED sample preparation of lipidic cubic phase embedded membrane protein crystals. *Nature communications*, 14(1), 1086.

Inaba K, et al. (2022) Molecular action of larvicidal flavonoids on ecdysteroidogenic glutathione S-transferase Noppera-bo in *Aedes aegypti*. *BMC biology*, 20(1), 43.

Hodder AN, et al. (2022) Basis for drug selectivity of plasmepsin IX and X inhibition in *Plasmodium falciparum* and *vivax*. *Structure (London, England : 1993)*, 30(7), 947.