Resource Summary Report

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HOLLOW

RRID:SCR_005729
Type: Tool

Proper Citation

HOLLOW (RRID:SCR_005729)

Resource Information

URL: http://hollow.sourceforge.net/

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Description: HOLLOW facilitates the production of surface images of proteins. HOLLOW is a portable command-line utility written in Python 2.4-2.7; it does not have any other dependencies (although running under the PyPy JIT interpreter, it runs much faster). The input is a PDB file. The output is a PDB file of dummy water atoms that forms a cast of the voids and channels of a protein. HOLLOW generates a surface from a cast of the protein surface. HOLLOW fills the interior spaces of a protein structure with dummy atoms defined on an overlapping grid. The surface generated by these dummy atoms can be shown to reproduce the surface of the protein at the ideal limit. The use of the surface of the dummy atoms allows us to focus on a specific piece of the interior surface. Simply by deleting dummy atoms, the interior surface can be trimmed to produce a custom portion of the interior space. For advanced coloring of the surface, the B-factor of the dummy atoms can be calculated as the average of the B-factor of the protein atoms surrounding the dummy atoms. This allows various colorings of the surface to be conveyed through the B-factor field of the PDB files. The volume filling representation facilitated by HOLLOW is meant to complement other programs that identify voids, pockets and channels, such as SPHGEN and CASTp, which identify binding sites but cannot produce output that can be rendered in standard molecular graphics software. HOLLOW can be used to help render these binding pockets.

Abbreviations: HOLLOW

Synonyms: HOLLOW - Volume Filling of Protein Structures, HOLLOW: Generating Accurate Representations of Channel and Interior Surfaces in Molecular Structures

Resource Type: software application, data visualization software, data processing software, software resource

Defining Citation: PMID:19014592

Keywords: surface image, protein, protein image, protein structure, image, channel surface, electrostatic surface, interior pathway surface, ligand-binding surface, molecular structure, python

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Resource Name: HOLLOW

Resource ID: SCR_005729

Alternate IDs: nlx_149186

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Ratings and Alerts

No rating or validation information has been found for HOLLOW.

No alerts have been found for HOLLOW.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Li M, et al. (2024) Structural insights into human EMC and its interaction with VDAC. Aging, 16(6), 5501.

Strauss J, et al. (2024) Functional and structural asymmetry suggest a unifying principle for catalysis in membrane-bound pyrophosphatases. EMBO reports, 25(2), 853.

Fu C, et al. (2024) Insight into binding of endogenous neurosteroid ligands to the sigma-1

receptor. Nature communications, 15(1), 5619.

Serrano A, et al. (2024) Unveiling the kinetic versatility of aryl-alcohol oxidases with different electron acceptors. Frontiers in bioengineering and biotechnology, 12, 1440598.

Lyu Y, et al. (2024) Engineering of a mammalian VMAT2 for cryo-EM analysis results in non-canonical protein folding. Nature communications, 15(1), 6511.

Ding M, et al. (2024) Probing plant signal processing optogenetically by two channelrhodopsins. Nature, 633(8031), 872.

Cinca-Fernando P, et al. (2024) Discovery, characterization, and synthetic potential of two novel bacterial aryl-alcohol oxidases. Applied microbiology and biotechnology, 108(1), 498.

Tajima S, et al. (2023) Structural basis for ion selectivity in potassium-selective channelrhodopsins. Cell, 186(20), 4325.

Morizumi T, et al. (2023) Structures of channelrhodopsin paralogs in peptidiscs explain their contrasting K+ and Na+ selectivities. Nature communications, 14(1), 4365.

Silberberg JM, et al. (2022) Inhibited KdpFABC transitions into an E1 off-cycle state. eLife, 11.

Melnikov I, et al. (2022) High-pressure crystallography shows noble gas intervention into protein-lipid interaction and suggests a model for anaesthetic action. Communications biology, 5(1), 360.

Kao WC, et al. (2022) Structural basis for safe and efficient energy conversion in a respiratory supercomplex. Nature communications, 13(1), 545.

Velazhahan V, et al. (2022) Activation mechanism of the class D fungal GPCR dimer Ste2. Nature, 603(7902), 743.

Demmer JK, et al. (2022) Structure of ATP synthase from ESKAPE pathogen Acinetobacter baumannii. Science advances, 8(7), eabl5966.

Heit S, et al. (2021) Structure of the hexameric fungal plasma membrane proton pump in its autoinhibited state. Science advances, 7(46), eabj5255.

Tillinghast J, et al. (2021) Structural mechanisms for gating and ion selectivity of the human polyamine transporter ATP13A2. Molecular cell, 81(22), 4650.

Silberberg JM, et al. (2021) Deciphering ion transport and ATPase coupling in the intersubunit tunnel of KdpFABC. Nature communications, 12(1), 5098.

Raj R, et al. (2020) Structural and biochemical characteristics of two Staphylococcus epidermidis RNase J paralogs RNase J1 and RNase J2. The Journal of biological chemistry, 295(49), 16863.

Kovalev K, et al. (2020) High-resolution structural insights into the heliorhodopsin family. Proceedings of the National Academy of Sciences of the United States of America, 117(8), 4131.

Coudray N, et al. (2020) Structure of bacterial phospholipid transporter MlaFEDB with substrate bound. eLife, 9.