

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

PoSSuM

RRID:SCR_006109

Type: Tool

Proper Citation

PoSSuM (RRID:SCR_006109)

Resource Information

URL: <http://possum.cbrc.jp/PoSSuM/>

Proper Citation: PoSSuM (RRID:SCR_006109)

Description: Relational database of all the discovered similar pairs in a huge number of protein-ligand binding sites with annotations of various types (e.g., CATH, SCOP, EC number, Gene ontology). They used a tremendously fast algorithm called SketchSort that enables the enumeration of similar pairs in a huge number of protein-ligand binding sites. They conducted all-pair similarity searches for 3.4 million known and potential binding sites using the proposed method and discovered over 24 million similar pairs of binding sites. PoSSuM enables rapid exploration of similar binding sites among structures with different global folds as well as similar ones. Moreover, PoSSuM is useful for predicting the binding ligand for unbound structures. Basically, the users can search similar binding pockets using two search modes: # Search K is useful for finding similar binding sites for a known ligand-binding site. Post a known ligand-binding site (a pair of PDB ID and HET code) in the PDB, and PoSSuM will search similar sites for the query site. # Search P is useful for predicting ligands that potentially bind to a structure of interest. Post a known protein structure (PDB ID) in the PDB, and PoSSuM will search similar known-ligand binding sites for the query structure.

Abbreviations: PoSSuM

Synonyms: PoSSuM - POcket Similarity Search Using Multiple-Sketches, Pocket Similarity Search using Multiple-Sketches (PoSSuM), PoSSuM Database, POcket Similarity Search Using Multiple-Sketches

Resource Type: data or information resource, database

Defining Citation: [PMID:22135290](#), [PMID:22113700](#)

Keywords: binding site, ligand-binding site, protein function, protein, prediction, small molecule, drug discovery

Funding: Japan Society for the Promotion of Science KAKENHI 21680025;
Japan Society for the Promotion of Science KAKENHI 23500374

Availability: Freely available, Acknowledgement required

Resource Name: PoSSuM

Resource ID: SCR_006109

Alternate IDs: nlx_151581

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260801T190946+0000

Ratings and Alerts

No rating or validation information has been found for PoSSuM.

No alerts have been found for PoSSuM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Blasdell KR, et al. (2024) Experimental infection of ringtail possums (*Pseudocheirus peregrinus*) with *Mycobacterium ulcerans*, the agent of Buruli ulcer. *Scientific reports*, 14(1), 25352.

Ishitani R, et al. (2024) Protein ligand binding site prediction using graph transformer neural network. *PloS one*, 19(8), e0308425.

Katuuramu DN, et al. (2023) Genetic control of flowering time and fruit yield in citron watermelon. *Frontiers in plant science*, 14, 1236576.

Tsuchiya Y, et al. (2023) PoSSuM v.3: A Major Expansion of the PoSSuM Database for Finding Similar Binding Sites of Proteins. *Journal of chemical information and modeling*, 63(23), 7578.

Lukianova AA, et al. (2022) *Pectobacterium versatile* Bacteriophage Possum: A Complex Polysaccharide-Deacetylating Tail Fiber as a Tool for Host Recognition in *Pectobacteriales* Schitoviridae. *International journal of molecular sciences*, 23(19).

Wang X, et al. (2022) ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. *Briefings in bioinformatics*, 23(2).

Bertucci EM, et al. (2021) Exposure to ionizing radiation disrupts normal epigenetic aging in Japanese medaka. *Aging*, 13(19), 22752.

Shirafkan F, et al. (2021) Moonlighting protein prediction using physico-chemical and evolutionary properties via machine learning methods. *BMC bioinformatics*, 22(1), 261.

Drobnjak I, et al. (2021) Physical and digital phantoms for validating tractography and assessing artifacts. *NeuroImage*, 245, 118704.

Westbrook JI, et al. (2021) Associations between double-checking and medication administration errors: a direct observational study of paediatric inpatients. *BMJ quality & safety*, 30(4), 320.

Schild DR, et al. (2019) The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. *Genome research*, 29(4), 590.

Lima DFT, et al. (2019) Outcome prediction with Physiological and Operative Severity Score for the enumeration of Mortality and Morbidity score system in elderly patients submitted to elective surgery. *Saudi journal of anaesthesia*, 13(1), 46.

Chen L, et al. (2019) A simplified scoring system for the prediction of pancreatoduodenectomy's complications: An observational study. *Medicine*, 98(1), e13969.

Klein R, et al. (2018) In silico identification and experimental validation of hits active against KPC-2 β -lactamase. *PloS one*, 13(11), e0203241.

Majka P, et al. (2018) A three-dimensional stereotaxic atlas of the gray short-tailed opossum (*Monodelphis domestica*) brain. *Brain structure & function*, 223(4), 1779.

Ledón-Rettig CC, et al. (2017) Asymmetric interactions between doublesex and tissue- and sex-specific target genes mediate sexual dimorphism in beetles. *Nature communications*, 8, 14593.

Ma S, et al. (2017) Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. *Scientific reports*, 7(1), 5557.

Ghorbanpour E, et al. (2017) FMNL2 with Functions Related to the Cytoskeleton is Partially Regulated by PAX6. *Journal of ophthalmic & vision research*, 12(4), 407.

Rasnitsyn A, et al. (2017) FOXC1 modulates MYOC secretion through regulation of the exocytic proteins RAB3GAP1, RAB3GAP2 and SNAP25. *PloS one*, 12(6), e0178518.

Majka P, et al. (2016) Possum-A Framework for Three-Dimensional Reconstruction of Brain Images from Serial Sections. *Neuroinformatics*, 14(3), 265.