

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## Phase

RRID:SCR\_014884

Type: Tool

### Proper Citation

Phase (RRID:SCR\_014884)

### Resource Information

**URL:** <https://www.schrodinger.com/Phase/>

**Proper Citation:** Phase (RRID:SCR\_014884)

**Description:** Pharmacophore modeling software to create 3D structure activity relationships, screen databases, and generate hits through establishing a chemical space occupied by active ligands. Used in drug design.

**Resource Type:** simulation software, software application, software resource

**Keywords:** drug, design, ligand, software, pharmacophore, modeling, FASEB list

**Availability:** Commercially available

**Resource Name:** Phase

**Resource ID:** SCR\_014884

**License URLs:** <https://www.schrodinger.com/terms-use>

**Record Creation Time:** 20220129T080322+0000

**Record Last Update:** 20260905T132751+0000

### Ratings and Alerts

No rating or validation information has been found for Phase.

No alerts have been found for Phase.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Pyun WY, et al. (2026) Nutrient Availability Dictates Cancer Metabolism-Based Therapeutic Responses to Nononcology Drugs. *Cancer research*, 86(5), 1194.

Weber MD, et al. (2024) Deep-pelagic fishes: Demographic instability in a stable environment. *Ecology and evolution*, 14(4), e11267.

Morley KI, et al. (2024) Wellbeing Impact Study of High-Speed 2 (WISH2): Protocol for a mixed-methods examination of the impact of major transport infrastructure development on mental health and wellbeing. *PloS one*, 19(2), e0298701.

Rácz A, et al. (2022) Consensus Virtual Screening Identified [1,2,4]Triazolo[1,5-b]isoquinolines As MELK Inhibitor Chemotypes. *ChemMedChem*, 17(2), e202100569.

Yaman Y, et al. (2021) A novel 2 bp deletion variant in Ovine-DRB1 gene is associated with increased Visna/maedi susceptibility in Turkish sheep. *Scientific reports*, 11(1), 14435.

Damen M, et al. (2021) Ancestral Origin of the First Indian Families with Myotonic Dystrophy Type 2. *Journal of neuromuscular diseases*, 8(4), 715.

Oliveira TM, et al. (2021) TLR4 and TLR8 variability in Amazonian and West Indian manatee species from Brazil. *Genetics and molecular biology*, 44(2), e20190252.

Mestiri S, et al. (2021) Genetic diversity of the North African population revealed by the typing of SNPs in the DRD2/ANKK1 genomic region. *Gene*, 777, 145466.

Sirous H, et al. (2020) Computer-Driven Development of an in Silico Tool for Finding Selective Histone Deacetylase 1 Inhibitors. *Molecules (Basel, Switzerland)*, 25(8).

Kidd KK, et al. (2020) The distinctive geographic patterns of common pigmentation variants at the OCA2 gene. *Scientific reports*, 10(1), 15433.

Anderson DE, et al. (2020) Global brain network dynamics predict therapeutic responsiveness to cannabidiol treatment for refractory epilepsy. *Brain communications*, 2(2), fcaa140.

Colussi S, et al. (2019) A single nucleotide variant in the promoter region of the CCR5 gene increases susceptibility to arthritis encephalitis virus in goats. *BMC veterinary research*, 15(1), 230.

Huang T, et al. (2019) Genome-wide association and evolutionary analyses reveal the formation of swine facial wrinkles in Chinese Erhualian pigs. *Aging*, 11(13), 4672.

Boussetta S, et al. (2019) Usefulness of COMT gene polymorphisms in North African populations. *Gene*, 696, 186.

Wang L, et al. (2018) A Study on the Association Between Polymorphisms in the Cytochrome P450 Family 17 Subfamily A Member 1 Gene Region and Type 2 Diabetes Mellitus in Han Chinese. *Frontiers in endocrinology*, 9, 323.

Mühlhausen S, et al. (2018) Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in *Ascoidea asiatica*. *Current biology : CB*, 28(13), 2046.

Lu N, et al. (2018) Single-nucleotide polymorphisms(SNPs) in a sucrose synthase gene are associated with wood properties in *Catalpa fargesii* bur. *BMC genetics*, 19(1), 99.

Martínez-Montes ÁM, et al. (2018) Using genome wide association studies to identify common QTL regions in three different genetic backgrounds based on Iberian pig breed. *PloS one*, 13(3), e0190184.

Mangiatordi GF, et al. (2017) Novel chemotypes targeting tubulin at the colchicine binding site and unbiassing P-glycoprotein. *European journal of medicinal chemistry*, 139, 792.

Sobjanek M, et al. (2015) -308 G/A TNF- $\alpha$  gene polymorphism influences the course of basal cell carcinoma in a Polish population. *Archives of medical science : AMS*, 11(3), 599.