

Resource Summary Report

Generated by [RRID](#) on Aug 2, 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: software resource, software application, simulation software

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: 20260801T190509+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 36 mentions in open access literature.

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

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.

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.

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.

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- α gene polymorphism influences the course of basal cell carcinoma in a Polish population. Archives of medical science : AMS, 11(3), 599.

Stanton DW, et al. (2014) Distinct and diverse: range-wide phylogeography reveals ancient lineages and high genetic variation in the endangered okapi (*Okapia johnstoni*). PloS one, 9(7), e101081.