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Data-driven rheology enables predictive embedded bioprinting

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Running title: Data-driven precise bioprinting

Supplementary File

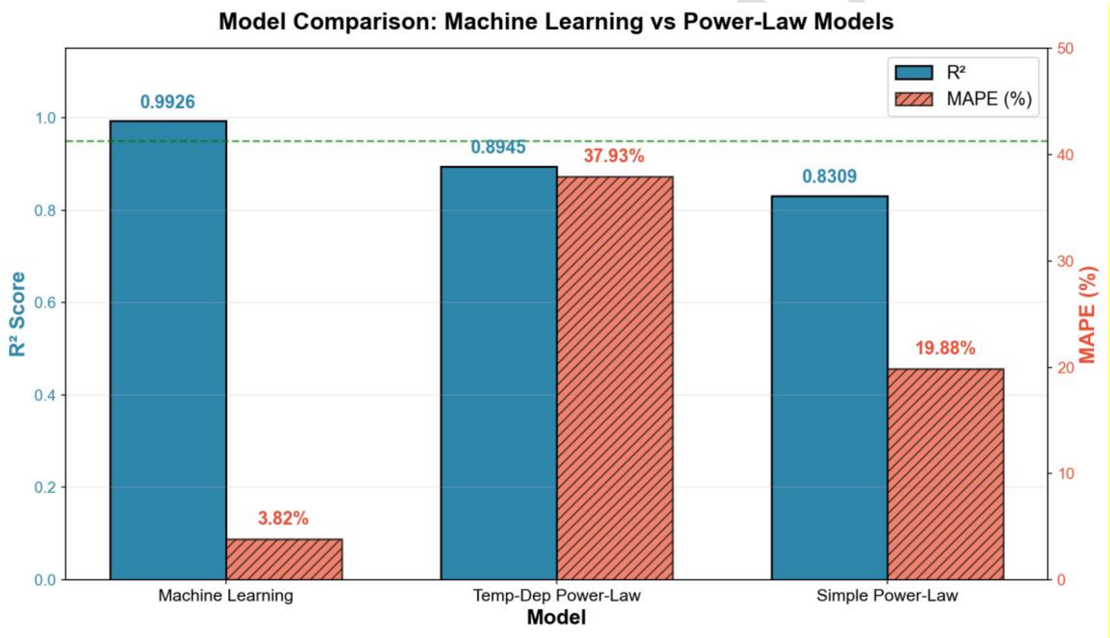

Figure S1. Column contrast chart of Machine Learning and Simple Power-Law, Temp-Dep Power-Law. To indicate the different fitting effect between those models, it shows that ML is better than PL in the rheological characteristics of fitting GelMA.

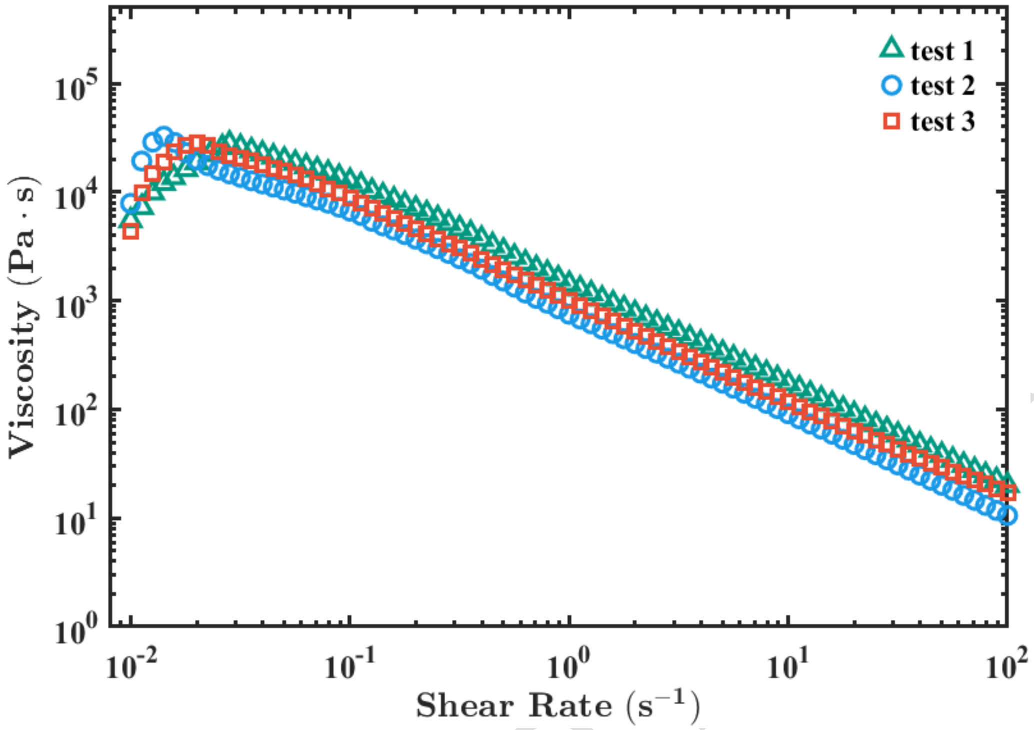

Figure S2. Repeatability assessment of rheological measurements at 25°C. Three independent measurements were performed under identical experimental conditions. The resulting flow curves exhibited consistent trends and comparable rheological responses across replicates, demonstrating satisfactory measurement repeatability.

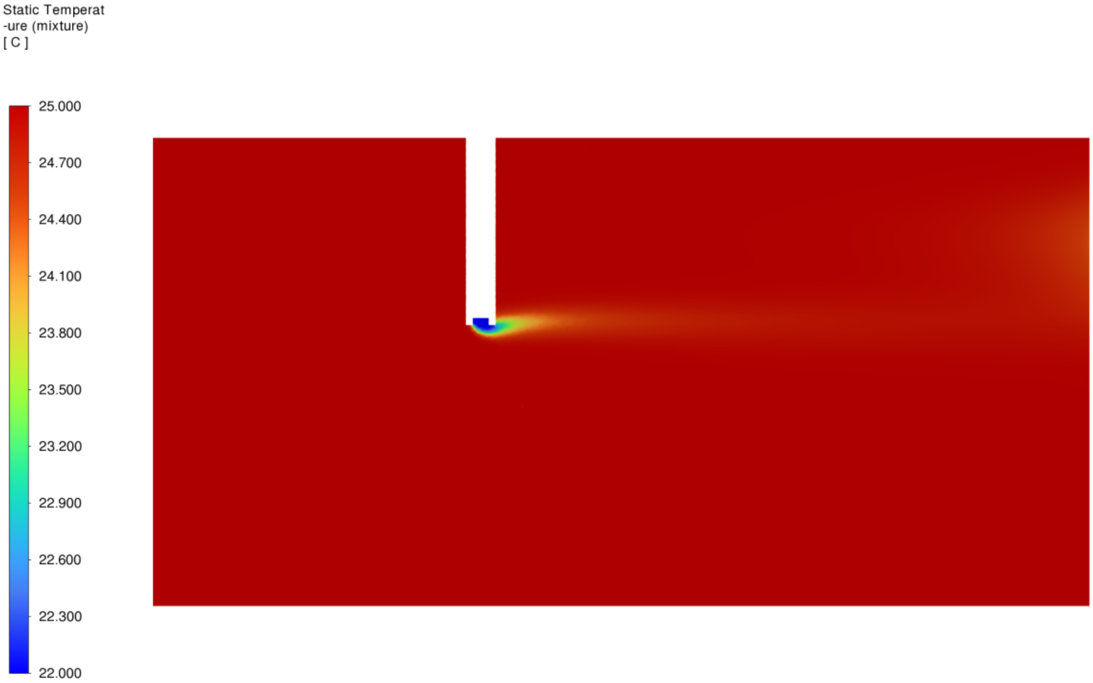

Figure S3. Temperature contour plot showing the transient heating process of the filament during deposition. The results indicate that the ink gradually warms up from 22°C to the ambient supporting bath temperature of 25°C over time.

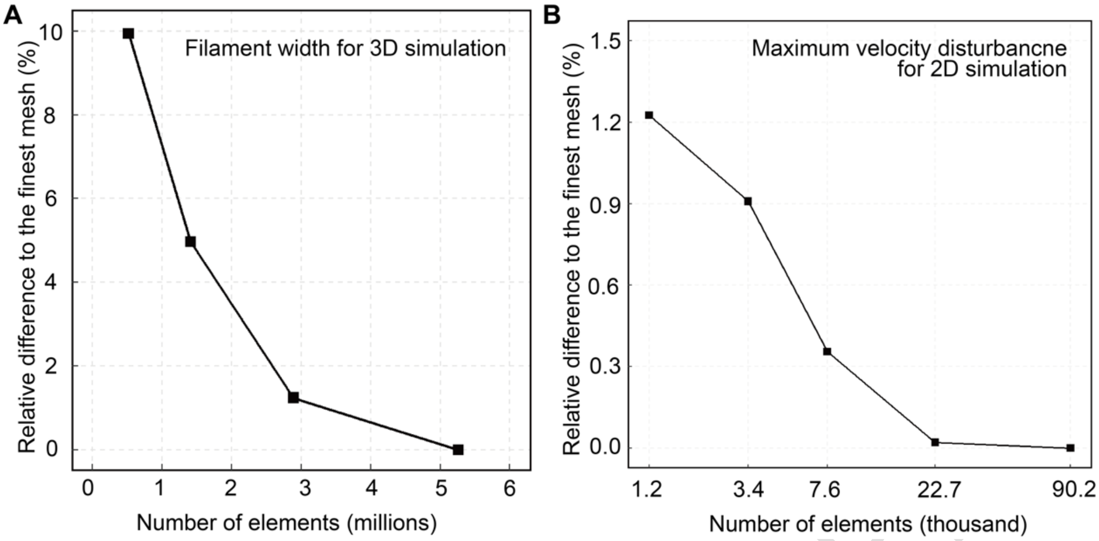

Figure S4. Mesh independence validation for numerical simulations. (A) Relative difference in predicted filament width as a function of the number of mesh elements (in millions) for the 3D simulation. (B) Relative difference in the maximum velocity disturbance as a function of the number of elements (in thousands) for the 2D simulation. Both plots demonstrate that the numerical results stabilize as the mesh is refined, ensuring the accuracy of the chosen mesh density.

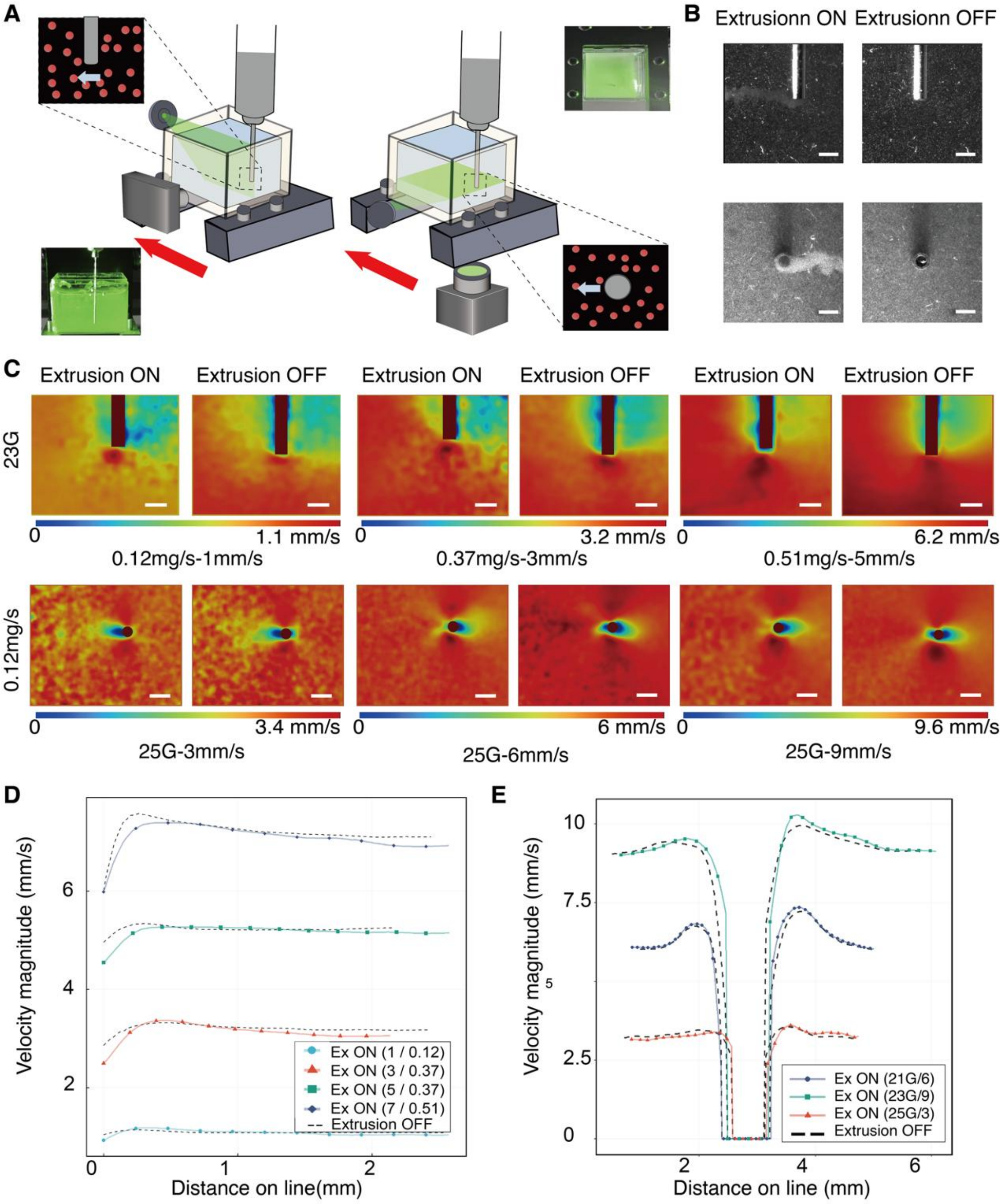

Figure S5. PIV experimental setup and multi-dimensional flow field analysis. (A) Schematic illustration of the PIV system, including the laser sheet orientation, camera positions for side and bottom views, and the nozzle movement in the supporting bath. (B) Representative raw PIV images. (C) Velocity magnitude counter for various needle gauges and printing parameters. (D-E) Quantitative comparison of velocity magnitude profiles along specific lines in the side view (D) and bottom view (E).

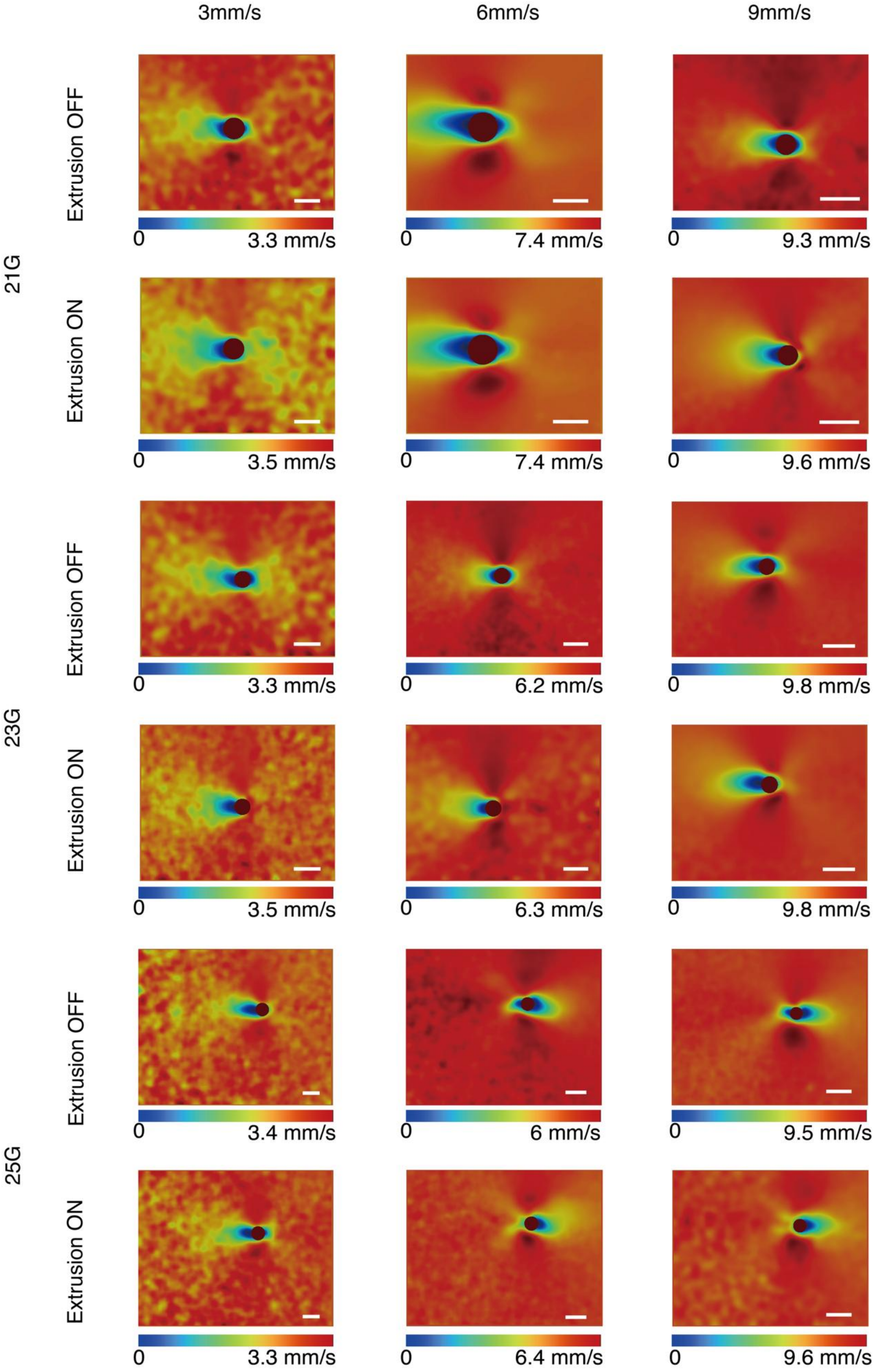

Figure S6. Influence of needle gauge and printing speed on the horizontal flow field

(Bottom view).

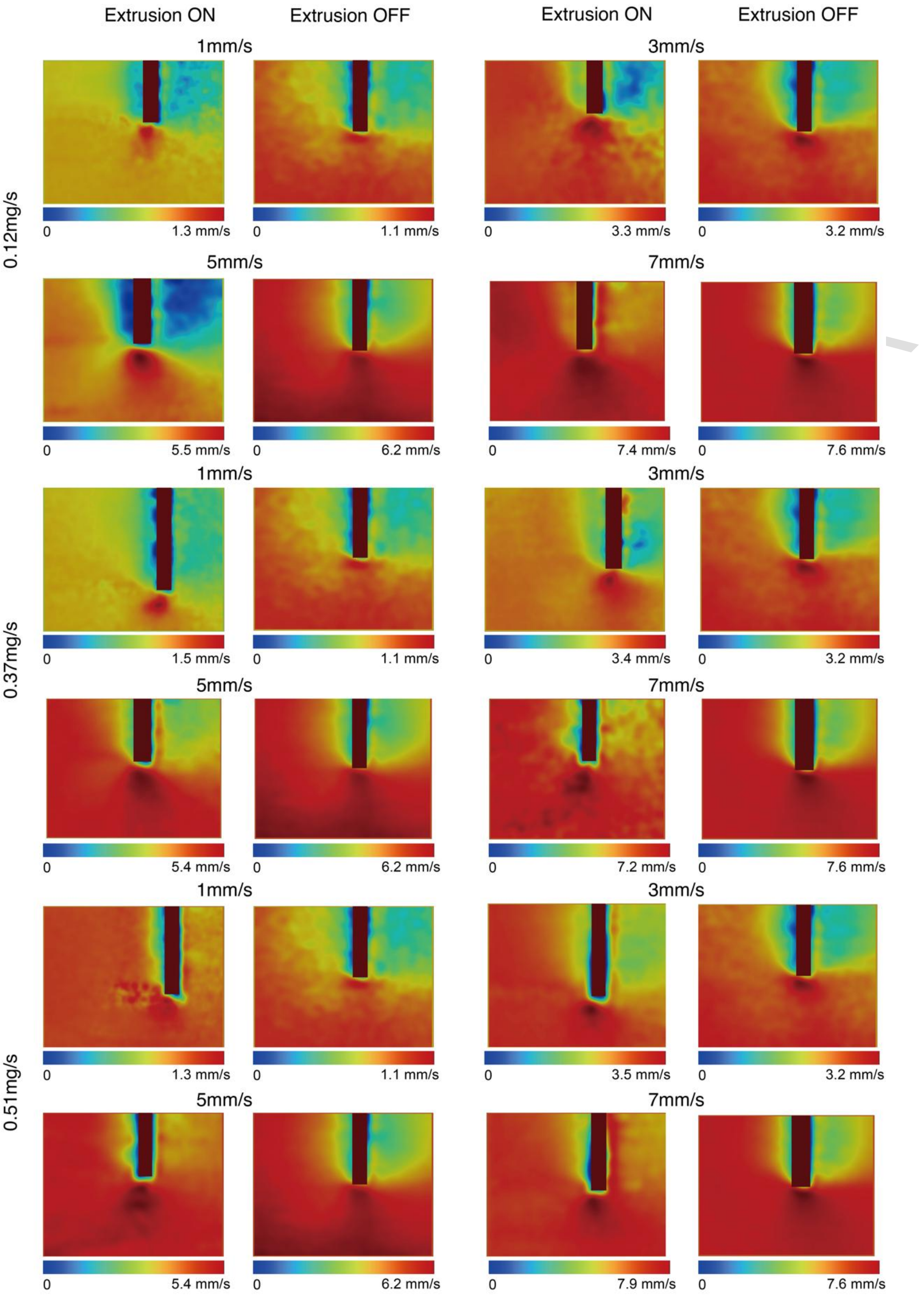

Figure S7. Effect of extrusion flow rate and printing speed on the vertical flow field (Side view).

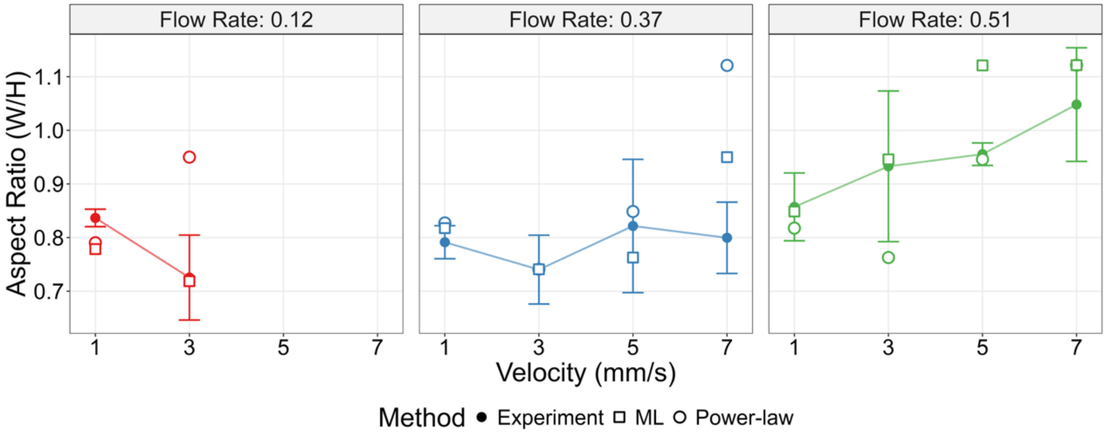

Figure S8. Comparison of filament aspect ratio (*W*/H) across experimental, analytical, and machine learning models. The plots show the aspect ratio as a function of printing velocity for three distinct flow rates. Data points represent experimental measurements, analytical predictions based on the Power-law model, and machine learning (ML) predictions (n = 3).

Figure S9. Comparative chart of different data quantities, showing that more than 315 well-distributed measurements are generally sufficient to achieve stable predictive performance.

Table S1 KEGG pathways enriched in the well-defined vs. over-stacked models

Category	Description	pvalue	p.adjust	group
Environmental Information Processing	Neuroactive ligand-receptor interaction	2.1474E-05	0.0027	Activated
Human Diseases	Hepatitis C	4.6674E-05	0.0028	Activated
Human Diseases	Influenza A	6.4949E-05	0.0028	Activated
Human Diseases	Herpes simplex virus 1 infection	0.0015	0.0468	Activated
Human Diseases	Epstein-Barr virus infection	0.0021	0.0534	Activated
Human Diseases	Measles	0.0025	0.0534	Activated
Organismal Systems	Renin-angiotensin system	0.0092	0.1356	Activated
Organismal Systems	NOD-like receptor signaling pathway	0.0103	0.1356	Activated
Human Diseases	Coronavirus disease - COVID-19	0.0107	0.1356	Activated
Metabolism	Tyrosine metabolism	0.0113	0.1356	Activated
nan	Hormone signaling	0.0117	0.1356	Activated
Metabolism	Tryptophan metabolism	0.0186	0.1980	Activated
Environmental Information Processing	Cell adhesion molecule (CAM) interaction	0.0352	0.3351	Activated
Organismal Systems	Renin secretion	0.0367	0.3351	Activated
Metabolism	Nucleotide metabolism	0.0450	0.3732	Activated
Human Diseases	Proteoglycans in cancer	0.0488	0.3732	Activated

Category	**Description**	**pvalue**	**p.adjust**	**group**
Metabolism	Arachidonic acid metabolism	0.0499	0.3732	Activated
Organismal Systems	Complement and coagulation cascades	0.0550	0.3732	Activated
Environmental Information Processing	Viral protein interaction with cytokine and cytokine receptor	0.0561	0.3732	Activated
Metabolism	Thiamine metabolism	0.0589	0.3732	Activated
Environmental Information Processing	cAMP signaling pathway	0.0612	0.3732	Activated
Metabolism	Selenocompound metabolism	0.0665	0.3866	Activated
Metabolism	Phenylalanine metabolism	0.0814	0.4429	Activated
Organismal Systems	Leukocyte transendothelial migration	0.0830	0.4429	Activated
Organismal Systems	Inflammatory mediator regulation of TRP channels	0.0965	0.4941	Activated
Organismal Systems	Vascular smooth muscle contraction	0.1145	0.5114	Activated
Environmental Information Processing	Cytokine-cytokine receptor interaction	0.1147	0.5114	Activated
Metabolism	beta-Alanine metabolism	0.1215	0.5114	Activated
Metabolism	Mucin type O-glycan biosynthesis	0.1215	0.5114	Activated

Category	**Description**	**pvalue**	**p.adjust**	**group**
Metabolism	Biosynthesis of cofactors	0.1264	0.5114	Activated
Organismal Systems	Adrenergic signaling in cardiomyocytes	0.1305	0.5114	Activated
Environmental Information Processing	Hippo signaling pathway	0.1332	0.5114	Activated
Human Diseases	Cushing syndrome	0.1387	0.5114	Activated
Human Diseases	African trypanosomiasis	0.1391	0.5114	Activated
Organismal Systems	Aldosterone-regulated sodium reabsorption	0.1426	0.5114	Activated
Metabolism	Glycine, serine and threonine metabolism	0.1495	0.5114	Activated
Human Diseases	Nicotine addiction	0.1495	0.5114	Activated
Environmental Information Processing	cGMP-PKG signaling pathway	0.1526	0.5114	Activated
Human Diseases	Hepatocellular carcinoma	0.1568	0.5114	Activated
Metabolism	Nicotinate and nicotinamide metabolism	0.1598	0.5114	Activated
Metabolism	Other types of O-glycan biosynthesis	0.1666	0.5201	Activated
nan	Virion - Hepatitis viruses	0.1867	0.5566	Activated
nan	Neuroactive ligand signaling	0.1870	0.5566	Activated

Category	**Description**	**pvalue**	**p.adjust**	**group**
Metabolism	Pyrimidine metabolism	0.2062	0.5653	Activated
Metabolism	Valine, leucine and isoleucine degradation	0.2062	0.5653	Activated
Human Diseases	Allograft rejection	0.2095	0.5653	Activated
Human Diseases	Graft-versus-host disease	0.2095	0.5653	Activated
Human Diseases	Diabetic cardiomyopathy	0.2164	0.5653	Activated
Genetic Information Processing	Viral life cycle - HIV-1	0.2254	0.5653	Activated
Human Diseases	Basal cell carcinoma	0.2254	0.5653	Activated
nan	Cornified envelope formation	0.2254	0.5653	Activated
Human Diseases	Type I diabetes mellitus	0.2316	0.5653	Activated
Human Diseases	Malaria	0.2347	0.5653	Activated
Human Diseases	Renal cell carcinoma	0.2471	0.5653	Activated
Metabolism	Drug metabolism - cytochrome P450	0.2532	0.5653	Activated
Organismal Systems	Cortisol synthesis and secretion	0.2532	0.5653	Activated
Human Diseases	Human immunodeficiency virus 1 infection	0.2538	0.5653	Activated
Human Diseases	Autoimmune thyroid disease	0.2592	0.5653	Activated
Organismal Systems	Gastric acid secretion	0.2623	0.5653	Activated

Category	Description	pvalue	p.adjust	group
Human Diseases	Pertussis	0.2682	0.5653	Activated
Organismal Systems	B cell receptor signaling pathway	0.2771	0.5653	Activated
Organismal Systems	Antigen processing and presentation	0.2946	0.5653	Activated
Organismal Systems	Insulin secretion	0.2946	0.5653	Activated
Cellular Processes	Peroxisome	0.2974	0.5653	Activated
Organismal Systems	Salivary secretion	0.2974	0.5653	Activated
Organismal Systems	GABAergic synapse	0.3088	0.5653	Activated
Organismal Systems	Taste transduction	0.3116	0.5653	Activated
Human Diseases	Viral myocarditis	0.3116	0.5653	Activated
Human Diseases	Morphine addiction	0.3144	0.5653	Activated
Organismal Systems	Circadian entrainment	0.3337	0.5653	Activated
Organismal Systems	Melanogenesis	0.3337	0.5653	Activated
Human Diseases	Hypertrophic cardiomyopathy	0.3337	0.5653	Activated
Human Diseases	AGE-RAGE signaling pathway in diabetic complications	0.3364	0.5653	Activated
Metabolism	Retinol metabolism	0.3391	0.5653	Activated
Human Diseases	Chagas disease	0.3418	0.5653	Activated
Human Diseases	Dilated cardiomyopathy	0.3418	0.5653	Activated

Category	**Description**	**pvalue**	**p.adjust**	**group**
nan	IgSF CAM signaling	0.3422	0.5653	Activated
Organismal Systems	Aldosterone synthesis and secretion	0.3445	0.5653	Activated
Environmental Information Processing	NF-kappa B signaling pathway	0.3524	0.5710	Activated
Human Diseases	Insulin resistance	0.3603	0.5765	Activated
Environmental Information Processing	TGF-beta signaling pathway	0.3655	0.5776	Activated
Environmental Information Processing	HIF-1 signaling pathway	0.3784	0.5804	Activated
Organismal Systems	Natural killer cell mediated cytotoxicity	0.3784	0.5804	Activated
Environmental Information Processing	TNF signaling pathway	0.3809	0.5804	Activated
Environmental Information Processing	Sphingolipid signaling pathway	0.4129	0.5967	Activated
Human Diseases	Staphylococcus aureus infection	0.4129	0.5967	Activated
Organismal Systems	Osteoclast differentiation	0.4153	0.5967	Activated
Environmental Information Processing	FoxO signaling pathway	0.4177	0.5967	Activated
Metabolism	Purine metabolism	0.4201	0.5967	Activated

Category	Description	pvalue	p.adjust	group
Human Diseases	Human papillomavirus infection	0.4246	0.5967	Activated
Cellular Processes	Apoptosis	0.4248	0.5967	Activated
Cellular Processes	Signaling pathways regulating pluripotency of stem cells	0.4341	0.5967	Activated
Human Diseases	Alcoholic liver disease	0.4365	0.5967	Activated
Human Diseases	Breast cancer	0.4501	0.5967	Activated
Environmental Information Processing	Phospholipase D signaling pathway	0.4546	0.5967	Activated
Human Diseases	Fluid shear stress and atherosclerosis	0.4546	0.5967	Activated
Human Diseases	Gastric cancer	0.4569	0.5967	Activated
Human Diseases	Systemic lupus erythematosus	0.4569	0.5967	Activated
Organismal Systems	Retrograde endocannabinoid signaling	0.4657	0.6021	Activated
Environmental Information Processing	mTOR signaling pathway	0.4744	0.6072	Activated
Cellular Processes	Efferocytosis	0.4850	0.6147	Activated
Cellular Processes	Tight junction	0.4976	0.6175	Activated
Environmental Information Processing	JAK-STAT signaling pathway	0.5017	0.6175	Activated
nan	Cadherin signaling	0.5018	0.6175	Activated
Cellular Processes	Necroptosis	0.5138	0.6183	Activated

Category	**Description**	**pvalue**	**p.adjust**	**group**
Environmental Information Processing	Wnt signaling pathway	0.5178	0.6183	Activated
Cellular Processes	Phagosome	0.5217	0.6183	Activated
Cellular Processes	Cellular senescence	0.5217	0.6183	Activated
Organismal Systems	Chemokine signaling pathway	0.5466	0.6419	Activated
Cellular Processes	Motor proteins	0.5540	0.6447	Activated
Human Diseases	Lipid and atherosclerosis	0.5876	0.6672	Activated
Human Diseases	Transcriptional misregulation in cancer	0.5910	0.6672	Activated
Human Diseases	Kaposi sarcoma-associated herpesvirus infection	0.5960	0.6672	Activated
Human Diseases	Viral carcinogenesis	0.6026	0.6672	Activated
Human Diseases	Chemical carcinogenesis - reactive oxygen species	0.6075	0.6672	Activated
Human Diseases	Chemical carcinogenesis - receptor activation	0.6107	0.6672	Activated
nan	Cytoskeleton in muscle cells	0.6139	0.6672	Activated
Cellular Processes	Regulation of actin cytoskeleton	0.6155	0.6672	Activated
Environmental Information Processing	Ras signaling pathway	0.6202	0.6672	Activated

Category	**Description**	**pvalue**	**p.adjust**	**group**
Human Diseases	Human T-cell leukemia virus 1 infection	0.6326	0.6738	Activated
Human Diseases	Salmonella infection	0.6416	0.6738	Activated
Human Diseases	Human cytomegalovirus infection	0.6460	0.6738	Activated
Environmental Information Processing	Calcium signaling pathway	0.6475	0.6738	Activated
Cellular Processes	Endocytosis	0.6659	0.6874	Activated
Environmental Information Processing	MAPK signaling pathway	0.7062	0.7232	Activated
Environmental Information Processing	PI3K-Akt signaling pathway	0.7796	0.7920	Activated
Human Diseases	Alzheimer disease	0.7982	0.8045	Activated
Human Diseases	Pathways of neurodegeneration - multiple diseases	0.8629	0.8629	Activated
Human Diseases	Platinum drug resistance	5.9477E-05	0.0086	Suppressed
nan	Cornified envelope formation	1.0212E-04	0.0086	Suppressed
Human Diseases	Fluid shear stress and atherosclerosis	2.5537E-04	0.0108	Suppressed
Metabolism	Drug metabolism - cytochrome P450	3.4198E-04	0.0108	Suppressed
Metabolism	Glutathione metabolism	3.6470E-04	0.0108	Suppressed

Category	**Description**	**pvalue**	**p.adjust**	**group**
Metabolism	Metabolism of xenobiotics by cytochrome P450	4.3976E-04	0.0108	Suppressed
Environmental Information Processing	HIF-1 signaling pathway	4.4967E-04	0.0108	Suppressed
Human Diseases	Chemical carcinogenesis - DNA adducts	9.5371E-04	0.0200	Suppressed
Metabolism	Drug metabolism - other enzymes	0.0013	0.0238	Suppressed
Genetic Information Processing	Ribosome	0.0017	0.0293	Suppressed
Human Diseases	Coronavirus disease - COVID-19	0.0020	0.0301	Suppressed

Table S2 GO pathways enriched in the well-defined vs. over-stacked models

Ontology	Description	pvalue	p.adjust	group
BP	cellular response to interferon-beta	7.0681E-20	1.2482E-16	Activated
BP	response to interferon-beta	6.8418E-19	6.0413E-16	Activated
BP	negative regulation of IP-10 production	5.1276E-08	2.7091E-05	Activated
BP	IP-10 production	7.6702E-08	2.7091E-05	Activated
BP	regulation of IP-10 production	7.6702E-08	2.7091E-05	Activated
BP	regulation of ribonuclease activity	2.7891E-07	8.2091E-05	Activated
BP	defense response to bacterium	4.5074E-07	1.1372E-04	Activated
BP	negative regulation of viral genome replication	1.8110E-06	3.9977E-04	Activated
BP	negative regulation of viral process	2.2683E-06	4.4510E-04	Activated
BP	regulation of nuclease activity	3.0351E-06	5.3048E-04	Activated
BP	regulation of heart rate	3.3042E-06	5.3048E-04	Activated
BP	regulation of blood circulation	5.8985E-06	8.6806E-04	Activated
BP	negative regulation of chemokine (C-X-C motif) ligand 2 production	7.3214E-06	8.9628E-04	Activated
BP	regulation of heart contraction	7.4857E-06	8.9628E-04	Activated

Category	Description	pvalue	p.adjust	group
BP	negative regulation of chemokine production	7.6128E-06	8.9628E-04	Activated
BP	positive regulation of cytosolic calcium ion concentration	8.8153E-06	9.7298E-04	Activated
BP	response to virus	1.1816E-05	0.0012	Activated
BP	regulation of blood pressure	1.5787E-05	0.0015	Activated
BP	defense response to protozoan	1.7550E-05	0.0016	Activated
BP	acute-phase response	1.9252E-05	0.0017	Activated
BP	regulation of viral genome replication	2.1042E-05	0.0018	Activated
BP	regulation of viral life cycle	2.2079E-05	0.0018	Activated
BP	negative regulation of heart rate	2.4525E-05	0.0019	Activated
BP	heart contraction	2.6098E-05	0.0019	Activated
BP	response to protozoan	2.7292E-05	0.0019	Activated
BP	heart process	3.6567E-05	0.0025	Activated
BP	positive regulation of interferon-beta production	3.7555E-05	0.0025	Activated
BP	positive regulation of blood pressure	5.4045E-05	0.0034	Activated
BP	regulation of innate immune response	5.5322E-05	0.0034	Activated
BP	positive regulation of monocyte chemotactic protein-1 production	5.7488E-05	0.0034	Activated

Category	Description	pvalue	p.adjust	group
BP	regulation of viral process	6.0864E-05	0.0035	Activated
BP	negative regulation of response to external stimulus	6.5945E-05	0.0036	Activated
BP	activation of innate immune response	7.2636E-05	0.0039	Activated
BP	viral genome replication	9.1360E-05	0.0047	Activated
BP	type I interferon-mediated signaling pathway	9.6189E-05	0.0047	Activated
BP	cellular response to type I interferon	9.6189E-05	0.0047	Activated
BP	negative regulation of innate immune response	1.0993E-04	0.0052	Activated
BP	negative regulation of heart contraction	1.1092E-04	0.0052	Activated
BP	negative regulation of type I interferon-mediated signaling pathway	1.2446E-04	0.0056	Activated
BP	interferon-beta production	1.3505E-04	0.0058	Activated
BP	regulation of interferon-beta production	1.3505E-04	0.0058	Activated
BP	negative regulation of blood circulation	1.3903E-04	0.0058	Activated
BP	response to type I interferon	1.4249E-04	0.0059	Activated

Category	Description	pvalue	p.adjust	group
BP	acute inflammatory response	1.5052E-04	0.0059	Activated
BP	chemokine (C-X-C motif) ligand 2 production	1.5467E-04	0.0059	Activated
BP	regulation of chemokine (C-X-C motif) ligand 2 production	1.5467E-04	0.0059	Activated
BP	defense response to virus	1.8895E-04	0.0067	Activated
BP	surfactant homeostasis	1.8928E-04	0.0067	Activated
BP	monocyte chemotactic protein-1 production	1.8928E-04	0.0067	Activated
BP	regulation of monocyte chemotactic protein-1 production	1.8928E-04	0.0067	Activated
BP	defense response to symbiont	1.9249E-04	0.0067	Activated
BP	response to interferon-alpha	2.0831E-04	0.0071	Activated
BP	negative regulation of immune response	2.3234E-04	0.0077	Activated
BP	interferon-mediated signaling pathway	2.4506E-04	0.0080	Activated
BP	positive regulation of type I interferon production	2.5645E-04	0.0082	Activated
BP	viral life cycle	2.9566E-04	0.0093	Activated

Category	Description	pvalue	p.adjust	group
BP	regulation of multicellular organism growth	3.0586E-04	0.0095	Activated
BP	positive regulation of multicellular organism growth	4.6970E-04	0.0143	Activated
BP	positive regulation of innate immune response	4.9582E-04	0.0148	Activated
BP	negative regulation of response to biotic stimulus	5.8995E-04	0.0174	Activated
BP	regulation of type I interferon-mediated signaling pathway	6.5484E-04	0.0190	Activated
BP	excitatory chemical synaptic transmission	6.9107E-04	0.0197	Activated
BP	positive regulation of response to biotic stimulus	7.4972E-04	0.0210	Activated
BP	endolysosomal toll-like receptor signaling pathway	8.3228E-04	0.0226	Activated
BP	regulation of chemokine production	8.3280E-04	0.0226	Activated
BP	regulation of transforming growth factor beta1 production	9.7547E-04	0.0261	Activated
BP	antiviral innate immune response	0.0010	0.0273	Activated
BP	regulation of systemic arterial blood pressure mediated by a chemical signal	0.0011	0.0284	Activated

Category	Description	pvalue	p.adjust	group
BP	regulation of tumor necrosis factor production	0.0011	0.0286	Activated
BP	chemokine production	0.0011	0.0286	Activated
BP	regulation of tumor necrosis factor superfamily cytokine production	0.0012	0.0289	Activated
BP	epithelial cell migration	0.0012	0.0289	Activated
BP	cytokine-mediated signaling pathway	0.0012	0.0289	Activated
BP	regulation of systemic arterial blood pressure	0.0012	0.0289	Activated
BP	viral process	0.0012	0.0289	Activated
BP	negative regulation of defense response	0.0013	0.0289	Activated
BP	epithelium migration	0.0013	0.0289	Activated
BP	tumor necrosis factor production	0.0013	0.0289	Activated
BP	tissue migration	0.0013	0.0289	Activated
BP	transforming growth factor beta1 production	0.0013	0.0289	Activated
BP	tumor necrosis factor superfamily cytokine production	0.0014	0.0300	Activated
BP	regulation of type I interferon production	0.0015	0.0322	Activated
BP	endothelial cell migration	0.0015	0.0322	Activated
BP	peptidyl-serine modification	0.0015	0.0322	Activated
BP	neutrophil migration	0.0016	0.0329	Activated

Category	Description	pvalue	p.adjust	group
BP	type I interferon production	0.0017	0.0352	Activated
BP	positive regulation of tumor necrosis factor production	0.0018	0.0366	Activated
BP	negative regulation of hydrolase activity	0.0018	0.0368	Activated
BP	regulation of systemic arterial blood pressure by circulatory renin-angiotensin	0.0019	0.0368	Activated
BP	spongiotrophoblast layer development	0.0019	0.0368	Activated
BP	positive regulation of tumor necrosis factor superfamily cytokine production	0.0019	0.0368	Activated
BP	cytosolic pattern recognition receptor signaling pathway	0.0021	0.0412	Activated
BP	cellular response to interferon-alpha	0.0023	0.0444	Activated
BP	negative regulation of peptidase activity	0.0024	0.0453	Activated
BP	nervous system process involved in regulation of systemic arterial blood pressure	0.0026	0.0469	Activated
BP	positive regulation of glycogen metabolic process	0.0026	0.0469	Activated
BP	positive regulation of transforming growth factor beta production	0.0026	0.0469	Activated

Category	Description	pvalue	p.adjust	group
BP	negative regulation of cytokine-mediated signaling pathway	0.0026	0.0474	Activated
BP	regulation of generation of precursor metabolites and energy	0.0028	0.0495	Activated
CC	high-density lipoprotein particle	2.7378E-04	0.0172	Activated
CC	cell-cell contact zone	3.2074E-04	0.0172	Activated
CC	plasma lipoprotein particle	5.0554E-04	0.0172	Activated
CC	lipoprotein particle	5.0554E-04	0.0172	Activated
CC	protein-lipid complex	6.1699E-04	0.0172	Activated
CC	intercalated disc	0.0018	0.0427	Activated
MF	adenylyltransferase activity	4.1542E-06	0.0012	Activated
MF	GTPase activity	1.5838E-05	0.0023	Activated
MF	ion channel regulator activity	1.4041E-04	0.0131	Activated
MF	channel regulator activity	1.8941E-04	0.0131	Activated
MF	double-stranded RNA binding	2.2945E-04	0.0131	Activated
MF	sodium channel regulator activity	3.0299E-04	0.0144	Activated
MF	nucleotidyltransferase activity	0.0016	0.0430	Activated
MF	ligand-gated monoatomic ion channel activity	0.0016	0.0430	Activated
MF	hormone activity	0.0017	0.0430	Activated

Category	Description	pvalue	p.adjust	group
MF	nucleoside monophosphate kinase activity	0.0017	0.0430	Activated
MF	cytokine activity	0.0017	0.0430	Activated
MF	ligand-gated channel activity	0.0018	0.0430	Activated
MF	nucleoside diphosphate kinase activity	0.0021	0.0470	Activated
BP	regulation of hormone secretion	1.1650E-06	0.0017	Suppressed
BP	peptide transport	1.3830E-06	0.0017	Suppressed
BP	amide transport	2.0224E-06	0.0017	Suppressed
BP	leukocyte chemotaxis	3.6884E-06	0.0019	Suppressed
BP	renal system process	3.9501E-06	0.0019	Suppressed
BP	peptide hormone secretion	5.4717E-06	0.0019	Suppressed
BP	hormone secretion	6.4641E-06	0.0019	Suppressed
BP	peptide secretion	6.7886E-06	0.0019	Suppressed
BP	cell chemotaxis	7.1578E-06	0.0019	Suppressed
BP	hormone transport	7.7767E-06	0.0019	Suppressed
BP	regulation of peptide hormone secretion	7.9677E-06	0.0019	Suppressed
BP	regulation of peptide secretion	9.2600E-06	0.0019	Suppressed
BP	regulation of peptide transport	9.8249E-06	0.0019	Suppressed
BP	regulation of blood pressure	1.6752E-05	0.0031	Suppressed
BP	positive regulation of leukocyte chemotaxis	2.1153E-05	0.0036	Suppressed

Category	Description	pvalue	p.adjust	group
BP	chemotaxis	2.3005E-05	0.0036	Suppressed
BP	taxis	2.3932E-05	0.0036	Suppressed
BP	positive regulation of urine volume	2.6353E-05	0.0036	Suppressed
BP	calcium ion transport	2.6394E-05	0.0036	Suppressed
BP	regulation of chemotaxis	3.3017E-05	0.0040	Suppressed
BP	leukocyte migration	3.4828E-05	0.0040	Suppressed
BP	negative regulation of smooth muscle cell migration	3.5341E-05	0.0040	Suppressed
BP	negative regulation of smooth muscle cell proliferation	3.6230E-05	0.0040	Suppressed
BP	regulation of leukocyte migration	3.9245E-05	0.0042	Suppressed
BP	second-messenger-mediated signaling	4.4063E-05	0.0045	Suppressed
BP	one-carbon metabolic process	4.8336E-05	0.0047	Suppressed
BP	regulation of systemic arterial blood pressure	4.9355E-05	0.0047	Suppressed
BP	regulation of mononuclear cell migration	5.1532E-05	0.0047	Suppressed
BP	protein homooligomerization	5.4697E-05	0.0048	Suppressed
BP	mononuclear cell migration	6.8533E-05	0.0055	Suppressed
BP	regulation of leukocyte chemotaxis	6.9008E-05	0.0055	Suppressed

Category	Description	pvalue	p.adjust	group
BP	regulation of body fluid levels	6.9427E-05	0.0055	Suppressed
BP	cellular response to gonadotropin stimulus	7.9967E-05	0.0062	Suppressed
BP	response to gonadotropin	1.1312E-04	0.0085	Suppressed
BP	regulation of T cell migration	1.2663E-04	0.0093	Suppressed
BP	regulation of insulin secretion	1.3172E-04	0.0094	Suppressed
BP	positive regulation of chemotaxis	1.9140E-04	0.0132	Suppressed
BP	regulation of renal system process	2.0372E-04	0.0137	Suppressed
BP	epithelial cell development	2.2984E-04	0.0147	Suppressed
BP	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	2.2984E-04	0.0147	Suppressed
BP	keratinization	2.3861E-04	0.0149	Suppressed
BP	intracellular calcium ion homeostasis	2.5730E-04	0.0157	Suppressed
BP	positive regulation of leukocyte migration	2.7108E-04	0.0161	Suppressed
BP	glutathione metabolic process	3.0612E-04	0.0178	Suppressed
BP	regulation of urine volume	3.3155E-04	0.0188	Suppressed
BP	regulation of lymphocyte migration	3.4455E-04	0.0192	Suppressed
BP	response to salt	3.5407E-04	0.0193	Suppressed

Category	Description	pvalue	p.adjust	group
BP	negative regulation of blood pressure	3.6501E-04	0.0193	Suppressed
BP	positive regulation of monocyte chemotaxis	3.6998E-04	0.0193	Suppressed
BP	protein complex oligomerization	3.8863E-04	0.0199	Suppressed
BP	insulin secretion	4.0658E-04	0.0199	Suppressed
BP	T cell migration	4.0851E-04	0.0199	Suppressed
BP	regulated exocytosis	4.1580E-04	0.0199	Suppressed
BP	cellular response to xenobiotic stimulus	4.1934E-04	0.0199	Suppressed
BP	calcium ion homeostasis	4.2834E-04	0.0199	Suppressed
BP	regulation of smooth muscle cell proliferation	4.4312E-04	0.0202	Suppressed
BP	smooth muscle cell proliferation	5.6345E-04	0.0253	Suppressed
BP	calcium-ion regulated exocytosis	6.1995E-04	0.0273	Suppressed
BP	regulation of monocyte chemotaxis	7.8303E-04	0.0335	Suppressed
BP	generation of precursor metabolites and energy	7.8494E-04	0.0335	Suppressed
BP	positive regulation of secretion by cell	8.2088E-04	0.0344	Suppressed
BP	endocrine system development	8.4296E-04	0.0348	Suppressed
BP	regulation of cardiac muscle cell contraction	0.0011	0.0412	Suppressed
BP	smooth muscle cell chemotaxis	0.0011	0.0412	Suppressed

Category	Description	pvalue	p.adjust	group
BP	regulation of serine-type endopeptidase activity	0.0011	0.0412	Suppressed
BP	negative regulation of serine-type endopeptidase activity	0.0011	0.0412	Suppressed
BP	regulation of serine-type peptidase activity	0.0011	0.0412	Suppressed
BP	negative regulation of serine-type peptidase activity	0.0011	0.0412	Suppressed
BP	regulation of T cell activation	0.0011	0.0426	Suppressed
BP	response to metal ion	0.0012	0.0433	Suppressed
BP	regulation of cell killing	0.0012	0.0433	Suppressed
BP	action potential	0.0012	0.0439	Suppressed
BP	regulation of regulated secretory pathway	0.0013	0.0465	Suppressed
BP	heart contraction	0.0013	0.0465	Suppressed
BP	regulation of protein secretion	0.0015	0.0497	Suppressed
CC	perikaryon	1.3362E-06	3.5543E-04	Suppressed
CC	postsynaptic membrane	1.5129E-05	0.0020	Suppressed
CC	apical plasma membrane	7.7054E-05	0.0068	Suppressed
CC	cornified envelope	3.3619E-04	0.0184	Suppressed
CC	transporter complex	3.4579E-04	0.0184	Suppressed
CC	cation channel complex	5.1879E-04	0.0230	Suppressed
CC	voltage-gated potassium channel complex	6.7999E-04	0.0258	Suppressed

Category	Description	pvalue	p.adjust	group
CC	collagen-containing extracellular matrix	0.0011	0.0303	Suppressed
CC	transmembrane transporter complex	0.0011	0.0303	Suppressed
CC	secretory granule	0.0011	0.0303	Suppressed
CC	potassium channel complex	0.0013	0.0307	Suppressed
CC	leading edge membrane	0.0014	0.0310	Suppressed
CC	basal part of cell	0.0015	0.0310	Suppressed
CC	juxtaparanode region of axon	0.0017	0.0319	Suppressed
CC	respirasome	0.0020	0.0355	Suppressed
CC	proximal dendrite	0.0023	0.0382	Suppressed
CC	germ cell nucleus	0.0025	0.0392	Suppressed
CC	basolateral plasma membrane	0.0027	0.0392	Suppressed
CC	basement membrane	0.0030	0.0418	Suppressed
MF	glutathione peroxidase activity	9.6045E-06	0.0024	Suppressed
MF	glutathione transferase activity	1.9301E-05	0.0024	Suppressed
MF	steroid delta-isomerase activity	2.6030E-05	0.0024	Suppressed
MF	oxidoreductase activity, acting on a sulfur group of donors, oxygen as acceptor	2.6030E-05	0.0024	Suppressed
MF	monocarboxylic acid binding	9.0860E-05	0.0058	Suppressed
MF	glutathione binding	9.4445E-05	0.0058	Suppressed
MF	peroxidase activity	2.5035E-04	0.0092	Suppressed

Category	Description	pvalue	p.adjust	group
MF	intramolecular oxidoreductase activity, transposing C=C bonds	2.5947E-04	0.0092	Suppressed
MF	fatty acid binding	2.6659E-04	0.0092	Suppressed
MF	oxidoreductase activity, acting on peroxide as acceptor	2.8356E-04	0.0092	Suppressed
MF	delayed rectifier potassium channel activity	2.9224E-04	0.0092	Suppressed
MF	transferase activity, transferring alkyl or aryl (other than methyl) groups	3.0130E-04	0.0092	Suppressed
MF	metal ion transmembrane transporter activity	3.6645E-04	0.0104	Suppressed
MF	oxidoreductase activity, acting on the CH-NH group of donors	4.0623E-04	0.0107	Suppressed
MF	hormone activity	6.8371E-04	0.0168	Suppressed
MF	voltage-gated monoatomic cation channel activity	7.7707E-04	0.0178	Suppressed
MF	carboxylic acid binding	8.2026E-04	0.0178	Suppressed
MF	antioxidant activity	0.0011	0.0207	Suppressed
MF	monoatomic ion gated channel activity	0.0011	0.0207	Suppressed
MF	gated channel activity	0.0012	0.0207	Suppressed
MF	organic acid binding	0.0012	0.0207	Suppressed
MF	voltage-gated potassium channel activity	0.0014	0.0242	Suppressed

Category	Description	pvalue	p.adjust	group
MF	14-3-3 protein binding	0.0020	0.0323	Suppressed
MF	oxidoreductase activity, acting on a sulfur group of donors	0.0023	0.0345	Suppressed
MF	peptidase regulator activity	0.0023	0.0345	Suppressed
MF	carbonate dehydratase activity	0.0025	0.0353	Suppressed
MF	toxic substance binding	0.0028	0.0372	Suppressed
MF	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	0.0028	0.0372	Suppressed
MF	intramolecular oxidoreductase activity	0.0031	0.0372	Suppressed
MF	G protein-coupled peptide receptor activity	0.0031	0.0372	Suppressed
MF	voltage-gated monoatomic ion channel activity	0.0032	0.0372	Suppressed
MF	voltage-gated channel activity	0.0032	0.0372	Suppressed
MF	potassium channel activity	0.0033	0.0372	Suppressed
MF	serine-type endopeptidase inhibitor activity	0.0041	0.0439	Suppressed
MF	peptide receptor activity	0.0042	0.0439	Suppressed
MF	transferase activity, transferring one-carbon groups	0.0043	0.0443	Suppressed