Kam Y J Zhang

List of Publications by Year in Descending Order

143 papers	7,682 citations	36 h-index	86 g-index
150 ext. papers	8,603 ext. citations	7.4 avg, IF	5.75 L-index

#	Paper	IF	Citations
143	Molecular dynamics simulations: Principles, methods, and applications in protein conformational dynamics **2022**, 439-454		1
142	In-Silico Design of a Novel Tridecapeptide Targeting Spike Protein of SARS-CoV-2 Variants of Concern.. *International Journal of Peptide Research and Therapeutics*, **2022**, 28, 28	2.1	3
141	Tumor Derived Extracellular Vesicles Drive T Cell Exhaustion in Tumor Microenvironment through Sphingosine Mediated Signaling and Impacting Immunotherapy Outcomes in Ovarian Cancer.. *Advanced Science*, **2022**, e2104452	13.6	0
140	TIRAP-mediated activation of p38 MAPK in inflammatory signaling.. *Scientific Reports*, **2022**, 12, 5601	4.9	2
139	A novel structure-based approach for identification of vertebrate susceptibility to SARS-CoV-2: Implications for future surveillance programmes.. *Environmental Research*, **2022**, 113303	7.9	1
138	Crystal structure of human acetylcholinesterase in complex with tacrine: Implications for drug discovery.. *International Journal of Biological Macromolecules*, **2022**, 210, 172-181	7.9	1
137	Piperidine-4-carboxamide as a new scaffold for designing secretory glutaminyl cyclase inhibitors. *International Journal of Biological Macromolecules*, **2021**, 170, 415-423	7.9	4
136	Evolutionary and codon usage preference insights into spike glycoprotein of SARS-CoV-2. *Briefings in Bioinformatics*, **2021**, 22, 1006-1022	13.4	7
135	Comprehensive Intrinsic Disorder Analysis of 6108 Viral Proteomes: From the Extent of Intrinsic Disorder Penetrance to Functional Annotation of Disordered Viral Proteins. *Journal of Proteome Research*, **2021**, 20, 2704-2713	5.6	4
134	Chemical similarity assisted search for acetylcholinesterase inhibitors: Molecular modeling and evaluation of their neuroprotective properties. *International Journal of Biological Macromolecules*, **2021**, 174, 466-476	7.9	2
133	Crystal Structure and Structure-Based Discovery of Inhibitors of the Nematode Chitinase Cht1. *Journal of Agricultural and Food Chemistry*, **2021**, 69, 3519-3526	5.7	6
132	The symmetric designer protein Pizza as a scaffold for metal coordination. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 945	4.2	2
131	A multidimensional computational exploration of congenital myasthenic syndrome causing mutations in human choline acetyltransferase. *Journal of Cellular Biochemistry*, **2021**, 122, 787-800	4.7	1
130	Targeting LIF/LIFR signaling in cancer. *Genes and Diseases*, **2021**,	6.6	3
129	Lean-Docking: Exploiting Ligands' Predicted Docking Scores to Accelerate Molecular Docking. *Journal of Chemical Information and Modeling*, **2021**, 61, 2341-2352	6.1	6
128	Understanding the molecular interactions of inhibitors against Bla1 beta-lactamase towards unraveling the mechanism of antimicrobial resistance. *International Journal of Biological Macromolecules*, **2021**, 177, 337-350	7.9	1
127	Insights into the evolutionary forces that shape the codon usage in the viral genome segments encoding intrinsically disordered protein regions. *Briefings in Bioinformatics*, **2021**, 22,	13.4	3

126	Identification of 1,2,4-Triazolylthioethanone Scaffold for the Design of New Acetylcholinesterase Inhibitors. *Molecular Informatics*, **2021**, 40, e2100020	3.8	
125	A variant in human AIOLOS impairs adaptive immunity by interfering with IKAROS. *Nature Immunology*, **2021**, 22, 893-903	19.1	9
124	A loss-of-function variant in SUV39H2 identified in autism-spectrum disorder causes altered H3K9 trimethylation and dysregulation of protocadherin β-cluster genes in the developing brain. *Molecular Psychiatry*, **2021**,	15.1	2
123	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. *Science Advances*, **2021**, 7,	14.3	2
122	Structure-based virtual screening of highly potent inhibitors of the nematode chitinase Cht1. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **2021**, 36, 1198-1204	5.6	2
121	Identification of Novel Cathepsin B Inhibitors with Implications in Alzheimer's Disease: Computational Refining and Biochemical Evaluation. *Cells*, **2021**, 10,	7.9	2
120	A Novel Therapeutic Peptide Blocks SARS-CoV-2 Spike Protein Binding with Host Cell ACE2 Receptor. *Drugs in R and D*, **2021**, 21, 273-283	3.4	6
119	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. *Briefings in Bioinformatics*, **2021**, 22,	13.4	1
118	Seven Amino Acid Types Suffice to Create the Core Fold of RNA Polymerase. *Journal of the American Chemical Society*, **2021**, 143, 15998-16006	16.4	4
117	Evolutionary Signatures Governing the Codon Usage Bias in Coronaviruses and Their Implications for Viruses Infecting Various Bat Species. *Viruses*, **2021**, 13,	6.2	4
116	ProFitFun: A Protein Tertiary Structure Fitness Function for Quantifying the Accuracies of Model Structures. *Bioinformatics*, **2021**,	7.2	1
115	Neuroprotective derivatives of tacrine that target NMDA receptor and acetyl cholinesterase - Design, synthesis and biological evaluation. *Computational and Structural Biotechnology Journal*, **2021**, 19, 4517-4537	6.8	4
114	Actin R256 Mono-methylation Is a Conserved Post-translational Modification Involved in Transcription. *Cell Reports*, **2020**, 32, 108172	10.6	4
113	Design of a peptide-based subunit vaccine against novel coronavirus SARS-CoV-2. *Microbial Pathogenesis*, **2020**, 145, 104236	3.8	110
112	A protein sequence fitness function for identifying natural and nonnatural proteins. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 1271-1284	4.2	5
111	EC330, a small-molecule compound, is a potential novel inhibitor of LIF signaling. *Journal of Molecular Cell Biology*, **2020**, 12, 477-480	6.3	4
110	A Series of Compounds Bearing a Dipyrido-Pyrimidine Scaffold Acting as Novel Human and Insect Pest Chitinase Inhibitors. *Journal of Medicinal Chemistry*, **2020**, 63, 987-1001	8.3	16
109	ATP7A Clinical Genetics Resource - A comprehensive clinically annotated database and resource for genetic variants in ATP7A gene. *Computational and Structural Biotechnology Journal*, **2020**, 18, 2347-2356	6.8	1

108	Mechanistic insights into the loss-of-function mechanisms of rare human D-amino acid oxidase variants implicated in amyotrophic lateral sclerosis. *Scientific Reports*, **2020**, 10, 17146	4.9	4
107	Identification of a Selective RelA Inhibitor Based on DSE-FRET Screening Methods. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	1
106	Improving ligand 3D shape similarity-based pose prediction with a continuum solvent model. *Journal of Computer-Aided Molecular Design*, **2019**, 33, 1045-1055	4.2	1
105	EC359: A First-in-Class Small-Molecule Inhibitor for Targeting Oncogenic LIFR Signaling in Triple-Negative Breast Cancer. *Molecular Cancer Therapeutics*, **2019**, 18, 1341-1354	6.1	17
104	Human Chitinases: Structure, Function, and Inhibitor Discovery. *Advances in Experimental Medicine and Biology*, **2019**, 1142, 221-251	3.6	13
103	Chemoinformatics and structural bioinformatics in OCaml. *Journal of Cheminformatics*, **2019**, 11, 10	8.6	3
102	Shape similarity guided pose prediction: lessons from D3R Grand Challenge 3. *Journal of Computer-Aided Molecular Design*, **2019**, 33, 47-59	4.2	6
101	Population-Based Sampling and Fragment-Based De Novo Protein Structure Prediction **2019**, 774-784		1
100	Human glutaminyl cyclase: Structure, function, inhibitors and involvement in Alzheimer's disease. *Pharmacological Research*, **2019**, 147, 104342	10.2	7
99	Computational design of symmetrical eight-bladed β-propeller proteins. *IUCrJ*, **2019**, 6, 46-55	4.7	25
98	EC313-a tissue selective SPRM reduces the growth and proliferation of uterine fibroids in a human uterine fibroid tissue xenograft model. *Scientific Reports*, **2019**, 9, 17279	4.9	0
97	A structural homology approach for computational protein design with flexible backbone. *Bioinformatics*, **2019**, 35, 2418-2426	7.2	4
96	A cross docking pipeline for improving pose prediction and virtual screening performance. *Journal of Computer-Aided Molecular Design*, **2018**, 32, 163-173	4.2	15
95	Advances in the Development of Shape Similarity Methods and Their Application in Drug Discovery. *Frontiers in Chemistry*, **2018**, 6, 315	5	56
94	Discovery of Fungal Denitrification Inhibitors by Targeting Copper Nitrite Reductase from Fusarium oxysporum. *Journal of Chemical Information and Modeling*, **2017**, 57, 203-213	6.1	15
93	Balancing exploration and exploitation in population-based sampling improves fragment-based de novo protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 852-858	4.2	14
92	Evolution-Inspired Computational Design of Symmetric Proteins. *Methods in Molecular Biology*, **2017**, 1529, 309-322	1.4	10
91	Computational design of a symmetrical β-trefoil lectin with cancer cell binding activity. *Scientific Reports*, **2017**, 7, 5943	4.9	23

90	Identification and structure-activity relationship of purine derivatives as novel MTH1 inhibitors. *Chemical Biology and Drug Design*, **2017**, 89, 862-869	2.9	6
89	Fragger: a protein fragment picker for structural queries. *F1000Research*, **2017**, 6, 1722	3.6	1
88	Fragger: a protein fragment picker for structural queries. *F1000Research*, **2017**, 6, 1722	3.6	2
87	Application of Shape Similarity in Pose Selection and Virtual Screening in CSARdock2014 Exercise. *Journal of Chemical Information and Modeling*, **2016**, 56, 965-73	6.1	22
86	Understanding the Assembly of an Artificial Protein Nanotube. *Advanced Materials Interfaces*, **2016**, 3, 1600846	4.6	6
85	A Novel Scaffold for Developing Specific or Broad-Spectrum Chitinase Inhibitors. *Journal of Chemical Information and Modeling*, **2016**, 56, 2413-2420	6.1	18
84	The Effect of F877L and T878A Mutations on Androgen Receptor Response to Enzalutamide. *Molecular Cancer Therapeutics*, **2016**, 15, 1702-12	6.1	48
83	Identification of new SUMO activating enzyme 1 inhibitors using virtual screening and scaffold hopping. *Bioorganic and Medicinal Chemistry Letters*, **2016**, 26, 1218-23	2.9	27
82	A pose prediction approach based on ligand 3D shape similarity. *Journal of Computer-Aided Molecular Design*, **2016**, 30, 457-69	4.2	13
81	Prospective evaluation of shape similarity based pose prediction method in D3R Grand Challenge 2015. *Journal of Computer-Aided Molecular Design*, **2016**, 30, 685-693	4.2	10
80	Advances in the development of SUMO specific protease (SENP) inhibitors. *Computational and Structural Biotechnology Journal*, **2015**, 13, 204-11	6.8	42
79	Synthesis, cholinesterase inhibition and molecular modelling studies of coumarin linked thiourea derivatives. *Bioorganic Chemistry*, **2015**, 63, 58-63	5.1	38
78	Biomineralization of a Cadmium Chloride Nanocrystal by a Designed Symmetrical Protein. *Angewandte Chemie - International Edition*, **2015**, 54, 9857-60	16.4	31
77	Hierarchical virtual screening approaches in small molecule drug discovery. *Methods*, **2015**, 71, 26-37	4.6	90
76	Biomineralization of a Cadmium Chloride Nanocrystal by a Designed Symmetrical Protein. *Angewandte Chemie*, **2015**, 127, 9995-9998	3.6	
75	Characterization of pH-induced transitions of Entamoeba histolytica D-phosphoglycerate dehydrogenase. *International Journal of Biological Macromolecules*, **2015**, 79, 284-9	7.9	1
74	The crystal and solution structure of YdiE from Escherichia coli. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 919-24	1.1	1
73	A fragmentation and reassembly method for ab initio phasing. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 304-12		14

72	Quality Assessment of Predicted Protein Models Using Energies Calculated by the Fragment Molecular Orbital Method. *Molecular Informatics*, **2015**, 34, 97-104	3.8	12
71	Improving fragment quality for de novo structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 2240-52	4.2	9
70	Discovery of small molecule inhibitors targeting the SUMO□SIM interaction using a protein interface consensus approach. *MedChemComm*, **2014**, 5, 783-786	5	6
69	Identification of sumoylation inhibitors targeting a predicted pocket in Ubc9. *Journal of Chemical Information and Modeling*, **2014**, 54, 2784-93	6.1	11
68	Identification of 1,2,5-oxadiazoles as a new class of SENP2 inhibitors using structure based virtual screening. *Journal of Chemical Information and Modeling*, **2014**, 54, 870-80	6.1	40
67	Computational design of a self-assembling symmetrical □propeller protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 15102-7	11.5	101
66	A rotation-translation invariant molecular descriptor of partial charges and its use in ligand-based virtual screening. *Journal of Cheminformatics*, **2014**, 6, 23	8.6	19
65	Pharmacophore modeling: advances, limitations, and current utility in drug discovery. *Journal of Receptor, Ligand and Channel Research*, **2014**, 81		22
64	Assay methods for small ubiquitin-like modifier (SUMO)-SUMO-interacting motif (SIM) interactions in vivo and in vitro using a split-luciferase complementation system. *Analytical Biochemistry*, **2014**, 448, 92-4	3.1	7
63	Combining in silico and in cerebro approaches for virtual screening and pose prediction in SAMPL4. *Journal of Computer-Aided Molecular Design*, **2014**, 28, 363-73	4.2	22
62	Computational Investigation of SENP:SUMO Protein-Protein Interaction for Structure Based Drug Design. *Molecular Informatics*, **2013**, 32, 267-80	3.8	4
61	Identification of small peptides inhibiting the integrase-LEDGF/p75 interaction through targeting the cellular co-factor. *Journal of Peptide Science*, **2013**, 19, 651-8	2.1	7
60	CDC25A-inhibitory RE derivatives bind to pocket adjacent to the catalytic site. *Molecular BioSystems* , **2013**, 9, 1026-34		4
59	Identification of quinazolinyloxy biaryl urea as a new class of SUMO activating enzyme 1 inhibitors. *Bioorganic and Medicinal Chemistry Letters*, **2013**, 23, 5145-9	2.9	16
58	The discovery of novel human androgen receptor antagonist chemotypes using a combined pharmacophore screening procedure. *ChemMedChem*, **2013**, 8, 644-51	3.7	23
57	Identification of sumoylation activating enzyme 1 inhibitors by structure-based virtual screening. *Journal of Chemical Information and Modeling*, **2013**, 53, 809-20	6.1	37
56	Investigation on the effect of key water molecules on docking performance in CSARdock exercise. *Journal of Chemical Information and Modeling*, **2013**, 53, 1880-92	6.1	35
55	Spectomycin B1 as a novel SUMOylation inhibitor that directly binds to SUMO E2. *ACS Chemical Biology*, **2013**, 8, 2635-42	4.9	68

54	Protein interface pharmacophore mapping tools for small molecule protein: protein interaction inhibitor discovery. *Current Topics in Medicinal Chemistry*, **2013**, 13, 989-1001	3	30
53	Design and pharmacology of a highly specific dual FMS and KIT kinase inhibitor. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 5689-94	11.5	61
52	Efficient sampling in fragment-based protein structure prediction using an estimation of distribution algorithm. *PLoS ONE*, **2013**, 8, e68954	3.7	20
51	Electrostatic similarities between protein and small molecule ligands facilitate the design of protein-protein interaction inhibitors. *PLoS ONE*, **2013**, 8, e75762	3.7	14
50	Glu-108 is essential for subunit assembly and dimer stability of D-phosphoglycerate dehydrogenase from Entamoeba histolytica. *Molecular and Biochemical Parasitology*, **2012**, 181, 117-24	1.9	11
49	Durandal: fast exact clustering of protein decoys. *Journal of Computational Chemistry*, **2012**, 33, 471-4	3.5	20
48	An integrated fragment based screening approach for the discovery of small molecule modulators of the VWF-GPIbα interaction. *Chemical Communications*, **2012**, 48, 11349-51	5.8	8
47	Novel protein-protein interactions between Entamoeba histolyticad-phosphoglycerate dehydrogenase and phosphoserine aminotransferase. *Biochimie*, **2012**, 94, 1676-86	4.6	5
46	Error-estimation-guided rebuilding of de novo models increases the success rate of ab initio phasing. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 1522-34		6
45	Computational fragment-based screening using RosettaLigand: the SAMPL3 challenge. *Journal of Computer-Aided Molecular Design*, **2012**, 26, 603-16	4.2	13
44	Role of conserved active site tryptophan-101 in functional activity and stability of phosphoserine aminotransferase from an enteric human parasite. *Amino Acids*, **2012**, 43, 483-91	3.5	8
43	Pharmacophore modelling as a virtual screening tool for the discovery of small molecule protein-protein interaction inhibitors. *Current Pharmaceutical Design*, **2012**, 18, 4586-98	3.3	19
42	A probabilistic fragment-based protein structure prediction algorithm. *PLoS ONE*, **2012**, 7, e38799	3.7	36
41	Accelerating ab initio phasing with de novo models. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 804-12		13
40	Entropy-accelerated exact clustering of protein decoys. *Bioinformatics*, **2011**, 27, 939-45	7.2	20
39	Clinical efficacy of a RAF inhibitor needs broad target blockade in BRAF-mutant melanoma. *Nature*, **2010**, 467, 596-9	50.4	1379
38	PAR: a PARallel and distributed job crusher. *Bioinformatics*, **2010**, 26, 2918-9	7.2	6
37	Scaffold-based discovery of indeglitazar, a PPAR pan-active anti-diabetic agent. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 262-7	11.5	115

36	Discovery of a selective inhibitor of oncogenic B-Raf kinase with potent antimelanoma activity. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 3041-6	11.5	1056
35	Scaffold-Based Drug Discovery **2007**, 129-153		6
34	Identification of a novel noncatalytic bicarbonate binding site in eubacterial beta-carbonic anhydrase. *Biochemistry*, **2006**, 45, 4351-61	3.2	91
33	Germline KRAS mutations cause Noonan syndrome. *Nature Genetics*, **2006**, 38, 331-6	36.3	562
32	Crystal Structure of Phosphodiesterase Families and the Potential for Rational Drug Design **2006**,		2
31	Phosphodiesterase-4 as a potential drug target. *Expert Opinion on Therapeutic Targets*, **2005**, 9, 1283-305	6.4	70
30	A family of phosphodiesterase inhibitors discovered by cocrystallography and scaffold-based drug design. *Nature Biotechnology*, **2005**, 23, 201-7	44.5	200
29	Keynote review: phosphodiesterase-4 as a therapeutic target. *Drug Discovery Today*, **2005**, 10, 1503-19	8.8	530
28	Bcl-XL mutations suppress cellular sensitivity to antimycin A. *Journal of Biological Chemistry*, **2004**, 279, 2159-65	5.4	61
27	Mcl-1 is required for Akata6 B-lymphoma cell survival and is converted to a cell death molecule by efficient caspase-mediated cleavage. *Oncogene*, **2004**, 23, 4818-27	9.2	121
26	Structural basis for the activity of drugs that inhibit phosphodiesterases. *Structure*, **2004**, 12, 2233-47	5.2	307
25	A glutamine switch mechanism for nucleotide selectivity by phosphodiesterases. *Molecular Cell*, **2004**, 15, 279-86	17.6	240
24	A Glutamine Switch Mechanism for Nucleotide Selectivity by Phosphodiesterases. *Molecular Cell*, **2004**, 15, 659	17.6	3
23	Multidimensional histograms for density modification. *Methods in Enzymology*, **2003**, 374, 188-203	1.7	
22	Accurate computer-based design of a new backbone conformation in the second turn of protein L. *Journal of Molecular Biology*, **2002**, 315, 471-7	6.5	70
21	Structures of the B1 domain of protein L from Peptostreptococcus magnus with a tyrosine to tryptophan substitution. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 480-7		54
20	Post-translational modification of the N-terminal His tag interferes with the crystallization of the wild-type and mutant SH3 domains from chicken src tyrosine kinase. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 759-62		39
19	Crystal structure of E. coli beta-carbonic anhydrase, an enzyme with an unusual pH-dependent activity. *Protein Science*, **2001**, 10, 911-22	6.3	131

18	Antimycin A mimics a cell-death-inducing Bcl-2 homology domain 3. *Nature Cell Biology*, **2001**, 3, 183-91	23.4	391
17	Single-site mutations induce 3D domain swapping in the B1 domain of protein L from Peptostreptococcus magnus. *Structure*, **2001**, 9, 1017-27	5.2	50
16	Conversion of monomeric protein L to an obligate dimer by computational protein design. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 10687-91	11.5	62
15	Biophysical characterization of recombinant human Bcl-2 and its interactions with an inhibitory ligand, antimycin A. *Biochemistry*, **2001**, 40, 4911-22	3.2	75
14	Crystallization and preliminary X-ray diffraction studies of mutants of B1 IgG-binding domain of protein L from Peptostreptococcus magnus. *Acta Crystallographica Section D: Biological Crystallography*, **2000**, 56, 506-8		4
13	Cloning, crystallization and preliminary characterization of a beta-carbonic anhydrase from Escherichia coli. *Acta Crystallographica Section D: Biological Crystallography*, **2000**, 56, 1176-9		14
12	A two-dimensional histogram-matching method for protein phase refinement and extension. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 1893-900		7
11	Density modification for macromolecular phase improvement. *Progress in Biophysics and Molecular Biology*, **1999**, 72, 245-70	4.7	199
10	The two-dimensional histogram as a constraint for protein phase improvement. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 1230-44		8
9	Mutation and modeling analysis of the Saccharomyces cerevisiae Swi6 ankyrin repeats. *Biochemistry* , **1998**, 37, 4437-50	3.2	12
8	Oncogene-dependent apoptosis in extracts from drug-resistant cells. *Genes and Development*, **1997** , 11, 1266-76	12.6	54
7	Combining constraints for electron-density modification. *Methods in Enzymology*, **1997**, 277, 53-64	1.7	95
6	Solid-state phase transition in the crystal structure of ribulose 1,5-bisphosphate carboxylase/oxygenase. *Acta Crystallographica Section D: Biological Crystallography*, **1994**, 50, 258-62		4
5	Ambiguities in ab initio phasing. *Science*, **1993**, 259, 1771-2	33.3	1
4	SQUASH - combining constraints for macromolecular phase refinement and extension. *Acta Crystallographica Section D: Biological Crystallography*, **1993**, 49, 213-22		34
3	The use of Sayre's equation with solvent flattening and histogram matching for phase extension and refinement of protein structures. *Acta Crystallographica Section A: Foundations and Advances*, **1990**, 46, 377-381		80
2	High Throughput Designing and Mutational Mapping of RBD-ACE2 Interface Guide Non-Conventional Therapeutic Strategies for COVID-19		6
1	Seven amino acid types suffice to reconstruct the core fold of RNA polymerase		1