

Quantum Kerr- (A) Ds Galilean Myers– Perr driven gravitational transformations for the anti-COVID-19 Roccuffirna™ drug design.

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Abstract

General methods to quantize reference frame transformations, to a “superposition of coordinate transformations” have been previously introduced on an array of recent observations developed through gravitational amplification of primeval density fluctuations generated in the exceedingly early phase of cosmic evolution. In this paper, we strongly combine machine learning characteristics to Quantum Kerr- (A) dS-Myers–Perry black microBlackHole-Inspired Gravitational for both Euclidean and Lorentzian signatures in Practice. I provide algorithms by means of mean percentile free energy ranking, in a new recall-based evaluation metric for the generation of an anti-COVID-19 small molecule combination of Roccuffirna™, Roccuttirna™, and Eplerotiffirna™ anti- (nCoV-19) ligands. In this paper, I show that the notion of entanglement and superposition are observer-dependent features in quantum circuit reference frames including Galilean transformation, and near-horizon symmetries ranging from supergravity theories to Lorentzian cryptographic signatures to enhance the Roccuffirna™’s gravity to trap the SARS-COV-2 viruses in practice.

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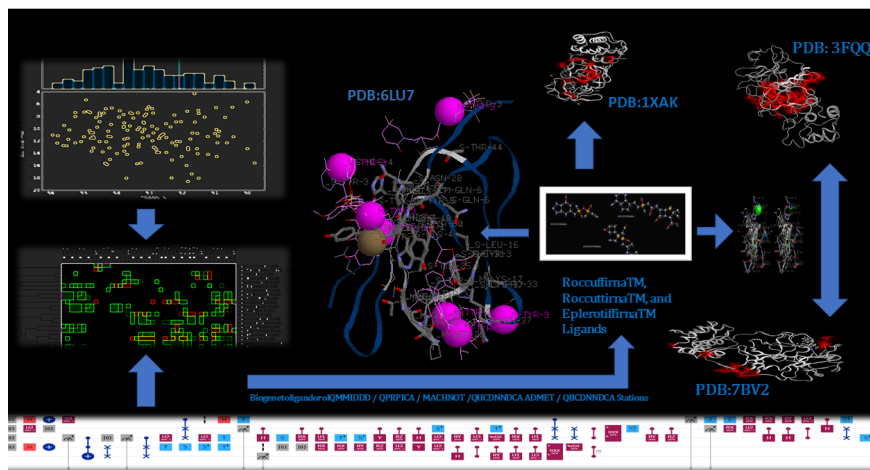
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ABSTRACT

General methods to quantize reference frame transformations, to a “superposition of coordinate transformations” have been previously introduced on an array of recent observations developed through gravitational amplification of primeval density fluctuations generated in the exceedingly early phase of cosmic evolution. In this paper, we strongly combine machine learning characteristics to Quantum Kerr- (A) dS-Myers–Perry black microBlackHole-Inspired

Gravitational for both Euclidean and Lorentzian signatures in Practice. I provide algorithms by means of mean percentile free energy ranking, in a new recall-based evaluation metric for the generation of an anti-COVID-19 small molecule combination of RoccuffirnaTM, RoccutirnaTM, and EplerotiffirnaTM anti- (nCoV-19) ligands. In this paper, I show that the notion of entanglement and superposition are observer-dependent features in quantum circuit reference frames including Galilean trans formation, and near-horizon symmetries ranging from supergravity theories to Lorentzian cryptographic signatures to enhance the RoccuffirnaTM's gravity to trap the SARS-COV-2 viruses in practice.



SIGNIFICANT STATEMENTS

In this original research paper, I write the Schrödinger equation in quantum reference frames. As a part of this project that the quantum canonical transformations are defined outside of the Hilbert space, we finally designed small molecules the RoccuffirnaTM's chemical structures that comprising the highest binding free energy docking values based on reliable comparisons of numerical cryptographical models with observed docking data by using Galilean Black Hole Transformations, Quantum chemistry phenomena, and Pharmacophoric Merging Hyper-algorithms. (31, 32, 37-43) As a by-product of the fact that the quantum canonical transformations are defined outside of the Hilbert space, I was able of the QMMM construction of the Roccuffirna small molecule by introducing numerical cosmological calculations to investigate different quantum chemistry phenomena.

INTRODUCTION

The emergence of a novel coronavirus infection causing new Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2),coronavirus (nCoV-19) has brought tremendous impact on worldwide health, (1, 2, 3, 4, 5) whilst the chemogenomic interactions between the virus and the human is widely recognized to be critical foundation in responding the current outbreak the of the COVID2019 disease. Systems using DNA as a one-time code pad in a steganographic approach have been described (15).In work by Gehani et al. they proposed use of DNA codes assembled from short oligonucleotide sequences, into one-time pads. They further assume that the one-time pads can be kept as a pre-shared secret. The approach relies on encoding the plaintext through a DNA substitution a bit-wise XOR function between the plaintext and the DNA sequence. They also propose that the language for creating the DNA ciphertext be disjoint from the plaintext. Gehani also proposes an approach with biological instantiation (5). (6, 7, 8, 9, 10, 11, 12)The virus has been named severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) (3) because the RNA genome is about 82% identical to that of the SARS coronavirus(SARS-CoV) ; both viruses belong to clade b of the genus Beta-coronavirus (1, 2) caused an outbreak of severe pulmonary disease in China, in the city of Wuhan, the capital of Hubei province and was initially detected in Himalayan palm civets(Guan et al., 2003) that may have

served as an amplification host. The civet virus contained a 29-nucleotide sequence not found in most human isolates that were related to the global epidemic and thus, can be considered as druggable targets. (1-4, 13, 14, 15, 16) It has been speculated that the function of the affected open reading frame (ORF 10) might have played an important role in the trans-species jump infections. (17, 18, 19, 20, 21) A similar virus was found later in horseshoe bat (13-20, 21, 22, 23, 24, and 25). Structural and biochemical characterizations have indicated to us that a 29-bp insertion in ORF 8 of bat-SARS-CoV genome, not found in most human SARS-CoV genomes of a common ancestor with civet SARS-CoV (11-17, 18-23, 24, 25, 26, 27). Numerical investigations and Equilibrium black-hole cryptography solutions to Einstein's Eqs have been known since the advent of general relativity. DNA signatures based on integration sites between the transgene insert and the flanking DNA make use of the same idea. While these types of signatures have been the paradigm of GMO detection for decades, this article strongly challenges the function of such signatures, especially relative to intended manipulations. Both traditionally and in the cyber-domain, signatures have long served as a valuable tool to guarantee the integrity and authenticity of the document being signed. However, the very concept of signatures in the cyber-realm first needed to be redressed as the Internet is Susceptible to intrusions that are not existent in the traditional setting. Analogously, it is argued here, that unique signature vulnerabilities exist in the biologic domain. A very recent study (Mueller, 2019) demonstrates that the existing DNA signature paradigm may be exploited via previously unrecognized for ms of attack (5). (29, 30) By studying geometrical and mathematical principles of the quantum fields in a black-hole background, on the geometric framework Hawking demonstrated that this is not a mere analogy and in fact quantum mechanically black holes in which astrophysical processes occur, are a thermodynamic system. (29, 30, 31, 32) (Quantitative) Structure-Activity Relationships((Q) SARs) Tools for artificial intelligence and data mining can derive in an objective and reproducible approximation of relative quantities and topological descriptors for finding eigenvectors, eigenvalues by applying general solutions of the wave equation of Lamarckian-Laplacian paired with advanced machine learning algorithms to formulate an extension of the weak equivalence principle in chemical entities for generalizing small molecules into multi-targeted scaffolds. (30, 31, 32, 33) The state of a physical system has no absolute quantum meaning but is only defined relative to pharmacophoric reference frames in a special-relativistic or in a general-relativistic context when describing the motion of the ligand-receptor system. The same system may be associated to different states in different reference frames, which are normally related via some reference frame transformation. From a physical point of view, a frame of reference is an abstraction of an idealized physical system: for example, an ideal rigid body can serve as a reference frame to define relative spatial distances and orientations of other objects. In classical physics, a coordinate transformation is used to transform the description of the system under consideration between two different reference frames. These transformations include, for example, spatial rotations and translations in space and time or constant relative motion of the frames (e. g., Galilean transformations). In general, the dynamical physical laws are invariant under some group of transformations. For instance, the laws of non-relativistic physics are invariant under Galilean transformations. In every physical laboratory situation, the reference frame is realized through a physical system. As any physical system, it ultimately behaves according to the laws of quantum mechanics. Therefore, one might see the standard treatment of reference-frame transformations as an approximation to a more fundamental set of transformations. Specifically, one should consider the possibility that one laboratory, from the perspective of another laboratory, might appear in a superposition or even become entangled with the system. Hence, the relationship between the two laboratories becomes more than a simple coordinate transformation between classical reference frames; it becomes a fundamentally quantum relationship. We may then speak about transformations between quantum reference frames (QRFs). For example, we can imagine that common virtual screening method and the fragmentizing of one chemical scaffold are fixed to a multi-targeted chemical entity that is in a superposition of position states with respect to the reference frame of other approved FDA small molecules. Can we meaningfully define transformations between such QRFs? Which transformations relate quantum states of pharmacophoric systems defined with respect to one chemical frame of reference to those pharmacophoric characters defined with respect to a second frame of reference? What are the black-hole solutions and dynamical physical laws are relatively invariant under such quantum symmetrical transformations? In this article, we discuss the various ways, singularities, and quantum information numerical methods about

extremely specific molecular modeling problems to symmetrize chemical models where as extremal black hole geometries allowed us to address the composition, organization, and dynamics of a quantum reference frame in a nanoscale, for the computation of topological links and tangles and invariants of knots, through a stochastic discrete optimization procedure to rule out possible topologies, in diverse dimensions and theories. (32, 33, 34, 35, 36, 37) We also investigated lead optimization docking protocols in quantum mechanics, that relies on the noiseless Subsystem reference frame method in combination with idealized 2D chemical symmetries to simplifying free energy assumptions with either idealized symmetries regarding the entropy-driven docking behavior, the new ligand’s pharmacometrics behavior, and the protein-ligand interactions among the protein-ligand complexes(38). (34, 35, 36, 37, 38, 39, 40) Our technique is motivated by a Bayesian based approach in quantum reference frames with in a quantum state as an outside for ce that tries to intercept and read the encoded chemical data which sometimes rendered biased fingerprint fragment where as Einstein’s chaotic as well Mixmaster behaviors can be studied in the context of Hamiltonian dynamics, with the Hamiltonian $2H = -p^2\Omega + p^2_{++} [?] [?] [?] Z M [?] [?] [?] CS (A) \cos \theta j_{++} [?] [?] [?] Z M [?] [?] [?] CS (A) \cos \theta j_{++} p^2_{-+} e4\Omega (V-1)$, to protect quantum states against undesired noise in terms of quantitative structure-activity relationship(QSAR). (38, 39, 40, 41, 42, 43) Here, for the first time we developed relational theories that predicts a fundamental decoherence mechanism by combining statistical significance, black-hole cryptography solutions to Einstein’s Eqs and putative visualizations of time emerges from a time-symmetric theory on virtual compound libraries for per for ming quantum cryptographic communications in a quantum system relative to the quantum reference frame for pharmacophoric systems generally. (31-42, 43) Moreover, our model circumvents the problem of the –collapse of the wave packet— as the probability interpretation is only ever applied to diagonal density operators. (30, 31-37) Turning to the dynamics, we propose an extension of the notion of covariance of the physical laws to include genuine quantum transformations, where one frame of reference is in a superposition of different relative positions, momenta, or velocities with respect to another frame of reference for generalizing chemical characters in a quantum pharmacophoric system. Here we investigated the conditions under which, in a quantum reference frame, and its own degrees of freedom, which can be in quantum superposition or entangled and evolve in time according to an account in terms of absolute quantities can provide a good approximation of relative quantities and topological descriptors for finding eigenvectors and eigenvalues of the combinatorial Lamarckian-Laplacian paired with advanced machine learning algorithms, such as the data mining, AI-Quantum computing, entanglement complexity guidelines for (Q) SAR requirements as well as per for mance implications, such as deep neural network(DNN), random forest (RF), and gradient boosting decision tree (GBDT), to facilitate their applications to quantitative toxicity and fragment based drug design predictions. (34, 35, 36-37) In this hybrid drug designing approach, we applied an operational formalism black-hole solutions to Einstein’s Eqs for per for ming relational reference frame theory quantum communications into neural matrix factorizations, cryptography, Schrödinger inspired docking algorithms, and other Lorentzian signatures driven Information-theoretic tasks to merge the pharmacophoric elements from different chemical and physical databases into the RoccuffirnaTM innovative structure to for m a rigid chemical scaffold with anti-COVID-19 properties (1, 4-22, 23-43, 44).

METHODS AND MATERIALS

Detailed methods are provided in the online version of this paper and include the following:

RESOURCE AVAILABILITY

Lead contact

Data and code availability

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Public Datasets, SARS-COV-2 motif peptide consensus strategy.

Screening library and COVID2019 targets.

METHOD DETAILS

- Pharmacophoric-ODEs fragmentating,merging and recoring of the selected Hit compounds: Biogenetoligandorol AI-microBlackHole heuristic algorithm.
- Roccuffirna free pharmacophoric system
- Geometric symmetries from a quantum reference multi-merged pharmacophoric frame.

RESULTS

In this computational drug design project we provided an extensive combination of toolboxes by applying black-hole solution to Einstein's Eqs for performing quantum communication, neural matrix factorizations, cryptography, Schrödinger inspired docking algorithms, and other Information-theoretic tasks in MathCast programming language, and compared these algorithms by means of mean percentile free energy ranking, in a new recall-based evaluation metric for the Insilco design of a Novel Series of RoccuffirnaTMQMMCoRoN-NARRFr anti-(nCoV-19) annotated ligands. (Figure S1a) . 3D Docking interactions of the selected NuBEE physical elements inside the PDB:6XS6, SARS-CoV-2 Spike D614G variant were combined to various general docking results including heuristic horizon topologies, into near-horizon pharmacophoric fragmentations as applied to Euclidean symmetries ranging from applied supergravity theories to a system of intrinsically positioned cables.(35, 36, 37, 38, 39) (Table S1). Docking energy rankings of the physical hit compoundsof Wyerone, bis-(5-for mylfurfuryl) ether, Monocrotaline, and Zeatin(Figure S1f), Methoxsalen, behenic acid, Bergapten, L-gamma -Glutamyl-S-allylthio-L-cysteine, Oleic Acid, Sursane, Hesperetin, Adenosine, and Eriodictyol (Figure S1g),Baicalein-7-methyl ether, Euglobal III, and the Linoleic Acid residues(Figure S1h), Atrazine, Genistein, Pregnenolone ligands (Figure S1i) when docked onto the SARS-COV-2 protein targets were applied and kinematically sTabstriangular bars generated when filtered before evaluation as extracted from the selected physical chemical databases. Structurally valid symmetricformations were then connected into smaller molecule components, holes, (40, 41, 42, 43, 44) and voidsjointed at their endsby hinged connections into Roccuffirna'schemical structure to trap computationally the SARS-COV-2 viruses in practice.

DISCUSSIONS

In this work we introduced an operationalfor malismand a relational reference frame theory that predicts a fundamental decoherence mechanism, by combining black-hole cryptography solutions to Einstein's Eqsfor performing quantum communication, neural matrix factorizations, and putative ligand-receptor visualizations to apply quantum mechanics from the point of view of a reference frame translated to a quantum pharmacophoric system of ((2S, 5R, 6R) -6-((2S) -2-amino-2- phenylacetamido) -3, 3- dimethyl-7-oxo- 4-thia-1- azabicyclo (3. 2. 0)heptane-2-carbonyloxy), ({ ((2-amino-6- oxo- 6, 9-dihydro-3H-purin-9-yl) oxy) (hydroxy)phosphoryl} oxy) phosphinic acid—chemical bridge, which we call quantum reference frame. (31-42, 43) This reference frame has an arrow of time emerges from a time-symmetric theory on virtual compound libraries and its own degrees of freedom, which can be in quantum superposition or entangled and evolve in time according to their own Hamiltonian with respect to the docking frame of reference. Moreover, our model adopts a relational view, according to which any reference frame is described as a quantum degree of freedom relatively to another reference frame, collapse of the wave packet and circumvents the problem of generalizing chemical characters to a quantum pharmacophoric system as the probability interpretation which was only ever applied to diagonal density operators. Hence, theframe of reference in this research paper by combining black-hole cryptography solutions to Einstein's Eqsfor performing quantum cryptographic communications is a quantum system relative to the quantum reference frame of a pharmacophoric system of ((2S, 5R, 6R) - 6-((2S) -2-amino-2- phenylacetamido) -3, 3- dimethyl-7-oxo- 4-thia-1- azabicyclo (3. 2. 0)heptane-2- carbonyloxy), ({ ((2-amino-6-oxo- 6, 9-dihydro-3H-purin-9-yl) oxy) (hydroxy)phosphoryl} oxy) phosphinic acid, much like the pharmacophoric system of ((2S, 5R, 6R) -6- ((2S)-2-amino-2- phenylacetamido) -3, 3-dimethyl-7-oxo- 4-thia-1- azabicyclo (3. 2. 0) heptane- 2-carbonyloxy), ({ ((2-amino-6-oxo- 6, 9-dihydro-3H-purin-9-yl)oxy) (hydroxy) phosphoryl} oxy) phosphinic acid that interprets a quantum system relative to the laboratory frame. This allows us to avoid assuming the existence of an external perspective of an absolute reference frame and choose a generalized parity-swap operator which acts as a piece of information that enables the sender of a message to encrypt the message and the receiver of a message to decrypt the

message (Hoffstein, Pipher, & Silverman, 2008) in such a way that the solutions of the Eqs of motion of pharmacophoric system C from the point of view of A are of opposite sign to those of the Eqs of motion of pharmacophoric system of((2S, 5R, 6R) - 6- ((2S) -2-amino-2- phenylacetamido) - 3, 3-dimethyl-7-oxo- 4-thia-1- azabicyclo(3. 2. 0) heptane-2- carbonyloxy), ({((2-amino-6- oxo-6, 9-dihydro- 3H-puri n-9-yl)oxy) (hydroxy) phosphoryl} oxy) phosphinic acid from the point of view of C. Considering that quantum cryptographical techniques will continue to advance drug discovery approaches to obtain the relational degrees of freedom from the very start physical degrees of freedom to be relational from the point of view of a chosen QRF. These Schrodinger inspired docking algorithms when combining with black-hole solution to Einstein's Eqs as seen from a QRF and other chemistry-theoretic tasks of the reference-frame transformation for finding topological descriptors, eigenvectors, and eigenvalues with advanced machine learning algorithms, such as the data mining to merge pharmacophoric elements used could be appropriate to design multi-targeted ligands-for other diseases as well.(METHODS AND MATERIALS) (Scheme of Eqs. 1-210),(METHODS AND MATERIALS) (Cluster of Eqs. 1-104)

Limitations of the study

Limitations still existed in the current study since Quantum computers are exceedingly difficult to engineer, build and program. QC could make current CADD tools more effective by helping to predict molecular properties with high accuracy. That can affect the development process in several ways, such as modeling how SARS-COV-2 proteins fold and how anti-viral drug candidates interact with biologically relevant proteins. I still believe that quantum computing is likely to transform only the very early stages of pharmaceutical R&D over the coming decades but that it will provide near-term benefits as the technology matures.

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AUTHOR CONTRIBUTIONS

Grigoriadis Ioannis's diverse contributions to the published work are accurate and agreed. Grigoriadis Ioannis has contributed to the below multiple roles:

- Conceptualization Ideas, formulation or evolution of overarching research goals and aims.
- Methodology, Development, or design of methodology; creation of models.
- Writing - Review & Editing, Preparation, creation and presentation of the published work by those from the original research group, specifically critical review, commentary, or revision including pre-or post-publication stages.
- Visualization, Preparation, creation, and presentation of the published work, specifically visualization/data presentation.
- Supervision, Oversight and leadership responsibility for the research activity planning and execution, including mentorship external to the core team.
- Project administration, Management, and coordination responsibility for the research activity planning, and execution.

DECLARATION OF INTERESTS

No potential competing interest was reported by the author.

REFERENCES

1. Hui DS. Epidemic and Emerging Coronaviruses (Severe Acute Respiratory Syndrome and Middle East Respiratory Syndrome). ClinChestMed. 2017;38 (1) :71-86.
2. Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, Novel Coronavirus from Patients with Pneumonia in China, 2019. N Engl J Med. 2020;382 (8) :727-33.

3. Paraskevis D, Kostaki EG, Magiorkinis G, Panayiotakopoulos G, Sourvinos G, Tsiodra S. Full-genome evolutionary analysis of the novel coronavirus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event. *InfectGenetEvol.* 2020;79:104212.
4. Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, G. genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet.* 2020;395 (10224) :565-74.
5. Mueller S. On DNA Signatures, Their Dual-Use Potential for GMO Counterfeiting, and a Cyber-Based Security Solution. *FrontBioengBiotechnol.* 2019;7:189. Published 2019 Aug 7. doi:10. 3389/fbioe. 2019. 00189
6. Ziebuhr J. Molecular biology of severe acute respiratory syndrome coronavirus. *Curr Opin Microbiol.* 2004;7 (4) :412-9.
7. Weis SR, Leibowitz JL. Coronavirus pathogenesis. *Adv Virus Res.* 2011;81:85-164.
8. Brian DA, Baric RS. Coronavirus genome structure and replication. *Curr Top Microbiol Immunol.* 2005;287:1-30.
9. Narayanan K, Huang C, Makino S. SARS coronavirus accessory proteins. *Virus Res.* 2008;133 (1) :113-21.
10. Arndt AL, Larson BJ, Hogue BG. A conserved domain in the coronavirus membrane protein tail is important for virus assembly. *J Virol.* 2010;84 (21) :11418-28.
11. Neuman BW, Kiss G, Kunding AH, Bhella D, Baksh MF, Connelly S, et al. A structural analysis of M protein in coronavirus assembly and morphology. *J Struct Biol.* 2011;174 (1) :11-22
12. Siu KL, Chan CP, Kok KH, Chiu-Yat Woo P, Jin DY. Suppression of innate antiviral response by severe acute respiratory syndrome coronavirus M protein is mediated through the first transmembrane domain. *Cell Mol Immunol.* 2014;11 (2) :141-9.
13. Schoeman D, Fielding BC. Coronavirus envelope protein: current knowledge. *Virol J.* 2019;16 (1) :69.
14. Pilon, A. C., Valli, M., Dametto, A. C. et al. NuBBEDB: an updated database to uncover chemical and biological information from Brazilian biodiversity. *Sci Rep* 7, 7215 (2017). <https://doi.org/10.1038/s41598-017-07451-x>
15. Ruch TR, Machamer CE. The coronavirus E protein: assembly and beyond. *Viruses.* 2012;4 (3) :363-82.
16. McBride R, van Zyl M, Fielding BC. The coronavirus nucleocapsid is a multifunctional protein. *Viruses.* 2014;6 (8) :2991-3018.
17. Chang CK, Hou MH, Chang CF, Hsiao CD, Huang TH. The SARS coronavirus nucleocapsid protein—forms and functions. *Antiviral Res.* 2014;103:39-50.
18. Yan R, Zhang Y, Li Y, Xia L, Guo Y, Zhou Q. Structural basis for the recognition of the SARS-CoV-2 by full-length human ACE2. *Science.* 2020.
19. Walls AC, Park YJ, Tortorici MA, Wall A, McGuire AT, Veesler D. Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. *Cell.* 2020.
20. Hoffmann M, Kleine-Weber H, Schroeder S, Kruger N, Herrler T, Erichsen S, et al. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. *Cell.* 2020.
21. Kang H, Bhardwaj K, Li Y, Palaninathan S, Sacchettini J, Guarino L, et al. Biochemical and genetic analyses of murine hepatitis virus Nsp15 endoribonuclease. *J Virol.* 2007;81 (24) :13587-97.
22. Bhardwaj K, Sun J, Holzenburg A, Guarino LA, Kao CC. RNA recognition and cleavage by the SARS coronavirus endoribonuclease. *J Mol Biol.* 2006;361 (2) :243-56.

23. Zhang L, Li L, Yan L, Ming Z, Jia Z, Lou Z, et al. Structural and Biochemical Characterization of Endoribonuclease Nsp15 Encoded by Middle East Respiratory Syndrome Coronavirus. *J Virol.* 2018;92 (22).
24. Ton AT, Gentile F, Hsing M, Ban F, Cherkasov A. Rapid Identification of Potential Inhibitors of SARS-CoV-2 Main Protease by Deep Docking of 1. 3 Billion Compounds. *MolInfor m.* 2020.
25. Waterhouse A, Bertoni M, Bienert S, Studer G, Tauriello G, Gumienny R, et al. SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic AcidsRes.* 2018;46 (W1) :W296-W303.
26. Wishart DS, Feunang YD, Guo AC, Lo EJ, Marcu A, Grant JR, et al. DrugBank 5. 0: a major update to the DrugBank database for 2018. *Nucleic AcidsRes.* 2018;46 (D1) :D1074-D82.
27. Tchesnokov EP, Feng JY, Porter DP, Gotte M. Mechanism of Inhibition of Ebola Virus RNA-Dependent RNA Polymerase by Remdesivir. *Viruses.* 2019;11 (4).
28. Al-Tawfiq JA, Al-Homoud AH, Memish ZA. Remdesivir as a possible therapeutic option for the COVID-19. *Travel Med Infect Dis.* 2020:101615.
29. Poulin D, Yard J (2007) Dynamics of a quantum reference frame. *N J Phys* 9 (5) : 156.
30. Skotiniotis M, Toloui B, Durham IT, Sanders BC (2013) Quantum Frameness for CPT Symmetry. *PhysRevLett* 111 (2) : 020504.
31. Giacomini F, Castro-Ruiz E, Brukner Č. Quantum mechanics and the covariance of physical laws in quantum reference frames. *Nat Commun.* 2019;10 (1) :494.
Published 2019 Jan 30. doi:10. 1038/s41467-018-08155-0
32. Poulin D (2006) Toy model for a relational formulation of quantum theory. *Int J TheorPhys* 45 (7) : 1189 - 1215.
33. Girelli F, Poulin D (2008) Quantum reference frames and deformed symmetries. *PhysRev D* 77 (10) : 104012.
34. Miyadera T, Loveridge L, Busch P (2016) Approximating relational observables by absolute quantities: a quantum accuracy-size trade-off. *J Phys. A* 49 (18) : 185301.
35. Loveridge L, Busch P, Miyadera T (2017) Relativity of quantum states and observables. *EPL (EurophysLett)* 117 (4) : 40004.
36. Kunduri HK, Lucietti J. Classification of Near-Horizon Geometries of Extremal Black Holes. *LivingRevRelativ.* 2013;16 (1) :8. doi:10. 12942/lrr-2013-8
37. Yoshida N. formation of the first generation of stars and blackholes in the Universe. *Proc JpnAcad Ser B Phys Biol Sci.* 2019;95 (1) :17-28. doi:10. 2183/pjab. 95. 002
38. Bertschinger E. Simulations of Structure formation in the Universe. *Annu. Rev. Astron. Astrophys.* 1998;36:599–654. doi: 10. 1146/annurev. astro. 36. 1. 599. (CrossRef) (Google Scholar)
39. Birrell ND, Davies PCW. *Quantum Fields in Curved Space.* Cambridge, U. K. : Cambridge University Press; 1982. (Google Scholar)
40. Baumgarte TD, Shapiro SL. On the Numerical Integration of Einstein S Field Eqs. *Phys. Rev. D.* 1999;59:024007. doi: 10. 1103/PhysRevD. 59. 024007. (CrossRef) (Google Scholar)
41. Anninos P, Masso J, Seidel E, Suen W-M, Tobias M. Dynamics of Gravitational Waves in 3D: for simulations, Methods, and Tests. *Phys. Rev. D.* 1997;56:842–858. doi:10. 1103/PhysRevD. 56. 842. (CrossRef) (Google Scholar)

42. Anninos P, Centrella J, Matzner R. Nonlinear Wave Solutions to the Planar Vacuum Einstein Eqs. *Phys. Rev. D*. 1991;43:1825–1838. doi: 10. 1103PhysRevD. 43. 1825. (PubMed) (CrossRef) (GoogleScholar)
43. Chou YC. A radiating Kerr black hole and Hawking radiation. *Heliyon*. 2020;6 (1) :e03336. Published 2020 Jan 31. doi:10. 1016j. heliyon. 2020. e03336
44. Marcus Johansson and Valera Veryazov Automatic procedure for generating symmetry adapted wave-functions. Division of Theoretical Chemistry, Lund University, Naturvetarvägen 14, P. O. B. 124, 221 00 Lund, Sweden.
45. Chambers C M. The Cauchy Horizon in Black Hole-de Sitter Spacetimes. In: Burko L M, Ori A, editors. *Internal Structure of Black Holes and Spacetime Singularities*. Bristol: Institute of Physics; 1998. [Google Scholar]
46. Compère G. The Kerr/CFT correspondence and its extensions. *Living Rev Relativ*. 2017;20 (1) :1. doi: 10. 1007s41114-017-0003-2. Epub 2017 Feb 27. PMID: 28690421; PMCID: PMC5479153.
47. Nalewajski, R. F. Quantum information descriptors in position and momentum spaces. *J Math Chem* 53, 1549–1575 (2015). [https:// doi. org10. 1007s10910-015-0505-7](https://doi.org/10.1007/s10910-015-0505-7)