

OLEG A. RAEVSKY - SCIENTIST, TEACHER, PERSON



V.Y. Grigorev¹, O.V. Tinkov², V.P. Kazachenko¹

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²*Shevchenko Transnistria State University, Tiraspol, Moldova*

Moscow, 2024

The activity of a scientist



Meeting of the International QSAR and Molecular Modeling Society Board, Boston (USA), August 1995.

Left to right: Prof. King (USA), Prof. Charton (USA), Dr. Magi (USA), Prof. Raevsky (Russia), Prof. Block (USA).

The activity of a scientist



Meeting on the Rhine (July 1993).

Seminar on Hydrogen Bonding. Left to right: Prof. Lawrence (France), Prof. Kerry (USA), Prof. Schneider (Germany), Prof. Abraham (UK), Prof. Raevsky (Russia).

The activity of a scientist



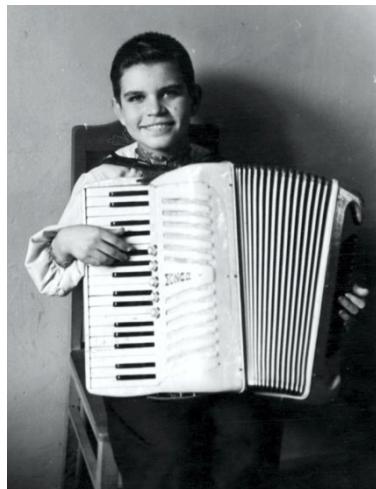
Final meeting of project leaders and collaborators of the International Science and Technology Center project, Liverpool, England, August 2010.

Standing left to right: Dr. A. Worth (Joint Research Center of the European Union, Italy), Prof. J.C. Dearden (John Moores University, Liverpool), and Prof. V.V. Poroikov (Institute of Biomedical Chemistry, Moscow).

Foreign colleagues/co-authors

- Prof. Dr. H.-J. Schneider, University of Saarbrucken, Germany
- Dr. K.-J. Shaper, Research Center Borstel, Germany
- Prof. Dr. J.R. Chretien, University of Orleans, France
- Dr. H. Van de Waterbeemd, F. Hoffmann-La Roche Ltd, Switzerland
- Prof. Dr. J.C. Dearden, University John Moore, Liverpool, England
- Dr. J. McFarland, Pfizer, Groton, USA
- Dr. E.E. Weber Environmental Protection Agency (EPA), USA
- Prof. Dr. R. Mannhold, University of Dusseldorf, Germany
- Dr. A. Worth, EU Joint Research Centre, Ispra, Italy

Education. The beginning of scientific work.



School, 1947-1957

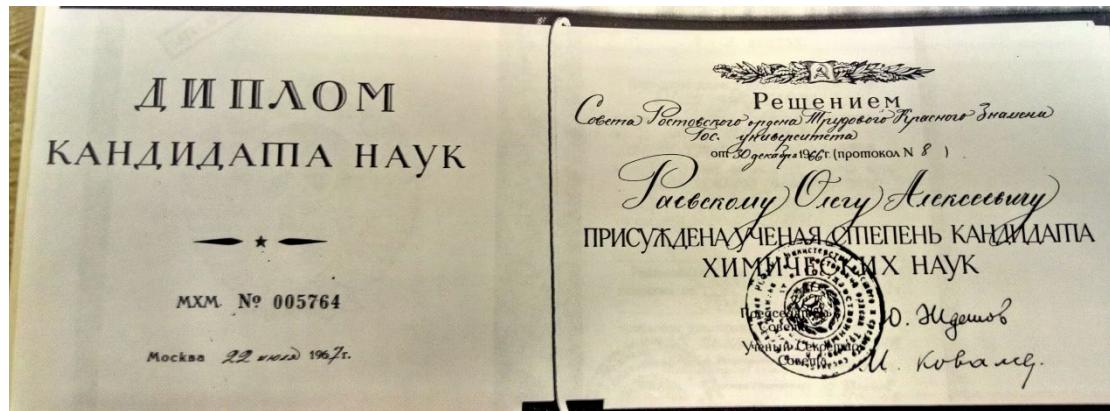


Rostov State
University,
1957-1962

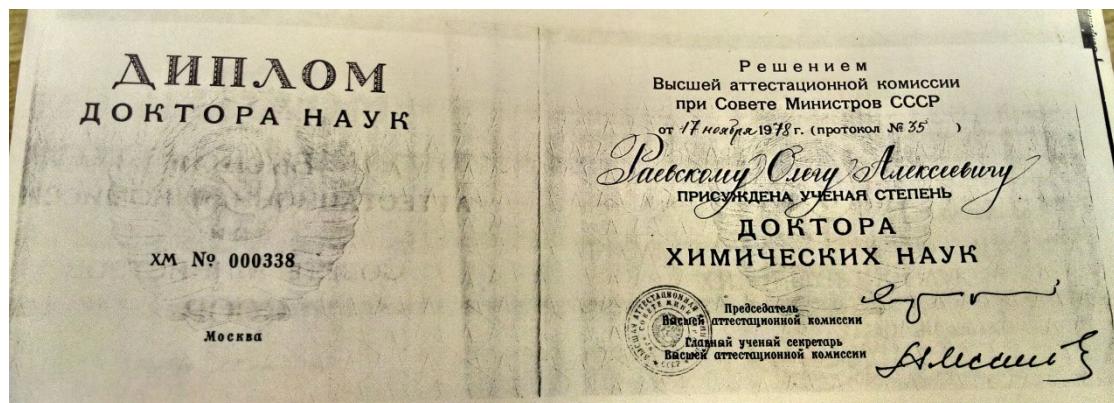


Institute of Organic and Physical Chemistry, 1962-1979

Education



PhD thesis (1966): "Physicochemical properties and structure of semithiosemicarbazones"



Doctoral dissertation (1978): "Spatial structure and intramolecular interactions in a series of acyclic organophosphorus compounds".

Work



Laboratory of Physico-Chemical
Research (1983)



Department of Computer Aided Molecular
Design (1991)



Department of Computer Aided
Molecular Design (2015)



Deputy Director of the IPAS RAS for research(2006)

Work

Research interests:

- Physical chemistry
- Spectroscopy
- Molecular modeling
- Study of the structure-property relationship
- Design and computer search for new physiologically active compounds
- Development of computer programs and creation of databases

Parameterization of H-bond (database)

File Edit Search View Tools Combinatorial libraries Diversity Drug-likeness Process structures Spectra Window Help

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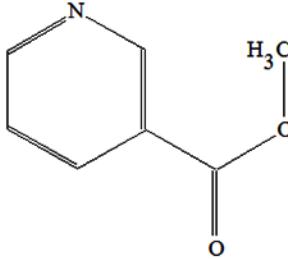
Hydrogen Bond thermodynamic
E-mail: raeovsky@ipac.ac.ru

Logical No. Mar Solvent Name H-bond d CAS ID H-bond Name H-bond

0000001	► CCl4	PHENOL	93-60-7	METHYL EST
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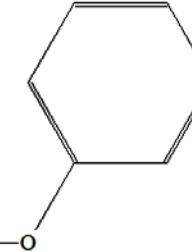
All data

Acceptor



Molecular weight acceptor
137.14
Brutto-formula acceptor
 $C_7H_7NO_2$
CAS ID H-bond acceptor
93-60-7
ID
1

Donor



Molecular weight donor
94.11
Brutto-Formula donor
 C_6H_6O
CAS ID H-bond donor
108-95-2
Solvent
CCl4

Name H-bond acceptor
METHYL ESTER 3-PYRIDINECARBOXYLIC ACID

Name H-bond donor
PHENOL

-Delta G	Method G	-Delta H	Method H	Complex D/A	Shift IR	Shift NMR	H-bond	Temperature	TYPE
7.92	IR	19.10	IR	1:1			1	298.15	OH...N

Authors
Szemik A., Zeegers-Huyskens Th.

Source
J. Mol. Struct.

Volume	Number	Year	Page
117		1984	265-273

Assignment
1

Comment

Parameterization of H-bond (model/scale)

Database : (CCl₄; 1:1; 163 H-donor; 195 H-acceptors; N=936)

Additive-multiplicative model:

E_a – enthalpy H-acceptor descriptor

E_d – enthalpy H-donor descriptor

C_a – free energy H-acceptor descriptor

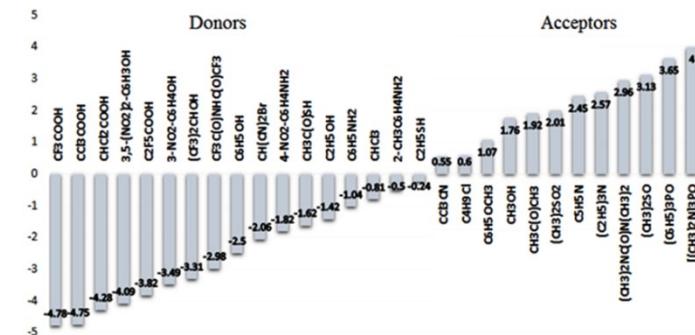
C_d – free energy H-donor descriptor

Standard H-donor: phenol ($E_d=-2.50$; $C_d=-2.50$)

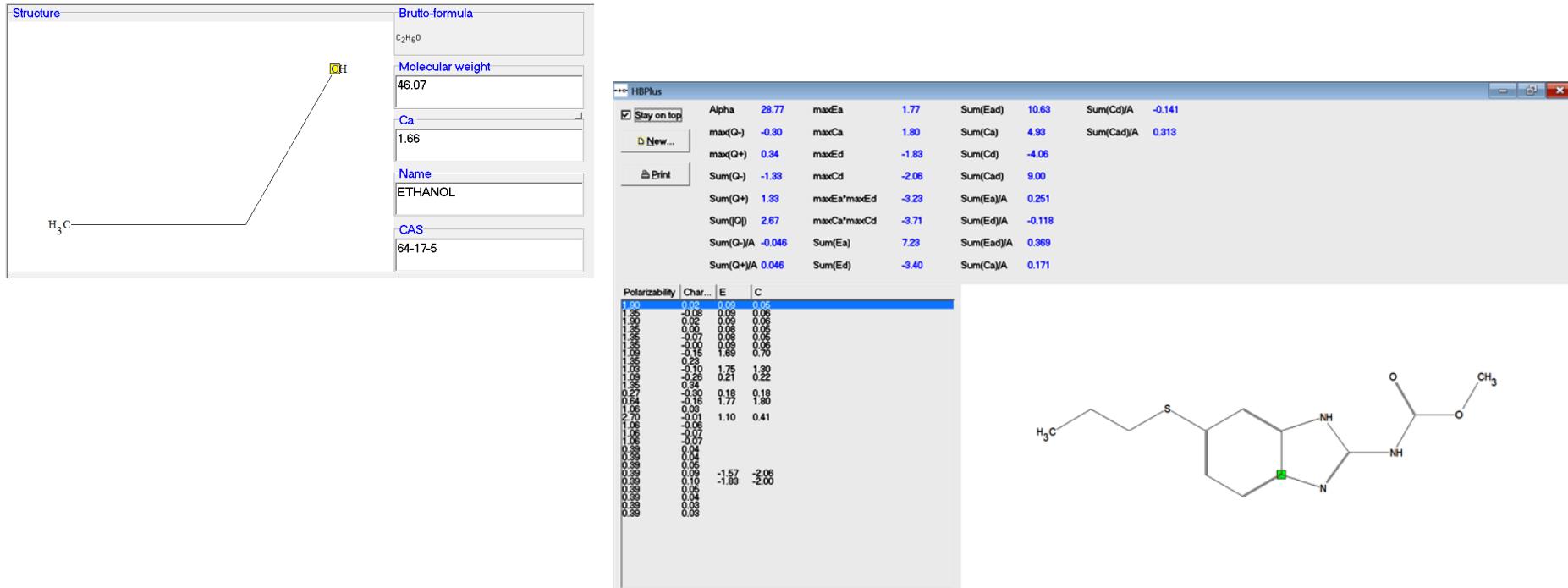
Standard H-acceptor : HMPA ($E_a=2.50$; $C_a=4.00$)

$$\Delta H(\text{kJ/mol}) = k_1 * E_a E_d + k_2; \quad k_1=4.96; \quad k_2=0.00$$

$$\Delta G(\text{kJ/mol}) = k_3 * E_a E_d + k_4; \quad k_3=2.43; \quad k_4=5.70$$



Parameterization of H-bond (HBPLUS)



Local Descriptors

$$C_D^{\max}$$

$$E_D^{\max}$$

$$C_A^{\max}$$

$$C_D^i E_D^i C_A^i E_A^i$$

Molecular Descriptors

$$\sum C_D$$

$$\sum E_D$$

$$\sum C_A$$

$$\sum C_A + \sum C_D$$

Composed Descriptors

$$\sum C_D / MW$$

$$\sum E_D / MW$$

$$\sum C_A / MW$$

$$(\sum C_A + \sum C_D) / MW$$

Parameterization of H-bond (QSAR)

Water solubility:

$\log S = 0.43(\pm 0.12) - 0.298(\pm 0.009)\alpha + 1.09(\pm 0.05)\sum C_a - 0.30(\pm 0.05)\sum C_d$
n=630; $r^2=0.90$; s=0.54

Acute toxicity (Guppy):

$\log LC_{50} = 5.14(\pm 0.12) - 0.259(\pm 0.008)\alpha + 0.79(\pm 0.03)\sum C_a$
n=90; $r^2=0.95$; s=0.32

Blood-brain barrier penetration:

RF_cv: n=1000; SN=0.824; SP=0.756; ACC=0.790

RF_test: n=100; SN=0.940; SP=0.700; ACC=0.820

Computer programs

HBPLUS (Hydrogen Bond PLUS): 2D H-bond descriptors

DNESTR (Design New Effective STructures): 2D molecular descriptors

MOLTRA (MOlecular TRansform Analysis): 3D H-bond descriptors

SLIPPER (Solubility LIPophilicity, PERmeability): solubility, lipophilicity, permeability

MOLDIVS (MOlecular DIVersity and Similarity): molecular similarity and diversity

DISCON (DIssociation CONstants): pKa

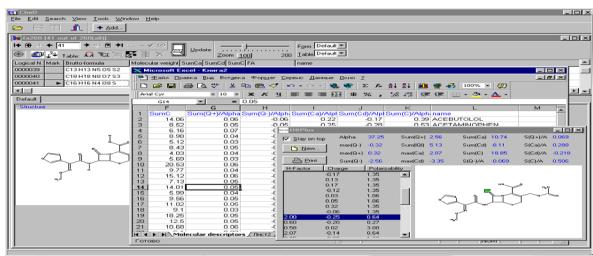
AMP (Arithmetic Mean Property)

LOREP (LOcal REgression Property)

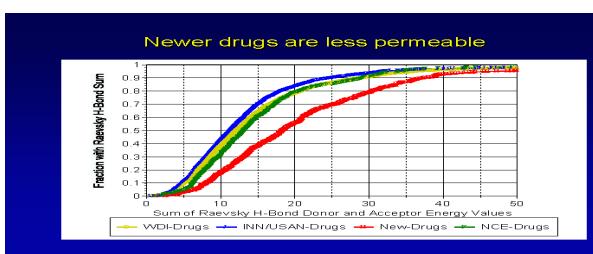
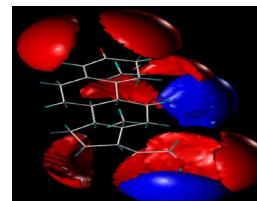
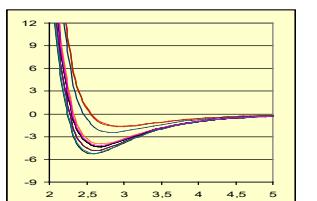
SOCR (Super Overlapping Cluster Regression)

HYBOT (HYdrogen BOnd Thermodynamics)

Complete description of hydrogen bonding for QSAR, Molecular Modelling and Drug Design on your desk!



output (/usr/people/vad/output.sdf)						
File Edit View Info Graph Options QSAR		Select Rows				
AutoFill Pick Points Show RowSet Select Rows		Select Cols Show Info				
0 of 363 Rows	0 of 18 Columns	3: Alpha	4: maxC*α	5: maxC*d	6: maxQ*α	7: maxQ*d
1: Cd-00000001		10.71	0.97	-2.50	0.11	-0.0
2: Cd-00000002		12.64	0.98	-2.18	0.11	-0.0
3: Cd-00000003		12.64	0.98	-2.18	0.11	-0.0
4: Cd-00000004		12.62	0.95	-1.17	0.11	-0.0
5: Cd-00000005		12.64	1.02	-2.40	0.11	-0.0
6: Cd-00000006		10.62	0.79	-2.01	0.21	-0.0
7: Cd-00000007		12.64	0.66	-2.92	0.12	-0.0
8: Cd-00000008		13.33	0.70	-2.94	0.11	-0.0
9: Cd-00000009		10.96	0.93	-2.56	0.15	-0.0
10: Cd-00000010		12.26	0.95	-2.45	0.26	-0.0
11: Cd-00000011		12.64	1.10	-2.42	0.11	-0.0



Program package HYBOT under Windows, UNIX, LINUX contains vast databases of thermodynamics parameters of H-bonding (15000 complexes), enthalpy and free energy factors (34000), the program for calculation of enthalpy and free energy of H-bonding as well as 16 two and 10 three dimensional original descriptor.

«Calculation of many different descriptors is possible using a range of commercially available software packages, such as Sybyl, Cerius2, Tsar, Malconn-Z, HYBOT etc.» (H. Waterbeemd, D.S. Smith, K. Beaumont, D.K. Walker. *J. Med. Chem.*, 44, 1313-1333 (2001)).

«We have used ABSOLV and three other commercial software packages (HYBOT-PLUS, Molecular modeling Pro and QsarIS) that calculate descriptors of similar classes, to model partitioning in the four solvent-water systems. Overall, HYBOT-PLUS gave the best results.» (J.C. Dearden, D. Bentley. *SAR QSAR Environ Res.*, 13, 185-197 (2002)).

C.A. Lipinski (Pfizer, Groton, USA) used the HYBOT descriptor Σ Cad as global measure of permeability for analysis of four data bases (WDI, INN/USAN0DRUGS, NSE DRUGS and New Drugs) and estimated that the “newer drugs are less permeable”. This declaration had essential influence on Drug Development projects of not only this company but also many others.

Database of the Institute of Physiologically Active Compounds (IPAC) of the Russian Academy of Sciences

File Edit Search View Tools Window Help

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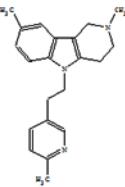
Logical No. Mat.Code
0000235 ► dimethob
0000236 CA-7502 TT-2128
0000237 FC-2974

Form 43 Table 43

Zoom 100 200

Common | AChE BChE CE | NMDAR MK-801 Ifenprodil | Mitochondrial membrane | Mitochondrial pore | Tubuline | SH-SY5Y | PI displacement | ABTS activity | ORAC

Structure



Brutto- f -Molecular Code

Comments

IC50(1)n IC50(2)n IC50(3)n IC50(4)m
IC50(5)n Tubuline
IC50(10) IC50(11)

Ligand_Name

Test(1) Target(1) Source_Organism(1) IC50_mkM(1) Inhibition_percent(1)
Test(2) Target(2) Source_Organism(2) IC50_mkM(2) Inhibition_percent(2)
Test(3) Target(3) Source_Organism(3) IC50_mkM(3) Inhibition_percent(3)
Test(4) Target(4) Source_Organism(4) IC50_mkM(4) Blockage_percent(4)
Test(5) Target(5) Source_Organism(5) IC50_mkM(5) Blockage_percent(5)
Test(6) Target(6) Source_Organism(6) Denormalization
Test(7) Target(7) Source_Organism(7) nMPT
Test(8) Target(8) Source_Organism(8) Tubuline_Polymerization
Test(9) Target(9) Source_Organism(9) IC100_mkM(9) Concentration_mkM(9) Glutam
Test(10) Target(10) Source_Organism(10) IC50_mkM(10) Displacement(1) percent(1) Concentration(1) mkM(1) Quench(2) perc
Test(11) Target(11) IC50_mkM(11) Quench(1) percent(1) Concentration(1) mkM(1) Quench(2) perc
Test(12) Target(12) Trolox_equivalent (12)

Database of IPAC RAS (tests)

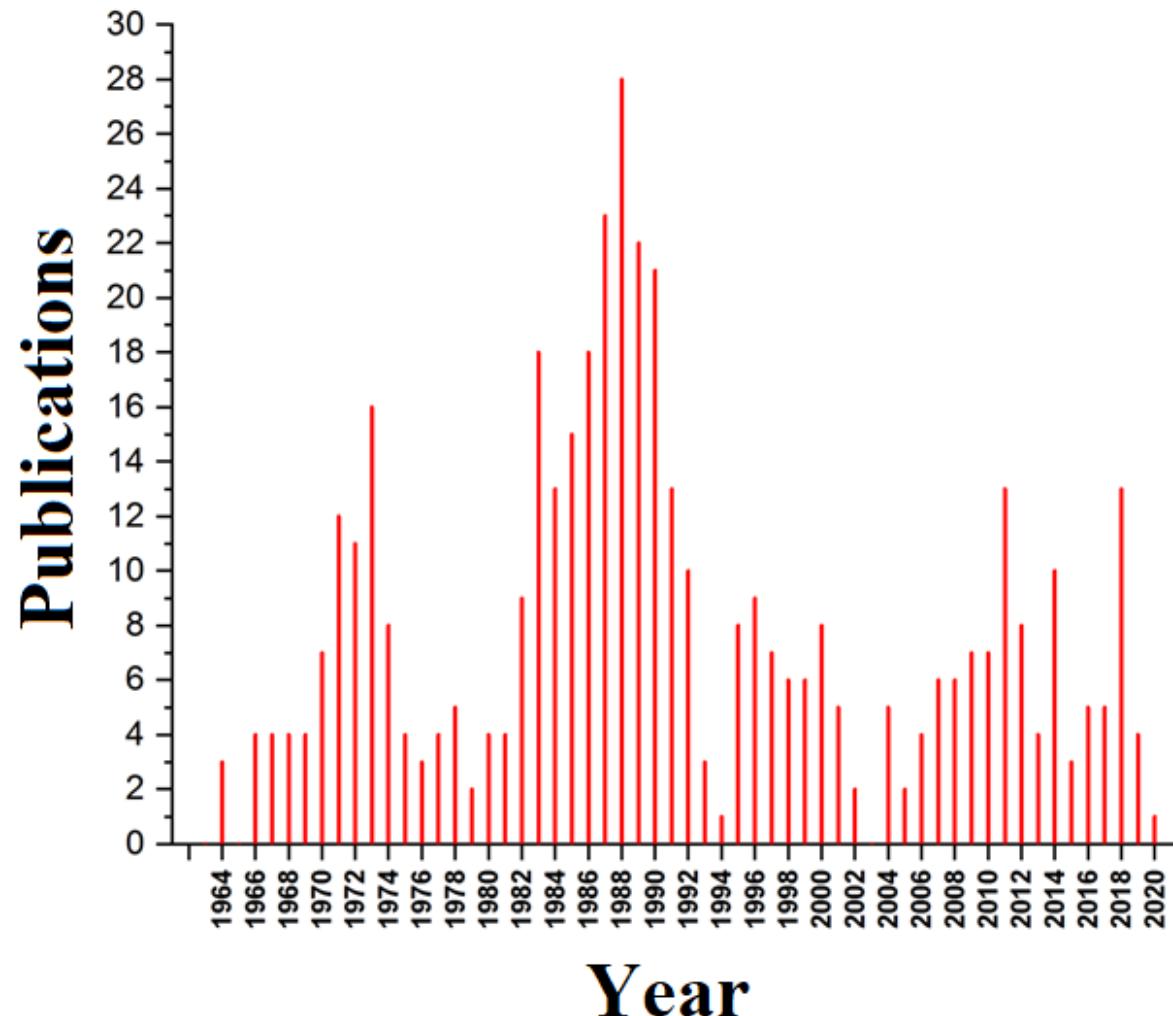
- acetylcholinesterase (AChE) inhibition
- butyrylcholinesterase (BChE) inhibition
- carboxylesterase (CE) inhibition
- N-methyl-D-aspartate (NMDA) receptor blockade, [³H]MK-801 binding site
- NMDA receptor blockade, [³H]ifenprodil binding site
- mitochondrial potential
- effect on opening of non-specific mitochondrial pore MPT (Mitochondrial permeability transition)
- tubulin polymerization
- cytotoxicity and protection from glutamate-induced toxicity
- inhibition of AChE-induced beta-amyloid aggregation
- antioxidant activity, ABTS test
- antioxidant activity, ORAC test

Publication activity (Russian Science Citation Index)

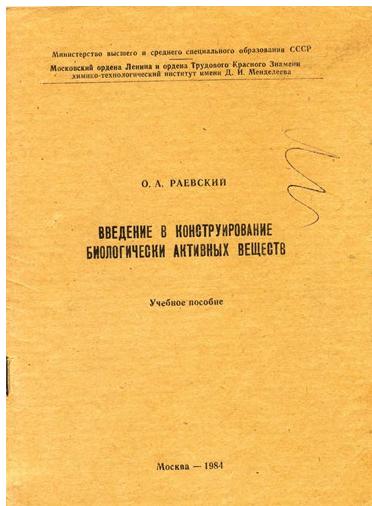
Number of publications : 454 (1964-2020)

Number of citations : 4687

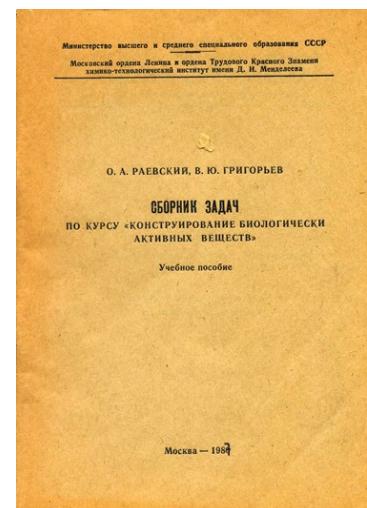
h-index : 27



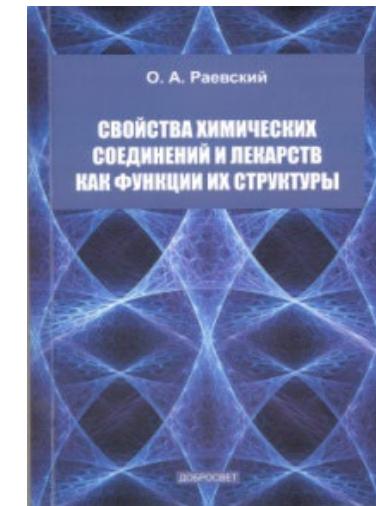
Publication activity



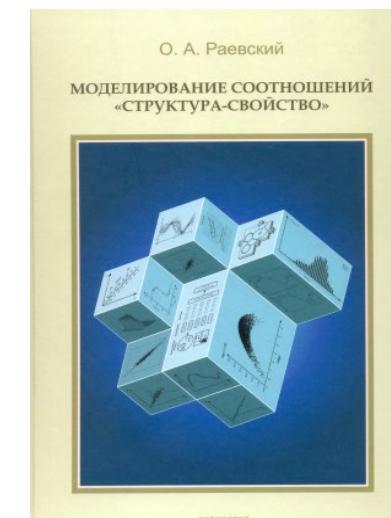
1984



1987



2013



2015

Most cited works (Russian Science Citation Index)

1. Van De Waterbeemd H., Camenisch G., Folkers G., Chretien J.R., Raevsky O.A. ESTIMATION OF BLOOD-BRAIN BARRIER CROSSING OF DRUGS USING MOLECULAR SIZE AND SHAPE, AND H-BONDING DESCRIPTORS // *J. Drug Target.* 1998. Vol. 6. P. 151-165.
2. Van Waterbeemd H.D., Camenisch G., Folkers G., Raevsky O.A. ESTIMATION OF CACO-2 CELL PERMEABILITY USING CALCULATED MOLECULAR DESCRIPTORS // *Quant. Struct.-Act. Relat.* 1996. Vol. 15. P. 480-490.
3. Raevsky O.A., Grigor'ev V., Kireev D., Zefirov N. COMPLETE THERMODYNAMIC DESCRIPTION OF H-BONDING IN THE FRAMEWORK OF MULTIPLICATIVE APPROACH // *Quant. Struct. –Act. Relat.* 1992. Vol. 11. P. 49-63.
4. Raevsky O.A. MOLECULAR STRUCTURE DESCRIPTORS IN THE COMPUTER-AIDED DESIGN OF BIOLOGICALLY ACTIVE COMPOUNDS // *Russ. Chem. Rev.* 1999. Vol. 68. P. 505-524.
5. McFarland J.W., Avdeef A., Berger C.M., Raevsky O.A. ESTIMATING THE WATER SOLUBILITIES OF CRYSTALLINE COMPOUNDS FROM THEIR CHEMICAL STRUCTURES ALONE // *J. Chem. Inf. Comput. Sci.* 2001. Vol. 41. P. 1355-1359.

Selected works of O.A. Raevsky in the field of computer molecular design in Russian can be downloaded from the link :

<https://new.ras.ru/upload/iblock/e23/ss3xm4zb5kbnioockwj3z72smie071j0.pdf?ysclid=m0f1jizolk18528432>

The Laboratory of Quantitative Structure-Activity Relationships (QSAR)

Main research areas:

- experimental study of the physicochemical properties of physiologically active compounds
- study of the relationship between the structure and biological activity of chemical compounds based on machine learning
- creation of new approaches to studying the “structure – property” relationship using fractal geometry and nonlinear dynamics methods

Interests, hobbies, travels



Chernogolovka, 2007



New York, 1995



Chernogolovka, 1991



Venice, 2007



Uglich, 1997

Thank you for your attention!