"BABEŞ-BOLYAI" UNIVERSITY CLUJ-NAPOCA FACULTY OF CHEMISTRY AND CHEMICAL ENGINEERING

Ph.D. THESIS SUMMARY

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TOPOLOGY OF THE NANOWORLD SUMMARY

"Imagination is more important than knowledge. For knowledge is limited to all we now know and understand, while imagination embraces the entire world, and all there ever will be to know and understand." Albert Einstein

> SCIENTIFIC COORDINATOR Prof. Dr. MIRCEA V. DIUDEA

CONTENTS

I. Chemical Graph Theory	Page
I.1. Basic Definitions in Graphs	1
I.2. Topological Matrices and Indices	3
I.2.1. Adjacency Matrix	3
I.2.2. Remote Adjacency Matrix	3
I.2.3. Distance Matrix	4
I.2.4. Detour Matrix	5
I.2.5. Wiener Matrices	6
I.2.6. Cluj Matrices	7
I.2.7. Reciprocal Matrices	8
I.2.8. Layer and Shell Matrices	8
I.2.8.1. Layer Matrices	8
I.2.8.2. Shell Matrices	9
I.3. Indices of Centrality	11
I.3.1. Centrality index	11
I.3.2. Ring Signature Index	11
I.4. Topological Symmetry	12
I.5. Counting Polynomials	13
I.5.1. Omega Polynomial	13
I.5.2. Cluj Polynomial	14
I.6. Spectral Graph Theory	15
I.6.1. Spectrum of Eigenvalues	15
I.6.2. Energy of Graphs	15
I.7. Polyhedra and Polytopes	16
II. Operations on Maps	23
II.1. Dual	23
II.2. Medial	23
II.3. Truncation	24
II.4. Polygonal mapping	24
II.5. Snub	25
II.6. Leapfrog	25

II.7. Quadrupling	
III. Teoretical QSAR background	
III.1. Statistical parameters in QSAR	
IV. Personal Contributions (Structural Chemistry)	
IV.1. Cell@cell higher dimensional structures	
IV.2. Covering in icosahedral clusters43	
IV.3. Covering in octahedral clusters47	
IV.4. Cube and Rh ₁₂ networks55	
IV.5. C ₆₀ related multi-shell clusters	
IV.6. Euler characteristic70	
IV.7. Applications of Spectral Theory76	
IV.7.1. In propellans76	
IV.7.2. In C ₄₀ Fullerenes79	
IV.8. Conclusions	
V. Personal Contributions (QSAR)	
V.1. QSAR study on phenothiazines92	
V.2. QSAR study on triptan class100	
V.3. QSAR study on sildenafil derivatives119	
V.4. QSAR study on cephalosporines	
V.5. QSAR study on penicillines138	
V.6. QSAR study on capsaicin derivatives142	
V.7. Conclusions149	
VI. Final Conclusions	
VI.1. General conclusions152	
VI.2. List of publications154	

Thesis Abstract

TOPOLOGY OF THE NANOWORLD is an attempt of introducing the complexity of the material nature seen at nano-level (10^{-9} m). Complex structures are designed by map operations starting from Platonic solids. Topological analysis was performed by topological symmetry tools, vertex centrality counting, vertex ring signature, RSI, and figure count, in agreement with the Euler's theorem. The main results are presented in two chapters of personal contribution, *IV*. *Structural Chemistry* and *V. QSAR studies*. The study resulted in 7 published articles, a chapter in a Springer book, 3 sent articles, 6 oral conference presentations, 3 conference posters.

Keywords: graph, multishell-cluster, vertex equivalence class, topological index, layer-matrix, centrality index, topological index, hypermolecule, TOPO GROUP CLUJ algorithm, cluster similarity prediction.

I. Chemical Graph Theory

Chemical Graph Theory is an interdisciplinary science, between Chemistry and Mathematics, with tools from Graph Theory, Set Theory and Statistics, in an attempt to solve difficult problems of Chemistry, like isomer enumeration, symmetry, and finally structure elucidation. Energetics of molecular or ionic structures, their stability and reactivity make the subject of Quantum Chemistry and is out of the aim of this thesis. For a better understanding of this work, some basic definitions in Graph Theory could be useful.

I.7. Polyhedra and Polytopes

A regular polyhedron is a highly symmetric structure, being vertex-transitive, edge-transitive and face-transitive (Coxeter, 1973). There are three symmetry groups: *tetrahedral*; *octahedral* (or cubic) and *icosahedral* (or dodecahedral).

There are five regular polyhedra, known as *Platonic solids* (Figure I.11): tetrahedron, cube, octahedron, dodecahedron and icosahedron can be written as {3,3}; {4,3}; {3,4}; {5,3} and {3,5} by using the basic (Schläfli,1901)



Fig. I.11. The Platonic solids, with symbols, vertex configurations and point group symmetry

Archimedean solids (Table I.4 and Figure I.12) are highly symmetric, semi-regular convex polyhedra, with two (or more) types of regular polygons meeting in identical vertices; they are vertex-transitive but not face-transitive.

No	Symbol	Polyhedron	Obtaining formula
1	TT	Truncated tetrahedron	<i>t</i> (<i>T</i>)
2	ТО	Truncated octahedron	t(O) = t(m(T))
3	TC	Truncated cube	t(C) = t(d(m(T)))
4	TI	Truncated icosahedron	$t(I) = t(d(p_5(T)))$
5	TD	Truncated dodecahedron	$t(D) = t(p_5(T))$
6	CO	Cuboctahedron	m(C) = m(O) = m(m(T))
7	ID	Icosidodecahedron	m(I) = m(D) = m(s(T))
8	RCO	Rhombicuboctahedron	$m(CO) = m(m(C)) = d(p_4(C))$
9	RID	Rhombicosidodecahedron	$m(ID) = m(m(I)) = d(p_4(I))$
10	TCO	Truncated cuboctahedron	t(CO) = t(m(m(T)))
11	TID	Truncated icosidodecahedron	t(ID) = t(m(s(T)))
12	SC	Snub cube	$s(C) = d(p_5(C))$
13	SD	Snub dodecahedron	$s(D) = d(p_5(D))$

Table I.4. Archimedean solids



Truncated Tetrahedron TT T_d



Truncated Octahedron TO O_h



Cuboctahedron Icosidodecahedron

CO





Truncated

Truncated

Cuboctahedron TCO

Fig. I.12. Archimedean solids





Icosidodecahedron TID

TC O_h



Truncated Cube

Rhombicuboctahedron

RCO



Snub cube SC



Truncated Dodecahedron TD I_h



Rhombicosidodecahedron

RID



Snub dodecahedron

SD



Truncated Icosahedron

 $\mathrm{TI}\,I_h$

Catalan solids (Catalan, 1865) (Figure I.13) are the duals of Archimedean solids. The Catalan solids are all face-transitive but not vertex-transitive.



Fig. I.13. Catalan solids

Generalization of a polyhedron to *n*-dimensions is called a polytope (Grünbaum, 2003; Coxeter, 1973). A regular 4-polytope can be written as { α , β , γ }, meaning: γ -polyhedra (of { α , β }) type meet at any edge of the polytope. There are six regular 4-polytopes: 5-Cell {3, 3, 3}, 8-cell {4, 3, 3}, 16-cell {3, 3, 4}, 24-cell {3, 4, 3}, 120-cell {5, 3, 3} and 600-cell {3, 3, 5}. Besides 24-cell, all can be associated to the Platonics. 5-Cell {3, 3, 3} and 24-cell {3, 4, 3} are self-dual.The others (8-cell & 16-cell), (120-cell & 600-cell) are pairs.

There are three types of convex regular polytopes in dimensions 5 and higher, as follows.

The *n*-simplex (Coxeter 1973), with the Schläfli symbol $\{3^{n-1}\}$, and the number of k-faces $\binom{n+1}{k+1}$, is a generalization of the triangle or tetrahedron to *n*-dimensions. A simplex may be defined as the smallest convex set containing the given vertices.

The *hypercube*, also called an *n*-cube and denoted Q_n , is a regular polytope with mutually perpendicular sides; it has the Schläfli symbol $\{4,3^{n-2}\}$ and the number of k-faces given by $2^{n-k}\binom{n}{k}$. After Cartesian product graph of *n* edges: $(K_2)^{\square n} = Q_n$, one obtains the hypercube.

The *n-orthoplex* or cross-polytope (Coxeter, 1973) has the Schläfli symbol $\{3^{n-2}, 4\}$ and the number of kfaces $2^{k+1}\binom{n}{k+1}$; it exists in any number of dimensions and is the dual of *n*-cube.

An *abstract polytope* is a structure which considers only the combinatorial properties of a traditional polytope: properties like angles, edge lengths, etc. are disregarded. No n-dimensional space, such as Euclidean space, is required within this theory, in which combinatorial properties are expressed as partially ordered sets or "posets". The poset theory originates in the PhD thesis of Schulte (1985, 2014) and next developed by McMullen and Schulte (2002).

II. Operations on Maps

A map M is a discretized surface domain; several operations on maps are used to modify the topology of a parent map. By running such operations the symmetry of parents is preserved.

II.1 Dual d

Dual: put a point in the center of each face of a map/polyhedron, join two such points if their corresponding faces share a common edge. It is the Poincaré dual d(M);



dD = I

Fig. II.1 Platonic solids as dual-pairs

II.2 Medial *m*

Medial: mark the midpoints of parent edges and join two such points if the edges span an angle while the parent vertices are cut off. Medial is a 4-connected graph, symmetric between the parent and its dual, that is mdM=mM, (Figure II.2). The figure sequence of transformed map is: {e, 2e, e+2}, with e being the number of edges in the parent map.



II.3 Truncation t

Truncation: cut off the neighborhood of each vertex by a plane close to the vertex, such that it intersects each edge incident in the point. The resulted truncated polyhedron is always a three-connected one (Figure II.3); its figure sequence is: $\{2e, 3e, e+2\}$.



t(C); 3.8² **Fig. II.3** Truncation of Cube (left) and Octahedron (right)



II.4 Polygonal mapping *p_n*

Add a new point in the center of each face. Put *n*-3 points on the boundary edges. Connect the central point with one vertex on each edge (the endpoints included. Figure II.4 illustrates examples of the p_n operations (Diudea and Nagy, 2007).



$$p_3 D$$
 $p_4 C = p_4 O$ $p_5 C_{60}$

Fig. II.4 Polygonal *p_n* operations on Dodecahedron

II.5 Snub s

Snub operation is the dual of p_5 operation: $sM = dp_5M$. Similar to the medial operation, sM = sdM. (Figure II.5).



Fig. II.5 Snub of Platonic solids

II.6 Leapfrog *l*

Leapfrog (or *tripling* or also *dual of kiss*) is a mixed operation (Eberhart, 1891; Fowler, 1986): lM = d(stM) = t(dM). (Figure II.6.)



Fig. II.6 The leapfrog l operation on a pentagonal face f_5 .

II.7 Quadrupling q

Quadrupling (Eberhart, 1891; Diudea and John, 2001), also named *chamfering* c (Conway notation) can be written as: $qM = t_{sel}(p_3M)$, where t_{sel} is the selective truncation of the central point added by stellation); (Figure II.7).



Fig. II.7. The Quadrupling q operation on a pentagonal face f_5 .

II.8 Septupling

Two septupling operations are known; they multiply seven times the vertices of a three-connected parent map: s_1 and s_2 .



Fig. II.9 Septupling of Platonic solids

II.9. Propelling

Join by a new point the vertices lying opposite diagonal in a rhomb of a Rh-cage to get Prp1 generation (possible A and B isomers, as there are two diagonals) (Diudea *et al*, 2017). In a second step, put a new point opposite to a vertex of degree higher than 2 and join the new point with the vertices of d = 2 surrounding that vertex of d > 2, (see Figure II.10).



 $d(mC_{60}).92$ $ppl(d(mC_{60}).92).214$ $ppl(ppl(d(mC_{60}).92).214).242$ Fig. II.10. Exemples of structures obtained by propelling

Several software programs were developed by TOPO GROUP CLUJ specialized in polyhedral tessellation and embedment in surfaces of various types, either as finite or infinite structures: TORUS, CageVersatile_CVNET, JSCHEM, Omega Polynomial Counter and NANO-Studio (Diudea *et al*, 2003; Stefu and Diudea, 2005; Nagy and Diudea, 2005; Cigher and Diudea, 2006; Nagy and Diudea, 2009).

Personal Contributions

IV. Structural Chemistry

IV.1 Cell@cell higher dimensional structures

Point-centered clusters represent cage-duals of polyhedra with the same number of cells around a central one; they are objects of Euclidean 4D-space (Fathalikhani *et al*, 2016 (Tables IV.1-8) using Euler-Poincare formula v-e+f=2(1-g). This idea can be extended to cages other than Platonics (Figure IV.1-8).



Figure IV.2. TP-derived structures

 Table IV.2.
 Figure count for clusters derived from TP cluster

T-structure	v	e	\mathbf{f}_3	\mathbf{f}_5	f_6	f	p_1	p_2	p_3	Μ	c	χ	Sym	<i>pk</i> ; (M)
TP.5	5	10	10	0	0	10	4	0	0	1	5	0	3	T; 0; 0 (P; T)
<i>d</i> (TP).10	10	30	30	0	0	30	4	4	0	2	10	0	3	T; Oct=AP ₃ ; 0 (T;O)
<i>m</i> (TP).10	10	30	30	0	0	30	4	4	0	2	10	0	3	T; Oct=Ap ₃ ; 0 (T;O)



d(OP).20 CO@((Ap4)₆;(T)₈)@C.20 **Fig. IV.3** . OP-derived structures



m(OP).18 O@((O)₈;(Py4)₆)@CO.18



t(OP).36 O@((TT)₈;(Py4)₆)@TO.36

Table IV.3. Figure count for clusters derived from OP cluster

OP-structure	v	e	f_3	f_5	\mathbf{f}_6	f	p_1	p_2	p ₃	М	с	χ	Sym	<i>k</i> ; (M)
OP.7	7	18	20	0	0	20	8	0	0	1	9	0	4	T;0;0 (P;O)
<i>d</i> (OP).20	20	60	44	12	0	56	8	6	0	2	16	0	4	T;Ap4;0 (CO;C)
<i>m</i> (OP).18	18	60	52	6	0	58	8	6	0	2	16	0	4	O; Py4 (Oct; CO)
<i>t</i> (OP).36	36	78	32	6	20	58	8	6	0	2	16	0	4	TT;Py4;0 (O;TO)

Table IV.4. Figure count for clusters derived from CP cluster

C-structure	v	e	\mathbf{f}_3	f_5	f_6	f	p_1	p ₂	p ₃	М	с	χ	Sym	<i>pk</i> ; (M)
CP.9	9	20	12	6	0	18	0	6	0	1	7	0	4	0;Py4; 0 (P;C)
<i>d</i> (CP).18	18	60	52	6	0	58	8	6	0	2	16	0	4	Oct; Py4 (Oct; CO)
<i>m</i> (CP).20	20	60	44	12	0	56	8	6	0	2	16	0	4	T;Ap4;0 (C; CO)
<i>t</i> (CP).40	40	80	32	6+6	12	56	8	6	0	2	16	0	4	T;HTO;0 (C; TC)



d(CP).18 O@((O)8;(Py4)₆)@CO.18

m(CP).20 C@((Ap4)₆;(T)8)@CO.20



t(CP).40 C@((HTO)₆;(T)₈)@TC.40

Figure IV.4.CP-derived structures

 Table IV.5. Figure count for clusters derived from IP cluster

IP-structure	v	e	f_3	f_5	f_6	f	p_1	p_2	p_3	М	с	χ	Sym	<i>p</i> _k ; (M)
IP.13	13	42	50	0	0	50	20	0	0	1	21	0	5	T; 0; 0 (P; I)
<i>d</i> (IP).50	50	150	110	24	0	134	20	12	0	2	34	0	5	T;AP5;0 (ID.30;D)
<i>m</i> (IP).42	42	150	130	60	12	142	20	12	0	2	34	0	5	Oct; Py5;0 (I;ID30)
<i>t</i> (IP).84	84	192	80	0	62	142	20	12	0	2	34	0	5	TT; Py5; 0 (I;C ₆₀)



d(IP).50 ID@((Ap5)₁₂;(T)₂₀)@D.50 m(DP).50=D@((Ap5)₁₂;(T)₂₀)@ID.50 **Fig IV.5**. IP-derived structures



m(IP).42I@((O)₂₀;(Py5)₁₂)@ID.42



t(IP).84 I@((TT)₂₀;(Py5)₁₂)@C₆₀.84



ID@ID.60 ID@((P5)₁₂;(P3)₂₀)@ID.60



T(4,12)Q4T5.96 Fig. IV.7 . Other cell-in-cell structures



 $C_{60}@C_{60}.120$ $C_{60}@((P5)_{12};(P6)_{20})@C_{60}.120$



Q6(TU(4,8)Q6T7).64

Table IV.7 Figure count for the objects in Figure IV.7.

Structure	0	1	f3	f4	f5	f6	2	р3	p5	р6	m	3	4	5	χ
ID@ID.60	60	150	40	60	24	0	124	20	12	0	2	34	0	0	0
$C_{60}@C_{60}.120$	120	240	0	90	24	40	154	0	12	20	2	34	0	0	0
$T(4,12)Q_4T_5.96$	96	240	0	216	0	0	216	0	0	0	0	84	12	0	0*
Q6.64	64	192	0	240	0	0	240	0	0	0	0	160	60	12	0
* in case of Torus, the right member of (2) gives all time zero, because the torus is a surface of genus $g=1$.															



Fig. IV.8. Sphere inversion by 4D-clusters: moving on the fourth dimension

IV.2. Covering in icosahedral clusters

Design of multi-shell cages

The operations sequence in building the cluster C750, achived by map operations is :

ts(*p*₄(C₆₀)).330; *s*₂(C₆₀).420; *ts*(*p*₄(C₆₀))@s₂(C₆₀).750 (Figure IV.9). Cluster C₇₅₀ is a spongy one, it is a C₂₀ tessellation:



 $ts(p_4(C_{60}))@(s_2(C_{60}).420).750$

 $C_{60}((C_{20})_{60}).750$



Fig.IV.9. Multi-shell structures on 750 atoms

Table IV.9. Symmetry of C_{750} : Automorphism group = $C_2 \times A_5 = Ih$; |Ih| = 120.

Class	Centrality signature (5;6)	No.Elements	Vertex degree	Atom type
1	0.0425537487829127	60	4	5^5
2	0.0425405656366799	30	4	5^5
3	0.0408741428983785	60	3	5^3
4	0.0403249632533878	60	4	5^6
5	0.0403215210989583	60	4	5^5.6
6	0.0403184110690464	60	4	5^5.6
7	0.0380980964599947	60	4	5^5
8	0.0380776127196794	60	4	5^5
9	0.0380525586272046	60	4	5^5
10	0.0363966020960237	60	3	5^3
11	0.0363899446618803	60	3	5^3
12	0.0363398403991418	120	3	5^3

The structure C_{810} (Figure IV.10) has alike structure with C_{750} , only that it has a C_{60} fullerene inside C_{750} , so $C_{810}=C_{60}@C_{750}$. When merged to the hollow of C_{750} (i.e. $ts(p_4(C_{60}))330$), C_{60} offer C_{20} and C_{24} cells, as shown in the structure $C_{60}(@((C_{20})_{12};(C_{24})_{20}).390$.

The substructures are given at the bottom of figures.





 $C_{60}@(C_{60}(C_{20})_{60}).810$



Fig. IV.10 C₈₁₀ and its components

A cluster of general formula M@M₁₂, namely $C_{408}=C_{84}@(C_{84})_{12}.408=t$ (Diu45).408 (Pârvan-Moldovan *et al*, 2014 – Figure IV.11) was obtained by truncation of Diudea's cluster Diu₄₅=IP@(IP)₁₂.45



 $(I@(TT_{20})@((I)_{12};TT_{20};TT_{30})@(Py5@TT_5)_{12}.408$

t(Diu₄₅).408



IP.13

Fig. IV.11 C_{408} and its components



t(IP).84



Diu45=IP@(IP)12.45



Fig. IV.13: Multi-shell clusters of Icosahedral symmetry C2 x A5 and rank higher than 3

IV. 3. Covering in octahedral clusters

The multi-shell structures in Figure IV.14 have been designed by truncating some Diudea's multi-shell clusters (Figure IV.15), named Diu_k , with *k* being the number of atoms; (Kooperazan-Moftakhar, 2015).





C₈₈@(C₇₂@(C:TO₄)₆.360).376 *t*(Diu₅₁).376



m(Diu₅₇).212



Figure IV.14 . Octahedral multi-shell structures.

The only structure made by Medial operation is $C_{44}@(C_{44})_6.212$, also named $m(\text{Diu}_{57}).212$ (Figure IV.14).

The structure $C_{72}@(C:TO_4)_6.360$ is a spongy one; its hollow fits precisely the cage $C_{72} = (4:6_4)_6; 6_8.72$ and also C_{88} , the last one being named C@TO_6.88 (i.e. six truncated octahedra joined at the faces of the cube).









Fig. IV.16. Cluster C_{424} and its substructures



 $p_{3}(C)P^{8}.15)@(p_{3}(C)P^{8}.15)_{6}.57$

 $(P^{^{8}}@Oct_{6}.15)@(P^{^{8}}@Oct_{6}.15)_{6}.57$

 $Diu_{57} = p_3(Diu_{51})$





Fig IV.18. Cluster Diu_{57} and its substructures (continued)



 $(P^{^{8}}@(O)_{6}.15)@(P^{^{8}}@(O)_{4}.13)_{6}.51$

 $m(p_3(\mathbf{C})\mathbf{P}^{^{14}}.15)\mathbf{P}^{^{8}}.51$



IV.4. Cube and Rh₁₂ networks

Filling the space by cube and its transforms by symmetry and/or map operations requires consideration of infinite networks and translational methods producing and investigating them.

As a seed, in this section, we take the small cluster $P^{8}@(O)_{6}@p_{3}C.15$, consisting of six octahedral shapes all meeting in the central vertex/point "P" of a capped/starred cube; shortly it is called $p_{3}CP.15$ (Pârvan-Moldovan and Diudea, 2015a, b). Its transforms, by dual, medial, truncation and leapfrog represent repeating units of the nets obtained applying these operations, either to the body centered cubic net or to the simple cubic *pcu* net (see CP.222.35 and C.222.27 in Figure IV.20





Fig. IV.21. Structural units transformed by map operations.



Fig. IV.21. Structural units transformed by map operations (continued)

The net/co-net unit pairs are as follows: *dual* net $(d(p_3(CP)).36 / d(P@(CP)_8).96; medial net <math>(m(p_3(CP)).44 / m(P@(CP)_8).94);$ truncate net $(t(p_3(CP)).88 / t(P@(CP)_8).172)$ and *leapfrog* net $(l(p_3(CP)).108 / l(P@(CP)_8).264);$









C₃₆.444.768.sel.432

Fig. IV.22. Cubic network transformed by dual



C₉₄.333.1480.sel.576



m(*st*CP).44



C₉₄.333.1480.sel.576

Fig. IV.23. Cubic network transformed by p_3



C₈₈.444.2392.sel.428







C₈₈.444.2392.sel.428

Fig. IV.24. Cubic network transformed by *t*



C264.333.2256.sel.576



P@8CP.35







C₂₆₄.333.2256.sel.576

Fig. IV.	.25. Cubic	network	transformed	by l
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	v	е	3(2)	4(2)	5/6/8(2)	2	1(3)	2(3)	3(3)	М	3	χ	k	<i>n</i> (3);(M);(4)
1	15	44	36	0	0	36	6	0	0	1	7	0	4	O;(P; <i>st</i> C)
2	36	84	20	36	8	64	6	8	0	2	16	0	4	C;hCO;(CO;TO)
3	96	240	64	102	6	172	12	8	6	2	28	0	4	C;CO;hmmC;(mmC)
4	44	108	36	36	0	72	6	0	0	2	8	0	4	CO;(C)
5	94	240	72	96	0	168	12	8	0	2	22	0	4	CO;C;(Rh ₁₂)
6	88	152	0	36	36	72	6	0	0	2	8	0	4	TO;(C)
7	172	302	0	72	72	144	12	0	0	2	14	0	4	TO;(Rh ₁₂)
8	108	180	44	0	36	80	6	0	0	2	8	0	4	TC;(TC)
9	264	480	136	6	96	238	20	0	0	2	22	0	4	TC;(<i>d</i> (<i>st</i> CO).48)

Table IV.18. Figure count in p_3 CP.15 derivatives

 $1 = p_3 \text{CP.15}; 2 = d(p_3(\text{CP})).36; 3 = d(\text{P}@8\text{CP}).96; 4 = m(p_3\text{CP}).44; 5 = m(\text{P}@8\text{CP}).94; 6 = t(p_3\text{CP}).88; 7 = t(\text{P}@8\text{CP}).172; 8 = l((p_3(\text{CP})).108; 9 = l(\text{P}@8\text{CP}).264.$





 $l(p_3(CP)).108/l(P@(CP)_8.264)$



 $t(p_3(CP)).88/t(P@(CP)_8).172$

Space filling by Rh₁₂ and related structures

In this section, attention will be focused on the rhombic dodecahedron, Rh_{12} .14, designed as the dual of medial of cube, d(mC).14 (or dual of cuboctahedron DCO).





 $l((Rh_{12}@12Rh_{12}).480$

Fig. IV.27. Space filling by cuboctahedron CO relatives



TCO@(6TC;8TT;12TCO).480

l(Rh₁₂@12Rh₁₂).480



l(Rh₁₂@12Rh₁₂).480.4

Fig. IV.28. TCO space filling

TT@4TCO.168





 $Rh_{12}@12Rh_{12}.94$



Fig. IV.29. Space filling by cuboctahedron CO relatives

IV.5. C₆₀ related multi-shell clusters

An elaborated structure, obtained by truncation of $\text{Diu}_{125}=p_3(\text{C}_{60}@d(\text{C}_{60})\text{P}^{32}).125$ cluster (Figure IV.30) is shown; it is detailed as $\text{C}_{1208}=t(\text{Diu}_{125}).1208=(d(\text{C}_{60}))@(\text{C}_{84})_{12};\text{C}_{100})_{20}).1208.$



 $t(\text{Diu}_{125}).1208$ $d(C_{60})@(C_{84})_{12};C_{100})_{20}.1208$
 $i(p_{3}(\text{Ap6})P).100$ i(P).84 $p_{3}(C_{60}@(d(C_{60})P^{^{32}}).125=\text{Diu}_{125})$

 i(P).13 $P@p_{3}(\text{Ap}_{6}).15$ $(d(C_{60}))@((TT)_{12};(T)T_{20})@C_{180}(I_{h}).244$

Fig. IV.30. C_{1208} and its components

Lable 17.23. Ealer formula for some of the studied elasters	Table IV.23.	Euler formula	for some of	the studied clusters
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Cluster	v	е	f_3	f_5	f_6	f	c1	c2	c3	c4	c5	с	χ	$M_k;[M]$
$d(C_{60}).32$	32	90	60	0	0	60	0	0	0	0	0	0	2	((3^5) ₁₂ ;(3^6) ₂₀)=St(Do)32
$C_{180}(I_h)$	180	270	0	12	80	92	0	0	0	0	0	0	2	(5.6^2)60;(6^3)120
$C_{540}(I_h)$	540	810	0	12	260	272	0	0	0	0	0	0	2	(5.6^2)60;(6^3)480
P@p ₃ (Ap ₅).13	13	42	50	0	0	50	20	0	0	0	1	21	0	T;0;0;0;[St(Ap5)=Ico.12]
C ₈₄	84	192	80	12	50	142	20	12	0	0	2	34	0	TT; Py5;0;0;[Ico; C ₆₀ (I _{<i>h</i>})]
P@p ₃ (Ap ₆).15	15	50	60	0	0	60	24	0	0	0	1	25	0	T;0;0;0;(<i>p</i> ₃ (Ap6))
C ₁₀₀	100	230	96	12	62	170	24	12	2	0	2	40	0	$[p_3(Ap_6); C_{72}(D_{6d})]$
C ₃₃	33	122	150	0	0	150	60	0	0	0	1	61	0	T;0;0; 0;(<i>p</i> ₃ (D)32)
Tr(C ₃₃).244	244	572	240	12	170	422	60	12	20	0	2	94	0	TT; Py_5 ; Py_6 ;0; [($d(C_{60})$,32; C_{180}]
C ₁₂₅	125	604	870	0	0	870	390	0	0	0	1	391	0	T;0;0;0; $(p_3(C_{60})92)$
C ₁₂₀₈	1208	3214	1560	12	950	2522	390	24	40	60	2	516	0	TT; (Py5;St(Ap5);

* Johnson object J₅₂; Py_k=Pyramid on k- basis; Ap_k=Antiprism on k-basis.



 $(d(\mathbf{C}_{60}))@((\mathbf{TT})_{12};(\mathbf{T})\mathbf{T}_{20})@\mathbf{C}_{180}(I_h).244$



TT.12 Fig.IV.31. C₂₄₄ and its components

D.20



 $C_{244} = t(Diu_{33}).244$

*p*₃ (DP^{^32}).33=Diu₃₃



IV.6. Euler characteristic

Genus g is involved in Euler characteristic determination of a closed orientable surface (g = the number of tori in a connected sum decomposition of the surface, or the number of handles or holes an object has) by the Poincaré formula

$$v - e + f = \chi = 2(1 - g)$$
 (2)

Euler characteristic can be computed for general surfaces as the alternating sum of figures of dimension/ rank k by finding a polygonization of the surface.

$$\chi = f_0 - f_1 + f_2 - f_3 + \dots, \tag{6}$$

Pairs of map operation

Theorem 1. Let $\{v, e, f\}$ and $\{n_1e+\delta, n_2e, n_3e\}$ be types of a parent polyhedron and its derivative polyhedron o(P) (obtained by a map operation o). Also, let both P and o(P) have the same Euler characteristic χ . Then, $\delta = \chi$ if and only if $(n_1 + n_3) = n_2$. (Pîrvan-Moldovan *et al*, 2016)

Corolary 1 (2). The dual of the generalized transform d(o(P)) will have the type: $\{n_3e, n_2e, n_1e+\chi\}$. This comes out from the property of Schläfli symbol that its reversal gives the symbol of the dual polyhedron.

Corolary 1 (3). Difference in the number of vertices of the transformed polyhedral graphs by selected pairs of map operations, o_1 and o_2 , equals the Euler characteristic of the embedding surface (Table IV.29-30): $|V(o_1(P))| - |V(o_2(P))| = \chi$.



Fig. IV.33. Operations applied on Cube C (top) and Dodecahedron D (bottom): vertex number differece: $\chi=2$ (Euler characteristic of the sphere).



Fig. IV.34. Operations acting on a square-tiled torus: vertex number differece: $\chi=0$ (Euler characteristic of the torus).



Fig. IV.35. Operations acting on a triple torus: vertex number differece: $\chi = -4$; g=3.



Fig. IV.36. Operations acting on a dodecahedral multi-torus: vertex number differece: $\chi = -20$; g=11.

The figure count for the structures in Figures IV.34-36 is given in Table IV.29.

Structure	v	е	f_3	f_4	f_5	f_6	f_7	f	χ	g	Diff
H6.8	48	96	0	48	0	0	0	48	0	1	-
<i>m</i> (H6.8)	96	192	0	96	0	0	0	96	0	1	-
<i>dm</i> (H6.8)	96	192	0	96	0	0	0	96	0	1	0
H ₃₄₀	340	510	0	0	12	118	36	166	-4	3	-
$dm(H_{340})$	506	1020	0	510	0	0	0	510	-4	3	-
$m({ m H}_{340})$	510	1020	340	0	12	118	36	506	-4	3	- 4
C ₂₈₀	280	420	0	0	0	0	120	120	-20	11	-
$p_4(C_{280})$	820	1680	0	840	0	0	0	840	-20	11	-
<i>l</i> (C ₂₈₀)	840	1260	0	0	0	280	120	400	-20	11	- 20

Table IV.29. Figure count for the objects in Figs. 2 to 4.



TTT57.104

 p_4 (TTT57.104).308

t(TTT57.104).312

l(TTT57.104).312

Fig. IV.37. Other example of pairs of operations

Table IV.30. Figure count in toroi	dal structures (Figures IV.37-38)
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Structure	v	e	f3	f4	f5	f6	f7	f8	f10	f12	f14	f	χ	g
H.1220	1220	1830	0	0	0	470	120	0	0	0	0	590	-20	11
t H.1220	3660	5490	1220	0	0	0	0	0	0	470	120	1810	-20	11
<i>p4</i> H.1220	3640	7320	0	3660	0	0	0	0	0	0	0	3660	-20	11

<i>l</i> H.1220	3660	5490	0	0	0	1690	120	0	0	0	0	1810	-20	11
C60	60	90	0	0	12	20	0	0	0	0	0	32	2	0
t C60	180	27	60	0	0	0	0	0	12	20	0	92	2	0
<i>p4</i> C60	182	360	0	180	0	0	0	0	0	0	0	180	2	0
<i>l</i> C60	180	270	0	0	12	80	0	0	0	0	0	92	2	0
H68_48	48	96	0	48	0	0	0	0	0	0	0	0	0	1
t H68_48	192	288	0	48	0	0	0	0	0	0	0	0	0	1
<i>p4</i> H68_48	192	384	0	192	0	0	0	0	0	0	0	0	0	1
<i>l</i> H68_48	192	288	0	48	0	0	0	48	0	0	0	96	0	1
TTT57	104	156	0	0	12	0	36	0	0	0	0	48	-4	3
t TTT57	312	468	104	0	0	12	0	0	0	6	42	152	-4	3
<i>p4</i> TTT57	308	624	0	312	0	0	0	0	0	0	0	312	-4	3
<i>l</i> TTT57	312	468	0	0	12	104	36	0	0	0	0	152	-4	3



Fig. IV.38. Operations acting on a C₆₀; vertex number differece: $\chi = 2$; g=0.

IV.7. Applications of Spectral Theory

IV.7.1. Propellans



Fig. IV.39. Triacontahedron and three disconnected polyhedra composing propellanes.

All the rings in propellanes are rhombs. As a general property, all the vertex classes represent nonconnected sets, thus the chromatic number equals the number of vertex classes. This property facilitates identification of vertex partitions as polyhedra and evaluation of their graph energy. A "binding" energy E_{bind} (in Beta units) can be calculated (see Table IV.31) for the parent graphs with respect to their independent partitions (*i.e.*, energy of composition, E_{compos}), by analogy with the quantum computations in molecular graphs.







Rh₃₀_PrpB.62





Rh₃₀_PrpAD.82

Fig.IV.41. Propellanes of the 2nd generation.



Rh₃₀_PrpACD.94





Rh₃₀_PrpBD.74



Rh₃₀_PrpBCD.94

	Cluster	Composition	ν	Е	E compos	$\rm E_{bind}$	λ max	λ min
1	Icosahedron		12	23.416			5	-2.236
2	Dodecahedron		20	29.416			3	-2.236
3	Icosidodecahedron		30	55.416			4	-2
4	Rh ₃₀	I+D	32	47.896	52.832	-4.936	3.873	-3.873
5	Rh ₃₀ _Prp1A	I+D+ID	62	71.872	108.248	-36.376	5	-5
6	Rh ₃₀ _Prp1B	I+D+ID	62	87.314	108.248	-20.934	4.583	-4.583
7	Rh ₃₀ _Prp2A	I+2D+ID	82	129.43	137.664	-8.234	5.269	-5.269
8	Rh ₃₀ _Prp2B	2I+D+ID	74	132.828	131.664	1.164	5	-5
9	Rh ₃₀ _Prp3A	2I+2D+ID	94	154.906	161.08	-6.174	5.568	-5.568
10	Rh ₃₀ _Prp3B	2I+2D+ID	94	162.292	161.08	1.212	5.349	-5.349

Table IV.31. Propellane relatives of Rh_{30} .32; Graph energy; $E_{bind} = E - E_{compos}$.

IV.7.2. C₄₀ Fullerenes

Graph energy in fullerene energy evaluation



Fig.IV.43. Plots of total energy/atom (in au) and strain energy/atom (in kcal/mol) vs the number of fused pentagons n_p .

QSPR models (Table IV.35-36) can be derived in a variety of combinations; the goal was to show that the graph energy of these fullerenes can be used to evaluate the quantum calculated molecular energy. Table IV.34 lists several combinations, including the energy of graphs and remote graphs, with and without the n_p parameter.

X_1	X_2	X ₃	\mathbb{R}^2	S
n _p			0.900	0.000662
SD _{E/atom}			0.849	0.000813
LEig			0.780	0.000981
n_p	E_1		0.916	0.000616
	D ₃		0.915	0.000617
n_p	E_1	LEig	0.924	0.000591
		D_3	0.921	0.000605
		C(Sh(D))	0.918	0.000614
SD _{E/atom}	LEig		0.897	0.000680
	D3D		0.882	0.000727
SD _{E/atom}	LEig	C(Sh(D))	0.918	0.000615
		D3D	0.907	0.000655

Table IV 25 D . 1 **n** /

IV.8. Conclusions on Chapter IV

The following results were presented:

- 1. The smallest clusters of dimension/rank 4
- 2. Clusters of icosahedral symmetry
- 3. Clusters of octahedral symmetry
- 4. Cube and Rh₁₂ networks
- 5. Clusters related to C_{60} fullerene
- 6. Energy of graphs in Propellanes
- 7. QSPR of C_{40} fullerenes using graph energies as descriptors

V. Personal Contributions (QSAR)

These QSAR studies were performed following Diudea's algorithm (Moldovan *et al*, 2008); it is based on the alignment of molecules over a hypermolecule (Balaban *et al*, 1980) and a correlation weighting procedure (Toropov *et al*, 2001,2002) coupled with a predictive validation of the model descriptors within similarity clusters (Willett, 1998) performed for each molecule in the test set.

V.1. QSAR study on phenothiazines

Phenothiazine is an organic heterocyclic compound, of the class of thiazines, with the brute formula $S(C_6H_4)_2NH$. Derivatives of phenothiazine revolutionized the field of psychiatry and allergy treatment.

Mol	CID	Name	Canonical Smiles	logP	LD50 mg/kg
1	2726	chlorpromazine	CN(C)CCCN1C2=CC=C2SC3=C1C=C(C=C3)Cl	5.41	14
2	2801	clomipramine	CN(C)CCCN1C2=CC=C2CCC3=C1C=C(C=C3)Cl	5.19	150
3	2995	desipramine	CNCCCN1C2=CC=CC=C2CCC3=CC=CC=C31	4.90	85
4	3089	fonazine/dimetothiazine	CC(CN1C2=CC=CC=C2SC3=C1C=C(C=C3)S(=O)(=O)N(C)C)N(C)C	3.34	190
5	3781	isothipendyl	CC(CN1C2=CC=CC=C2SC3=C1N=CC=C3)N(C)C	3.66	62
6	4066	mequitazine	C1CN2CCC1C(C2)CN3C4=CC=CC=C4SC5=CC=CC=C53	4.70	54
7	4744	perazine	CN1CCN(CC1)CCCN2C3=CC=CC=C3SC4=CC=CC=C42	4.10	185
8	4747	periciazine	C1CN(CCC10)CCCN2C3=CC=C3SC4=C2C=C(C=C4)C#N	3.52	115
9	4748	perphenazine	C1CN(CCN1CCCN2C3=CC=CC=C3SC4=C2C=C(C=C4)Cl)CCO	4.20	64
10	4917	prochlorperazine	CN1CCN(CC1)CCCN2C3=CC=C3SC4=C2C=C(C=C4)Cl	4.88	120
11	4926	promazine	CN(C)CCCN1C2=CC=CC=C2SC3=CC=CC=C31	4.55	140
12	4927	promethazine	CC(CN1C2=CC=CC=C2SC3=CC=CC=C31)N(C)C	4.81	124
13	5452	thioridazine	CN1CCCCC1CCN2C3=CC=CC=C3SC4=C2C=C(C=C4)SC	5.90	65
14	5566	trifluoperazine	CN1CCN(CC1)CCCN2C3=CC=C3SC4=C2C=C(C=C4)C(F)(F)F	5.03	120
15	6075	mepazine/pecazine	CN1CCCC(C1)CN2C3=CC=CC=C3SC4=CC=CC=C42	5.60	140
16	6077	acetylpromazine	CC(=O)C1=CC2=C(C=C1)SC3=CC=CC=C3N2CCCN(C)C	4.20	350
17	6761	pipamazine	C1CN(CCC1C(=O)N)CCCN2C3=CC=CC=C3SC4=C2C=C(C=C4)Cl	4.40	80
18	10646	pyrathiazine	C1CCN(C1)CCN2C3=CC=CC=C3SC4=CC=CC=C42	4.70	190
19	14670	prothypendyl	CN(C)CCCN1C2=CC=C2SC3=C1N=CC=C3	3.40	135
20	14677	methdilazine	CN1CCC(C1)CN2C3=CC=CC=C3SC4=CC=CC=C42	5.23	183
21	16414	7-hidroxyclorpromazine	CN(C)CCCN1C2=C(C=C(C=C2)O)SC3=C1C=C(C=C3)Cl	4.80	119
22	19396	oxomemazine	CC(CN1C2=CC=CC=C2S(=O)(=O)C3=CC=CC=C31)CN(C)C	3.40	185
23	19675	piperacetazine	CC(=0)C1=CC2=C(C=C1)SC3=CC=CC=C3N2CCCN4CCC(CC4)CCO	4.21	98
24	65535	diethazine	CCN(CC)CCN1C2=CC=CC=C2SC3=CC=CC=C31	4.90	225
25	65750	chlorproethazine	CCN(CC)CCCN1C2=CC=CC=C2SC3=C1C=C(C=C3)Cl	5.90	90
26	68223	fenethazine	CN(C)CCN1C2=CC=CC=C2SC3=CC=CC=C31	4.20	115
27	69500	difazin	CCN(CC)CC(=0)N1C2=CC=CC=C2SC3=CC=CC=C31	3.80	210
28	70413	opromazine	CN(C)CCCN1C2=CC=C2S(=O)C3=C1C=C(C=C3)C1	3.90	163
29	72287	levomepromazine	C[C@@H](CN1C2=CC=C2SC3=C1C=C(C=C3)OC)CN(C)C	4.68	58.5
30	94280	dimetacrine	CC1(C2=CC=CC=C2N(C3=CC=CC=C31)CCCN(C)C)C	4.96	206

Table V.1. Studied phenothiazines with their name, CID, properties logP and LD₅₀.



Fig. V.1. Hypermolecule comprising the features of the dataset

Basic equations that describe the relationships between values of property or biological activity of compounds and their structures were obtained:

$$logP= 59.096+SD_{logP};$$
 n=30; R²=0.946; s=0.165; F=488.078 (1)

$$LD_{50}=9113.289+SD_{LD50};$$
 n=28; R²=0.956; s=13.964; F=566.487 (2)

(molecules 1 and 23 were outliers, residual value>2s)

QSAR models (for case log P)

The models were performed on the training set (structures 11-30) and the best results (in decreasing order of R^2) are listed below in Tables V.3 and V.4 (Pîrvan-Moldovan, 2016).

Monovariate regression	$logP=57.266+0.966\times SD_{logP}$	(3)
	n=20; R ² =0.946; s=0.172; F=317.170	
Bivariate regression	$logP = 57.299 + 0.968 \times SD_{logP} + 3.54 \times 10^{-5} \times IP[CfMax]$	(4)
	n=20; R ² =0.949; s=0.173; F=157.155	
Trivariate regression	$logP=56.341+0.948\times SD_{logP}+1.26\times 10^{-}\times IP[CfMin]+0.097\times Chem.pot.$	(5)
	n=20; R ² =0.951; s=0.174; F=103.820	

QSAR models (for case LD₅₀) (https://www.drugbank.ca/)

The models were performed on the training set and the best results (in decreasing order of R^2) are listed below in Tables V.5 and V.6.

Monovariate regression	$LD_{50}=9444.65+1.037\times SD_{LD50}$	(6)
	n=19; R ² =0.940; s=13.534; F=265.126)	
Bivariate regression	$\label{eq:lds} \begin{split} LD_{50} = & 9415.945 + 1.033 \times SD_{LD50} - 0.0266 \times IE[CfMax] \\ n = & 19; \ R^2 = & 0.943; \ s = & 13.607; \ F = & 131.573) \end{split}$	(7)
Trivariate regression	$LD_{50}\!\!=\!\!9606.267\!+\!1.055\!\times\!\!SD_{LD50}\!\!-\!0.2024\!\times\!IE[CfMax]\!+\!0.047\!\times\!Distance$	(8)
	n=19; R ² =0.947; s=13.498; F=89.557	

Models validation

(a) Leave-one-out

The performances in leave-one-out analysis (Jäntschi, 2005) related to the models listed as best in Tables are shown in Tables V.7 and V.8.

Table V.7. Leave-one-out analysis for the best logP models

	Descriptors	Q^2	$R^2 - Q^2$
1	$\mathrm{SD}_{\mathrm{logP}}$	0.938	0.008
2	SD _{logP} , IP[CfMax]	0.928	0.021
3	SD _{logP} , IP[CfMin], Chem.pot.	0.910	0.041

Table V.8. Leave-one-out analysis for the best LD₅₀ models

	Descriptors	Q^2	R^2 - Q^2
1	SD _{LD50}	0.931	0.009
2	SD _{LD50} , IE[CfMax]	0.925	0.018
3	SD _{LD50} , IE[CfMax], Distance	0.919	0.030

(b) External Validation



Fig.V.3. The plot $logP_{exp}$ vs. $logP_{calc.}$ for the test set (external validation).



Fig.V.4. The plot LD_{50exp} vs. LD_{50calc}. for the test set (external validation)

From Figures V.3 and V.4 one can see that our models show a good predictive ability.

(c) Similarity Cluster Validation



Fig.V.5. The plot $logP_{exp}$ vs. $logP_{calc}$ (by clusters of similarity) for the test set



Fig. V.6. The plot LD_{50} vs. LD_{50calc} (by clusters of similarity) for the test set

V.2. QSAR study on triptan class

Sumatriptan, $C_{14}H_{21}N_3O_2S$, is a synthetic drug included in the triptan class used for the treatment of migraine.

Molecule	XLogP3	CID	Canonical SMILES
1	0.9	5358	CNS(=0)(=0)CC1=CC2=C(C=C1)NC=C2CCN(C)C
2	2	4440	CNS(=0)(=0)CCC1=CC2=C(C=C1)NC=C2C3CCN(CC3)C
3	4 1	77993	CN1CCC[C@@H]1CC2=CNC3=C2C=C(C=C3)CCS(=O)(=O)C4=CC=CC=C4
4	1.2	100/3/01	CN1CCCN(S1(-0)-0)CC2-CC2-C(C-C2)NC-C2CCN(C)C
4	1.2	10043491	CN1CCCN(S1(-0)-0)CC2-CC3-C(C-C2)NC-C3CCN(C)C
5	1.9	24955	CCNTCCN(ST(=0)=0)CCC2=CCS=C(C=C2)NC=CSCCN(C)C
6	2.2	34855	CU=CU=C(U=U)NU=U2UN(U)U
7	1.2	10257	CN(C)CCC1=CNC2=C1C=C(C=C2)O
8	2.7	10340828	CN(C)CCC1=CNC2=C1C=C(C=C2)N3CCN(S3(=O)=O)CC4=CC=CC=C4
9	-1.2	439280	C1=CC2=C(C=C1O)C(=CN2)C[C@@H](C(=O)O)N
10	0.1	11722814	CN1CCN(S1(=O)=O)CC2=CC3=C(C=C2)NC=C3CCN
11	1.4	10404770	CN(C)CCC1=CNC2=C1C=C(C=C2)CCN3CCNS3(=O)=O
12	1.9	9998879	CC(C)N1CCN(S1(=0)=0)CC2=CC3=C(C=C2)NC=C3CCN(C)C
13	1.6	123606	CN(C)CCC1=CNC2=C1C=C(C=C2)CS(=O)(=O)N3CCCC3
14	2.3	9802530	CN(C)CCC1=CNC2=C1C=C(C=C2)OS(=O)(=O)C(F)(F)
15	3	10618751	CCN(CC)CCC1=CNC2=C1C=C(C=C2)OS(=O)(=O)C(F)(F)F
16	0.5	4713248	CNS(=0)(=0)C1=CC2=C(C=C1)NC=C2CCN(C)C
17	3.9	9954663	C1CCN(C1)CCC2=CNC3=C2C=C(C=C3)C4=CCN(CC4)S(=O)(=O)C5=CC=CC=C
18	1.5	18423663	CNS(=0)(=0)CC1=CC2=C(C=C1)NC=C2CC3CCCN3C
19	1	18423665	CNS(=O)(=O)CC1=CC2=C(C=C1)NC=C2CC3CCCN3
20	4.6	11177383	CC(C)C1=CC=C(C=C1)S(=O)(=O)NC2=CC3=C(C=C2)NC=C3CC4CCCN4C
21	1.5	12822482	C1=CC=C(C=C1)S(=O)(=O)NCC2=CC3=C(C=C2)NC=C3CCN
22	2.3	53644294	C1CN(CC1CNCC2=CC=CC=C2)CCC3=CNC4=C3C=C(C=C4)CS(=O)(=O)N
23	4.3	19422723	CN1CCCC1CC2=CNC3=C2C=C(C=C3)C(=C)S(=O)(=O)C4=CC=CC=C4
24	2.9	67923722	CNS(=0)(=0)C(CC1=CC=CC=C1)C2=CC3=C(C=C2)NC=C3CCN(C)C
25	3	44400804	C1CC(NC1)CC2=CNC3=C2C=C(C=C3)NS(=O)(=O)C4=CC=CC=C4
26	2.2	13475733	C1=CC=C(C=C1)CNS(=O)(=O)CCC2=CC3=C(C=C2)NC=C3CCN
27	1.4	13286052	C1=CC=C(C=C1)CNS(=O)(=O)CC2=CC3=C(C=C2)NC=C3CCN
28	1.5	13286055	C1=CC=C(C=C1)NS(=O)(=O)CC2=CC3=C(C=C2)NC=C3CCN
29	1.4	12822479	C1=CC=C(C=C1)CS(=O)(=O)NCC2=CC3=C(C=C2)NC=C3CCN
30	3.3	12082798	CN1CCC(=CC1)C2=CNC3=C2C=C(C=C3)CCS(=O)(=O)N(C)CC4=CC=CC=C4
31	2.4	105/12//	CNS(=0)(=0)CC1=CC2=C(C=C1)NC=C2CCN(C)CC3=CC=CC=C3
32	5	10203969	CICUN(CI)CUC2=UNC3=C2U=C(C=C3)NS(=O)(=O)(4=CU=C(C=C4)C5=CC=C5
24	2.1	102242445	CUUI=UNU2=UIU=U(U=U2)US(=U)(=U)N3UUUUS
25	3.0	77250860	CNICCCUC2=CNC3=C2C=C(C=C3)/C=C/S(=O)(=O)C4=CC=C4
26	1.8	76115652	COCC1CCN(C1)CC2=C(C=C1)NC=C2CCC3CCCN3C
27	2.0	70113032	CUCC1CCN(C1)CC2 = CNC3 = C2C = C(C = C3)CS(=O)(=O)N(C)C
39	15	11800037	CN1CCC(CC1)C2-CNC3-C2N-C(C-C3)OS(-O)(-O)C
39	1.5	71315712	CNCCC1 - CNC2 - C1C - C(C - C2)CS(-0)(-0)C
40	3.6	70946434	CN1CCCC1C2=CNC3=C2C=C(C=C3)CCS(=O)(=O)C4=CC=CC=C4
41	2	70836771	CN(CCC1=CNC2=C1C=C(C=C2)CS(=O)(=O)N3CCCC3)CF
42	1.9	70932894	C(C1=CNC2=C1C=C(C=C2)CS(=O)(=O)(N3CCCC3)N(C)C
43	1.7	67834586	CC(C1=CC2=C(C=C1)NC=C2CC3CCCN3)S(=O)(=O)NC
44	1.6	67767267	CC1(CN(S(=0)(=0)N1)CC2=CC3=C(C=C2)NC=C3CCN(C)C)C
45	4.8	67424557	C1CC(N(C1)CI)CC2=CNC3=C2C=C(C=C3)CCS(=O)(=O)C4=CC=CC=C4
46	5.4	67125361	CCCC(CC1=CC2=C(C=C1)NC=C2CC3CCCN3C)S(=O)(=O)C4=CC=C4
47	1.2	66617669	CC(C)(CC1=CNC2=C1C=C(C=C2)CS(=O)(=O)N3CCCC3)N
48	0.6	54293224	C1CC(NC1)CC2=CNC3=C2C=C(C=C3)CS(=O)(=O)N
49	0.8	54277349	CNS(=0)(=0)CC1=CC2=C(C=C1)NC=C2C3=CCN(CC3)C
50	1.8	54043760	CNS(=O)(=O)CCC1=CC2=C(C=C1)NC=C2C[C@H]3CCCN3
51	3.8	44400787	CC1=CC=C(C=C1)S(=O)(=O)NC2=CC3=C(C=C2)NC=C3CC4CCCN4C
52	0.6	10448821	CC1(CN(S(=O)(=O)N1)CC2=CC3=C(C=C2)NC=C3CCN)C
53	2.4	23192135	CN1CCCC1CC2=CNC3=C2C=C(C=C3)CCS(=O)(=O)N(C)C
54	1.2	22924406	CN1CCC(=CC1)C2=CNC3=C2C=C(C=C3)CCS(=O)(=O)N
55	1.8	22371684	CC(C1=CC2=C(C=C1)NC=C2CC3CCCN3C)S(=O)(=O)N
56	2.8	21852525	CC(C)(C)NS(=O)(=O)CC1=CC2=C(C=C1)NC=C2CC3CCCN3C
57	1.6	20066734	CNS(=0)(=0)CCC1=CC2=C(C=C1)NC=C2C3=CCN(CC3)C
58	1.9	19970226	CN1CCCC1CC2=CNC3=C2C=C(C=C3)CCS(=O)(=O)N
59	4	19970209	CC(C1=CC2=C(C=C1)NC=C2CC3CCCN3C)S(=O)(=O)C4=CC=CC=C4
60	3.6	19041599	C1CC(NC1)CC2=CNC3=C2C=C(C=C3)CCS(=O)(=O)C4=CC=CC=C4



Fig.V.7.a. HM designed for molecules that have S at 2 atoms distance from indole



Fig. V.7.c. HM designed for molecules that have S at 3 atoms distance from indole

Basic equations that describe the relationships between values of property of 30, respectively 20 compounds and their structures were obtained; molecules 5, 9 and 10 are outliers.

$$logP=-15.734+0.999\times SD_{logP}; n=30, R^{2}=0.927, s=0.321, F=355.73$$
(13)

$$n=20, R^2=0.9998, s=0.017, F=119140$$
 (14)

QSAR models in set "2" (for case logP)

 $logP=13.628+SD_{logP};$

The models were performed on the training set and the best results (in decreasing order of R^2) are listed in Table V.12.

QSAR models:

Monovariate regression	$logP=-15.294+0.978 \times SD_{logP}$	(15)
	$n=21, R^2=0.952, s=0.280$	
Bivariate regression	$logP=-16.582+1.124\times SD_{logP} -0.029\times N$	(16)
	n=21, R ² =0.966, s=0.242	
Trivariate regression	$logP=-16.582+1.154\times SD_{logP} -0.032\times N-0.431\times HOMO$	(17)
	$n=21, R^2=0.969, s=0.237$	

Models validation

a. Internal validation

The performances in leave-one-out analysis related to the models listed as best are shown in Table V.13.

Table V.13. Leave-one-out analysis for the best logP models						
	Descriptors	R^2	Q^2	R^2 - Q^2		
1	$\mathrm{SD}_{\mathrm{logP}}$	0.952	0.944	0.009		
2	$\mathrm{SD}_{\mathrm{logP}},\mathrm{N}$	0.966	0.955	0.012		
3	SD _{logP} , N, HOMO	0.969	0.956	0.014		

b. External Validation



Fig.V.8. The plot $logP_{exp}$ vs. $logP_{calc.}$ f or the test set (external validation).

c. Similarity Cluster Validation



Fig. V.9. The plot $logP_{exp}$ vs. $logP_{calc.}$ for the test set (similarity cluster validation).

QSAR models in set "2" for case Binding Affinity

Ligand-protein binding is based on intermolecular forces, like ionic bonds, hydrogen bonds and Van der Waals forces. After association of docking could take place the dissociation, being a reversible process. The rate of binding is called affinity. BA values were obtained by molecular docking procedure using AutoDock 4.2.6 (Morris *et al*, 2009)

Basic equation that describes the relationships between 32 compounds Binding Affinity values and their structures is obtained.

Binding Affinity=-11.827+SD_{BA} (kcal/mol);
$$n=32, R^2=0.915, s=0.253, F=324.639$$
 (18)

Model validation

After similarity analysis was determined molecules cluster for the chosen ligand to test. Each cluster includes the same number of molecules. In Table V.17 are some similarity results obtained using TOPOCLUJ software.



Fig.V.10. The plot BA_{exp} vs. $BA_{calc.}$ for the test set (similarity cluster validation).

The plot BA_{exp} vs. $BA_{calc.}$ for the test set (Fig.V.10) shows a good correlation between experimental data and calculated ones.

Predicting Binding Affinity for new ligands

Three new molecules for each set have been proposed, each of them was included in its own set for calculating SD_{logP} (Table V.25). Every new ligand was compared with its set, different clusters were made, different predicting models were established.

			1 1	8	
New	Average BA		Predicted BA	Docking BA	Average BA of conformes
ligand	(kcal/mol)	$\mathrm{SD}_{\mathrm{BA}}$	(kcal/mol)	(kcal/mol)	(kcal/mol)
2a	-7.30	9.494	-8.26	-8.7	-7.9
2b	-7.23	9.297	-8.27	-8.8	-8.3
2c	-7.18	9.829	-7.82	-8.9	-8.5
3a	-7.46	6.998	-7.49	-8.4	-7.8
3b	-7.49	7.004	-7.52	-8.0	-7.6
3c	-7.46	6.480	-8.02	-8.1	-7.8



Fig.V.13. The plot BA_{docking} vs. SD_{BA} for the set "2"



Fig.V.14. The plot $BA_{docking}$ vs. SD_{BA} for the set "3"

Concluding, it is possible to predict activities of untested congeneric molecules if the study is based on good experimental results.

V.3. QSAR study on sildenafil derivatives

Sildenafil, $C_{22}H_{30}N_6O_4S$, is a strong and selective inhibitor of cGMP-specific phosphodiesterase type 5 (PDE5), an enzyme that sustains degradation of cyclic guanosine monophosphate (cGMP), which adjusts blood flow in the corpus cavernosum.

A 40 molecules set was downloaded from a (https://pubchem.ncbi.nlm.nih.gov) database, Table V.26.

Tabl	able V.26. List of studied sildenafil derivatives with their CID and properties logP and TPSA.							
#	CID	Canonical SMILES	XLogP	TPSA (A ²)				
1	5212	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC)C	1.5	118				
2	44440137	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCC(CC4)P(=O)(OCC)OCC)OCC)CCC)C	2.7	150				
3	44440128	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)CP(=O)(O)OCC)OCCC)C	-1.1	164				
4	44391946	CCC1=C2C(=NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC)N(N1)C5CCCC5	2.6	115				
5	110634	CCCC1=NC(=C2N1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)CC)OCC)C	2.5	118				
6	44391895	CCCN1C2=NC(=NC(=O)C2=C(N1)CC)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC	2.2	115				
7	44402347	CCOC1=C(C=C(C=C1)S(=O)(=O)N2CCN(CC2)C)C3=NC(=O)C4=C(N3)N5C=CC=C(C5=N4)C	2.5	117				
8	44402480	CCOC1=C(C=C(C=C1)S(=O)(=O)N2CCN(CC2)C)C3=NC(=O)C4=C(N3)N5C=C(C=CC5=N4)C	2.5	115				
9	44402581	CCN1CCN(CC1)S(=0)(=0)C2=CC(=C(C=C2)OCC)C3=NC(=0)C4=C(N3)N5C(=CC=CC5=N4)C	2.9	117				
10	45266248	CCOC1=C(C=C(C=C1)S(=O)(=O)N2CCN(CC2)C)C3=NC(=O)C4=C(N3)N5C=CC=CC5=N4	2.2	117				
11	9913987	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCC(CC4)C(=O)N)OCC)C	1	157				
12	44381943	CCCN1C=NC2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCCC	1.8	118				
13	45267330	CCCC1=C(C=C(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC)O)OC	3.2	129				
14	72543811	CCCC1=NN(C2=C1N=C(N=N2)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC)C	1.4	115				
15	118728651	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)NCCCCO)OCC)C	1.5	143				
16	118728655	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)NCCN(CC)CC)OCC)C	2.3	126				
17	118728656	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)NCCCN(C)C)OCC)C	1.9	126				
18	9935230	CCCC1=NC(=C2N1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC)CC	2.5	118				
19	10227317	CCCC1=C2NC(=NC(=O)N2C(=N1)C)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC	2.1	118				
20	10277925	CCN1CCN(CC1)S(=0)(=0)C2=CN=C(C(=C2)C3=NC(=0)C4=NN5CCCCC5=C4N3)OCC	0.6	130				
21	11540832	CCC1=C2C(=O)N=C(NN2C(=N1)C3CCCC3)C4=C(C=CC(=C4)S(=O)(=O)N5CCN(CC5)C)OCC	3	118				
22	9955904	CCCN1C=NC2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC	1.2	118				
23	9956558	CCCN1C2=NC(=NC(=O)C2=C(N1)C)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC	1.8	115				
24	24859502	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C5CCCCC5)OCC)C	3.3	118				
25	70687499	CCOC1=C(C=C(C=C1)S(=O)(=O)N2CCN(CC2)C)C3=NC(=O)C4=C(N3)C=NN4C	0.3	118				
26	9845589	CCCC1=NN(C2=C1NC(=NC2=O)C3=CC(=CC=C3)S(=O)(=O)N4CCN(CC4)C)C	1.1	108				
27	1896867	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCCCC4)OCC)C	2.5	114				
28	53956764	CCOC1=C(C=C(C=C1)S(=O)(=O)N2CCN(CC2)C)C3=NC(=O)C4=C(N3)C(=NN4C)	0.7	118				
29	10072962	CCCC1=C2C(=NN1)C(=O)N=C(N2)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC	1.5	128				
30	10141109	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CC(NC(C4)C)C)OCC)C	1.9	126				
31	10228242	CCCC1=NN(C2=C1NC(=NC2=S)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C)OCC)C	2.1	133				
32	12018718	CCCC1=NC(=C2N1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCNCC4)OCC)C	1.6	126				
33	24756844	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)CC)OCC)C	1.8	118				
34	56841591	CCCC1=NN(C2=C1NC(=NC2=S)C3=C(C=CC(=C3)S(=O)(=O)N4CC(NC(C4)C)C)OCC)C	2.5	141				
35	25209618	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCN(CC4)C5CCCC5)OCC)C	2.8	118				
36	102582026	CCCC1=NN(C2=C1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N4CCNCC4)OCCC)CC	1.8	126				
37	23449792	CCCCOC1=NC=C(C=C1C2=NC(=O)C3=NNC(=C3N2)CC)S(=O)(=O)N4CCN(CC4)CC	1.6	141				
38	22893606	CCCCCC1=NC(=C2N1NC(=NC2=O)C3=C(C=CC(=C3)S(=O)(=O)N(CC)CC)OCC)C	4.1	115				
39	23522695	CCCC1=C2NC(=NC(=O)N2C(=N1)C)C3=C(C=CC(=C3)S(=O)(=O)N4CCCCC4)OCC	3.1	114				
40	23522716	CCCC1=C2NC(=NC(=O)N2C(=N1)C)C3=C(C=CC(=C3)S(=O)(=O)NO)OCC	1.6	143				

Diudea's algorithm is followed in this study, too.

- Downloading from a database of molecular structures; spliting in training set and test set.
- Geometry optimization (Energy and partial charges calculation)
- Global/local descriptors/indices calculation
- Hypermolecule and its vectors calculation (more than one alignments)
- Correlation weighting and data reduction
- Sum descriptor SD calculation
- QSAR Models (Toplis & Costello; Chance correlation)
- Internal&External validation
- Similarity clusters calculation
- Prediction/validation by similarity clusters



Fig.V.14.b. Hypermolecule comprising the features of the dataset

Basic equations on entire molecules set was obtained. From logP point of view, molecule 32 is an outlier.

$logP=16.901+SD_{logP};$	n=39, R ² =0.934, s=0.245, F=525.792	(21)
TPSA=207.877+0.989×SD _{TPSA} ;	n=37, R ² =0.925, s=0.323, F=433.889	(22)

QSAR models with 1 variable

In training set basic equations were obtained.

$logP=17.121+1.0108 \times SD_{logP};$	$n=26$, $R^2=0.953$, $s=0.228$, $F=485.105$	(23)
TPSA=210.063+0.987×SD _{TPSA} ;	n=26, R ² =0.953, s=2.954, F=486.036	(24)

Conclusions to Tables V.29-30: Although R^2 increases, standard error is not decreasing. It is obvious that standard error (monovariate model) < standard error (bivariate model)< standard error (trivariate model), so the most simple models are to be used in future predictions (Eq. 23 and 24).

	logP Descripto	rs	R^2	S	F
$\mathrm{SD}_{\mathrm{logP}}$			0.9529	0.2279	485.1048
$\mathrm{SD}_{\mathrm{logP}}$	LUMO		0.9535	0.2311	235.9656
$\mathrm{SD}_{\mathrm{logP}}$	LUMO	Detour	0.9537	0.2359	151.0588

Table V.31. Statistical parameters of multilinear regression in logP study

Table V.32. Statistical parameters of multilinear regression in TPSA study

	TPS	A Descriptors	\mathbf{R}^2	S	F
SD_{TPSA}			0.9529	2.9541	486.0361
$\mathrm{SD}_{\mathrm{TPSA}}$	HOMO		0.9546	2.9634	241.9298
$\mathrm{SD}_{\mathrm{TPSA}}$	HOMO	logWkOp[Adj.Det.D3D]	0.9554	3.0033	157.1547

Models validation

Internal validation LOO

 Q^2 is the corresponding R^2 to the prediction.

Descriptor	R^2	Q^2	R^2-Q^2
$\mathrm{SD}_{\mathrm{logP}}$	0.9529	0.9468	0.0061
$\mathrm{SD}_{\mathrm{TPSA}}$	0.9529	0.9481	0.0048

External validation

It makes up clusters of similarity (within the molecules of the learning set) for each of the test-molecules; it generates models for the test clusters (excluding the leaders of similarity); it predicts the activity values for the test-molecules (individual, on each similarity cluster) (Table V.34).



Fig. V.15. The plot $logP_{exp}$ vs. $logP_{calc.}$ for the test set (external validation).



Fig. V.16. The plot $TPSA_{ext}$ vs. $TPSA_{calc.}$ for the test set (external validation).

Similarity Cluster Validation

The principle of clusters composition was the same. Only molecules with similarity over 80% were retained. Based on similarity clusters, calculated values of logP and TPSA were obtained (Table V.36-37).

Figures V.17-18 show the degree of correlation between experimental values of studied properties and calculated ones.



Fig.V.17. The plot $logP_{exp}$ vs. $logP_{calc.}$ for the test set (cluster similarity validation).



Fig.V.18. The plot TPSA_{ext} vs. TPSA_{calc.} for the test set (similarity cluster validation).

Prediction of logP (R^2 =0.902), and TPSA (R^2 = 0.867), is more accurate when using the similarity clusters, compared to the classical external validation of the model.

V.4. QSAR study on cephalosporines

The cephalosporins are a class of β -lactam antibiotics were discovered in 1945 by the Italian pharmacologist Giuseppe Brotzu and were first sold in 1964. Cephalosporins are bactericidal and have the same mode of action as other β -lactam antibiotics (penicillins), but are less susceptible to β -lactamases.

				logP		PS.	A		
Mol	Name	CID	Pubchem	AlogPS	Ichem	PubChem	Ichem	Polarizability (A^3)	Refractivity (A^3)
1	Cefacetrile	91562	-0.5	-0.52	-1.78	162	136.80	31.32	77.51
2	Cefaclor	51039	-1.8	0.85	-2.31	138	112.73	35.11	89.56
3	Cefadroxil	47965	-2.1	0.51	-2.45	158	132.96	35.86	90.95
4	Cefalotin	6024	-0.4	0.63	0.02	167	113.01	37.22	93.79
5	Cefamandole	456255	-0.9	-0.05	0.03	201	150.54	42.45	126.65
6	Cefapirin	30699	-1.1	0.18	-2.00	177	125.90	40.63	122.43
7	Cefazolin	33255	-0.4	-0.40	-1.52	235	156.09	41.44	119.86
8	Cefdinir	6915944	0	0.02	-1.69	212	158.21	36.12	94.34
9	Cefditoren	9870843	0.7	1.70	-0.15	242	160.10	49.19	124.18
10	Cefepime	5479537	-0.1	-0.37	-4.29	204	150.04	47.53	141.98
11	Cefixime	5362065	-0.7	0.25	-1.18	238	184.51	41.62	104.91
12	Cefmenoxime	9570757	0	-0.13	-0.83	270	190.81	47.04	133.51
13	Cefmetazole	42008	-0.6	-0.38	-0.65	239	163.33	44.50	124.57
14	Cefonicid	43594	-1.9	-0.71	-2.51	264	204.91	47.96	136.58
15	Cefoperazone	44187	-0.7	-0.11	-0.90	271	220.26	62.82	169.06
16	Ceforanide	43507	-3.2	-1.35	-3.17	244	193.63	49.27	139.87
17	Cefotaxime	5742673	-1.4	0.14	-1.41	227	173.51	41.77	105.11
18	Loracarbef	5284585	-1.7	0.55	-2.40	113	112.73	32.61	86.64
19	Cefotiam	43708	-2.4	-0.33	-3.09	251	172.46	49.87	142.34
20	Cefpiramide	636405	-0.1	0.53	0.22	259	212.76	58.79	164.81
21	Cefpodoxime	6335986	-1.4	0.05	-1.19	210	156.44	39.90	100.71
22	Cefprozil	5281006	-1.4	0.94	-1.92	158	132.96	39.35	101.27
23	Cefradine	38103	0.4	0.70	-2.45	138	112.73	33.19	92.00
24	Ceftazidime	5481173	0.4	-1.21	-4.12	245	191.22	51.06	143.88
25	Ceftizoxime	6533629	0	0.40	-0.85	201	147.21	35.38	89.90
26	Ceftobiprole	6918430	-3.7	-1.27	-4.53	250	203.44	50.41	131.04
27	Ceftolozane	53234134	-3.2	-1.20	-8.68	356	302.21	62.09	194.51
28	Ceftriaxone	5479530	-1.3	0.01	-1.79	288	208.98	51.47	128.47
29	Cefuroxime	5479529	-0.2	-0.24	-0.90	199	173.76	38.75	97.17
30	Cephalexin	27447	0.6	0.55	-2.14	138	112.73	32.52	89.97
31	Cephaloglycin	19150	-3	0.54	-2.90	164	139.03	37.64	99.90

Table V.38. Downloaded drugs from cephalosporins family (https://pubchem.ncbi.nlm.nih.gov)

Hypermolecule (Figure V.19.a-b) building was realized using some special features of NanoStudio software, "Connect" and "Identification", atom by atom of each structure.



Fig.V.19.a. Hypermolecule, comprising the features of the dataset

Basic equation performed on entire set

$logP= 16.415+0.998 \times SD_{logP};$ n=27; J	$^{2}=0.865; s=0.435; F=160.164$ (25)
--	---------------------------------------

QSAR Models

Mathematical models generated in training set are illustrated in Eq. 26-28.

Model validation

Internal validation LOO

D_1	D_2	D_3	R^2	Q^2	$R^2 - Q^2$
$\mathrm{SD}_{\mathrm{logP}}$			0.875	0.845	0.030
$\mathrm{SD}_{\mathrm{logP}}$	D3D		0.902	0.866	0.036
$\mathrm{SD}_{\mathrm{logP}}$	D3D	TE/N	0.923	0.874	0.049

External validation of trivariate model on the test set, using Eq.28, conducts to result plotted in Figure V.20.



Fig. V.20. The plot $logP_{exp}$ vs. $logP_{calc.}$ for the test set (external validation).

5. QSAR study on penicillines

 β -Lactam antibiotics inhibit the formation of peptidoglycan links in the bacterial cell wall; this is realized through binding of the four-membered β -lactam ring of penicillin to the enzyme DD-transpeptidase. It cannot catalyze formation of these cross-links, the imbalance between cell wall production and degradation causes the cell to die.



Fig. V.21.a Hypermolecule comprising the features of the dataset

Table V.44 lists 40 structures sharing the β -lactam ring.

Mol	CID	Name	MW	XlogP3	LD50 rat, oral	Canonical SMILES
1	5493108	AC1NUTQ9	463.51	-2.9	2310.0	CC1(C(N2C(S1)C(C2=0)NC(C3=CC=CC=C3)C(=0)NC(=0)C(CC(=0)N)N)C(=0)O)C
2	5745669	AC1NX6WR	479.51	-3.7	4610.0	CC1(C(N2C(S1)C(C2=O)NC(C3=CC=C(C=C3)O)C(=O)NC(=O)C(CC(=O)N)N)C(=O)O)C
3	5745670	AC1NX6WT	477.54	-2.7	2280.0	CC1(C(N2C(S1)C(C2=0)NC(C3=CC=CC=C3)C(=0)NC(=0)C(CC(=0)N)NC)C(=0)O)C
4	71365	Almecillin PenO	330.42	1.8	~	CC1(C(N2C(S1)C(C2=0)NC(=0)CSCC=C)C(=0)0)C
5	36273	Amdinocillin	325.43	2.1	1544.3	CC1(C(N2C(S1)C(C2=0)N=CN3CCCCCC3)C(=0)0)C
6	33613	Amoxicillin	365.40	-2	1703.6	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=C(C=C3)0)N)C(=0)0)C
7	6249	Ampicillin	349.41	-1.1	1562.0	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=CC=C3)N)C(=0)O)C
8	71961	Aspoxicillin	493.54	-3.4	8000.0	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=C(C=C3)0)NC(=0)C(CC(=0)NC)N)C(=0)0)C
9	15574941	Azidocillin	375.40	2.8	2132.9	CC1(C(N2C(S1)C(C2=O)NC(=O)C(C3=CC=CC=C3)N=[N+]=[N-])C(=O)O)C
10	5284519	Azlocillin	461.49	0.1	2183.8	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=CC=C3)NC(=0)N4CCNC4=0)C(=0)0)C
11	441397	Bacampicillin	465.52	2.7	2073.3	CCOC(=0)OC(C)OC(=0)C1C(SC2N1C(=0)C2NC(=0)C(C3=CC=CC=C3)N)(C)C
12	6196	Oxacillin	401.44	2.4	1658.3	CC1=C(C(=NO1)C2=CC=CC)C(=O)NC3C4N(C3=O)C(C(S4)(C)C)C(=O)O
13	20824	Carbenicillin	378.40	1.1	1459.9	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=CC=C3)C(=0)0)C(=0)0)C
14	33672	Carfecillin	454.50	3	980.0	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=CC=C3)C(=0)OC4=CC=CC=C4)C(=0)O)C
15	6098	Cloxacillin	435.88	2.4	1994.6	CC1=C(C(=N01)C2=CC=CC=C2CI)C(=0)NC3C4N(C3=0)C(C(S4)(C)C)C(=0)O
16	19003	Cyclacillin	341.43	1.3	1864.3	CC1(C(N2C(S1)C(C2=0)NC(=0)C3(CCCCC3)N)C(=0)0)C
17	18381	Dicloxacillin	470.33	2.9	1994.6	CC1=C(C(=N01)C2=C(C=CC=C2CI)CI)C(=0)NC3C4N(C3=0)C(C(S4)(C)C)C(=0)O
18	71797	Ephicillin	433.57	2.9	~	CCN(CC)CCOC(=0)C1C(SC2N1C(=0)C2NC(=0)CC3=CC=CC=C3)(C)C
19	6438232	Flavicidin PenF	312.38	1.9	2000.0	CCC=CCC(=0)NC1C2N(C1=0)C(C(S2)(C)C)C(=0)O
20	12314049	Heptylpenicillin PenA	342.45	3.5	2000.0	CCCCCCCC(=0)NC1C2N(C1=0)C(C(S2)(C)C)C(=0)0
21	6087	Meticillin	380.42	1.2	1889.3	CC1(C(N2C(S1)C(C2=0)NC(=0)C3=C(C=CC=C3OC)OC)C(=0)O)C
22	36921	Ticarcillin	384.43	0.8	1459.1	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CSC=C3)C(=0)0)C(=0)0)C
23	656511	Mezlocillin	539.58	-0.2	2500.3	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=CC3)NC(=0)N4CCN(C4=0)S(=0)(=0)C)C(=0)O)C
24	8982	Nafcillin	414.48	2.9	2120.8	CCOC1=C(C2=CC=CC=C2C=C1)C(=O)NC3C4N(C3=O)C(C(S4)(C)C)C(=O)O
25	180562	O-Chlorophenoxymethyl penicillin	384.38	2.7	~	CC1(C(N2C(S1)C(C2=0)NC(=0)COC3=CC=CC=C3Cl)C(=0)0)C
26	6439405	Octenoylpenicillin	340.44	3	~	CCCCC=CCC(=0)NC1C2N(C1=0)C(C(S2)(C)C)C(=0)O
27	5852	Penicillamine	149.21	-1.8	2029.0	CC(C)(C(C=0)0)N)S
28	115163	Pivmecillinam	439.57	3.1	2187.4	CC1(C(N2C(S1)C(C2=0)N=CN3CCCCCC3)C(=0)OCOC(=0)C(C)(C)C)C
29	167942	p-Hydroxy penicillin	366.39	1.7	~	CC1(C(N2C(S1)C(C2=0)NC(=0)COC3=CC=C(C=C3)O)C(=0)O)C
30	150610	Ertapenem	475.52	-1.5	2080.3	CC1C2C(C(=0)N2C(=C1SC3CC(NC3)C(=0)NC4=CC=CC(=C4)C(=0)0)C(=0)0)C(C)0
31	5904	Benzylpenicillin PenG	334.39	1.8	1652.3	CC1(C(N2C(S1)C(C2=0)NC(=0)CC3=CC=CC=C3)C(=0)0)C
32	123630	Tazobactam	300.29	-2	1810.0	CC1(C(N2C(S1(=0)=0)CC2=0)C(=0)0)CN3C=CN=N3
33	120720	Penicillin X (III)	350.39	1.5	1652.3	CC1(C(N2C(S1)C(C2=0)NC(=0)CC3=CC=C(C=C3)0)C(=0)0)C
34	71724	Adicillin PenN	359.40	-2.5	2000.0	CC1(C(N2C(S1)C(C2=0)NC(=0)CCCC(C(=0)0)N)C(=0)0)C
35	107556	Amylpenicillin PenDF	314.40	2.4	2000.0	CCCCCC(=0)NC1C2N(C1=0)C(C(S2)(C)C)C(=0)O
36	21319	Flucloxacillin	453.87	2.6	2083.4	CC1=C(C(=N01)C2=C(C=CC=C2CI)F)C(=0)NC3C4N(C3=0)C(C(S4)(C)C)C(=0)O
37	443387	Hetacillin	389.47	-0.6	1851.4	CC1(C(N2C(S1)C(C2=0)N3C(=0)C(NC3(C)C)C4=CC=CC=C4)C(=0)0)C
38	6869	Phenoxymethylpenicillin	350.39	2.1	1895.3	CC1(C(N2C(S1)C(C2=0)NC(=0)COC3=CC=CC=C3)C(=0)0)C
39	43672	Piperacillin	517.56	0.5	2392.5	CCN1CCN(C(=0)C1=0)C(=0)NC(C2=CC=C2)C(=0)NC3C4N(C3=0)C(C(S4)(C)C)C(=0)O
40	33478	Pivampicillin	463.55	2.9	1919.3	CC1(C(N2C(S1)C(C2=0)NC(=0)C(C3=CC=CC=C3)N)C(=0)OCOC(=0)C(C)(C)C)C

Table V.44. penicillin derivatives with their CID and properties logP and LD₅₀.(https://pubchem.ncbi.nlm.nih.gov)

There are 5 molecules with unknown biological activity. The purpose of this study is to predict their activities.

Average value of LD_{50} of entire set is 2167 mg/kg; this value is taken in consideration in SD_{LD50} determination.

Basic equation is obtained, molec 14 being an outlier.

$$LD_{50}=1997.8+0.992\times SD_{LD50};$$
 n=39, R²=0.954, s=233.751, F=761.981 (29)
The model used for prediction is by Eq.30 described.

$$LD_{50}=1994.253+0.999\times SD_{LD50};$$
 n=34, R²=0.961, s=230.279, F=791.147 (30)

Model validation



Fig. V.22. The plot LD₅₀=*f*(SD_{LD50})

The calculated values (predicted) of LD_{50} for those 5 molecules range successfully among the external values.

V.6. QSAR study on capsaicin derivatives

Capsaicin, $C_{18}H_{27}O_3N$, and several related compounds are called *capsaicinoids* and are produced as secondary metabolites by chili peppers.

The studied molecules downloaded from PubChem are listed in Table V.47.

Mol	CID	Canonical SMILES	XlogP3	$TPSA(A^2)$
1	1548943	CC©C=CCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	3.6	58.6
2	42759	CCCCCCCNC(=0)C1=CC(=C(C=C1)0)OC	4.1	58.6
3	2998	CCCCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	4.2	58.6
4	3041745	CCCCCCCNC(=0)CC1=CC(=C(C=C1)0)OC	4.2	58.6
5	69336196	CCCCCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	2.8	67.8
6	10090630	CC(=CCCC(=CCC(=O)NCC1=CC(=C(C=C1)O)OC)C)C)C	5.8	58.6
7	25201160	CC(=CCCCCC(=O)NCC1=CC(=C(C=C1)O)OC)C	3.4	58.6
8	68413664	CCCCCCCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	5.0	70.6
9	3065261	CCCCCCCCCCC(=O)CC1=CC(=C(C=C1)O)OC	4.7	58.6
10	169252	CCCCCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	4.7	58.6
11	3053256	CCCCCCCCCC(=0)NCC1=CC(=C(C=C1)O)OC	5.8	58.6
12	160785	COC1=C(C=CC(=C1)CNC(=O)CCCCCCCC=C)O	4.8	58.6
13	206278	CCCCCCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	5.3	58.6
14	3021470	CCCC(=O)NCC1=CC(=C(C=C1)O)OC	1.5	58.6
15	3022073	CCCCC(=0)NCC1=CC(=C(C=C1)0)OC	2.0	58.6
16	46887832	CC1CCC(C(C1)NC(=O)NCC2=CC(=C(C=C2)O)OC)C©C	4.0	70.6
17	68414474	COC1=C(C=CC(=C1)CNC(=O)NCC2=CC=CC=C2)O	1.3	70.6
18	3041816	CCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	2.6	58.6
19	68760229	COC1=C(C=C(C=C1)CNC(=O)O)O	0.7	78.8
20	67419566	CC©©N(CC1=CC(=C(C=C1)O)OC)C(=O)O	1.9	70.0
21	22245803	CC©©OC(=0)NC1=CC(=C(C=C1)OC)O	2.2	67.8
22	5149140	CCCCCCCC(=O)NCC1=CC(=C(C=C1I)O)OC	4.8	58.6
23	168836	CC©CCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	3.9	58.6
24	9839519	CC©C=CCCCCC(=O)OCC1=CC(=C(C=C1)O)OC	4.2	55.8
25	101751387	CC(CCCCCC(=O)NCC1=CC(=C(C=C1)O)OC)CO	3.0	78.8
26	20058472	CCCCCCCNC(=0)C©C1=CC(=C(C=C1)O)OC	4.7	58.6
27	66552406	CCCCCCCCCCC(=0)C©C1=CC(=C(C=C1)0)OC	5.3	58.6
28	107982	CC©CCCCCC(=O)NCC1=CC(=C(C=C1)O)OC	4.4	58.6
29	4446034	CCCCCCCC(=O)NCC1=CC=CC=C1	4.6	29.1
30	44398654	CCCCCCCC(=O)NCC1=CC(=C(C(=C1)OC)O)CC	5.0	58.6
31	66552464	CCCCCCCC(=O)NC©C1=CC(=C(C=C1)O)OC	4.6	58.6
32	11630698	CC©CC=CCCC(=0)NCC1=CC(=C(C=C1)0)OC	3.1	58.6
33	11486920	CCCCCCCC(=0)NCC1=C(C(=C(C=C1)0)OC)I	4.8	58.6
34	122189959	COC1=CC=C(C=C1)CC(=O)NCC2=CC(=C(C=C2)O)O	1.9	78.8
35	52944666	CC©©C1=CC=C(C=C1)CNC(=0)CC2=CC(=C(C=C2)0)OC	3.9	58.6
36	71541380	CN©CCNC(=0)CC1=CC(=C(C=C1)0)OC	0.8	61.8
37	15068906	CC1=CC(=CC=C1)CCNC(=O)CC2=CC(=C(C=C2)OC)OC	3.4	47.6
38	9566808	CC(=NNC(=0)CC1=CC(=C(C=C1)OC)OC)C2=CN=CC=C2	1.9	72.8
49	71748835	CC©(C=CCCCCC(=O)NCC1=CC(=C(C=C1)O)OC)O	2.2	78.8

 Table V.47. Capsaicin derivatives with their CID, properties logP and TPSA.(https://pubchem.ncbi.nlm.nih.gov)



Fig.V.23.a. Hypermolecule comprising the features of the dataset

Basic equation (31) was performed on entire set

$$logP=4.377+SD_{logP}$$
; n=40; R²=0.791; s=0.644; F=143.535 (31)

QSAR Models

40

Following already classic Diudea's algorithm, the QSAR model were established (Eq. 32-34)

Monovariate regression	$logP=4.381+0.992\times SD_{logP}$	(32)
	n=28; R ² =0.815; s=0.672; F=114.300	
Bivariate regression	$logP=5.045+1.012\times SD_{logP}-3.461\times Charges$	(33)
	n=28; R ² =0.834; s=0.647; F=63.013	
Trivariate regression	$logP=7.301+0.861 \times SD_{logP}-2.856 \times Charges+0.014 \times TE/N$	(34)
	n=28; R ² =0.846; s=0.637; F=43.997	

Models validation

Internal validation LOO

Table V.51. LOO analysis result
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D_1	D_2	D ₃	R^2	Q^2	R^2 - Q^2
$\mathrm{SD}_{\mathrm{logP}}$			0.815	0.791	0.024
$\mathrm{SD}_{\mathrm{logP}}$	Charges		0.834	0.798	0.037
$\mathrm{SD}_{\mathrm{logP}}$	Charges	TE/N	0.846	0.801	0.045

56

External validation of trivariate model, eq.34



Fig.V.24. The plot $logP_{exp}$ vs. $logP_{calc.}$ for the test set (external validation).

Similarity Cluster Validation

The monovariate correlation for logP is plotted in Figure 25.



Fig.V.25. The plot $logP_{ext}$ vs. $logP_{calc.}$ for the test set (similarity cluster validation).

Prediction of logP ($R^2=0.903$) is more accurate when using the similarity clusters, compared to the classical external validation of the model ($R^2=0.712$).

V.7. QSAR conclusion

The paradigm of Corvin Hansch "similar molecules exhibit similar biological activity" is basic idea of QSAR studies. It does not represent a causalily relating structure and activity, but is simply a statistics.

We stress here that our goal was not to find the best models but to test an algorithm (developed at TOPO Group CLUJ), a methodology enabling an "ad-hoc" best prediction, within the "hypermolecule simulation of the biological receptor and regression weighting" of independent variables; the predictability of models in external sets is thus not necessary.

Predictions by similarity clustering is a special case of Leave-one-out procedure, where one molecule property is predicted by its similarity cluster computed among initial database molecules, this enabling the cluster to be congeneric, as initially asked by C. Hansch.

Good results we obtained on several sets of molecules taken from PubChem and other data bases.

We stress that our approach is not looking for predictability of QSAR equations in any data set. Our work is focused on ad-hoc best prediction on a study case.

Prediction could be made for molecules that have no external activity taking the mean value of the set. Some descriptor can be calculated and then their activity predicted, some exemples been given in this thesis.

Six sets of bioactive organic molecules were studied and presented in this chapter:

1. Phenothiazines

4. Cephalosporins

- 2. Sumatriptans
- 3. Sildenafils

- 5. Penicilline
- 6. Capsaicines

VI. Final Conclusions

VI.1. General Conclusions

Within this Thesis,

- 1. Design of various multi-shell clusters of icosahedral and octahedral symmetry was accomplished by map operations and their structure described by enumerating the substructures (*i.e.*, figure counting), which enabled to establish their rank (3D or higher).
- 2. Equivalence classes of figures (vertices/atoms, edges/bonds, facets of higher rank) in icosahedral, octahedral or rhombohedral clusters have been solved by using the centrality topological index, which provides an image of atom distribution according to molecular centrality. Classes were confirmed by group symmetry calculations obtained by permutations in the adjacency matrix. Equivalence class counting is related to "topological symmetry", that is the maximum possible symmetry achievable by a molecular structure.

- 3. Energy of graphs was computed from the eigenvalues in propellanes (a new class of rhomboidal polytopes) and applied in a QSPR study performed on C_{40} fullerenes.
- QSAR studies were performed in 6 classes of organic compounds with biological activity: phenothiazines, triptans, sildenafil derivatives, cephalosporines, penicillines, capsaicin derivatives.
- 5. Research resulted in 8 published articles, a chapter in a Springer book, 3 sent articles, 6 oral conference presentations, 3 conference posters

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