

Index

a

A_S+logP 394, 396–399, 401
ab initio methods 266, 388
 AB/LogP 359, 368–370, 375
 Abraham's descriptors 383
 absolute configuration 6
 ABSOLV 343, 383, 396–399, 401–402
 absorption in humans 128, 145–146
 absorption 25–26, 28–35, 37–47, 49–51, 55–57, 61, 63, 78–81, 83, 85, 96–98, 107, 112–115, 118, 119, 124–125, 128, 131–132, 134, 141–142, 145–148, 151–153
 absorption/permeability 131
 accessible surface area 387–388, 391, 404
 accuracy extender 368
 ACD/LogP 359, 367–368, 370, 375, 378–379
 acetylcholine 11–17, 22
 acid–base equilibria 287
 acids 266–268, 278
 acquisition process 455–456
 adaptability 10–15, 17, 19
 adaptability of acetylcholine 12, 14
 adjacency matrix 87
 ADME 25–28, 36, 39, 41–46, 48, 50–52, 55–56, 79, 81, 403, 406, 408, 410, 412–413, 419, 427, 430–432, 435–437
 ADME Boxes 323, 328
 ADMET prediction 428
 ADMET 85, 96–97, 315, 325, 327–328, 331–332, 357–358, 376, 406–407, 415, 419–420, 428, 432, 436, 441–442
 α_1 -adrenoceptors 3, 19
 aggregation 57, 72–73, 79, 82
 agrochemicals 283
 alignment media 209, 211, 218–221, 248
 alignment tensors 223–224

aliphatic proximity 364–365
 alkane–water partitioning 34
 ALL-QSAR 104
 ALMOND 197
 ALOGP98 371ff, 375, 444
 ALOGPS 394, 396–399, 401, 405–406, 428–429, 436
 amorphous 259, 262, 271–272, 274–277, 280–281
 anisotropic medium 11, 14, 16
 anisotropic NMR parameters 209, 225, 242
 anisotropic 322, 324–326
 anticancer compounds 102
 apparent partition coefficient 64–65
 3D approaches 382
 AQUAFAC 305
 AQUASOL Data Base 302
 aquatic toxicity 149, 154
 aqueous boundary layer 55, 57–58, 74
 aqueous solubility 93, 107
 aqueous solution 198
 arithmetic average model 381, 395
 aromaticity 400–401
 artificial membranes 25, 28, 36–38
 artificial neural network 85, 93
 assignment 208–209, 217, 223, 228, 245, 249, 251
 associative neural networks 397, 405–406
 atom-based methods 371–373, 375
 atom/fragment contribution 357, 363, 378
 atom types 91, 371–374
 ATP-binding cassette 97
 Avdeef–Bucher equation 60

b

bases 266, 268–269
 basic group parameters 361–362

- Bayesian neural network 37
 - BBB penetration 112, 115–116, 119
 - benchmarking 394–397, 399–402, 406
 - biliary excretion 33
 - Bioactive conformation 159, 187f, 192–202, 210, 237
 - bioavailability area 115
 - bioavailability radar plots 118
 - bioavailability
 - 29, 41, 43, 115, 117–118, 123, 125–126
 - bioequivalence studies 32
 - biopartitioning micellar chromatography (BMC) 25, 39, 50
 - Biopharmaceutics Classification System (BCS) 25, 32, 45, 55–56, 127, 147
 - BioPrint 428
 - biosensors 40
 - Bjerrum plot 60, 80
 - blood–brain barrier (BBB) 33–35, 41, 55, 74–75, 85, 96, 112, 357–358, 407, 411, 429
 - blood–lumen barrier 56
 - boiling point 7, 10
 - bond angles 161, 164–166
 - bond lengths 161, 164–165, 173
 - BOSS 297, 306
 - branch bonds 364–365
 - brickdust 273–275, 277–278
 - Brij35 [polyoxyethylene(23)lauryl ether] 39
- C**
- Caco-2 monolayer 32, 34, 39
 - Caco-2 studies 32
 - Caco-2 25–26, 29, 32, 38, 42, 44, 46–48, 55, 57–58, 74, 80, 85, 98, 111–112, 115, 124, 441, 444
 - calculated lipophilicity potential (CLIP) 391
 - calculated solubility 32
 - Cambridge Crystallographic Database 158
 - Cambridge Structural Database 139, 152
 - capillary electrophoresis (CE) 347–349
 - carbon atom contributions 367
 - carboxylic acids 59, 82
 - carcinogenicity 99–100, 102, 108
 - carnosinase 11, 15–18, 23
 - carnosine 11–12, 15–18, 22
 - center atoms 362
 - central nervous system (CNS) 25, 41, 51, 115, 441, 444
 - Cerius² 42, 92, 95, 100, 103, 105, 372
 - chain bonds 364, 365
 - chain conjugation 360
 - charge density σ 294
 - CHARMM 240, 253, 297
 - chemical filters 445
 - chemical libraries 10, 86f, 97, 102ff, 102–106
 - chemical space 10, 21–22
 - Chemistry Development Kit 120, 126
 - ChemProp 383
 - chromatographic hydrophobicity index (CHI) 82, 341, 416
 - chromatographic methods 416, 419
 - Cisplatin 102
 - CLASS 449, 460
 - Classification And Regression Trees (CART) 96, 444, 458
 - classification problem 442, 453, 457
 - classification 442, 444, 453–454, 456–458, 460
 - Clog *P* 326
 - CLOGP 37, 98, 298, 306, 309, 359, 363–367, 370, 375, 379, 391, 394, 399, 402, 441, 443–444, 449–453, 460
 - close contact ratio 157, 173, 177
 - CNS rule-of-thumb 41
 - Collander relationship 29
 - column length 338, 344ff
 - combichem 442
 - combinatorial libraries 27, 34, 41
 - combinatorial problem 195
 - combinatorial QSAR 42, 52
 - CoMFA 392, 404
 - composition 5–6
 - compound collection 449, 455, 460
 - computable properties 6
 - computational approaches 408, 411, 425, 430, 432
 - Computer Automated Structure Evaluation (CASE) 361
 - computer-aided drug design 128
 - CONCORD 173, 176–178, 180–181
 - configuration 208–209, 222–223, 227–228, 236, 249
 - conformation 9, 12, 16, 18, 34, 87, 112, 157–176, 179ff, 183, 187f, 190–202, 208–210, 228f, 238–245, 306, 388f
 - conformational analysis 183–188, 191–195, 202ff, 208, 243
 - conformational behavior 7–8, 14, 17
 - conformational cluster 12–14
 - conformational energy cutoffs 187
 - conformational energy penalty 188ff, 197
 - conformational lock 198f
 - conformational profile of acetylcholine 11–12
 - conformational restriction 198
 - conformer 10ff, 10–16, 112, 115ff, 115–119, 159, 183, 185ff, 192–198

- conjugated multiheteroatomic effects 362
 connectivity 5–6
 consensus or ensemble models 42
 constitution 5–6, 208, 236
 constitutional isomer 6
 constructionistic approaches 359
 continuum solvation models 382, 386
 conventional apolar stationary phases 334
 CORCEMA 216, 247
 core 363, 391
 CORINA 122, 159, 162–163, 166–167,
 171–173, 176–181, 393, 396–397
 correction factors 358, 363–364, 367, 369,
 371, 374
 correlation time 212–216, 229–232, 234,
 236
 COSMOfrag 308, 310, 388, 396, 398–399,
 403
 COSMO-RS 293, 295
 cosolvent methods 60–61
 Coulomb interactions 288, 293
 cross-correlated relaxation 207, 209, 229,
 251–252
 cross-relaxation rates 213, 215–6, 232, 235,
 252
 cross-sectional area 25, 33
 crowding 364, 366
 crystal structure 290, 308
 crystalline 259, 263–264, 271–272, 274–277,
 279, 281, 288–290
 CSlogP 421, 423, 435
 cyclic voltammetry 32
 cyclohexane 408, 411, 424
 cyclooxigenase 85, 96
 cytochrome P450 85, 100, 108
 cytotoxicity 40
- d**
- δ connectivity index 88
 Debye–Hückel theory 59
 decoupling of resonance 360
 density functional theory 381, 387
 deprotonation 6
 DEREK 99–100, 102, 108
 descriptors 128–131, 134–136, 138, 141–
 154, 159
 2D descriptors 397
 dibutyl ether 411
 dichloroethane 411, 416, 423, 431
 dihedral angles 11–12
 dihedral bond angles 209
 dimethylsulfoxide (DMSO) 38, 55, 60, 207,
 212, 257, 348, 407, 415
 dipolar interaction 211–212, 218, 229, 251
 dipolar ion effects 362
 dipolar relaxation 212–213, 229, 235
 dipole moment 15, 19f, 122, 278, 316f, 385
 dissolution 30, 32, 36–37, 44–45
 distance geometry 207, 210, 236–237, 252
 distance H-bond potentials 128, 136
 distance matrices 238
 distance matrix 88
 distribution coefficients 26, 35–36, 315,
 320, 332, 381, 385, 389, 399, 406–409,
 414, 421, 423, 425, 426, 435–436
 DMPK 25–28, 42
 DMSO solubility 258, 267, 271, 276–277,
 279–280, 282, 308
 dopamine D₂ 446
 dopamine receptor 94
 dopamine transporter 93, 107
 Dragon 92, 96–98, 100, 102
 drug solubility prediction 283, 287,
 289–291, 308
 drug solubility 257
 drug transport 112–114, 119, 124, 126
 drug-like compounds 96–97, 288–290, 305,
 307–308
 drug-like properties 40–41, 44, 50
 drug-likeness 112, 123, 125, 442–445,
 453–454, 457–460
 duplicate removal parameter 193–194
 dynamic QSAR 11, 19, 21, 23
 Dyrssen dual-phase potentiometric log P_{oct}
 technique 64
- e**
- E*- and *Z*-descriptors 6
E-Dragon 92
 effective lipophilicity 36
 electron density 9
 electronegativity facing bulk 360
 electronic effects through π -bonds 361,
 364, 366
 electronic strength 366
 electrostatic solvation energy 388
 electrostatically collapsed 190
 electrotopological indices 6
 electrotopological state (*E*-state) 85ff, 304,
 310, 393
Elog D 26, 37
 enantiomerism 6
 energy cutoffs 187, 190, 195, 197
 equatorial/axial ring substituents 169
E-state 87–103
 Estrogen receptors 104
 exchange-transferred experiments 209,
 230–231, 235

experimental value adjusted 357, 364
 extended Collander equations 37
 extension of aromaticity 364, 366

f

factorization 316, 322–324
 FaSSiF 25, 32
 field effect 366
 file formats 178, 181
 flexibility 237, 252, 291, 324
 flexible nitrogen 171
 fluorosomes 38, 40
 force fields 184, 187, 237, 239–240, 253, 296
 four components of SAR and QSAR studies 4
 Fourier transform methods 265
 fraction absorbed (FA) 111, 114, 128, 146
 fragment valence type 361, 366
 fragmental contributions 367
 fragmental methods 359, 361, 363, 365, 367, 369, 373, 378–379
 fragmentation rules 364–365, 367, 370
 freeze–thaw cycles 276–277, 280–281

g

Gasteiger–Hückel scheme 317
 gastrointestinal absorption 35
 gastrointestinal tract 55–56
 general solubility equation 283, 289, 308
 Generalized Born 386–387, 390, 403
 Generalized Born/surface area 183, 190
 genotype, molecular 5–9
 geometric π -diastereomerism 6
 geometric descriptors 11, 19–20
 geometric features 8, 11
 Ghose–Crippen approach 371–373
 Ghose–Crippen atom types 454
 Gibbs free energy 286, 382, 385
 Gibbs' pK_a 57–58, 69, 71
 global minimum conformation 162, 187f, 192f
 Good buffers 62, 72
 gradient approaches 339, 341, 343, 345, 347
 graph molecular connectivity 392
 greaseballs 273–274, 277–278
 GRID 137, 139, 149, 152
 GROMACS 223, 239
 GROMOS 239f
 group contribution methods 283, 298
 GVK BIO 195, 196, 443, 446, 449–452, 455–456, 458

gyromagnetic ratio 212, 219, 229, 235

h

H-bond acceptors 41, 118, 127–128, 130, 136, 138, 138f, 141, 144–146, 148–149, 151, 274, 300, 335, 367, 443
 H-bond donors 41f, 93f, 96–97, 118, 127–128, 130, 132–133, 135–136, 138, 138f, 145–146, 150, 274, 300, 335, 389, 443
 H-bond indicators 128–129, 133
 H-bond potentials 128, 136–137, 139, 141–142, 152
 H-bonding 9, 12, 25, 29, 32, 34–35, 112–113, 117–119, 122, 128–143, 146–149, 274, 278–281, 304, 361, 363, 366f, 367, 369–370, 385–388, 397, 401, 411, 417
 H-bonding fields 10
 H-bonding interactions 9
 3D H-bonding parameters 134
 Henderson–Hasselbalch equation 56–57, 59, 68–70, 72, 78–79
 Henderson–Hasselbalch relationship 36
 hepatitis C virus NS5B 199–200, 205
 HEPES 55, 62
 hERG potassium channel 327
 HE-state 85, 89–94, 96, 98, 100
 heteronuclear couplings 221
 heteronuclei 209, 222, 227, 249
 hexadecane membrane (HDM) 25, 39
 hierarchical clustering 370
 high-performance liquid chromatography (HPLC) 63, 277, 331, 340, 407, 415, 432–433
 high-quality ligand–protein complexes 188, 193
 high-throughput screening (HTS) 25, 27, 44, 49–50, 117, 183, 201–203, 257, 282, 441–442, 459
 HIV-1 protease 93–94, 107
 holonomic constraints 236, 238
 HPLC 262, 269–271, 277f, 340, 347, 415–420
 human ether-a-go-go-related gene (hERG) 315, 327
 human intestinal absorption 85, 97–98
 human oral absorption data 30, 35
 human serum albumin (HSA) 25, 30, 85, 98
 HYBOT 35, 42, 127, 132–133, 136, 138–139, 141, 143–145, 147–148, 151–154, 384
 hybridization 361, 367, 372–374, 393

hydrophobic carbons 373
 hydrophobic effect 9
 hydrophobic interactions (HINT) 378, 391
 hydrophobically collapsed 191
 hydrophobicity fields 9
 hydrophobicity 35, 37, 46, 323–324, 326, 329, 357–358, 377–378

i

immobilized artificial membranes (IAM) 25, 37, 85, 98, 332–333, 351–352, 407, 418, 433–434
 immobilized liposome chromatography (ILC) 25, 39
in combo 43, 44, 52, 83
in silico PAMPA 39
in silico prediction methods 284, 289
 indicator variables 128, 131, 150
 indicator 128–131, 133–134, 149–150
 INSIGHT 240, 157, 302, 322
 intermolecular forces 318, 319, 323
 intermolecular interactions 9
 intestinal absorption 56, 112, 114–115, 119, 124
 intestinal fluid solubility 261
 intramolecular effects 9
 intramolecular interaction contributions 367
intrinsic lipophilicity 35–36
 intrinsic solubility 286–287
 intrinsic state 86–87, 89–90, 92
 inverse QSAR 103
 ionic bonds 9
 ionization constant 55–65, 76, 80
 ionization properties 266
 ionization reactions 58
 ionization 26, 30, 32–33, 35
 ion-pair partition 64–66, 78
 ion-pairing 410, 412, 421, 423–425, 427, 435
 isocratic conditions 333, 335, 337, 339
 isolating carbon 357, 365, 370
 isotropic medium 11, 14, 16
 isotropic 322, 324–326

j

J-couplings 208–209, 211, 226–227, 242–243, 247, 249
 JOELib 120, 126

k

Kamlet–Abraham’s acidity parameters 133
 Karplus relation 211, 226–228

Kier–Hall electronegativity 85, 89–90
 kinetic solubility 259, 262–264, 273, 275
 KLOGP 359, 362
k-nearest neighbors 85, 99
 KOWWIN 359, 363–364, 375

l

Larmor frequency 212, 218
 lazy learning 85, 104, 108
 lead-like paradigm 444
 lead-likeness 441, 443, 445, 457
 LeadScope 457, 460
 LEKC 332, 350
 LIBRARY mode 399, 428–429
 ligand efficiency 441, 450–453, 457, 460
 light scattering 265f, 273–274
 linear discriminant analysis 85, 97, 105
 linear line notations 6
 linear solvation energy relationship (LSER) 335, 382
 linear solvent strength (LSS) 340
 Lipinski’s rule of five 33, 443
 lipophilicity fields 9
 lipophilicity indices 332–333, 340, 343, 352
 lipophilicity range 20
 lipophilicity 9, 13, 15–16, 18, 20, 22, 28–30, 33, 35–37, 39–41, 313, 315–329, 357–358, 360, 376–377, 379, 381–384, 390–394, 402, 404–406, 408, 410, 412–420, 423–424, 427, 429, 430–436, 446, 448–449
 liposome electrokinetic chromatography 332
 liposomes 40, 57, 67, 78
 liquid-state properties 7
 local energy minimization 185
 local lymph node assay 85, 100
 log *D* 398–400, 406, 408, 410–419, 423, 425–433, 436–437
 log *D*_{oct}-pH lipophilicity profiles 65–66
 log *D*-pH plots 36
 log *k*_w 333–336, 337–343, 346, 416–417
 Δlog *P* 26, 34
 log *P* increments 367
 log *P* 10, 12–16, 18–22, 111, 114–115, 118, 121–122, 357–368, 370–379, 381–386, 388–392, 394–395, 398–406, 441, 443–444, 446–450, 454
 log *P*_{oct} 63–64, 332–338, 343, 347–350, 408–413, 419
 log *P*_{ow} 283, 289, 291, 297–299, 301, 306–307

- long-range interactions 371
- low-energy conformational ensembles 192
- m**
- macroscopic properties 10
- Madin-Darby canine kidney 38, 55, 57
- magic constant 357, 360–361
- marketed drugs 443, 449–450
- mass spectrometry 271, 344, 415, 419
- maximum absorbable dose (MAD) 25, 31
- MD 381–382, 389–390, 392, 396, 401, 406
- MDL Comprehensive Medicinal Chemistry 441, 443, 458
- MDL Drug Data Report 441, 443, 458
- MEEKC 332, 348–350, 354
- MEKC 332, 348–350
- melting point 7, 10, 283, 289
- membrane model 11, 14, 16
- membrane pK_a 57
- Merck molecular force fields 183, 188, 204
- MES 55, 62
- micellar electrokinetic chromatography (MEKC) 25, 39
- microemulsion electrokinetic chromatography 332, 355, 407, 418, 433
- MIMUMBA 166
- minimization 185, 187
- missing fragments 359, 368, 378
- mixed-charge aggregate 73
- MLOGP 392, 395–398, 401
- MLP 357–358, 381–383, 390–391
- mobile order and disorder 127, 142, 151
- MOLCAD 371–372
- Molconn-Z 92, 95, 100, 104
- molecular complexity 444, 448, 450, 458
- molecular connectivity indices 86, 88, 89, 101
- molecular core features 5
- molecular descriptors 10, 19, 113, 115–117, 120–126
- molecular dynamics (MD) 3, 11, 207, 210, 247, 251, 253, 283, 296, 309, 382
- molecular electronegativity topological distance vector 92
- molecular electrostatic potentials 8–9, 22, 38, 39
- molecular environment 7, 19
- molecular force fields (MFF) 188, 190
- molecular genotype 5, 6, 9
- molecular geometry 184
- molecular graphs 87, 106–107
- molecular H-bonding potential 52, 127
- molecular interaction fields 39
- molecular lipophilicity potential (MLP) 382
- molecular phenotype 6, 7
- molecular polarizability 128, 143, 147, 149
- molecular properties 7, 9–11, 13, 19
- molecular sensitivity 11, 19, 41, 49
- molecular size and shape 33
- molecular size 382–383, 385, 390, 401, 403
- molecular structure 3, 5, 10, 22
- molecular surface area 9
- molecular surface 111–112, 115, 119, 123–125
- molecular topology 86, 105
- molecular volume 9
- molecular weight 6, 441, 443
- molecular 3–18
- MolSurf 42
- MOLTRA 138, 152
- Monte Carlo 3, 10, 283, 296, 309
- multidimensional hyperspace 10
- multihalogenation 360
- multiple linear regression 85, 93
- multiple parallel synthesis 441–442
- multivariate adaptive regression splines 85–86, 98, 107
- mutagenicity 99–102
- Mycobacterium tuberculosis* 95
- n**
- National Toxicology Program 102
- N*-dimensional objects 21
- nephelometric turbidity units 266
- nephelometry 265–266
- neural networks 302, 394, 397, 399, 405–406
- neuropeptide Y 85, 95, 107
- neutral compounds 266, 269
- new chemical entities (NCEs) 146, 419–420
- NMR parameters for conformational analysis 211
- nuclear magnetic resonance 157–158, 207–208, 246
- nuclear Overhauser effect 209, 246–247, 251
- o**
- observable properties 6
- obtaining bioactive conformations
- octadecylsilane (ODS) 335, 416
- octanol 402–420
- octanol pK_a 57–58, 66
- octanol–water partition coefficient 55, 63
- octanol–water volume ratio 65
- Oie–Tozer equation 30

- OMEGA 160, 163, 175, 181, 186–187, 193–196, 201, 203–204
- o-nitrophenyl octyl ether 431, 462
- OpenEye 446, 459
- optimal prediction space (OPS) 393
- optimization process of potential leads 26
- oral absorption 28–35, 38, 40–42, 51, 118, 147, 259, 261, 263–264, 267–270, 272–273, 275–276, 281
- oral bioavailability 98
- oral drugs 443–444, 449–450, 460–461
- organic modifiers 337–339
- Ostwald's rules 272
- oxidation state 372
- p**
- PAMPA 25–26, 28–29, 37–39, 55, 57–58, 74–75, 77–78, 81, 83, 419
- paracellular 33
- parallel artificial membrane permeation assay (PAMPA) 25, 28, 55, 57
- paramagnetic relaxation enhancement 207, 231, 235
- partial least squares 86, 95, 107
- partition coefficient 321, 325–326, 357–358, 371, 374, 377–379, 408–409, 411, 416–417, 419, 421–426, 431–433, 435
- partition coefficients measurement 63
- partitioning 7, 9, 142–145, 149, 153
- passive diffusion 34, 38
- Pauling electronegativity 92
- PBPK modeling 32, 40
- PerlMol 120
- permeability 28–35, 37–42, 56–58, 74–80, 82–83, 127, 131, 134, 145–147, 150–153, 325–326
- permeation 411–412, 418–419, 421, 423, 431, 434, 435
- pesticides 283, 309
- P-glycoprotein (P-gp) 25, 34
- P-glycoprotein 86, 97–98, 107
- pH gradient 56, 267
- pH method 37
- pharmacophore 180, 192, 194, 442
- pharmacophore analysis 457
- pharmacophore searching 180, 192, 194
- phenotype space 7
- pH-metric titration 60
- phosphatidylcholine 67, 331, 336
- phospholipidosis 40
- phospholipids 40
- pH-partition antithesis 57, 80
- pH-partition hypothesis 56–57, 77, 266, 268
- pH-partition theory 32, 421
- Physicians' Desk Reference 102, 441, 443, 458
- physicochemical profiling 58, 78, 81
- physicochemical properties 5, 11–15, 18–21, 25–28, 30, 42
- physiologically based pharmacokinetic modeling 25
- PHYSPROP 302, 303, 388, 394–395, 404–405
- pK_a prediction methods and software 63
- pK_a predictions 33
- pK_a 7, 20–22, 26, 30, 32–33, 35–37, 63, 65–67, 69, 71, 73–75, 77, 288
- plasma protein binding (PPB) 26, 30
- point charges 316–318, 322, 324
- polar fragments 112–113, 119, 365–366
- polar interactions 324
- polar surface area (PSA) 3, 9, 13, 16f, 18–20, 25, 34–35, 111–123, 128f, 136, 444, 446–448
- polar surface area 3, 19, 441, 444, 458
- polarizability 9, 384–385, 388, 392
- polarization 9
- polymorphs 286
- potentials 128, 136–137, 139–142, 149, 152
- potentiometric method 58, 61, 64, 415–416, 432
- potentiometric titration 37
- predictive power 375, 379
- principal component analysis 62
- principal component regression 86, 95
- property range and distribution 11, 19
- property ranges 16, 448–449, 453, 457
- property space 7, 10–12, 14–16, 18–23
- property-based approaches 358, 395, 397, 399
- Protein Data Bank 157–158, 181, 183, 187, 204
- protonation 6
- proximity effect 360, 362
- pseudoatom types 373
- pseudo-contact shifts 211
- PubChem 456, 460
- q**
- QikProp 297, 301, 306, 309–310, 382, 389–390, 396–399, 404
- QLOGP 385–386, 396, 398–399, 401
- QSAR Modeling 42
- QSAR tool 42
- quality control 173

- quantitative structure–activity relationship (QSAR) 3–4, 11, 19, 22, 25, 36, 86, 107, 111–113, 116, 121–122, 125–128, 131, 134, 138, 142, 145, 148–154, 157–158, 183, 196, 315, 326, 331, 342, 343, 354, 357–358, 376–379, 381, 384, 404, 408, 431, 434
- quantitative structure–pharmacokinetic relationships 99, 108
- quantitative structure–property relationship (QSPR) 86, 283, 291–310, 408
- QuantlogP 389, 396–398
- quantum chemical calculations 385, 387
- r**
- R- and S-descriptors 6
- range 10–13, 15, 18–22
- recognition forces 9
- recursive feature elimination 86, 98, 104
- recursive partitioning 86, 105
- reductionistic approaches 359
- Rekker's fragmental constant approach 37
- relevant conformational ensembles 187
- ReLiBase+ 188
- residual chemical shift anisotropy 207, 211, 225
- residual dipolar couplings 209, 247, 248–250
- residual quadrupolar couplings 211
- resonance interaction 360
- restrained molecular dynamics calculations 210
- retention factors 333–335, 337–338, 352, 354
- retention time 333, 339–347
- reversed-phase high-performance liquid chromatography 35
- reversed-phase liquid chromatography 332, 353
- reverse-phase high-performance liquid chromatography 262
- reversible processes 6
- ridge regression 86, 95
- rigid-body docking 194
- rigidity 291
- rigidity of carnosine 16
- ring bonds 364–365
- ring closure 198–200
- ring conformations 162, 164, 168
- ring templates 162, 166–168
- root mean square deviation 19
- root mean square error 283, 288
- root mean square 157, 174, 183, 190
- rotatable bonds 185, 188, 190, 195–198
- Rule-of-3 443
- Rule-of-5 33, 41, 118, 131, 147, 413, 443, 451
- s**
- σ profile 294–296
- σ/ρ fragment interaction 361, 366
- safety/toxicity 26–27
- SANALOGP_ER 361
- SARVision 457
- SAS 3, 13, 16, 18, 20
- saturation transfer difference 207, 231, 252
- scaffold hopping 200–202
- SDFFile 176, 178
- secondary algorithms 368
- sensitivity and range descriptors 21
- σ_f system 359–361, 366
- shake-flask 37, 63, 65, 69–70, 81–82, 414
- shape-based scaffold hopping 200
- shape-matching techniques 201
- SHAPES 235, 252
- similarity indices of spectra
- simulated annealing 217, 237, 243
- single conformation 196–197
- single gradient run 340–341
- SLAPSTIC 236
- SLIPPER 382–384, 396–399, 402
- slope 57, 65, 69, 73, 76–77, 289, 334–335, 337–338, 347
- SMARTS 183, 187, 372, 446
- SMILES 120, 159, 178–179, 181
- sodium dodecyl sulfate 39
- soft independent modeling of class analogy (SIMCA) 86, 105
- software 186, 204
- solid-state properties 10, 270
- solubility 7, 10, 26, 30–33, 56–58, 60–61, 68–73, 78–82, 128, 143–144, 147–148, 151–153, 283–292, 296–310
- solubility assay 258–259, 262–265, 272–273, 275–276
- solubility prediction 32
- solvation 112, 142, 144–146, 149, 184, 187–188, 190–191, 283, 288, 291–293, 297, 301, 304, 308–310, 382–384, 387–390
- SPARC 382, 384–385, 396, 398, 400, 402
- SPARTAN 102
- special *ortho* effects 364, 366
- spectral properties 7
- spectrophotometric measurements 61
- spectrophotometric method 58, 81
- StarList 363, 375, 383, 393–395, 399–400

- starting 3D structure 186
 stationary phase 322, 332–339, 346,
 348–349, 416–418
 stereo centers 172, 176, 179
 stereo descriptors 159, 178
 stereoelectronic features 9
 stereoisomer 6
 stereostructure 209
 steric index 362
 stochastic algorithm 185
 1D strings 21
 structural analog approach 362
 structural factors 364–365, 370
 structure–activity relationship 3, 22, 257,
 263
 4D structures 21
 substructure-based approaches 358, 375
 supercooled liquid 289, 291–293, 298–299,
 307
 superfragments 368–370
 support vector machines 86, 98, 108
 surface activity measurements 33, 40
 surface plasmon resonance (SPR) 25, 40
 SYBYL 42, 136, 152, 177–178, 181, 240
 symbolic drawings 158
 system dwell volume 342, 344, 347
 systematic algorithm 185
- t**
- tautomeric equilibrium 7
 tautomerism 5–6, 8
 tautomerization effects 362
 tautomers 288, 400
 temperature 285–286, 288–291, 294, 298
 thermodynamic aqueous solubility 259,
 263
 thermodynamic property 285
 thin-layer chromatography 35, 332
 three-dimensional H-bond descriptors 134
 three-dimensional structure generation 157
 titration curve 60, 79
 TLOGP 393, 395–396, 398
 TOPKAT 99, 100, 102, 108
 topological descriptors 381, 392–393
 topological indices 6, 87, 88, 91–99, 101,
 104–107
 topological PSA 114, 119, 444
torsade de pointes 86, 98
 torsion angles 162, 166, 176–177, 179, 185
 total clearance 85, 99
 toxicity data 99
 toxicokinetic properties 41
 transcellular absorption potential 38
 transporter proteins 30, 34
- trivalent nitrogen 170, 179
 TSAR 371–372
 Tween-80 264
 two gradient runs 340–341, 346
 two-dimensional H-bond descriptors
 129–131
 two-dimensional thermodynamics
 descriptors 131
- u**
- unidimensional codes 6
 UNIFAC 298, 309
 unstirred water layer 38–39
- v**
- van der Waals interactions 9, 224, 288,
 293
 VEGA 391, 396–400, 402, 404
 VEKC 331, 332, 348–350
 vesicular electrokinetic chromatography
 331–332, 355
 Virtual Computational Chemistry Laboratory
 396, 402, 406
 virtual docking 117
 Virtual Screening of Chemical Libraries
 103–104
 virtual screening 103–105, 108, 112,
 117–119, 122, 124–126
 viscosity 10
 VLOGP 393, 396–399, 401, 406
 volatilization 288
 VolSurf 37, 42, 323, 329, 392, 405
 volume of distribution 26, 30
- w**
- Walden's rule 289–291
 water solubility 117–118, 147, 153,
 258–259, 261, 263–264, 270, 275, 277–278
 World Drug Index 41, 119, 127, 146, 441,
 443, 458
- x**
- XLOGP 371–375
 XPLORE-NIH 217, 223
 X-ray absorption spectroscopy 142
 X-ray crystallography 157–158
 X-ray Raman scattering 142
- y**
- Y-fragments 365
- z**
- zwitterions 267, 270, 278, 288, 364,
 398–400, 419

