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Impact of Dynamically Exposed Polarity on Permeability and Solubility of Chameleonic Drugs Beyond the Rule of 5

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3 **Keywords:** Beyond rule of 5, macrocycle, polar surface area, conformational flexibility,
4 permeability, solubility, molecular chameleon
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9 **ABSTRACT:** Conformational flexibility has been proposed to significantly affect drug
10 properties outside rule-of-5 (Ro5) chemical space. Here, we investigated the influence of
11 dynamically exposed polarity on cell permeability and aqueous solubility for a structurally
12 diverse set of drugs and clinical candidates far beyond the Ro5, all of which populated
13 multiple distinct conformations as revealed by X-ray crystallography. Efflux-inhibited
14 (passive) Caco-2 cell permeability correlated strongly with the compounds' minimum
15 solvent-accessible 3D polar surface areas (PSA), while aqueous solubility depended less on
16 the specific 3D conformation. Inspection of the crystal structures highlighted flexibly linked
17 aromatic side chains and dynamically forming intramolecular hydrogen bonds as particularly
18 effective in providing “chameleonic” properties that allow compounds to display both high
19 cell permeability and aqueous solubility. These structural features, in combination with
20 permeability predictions based on the correlation to solvent-accessible 3D PSA, should
21 inspire drug design in the challenging chemical space far beyond the Ro5.
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40 **INTRODUCTION**

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43 Improved selection of novel disease-associated drug targets has been highlighted as the most
44 important factor for success in drug discovery.¹ Unfortunately, half of all targets assumed to
45 be involved in human disease have been classified as “difficult to drug”^{2, 3} with traditional
46 small molecules, i.e. ligands that reside in the chemical space defined by Lipinski's rule of 5
47 (Ro5).^{4, 5} However, recent investigations have revealed that macrocycles,⁶⁻¹⁰ and other
48 compounds outside Ro5 chemical space,^{11, 12} provide improved opportunities for modulation
49 of difficult to drug targets. In particular, compounds residing in what has been termed
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3 beyond-rule-of-5 (bRo5) space^{12, 13} are better suited for modulation of targets that have large,
4 flat and groove-shaped binding sites, for instance protein-protein interactions. Understanding
5 how to design and optimize orally administered compounds in bRo5 space is therefore
6 essential for future success in drug discovery, especially for intracellular targets that are not
7 accessible to biologics.
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14 Recently, three datasets have been analyzed to provide insight into the outer limits of
15 chemical space in which pharmacokinetic risks may be managed and novel cell-permeable
16 and orally bioavailable drugs have a reasonable chance of being discovered.^{11, 14, 15} The
17 datasets consist of *i*) approved drugs and clinical candidates in bRo5 space,¹¹ *ii*) carefully
18 designed libraries of cyclic peptides¹⁴ and *iii*) compounds from preclinical drug discovery
19 projects.¹⁵ High-level analyses of these datasets have revealed that MW may be increased up
20 to approximately 1,000 Da, topological polar surface area (TPSA) to 250 Å², the number of
21 rotatable bonds to 20 and the number of hydrogen bond acceptors (HBA) to 15. However,
22 lipophilicity should be controlled in drug-like space (e.g. cLogP between 3 and 6), in
23 particular at high MW,^{14, 15} and few orally available drugs have more than six hydrogen bond
24 donors (HBD).^{11, 15} More detailed analyses of the same datasets,^{11, 14, 15} additional sets of
25 macrocyclic peptides,¹⁶⁻²⁴ and de novo designed macrocycles inspired by natural products^{25, 26}
26 have also begun to reveal the molecular properties, structural features and functional groups
27 that allow cell permeability in this non-traditional drug space. These studies have highlighted
28 reduction of polarity by N-alkylation of solvent-exposed amide bonds, shielding of polar
29 groups by bulky side chains and induction of intramolecular hydrogen bonds (IMHB) as
30 effective tactics that may be used to increase cell permeability. However, these tactics often
31 suffer from the drawback of decreasing solubility in aqueous media.²⁷
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53 Case studies of cyclosporin A,²⁸ a cyclic peptide model system,²¹ and a set of stereoisomeric
54 de novo designed macrocycles²⁵ have revealed that bRo5 compounds that dynamically
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3 expose or shield polarity can combine high permeability and aqueous solubility, in contrast to
4 analogues that are rigid or for which the molecular properties do not vary among
5 conformations.²⁶ Conformational flexibility may thus provide “chameleonic”, environment-
6 dependent properties to compounds, for instance by enabling them to transiently form IMHBs
7 and present a less polar surface when crossing the lipophilic cell membrane, while a more
8 polar surface with exposed hydrogen bonding functionalities is displayed in aqueous
9 environments.²⁸⁻³⁵ Recent analyses of crystal structures of drugs in bRo5 space have revealed
10 significant conformational differences that result in large variations in the 3D polar surface
11 area (PSA), suggesting that conformational flexibility may be of general importance for
12 compound properties in this space.^{12, 27, 29} It was proposed that adequate solubility in bRo5
13 space requires compounds to have a PSA of $\geq 0.2 \times MW$,²⁹ while early studies in the field
14 have revealed that PSA should be $\leq 140 \text{ \AA}^2$ for satisfactory passive cell permeability.^{36, 37}
15 These two guidelines indicate that compounds with MW >700 Da must be chameleonic, i.e.
16 be able to adapt their PSA to the environment, in order to satisfy both criteria.^{27, 29} This
17 appealing hypothesis has, however, not been experimentally tested beyond the few specific
18 examples listed above.^{21, 25, 28}

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20 Here, our aim was to investigate to what extent conformation-dependent, dynamically
21 exposed polarity provides chameleonic physicochemical properties to orally available drugs
22 in bRo5 space, and what substructural features stand out as important for such chameleonic
23 behavior. First, we determined how 2D PSA (TPSA; calculated directly from the connectivity
24 of a compound) and 3D PSA (derived from 3D conformers) varied with increasing MW for
25 drugs listed in the DrugBank database, so as to get an overview of how polarity is exposed or
26 hidden in different regions of chemical space. Then we selected 24 compounds representing
27 the major chemical classes of orally available drugs and clinical candidates,¹¹ covering both
28 macrocyclic and non-macrocyclic structures of natural product-derived and *de novo*-designed
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3 origins. The compounds showed varying degrees of conformational flexibility as revealed by
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5 multiple X-ray crystal structures. We identified a training set of eleven compounds and
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7 measured cell permeability, solubility, lipophilicity and pK_a under consistent experimental
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9 conditions so that data were unaffected by inter-laboratory variation. Quantitative models of
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11 how exposed polarity of experimentally confirmed conformations correlated to cell
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13 permeability and solubility were derived and validated using literature data. Finally,
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15 inspection of the crystal structures for all 24 drugs and clinical candidates provided an
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17 assessment of the nature and prevalence of dynamically formed intramolecular interactions
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19 that result in variations of 3D PSA.
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25 **RESULTS AND DISCUSSION**

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28 **Conformational Flexibility and Burying of Polar Surface Area in bRo5 Space.** The
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30 number of rotatable bonds (NRotB) provides an indication of a compound's conformational
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32 flexibility. Analysis of approved orally administered drugs reveals, as may have been
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34 expected, that NRotB increases with increasing MW (Figure 1A). Oral drugs in bRo5 space
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36 have a significantly higher mean NRotB than oral drugs with MW 100-500 Da ($p < 0.0001$).
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38 In addition, all oral drugs in bRo5 space have ≥ 5 NRotB, highlighting that oral drugs in this
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40 chemical space show some degree of conformational flexibility, which could provide them
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42 with chameleonic physicochemical properties.
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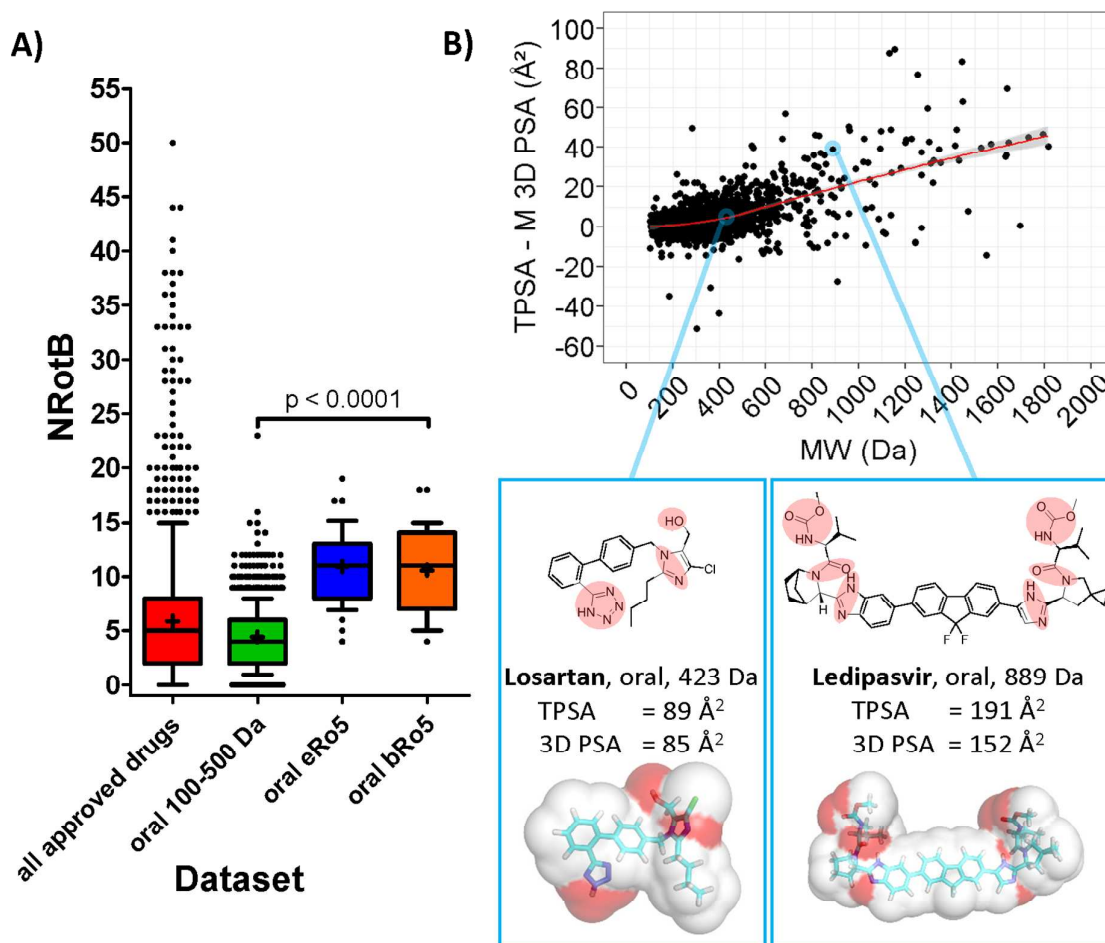


Figure 1. A) Distribution of number of rotatable bonds (NRotB) for all approved drugs in DrugBank (mean 5.9, sd 5.5, n=1814) followed by orally administered, approved drugs having MWs of 100-500 Da from DrugBank (mean 4.4 sd 3.0, n=788), oral drugs in extended Ro5 space¹¹ (500-700 Da; mean 10.9, sd 3.3, n=38) and oral drugs in bRo5 space¹¹ (>700 Da; mean 10.6 sd3.9, n=34, $p < 0.0001$ for t-test comparison to approved oral 100-500 Da drugs). Whiskers and boxes show the 10th, 25th, 50th, 75th and 90th percentiles, means are shown as a crosses and outliers as black dots. B) Difference between 2D TPSA and molecular 3D PSA (M 3D PSA) for calculated low energy conformations of all approved drugs in the DrugBank database with molecular weight (MW) 100-2000 Da, plotted versus MW. The data is fitted to a local linear regression function (LOESS, red line), showing how the difference in polar surface area changes with increasing MW. The regression standard error is shown as gray

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3 shading. Structures and molecular properties are included for losartan and ledipasvir, as
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5 examples of drugs in Ro5 and bRo5 space, respectively.
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10 Polar surface area is an established predictor of cell permeability^{36,37} and, as discussed above,
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12 a conformation-dependent variation in PSA may be essential for drug-like properties in bRo5
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14 space.^{12, 27, 29, 38} To evaluate if PSA increasingly depends on conformational preferences with
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16 increasing MW, we calculated TPSA for all approved drugs having MWs of 100-2000 Da in
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18 the DrugBank database³⁹ and compared it to a 3D molecular PSA calculated for the predicted
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20 low energy conformations using the same atom and surface definition as for TPSA (Figure
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22 1).⁴⁰ For typical small molecule drugs (MW <500 Da; exemplified by losartan in Figure 1),
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24 the PSA predicted from 2D fragment contributions (TPSA) expectedly corresponds well to
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26 molecular PSA calculated from 3D structures (standard deviation = 5.8 Å² for drugs 100-500
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28 Da). Hence, and also since it is rapidly calculated for large compound libraries, TPSA has
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30 found widespread use in Ro5 drug discovery. However, at MWs above 500 Da the difference
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32 between TPSA and molecular 3D PSA begins to increase linearly, indicating a conformation-
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34 dependent variability in PSA that is not captured by TPSA. Thus, in general, polarity is
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36 buried to an increasing degree as molecular size, structural complexity and often also
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38 flexibility increases farther into bRo5 space,⁴¹ as exemplified by ledipasvir (Figure 1). This
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40 observation provides initial support for the hypothesis that dynamic exposure of polarity may
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42 be of general importance for physicochemical properties in bRo5 space.
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49 **Compound and Structural Data Selection.** Because of the difficulty of accurately
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51 predicting the conformational landscape for compounds outside the Ro5 by computational
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53 methods,^{42, 43} we assessed compound flexibility from available X-ray crystal structures.
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55 Arguably, these may not exhaustively cover the respective conformational landscapes
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3 because of crystal packing effects and limitations in the availability of structural data.^{44, 45}
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5 However, the approach has the clear benefit of being directly based on experimentally
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7 verified conformations.^{12, 24, 33} Out of the 11 major chemical classes of orally available drugs
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9 and clinical candidates in bRo5 space¹¹ we therefore selected a *crystal structure set*
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11 consisting of 24 compounds, originating from seven of the 11 major classes plus one
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13 additional cyclic peptide and one natural product (Table 1). Among these 24 compounds we
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15 also selected a *training set* and a *test set* consisting of 11 and eight compounds, respectively.
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17 Cell permeability, solubility and LogD were determined for the drugs and clinical candidates
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19 in the training set, while cell permeability was retrieved from the literature for the compounds
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21 in the external test set. All compounds in the crystal structure set were used in the analysis of
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23 what substructural features drive the conformational differences observed for each of the
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25 compounds.
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29 Compounds were included in the crystal structure dataset if at least two high resolution
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31 crystal structures were available in the Protein Data Bank (PDB, <3.5 Å resolution) or the
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33 Cambridge Structural Database (CSD) that represented different conformations (heavy atom
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35 RMSD >0.75 Å between conformers). The crystal structures from the PDB were inspected to
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37 ensure that all conformations had well defined electron densities, high occupancies,
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39 temperature factors similar to target side chains adjacent to the ligand in the binding site and
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41 unstrained geometries. Overall, the 24 compounds in the crystal structure dataset included six
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43 orally administered erythronolides, six HIV-1 protease inhibitors, three HCV NS3/4A
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45 protease inhibitors, four rifamycins, two cyclic peptides and three additional natural products
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47 from different bRo5 classes (Table 1; Table S1). The 24 compounds had MWs that were
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49 evenly distributed between 500 and 900 Da, except for the two cyclic peptides which had
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51 significantly higher MWs. TPSA increased proportionally with MW from 120 to 360 Å²,^{11, 29}
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53 while cLogP remained centered at 3-5 (Figures 2, and Figure S1). These relationships for
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TPSA and cLogP are also characteristic for the comprehensive list of 85 orally administered drugs and clinical candidates identified in bRo5 space;¹¹ thus the selected compounds provide a representative and structurally diverse coverage of this property space. The number of crystal structures retrieved for each of the compounds ranged from two to 51, all of which were retained for subsequent analyses. After clustering similar conformations (RMSD <0.75 Å) the numbers of distinct conformations ranged from two to five for the different compounds. The effective flexibility assessed, i.e. the sampled conformational space, varied from low (heavy atom RMSD = 0.82 Å between the most different conformers) for some compounds to significantly larger (6.13 Å) for others. The crystal structure set, as well as the training and test sets contained within it, was therefore selected to display a range of conformational flexibilities, as revealed by the experimentally determined X-ray structures.

Table 1. Structural and conformational features of the compounds included in the crystal structure dataset,^a the training set^b and the external test set^c

Class	Name ^{a,b,c}	macrocycle	n° structures	n° conformers ^d	Max RMSD ^e (Å)	MW (Da)	TPSA ^f (Å ²)
Erythronolides	Azithromycin	Y	7	3	3.14	749	180
	Clarithromycin	Y	14	3	3.13	748	183
	Dirithromycin	Y	4	2	0.82	835	194
	Erythromycin	Y	10	4	1.94	734	194
	Roxithromycin	Y	3	2	3.96	837	217
	Telithromycin	Y	5	2	6.13	812	172
HIV-1 Inhibitor	Atazanavir		12	4	3.30	705	171
	Darunavir		51	5	3.78	548	140
	<i>Indinavir</i>		16	4	2.00	614	119
	Lopinavir		10	4	1.72	629	120

		Ritonavir	17	5	3.96	721	146	
		Saquinavir	29	3	3.90	671	168	
	NS3/4A Inhibitor	Asunaprevir	4	2	3.02	748	194	
		<i>Faldaprevir</i>	2	2	4.54	870	201	
		Telaprevir	5	3	1.45	680	180	
		Rifabutin	Y	2	2	1.22	847	210
	Rifamycin	Rifampicin	Y	8	3	1.56	823	220
		Rifapentin	Y	2	2	0.98	877	220
		<i>Rifaximin</i>	Y	7	2	1.64	786	201
		<i>Actinomycin D</i>	Y	12	2	3.92	1255	356
	Cyclic peptides	<i>Cyclosporin A</i>	Y	18	9	5.97	1203	279
		<i>Tacrolimus</i>	Y	6	5	3.72	804	178
	Other natural products	<i>Paclitaxel</i>	Y	3	2	3.51	854	221
		<i>Vinblastine</i>		4	2	0.92	811	157

^aAll compounds were included in the crystal structure dataset. ^bThe compounds in bold were included in the training set and their permeability across Caco-2 cell monolayers, solubility, logD and pK_a were determined as described in the Experimental Section. ^cThe compounds in italics were used as an external test set with efflux-inhibited cell permeabilities across Caco-2 cell monolayers compiled from the literature.⁴⁶⁻⁵² ^dThe number of distinct conformers was determined by clustering the available crystal structures, using a threshold of 0.75 Å for the root mean squared deviation (RMSD) of the heavy atom alignment. ^eMaximum RMSD of the heavy atom alignment of crystal structures representing the two most diverse conformations. ^fTPSA was calculated using the method reported by Ertl, et al.⁴⁰ as implemented in Instant J Chem v6.2.0.953. Crystal structure database identifiers for all evaluated structures are available in Table S1.

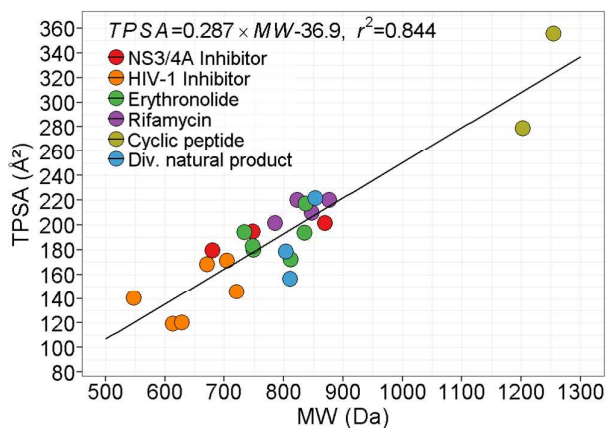


Figure 2. Topological polar surface area (TPSA, Å²) versus molecular weight (MW, Da) for the selected erythronolides, rifamycins, HIV-1, HCV NS3/4A protease inhibitors, cyclic peptides and other natural products. TPSA was calculated using the method reported by Ertl, et al.⁴⁰ as implemented in Instant J Chem v6.2.0.953.

The 11 compounds in the training set were obtained from the erythronolide and rifamycin classes of natural product derived antibacterials, and the *de novo* designed antiviral HIV-1 protease and HCV NS3/4A protease inhibitors (in boldface in Table 1). This selection was made as multiple crystal structures are available for several members of these four structural classes. In addition, most members of these classes were commercially available, allowing us to generate in-house solubility, lipophilicity and cell permeability data for them under consistent conditions. The selection led to that both macrocyclic and non-macrocyclic compounds were included in the training set. The 8 compounds in the external test set (in italics in Table 1) included compounds from three of the four classes in the training set, compounds from an additional three of the major bRo5 classes (the cyclosporins, ascomycins and taxanes) as well as one additional cyclic peptide (actinomycin D) and one additional natural product (vinblastine).⁴⁶⁻⁵² Compounds were included in the test set if their efflux-inhibited cell permeability had been reported in the literature, and if multiple crystal

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3 structures were available for each of them. All but three of the compounds in the training and
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5 tests sets had MWs in the range where achieving both good aqueous solubility and cell
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7 permeability has been proposed to be contingent on conformational flexibility, i.e. in the
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9 difficult bRo5 space at 700 Da or above. The 16 compounds with MW >700 Da constitute
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11 19% of all orally administered drugs and clinical candidates found in bRo5 space in our
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13 recent analysis.¹¹
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19 **Cell Permeability.** Permeability across intestinal epithelial cell monolayers was measured in
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21 the Caco-2 cell model for the 11 training set compounds. Monolayer permeabilities (P_{app})
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23 were determined at pH 7.4 in the apical-to-basolateral (AB) and basolateral-to-apical (BA)
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25 directions, and efflux ratios ($P_{app} BA / P_{app} AB$) were used to assess the impact of carrier-
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27 mediated transport processes (Table 2). In addition, passive-diffusive cell monolayer
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29 permeabilities ($P_{app} AB +inh$ and $P_{app} BA +inh$) were estimated by including an inhibitor
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31 cocktail of quinidine, sulfasalazine and benzobromarone that targets the three major efflux
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33 transporters in the intestinal epithelium: P-glycoprotein, (MDR1/P-gp; ABCB1), breast
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35 cancer resistance protein (BCRP; ABCG2) and multidrug-resistance associated protein 2
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37 (MRP2, ABCC2). Cell permeabilities determined in the absence of inhibitors ($P_{app} AB$)
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39 ranged from low ($<1 \times 10^{-6}$ cm/s) for saquinavir, telaprevir and three of the erythronolides to
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41 medium (10.9×10^{-6} cm/s) for atazanavir. All compounds were significantly affected by
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43 apical efflux transporters, with efflux ratios (ER) ranging from 11 for azithromycin to >500
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45 for saquinavir; this considerable transporter-mediated efflux was consistent with previous
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47 analyses of cellular permeability in bRo5 space.^{11, 27} Accordingly, apical-to-basolateral cell
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49 permeabilities determined in the presence of the inhibitor cocktail were significantly higher
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51 than the corresponding uninhibited permeabilities for all compounds. Residual efflux was
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53 observed, to different extents, also in the presence of the inhibitor cocktail (Table 2). This
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was particularly pronounced for saquinavir (residual ER 27.8); thus, the permeability estimate is not representative of the passive transcellular permeability and saquinavir was, consequently, excluded from the modeling of passive cell permeability.

Table 2. Experimental Caco-2 permeability data for the bRo5 drugs and clinical candidates included in the training set.

Class	Name	$P_{app} AB^a$ ($\times 10^{-6}$ cm/s)	SEM	ER ^b	$P_{app} AB$ +inh ^{a,c}		
					($\times 10^{-6}$ cm/s)	SEM	ER +inh ^{b,c}
Erythronolides	Azithromycin	1.8	0.4	11	2.8	0.1	7.9
Erythronolides	Clarithromycin	2.7	0.3	28	28.2	1.3	1.2
Erythronolides	Erythromycin	0.58	0.03	33	1.5	0.1	1.5
Erythronolides	Roxithromycin	0.90	0.04	57	11.9	1.6	1.0
Erythronolides	Telithromycin	0.20	0.02	203	4.3	0.1	3.9
HIV-1 inh.	Atazanavir	10.9	0.2	40	71.8	2.1	2.3
HIV-1 inh.	Ritonavir	8.7	0.3	142	232	40	2.1
HIV-1 inh.	<i>Saquinavir</i> ^d	0.52	0.1	585	5.0	0.2	28
NS3/4A inh.	Asunaprevir	3.4	0.4	272	48.0	5.7	4.1
NS3/4A inh.	Telaprevir	0.41	0.1	199	7.1	0.4	4.0
Rifamycin	Rifampicin	1.6	0.02	19	1.0	0.1	14.4

^a $P_{app} AB$: permeability in the apical-to-basolateral (AB) direction across Caco-2 cell monolayers. ^bER: efflux ratio ($P_{app} BA / P_{app} AB$). ^cDetermined in the presence of a cocktail of inhibitors (quinidine, sulfasalazine and benzobromarone, noted by +inh) of efflux transporters. ^dExcluded from modeling of permeability. All measurements were performed in triplicate, except for saquinavir and ritonavir (n=6, repeated with consistent results because of excessive mass balance in the uninhibited experiment). Measurements in both transport directions were performed both in the absence and presence of a cocktail of efflux transporter inhibitors.

Solubility, Lipophilicity and pK_a. Solubility was determined in potassium phosphate buffer at pH 7.4 using amorphous material, and LogD was measured in a miniaturized shake-flask assay using DMSO stock solutions (Table 3). pK_a was determined potentiometrically, or calculated using MoKA v.2.6.5 for atazanavir and ritonavir, for which low solubilities prevented experimental pK_a determination. All compounds except for telaprevir contained acidic and/or basic functionalities; seven were predominantly charged at a physiological pH of 7.4 and four were neutral. Seven of the 11 compounds had high solubilities (>100 μM) and all of them were charged and had lipophilicities in the preferred drug-like range (LogD_{7.4} = appr. 1–3). The remaining four compounds had lower solubilities (<25 μM), most likely as a result of their higher lipophilicities (LogD_{7.4} >3.8).

Table 3. Experimentally determined physicochemical properties for the bRo5 drugs and clinical candidates included in the training set.

Class	Name	Solubility (SEM) ^a (μM)	LogD _{7.4} (SEM) ^b	pK _a ^c	Ionization state at pH 7.4
Erythronolide	Azithromycin	1920 (135)	1.1 (0.1)	8.69, 9.45	2+
Erythronolide	Clarithromycin	746 (47)	1.6 (0.1)	9.10	1+
Erythronolide	Erythromycin	1405 (81)	0.9 (0.4)	8.87	1+
Erythronolide	Roxithromycin	1510 (24)	1.8 (0.1)	9.13	1+
Erythronolide	Telithromycin	1960 (141)	2.1 (0.1)	4.91, 8.69	1+
HIV-1 inh.	Atazanavir	2.4 (0.5)	4.2 (0)	5.01*	neutral
HIV-1 inh.	Ritonavir	0.3 (0.1)	4.6 (0.1)	2.43*, 3.45*	neutral
HIV-1 inh.	Saquinavir	24.5 (3.5)	4.7 (0.2)	7.16	neutral
NS3/4A inh.	Asunaprevir	160 (25)	3.1 (0.1)	5.7	1-
NS3/4A inh.	Telaprevir	4.3 (0.1)	3.8 (0.2)	-	neutral
Rifamycin	Rifampicin	183 (8.0)	1.3 (0.1)	2.97, 7.50	zwitterion

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3 ^aStandard error based on four repeats. ^bRelative standard error based on 3–6 repeats.

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5 ^cMeasured by potentiometry; based on three repeats with SEM<0.03. Values marked with an
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7 asterisk (*) were calculated with MoKa v.2.6.5. ADMET Predictor v7.2 provided similar
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9 values, i.e. 4.63 for atazanavir and 2.47 and 4.46 ritonavir.
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14 **Models for Predicting Cell Permeability and Solubility.** We assessed if 2D or 3D PSA
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16 measures could explain the balance between cell permeability and solubility for the bRo5
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18 drugs in the training set, and if quantitative models could be derived for these properties.
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20 When calculating 3D PSA, the impact of including polarity originating from partially charged
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22 atoms was compared to the traditional approach focused on oxygen, nitrogen and their
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24 attached hydrogen atoms.³⁸ Throughout this analysis TPSA was calculated as described by
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26 Ertl,⁴⁰ using the implementation in InstantJChem. Different programs (MOE, CDK, Spartan
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28 and PyMol) and different methods for atom type selection and partial charge calculation
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30 (using PM3, MMFF and Gasteiger methods) were initially explored for 3D PSA calculation.
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32 PyMol was selected because of its open-source accessibility and flexibility in defining
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34 surface area and atoms for the PSA calculation (commands available in SI). Thus, in the
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36 presented analyses PSA was calculated by three distinct approaches: i) 2D TPSA, assigning
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38 as polar atoms any N, O, or their attached H, ii) molecular 3D PSA (i.e. the surface area
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40 accessible to a probe of zero radius) and iii) solvent-accessible 3D PSA (i.e. the surface area
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42 accessible to a water-sized probe of 1.4 Å radius). The two 3D PSA methods were applied to
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44 all conformations, i.e. to all crystal structures, of each compound. Definitions that expanded
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46 the list of included atoms with atoms having PM3 calculated partial charges above specified
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48 thresholds were also investigated for the two 3D approaches—thereby also incorporating
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50 moderately polar atoms in the PSA (cf. next section). All regressions discussed can be found
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3 in section 2 of the Supporting Information along with r^2 , leave-one-out q^2 , p -values and
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5 RMSD of training and test sets.
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9 Efflux-inhibited (passive) permeability (P_{app} AB +inh) showed only a modest correlation with
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11 TPSA in our dataset ($r^2=0.36$, $p=0.068$; Figure 3A) and a moderate correlation with $\text{LogD}_{7.4}$
12
13 ($r^2 = 0.63$, $p = 0.0061$, Figure S2). Use of *molecular* 3D PSAs improved the correlation with
14
15 P_{app} AB +inh slightly as compared to TPSA, whereas *solvent-accessible* 3D PSAs gave the
16
17 best correlations (Figure S3A). Notably, the correlation obtained using solvent-accessible 3D
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19 PSA with the traditional definition of polar atoms (i.e. N, O and attached H) ($r^2=0.26$,
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21 $p=0.14$) was significantly improved by including moderately polar atoms when calculating
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23 PSA. An optimal correlation was obtained when atoms with absolute partial charges >0.6
24
25 were included as polar, giving an r^2 of 0.90 ($p=3.1 \times 10^{-5}$) for solvent-accessible 3D PSA
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27 (Figure 3B). The statistical validity of the correlation was demonstrated by a permutation
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29 procedure, in which the order of the dataset was randomly shuffled 20,000 times (i.e., each
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31 permeability measurement was randomly associated with one PSA value from the dataset). In
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33 no case did the resulting permuted r^2 reach the observed value of 0.90; this corresponds to an
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35 empirical $p < 5 \times 10^{-5}$.
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40 Importantly, the minimum solvent-accessible 3D PSA for each compound was consistently
41
42 better correlated with efflux-inhibited permeability ($\log P_{app}$ AB +inh) than were the
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44 corresponding maximum or average PSAs, regardless of the partial charge threshold (Figure
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46 S3A). This observation is consistent with conformation-dependent shielding of polar
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48 functional groups as the compounds pass through the lipophilic cell membrane interior. It
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50 also indicates that solvent-accessible 3D PSA and correct polar atom selection are important
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52 factors to achieve optimal predictive power for passive cell permeability in bRo5 space.
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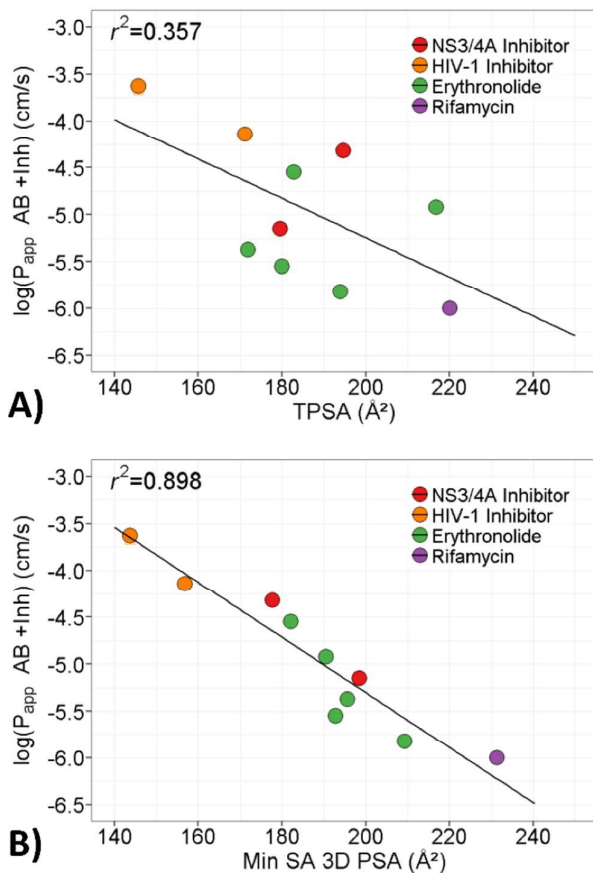


Figure 3. Permeability of the training set compounds [$\log(P_{app} AB + inh)$ cm/s] and its correlation to A) topological PSA (TPSA, \AA^2) and B) minimum solvent-accessible 3D PSA (Min SA 3D PSA, \AA^2) calculated from N, O and attached H atoms with inclusion of atoms with absolute partial charges >0.6 (as calculated by the PM3 method) as polar. The colored bar indicates the SEM for ritonavir; all other compounds had SEM within the size of the symbols. Models were derived from the minimum and maximum solvent-accessible 3D PSA across all conformations for the training set drugs. Refer to Figure S3 for models from alternative PSA definitions, including molecular and solvent accessible 3D PSA that includes atoms based on other partial charge thresholds. **Correlations:** $\log(P_{app} AB + Inh) = -0.02098 \times TPSA - 1.0492$, $r^2 = 0.36$, $p = 0.068$, $LOO q^2 = 0.071$ and $\log(P_{app} AB + Inh) = -0.02943 \times Min SA 3D PSA + 0.5825$ (atoms with absolute partial charges >0.6 were included as polar), $r^2 = 0.90$, $p = 3.1 \times 10^{-5}$, $LOO q^2 = 0.85$.

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6 The use of minimally exposed polarity in explaining permeability bRo5 was further validated
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8 using the eight drugs and clinical candidates in the external test set (Table 1, Supporting
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10 Table S3). In line with the observations from the training compounds, the minimum solvent-
11
12 accessible 3D PSA gave the best predictions for the efflux-inhibited cell permeabilities of the
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14 compounds in the test set (Figure 4, RMSE = 0.71, corresponding to 5.1-fold average error).
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16 The largest deviation was seen for paclitaxel, which is attributable to that its minimum
17
18 solvent-accessible PSA was outside the range seen in the training data. Excluding paclitaxel
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20 decreased the average error to 0.59 (3.9-fold), comparable to the predictivity of more
21
22 complex structure-permeability models in bRo5 space.²⁵ Notably, the two bRo5 peptides
23
24 cyclosporine A and actinomycin D differed from the training compounds by being
25
26 substantially larger (MW = 1203 and 1255 Da, in contrast to 680–840 Da in the training set)
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28 and containing more polar atoms (TPSA = 279 and 356 Å², compared to 146–220 Å²). Still,
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30 permeability was well predicted for both cyclic peptides by their minimally exposed solvent-
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32 accessibly 3D PSA (1.2 and 1.6-fold deviations from the average efflux-inhibited
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34 permeability reported).
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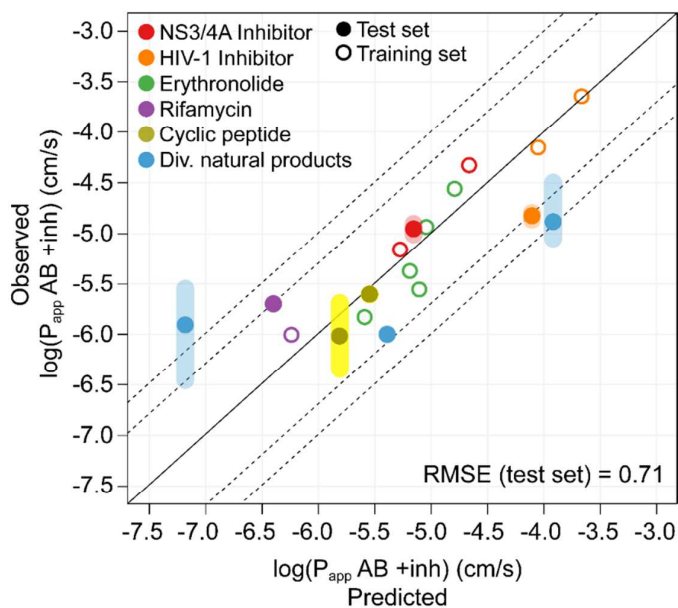
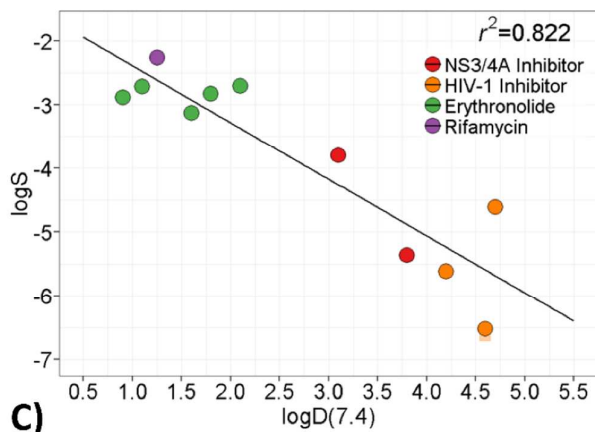
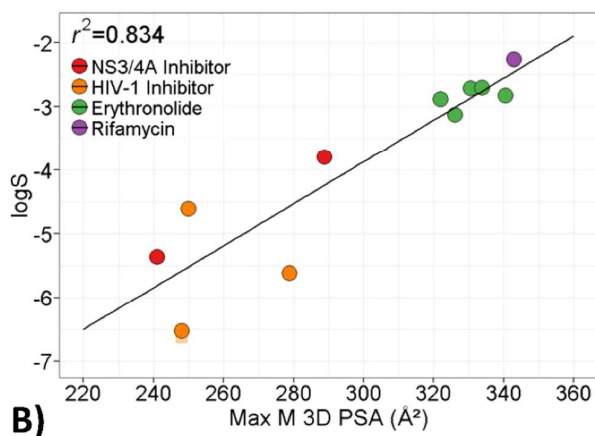
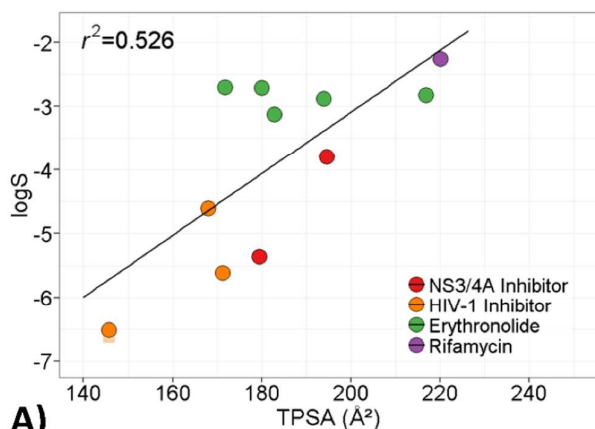


Figure 4. Permeability predictions for the external test set. Predictions are based on the correlation between efflux-inhibited Caco-2 cell permeability and solvent-accessible 3D PSA for the compounds in the training set (hollow circles, c.f. correlation in legend of Figure 3B). This correlation was used to predict the permeability for the external test set (solid circles). Colored bars for the test set indicate the range of observed permeabilities for these compounds. The solid line indicates the line of unity, and inner and outer dashed lines indicate 5- and 10-fold errors, respectively. The root mean squared error of prediction (RMSE) for the test set was 0.71 (5.1-fold). This was reduced to 0.59 (3.9-fold) if paclitaxel was excluded, the PSA of which was outside the range in the training data.

In comparison to cell permeability, aqueous solubility was somewhat better explained by TPSA ($r^2 = 0.53$, $p = 0.01$; Figure 5A). Again, the correlation improved substantially when the three-dimensional structure was taken into account. As for permeability, the optimal PSA definition included moderately polar atoms (absolute partial charges >0.5 , Figure 5B), further supporting a role of these in interactions with the surrounding medium. For solubility,

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3 however, much smaller differences were obtained when the minimum or maximum 3D PSA
4 for the compounds in the training set was used ($r^2 = 0.83$, $p < 1 \times 10^{-3}$, Figure S3B). Also,
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6 molecular surface areas gave better correlations than solvent-accessible areas. Since the
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8 former are less sensitive to conformational variation, the improved correlation suggests that
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10 the overall polarity in the molecule, rather than a single, specific conformation is the most
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12 predictive for solubility. These observations may therefore reflect a more extensive
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14 conformational sampling in aqueous media than in a lipid membrane environment. This
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16 hypothesis is tentatively supported by studies of two of the very few well characterized
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18 molecular chameleons, i.e. cyclosporin A⁵³ and a de novo designed macrocycle,²⁵ both of
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20 which have been found to display such environment dependent conformational flexibility.
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22 Similar to the permeability model above, the probability of obtaining a solubility model with
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24 $r^2 \geq 0.83$ using randomly permuted data was low ($p = 0.0003$). A strong correlation was
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26 observed between aqueous solubility and experimentally determined $\log D_{7.4}$ ($r^2 = 0.82$,
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28 $p = 1.2 \times 10^{-4}$; Figure 5C). Similarly, adding a calculated lipophilicity descriptor (cLogP) to the
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30 model based on the optimal calculated 3D PSA improved the correlation ($r^2 = 0.90$,
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32 $p = 8.4 \times 10^{-5}$, Figure S4B).
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46 **Figure 5.** Solubility (logS) and its correlation to A) topological PSA (TPSA, Å²) and B)
47 maximum molecular 3D PSA (Max M 3D PSA, Å²) calculated from N, O and attached H
48 atoms with inclusion of atoms with absolute partial charges >0.5 (as calculated by the PM3
49 method) as polar and C) experimental LogD_{7.4}. The colored bar indicates the SEM for
50 ritonavir; all other compounds had SEM within the size of the symbols. Models were derived
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3 from the minimum and maximum molecular 3D PSA across all conformations for the 11
4 selected drugs. Refer to Figure S3 for models from alternative PSA definitions, including
5 molecular and solvent-accessible 3D PSA that includes atoms based on other partial charge
6 thresholds **Correlations:** $\log S = 0.04836 \times TPSA - 12.7623$, $r^2 = 0.53$, p-value = 0.012, LOO
7 $q^2 = 0.35$ and $\log S = 0.03290 \times Max\ M\ 3D\ PSA - NOH+0.5 - 13.738$, $r^2 = 0.83$, p-value =
8 $8.66e-5$, LOO $q^2 = 0.74$ and $\log S = -0.8912 \times \log D(7.4) - 1.4975$, $r^2 = 0.82$, p-value = $1.17e-$
9 4 , LOO $q^2 = 0.71$.

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21 **Compound- and Conformation-Dependent Variation in Molecular Properties.** Multiple
22 sequential processes affect the permeability of drugs across cell membranes. Desolvation
23 occurs as the drug leaves the extracellular aqueous environment and is followed by
24 interactions with phospholipid head groups before it penetrates into the hydrophobic
25 membrane interior. Then a similar but reversed sequence of events take place as the drug
26 enters the cytosol. Each of these steps are likely differently affected by the drug's molecular
27 properties. We were therefore intrigued by the fact that such a strong correlation to cell
28 permeability was obtained using the minimally solvent-exposed 3D PSA as a single
29 descriptor.

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41 For example, the molecular radius of gyration and other descriptors reflecting the cross-
42 sectional area of the permeant have been shown to be important factors in membrane
43 permeability,^{41, 54, 55} presumably reflecting the cost of forming cavities as the drug penetrates
44 the phospholipid membrane. However, in our dataset, the radius of gyration was constrained
45 to a relatively narrow interval (4.8–5.9 and 4.8–6.1 Å in the minimum-radius conformations
46 of the training and test set compounds, respectively), suggesting a similar energetic cost for
47 cavity formation (Figure S5A). Most compounds also displayed a relatively small variation
48 between conformations, with the maximum radii being, on average, 1.06 times larger than the
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3 minimum ones. The total solvent-accessible surface areas were also relatively similar
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5 between compounds (898–1024 and 937–1317 Å² in the minimum-surface area
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7 conformations for the training and test set, respectively) and between conformations of these
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9 (average fold-difference of 1.05 between maximum and minimum conformations, Figure
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11 S5B).
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14 In contrast, the minimum solvent-accessible 3D PSA varied more between compounds (143–
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16 231 and 153–263 Å² for the training and test set conformations, respectively, Table S2 and
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18 Figure S5B). Also, PSA was more conformation-dependent, on average displaying 1.2-fold
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20 differences in exposed PSA. Differences in PSA ranged from quite small for roxithromycin
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22 and indinavir (Δ PSA: 7 and 13 Å², respectively) to very large for rifampicin, telithromycin,
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24 actinomycin D, faldaprevir and cyclosporin A (Δ PSA: 59, 60, 62, 72, and 79 Å²). The
25
26 average difference of 37 Å² in our dataset roughly corresponds to a shielding of 3–4 polar
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28 atoms in the minimum as compared to the maximum solvent-accessible conformation.
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32 The impact of dynamically exposed 3D PSA that we observe in the present dataset potentially
33
34 arises from the dual role of polar interactions in desolvation and resolvation and in the energy
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36 barrier for the drugs to cross the hydrophobic membrane interior. Compounds that have
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38 multiple energetically favorable conformations may thus attain lower desolvation costs and
39
40 lower penetration barriers by adopting the most favorable (i.e. the least polar) conformation
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42 when permeating cell membranes. Although this cannot be decisively concluded, the fact that
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44 our dataset samples from 7 of 11 major structural classes in which orally bioavailable bRo5
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46 drugs have been categorized suggests that such chameleonic behavior may be a general
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48 feature of drugs in the oral bRo5 subspace.
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3 **Influence of Polar Atom Selection on PSA.** Interestingly, the optimal polar atom selection
4 threshold for modeling permeability and solubility included atoms with absolute partial
5 charges >0.6 and >0.5 , respectively. This resulted in some atoms that would not normally be
6 selected as polar being included in the polar surface area, for instance atoms adjacent to polar
7 groups but also some terminal methyl carbon atoms (but not their attached hydrogens). A
8 logical explanation for these findings is that at very low thresholds, polar atoms in addition to
9 the typical N, O and attached H are taken into account, but also atoms which are not
10 genuinely polar, thereby reducing the correlations. At high thresholds (absolute partial
11 charge >0.8), some genuinely polar atoms are excluded, again decreasing the correlation to
12 permeability and solubility. This also manifests as a loss of the conformation-dependence in
13 the PSA-permeability relationship, i.e. minimum and maximum PSA show equally poor
14 correlation with permeability (Figure S3). The partial charge threshold affected the PSA for
15 most compounds in the dataset, with differences ranging from 15 to 73 Å² (mean \pm SD: 46
16 ± 20 Å²) between the least inclusive PSA definition (N, O and attached H) and the optimal
17 partial-charge threshold of >0.6 for minimum or maximum solvent-accessible 3D PSAs. Our
18 results thus suggest that not only the conformation and orientation (exposure) of polar atoms,
19 but also the different distribution of charge on atoms between conformations is important for
20 accurate prediction of permeability and solubility.
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45 **Structural Consequences of Conformational Flexibility.** The crystal structures presenting
46 minimum and maximum solvent-accessible 3D PSA for each compound were systematically
47 analyzed to determine what substructural features drive these conformational differences.
48 Conformational changes occurred in the core skeleton for half of the 24 compounds in our
49 crystal structure dataset, and most compounds had changes in the orientation of their side
50 chains (Figure 6A). Most conformational variation originated from freely rotatable bonds
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3 (bonds directly connected to an amide are not included), both for compounds with
4 conformational changes in the core and for those with changes in the side chains.
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6 Additionally, eight compounds displayed flexibility involving bonds directly connected to an
7 amide, while cycloalkane moieties changed conformation in three compounds. For example,
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9 telaprevir has an *N*-cyclopropyl amide that undergoes rotation of both its linked bonds,
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11 resulting in the amide oxygen's solvent-accessible 3D PSA as well as that of an adjacent
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13 carbonyl group becoming buried. Two of the three compounds that buried 3D PSA through
14
15 conformational changes in cycloalkane moieties were from the rifamycin class: rifampicin
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17 forms an IMHB when its piperazine group adopts a boat-like conformation, and in rifabutin
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19 the piperidine NH is occluded by a neighboring bulky lipophilic side chain when the
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21 piperidine adopts an alternate chair-like conformation. Thus, even though cycloalkyl groups
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23 and amides are semi-rigid functional groups, they can still adopt multiple stable, low-energy
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25 conformations with different solvent-accessible 3D PSA. It may be speculated that this semi-
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27 rigidity might make these and other semi rigid groups particularly useful in design of multi-
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29 conformer "chameleonic" compounds.
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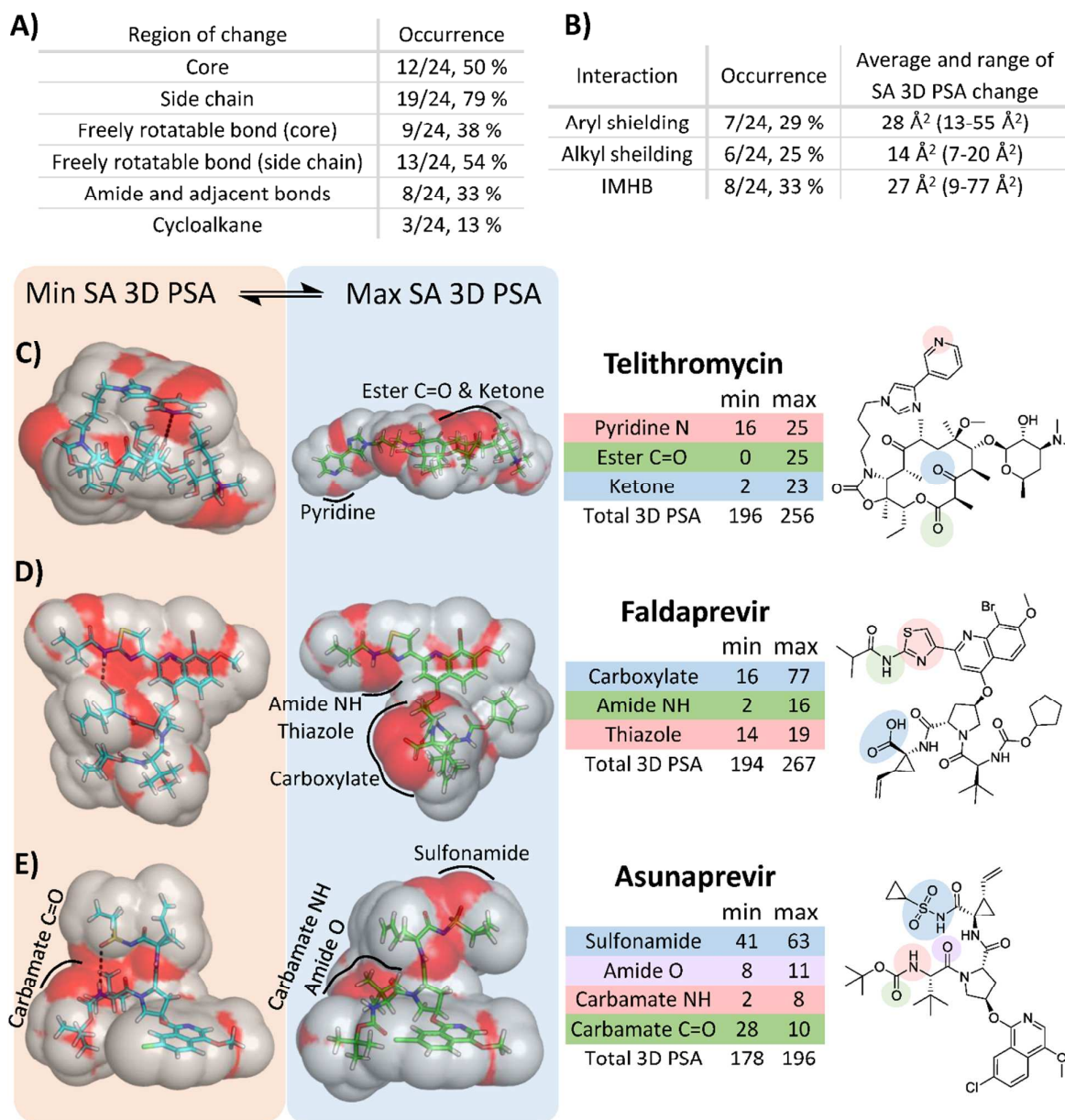


Figure 6. Conformational changes in crystal structures that display minimum and maximum solvent-accessible 3D polar surface area (Min and Max SA 3D PSA). A) Summary of substructural regions from which flexibility originates in the 24 investigated drugs and clinical candidates. B) Interactions formed in the minimum PSA structures as compared to those displayed in the maximum PSA structure. Crystal structures of C) telithromycin (1YIJ and 1P9X), D) faldaprevir (MEBYEZ and 3P8N) and E) asunaprevir (MIYWOI and 4WH6) with conformations shown that display minimum (orange box) and maximum (blue box)

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3 solvent-accessible 3D PSA. The structures are shown as sticks (carbons blue/green, nitrogens
4 dark blue, oxygens red, sulfurs yellow and hydrogens white) with solvent-accessible surface
5 area shown as red (polar) and white (non-polar). Solvent-accessible 3D PSA (SA 3D PSA,
6 \AA^2) was calculated from N, O and attached H atoms with inclusion of atoms with absolute
7 partial charges >0.6 (as calculated by the PM3 method) as polar. Polar and IMHB
8 interactions are shown as dotted black lines. Polar functional groups that are differently
9 exposed depending on conformation (leading to differences in 3D PSA) are outlined and
10 labeled in the 3D molecular structure, detailed in the accompanying tables and shaded in the
11 2D structures.
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26 Bulky side chains can be used to hide adjacent PSA in a non-polar environment, but this may
27 lead to reduced solubility,^{19, 22, 27} unless conformational flexibility allows re-exposure of the
28 hidden PSA in aqueous environments.^{21, 25} In half of the compounds in our crystal structure
29 dataset, one or more bulky side chains occluded polar functionalities in the minimum 3D
30 PSA conformation, but not in the corresponding maximum PSA conformation (Figure 6B).
31 Six of the affected compounds were from the de novo designed HIV and HCV protease
32 inhibitor series, while the remaining six were in the natural product derived and cyclic
33 peptide classes. The largest change in PSA was observed in telithromycin, in which the
34 aromatic side chain folds over the polar macrocyclic core and shields a significant amount of
35 solvent-accessible 3D PSA (55\AA^2 , Figure 6C).
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48 Flexibly attached aromatic rings such as the one in telithromycin accounted for half of all
49 such events of dynamic shielding of PSA, and lead to occlusion of an average of 28\AA^2 of
50 solvent-accessible 3D PSA. Alkyl shielding was equally common but shielded less PSA
51 (average of 14\AA^2). Alkyl shielding is best exemplified by faldaprevir's isopropyl and
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3 vinylcyclopropyl side chains (Figure 6D). Though relatively rigid, upon formation of a
4 charge-reinforced IMHB, these alkyl groups contribute to further reductions in 3D PSA.
5 Interestingly, most instances of aryl shielding (5/7) came from the *de novo* designed HIV-1
6 and HCV NS3/4A protease inhibitors, and the remaining two instances came from the
7 designed aryl side chains of telithromycin and paclitaxel. Alkyl shielding came
8 predominantly from natural product and cyclic peptide classes. We hypothesize that the
9 higher shielding of PSA by aromatic groups is partly due to their size and rigidity, but also to
10 the ability of aromatic groups to participate in weak dipole or weak IMHB interactions with
11 polar groups that can stabilize their conformational shielding.⁵⁶ Preliminary support for this
12 can be seen in telithromycin, where the flexible aromatic side chain folds directly over the
13 ketone and a weak dipole- π -interaction can be formed (Figure 6C). Flexibly linked aromatic
14 side chains may therefore be particularly useful in design of “chameleonic” compounds that
15 display a dynamic solvent-accessible 3D PSA when adapting to different environments.
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31 Formation of IMHBs is another theme that has been highlighted for reduction of PSA and a
32 subsequent increase of cell permeability.²⁸⁻³⁵ Motifs for formation of five to eight-membered
33 IMHB pseudoring systems have been derived by exhaustive analysis of crystal structure
34 databases and may serve as inspiration in drug design.³³ However, as noted, IMHBs that are
35 stable in both polar and non-polar environments (static IMHBs) can reduce solubility in
36 aqueous environments.^{19, 26, 27, 33} Indeed, just under half (10/24) of the drugs and clinical
37 candidates investigated herein made 1-4 IMHBs that were unchanged between the
38 conformations exposing the minimum and maximum solvent-accessible 3D PSA. All
39 compounds with such stable IMHBs were from the natural product and cyclic peptide classes.
40 For drug design purposes, dynamic—as opposed to static—IMHBs are of greater interest as
41 they potentially allow for both high solubility and permeability.^{27, 29, 33, 57} Eight of the 24
42 analyzed compounds formed additional IMHBs in their minimum solvent-accessible 3D PSA
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3 conformation that were not formed in the maximum PSA conformation. Six of these
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5 compounds were from the natural product classes, while two were de novo designed drugs.
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7 This indicates that natural products may have evolved to take advantage of both static and
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9 dynamic IMHBs for reduction of compound polarity, but also that medicinal chemists have
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11 not yet capitalized on dynamic IMHBs to their full potential when designing drug candidates
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13 in bRo5 space.
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16 The average solvent-accessible 3D PSA hidden by dynamic IMHBs was 27 \AA^2 , but this
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18 number varied considerably from 9 to 77 \AA^2 between different compounds (Figure 6B). The
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20 surprisingly large PSA reduction of 77 \AA^2 originates from faldaprevir, which makes a charge-
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22 reinforced IMHB between its carboxylate and isobutyramide NH (Figure 6D). Faldaprevir
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24 displays an interesting synergy between the two most prevalent methods for burying solvent-
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26 accessible 3D PSA, as the two polar groups are highly exposed in the maximum 3D PSA
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28 conformation but shielded by the bulky side chains in the hydrogen bonded minimum PSA
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30 conformation.
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34 When examining the substructural motifs present in these dynamic shielding events, a diverse
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36 range of functional groups as well as sizes and distances between the groups was seen.
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38 Dynamic IMHBs formed pseudorings in eight compounds, where all but three of the eleven
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40 instances had 10-17 atoms in the pseudoring. This indicates opportunities to extend the use of
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42 dynamic IMHBs in design beyond motifs based on five to eight-membered pseudorings,³³
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44 many of which are stable in different environments. Amide NH (5/11 instances) and amide
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46 CO (4/11 instances) were the most common donors and acceptors. All but one of the
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48 dynamically formed IMHBs contained two or more rotatable bonds, predominantly centered
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50 around sp^3 -hybridized carbon atoms within the IMHB ring. In addition, all dynamically
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52 formed IMHB contained rigidifying functional groups such as amides, alkyl rings, aryl rings,
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54 esters and carbon-carbon double bonds. There is no doubt that a subtle play between rigid and
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flexible elements is required to obtain dynamic, environment-dependent IMHBs. The most common motif in aryl shielding events involved 6-atom linkers between the polar group and the aryl ring (3/7 instances), with the remainder of the events ranging between 4 and 15 atoms in the linker. Phenyl groups accounted for the majority of aryl groups (6/7 aryl groups), probably due to their prevalence in the dataset, while polar groups were more diverse and included carbamates, hydroxyl groups, amides, sulfonamides and ketones. Finally, dynamic IMHBs were equally frequent between side chains as within cores (each 5/11 instances), while aryl shielding of polar groups were more frequent between side chains than side chain to core.

Predicting the Effect of Dynamic Polarity Exposure on Permeability. The average effect of the different intramolecular interactions on polar surface area—when combined with our model correlating passive cell permeability to solvent accessible 3D PSA—provide an opportunity to predict the average impact from each intramolecular interaction on passive cell permeability. Accordingly, aryl shielding and IMHB formation led to an average of 28 and 27 Å² reduction in solvent accessible 3D PSA, respectively, which is predicted to yield ~6-7 fold improvement in permeability. Alkyl shielding, on the other hand, had a much lower average effect on 3D PSA of 14 Å², and is expected to increase passive permeability ~2-3 fold.

The largest variations in solvent accessible 3D PSA were observed for cyclosporin A (79 Å²) and faldaprevir (77 Å²), both of which were included in the external test set. Notably, their minimum solvent accessible 3D PSA (208 and 194 Å², respectively) corresponds to predicted Caco-2 cell permeabilities of 2.9×10^{-6} and 7.5×10^{-6} cm/s, which both compare favorably to experimental Caco-2 data (2.5×10^{-6} cm/s for cyclosporin A; $8\text{--}11 \times 10^{-6}$ cm/s in two independent studies for faldaprevir^{49, 51}). The >75 Å² lower solvent accessible 3D PSAs of

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3 these compounds' least polar conformations, as compared to their most polar ones,
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5 corresponds to a predicted >180-fold improvement in permeability. This may well explain
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7 why the observed permeabilities are much greater than would be expected from the 2D TPSA
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9 for these structurally very different compounds, and suggests a considerable potential of
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11 incorporating dynamic IMHBs and aryl/alkyl shielding in compound design. In addition, the
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13 correlation between permeability and solvent-accessible 3D PSA allows calculation of upper
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15 limits of 3D SA PSA that are compatible with satisfactory cell permeabilities. Thus,
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17 moderate-to-high cell permeabilities (P_{app} AB +Inh ranging from 1 to 10×10^{-6} cm/s) that are
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19 predictive of medium-to-high absorption from the intestine,⁵⁸ translate into solvent accessible
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21 PSAs ranging from ≤ 220 to $\leq 190 \text{ \AA}^2$ when atoms with partial charges >0.6 are included in the
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23 PSA definition.
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30 CONCLUSIONS

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32 Our analysis of drugs in the DrugBank database revealed a trend that PSA is buried in
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34 minimum energy conformations when MWs exceed 500-700 Da. This indicates that
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36 conformation dependent PSA is a common feature of larger drugs, which may allow them to
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38 behave as molecular chameleons that adapt their properties to their environment.^{27, 29, 31, 32}
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40 The potential for conformational flexibility to provide chameleonic properties was further
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42 investigated by analysis of 24 orally administered drugs and clinical candidates, 19 of which
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44 had properties residing in bRo5 space. Examination of multiple crystal structures for each
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46 compound revealed that polar functionality was buried to various extents and that solvent
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48 accessible 3D PSA varied by up to 79 \AA^2 between conformations.
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52 The minimum solvent-accessible 3D PSA calculated from the crystal structures of the drugs
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54 and clinical candidates in our training set displayed an excellent correlation with passive cell
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3 permeability. This correlation also applied to an external test set of additional drugs and
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5 clinical candidates in bRo5 space. Altogether, these findings suggest that the minimum
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7 solvent-accessible 3D PSA for relevant conformations can be used to predict cell
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9 permeability in bRo5 space, *provided that* conformations in a lipid-like environment can be
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11 calculated with reasonable accuracy. Accurate procedures for conformational sampling of
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13 macrocyclic peptides were reported most recently,⁵⁹ which provides hope that breakthroughs
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15 may also be made for conformational sampling of druglike compounds in bRo5 space in the
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17 near future. Solubility, which is also crucial for oral administration, was found to be less
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19 conformation-dependent, with similar correlations for minimum, average and maximum
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21 exposed PSA. This may reflect a greater conformational flexibility in aqueous than in lipid
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23 membrane environments, as has been suggested for cyclosporin A.⁵³ Importantly, correlations
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25 for both permeability and solubility were significantly improved when partially charged
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27 atoms were included in the calculations of PSA, as compared to predictions based solely on
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29 nitrogen, oxygen and attached hydrogen atoms.
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34 Current knowledge of how to incorporate conformational flexibility in design of chameleonic
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36 drugs is limited. Our inspection of crystal structures suggests that approaches based on
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38 incorporation of flexibility in attached side chains of macrocycles as well as non-macrocycles
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40 are more likely to be successful in providing chameleonic properties than attempts to adjust
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42 flexibility in the backbone. In particular, flexibly linked aromatic side chains have been
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44 employed successfully in de novo designed drugs, but also in modification of natural
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46 products. Environment-dependent, dynamic IMHBs were more frequent in the natural
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48 products studied herein than in the de novo designed drugs. The finding that most dynamic
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50 IMHBs observed in our dataset involved pseudorings with more than ten members indicates a
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52 scope for utilization in compound design beyond the five to eight-membered pseudoring
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54 motifs already highlighted by others.³³ Incorporation of dynamic IMHBs and flexibly linked
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3 aromatic side chains was predicted to improve permeability by ~6-7 fold per effective
4 interaction, whereas aliphatic side chains only provide a ~2-3 fold improvement.
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6 Significantly greater improvements may be obtained, as illustrated by the charge-reinforced
7 IMHB of faldaprevir. However, if intramolecular interactions are not flexibly formed, any
8 improvement in permeability is likely to be accompanied by reduced solubility.^{19, 26, 27}
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14 In conclusion, it is becoming increasingly clear that traditional 2D descriptors such as TPSA,
15 HBA and HBD fail to effectively capture the properties that impart cell permeability and oral
16 absorption to chameleonic compounds in bRo5 space. Instead, it appears that conformational
17 preferences and flexibility must be considered, and that use of 3D descriptors provides
18 significant advantages.^{31, 32} 3D descriptors such as the radius of gyration (R_{gyr}),⁴¹ the degree
19 of IMHB formation,⁶⁰ and free energies of desolvation⁶¹ have showed promise, and a
20 procedure relying on a combination of QSPR modeling and assessment of the polarity of
21 conformational ensembles was recently presented.²⁵ As described herein, the minimum
22 solvent-accessible 3D PSA gave the best correlation to cell permeability when moderately
23 polar atoms were included in the PSA calculation. Compounds that adopt one or several
24 conformations that expose less than 190-220 Å² solvent-accessible 3D PSA are likely to
25 display medium-to-high oral absorption, provided that the compounds are not associated with
26 major transporter-mediated efflux. We are therefore optimistic that progress in
27 conformational sampling of compounds in bRo5 space, e.g. as recently demonstrated for
28 macrocyclic peptides,⁵⁹ in combination with introduction of more informative 3D descriptors
29 will continue to improve our insight into what determines drug-like properties in this space.
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31 Rational design also of non-peptidic drugs in bRo5 space that can be administered orally may
32 thus become a reality in a not too distant future.
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56 **EXPERIMENTAL SECTION**

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3 **Source of Drugs and Clinical Candidates.** Atazanavir sulfate, azithromycin,
4 clarithromycin, erythromycin, roxithromycin, ritonavir and telaprevir were purchased from
5 Selleckchem. Asunaprevir was from Medchemtronica, rifampicin from Sigma, saquinavir
6 from MedChem Express, and telithromycin from TOKU-E, respectively. All compounds had
7 a purity >95.8%.
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15 **Calculating PSA for Drugs in DrugBank.** The DrugBank dataset³⁹ was downloaded on
16 22/01/2017 and filtered to contain drugs with MW 100 Da – 2000 Da. TPSA and molecular
17 3D PSA were calculated in InstantJChem v6.2.0.953 and Pymol 1.7.0.1, respectively, while
18 low energy 3D conformers were calculated in Corina v3.2.
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26 **3D Conformer Preparation from Experimental Data.** The IUPAC names, SMILES and
27 common synonyms were obtained for the 24 compounds from the ChemSpider database
28 (www.chemspider.com). All instances of crystal structure data for the 24 compounds were
29 extracted from the PDB (www.rcsb.org/pdb) and CSD (www.ccdc.cam.ac.uk), using searches
30 by common name, synonyms, and chemical structure. From the PDB, only crystal structures
31 with a resolution < 3.5 Å were considered. They were inspected visually to ensure that all
32 conformers that were included had well defined electron densities for the drug or clinical
33 candidate. Conformers were also checked to ensure that there were no steric clashes of the
34 ligand with the protein and that the ligand geometry was not strained, ligand atom
35 occupancies were not low, and temperature factors were similar to the adjacent side chain
36 atoms of the protein structure. The structures were initially analyzed in MOE v 2014.10
37 (Chemical Computing Group, www.chemcomp.com) and hydrogen atoms were added
38 according to the measured or predicted major ionization state at pH 7.4. The structures were
39 relaxed in the MMFF94x force field with a Born implicit electrostatic model ($\epsilon = 80$), with
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3 maximum deviation from the original structures set to RMSD ≤ 0.5 Å. Partial charges were
4 then calculated in Spartan 14 v1.1.4 using the PM3 semi-empirical method. The structures
5 were aligned by heavy atoms using MOE and pairwise heavy atom RMSD was calculated
6 using the mol_rmsd svl plugin. Conformers were clustered using a heavy atom RMSD
7 threshold of 0.75 Å.
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15 **Molecular Descriptor Calculations** Topological polar surface areas (TPSA) were calculated
16 from SMILES structural representation using the method of Ertl et al.⁴⁰, as implemented in
17 InstantJChem v6.2. cLogP was also calculated in InstantJChem v6.2. Three-dimensional PSA
18 was calculated in PyMol v1.7.0.1, using molecular surface areas calculated from atomic van
19 der Waal's radii, or solvent-accessible surface areas calculated using a solvent molecule
20 radius of 1.4 Å. Atoms were assigned as 'polar' either based solely on atom type (O, N, and
21 attached H), or by also including atoms with absolute partial charges from the PM3 semi-
22 empirical method above a defined threshold. Three dimensional PSA was calculated for all
23 crystal structures of each of the 24 compounds in the crystal structure dataset. Further details,
24 settings and commands are available in the supporting information.
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39 **Caco-2 Cell Permeability Assay.** Caco-2 cells (originally obtained from the American Type
40 Culture Collection; ATCC), passage 95-105, were maintained in Dulbecco's modified
41 Eagle's medium (DMEM), containing 10 % fetal calf serum and 1 % non-essential amino
42 acids. Cells were cultured on Transwell polycarbonate filters (diameter 12 mm, pore size 0.4
43 μm) as previously described.⁶² Briefly, cells were seeded at a density of 0.5×10^6 cells/filter
44 and maintained in DMEM with 10 % fetal calf serum, 1 % non-essential amino acids, 100
45 units/ml penicillin and 100 $\mu\text{g/ml}$ streptomycin, for 21 days prior to permeability
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3 Permeability measurements were performed as previously described.⁶² Briefly, culture
4 medium was replaced with preheated Hank's Balanced Salt Solution (HBSS) buffered with
5 HEPES to pH 7.4, 30 minutes prior to the start of the experiment. For measurements of
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7 efflux-inhibited permeability, a cocktail of 50 μ M quinidine, 20 μ M sulfasalazine and 30 μ M
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9 benzbromarone was included in the preincubation cocktail, and also in the donor and receiver
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11 solutions during the permeability experiment.
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16 Apparent permeability was measured, at a compound concentration of 1-2 μ M, in both
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18 apical-to-basolateral (A-B) and basolateral-to-apical (B-A) direction at pH 7.4 using a
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20 shaking speed of 500 rpm. Immediately after the start of the experiment a sample was
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22 removed from the donor compartment (C_0), and subsequent samples were taken from the
23
24 receiver compartment at 15, 30 and 60 min. At the end of the experiment ($t=60$ min), a
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26 sample was removed from the donor chamber (C_f) for mass balance calculation. Compound
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28 concentrations were analyzed by LC-MS/MS (see Analytical procedure below) using eight-
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30 point standard curves. Values reported in Table 2 are means of three repeats, except for
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32 saquinavir and ritonavir ($n=6$, because of excessive mass balance in the uninhibited
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34 experiment).
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39 The apparent permeability coefficient (P_{app}) of the compounds was calculated as:
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$$41 \quad \quad \quad \frac{dQ}{dt}$$
$$42 \quad P_{app} = \frac{dQ/dt}{C_0 \times A}$$

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49 where dQ/dt is the linear rate of appearance of drug in the receiver compartment, A is the
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51 surface area of the filter, and C_0 is the initial drug concentration in the donor compartment.
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53 Efflux ratios (ERs) were calculated from the permeabilities in the basolateral-to-apical (BA)
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55 and apical-to-basolateral (AB) directions as:
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$$ER = \frac{P_{app} BA}{P_{app} AB}$$

To confirm the integrity of the monolayer, the permeability of [¹⁴C]mannitol was determined in parallel to the test compound, and the trans-epithelial electrical resistance (TEER) was monitored before and after each permeability experiment.

Solubility Measurements. Solubility was determined in 100 mM potassium phosphate buffer, pH 7.4. Solid material was weighed into glass HPLC vials and 400-500 μl potassium phosphate buffer was added, resulting in saturated solutions. Samples were equilibrated for at least 20 h at 37 °C in a heater-shaker at 900 rpm. After equilibration, samples were centrifuged at 10 000×g for 20 min to remove remaining particulate matter. The resulting supernatants were diluted 20- to 5000-fold in potassium phosphate buffer, and analyzed by LC-MS/MS using eight-point standard curves (see Analytical procedure below). Values reported in Table 3 are means of four determinations.

Octanol-buffer Partitioning Measurements. Octanol-buffer partition coefficients (logD) were determined using a miniaturized shake-flask procedure based on the traditional shake flask technique.⁶³ 1-Octanol (HPLC grade ≥99 %, Sigma-Aldrich) and potassium phosphate buffer (KP) 10 mM, pH 7.4 (p.a. grade, Merck), were pre-saturated with each other by stirring overnight. Subsequently, the two layers were separated and stored for use in the assay. Two phase ratios (1:3 and 1:6 [KP:octanol]) were used, with total assay volume of 1.2 ml. The assay was started by pipetting 1 μl of each test compound into a 2 ml HPLC glass vial, to which octanol and KP buffer was added. The vials were sealed and shaken at 900 rpm in a V 2000 heater-shaker at ambient temperature (ca 23 °C) overnight. The vials were centrifuged at 3500 rpm for 20 min and then equilibrated in dark for an additional 24 h. Subsequently, the octanol phase was carefully separated from the aqueous phase using a pipette. Aliquots of the samples were diluted (125× and 2.5× for the octanol phase and

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3 aqueous phase, respectively). Compound concentrations in each phase were analyzed by LC-
4 MS/MS using eight-point standard curves (see Analytical procedure below). Values reported
5 in Table 3 are means of three to six repeats.
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10 **Analytical Procedure.** Analysis was conducted on an Acquity UPLC coupled to a XEVO
11 TQ triple-quadrupole mass spectrometer (both from Waters Corp., Milford, MA) with
12 positive or negative electrospray ionization. For chromatographic separation, either a C18
13 BEH 1.7 μm or a HSS T3 1.8 μm column (both from Waters Corp.) was used, with a general
14 gradient of 1 % to 90 % of mobile phase B over a total running time of 2 min. Mobile phase
15 A consisted of 5 % acetonitrile and 0.1 % formic acid in purified water, and mobile phase B
16 of 0.1 % formic acid in 100 % acetonitrile. The flow rate was set to 0.5 ml/min and 5 μL of
17 the sample was injected. Warfarin was used as internal standard throughout the analysis.
18 Mass spectrometric settings were optimized for each compound and are listed in
19 Supplementary Table S4.
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34 **Determination of pKa.** Acid dissociation constants were measured potentiometrically using
35 a SiriusT3 instrument (Sirius Analytical Instruments) equipped with a Ag/AgCl double
36 junction reference pH electrode and a turbidity sensing device. Titration experiments were
37 conducted in 0.15 M KCl solution under nitrogen atmosphere at a temperature of 25 ± 1 $^{\circ}\text{C}$.
38 All tests were performed using standardized 0.5 M KOH and 0.5 M HCl as titration reagents.
39 For low-solubility compounds, $\text{p}K_{\text{a}}$ values were determined in water-methanol mixtures (30-
40 70 % methanol v/v) and extrapolated to pure aqueous conditions using the Yasuda-
41 Shedlovsky method.⁶⁴ For compounds where experimental determination was precluded
42 because of low aqueous solubility (atazanavir and ritonavir), or no sample (such as with the
43 test set) dissociation constants were predicted with MoKA v.2.6.5. (www.moldiscovery.com).
44 Reported experimental values are means of three determinations
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ASSOCIATED CONTENT

Supporting information

The Supporting Information is available free of charge on the ACS Publications website.

Methods for calculation of 3D PSA. Models for permeability and solubility. Additional figures and tables referred to in the article. Molecular formula strings (CSV).

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Author Contributions

M.R.S. and B.D. made equal contributions to the manuscript. The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

Notes

The authors declare no competing financial interest.

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ABBREVIATIONS USED

1
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3 AB, apical-to-basolateral; BA, basolateral-to-apical; BCRP, breast cancer resistance protein;
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5 bRo5, beyond rule of 5; CSD, Cambridge Structural Database; ER, efflux ratio; IMHB,
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7 intramolecular hydrogen bond; MRP2, multidrug-resistance associated protein 2; M 3D PSA,
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9 molecular 3D PSA; P_{app} , permeability across Caco-2 cell monolayers; R_{gyr} , radius of
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11 gyration; SEM, standard error of the mean; TPSA, topological polar surface area.
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