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A freely available crystallisation data set and its application in machine learning

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Supplementary material and methods

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Accurate mass measurements

Chromatographic separation was performed on a Hypersil GOLD column (Thermo Scientific, Reinach BL, Switzerland) (1.9um, 100x 1.0 mm i.d.). LC–MS was executed using a Thermo Scientifc Ultimate 3000 LC system (Thermo Scientific, Reinach BL, Switzerland). 1 µl sample was injected in microliter pickup mode. The mobile phase solvents for binary gradient elution had the following compositions: water + 0.05% formic acid + 3.75 mM ammonium acetate (solvent A) and acetonitrile + 0.04% formic acid (solvent B). The gradient elution program started with 95% A, increased to 100% B over 5 min, was maintained at 100% B for 2 min, increased to 95% A in 6 seconds, and then kept at 95% A for another 2 minutes for column equilibration. The separation was performed at 40° C using a flow rate of 150 ul/min. The LC system was coupled to a Q Exactive Plus Mass Spectrometer (Thermo Scientific, Reinach BL, Switzerland). Spectra were acquired using electrospray ionisation in positive and negative ion mode, using a resolution setting of 35,000 at m/z 200. High mass accuracy was obtained by using a lock mass.



Fig. S1 – Extracted CSD solvents. Shown are the relative frequencies of single solvent experiments in the CSD in white. The x-axis is log-scaled to improve visibility.



Fig. S2 – Cluster sizes. Shown is the number of molecules found within each of the largest 50 clusters.



Fig. S3 – Basic scaffolds for public compound clusters. Shown are the general scaffolds of each cluster for the OXDB data set. Compounds in each cluster vary only in the individual R-groups.



Fig. S4 – ER Diagram. Shown is the entity-relationship diagram for the OracleSQL data base used to store all experiments and their outcomes. This also includes advanced functionality for storage of x-ray diffraction sets and outcomes.

Table S1 – Data base fields for the public compound data. This table lists the individual fields of the data set for the public compounds, supplied with the ESI.

Field	Description							
PID	project ID							
SMILES	SMILES string for compound							
Cluster	assigned cluster							
Number	number in cluster							
Molweight	molecular weight in g/mol							
S-MeOH	solubility in methanol							
S-EtOH	solubility in ethanol							
S-iPrOH	solubility in iso-propanol							
S-ACT	solubility in acetone							
S-EMK	solubility in ethyl-methylketone							
S-iBMK	solubility in iso-butyl-methylketone							
S-EA	solubility in ethyl acetate							
S-tBME	solubility in tert-butyl-methylether							
S-THF	solubility in tetrahydrofurane							
S-CHCI3	solubility in chloroform							
S-TOL	solubility in toluene							
S-ACN	solubility in acetonitril							
S-NiMe	solubility in nitromethane							
S-DMF	solutiblity in dimethylformamide							
S-MCB	solubility in chlorobenzene							
S-DCM	solubility in dichlormethane							
S-DEE	solubility in diethylether							
S-HEX	solubility in hexane							
C-MeOH	crystal propensity in methanol							
C-EtOH	crystal propensity in ethanol							
C-iPrOH	crystal propensity in iso-propanol							
C-ACT	crystal propensity in acetone							
C-EMK	crystal propensity in ethyl-methylketone							
C-IBMK	crystal propensity in iso-butyl-methylketone							
C-EA	crystal propensity in etnyl acetate							
C-tBME	crystal propensity in tert-butyi-methylether							
C-THF	crystal propensity in tetranydroturane							
C-CHCI3	crystal propensity in chloroform							
C-TOL	crystal propensity in toluene							
C-ACN	crystal propensity in acetonitril							
C-NiMe	crystal propensity in nitromethane							
C-DMF	crystal propensity in dimethylformamide							

Purity	determined LCMS purity of sample
C-HEX	crystal propensity in hexane
C-DEE	crystal propensity in diethylether
C-DCM	crystal propensity in dichlormethane
C-MCB	crystal propensity in chlorobenzene

Table S2 – Raw data for statistics of the in-house and the public data. Shown are the solubility and crystallinity class distributions for the combined data from the in-house data set and the public compounds.

		MeOH	EtOH	iPrOH	ACT	EMK	iBMK	EA	tBME	THF	CHCI3	TOL	ACN
Solubility	RS KS TS PS	555 970 315 122	361 426 320 135	240 310 412 130	479 764 226 139	368 390 190 101	282 382 265 183	273 336 246 190	121 129 67 325	538 314 141 70	450 274 79 180	179 325 251 273	343 572 332 175
Crystallinity	XX YX CT DR FI AM	575 155 303 255 270 398	349 110 214 130 232 207	287 107 210 85 144 258	430 133 312 131 210 392	285 104 164 73 88 335	307 110 150 99 61 385	321 132 188 106 92 206	115 120 91 125 47 145	140 69 113 55 93 593	150 96 211 142 51 333	283 163 133 150 49 250	466 130 230 129 119 348

Exemplary Code

while we cannot provide the full data set for reasons of confidentiality, this code snippet shows an equivalent approach to model generation based only on the publicly available data. Due to the limited amount of training data, results will vary in comparison to the main manuscript.

```
import rdkit
from rdkit import Chem
from rdkit.Chem import rdMolDescriptors
from sklearn import cross_validation
from sklearn.ensemble import RandomForestClassifier
# function used to convert solubility and crystallisation assessments to numeric values
def convertToNumeric(x):
    typeDict={'XX':1,'YX':1,'CT':0,'FI':0,'DR':0,'AM':0,'RS':1,'KS':1,'TS':1,'PS':0,'NA':-1}
return typeDict[x]
```

mlData=[]

```
# read in of molecules in SMILES format
suppl=Chem.SmilesMolSupplier('/home/DB.csv', smilesColumn=1, nameColumn=2, delimiter=',')
# property flags
sProperties=['S-MeOH','S-EtOH','S-iPrOH','S-ACT','S-EMK','S-iBMK','S-EA','S-tBME','S-THF','S-
CHC13', 'S-TOL', 'S-ACN']
cProperties=['C-MeOH','C-EtOH','C-iPrOH','C-ACT','C-EMK','C-iBMK','C-EA','C-tBME','C-THF','C-
CHCl3', 'C-TOL', 'C-ACN']
# generate fingerprints and convert solubility and crystallisation results to binary
for m in suppl:
   if not m: continue
   temp=[m,[],[]]
   for i in sProperties:
       temp[1].append(convertToNumeric(m.GetProp(i)))
   for i in cProperties:
       temp[2].append(convertToNumeric(m.GetProp(i)))
   temp.append(rdMolDescriptors.GetMorganFingerprintAsBitVect(m,4,nBits=4096))
   mlData.append(temp)
# test/train split & model generation as well as prediction. The variable s determines the
predicted solvent (MeOH=0, EtOH=1, etc...)
s=0
x_train, x_test, y_train, y_test = cross_validation.train_test_split([x[3] for x in mlData if
x[2][s]>-1],[x[2][s] for x in mlData if x[2][s]>-1],test_size=.50)
treeClassifier=RandomForestClassifier(class_weight='auto',n_estimators=1000, max_features=None,
n_jobs=-1, oob_score=True, criterion='gini')
treeClassifier.fit(x train,y train)
pred=treeClassifier.predict(x test)
```

ESI separate files

Data base

The results for all crystallisation experiments can be found as a CSV file separate to the supplementary. For a description of the denoted fields in the data base, see Table S1.