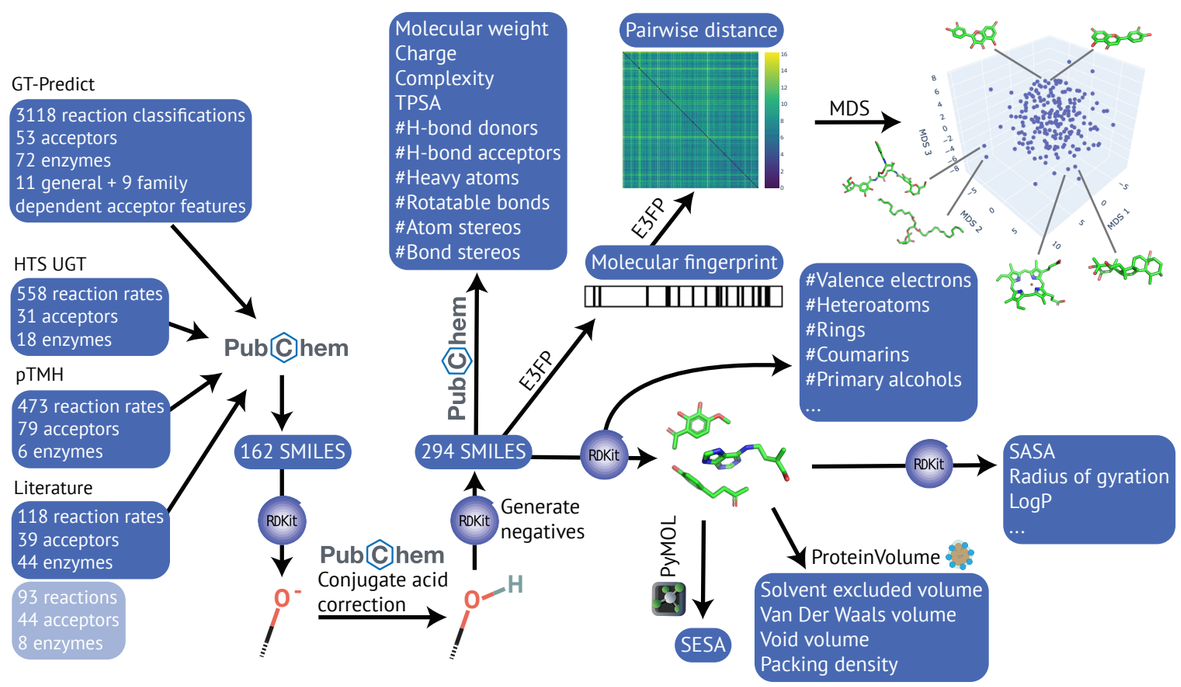
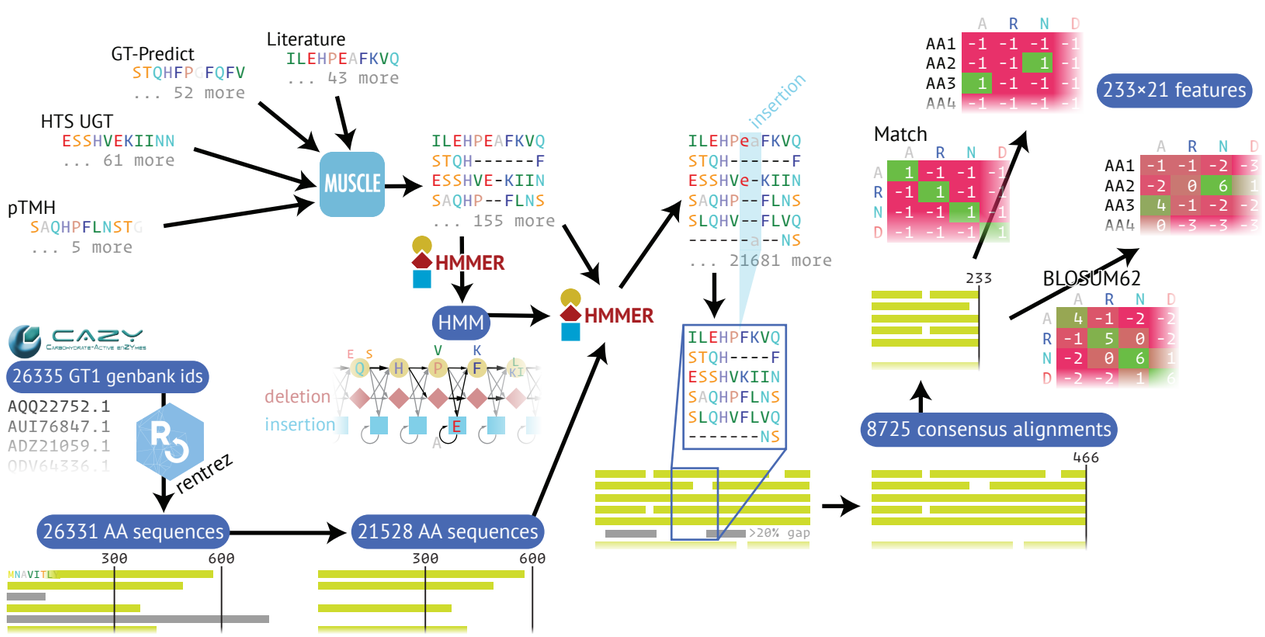

GT-Predict
3118 reaction classifications
53 acceptors
72 enzymes
11 general + 9 family dependent acceptor features
HTS UGT
558 reaction rates
31 acceptors
18 enzymes
pTMH
473 reaction rates
79 acceptors
6 enzymes
Literature
118 reaction rates
39 acceptors
44 enzymes
93 reactions
44 acceptors
8 enzymes
PubChem
162 SMILES
RDKit
PubChem
Conjugate acid correction
Generate negatives
294 SMILES
PubChem
Molecular weight
Charge
Complexity
TPSA
#H-bond donors
#H-bond acceptors
#Heavy atoms
#Rotatable bonds
#Atom stereos
#Bond stereos
E3FP
Molecular fingerprint
Pairwise distance
MDS
#Valence electrons
#Heteroatoms
#Rings
#Coumarins
#Primary alcohols
...
PyMOL
SESA
ProteinVolume
Solvent excluded volume
Van Der Waals volume
Void volume
Packing density
SASA
Radius of gyration
LogP
...


GT-Predict
STQHFPSFQFV
... 52 more
Literature
ILEHPEAFKVQ
... 43 more
HTS UGT
ESSHVEKIINN
... 61 more
pTMH
SAQHPFLNSTG
... 5 more
MUSCLE
ILEHPEAFKVQ
STQH------F
ESSHVE-KIIN
SAQHP--FLNS
... 155 more
HMMER
HMM
HMMER
CAZY
26335 GT1 genbank ids
AQQ22752.1
AUI76847.1
ADZ21059.1
QDV64336.1
rentrez
26331 AA sequences
21528 AA sequences
deletion
insertion
insertion
ILEHPeaFKVQ
STQH------F
ESSHVe-KIIN
SAQHP--FLNS
SLQHV--FLVQ
-------s--NS
... 21681 more
ILEHPFKVQ
STQH----F
ESSHVKIIN
SAQHPFLNS
SLQHVFLVQ
-------NS
>20% gap
8725 consensus alignments
233
466
Match
233×21 features
BLOSUM62