# Main Compound-Target Pair Information

Column Name	Type	Information about	Based on	Comments
parent_molregno	Int			Mapped from activities through
				molecule_hierarchy
parent_chemblid	String			
parent_pref_name	String			
max_phase	Float			
first_approval	Int	Compound	ChEMBL:	
usan_year	Int	Compound	molecule_dictionary	
black_box_warning	Int			
prodrug	Int			
oral	Int			
parenteral	Int			
topical	Int			
tid	Int		ChEMBL: assays	
mutation	String		ChEMBL: variant_sequences	
target_chembl_id	String		ChEMBL: target_dictionary	
target_pref_name	String	Target		
target_type	String			
organism	String			
tid_mutation	String		<tid>_<mutation></mutation></tid>	
cpd_target_pair	String		<pre><parent_molregno>_<tid></tid></parent_molregno></pre>	
cpd_target_pair_mutation	String	Compound-Target Pair	<pre><parent_molregno></parent_molregno></pre>	
			<tid_mutation></tid_mutation>	

### Aggregated Values

Aggregated per compound-target pair using parent\_molregno and tid\_mutation.

- \_BF: based on pchembl\_value\_mean\_BF (based on binding + functional assays)
- \_B: based on pchembl\_value\_mean\_B (based on binding assays)

Column Name	Type	Information about	Based on	Comments
pchembl_value_mean_BF	Float			Mean pchemb_value for the compound-target
pchembl_value_mean_B	Float		ChEMBL: pchembl values in activities in initial query	pair
pchembl_value_max_BF	Float			Maximum pchemb_value for the compound-
pchembl_value_max_B	Float		(dropped after aggregation)	target pair
pchembl_value_median_BF	Float		(dropped arter aggregation)	Median pchemb_value for the compound-
pchembl_value_median_B	Float			target pair
first_publication_cpd_target_	Int		ChEMBL: year values in docs in initial query (dropped after aggregation)	first publication in ChEMBL with this compound-target pair
pair_BF				
first_publication_cpd_target_	Int			
pair_B				
first_publication_cpd_target_	Int			first publication in ChEMBL with this
pair_w_pchembl_BF				compound-target pair and an associated
first_publication_cpd_target_	Int			pchembl value
pair_w_pchembl_B				penemoi vaiue

### DTI (Drug-Target Interaction) Annotations

Assigned based on cpd\_target\_pair, does not include mutation information.

Column Name	Type	Information about	Based on	Comments
therapeutic_target	Bool	Target	ChEMBL: drug_mechanism	Is the target in the drug mechanism table?
			table	
DTI	String	Compound-Target Pair	Assigned as per rules layed out	Drug target interaction annotation
			in code / comments / below	

#### Mechanism to assign the DTI annotations

in drug_mechanism	max_phase?	therapeutic target?	DTI annotation	Explanation
table?				
	4	_	D_DT	drug - drug target
	3	_	C3_DT	clinical candidate in phase 3 - drug target
Yes	2	_	C2_DT	clinical candidate in phase 2 - drug target
	1	_	C1_DT	clinical candidate in phase 1 - drug target
	$ $ < 1 $^{[1]}$	_	C0_DT	compound in unknown clinical phase - drug target
No	_	Yes	DT	drug target
	_	No	NDT	not drug target

Is the compound-target pair in the drug\_mechanisms table? = Is it a known relevant compound-target interaction?

What is the max\_phase of the compound?  $\hspace{1cm}=$  Is it a drug / clinical compound?

Is the target in the drug\_mechanisms table? = Is it a therapeutic target?

 $^{[1]}$  There are three possible annotations in ChEMBL with max\_phase not between 1 and 4:

0.5 = early phase 1 clinical trials

-1 = clinical phase unknown for drug or clinical candidate drug, i.e., where ChEMBL cannot assign a clinical phase

 $\operatorname{NULL}$  = preclinical compounds with bioactivity data

All three are grouped together into the annotation C0\_DT.

# Compound and Target Properties Based on ChEMBL Data

Column Name	Type	Information about	Based on	Comments
first_publication_cpd	Int		ChEMBL: docs	first appearance of the compound in the
				literature
mw_freebase	Float			
alogp	Float			
hba	Int			
hbd	Int			
psa	Float			
rtb	Int			
ro3_pass	String			
num_ro5_violations	Int			
cx_most_apka	Float			
cx_most_bpka	Float			
cx_logp	Float		ChEMBL: compound_properties	
cx_logd	Float	Compound		
molecular_species	String			
full_mwt	Float			
aromatic_rings	Int			
heavy_atoms	Int			
qed_weighted	Float			
mw_monoisotopic	Float			
full_molformula	String			
hba_lipinski	Int			
hbd_lipinski	Int			
num_lipinski_ro5_violations	Int			
standard_inchi	String		ChEMBL: compound_structures	
standard_inchi_key	String			
canonical_smiles	String			

### Compound and Target Properties Based on ChEMBL Data cont.

\_BF: based on pchembl\_value\_mean\_BF (based on binding + functional assays)

\_B: based on pchembl\_value\_mean\_B (based on binding assays)

Column Name	Type	Information about	Based on	Comments
LE_BF / LE_B	Float			
BEI_BF / BEI_B	Float		Calculated based on	Ligand efficiency metric
SEI_BF / SEI_B	Float	Compound	pchembl_value_mean	nigand enteries metric
LLE_BF / LLE_B	Float			
atc level1	String		ChEMBL: atc_classification,	Anatomical Therapeutic Chemical
_	String		molecule_atc_classification	(ATC) classification, level 1
target_class_l1	String	Target	ChEMBL: protein_classification,	Target class, level 1
target_class_l2	String	Target	protein_family_classification	Target class, level 2

# RDKit-Based Compound Descriptors

Column Name	Type	Information about	Based on	Comments
fraction_csp3	Float			
num_heteroatoms	Int			
num_stereocentres	Int			
ring_count	Int			
num_aliphatic_rings	Int			
num_aliphatic_carbocycles	Int			
num_aliphatic_heterocycles	Int		canonical_smiles + built-in RDKit methods	
num_aromatic_rings	Int		RDKIt methods	
num_aromatic_carbocycles	Int			
num_aromatic_heterocycles	Int	Compound		
num_saturated_rings	Int			
num_saturated_carbocycles	Int			
num_saturated_heterocycles	Int			
aromatic_atoms	Int			
aromatic_c	Int		canonical_smiles + RDKit-	
aromatic_n	Int		based methods	
aromatic_hetero	Int			
scaffold_w_stereo	String		canonical_smiles + built-in	
scaffold_wo_stereo	String		RDKit methods	

### **Annotations for Filtering**

The columns based on the calculated subsets are only available in the full dataset to facilitate the filtering into subsets.

Column	Type	Information about	Based on	Comments
Name				
in_dm_table	Bool		ChEMBL:	Is the compound-target pair (cpd_target_pair) in the drug mechanism table?
			drug_	
			mechanism	
keep_for_	Bool			Rows to keep if interested in information based only on binding assays + the
binding				drug_mechanism table. True if pchembl_value_mean_B (based on binding as-
				says) exists or if in_dm_table == True, i.e., the pair is in the drug mechanism
				table.
BF_100	Bool			binding + functional data; at least 100 comparator compounds* per target
BF_100_	Bool			binding + functional data; at least 100 comparator compounds* per target; at least
$c_dt_d_dt$		Compound-Target Pair		one compound annotated with D_DT or C_DT (C0_DT, C1_DT, C2_DT,
				C3_DT) per target
BF_100_d_dt	Bool			binding + functional data; at least 100 comparator compounds* per target; at least
			calculated	one compound annotated with D_DT per target
B_100	Bool		subsets	binding data only; at least 100 comparator compounds* per target
B_100_	Bool			binding data only; at least 100 comparator compounds* per target; at least one com-
$c_dt_d_dt$				pound annotated with D_DT or C_DT (C0_DT, C1_DT, C2_DT, C3_DT)
				per target
B_100_d_dt	Bool			binding data only; at least 100 comparator compounds* per target; at least one
				compound annotated with D_DT per target

<sup>\*</sup> comparator compounds must have a pchembl value but don't have a specified max\_phase or DTI annotation, i.e., drugs and clinical candidates are counted as comparator compounds as well