



FOUNDATIONS
ADVANCES

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Supporting information for article:

Extension of the transferable aspherical pseudoatom data bank for the comparison of molecular electrostatic potentials in structure–activity studies

Prashant Kumar, Barbara Gruza, Sławomir Antonii Bojarowski and Paulina Maria Dominiak

SUPPORTING INFORMATION

Extension of the transferable aspherical pseudoatom data bank for the comparison of molecular electrostatic potentials in structure–activity studies

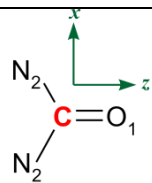
Prashant Kumar, Barbara Gruza, Sławomir Antoni Bojarowski, Paulina Maria Dominiak*

Biological and Chemical Research Centre, Department of Chemistry, University of Warsaw, ul. Żwirki i Wigury 101, 02-089, Warszawa, Poland

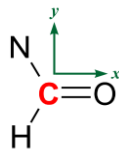
E-mail: pdomin@chem.uw.edu.pl; Phone: +48 22 55 26 714

Table 1S. Atom types in the UBDB2018 databank. The *D* symbol represents dummy atom required for coordinate system definition. The first letter in the atom type code goes for a chemical element symbol. The T letter marks atom types which need further improvement in atom type definition or more entries from model molecules to confirm parametrization. The meaning of atom labelling of the Nearest and Next-Nearest Neighbour Atom Types is given in the [Table 2S](#).

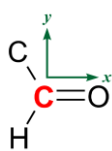
Carbon				
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C301	C302	C303	C510	C304
C305	C306*	C307	C523	C314-T



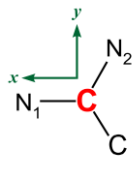
C308



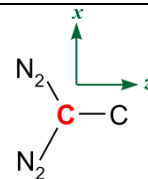
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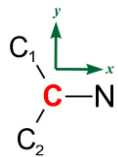
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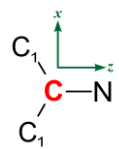
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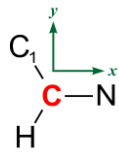
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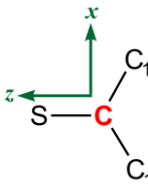
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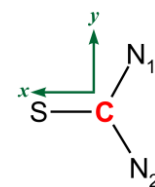
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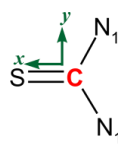
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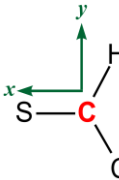
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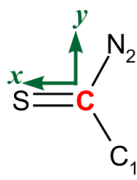
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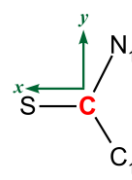
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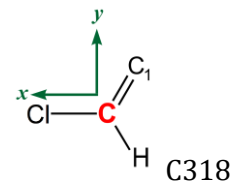
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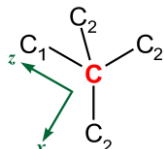
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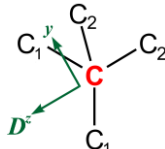
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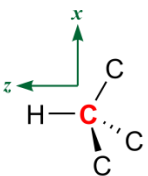
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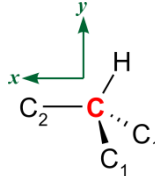
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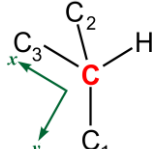
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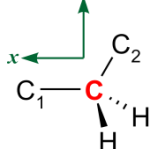
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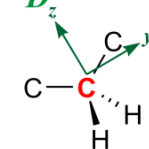
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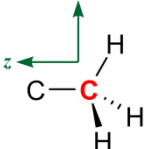
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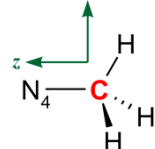
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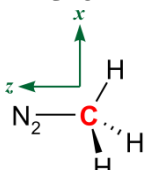
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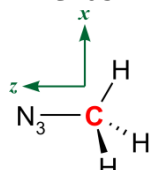
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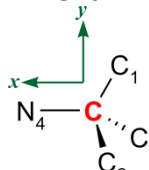
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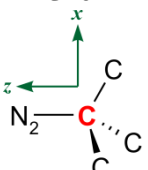
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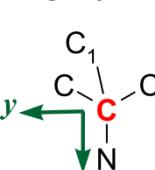
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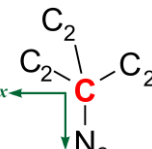
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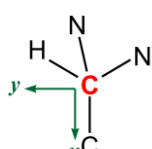
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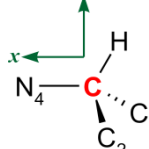
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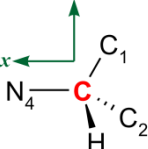
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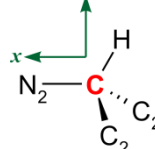
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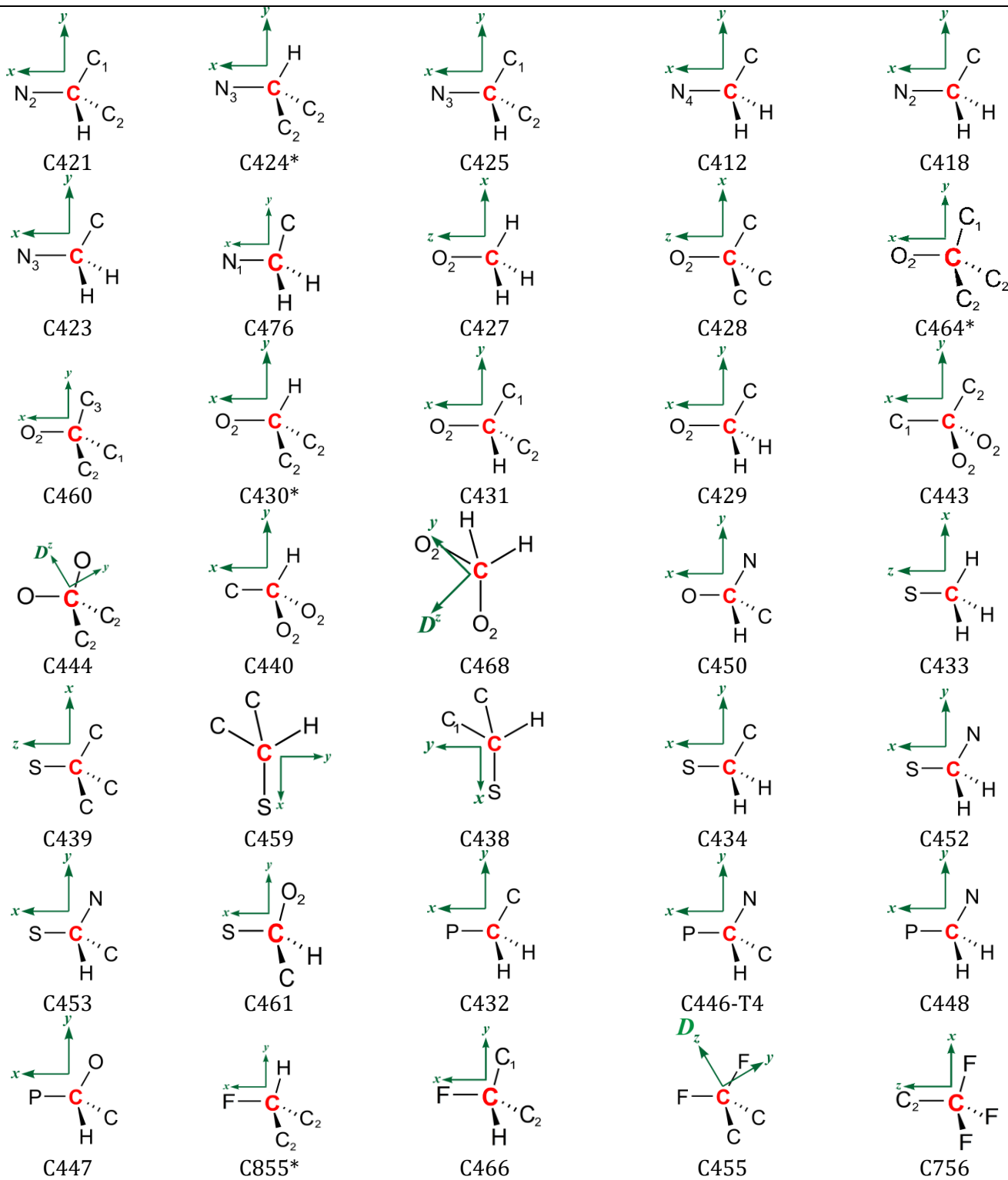
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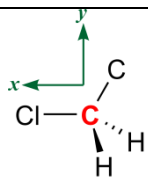


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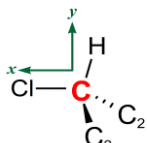


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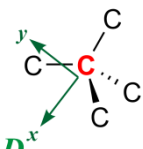




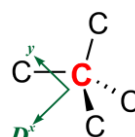
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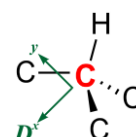
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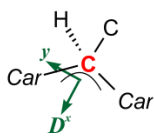
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C465-6M



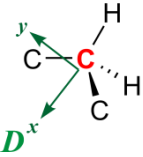
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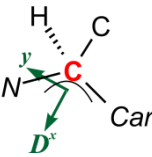
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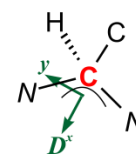
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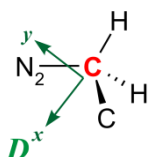
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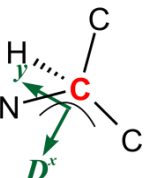
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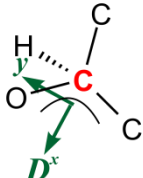
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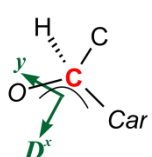
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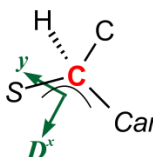
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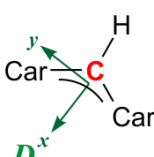
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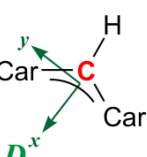
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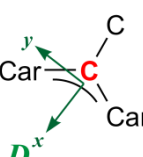
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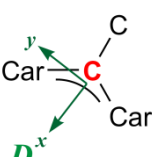
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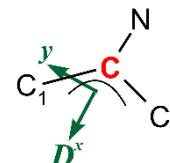
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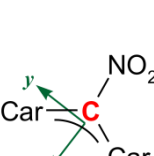
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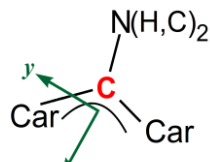
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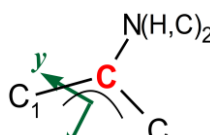
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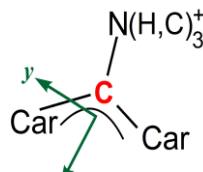
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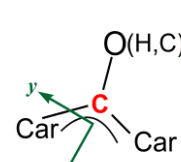
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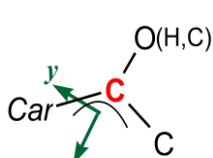
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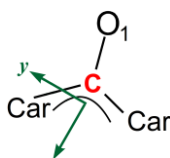
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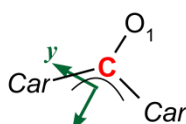
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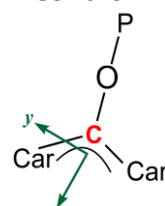
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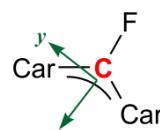
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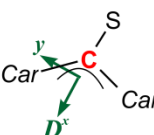
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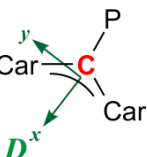
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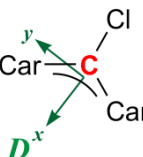
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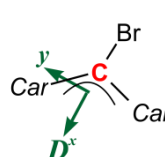
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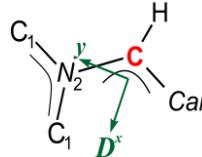
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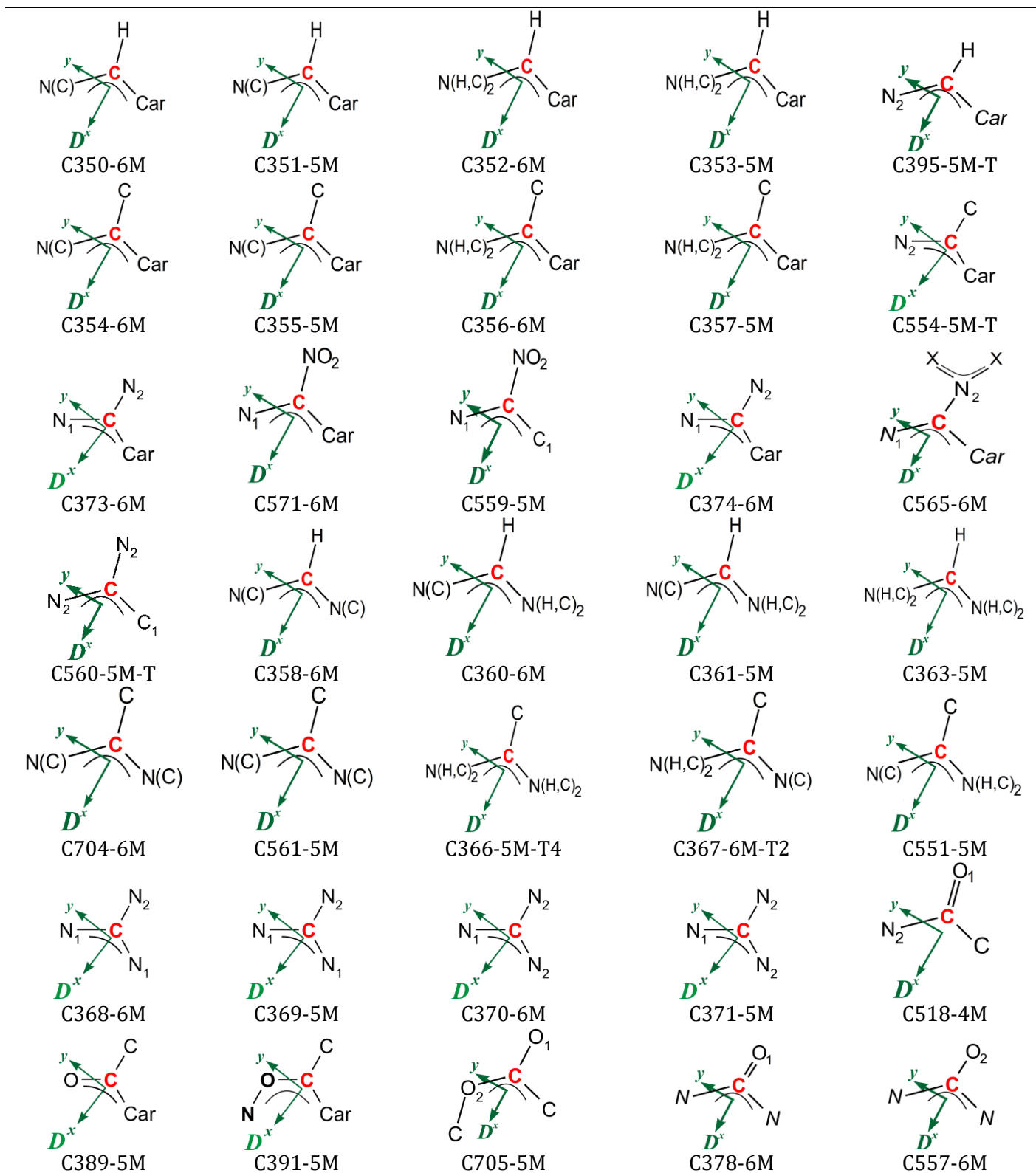
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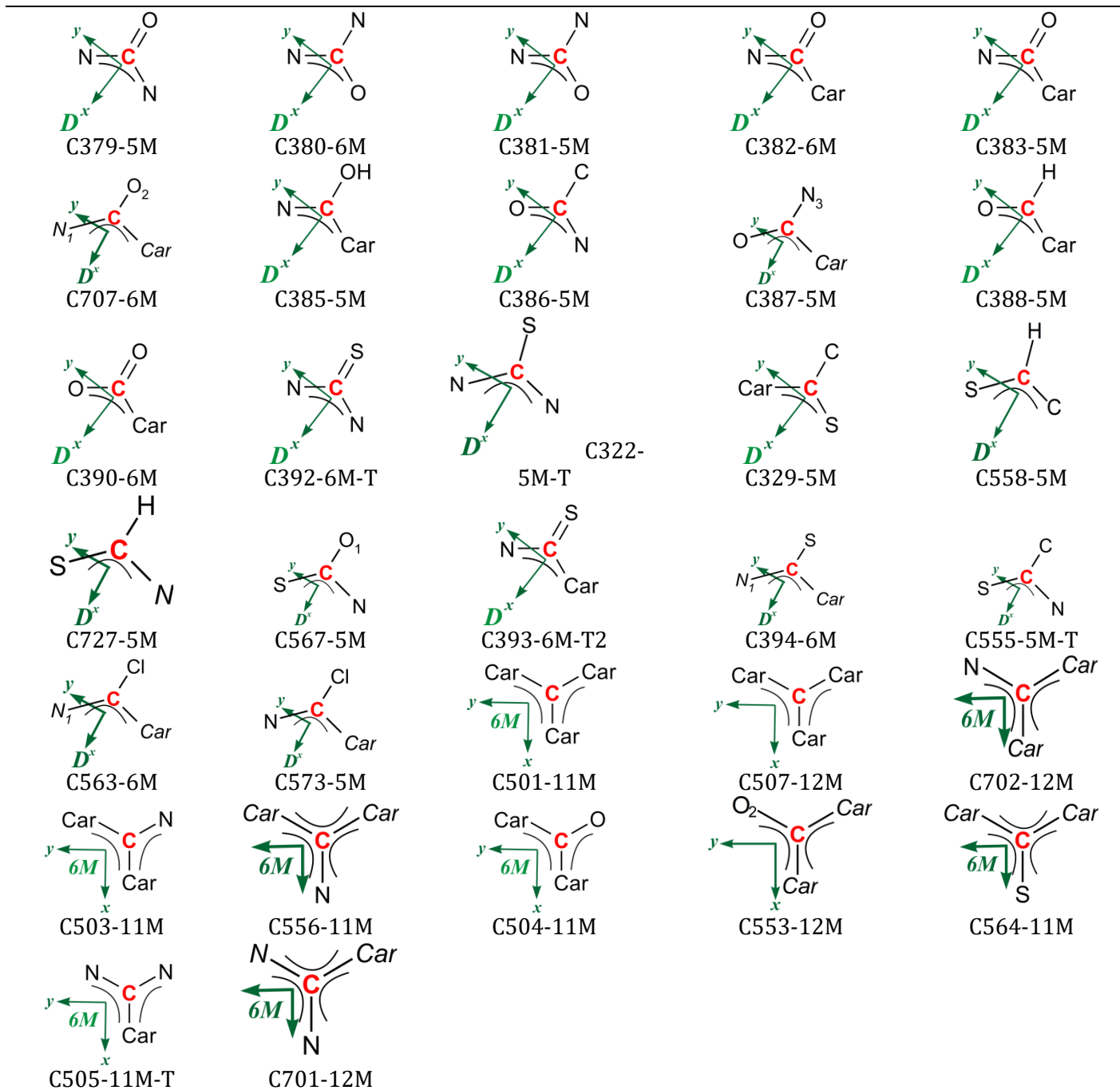


C347-6M

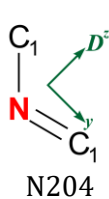
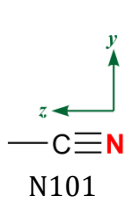


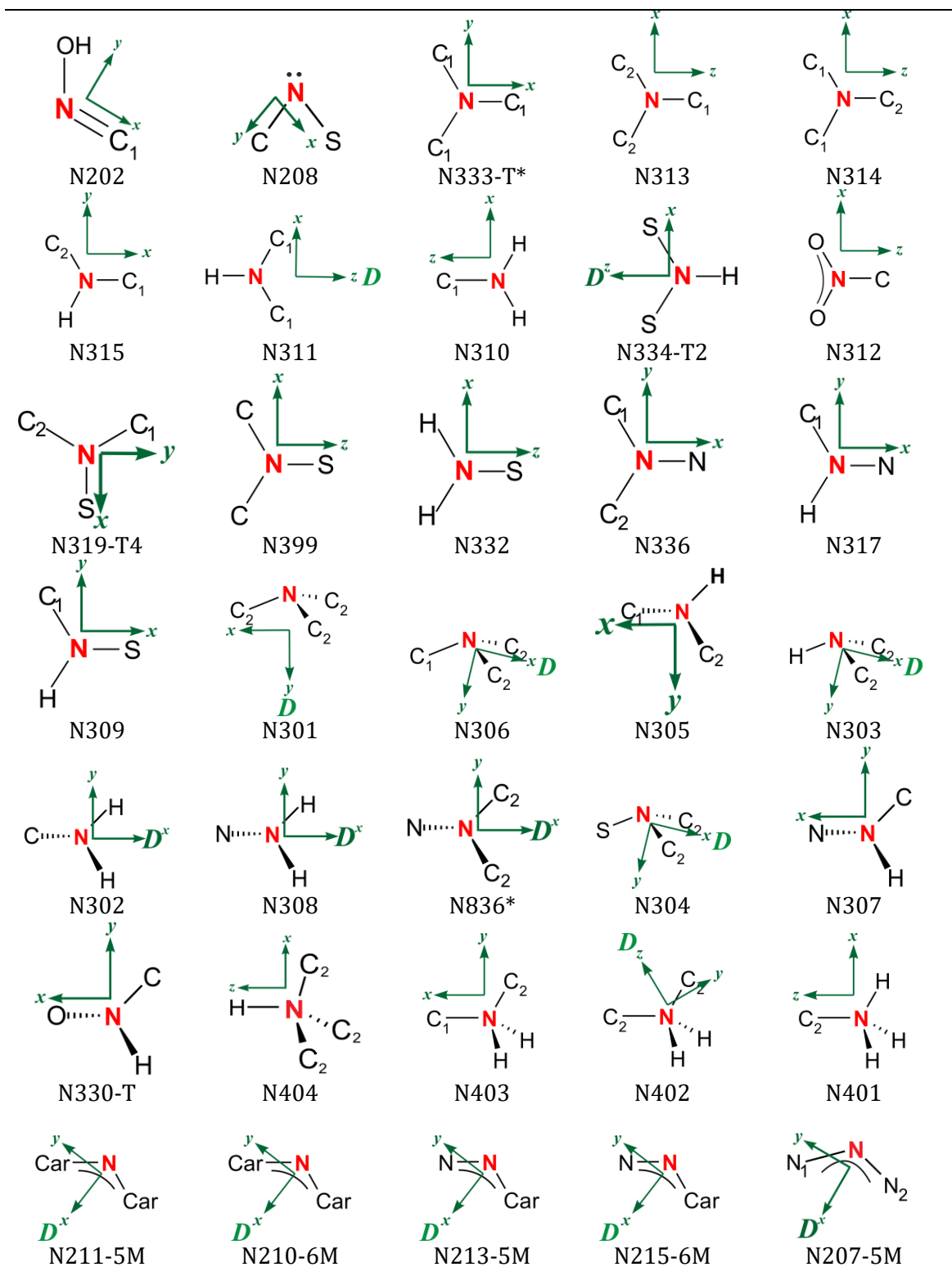
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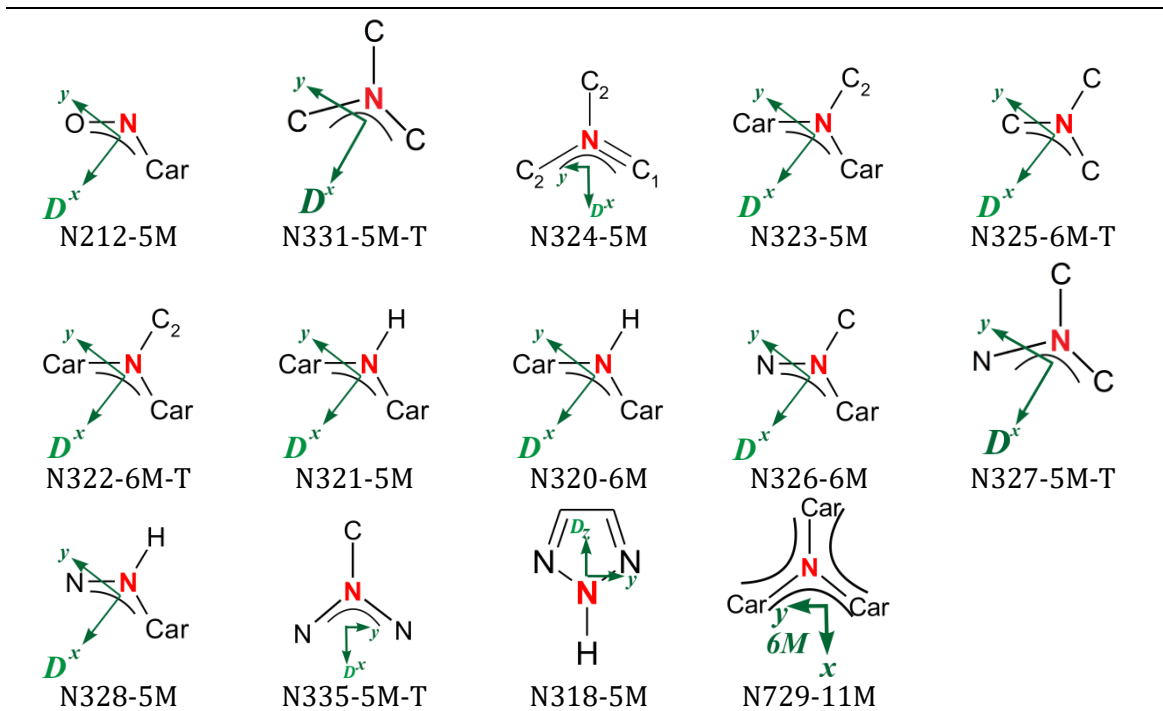




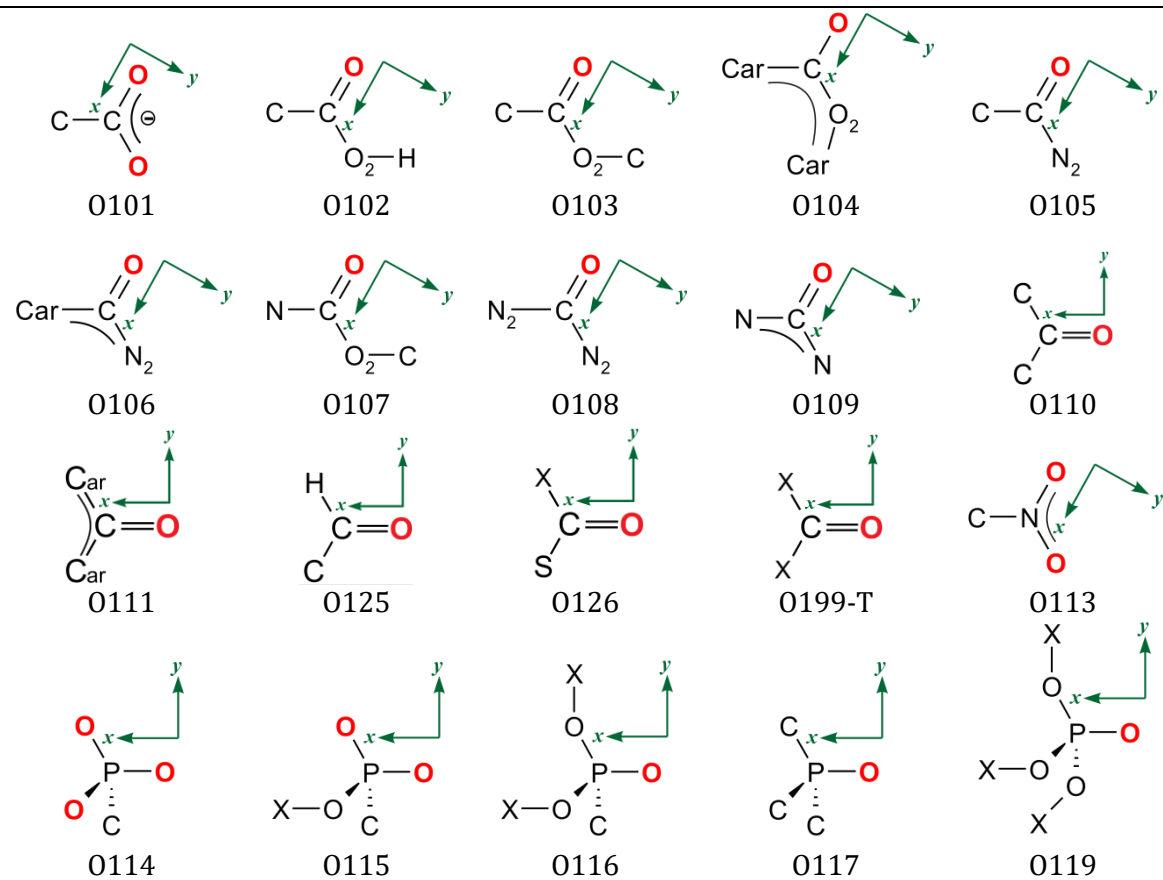
Nitrogen

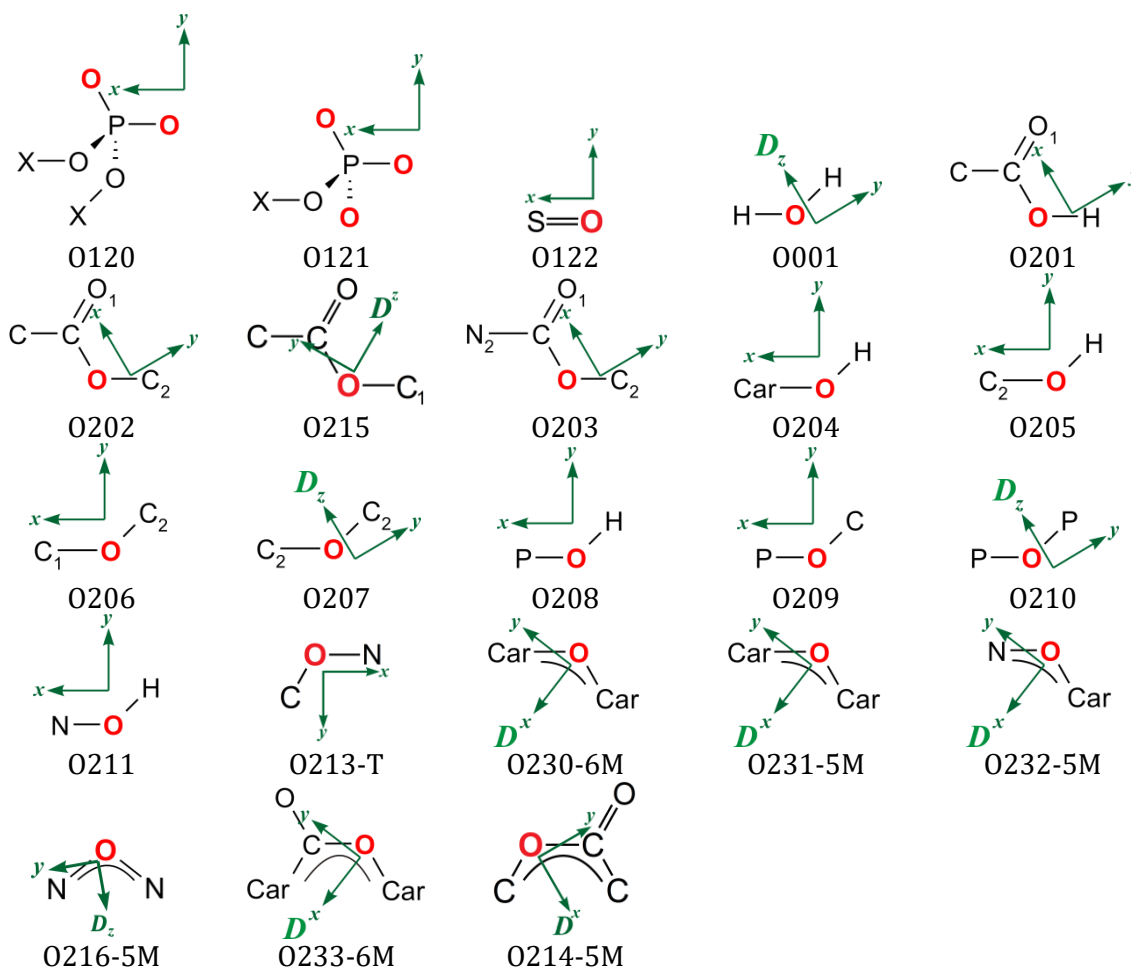




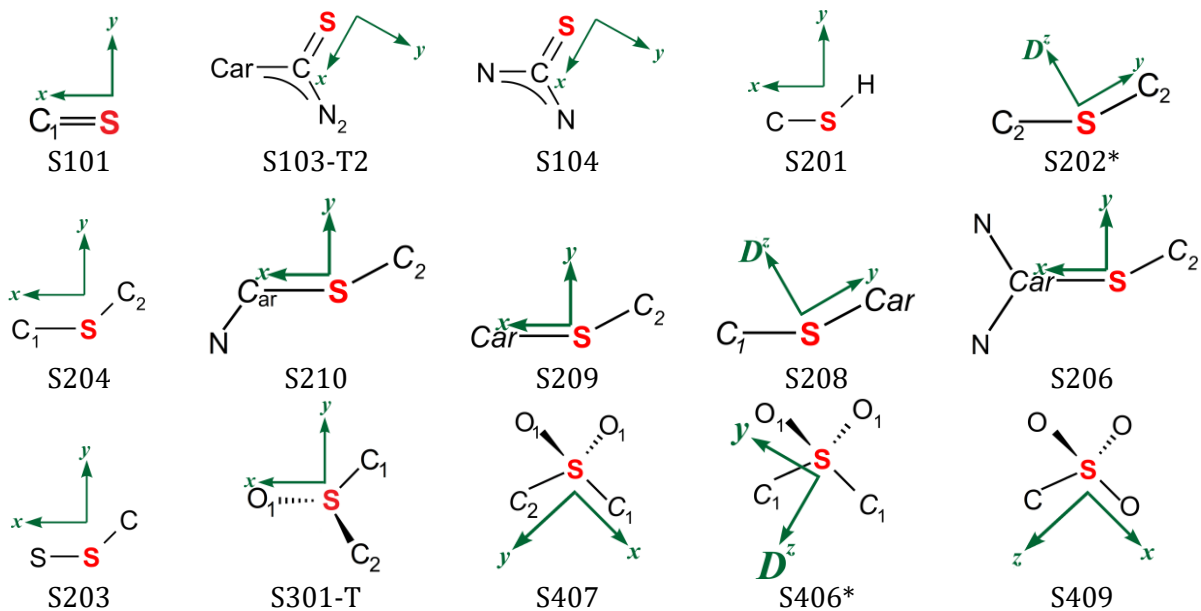


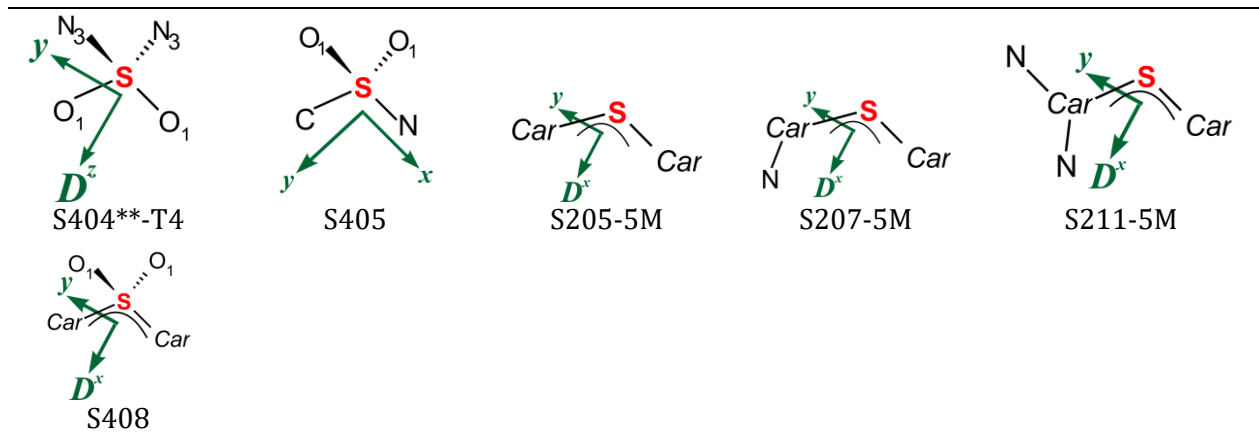
Oxygen



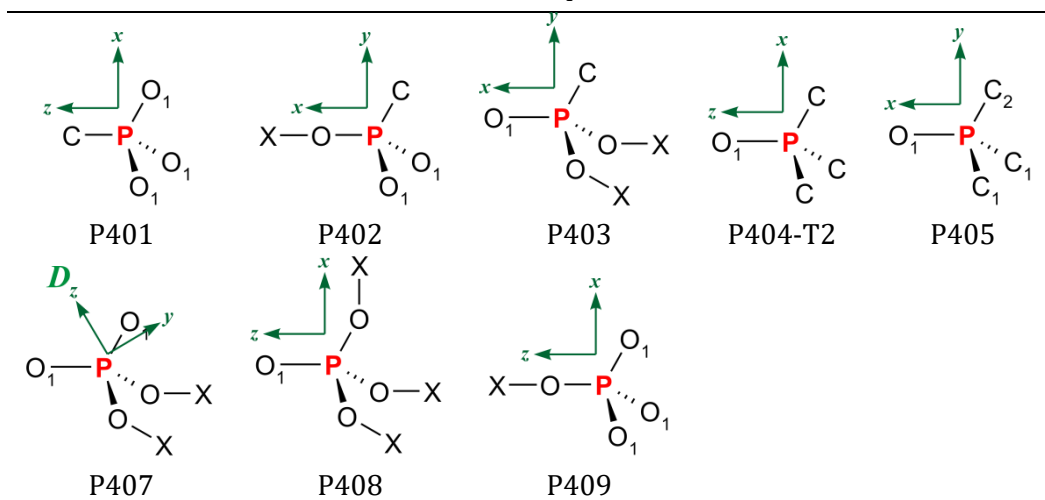


Sulphur





Phosphorus

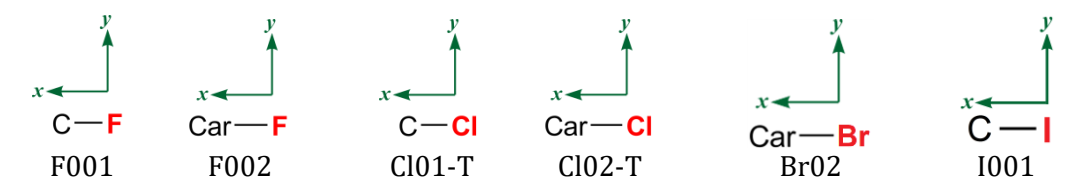


Fluorine

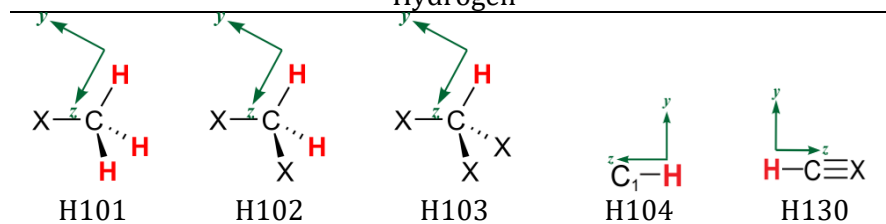
Chlorine

Bromine

Iodine



Hydrogen



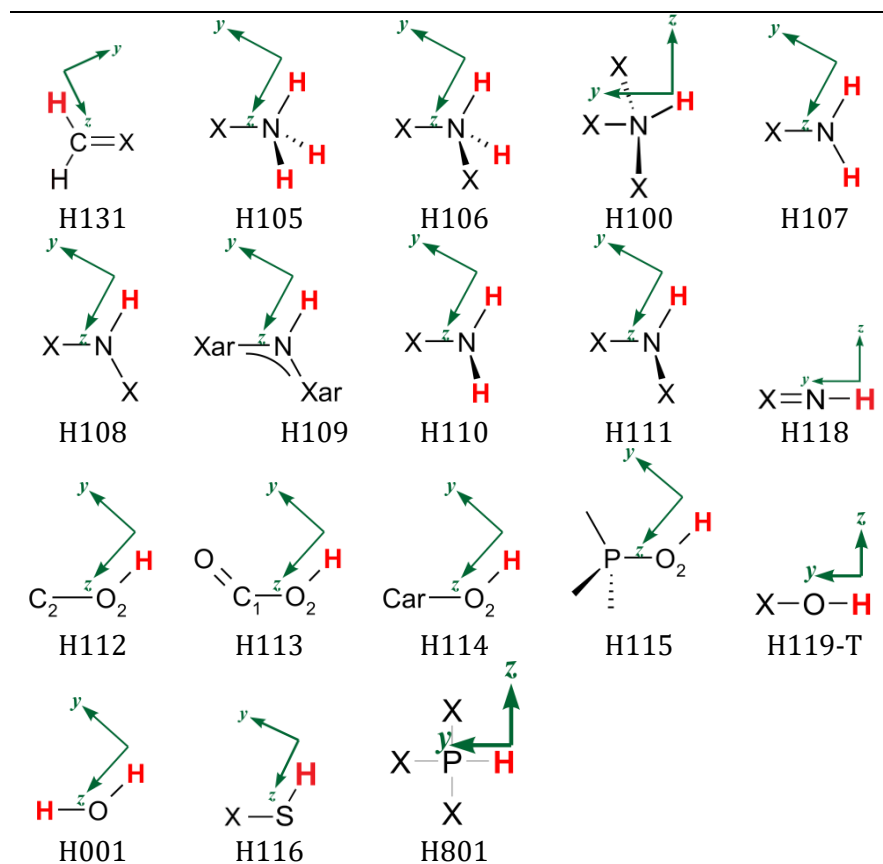


Table 2S. Labelling of the Nearest and Next-Nearest Neighbour Atom Types used in [Table 1S](#).^a

<i>C</i>	any carbon
<i>C</i> ₁	Csp ² aromatic and nonaromatic
<i>C</i> ₂	Csp ³
<i>C</i> ₃	Csp ¹
<i>Car</i>	Csp ² in planar ring
<i>N</i>	any nitrogen
<i>N</i> ₁	Nsp ² (2)
<i>N</i> ₂	Nsp ² (3)
<i>N</i> ₃	Nsp ³ (3)
<i>N</i> ₄	Nsp ³ (4)
<i>O</i> ₁	Osp ² (1)
<i>O</i> ₂	Osp ³ (2)
<i>X</i>	any non-hydrogen atom; in the case of <i>CPO</i> ₃ and <i>CPO</i> ₄ groups carbon or hydrogen atoms

* - there can be two *C*₁ atoms, two *C*₂ atoms or two *C*₃ atoms
 ** - there can be two *N*₁ atoms, two *N*₂ atom, two *N*₃ atoms or two *N*₄ atoms
nM - indicates number of neighbours
T - simplified atom definition

^a numbers in parentheses represent number of bonds to the atoms

Table 3S. Cambridge Structural Databank REFCODES for model molecules used to build the UBDB2018.

ABABIP	ABABOW	ABACAJ	ABAFUG	ABAHUI	ABALAS	ABALIA
ABATOO	ABEBUE	ABEFAO	ABEHEV	ABEKAV	ABEKEY	ABEKEZ
ABELAV	ABELEZ	ABEROP	ABIMUT	ABIPIL	ABIVUD	ABIZAM
ABUBEE	ABUGOT	ABUQAP	ABUQOD	ABURAQ	ABUTAS	ACACOX
ACAJEV	ACAMOX	ACANAC11	ACAYUY	ACAZOV	ACECAN	ACENAZ
ACERIK01	ACETSC10	ACEZIR99	ACGLUA11	ACICUK	ACIDAR	ACIDOH
ACIHEB	ACIMDC99	ACINDN	ACIRAG	ACIROU	ACIXAN	ACOREP
ACRLAC02	ACSALA01	ACUPUL	ACUZAZ99	ACXMPR	ACYHXA01	ADAGOC
ADAHET	ADAJUK01	ADAKUM	ADALAT	ADAVUW	ADAZOV	ADEKUQ
ADENCH99	ADEPAB	ADHELA10	ADIHUR	ADIMIK	ADINAD	ADITAI
ADOJAG	ADOJEI	ADONAK	ADOPIU	ADOTUJ	ADPOSD	ADULUG
ADUNAO	ADUQAS	ADUWIF	ADUXAY	ADUZAB	AEPHOS02	AFALIC
AFALUO	AFAMID	AFAYOV	AFCYDP	AFEJEC	AFEPIL	AFETEL
AFEVOW	AFEWIS	AFEZIV	AFIFOK	AFIFUR	AFIGEC	AFINAG01
AFIPIQ	AFIPOW	AFIZAS01	AFOBIH	AFOCEF	AFUGEP	AFUNEW
AFUVOM	AFUVUS	AFUYIJ	AGAGUK	AGASUY	AGEKII	AGESIO
AGIBAV	AGOCII99	AGODAD	AGONAN	AGOXOL	AGUPID	AHATAG
AHATEK	AHEBUL	AHECEW	AHECIB	AHEJAZ08	AHETOX	AHETUD
AHICIF	AHICUR	AHIKEI	AHOJIQ	AHOWOL	AHUBEM	AHUFEP
AHUZEI	AIPEPN20	AJACAP	AJACEV	AJACIX	AJAFIC	AJANAC
AJEVAN	AJEVOB	AJIDAA	AJIVIZ	AJIXIC	AJOGUC	AJOPOE01
AJUDAL	AKALAZ	AKAXAL99	AKENIO	AKEQOX	AKETUG	AKIFEF
AKILAH	AKIWOG	AKOCAE	AKOCEJ	AKOCOU	AKOPAT	AKOWAY
AKUMEA	AKUROO	AKUVEI	AKUVIM	ALAGUR	ALASAI	ALAYIW
ALAZAO	ALECIE	ALEVES	ALOVUS01	ALPHAGLY	ALUGOF	AMADAU
AMAPTZ	AMDPIM	AMEFEF	AMEGIK	AMELOU	AMELUA	AMIHXF
AMIMZA10	AMITEW	AMUMIG	ANISAT	ANTZOL10	ANUDOD	APAPYR
APEJEM	APEKEM	APEKIQ	APELAJ	APELEN	APEMOZ	APIFAH
APIPAS	APITEA	APOXOS01	APOYIO	APURAE99	AQANAI	AQARIU
AQECAA	AQEDUW	AQERAQ	AQEWOI	AQIGOW	AQINET	ARABUQ
ARACYP	ARADEC	ARBIMC10	ARCLAM01	ARFCYT99	ARGIND11	ARIQAV
AROJAU	AROMAV	AROMID	AROQEF	AROWIP	ARUBIY	ARUWEQ
ASABAZ	ASAXOJ	ASIJIW	ASIJIX	ASIYOR	ASOCOA	ASOTIM
ASOTUX	ASTROM99	ASULOP98	ASULOP99	ASUQOW	ATADUW	ATAXUO
ATAXUP	ATDZSA04	ATESIB	ATIXIM	ATIXUY	ATONOO	ATOVAG
ATOXEM	ATUBEX	ATUGAZ	ATUTAK99	ATZTHD10	AVAGIN	AVAKAK
AVEPAU	AVOTUA	AVOVIQ	AVUGUV	AVULIM	AVUSAN	AVUXAS
AWATUO	AWEBEL	AWELOE	AWENIB02	AWETED	AWIQEE	AWOLOP
AWOSOU	AWUBIF	AWUREQ	AWUYUM	AXADUZ	AXAFOV	AXAJUF
AXALAM	AXALAN	AXALOB	AXAMAN	AXANOD	AXAXED	AXEMIA
AXFSUR	AXIMEZ	AYECAJ	AYEFUF	AYIKID	AYOHEB	AYOHIF

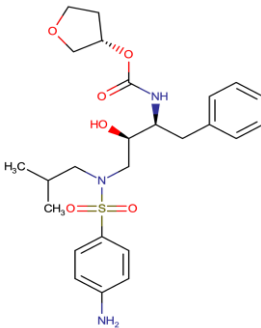
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AZOMOS	AZOPIP	AZOQUC	AZOROX	AZUCAA	AZUMOY	AZURAC01
AZURUI99	BACXOV	BADQIG	BAFLOL	BAFTAE	BAGTUA	BAGVAI
BAJYIV	BAKFUO	BAKLEG	BAKLUW	BALGUR	BALMOR	BALPIN
BAMDIC	BANFIG	BANKUW	BANLEH	BANNEL	BANPAK	BAQHOS01
BARCOX	BARFIJ	BATJUC	BATSUK	BATVAU	BAVBOP	BAWHEO
BAYGOZ	BAYYAB	BAZNEV	BCBANN01	BCZNON	BDIXNA	BEBLAW
BEBWEK	BEBWOU	BECGOF	BECRUY	BECYAL	BEDBAP	BEDDOE
BEFSUA	BEGLAC	BEGVOA	BEHDUO	BEKBOJ98	BEKBOJ99	BEMDAZ97
BEMDAZ98	BEMDAZ99	BEMFOO	BEMFUU	BENTEU	BEPRAP99	BERFUZ
BERHEL	BERXAY	BESLOC	BESNUI	BESPUL	BESYEF	BEWHUG
BEWQAV01	BEWQOK	BEXGEQ	BEXLIB	BEXMIA	BEXWEI	BEYPUR
BEYVEH	BEZGES	BIBTAI	BIBXUG	BICBIZ	BICSUC	BIDJON
BIDMIK97	BIDMIK98	BIDMIK99	BIFPIP	BIFTUH	BIFVET	BIFXUK
BIGUAN01	BIJSIX96	BIJSIX97	BIJSIX98	BIJSIX99	BIMSNO	BIMTIB
BIPTID01	BISDIQ	BIWWIO	BIZDUK	BIZWIS	BIZYAL01	BOCDOM
BOCPUE	BODCED	BOGQOE	BOHWUR	BOLYUW	BONLOG	BONVIL
BOPTZO	BOQJEW98	BOQJEW99	BOQVIM01	BOQYEN	BORHAS	BOTZOA
BOVYIV	BOWYOC	BOXGIE99	BOXKEE99	BOXWOA	BOYHIG	BOYZUL
BOZDIE	BUDPEW01	BUDYAB	BUDYEF	BUFDEM	BUFGIS	BUFTED
BUGDEM	BUGKIY	BUGMIZ	BUGXUW	BUHJAP	BUKKUP	BUKYIP
BULXOX	BUQCAT	BUQLAC	BUQMUX	BURFIF	BURKUU	BURZUJ
BUSJIJ	BUSPEK	BUSZUM	BUTFUT	BUWNOW	BUWSAN	BUWSAO
BUXFEG	BUYLAJ	BZOXZT	BZTZAD	CAACTY	CABPYR11	CABSIH10
CABZIR	CADMAW	CAGGUM	CAINSP95	CAINSP96	CAINSP97	CAINSP98
CAKRIQ	CALJIK	CAMVES98	CAMVES99	CAMZOG	CANCAW	CANDEB01
CANELL01	CAPROA	CAQYIE01	CARZAX	CASBAA	CASFAE	CATXOK98
CATXOK99	CAVGEL	CAVQUM	CBOHAZ	CEBNIG	CECHEY	CEDDIA01
CEDGUO	CEDROU	CEFTOW	CEGBUN	CEGKEG	CEGVER	CEHSIR
CEJSEP	CELLAI	CERJEP	CEVYEH95	CEVYEH96	CEVYEH97	CEVYEH98
CEVYEH99	CEWCAI10	CEYCIS99	CEYNEZ	CEZQII	CHPYRD	CHXIQL
CIBTUD	CIBVEP	CIDBIB	CIDHON	CIFTES	CIJZAX	CIJZUR
CINLOC	CINTOK	CIPMOE	CIPVII	CIPWOO	CIQCUA	CIQGEP
CIQHOB	CIQHUH	CIQJES	CIQYEH	CIRLEW	CIWVAH	CIWWAG
CIXWEL	CIZDUK02	CIZRUY	CIZYEP	CMPHOA10	CMTAZP	CNOXPA
COCVIZ	CODPIU	CODPOA	CODYUP10	COHBOQ	COHKOZ	COHNES99
COJMUJ	COJXIK	COJXUW	COLLEW	COMXAD97	COPHEU	COPREE10
CORSUY	CORWAI	COSFAR	COSKAX	COVXEQ	COXZAS10	COYROZ
COZKAD	COZKEH	COZKIL	CUCHUD	CUCVAY	CUDFOW	CUJQED
CUMQEI	CUNTAG	CUQVIU	CURPAI	CUYKEM01	CYTIAC	CYTIDI11
CYTOSC99	DABKOI	DABSOR	DADWEN	DAFTEK99	DAJWOB	DAPJAG
DAQHOS98	DAQHOS99	DAQYAV99	DASRIY	DASTAS	DASYEC99	DATTAU
DAXCAG01	DAYKAQ	DAYWEF	DAZVAB10	DEBHEX01	DECKUR	DELZAW
DEMYIE	DEPXUR	DERFAI	DERRIC	DESWUT	DETD0V	DETF0X

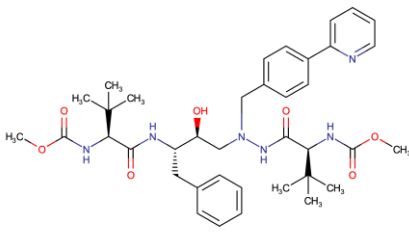
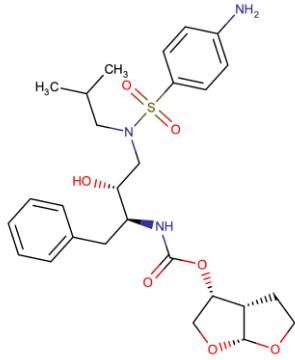
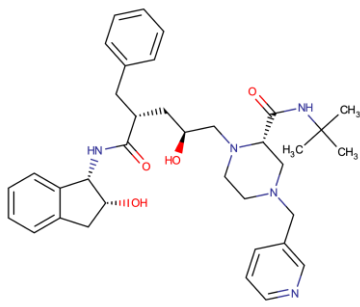
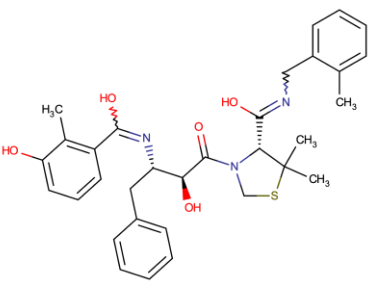
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DIKWIE	DINFAH01	DIPGIS12	DIUREA05	DIYHIC	DNBZFX01	DNPIMZ
DOBBIH	DOCYPO03	DODNUF	DOGBIK99	DOLBUC	DOMJUM	DOMQUS
DOQSUX01	DOTTIQ	DOVTAJ	DOWDEY98	DOWDEY99	DOXPOV	DOYNOU
DOZKOU	DOZMIO	DOZRIV	DUBCEI	DUBSID	DUCXAB	DUHMAW
DUHWAF	DUKSOR98	DUKSOR99	DUQPAH	DURYAS	DUSXOF	DUVGUX
DUXWIC	DUZYED	EKOKEU	ELEYID98	ELEYID99	ELINOC	EQONAZ
ERAHAG98	ERAHAG99	ESAMIU	EVENIC99	EVOTUE	EXOFOM95	EXOFOM96
EXOFOM97	EXOFOM98	EXOFOM99	FAGNEG99	FAGSUB	FAKKAD	FALBEA
FANYAV	FAPKEN99	FAVWIJ	FAWKUL	FAXPOJ99	FAZRAZ	FAZRED99
FECLUU	FECMEF	FECQAF	FEDBOF	FEFMAF	FEGSEP	FEHRIU
FEJJEJ	FELCIK	FEPNAP	FESPAU99	FESPEY	FESPOK	FETZEJ97
FETZEJ98	FETZEJ99	FEVQED	FICWAQ99	FICYOG	FIKCEI98	FIKCEI99
FIMPEW	FIPPEB	FIQKAS99	FISKIC99	FITJEX	FIWCOF	FLYITU
FOJQUQ02	FOKRUS	FOKWEI	FONFIY99	FONMOL	FORHAV	FORMYB01
FOVWAO	FOWREP	FOWVIX	FOYNUC	FOYXIA99	FUBWIJ	FUFYIP
FUFZAH	FUGJUM01	FUGQON01	FUNNUZ	FUNXAP	FUPDAX	FUQSAN
FUSDII	FUSNOY	FUTKUC	FUTLEN	FUWMOA	FUWTOG	FUXMES
FUXPIZ	FUYMES	GACTEM	GAFNAC	GAGSIR05	GAHCEY	GAHTEO
GAKGEE99	GAKPEN	GAKPIR	GAKZIC	GALHUX	GAMGAD	GAMKEK
GAMMOX	GARVOK99	GATPAS	GECLUX	GEDLEH98	GEDLEH99	GEDPIP98
GEDPIP99	GEFBIE	GEFTES	GEFTIW	GEJBIH99	GEJKUC97	GEJKUC98
GEJKUC99	GELGIN01	GELHIO10	GEPPIA	GERDOW98	GERDOW99	GERFEO
GETBOX	GEVREE	GEXQEF	GEYPOP	GEZVUC	GICCOK	GIMKAO
GIPCAL	GIQNOL	GIQYEK	GIQZOV	GIRKOI	GISLIF	GLCTSM
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GUSOIE	GUSXEZ	GUVCAD	GUWCOQ	GUXLAO	HABTEJ	HAFHIF97
HAFHIF98	HAFHIF99	HAJSAN	HAMROE	HAMZIF	HANLEP	HASVII
HEGFIJ95	HEGFIJ96	HEGFIJ97	HEGFIJ98	HEGFIJ99	HEGKIO	HEJCEE
HEMYON	HEPDUC	HEVDAO	HEXZEQ	HEZVEN	HIDXIB	HIFQES
HIFWOI	HISAPH97	HISAPH98	HISAPH99	HISTAN	HISTCM12	HISTPA1098
HIXGEA	HIYDIC	HIYJU099	HOHCOX	HOHGER	HOJKUO	HONLON
HOPJUR	HOQZAQ	HORN099	HORTAJ	HORZAQ	HORZOE	HORZUK
HOWYUP	HOYPER	HUGGEX	HUSCAZ98	HUSCAZ99	HUSNEP	HUXZOR
HYPRCX	HYPTHO	IBOCOT	IFIDUW97	IFIDUW98	IFIDUW99	IFIFAE
IGAYUK99	IGIHAI	IHIWIH	IJICIN97	IJICIN98	IJICIN99	IJIZAC
ILIDAI	ILOPUU	ILOQEH	INAYIH	INIFUI	IRISUY01	ISAXUX
ISOGAY	ISOGII	ISOGOO	ITEJEY	ITEMUR	ITESIL	ITICAR
ITIGAV	ITINOQ	ITUTEY	IVOMIR	IWIDEZ	IWILAB	IWOKEM
IWUGIQ	IXAXOW	IYAYIQ	JABCEX	JABMAD	JABSEN	JAFJAB98
JAFJAB99	JALQET	JAPPEV	JATWUW	JAXSEH	JAYNIG99	JEDBUQ
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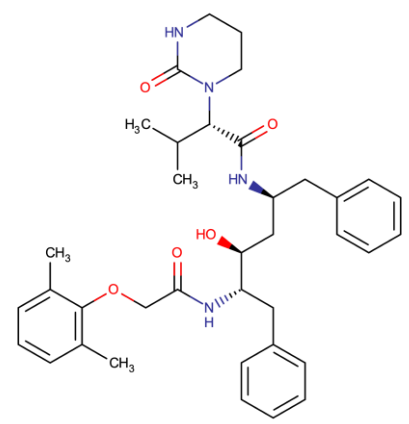
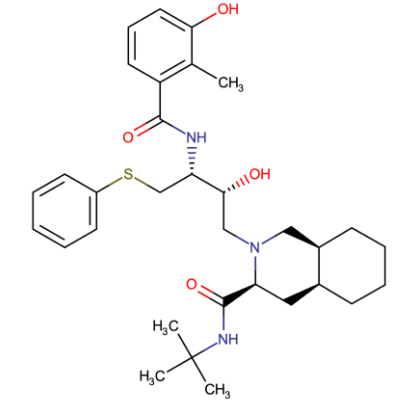
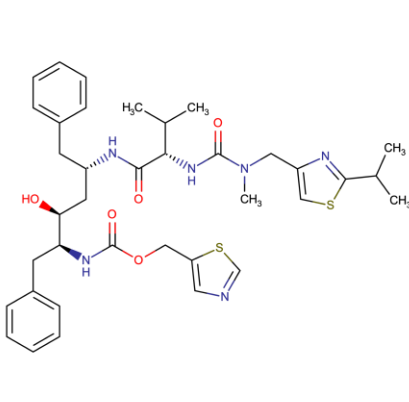
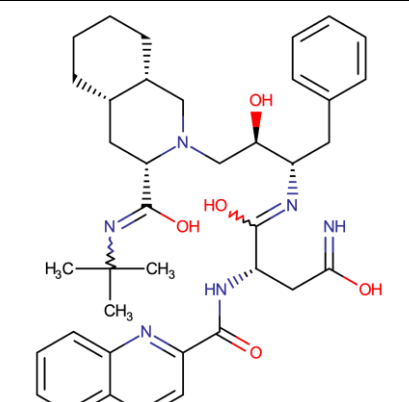
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JOWWIB	JOXDEF	JUDWEK	JUKNIO	JULXEV	JULZEX	JUMMEL
JUNBEB	JUPLOX	JURDIL	JURLIR	JURZED	KACTUE99	KADPUA
KAKLUE	KAPWAZ	KASNOH	KAYWIR01	KECFIJ	KECGO099	KEHZAY98
KEHZAY99	KEPHUI	KEPNUO	KERKIO1	KETLAX	KETSAF	KEZREM
KGULAM	KICJEL99	KIHVAY97	KIHVAY98	KIHVAY99	KIHVEC	KIKKIZ
KIMNID99	KISGAW	KITREK	KIWVIW	KOCHOZ	KOFKUL98	KOFKUL99
KOFLOG	KOJGUM	KOKBER98	KOMHAV01	KOTPEO	KOTXAU	KOVCAZ
KULREP	KUMZOJ	KUNBAY	KUNBIG	KUPGIN	KUPZUS	KUQBEF
KUSQEW	KUSQIA	KUTHOW	KUVYAC	KUXXUY	KUYBAJ	LABRUB98
LABRUB99	LABVIT98	LABVIT99	LALNIN03	LAPFIR98	LAPFIR99	LARGPH97
LARGPH98	LARGPH99	LAVHAR	LAXTIO98	LAXTIO99	LAXYOY98	LAXYOY99
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MOGZAK	MOGZEO	MOPMOT96	MOPMOT98	MOPMOT99	MOSRUH99	MOTJOU
MPHTAZ11	MPROLA10	MSMNIT	MUBVOV	MUGKAA01	MUHCOH98	MUHCOH99
MUJBIE	MUJTAM	MULFIK	MUNVAS98	MUNVAS99	MURYED99	MURYIH99
MUSYIJ	MUTDOW	MUYUYA	MUZNEC	NAFHUY	NAGGEH	NAGLEN98
NAGLEN99	NAJQOG	NALCYS02	NAMZAC	NAPRLA02	NARGIX99	NEFGAG98
NEFGAG99	NEQNIG	NETGIC97	NETGIC98	NETGIC99	NEZNAH	NIPBEV
NITRBE01	NIYDOO01	NMACEP01	NOKNOR	NOLHIF01	NOREPH01	NOWCAD99
NOZXEF	NUHJIK	NUHKIL	NUNFIL	NUPTAV	NURCEJ	NUTGEO99
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OJUHOS	OJUHUY	OKESOM	OKETUT	OLINEE	OQODOP	OQUPEW
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PABSOC	PAGXOL99	PAKWON	PAYWIX	PEFDOT	PEXTAN98	PEYSES
PHOGLY04	PINPAD01	PIPVAL	PIYKIR	PIZHAH	POBMIC	POJQEK98
POMDAW	PONTIV99	POTHRE01	POVKIU	PROAPH02	PUKVOI	PUMYIH
PUNJOZ	PURBAH	PURBEL	PURQOK	PURREB	PUSVIK	PUSYOT
QACLAH	QAFTUN	QAKWAB99	QANJUL98	QANJUL99	QAXDEY99	QAXDIC99
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QIJHUM98	QIJHUM99	QINGAV	QOTNAP	QUBVUE97	QUBVUE98	QUBVUE99
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RAXKAD96	RAXKAD97	RAXKAD98	RAXKAD99	RECZIJ	REDTUR	RESTOY
RIPGEE	RIQKEH	RISCUR	RIWBUV	RIWLAK99	RODFAR99	RUKCEH
RULHIR	RUNGAK	RUWFEU	SADMEQ99	SADMUG99	SAFFEK	SAHBUZ99
SAKHUI	SANPEE	SARZAM	SASBIX98	SASBIX99	SATCEW99	SATNAC
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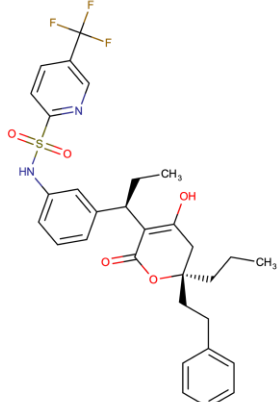
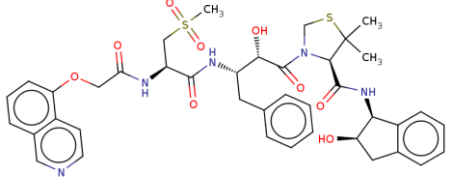
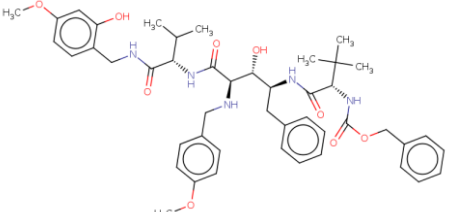
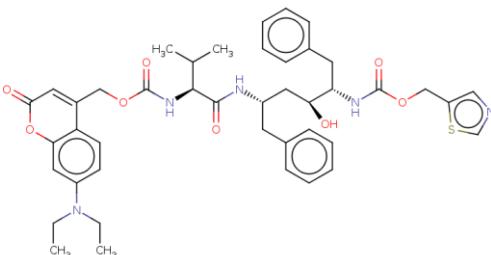
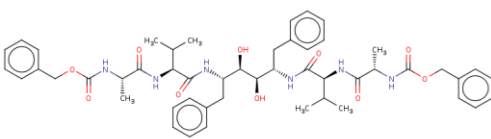
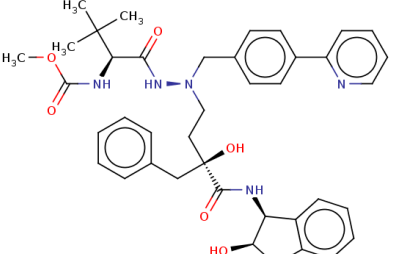
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SULBOS	SULSIC	SUMPAR99	SUNWUV	SURREC	TAHJIV99	TEDZUY
TEJDAN96	TEJDAN97	TEJDAN98	TEJDAN99	TEJMOK98	TEJMOK99	TEJNEB95
TEJNEB96	TEJNEB97	TEJNEB98	TEJNEB99	TEKNAY97	TEKNAY98	TEKNAY99
TEQZAR01	TERMIM99	TERNOT99	TERYAQ01	TERYAQ02	TEVHEH01	TIRPAL
TIXPIZ	TMEYPH	TODNUV97	TODNUV98	TODNUV99	TONQA099	TOZLOJ
TPHCUR97	TPHCUR98	TPHCUR99	TPYPOP10	TUBERC01	TUDMOU99	TUGWUN
TUGXAU	TUNTUT	TURYIQ	TURZEN	TUSVEK	TUWVOY	TUYWUH
UHAWUV	UNOCAB	VAFVUU	VALTUX97	VALTUX98	VANREH	VANRIL
VARNIM	VASSAL	VEFZIP	VEGKIB97	VEGKIB98	VEGKIB99	VELTIQ
VIGNII97	VIGNII98	VIGNII99	VINXAS	VIOLME98	VIOLME99	VIRYEA
VISVIC	VOCKIH	VOJJIN98	VOJJIN99	VOMKOZ	VOMZAY	VOVSAA
VOWGAP	VOWTEG98	VOWTEG99	VUMMIZ	VUMMOF	VUMMUL	VUPJUM
VUWCEW	VUXKAA99	VUXKEE	VUXKII	VUXKOO	VUXLAB	VUXLEF
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WEBFISmol1	WEJBIW	WEKHEA02	WELWUF	WEPMAH	WETNAK	WEVKEO
WIFREI	WIPCAZ98	WIPCAZ99	WIZZEL	WOBXAM	WOCSAI99	WOGWEV
WOLRUK	WOMCAC	WOMYEC	WONJAK	WOQZOR94	WOQZOR95	WOQZOR96
WOQZOR97	WOQZOR98	WOQZOR99	WOTZEK99	WOVXOU01	WUCZOL	WUKWEF
WUKWIJ	WUQPAB	WUSJEZ	WUXBIA99	XACMEBZ	XAJNIG	XANOPT99
XATXEV98	XATXEV99	XAZWOL99	XEGLAW98	XEGLAW99	XIHSEM96	XIHSEM97
XIHSEM98	XIHSEM99	XODXOF	XOPNEV	XORNOH	XOWGOF98	XOWGOF99
XOYFIA	XUCHAE	XUHQUM	XUJWUU	XUQPIK	XURNIJ	XUSTUC
XUTCEW	XUTDEX	XUZJUX01	YAJZUF	YALLON99	YANQEK99	YAYDAD
YAYSOH	YEHYOZ	YEMFOL99	YENKEH	YEQCIG98	YEQCIG99	YIRNOC
YOPSUR	YURNAA	ZAYJOY	ZAYPAQ99	ZEHKEC	ZEJMOQ99	ZETKUE
ZIKFOO99	ZILHOR02	ZONFOX	ZOZWAM	ZUMHUM	ZUPPAD	ZURLOP
ZUSXAO	ZUTFOL	ZUTKAC	ZUTKEG	ZZZSBA97	ZZZSPS99	ZZZUEE04

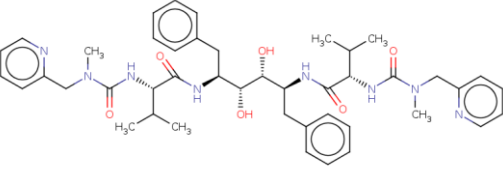
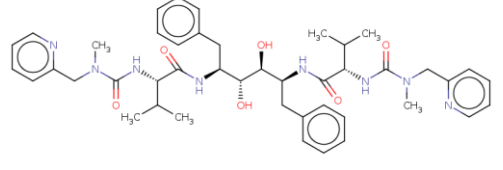
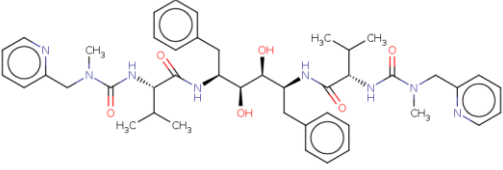
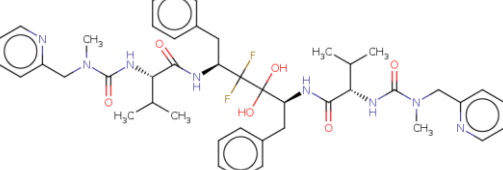
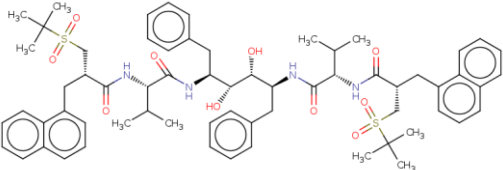
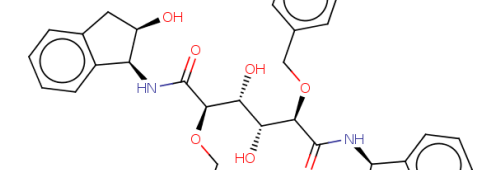
Table 4S. HIV-1 protease inhibitor compounds from the BindingDB database used in this study.

ID	Chemical Formula	Name	2D scheme
Amprenavir	C ₂₅ H ₃₅ N ₃ O ₆ S	Amprenavir	 <p>The image shows the 2D chemical structure of Amprenavir. It features a central nitrogen atom bonded to a methyl group, a methoxy group, and a chain containing a hydroxyl group, a benzyl group, and a hydroxamic acid group. The hydroxamic acid group is further substituted with a tetrahydrofuran ring. A sulfonamide group is attached to the nitrogen chain, which is in turn connected to a para-aminophenyl ring.</p>

Atazanavir	C ₃₈ H ₅₂ N ₆ O ₇ Atazanavir	 <p>The chemical structure of Atazanavir is a complex molecule featuring a central piperazine ring. It is substituted with a 4-(pyridin-2-yl)phenyl group, a 2-hydroxy-1-phenylethyl group, and a 2-(2S,3S)-2-methyl-3-methylbutanamide group. The piperazine ring also has a methyl group and a methoxycarbonyl group attached to it.</p>
Darunavir	C ₂₇ H ₃₇ N ₃ O ₇ S Darunavir	 <p>The chemical structure of Darunavir consists of a central piperazine ring. It is substituted with a 4-aminophenyl group, a 2-hydroxy-1-phenylethyl group, and a 2-(2S,3S)-2-methyl-3-methylbutanamide group. The piperazine ring also has a methyl group and a methoxycarbonyl group attached to it.</p>
Indinavir	C ₃₆ H ₄₇ N ₅ O ₄ Indinavir	 <p>The chemical structure of Indinavir features a central piperazine ring. It is substituted with a 2-hydroxy-1-phenylethyl group, a 2-(2S,3S)-2-methyl-3-methylbutanamide group, and a 2-(2S,3S)-2-methyl-3-methylbutanamide group. The piperazine ring also has a methyl group and a methoxycarbonyl group attached to it.</p>
JE-2147	C ₃₂ H ₃₇ N ₃ O ₅ S JE-2147	 <p>The chemical structure of JE-2147 is a complex molecule featuring a central piperazine ring. It is substituted with a 2-hydroxy-1-phenylethyl group, a 2-(2S,3S)-2-methyl-3-methylbutanamide group, and a 2-(2S,3S)-2-methyl-3-methylbutanamide group. The piperazine ring also has a methyl group and a methoxycarbonyl group attached to it.</p>

Lopinavir	$C_{37}H_{48}N_4O_5$	Lopinavir	 <p>The chemical structure of Lopinavir features a central piperidine ring. One nitrogen atom of the piperidine is part of a secondary amide group, which is further substituted with a 2,6-dimethylphenyl group. The other nitrogen atom of the piperidine is substituted with a 1-phenylethyl group. The 1-phenylethyl group is also substituted with a 2-hydroxy-1-phenylethyl group, which is in turn substituted with a 2,6-dimethylphenyl group.</p>
Nelfinavir	$C_{32}H_{45}N_3O_4S$	Nelfinavir	 <p>The chemical structure of Nelfinavir consists of a piperidine ring fused to a decalin system. The piperidine nitrogen is substituted with a 2,6-dimethylphenyl group. The decalin system is substituted with a 2-hydroxy-1-phenylethyl group, which is further substituted with a 2,6-dimethylphenyl group. A sulfur atom is attached to the 2,6-dimethylphenyl group via a methylene bridge.</p>
Ritonavir	$C_{37}H_{48}N_6O_5S_2$	Ritonavir	 <p>The chemical structure of Ritonavir is a complex molecule featuring a piperidine ring. The piperidine nitrogen is substituted with a 2,6-dimethylphenyl group. The piperidine ring is also substituted with a 2-hydroxy-1-phenylethyl group, which is further substituted with a 2,6-dimethylphenyl group. A sulfur atom is attached to the 2,6-dimethylphenyl group via a methylene bridge.</p>
Saquinavir	$C_{38}H_{50}N_6O_5$	Saquinavir	 <p>The chemical structure of Saquinavir features a piperidine ring. The piperidine nitrogen is substituted with a 2,6-dimethylphenyl group. The piperidine ring is also substituted with a 2-hydroxy-1-phenylethyl group, which is further substituted with a 2,6-dimethylphenyl group. A sulfur atom is attached to the 2,6-dimethylphenyl group via a methylene bridge.</p>

<p>Tipranavir</p>	<p>$C_{31}H_{33}F_3N_2O_5S$ Tipranavir</p>	 <p>The structure of Tipranavir features a central chromane ring system. It is substituted with a 4-(trifluoromethyl)phenylsulfonamide group, a methyl group, a hydroxyl group, a propyl group, and a benzyl group.</p>
<p>Cmpd7</p>	<p>$C_{40}H_{45}N_5O_9S_2$ KNI-10075</p>	 <p>The structure of KNI-10075 is a complex molecule with a central chromane core. It includes a methylsulfonamide group, a benzyl group, and a 1,2,3,4-tetrahydroquinoline ring system.</p>
<p>Cmpd42</p>	<p>$C_{46}H_{59}N_5O_9$ SDZ283-910</p>	 <p>The structure of SDZ283-910 is a complex molecule with a central chromane core. It features multiple amide linkages, methyl groups, and a 4-methoxyphenyl group.</p>
<p>Cmpd45</p>	<p>$C_{43}H_{51}N_5O_8S$</p>	 <p>The structure of Cmpd45 is a complex molecule with a central chromane core. It includes a diethylamino group, a methyl group, and a thiazole ring system.</p>
<p>Cmpd50</p>	<p>$C_{50}H_{64}N_6O_{10}$ TL-3, C2 symmetric inhibitor</p>	 <p>The structure of TL-3, C2 symmetric inhibitor is a complex molecule with a central chromane core. It features two benzyl groups and a 1,2,3,4-tetrahydroquinoline ring system.</p>
<p>Cmpd65</p>	<p>$C_{40}H_{47}N_5O_6$</p>	 <p>The structure of Cmpd65 is a complex molecule with a central chromane core. It includes a methyl group, a hydroxyl group, and a 1,2,3,4-tetrahydroquinoline ring system.</p>

Cmpd92	C ₄₄ H ₅₈ N ₈ O ₆	
Cmpd93	C ₄₄ H ₅₈ N ₈ O ₆	
Cmpd95	C ₄₄ H ₅₈ N ₈ O ₆	
Cmpd97	C ₄₄ H ₅₆ F ₂ N ₈ O ₆	
Cmpd115	C ₆₄ H ₈₂ N ₄ O ₁₀ S ₂	
Cmpd120	C ₃₈ H ₄₀ N ₂ O ₈	

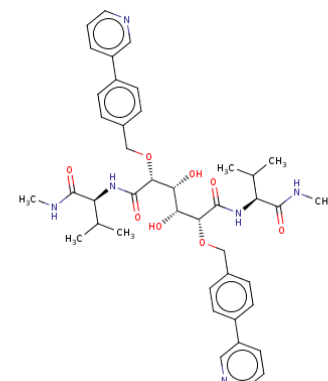
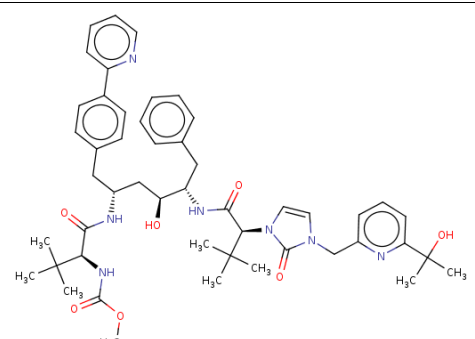
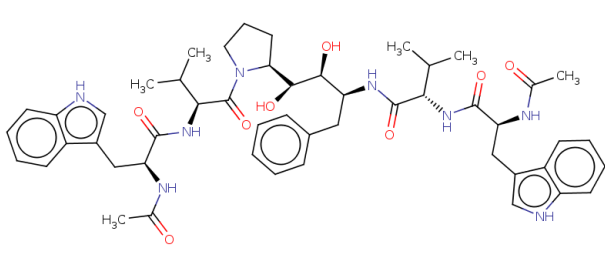
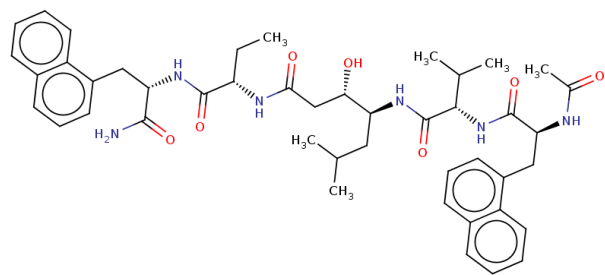
Cmpd127	$C_{42}H_{52}N_6O_8$ 
Cmpd188	$C_{49}H_{63}N_7O_7$ 
Cmpd213	$C_{50}H_{64}N_8O_8$ 
Cmpd251	$C_{45}H_{58}N_6O_7$ 

Table S5. Statistical descriptors of carbon, nitrogen, oxygen, sulfur and hydrogen pseudoatom values for atomic charge (e) computed for groups (C, N, O, S and H, respectively) and sub-groups divided basing on number of first neighbours (X_1 for one neighbour, X_3 for two, X_3 for three and X_4 for four, where X stands for label of element type) of pseudoatoms used to build the UBDB2018 databank. Trimmed mean - mean by dropping the top and bottom trim fraction by 10%. MAD - Median Absolute Deviation which is a robust measure of how spread out a set of data is ($MAD = median(|Y_i - median(Y_i)|)$). SE- standard error, the approximate standard deviation of a statistical sample population ($SE = \frac{\sigma}{\sqrt{n}}$).

	n	Mean	Standard deviation	Median	Trimmed mean	MAD	Min value	Max value	Range	Skew	Kurtosis	SE
Carbon												
C	12627	0.11	0.19	0.08	0.10	0.19	-0.57	0.78	1.35	0.33	0.05	0.00
C_2	177	-0.27	0.24	-0.36	-0.28	0.25	-0.57	0.25	0.82	0.30	-1.54	0.02
C_3	7289	0.00	0.11	0.00	0.00	0.12	-0.38	0.57	0.95	0.32	0.42	0.00
C_4	5161	0.27	0.16	0.26	0.27	0.17	-0.50	0.78	1.29	-0.13	0.06	0.00
Nitrogen												
N	2433	-0.01	0.09	-0.02	-0.01	0.08	-0.29	0.43	0.72	0.65	1.53	0.00
N_1	91	0.24	0.06	0.23	0.24	0.05	0.07	0.43	0.36	0.23	0.69	0.01
N_2	807	-0.03	0.06	-0.03	-0.03	0.05	-0.27	0.26	0.54	0.07	1.29	0.00
N_3	1420	0.00	0.08	-0.01	0.00	0.08	-0.29	0.33	0.62	-0.01	0.52	0.00
N_4	115	-0.12	0.07	-0.12	-0.12	0.05	-0.26	0.12	0.38	0.74	1.63	0.01
Oxygen												
O	3411	-0.20	0.08	-0.20	-0.20	0.08	-0.56	0.01	0.57	-0.70	1.74	0
O_1	1889	-0.19	0.09	-0.16	-0.18	0.08	-0.56	0.01	0.57	-1.08	1.37	0
O_2	1522	-0.22	0.05	-0.22	-0.22	0.05	-0.43	-0.01	0.42	0.21	0.78	0
Sulfur												
S	390	-0.24	0.16	-0.30	-0.25	0.12	-0.50	0.11	0.61	0.70	-0.97	0.01
S_1	56	-0.40	0.04	-0.40	-0.40	0.04	-0.50	-0.29	0.21	-0.07	0.60	0.01
S_2	229	-0.31	0.07	-0.32	-0.32	0.07	-0.44	-0.05	0.39	0.66	0.57	0.00
S_3	13	-0.05	0.04	-0.06	-0.05	0.04	-0.10	0.04	0.14	0.56	-1.03	0.01
S_4	92	0.02	0.04	0.02	0.02	0.04	-0.10	0.11	0.21	-0.06	0.08	0.00
Hydrogen												
H	9389	-0.02	0.10	-0.05	-0.03	0.07	-0.35	0.36	0.7	1.04	0.41	0

Table S5. Minimal (V_{\min} , e bohr⁻¹) and maximal (V_{\max} , e bohr⁻¹) values of potential, root mean square errors (RMSE, e bohr⁻¹) and correlation coefficients (Corr. Coef.) for molecular electrostatic potential grids computed from the UBDB, IAM and aug-PROmol models compared to the referential B3LYP/6-31G** method (REF). Molecules ordered according to the rising value of RMSE for UBDB.

	REF		UBDB				IAM				aug-PROmol			
	V_{\min}	V_{\max}	V_{\min}	V_{\max}	Corr.Coeff	RMSE	V_{\min}	V_{\max}	Corr.Coeff.	RMSE	V_{\min}	V_{\max}	Corr.Coeff.	RMSE
Cmpd127	-0.1061	97.49	-0.0935	99.91	0.9997	0.0085	0.0000	64.73	0.9742	0.0798	-0.1066	100.14	0.9986	0.0205
Cmpd50	-0.0838	123.14	-0.0963	125.41	0.9997	0.0087	0.0000	65.58	0.9750	0.0808	-0.0970	125.72	0.9987	0.0214
Cmpd97	-0.0974	115.35	-0.1180	114.54	0.9997	0.0093	0.0000	57.39	0.9772	0.0824	-0.1188	114.67	0.9985	0.0232
Cmpd92	-0.1004	209.16	-0.0955	207.39	0.9997	0.0100	0.0000	49.72	0.9163	0.1711	-0.1235	207.58	0.9986	0.0248
Cmpd95	-0.0977	163.41	-0.1004	163.70	0.9997	0.0105	0.0000	64.84	0.9546	0.1330	-0.1227	164.02	0.9987	0.0254
Lopinavir	-0.1054	167.21	-0.1175	56.36	0.9997	0.0106	0.0000	56.58	0.9543	0.1170	-0.1369	167.09	0.9985	0.0237
Cmpd93	-0.1051	83.70	-0.1008	83.70	0.9997	0.0107	0.0000	53.33	0.9916	0.0559	-0.1257	83.84	0.9983	0.0270
Cmpd188	-0.0968	103.79	-0.0766	103.54	0.9997	0.0110	0.0000	64.74	0.9810	0.0823	-0.1048	103.85	0.9986	0.0254
Cmpd251	-0.0894	190.82	-0.0951	196.99	0.9997	0.0112	0.0000	64.83	0.9210	0.1776	-0.1149	197.34	0.9987	0.0259
Saquinavir	-0.1031	69.81	-0.1167	70.61	0.9995	0.0121	0.0000	63.55	0.9945	0.0424	-0.1292	70.85	0.9981	0.0252
Cmpd213	-0.0970	87.12	-0.1152	87.47	0.9994	0.0128	0.0000	57.98	0.9841	0.0688	-0.1209	87.50	0.9985	0.0237
Atazanavir	-0.0859	116.93	-0.0849	119.26	0.9996	0.0128	0.0000	64.30	0.9812	0.0840	-0.1143	119.05	0.9986	0.0258
Cmpd45	-0.0939	126.85	-0.1023	126.82	0.9994	0.0131	0.0000	61.56	0.9737	0.0887	-0.1066	126.92	0.9987	0.0224
Cmpd120	-0.0838	54.99	-0.1159	56.13	0.9994	0.0138	0.0000	50.92	0.9954	0.0411	-0.1155	56.27	0.9985	0.0228
Cmpd115	-0.0778	117.20	-0.0954	114.61	0.9995	0.0138	0.0000	58.07	0.9823	0.0812	-0.1023	114.74	0.9984	0.0269
Cmpd42	-0.1063	55.70	-0.0890	55.66	0.9992	0.0140	0.0000	55.93	0.9941	0.0411	-0.1155	55.59	0.9983	0.0222
JE-2147	-0.0839	158.16	-0.0971	65.13	0.9993	0.0149	0.0000	158.47	0.9977	0.0322	-0.0993	158.42	0.9987	0.0228
Cmpd65	-0.0901	153.02	-0.1156	152.24	0.9993	0.0151	0.0000	63.83	0.9614	0.1118	-0.1091	152.04	0.9985	0.0240
Indinavir	-0.1026	132.80	-0.1309	134.19	0.9993	0.0153	0.0000	62.84	0.9656	0.1098	-0.1117	134.39	0.9984	0.0265
Darunavir	-0.0829	221.02	-0.0970	218.62	0.9996	0.0154	0.0000	115.03	0.8814	0.2639	-0.1152	218.87	0.9989	0.0265
Ritonavir	-0.1003	97.97	-0.1021	98.14	0.9993	0.0157	0.0000	65.49	0.9827	0.0764	-0.1304	98.32	0.9987	0.0229
Amprenavir	-0.0836	232.94	-0.0959	220.05	0.9995	0.0161	0.0000	64.70	0.9048	0.1924	-0.1088	220.18	0.9983	0.0262
Nelfinavir	-0.0961	75.50	-0.1342	75.32	0.9991	0.0164	0.0000	50.60	0.9883	0.0581	-0.1223	75.63	0.9984	0.0238
Cmpd7	-0.1070	64.99	-0.1045	63.66	0.9986	0.0219	0.0000	63.82	0.9957	0.0417	-0.1089	63.67	0.9983	0.0263
Tipranavir	-0.0910	64.47	-0.1172	64.29	0.9961	0.0322	0.0000	56.66	0.9963	0.0342	-0.1079	64.36	0.9984	0.0236

Table S6. The statistical quantitative descriptors of electrostatic potential at the van der Waals surface (Positive Average Potential (V_{av}^+ , e bohr⁻¹), Negative Average Potential (V_{av}^- , e bohr⁻¹) and their variance (σ^+ , σ^- , e bohr⁻¹), Average Deviation (π , e² bohr⁻²), Minimal (V_{min} , e bohr⁻¹) and maximal (V_{max} , e bohr⁻¹) values of potential evaluated as described in the original paper by Politzer et al. (Murray & Politzer, 1998; Formis *et al.*, 2000) using van der Waals surface thickness of 0.3 bohr.

	REF							
	V_{av}^+	σ^+	V_{av}^-	σ^-	Vav.	π	V_{max}	V_{min}
Cmpd127	0.0173	0.0148	-0.0218	0.0175	0.0005	0.0194	0.0982	-0.0896
Cmpd50	0.0182	0.0142	-0.0196	0.0164	0.0005	0.0177	0.0861	-0.0725
Cmpd97	0.0178	0.0122	-0.0205	0.0188	0.0005	0.0191	0.0794	-0.0840
Cmpd92	0.0165	0.0113	-0.0208	0.0192	0.0005	0.0187	0.0654	-0.0855
Cmpd95	0.0166	0.0128	-0.0189	0.0181	0.0005	0.0176	0.0834	-0.0839
Lopinavir	0.0121	0.0095	-0.0172	0.0164	0.0004	0.0145	0.0802	-0.0934
Cmpd93	0.0174	0.0130	-0.0211	0.0197	0.0006	0.0192	0.0786	-0.0895
Cmpd188	0.0151	0.0113	-0.0189	0.0162	0.0004	0.0162	0.0746	-0.0801
Cmpd251	0.0190	0.0150	-0.0214	0.0178	0.0005	0.0196	0.0853	-0.0754
Saquinavir	0.0158	0.0126	-0.0226	0.0222	0.0007	0.0191	0.0673	-0.0908
Cmpd213	0.0169	0.0145	-0.0221	0.0178	0.0005	0.0196	0.0762	-0.0817
Atazanavir	0.0152	0.0113	-0.0198	0.0178	0.0004	0.0170	0.0779	-0.0745
Cmpd45	0.0178	0.0115	-0.0209	0.0179	0.0005	0.0190	0.0656	-0.0833
Cmpd120	0.0173	0.0155	-0.0220	0.0159	0.0005	0.0197	0.0951	-0.0723
Cmpd115	0.0185	0.0130	-0.0215	0.0158	0.0004	0.0194	0.0819	-0.0700
Cmpd42	0.0158	0.0129	-0.0206	0.0174	0.0005	0.0181	0.0880	-0.0878
JE-2147	0.0117	0.0091	-0.0147	0.0112	0.0002	0.0131	0.0795	-0.0703
Cmpd65	0.0140	0.0096	-0.0189	0.0165	0.0004	0.0161	0.0666	-0.0807
Indinavir	0.0154	0.0105	-0.0222	0.0195	0.0005	0.0171	0.0685	-0.0860
Darunavir	0.0203	0.0136	-0.0236	0.0192	0.0006	0.0205	0.0839	-0.0766
Ritonavir	0.0166	0.0114	-0.0208	0.0189	0.0005	0.0180	0.0693	-0.0859
Amprenavir	0.0186	0.0148	-0.0238	0.0193	0.0006	0.0202	0.0810	-0.0730
Nelfinavir	0.0168	0.0133	-0.0221	0.0192	0.0005	0.0183	0.0822	-0.0831
Cmpd7	0.0219	0.0154	-0.0218	0.0159	0.0005	0.0219	0.1044	-0.0913
Tipranavir	0.0175	0.0132	-0.0190	0.0171	0.0005	0.0172	0.0841	-0.0799

Table S6. Cont.

	UBDB								aug-PROMol						
	V_{av}^+	σ^+	V_{av}^-	σ^-	Vav.	π	V_{max}	V_{min}	V_{av}^+	σ^+	V_{av}^-	σ^-	Vav.	V_{max}	V_{min}
Cmpd127	0.0214	0.0157	-0.0256	0.0189	-0.0050	0.0236	0.0963	-0.0845	0.0233	0.0175	-0.0275	0.0211	0.0020	0.1225	-0.0864
Cmpd50	0.0237	0.0166	-0.0246	0.0193	0.0031	0.0237	0.0944	-0.0858	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Cmpd97	0.0222	0.0147	-0.0260	0.0212	-0.0004	0.0240	0.0821	-0.1051	0.0208	0.0143	-0.0262	0.0230	0.0014	0.1021	-0.1089
Cmpd92	0.0200	0.0138	-0.0242	0.0190	-0.0011	0.0220	0.0806	-0.0836	0.0208	0.0141	-0.0267	0.0235	-0.0015	0.0840	-0.1003
Cmpd95	0.0211	0.0155	-0.0234	0.0190	0.0005	0.0221	0.0966	-0.0888	0.0207	0.0152	-0.0254	0.0214	0.0009	0.1011	-0.1005
Lopinavir	0.0144	0.0110	-0.0240	0.0212	-0.0008	0.0193	0.0788	-0.1116	0.0211	0.0144	-0.0295	0.0268	0.0015	0.1093	-0.1131
Cmpd93	0.0227	0.0164	-0.0253	0.0197	-0.0004	0.0239	0.0931	-0.0892	0.0207	0.0155	-0.0274	0.0243	0.0005	0.0993	-0.1042
Cmpd188	0.0227	0.0161	-0.0211	0.0154	0.0027	0.0218	0.0915	-0.0668	0.0194	0.0137	-0.0232	0.0188	0.0039	0.1078	-0.0855
Cmpd251	0.0207	0.0154	-0.0249	0.0208	0.0005	0.0227	0.0899	-0.0847	0.0260	0.0205	-0.0298	0.0230	0.0047	0.1333	-0.0942
Saquinavir	0.0216	0.0130	-0.0361	0.0267	-0.0014	0.0290	0.0947	-0.1045	0.0202	0.0143	-0.0327	0.0290	-0.0002	0.0874	-0.1131
Cmpd213	0.0211	0.0174	-0.0262	0.0234	-0.0063	0.0238	0.0861	-0.1069	0.0212	0.0158	-0.0297	0.0220	-0.0006	0.0929	-0.1010
Atazanavir	0.0192	0.0110	-0.0262	0.0188	-0.0006	0.0223	0.0721	-0.0810	0.0186	0.0122	-0.0266	0.0209	0.0019	0.0911	-0.0951
Cmpd45	0.0270	0.0155	-0.0291	0.0201	0.0028	0.0276	0.0873	-0.0892	0.0207	0.0139	-0.0252	0.0202	0.0032	0.0936	-0.0912
Cmpd120	0.0214	0.0124	-0.0338	0.0231	-0.0039	0.0279	0.0739	-0.1053	0.0222	0.0182	-0.0280	0.0210	-0.0016	0.1223	-0.0961
Cmpd115	0.0209	0.0152	-0.0231	0.0206	0.0006	0.0219	0.0840	-0.0869	0.0226	0.0160	-0.0268	0.0196	0.0038	0.1279	-0.0846
Cmpd42	0.0258	0.0181	-0.0249	0.0180	-0.0034	0.0252	0.1068	-0.0794	0.0208	0.0154	-0.0260	0.0201	0.0018	0.1038	-0.0982
JE-2147	0.0193	0.0119	-0.0261	0.0190	-0.0022	0.0001	0.0734	-0.0914	0.0265	0.0162	-0.0255	0.0196	0.0088	0.1038	-0.0812
Cmpd65	0.0195	0.0130	-0.0282	0.0214	-0.0004	0.0241	0.0705	-0.1098	0.0173	0.0110	-0.0258	0.0206	0.0000	0.0775	-0.1057
Indinavir	0.0219	0.0132	-0.0277	0.0221	0.0014	0.0241	0.0870	-0.1146	0.0200	0.0124	-0.0291	0.0240	0.0036	0.0916	-0.1017
Darunavir	0.0247	0.0166	-0.0284	0.0220	0.0025	0.0259	0.1023	-0.0881	0.0253	0.0168	-0.0290	0.0227	0.0055	0.1074	-0.0968
Ritonavir	0.0290	0.0183	-0.0274	0.0210	0.0072	0.0274	0.0971	-0.0882	0.0193	0.0130	-0.0276	0.0238	0.0025	0.0846	-0.1056
Amprenavir	0.0238	0.0179	-0.0295	0.0226	0.0016	0.0260	0.1009	-0.0874	0.0238	0.0171	-0.0294	0.0221	0.0039	0.0900	-0.0915
Nelfinavir	0.0291	0.0171	-0.0342	0.0289	0.0022	0.0339	0.1133	-0.1278	0.0220	0.0157	-0.0290	0.0251	0.0030	0.0929	-0.1050
Cmpd7	0.0270	0.0208	-0.0314	0.0242	0.0024	0.0292	0.1142	-0.0970	0.0266	0.0187	-0.0275	0.0190	0.0016	0.1533	-0.0925
Tipranavir	0.0178	0.0114	-0.0229	0.0262	0.0056	0.0457	0.1093	-0.1094	0.0229	0.0165	-0.0224	0.0205	0.0073	0.1003	-0.0918