wwPDB X-ray Structure Validation Summary Report (i)

Aug 6, 2023 – 11:07 AM EDT

PDB ID	:	1KKQ
Title	:	Crystal structure of the human PPAR-alpha ligand-binding domain in complex with an antagonist GW6471 and a SMRT corepressor motif
Authors	:	Xu, H.E.; Stanley, T.B.; Montana, V.G.; Lambert, M.H.; Shearer, B.G.; Cobb, J.E.; McKee, D.D.; Galardi, C.M.; Nolte, R.T.; Parks, D.J.
Deposited on	:	2001-12-10
Resolution	:	3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

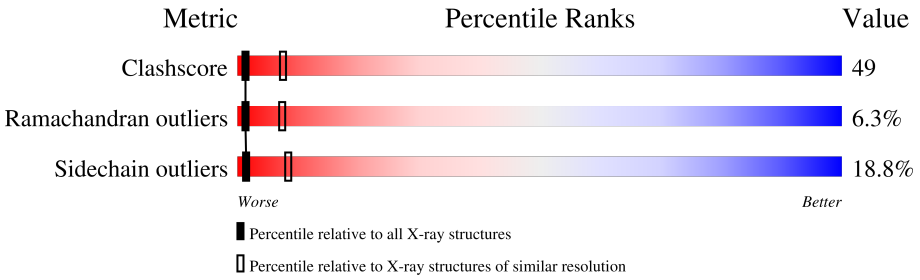
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	269	38% 48% 14%
1	B	269	43% 43% 12% •
1	C	269	39% 44% 13% •
1	D	269	44% 39% 15% •
2	E	19	16% 37% 37% 11%
2	F	19	32% 32% 32% 5%
2	G	19	37% 42% 21%
2	H	19	47% 26% 21% 5%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9606 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

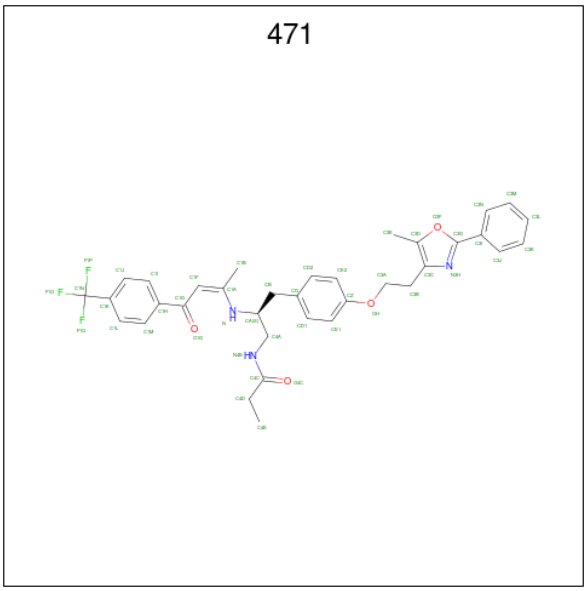
- Molecule 1 is a protein called PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	0	0
			2128	1365	357	388	18			
1	B	269	Total	C	N	O	S	0	0	0
			2128	1365	357	388	18			
1	C	269	Total	C	N	O	S	0	0	0
			2128	1365	357	388	18			
1	D	269	Total	C	N	O	S	0	0	0
			2128	1365	357	388	18			

- Molecule 2 is a protein called NUCLEAR RECEPTOR CO-REPRESSOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	19	Total	C	N	O	S	0	0	0
			145	94	24	25	2			
2	F	19	Total	C	N	O	S	0	0	0
			149	97	25	25	2			
2	G	19	Total	C	N	O	S	0	0	0
			145	94	24	25	2			
2	H	19	Total	C	N	O	S	0	0	0
			145	94	24	25	2			

- Molecule 3 is N-((2S)-2-({(1Z)-1-METHYL-3-OXO-3-[4-(TRIFLUOROMETHYL) PHENYL]PROP-1-ENYL}AMINO)-3-{4-[2-(5-METHYL-2-PHENYL-1,3-OXAZOL-4-YL)ETHOXY]PHENYL}PROPYL)PROPANAMIDE (three-letter code: 471) (formula: $C_{35}H_{36}F_3N_3O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C F N O 45 35 3 3 4	0	0
3	B	1	Total C F N O 45 35 3 3 4	0	0
3	C	1	Total C F N O 45 35 3 3 4	0	0
3	D	1	Total C F N O 45 35 3 3 4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	61	Total O 61 61	0	0
4	B	108	Total O 108 108	0	0
4	C	55	Total O 55 55	0	0
4	D	87	Total O 87 87	0	0
4	E	4	Total O 4 4	0	0
4	F	10	Total O 10 10	0	0
4	G	1	Total O 1 1	0	0
4	H	4	Total O 4 4	0	0

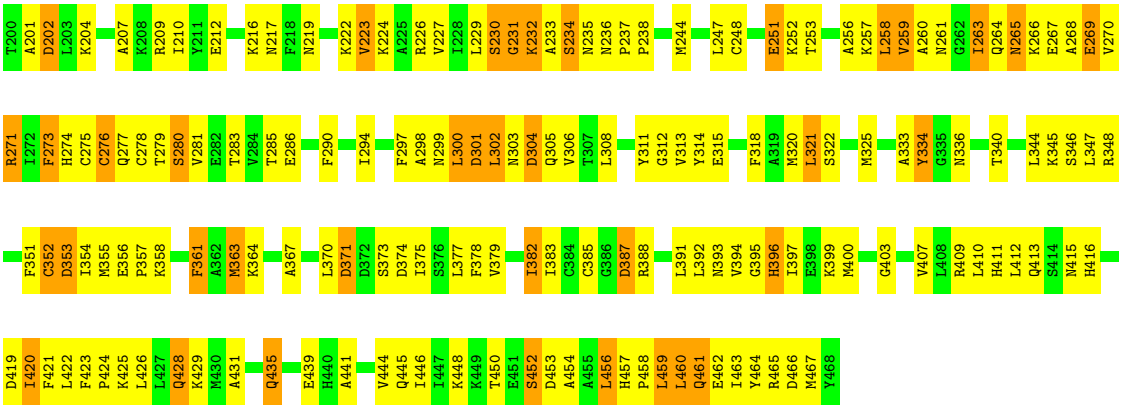
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

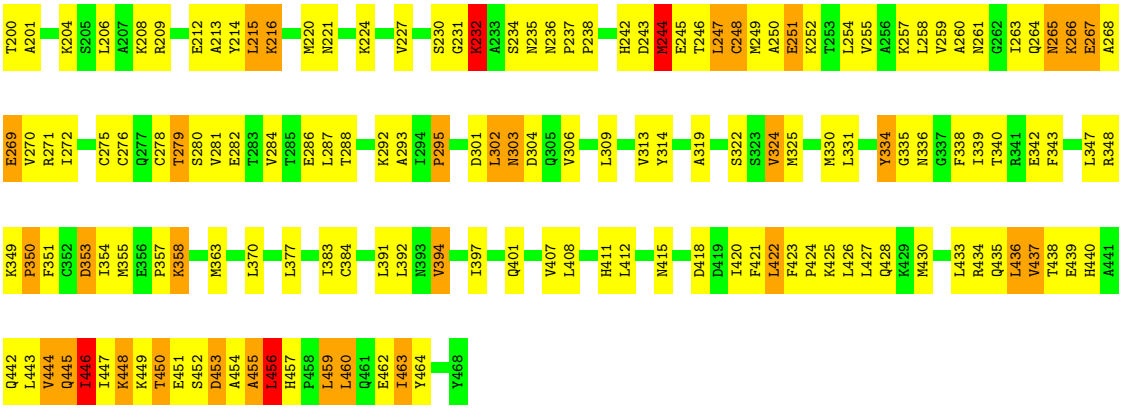
• Molecule 1: PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR

Chain A:



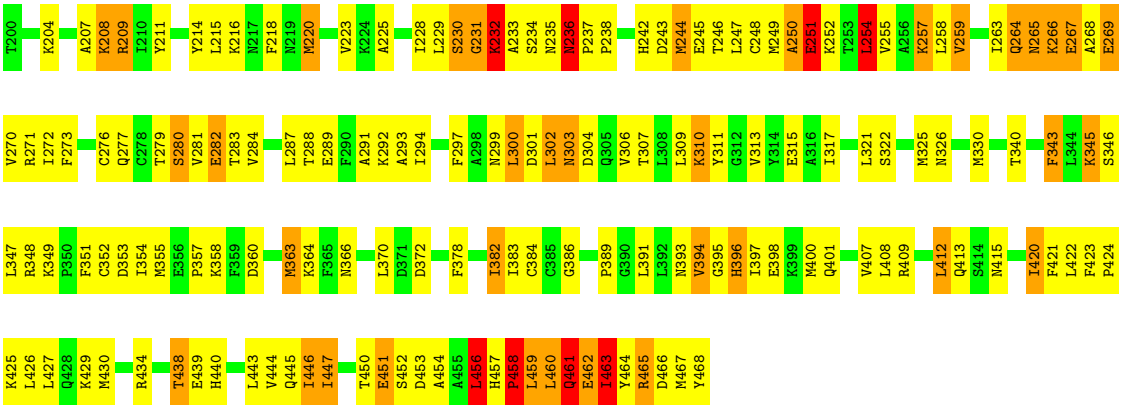
• Molecule 1: PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR

Chain B:



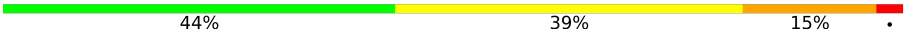
• Molecule 1: PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR

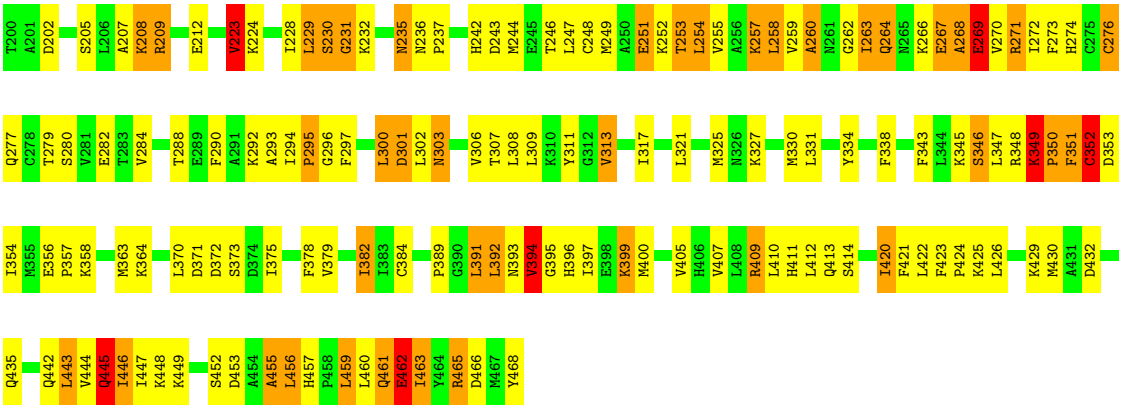
Chain C:



• Molecule 1: PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR

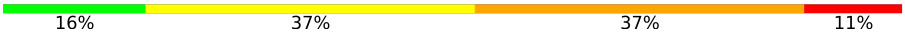
Chain D:





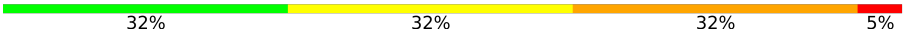
• Molecule 2: NUCLEAR RECEPTOR CO-REPRESSOR 2

Chain E:



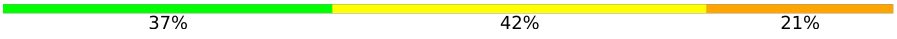
• Molecule 2: NUCLEAR RECEPTOR CO-REPRESSOR 2

Chain F:



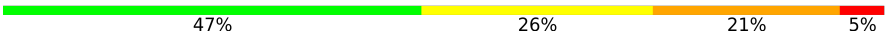
• Molecule 2: NUCLEAR RECEPTOR CO-REPRESSOR 2

Chain G:



• Molecule 2: NUCLEAR RECEPTOR CO-REPRESSOR 2

Chain H:


47%
26%
21%
5%


N682
M683
G684
L685
E686
I689
R690
L693
Y697
D698
Q699
W700

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	103.41Å 112.77Å 123.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.99 – 3.00	Depositor
% Data completeness (in resolution range)	98.8 (20.99-3.00)	Depositor
R_{merge}	0.02	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNX 2000	Depositor
R, R_{free}	0.258 , 0.290	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9606	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 471

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.40	0/2166	0.79	2/2920 (0.1%)
1	B	0.42	0/2166	0.82	2/2920 (0.1%)
1	C	0.39	0/2166	0.79	6/2920 (0.2%)
1	D	0.44	0/2166	0.78	3/2920 (0.1%)
2	E	0.63	0/147	0.99	1/195 (0.5%)
2	F	0.43	0/151	1.01	1/199 (0.5%)
2	G	0.55	0/147	1.17	2/195 (1.0%)
2	H	0.45	0/147	0.91	0/195
All	All	0.42	0/9256	0.81	17/12464 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	451	GLU	N-CA-C	-7.76	90.04	111.00
2	F	695	GLY	N-CA-C	7.60	132.10	113.10
1	C	461	GLN	N-CA-C	-7.52	90.69	111.00
1	B	267	GLU	N-CA-C	-7.34	91.18	111.00
1	D	236	ASN	N-CA-C	-7.16	91.66	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	349	LYS	Mainchain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2128	0	2168	199	0
1	B	2128	0	2168	206	0
1	C	2128	0	2168	222	0
1	D	2128	0	2168	206	0
2	E	145	0	138	36	0
2	F	149	0	149	39	0
2	G	145	0	138	29	0
2	H	145	0	138	18	0
3	A	45	0	36	1	0
3	B	45	0	35	8	0
3	C	45	0	36	2	0
3	D	45	0	35	3	0
4	A	61	0	0	3	0
4	B	108	0	0	5	0
4	C	55	0	0	7	0
4	D	87	0	0	8	0
4	E	4	0	0	1	0
4	F	10	0	0	3	0
4	G	1	0	0	1	0
4	H	4	0	0	1	0
All	All	9606	0	9377	916	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 49.

The worst 5 of 916 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:688:ILE:HD13	2:G:689:ILE:N	1.32	1.43
1:D:348:ARG:O	1:D:349:LYS:CG	1.74	1.35
2:G:685:LEU:O	2:G:688:ILE:CD1	1.92	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:GLU:HG3	1:A:348:ARG:HH11	1.09	1.16
1:D:348:ARG:O	1:D:349:LYS:HG2	1.33	1.14

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	267/269 (99%)	205 (77%)	46 (17%)	16 (6%)	1 9
1	B	267/269 (99%)	222 (83%)	31 (12%)	14 (5%)	2 12
1	C	267/269 (99%)	198 (74%)	50 (19%)	19 (7%)	1 5
1	D	267/269 (99%)	214 (80%)	35 (13%)	18 (7%)	1 6
2	E	17/19 (90%)	9 (53%)	6 (35%)	2 (12%)	0 1
2	F	17/19 (90%)	11 (65%)	5 (29%)	1 (6%)	1 9
2	G	17/19 (90%)	14 (82%)	2 (12%)	1 (6%)	1 9
2	H	17/19 (90%)	14 (82%)	2 (12%)	1 (6%)	1 9
All	All	1136/1152 (99%)	887 (78%)	177 (16%)	72 (6%)	1 7

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	234	SER
1	A	256	ALA
1	A	346	SER
1	B	448	LYS
1	B	455	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	234/235 (100%)	190 (81%)	44 (19%)	1 8
1	B	234/235 (100%)	193 (82%)	41 (18%)	2 10
1	C	234/235 (100%)	202 (86%)	32 (14%)	3 17
1	D	234/235 (100%)	189 (81%)	45 (19%)	1 8
2	E	12/15 (80%)	4 (33%)	8 (67%)	0 0
2	F	13/15 (87%)	7 (54%)	6 (46%)	0 0
2	G	12/15 (80%)	8 (67%)	4 (33%)	0 1
2	H	12/15 (80%)	7 (58%)	5 (42%)	0 0
All	All	985/1000 (98%)	800 (81%)	185 (19%)	1 8

5 of 185 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	463	ILE
1	D	382	ILE
1	D	209	ARG
1	D	269	GLU
1	D	414	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	440	HIS
1	D	299	ASN
1	C	445	GLN
1	D	242	HIS
1	D	393	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	471	C	777	-	43,48,48	2.01	15 (34%)	52,66,66	1.35	4 (7%)
3	471	D	778	-	43,48,48	1.97	16 (37%)	52,66,66	1.50	5 (9%)
3	471	A	775	-	43,48,48	1.98	16 (37%)	52,66,66	1.23	5 (9%)
3	471	B	776	-	43,48,48	2.00	15 (34%)	52,66,66	1.70	7 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	471	C	777	-	-	9/34/39/39	0/4/4/4
3	471	D	778	-	-	5/34/39/39	0/4/4/4
3	471	A	775	-	-	9/34/39/39	0/4/4/4
3	471	B	776	-	-	9/34/39/39	0/4/4/4

The worst 5 of 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	777	471	C1H-C1G	-6.22	1.40	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	776	471	C1H-C1G	-6.10	1.40	1.49
3	A	775	471	C1H-C1G	-5.81	1.40	1.49
3	D	778	471	C1H-C1G	-5.81	1.40	1.49
3	B	776	471	C1A-N	4.53	1.39	1.33

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	778	471	C4A-CA-N	5.82	121.89	109.05
3	B	776	471	C1B-C1A-N	5.79	125.31	118.82
3	B	776	471	C4A-CA-N	5.78	121.82	109.05
3	B	776	471	C1F-C1A-N	-4.97	117.31	121.29
3	D	778	471	C1B-C1A-N	4.89	124.30	118.82

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	775	471	N4B-C4A-CA-CB
3	B	776	471	C4A-CA-N-C1A
3	B	776	471	N4B-C4A-CA-N
3	C	777	471	N4B-C4A-CA-N
3	C	777	471	C1F-C1G-C1H-C1I

There are no ring outliers.

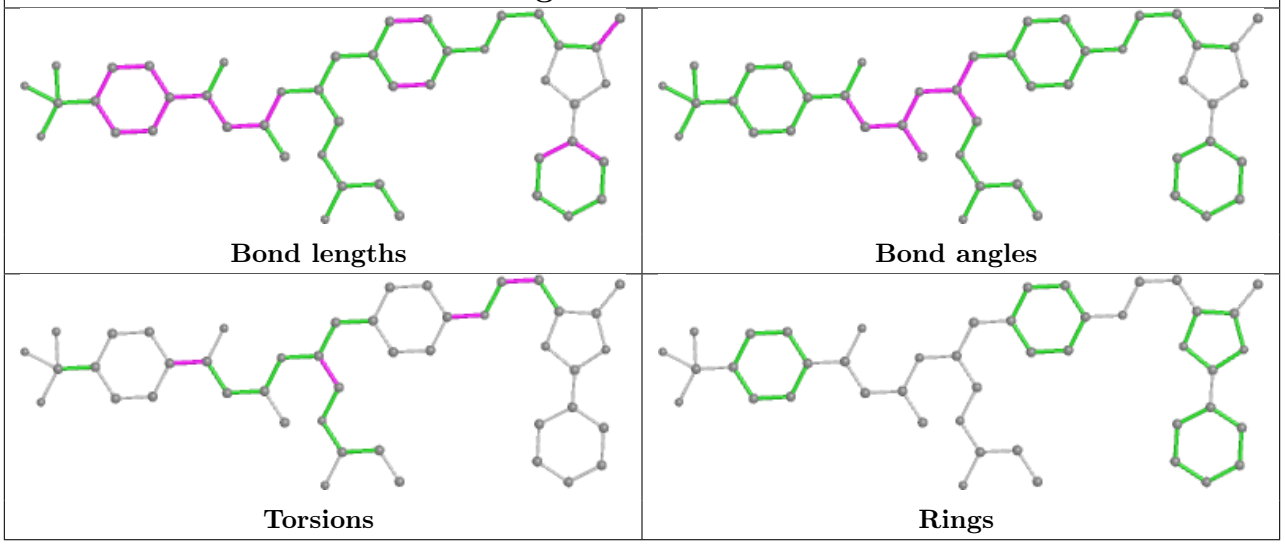
4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	777	471	2	0
3	D	778	471	3	0
3	A	775	471	1	0
3	B	776	471	8	0

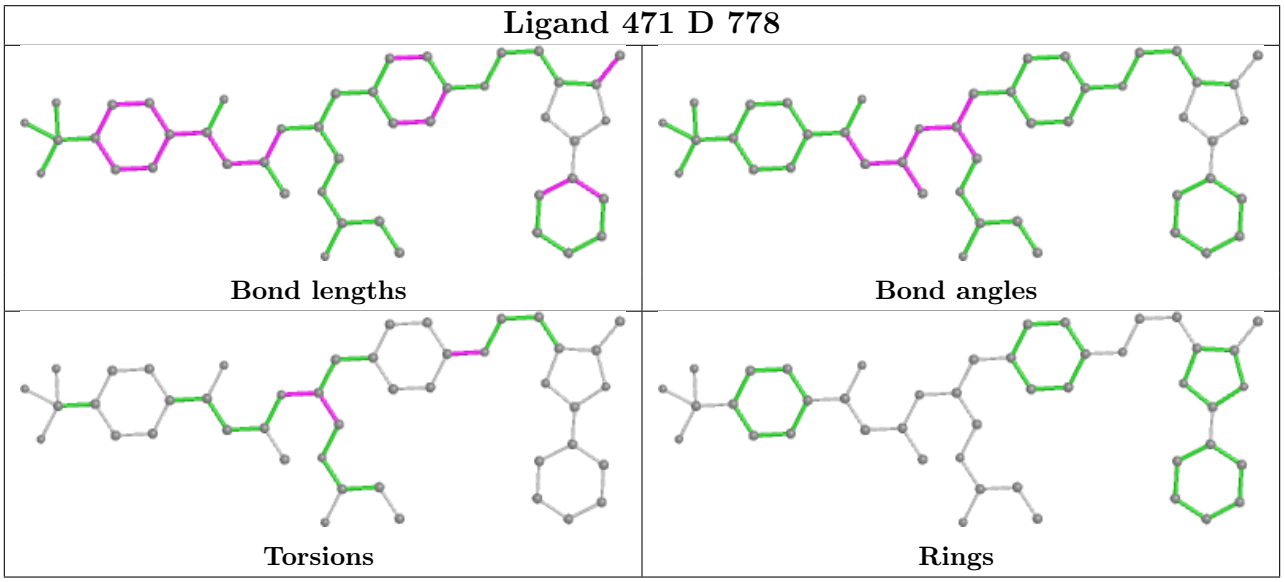
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

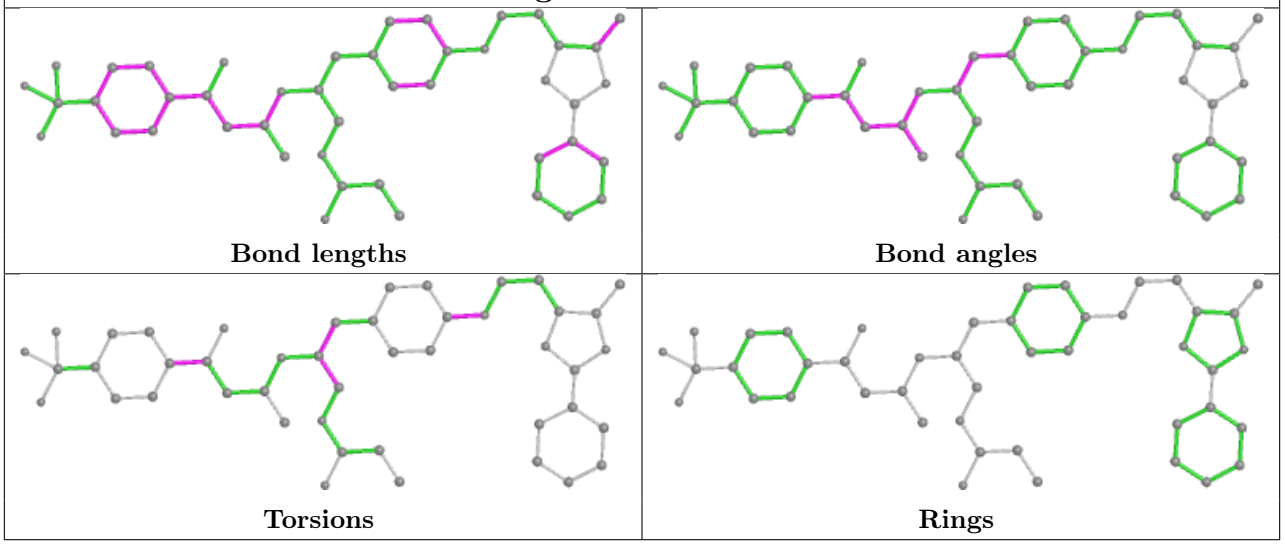
Ligand 471 C 777



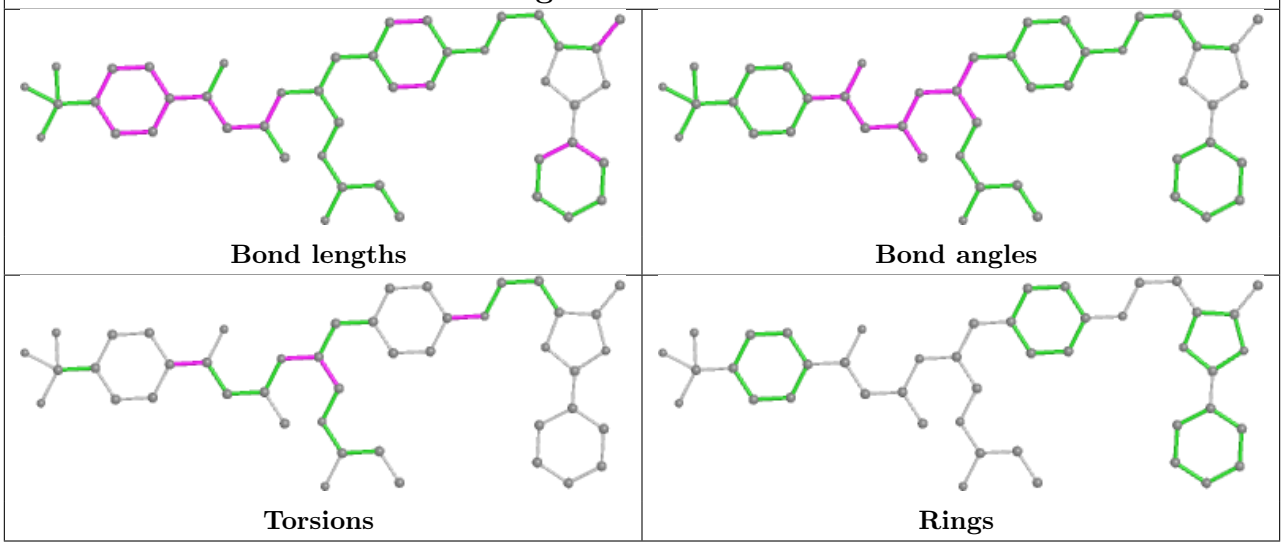
Ligand 471 D 778



Ligand 471 A 775



Ligand 471 B 776



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.