Full wwPDB X-ray Structure Validation Report ⓘ

Aug 28, 2023 – 03:07 AM EDT

PDB ID	:	3KME
Title	:	Crystal structure of catalytic domain of TACE with phenyl-pyrrolidinyl-tartrate inhibitor
Authors	:	Orth, P.
Deposited on	:	2009-11-10
Resolution	:	1.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ 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 ⓘ) were used in the production of this report:

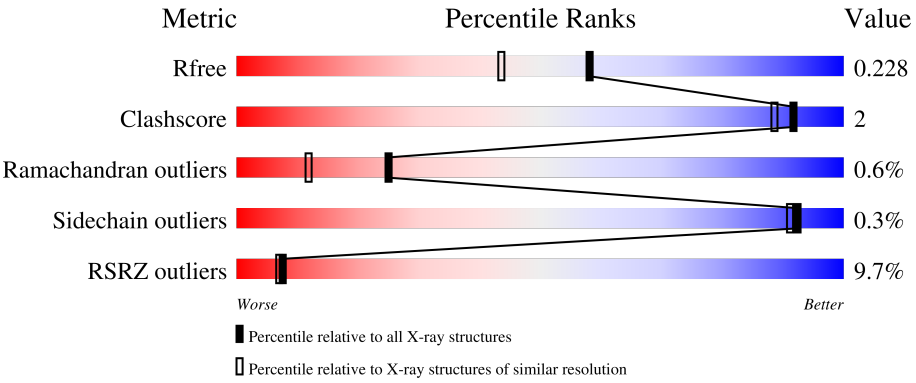
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 1.85 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))
R_{free}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	270	6% 91% · 6%
1	B	270	13% 89% 6% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	INN	A	485	-	X	-	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4256 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 TNF-alpha-converting enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	1	0
			1963	1240	326	384	13			
1	B	254	Total	C	N	O	S	0	1	0
			1933	1222	322	376	13			

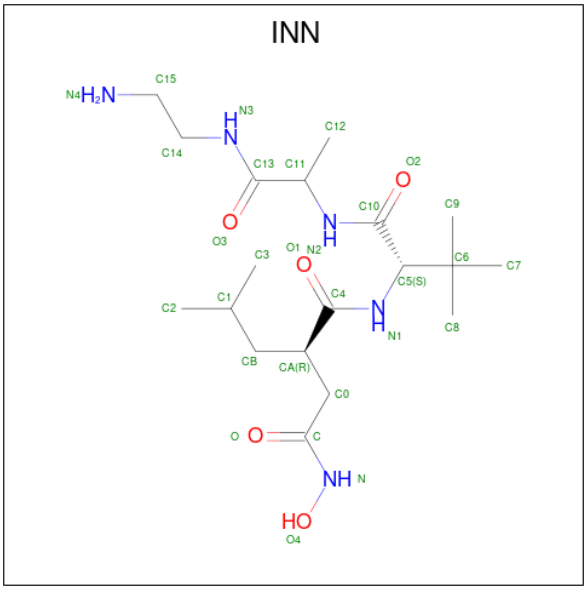
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	266	ALA	SER	engineered mutation	UNP P78536
A	353	GLY	VAL	engineered mutation	UNP P78536
A	452	GLN	ASN	engineered mutation	UNP P78536
A	477	GLY	-	expression tag	UNP P78536
A	478	SER	-	expression tag	UNP P78536
A	479	HIS	-	expression tag	UNP P78536
A	480	HIS	-	expression tag	UNP P78536
A	481	HIS	-	expression tag	UNP P78536
A	482	HIS	-	expression tag	UNP P78536
A	483	HIS	-	expression tag	UNP P78536
A	484	HIS	-	expression tag	UNP P78536
B	266	ALA	SER	engineered mutation	UNP P78536
B	353	GLY	VAL	engineered mutation	UNP P78536
B	452	GLN	ASN	engineered mutation	UNP P78536
B	477	GLY	-	expression tag	UNP P78536
B	478	SER	-	expression tag	UNP P78536
B	479	HIS	-	expression tag	UNP P78536
B	480	HIS	-	expression tag	UNP P78536
B	481	HIS	-	expression tag	UNP P78536
B	482	HIS	-	expression tag	UNP P78536
B	483	HIS	-	expression tag	UNP P78536
B	484	HIS	-	expression tag	UNP P78536

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

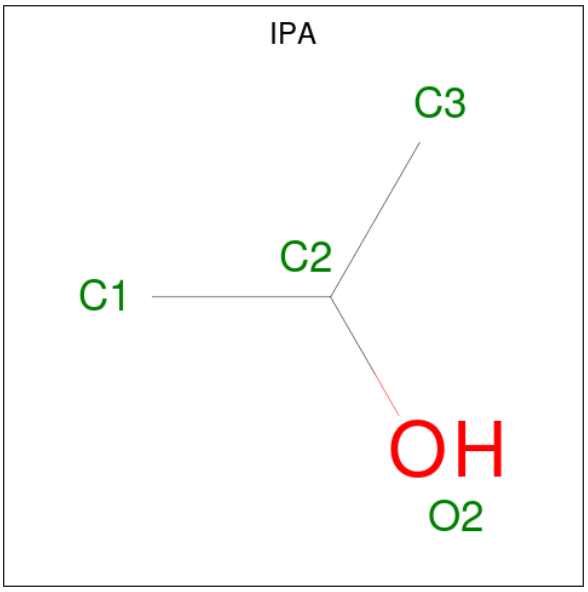
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is N-{(2R)-2-[2-(hydroxyamino)-2-oxoethyl]-4-methylpentanoyl}-3-methyl-L-valyl-N-(2-aminoethyl)-L-alaninamide (three-letter code: INN) (formula: $C_{19}H_{37}N_5O_5$).



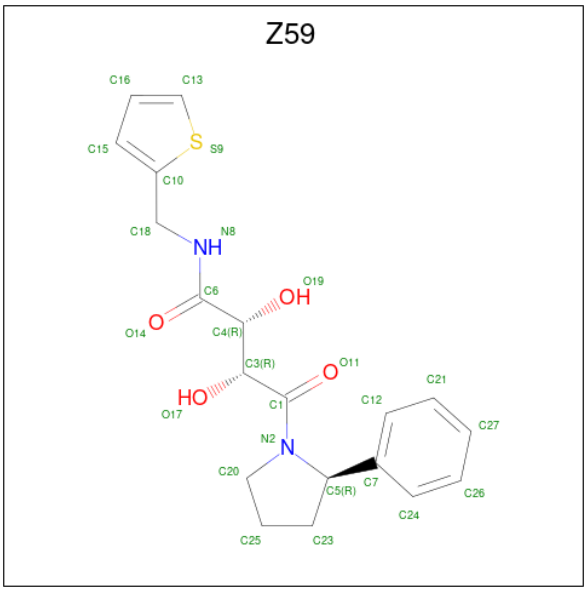
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 29 19 5 5	0	0

- Molecule 4 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
4	A	1	4	3	1		0	0

- Molecule 5 is (2R,3R)-2,3-dihydroxy-4-oxo-4-[(2R)-2-phenylpyrrolidin-1-yl]-N-(thiophen-2-ylmethyl)butanamide (three-letter code: Z59) (formula: $C_{19}H_{22}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	B	1	26	19	2	4	1	0	0

- Molecule 6 is water.

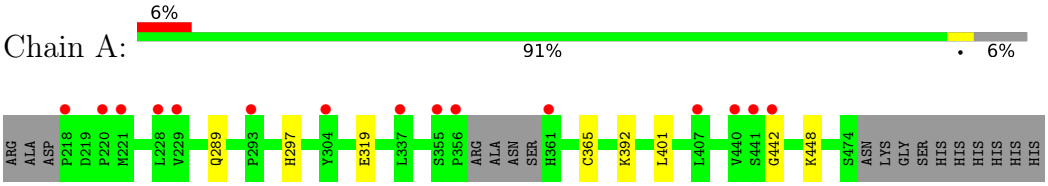
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	181	Total O 181 181	0	0
6	B	118	Total O 118 118	0	0

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

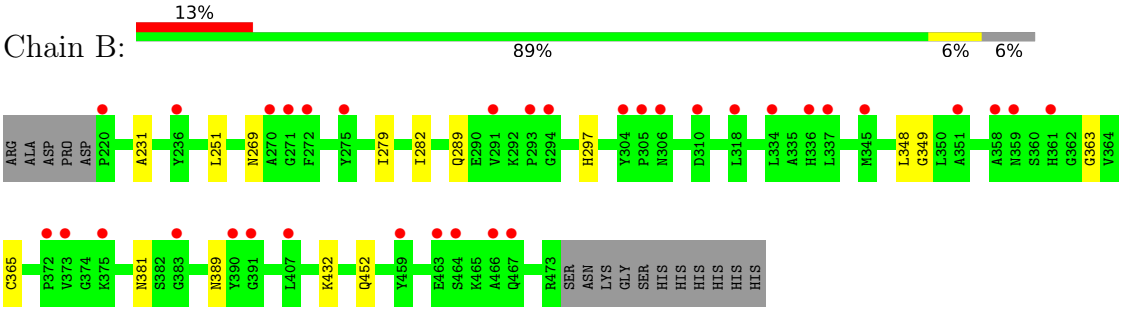
• Molecule 1: TNF-alpha-converting enzyme

Chain A:



• Molecule 1: TNF-alpha-converting enzyme

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	71.48Å 76.21Å 104.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.09 – 1.85 30.92 – 1.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (27.09-1.85) 99.3 (30.92-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.06 (at 1.85Å)	Xtriage
Refinement program	BUSTER 2.9.2	Depositor
R, R_{free}	0.200 , 0.225 0.202 , 0.228	Depositor DCC
R_{free} test set	956 reflections (1.94%)	wwPDB-VP
Wilson B-factor (Å^2)	30.6	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 43.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4256	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: INN, IPA, Z59, ZN

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	0.51	0/2011	0.63	0/2720
1	B	0.48	0/1979	0.62	0/2687
All	All	0.50	0/3990	0.63	0/5407

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1963	0	1841	3	0
1	B	1933	0	1764	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	29	0	35	0	0
4	A	4	0	8	0	0
5	B	26	0	20	1	0
6	A	181	0	0	1	0
6	B	118	0	0	1	0
All	All	4256	0	3668	12	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 2.

All (12) 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)
1:B:348:LEU:HD21	1:B:389:ASN:HB2	1.87	0.56
1:A:401:LEU:HD21	1:A:448:LYS:HG2	1.93	0.51
1:B:269:ASN:HD21	1:B:452:GLN:HE22	1.57	0.50
1:B:269:ASN:ND2	1:B:452:GLN:HE22	2.11	0.48
1:B:363:GLY:O	1:B:381:ASN:HA	2.18	0.44
1:A:289:GLN:HG2	1:A:297:HIS:CG	2.54	0.43
1:B:231:ALA:HB2	1:B:251:LEU:HD11	2.01	0.43
1:A:319:GLU:HG3	6:A:161:HOH:O	2.18	0.42
1:B:289:GLN:HG2	1:B:297:HIS:CG	2.55	0.42
1:B:279:ILE:HG21	1:B:282:ILE:HG13	2.01	0.42
1:B:349:GLY:O	5:B:485:Z59:H3	2.20	0.41
1:B:432:LYS:HE3	6:B:552:HOH:O	2.21	0.41

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	250/270 (93%)	243 (97%)	5 (2%)	2 (1%)	19 7
1	B	253/270 (94%)	247 (98%)	5 (2%)	1 (0%)	34 19
All	All	503/540 (93%)	490 (97%)	10 (2%)	3 (1%)	25 12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	442	GLY
1	A	365	CYS
1	B	365	CYS

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	205/230 (89%)	204 (100%)	1 (0%)	88 86
1	B	193/230 (84%)	193 (100%)	0	100 100
All	All	398/460 (86%)	397 (100%)	1 (0%)	92 91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	392	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	281	GLN
1	A	471	GLN
1	B	359	ASN
1	B	361	HIS
1	B	452	GLN
1	B	471	GLN

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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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	$\#\|Z\| > 2$
4	IPA	A	7	-	3,3,3	0.93	0	3,3,3	1.08	0
3	INN	A	485	2	28,28,28	5.64	23 (82%)	36,38,38	4.42	22 (61%)
5	Z59	B	485	2	28,28,28	3.10	14 (50%)	32,38,38	2.74	11 (34%)

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	INN	A	485	2	-	5/40/40/40	-
5	Z59	B	485	2	-	1/23/35/35	0/3/3/3

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	485	INN	C0-C	-9.70	1.29	1.51
3	A	485	INN	C6-C5	9.59	1.69	1.56
3	A	485	INN	C4-N1	-9.17	1.13	1.34
3	A	485	INN	C8-C6	9.08	1.73	1.53
5	B	485	Z59	C12-C7	8.53	1.52	1.39
3	A	485	INN	O2-C10	-7.71	1.08	1.23
3	A	485	INN	CB-CA	7.65	1.71	1.53
3	A	485	INN	C0-CA	7.19	1.68	1.53
5	B	485	Z59	C3-C1	7.12	1.60	1.53
3	A	485	INN	C5-N1	6.60	1.55	1.45
3	A	485	INN	CA-C4	6.36	1.62	1.51
3	A	485	INN	C10-N2	6.15	1.47	1.34
3	A	485	INN	C-N	6.14	1.39	1.32
3	A	485	INN	C11-N2	5.97	1.57	1.45
3	A	485	INN	C5-C10	5.67	1.64	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	485	Z59	C18-N8	5.32	1.56	1.46
5	B	485	Z59	C18-C10	5.28	1.57	1.51
3	A	485	INN	C7-C6	-5.12	1.42	1.53
3	A	485	INN	CB-C1	4.60	1.72	1.52
3	A	485	INN	C13-N3	4.34	1.43	1.33
3	A	485	INN	C12-C11	3.96	1.63	1.52
3	A	485	INN	O3-C13	-3.94	1.15	1.23
3	A	485	INN	O1-C4	3.55	1.30	1.23
5	B	485	Z59	O11-C1	3.31	1.28	1.22
5	B	485	Z59	C15-C10	3.22	1.46	1.37
5	B	485	Z59	C6-N8	3.17	1.40	1.33
3	A	485	INN	O-C	3.04	1.29	1.23
5	B	485	Z59	C24-C7	2.94	1.43	1.39
5	B	485	Z59	C16-C13	2.70	1.42	1.34
3	A	485	INN	C11-C13	-2.63	1.46	1.52
5	B	485	Z59	C21-C12	2.60	1.44	1.38
5	B	485	Z59	O19-C4	2.56	1.47	1.42
3	A	485	INN	C3-C1	2.53	1.65	1.51
5	B	485	Z59	C4-C6	2.25	1.57	1.52
5	B	485	Z59	C1-N2	2.14	1.39	1.34
5	B	485	Z59	C26-C24	2.14	1.43	1.38
3	A	485	INN	C2-C1	2.04	1.62	1.51

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	485	INN	C5-C10-N2	-10.08	98.16	116.26
3	A	485	INN	O2-C10-N2	9.89	141.24	122.93
3	A	485	INN	O1-C4-CA	-8.99	110.42	122.12
3	A	485	INN	CA-CB-C1	-8.75	95.57	115.68
5	B	485	Z59	C3-C4-C6	8.48	118.16	109.10
5	B	485	Z59	C21-C12-C7	-6.88	112.14	120.65
3	A	485	INN	O-C-N	-6.46	115.33	123.27
3	A	485	INN	C6-C5-C10	-6.33	106.87	112.81
3	A	485	INN	O-C-C0	6.04	130.34	121.50
5	B	485	Z59	C18-N8-C6	5.79	130.67	122.34
3	A	485	INN	CB-CA-C4	5.44	119.06	109.44
3	A	485	INN	C9-C6-C7	5.22	118.94	108.80
3	A	485	INN	C8-C6-C5	-4.81	99.97	109.70
3	A	485	INN	C11-N2-C10	-4.72	111.08	121.29
3	A	485	INN	CA-C0-C	-4.59	103.40	112.10
3	A	485	INN	C13-C11-N2	-4.10	101.45	111.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	485	INN	C3-C1-CB	-3.80	97.14	111.11
5	B	485	Z59	C16-C13-S9	-3.61	110.06	112.98
3	A	485	INN	C0-CA-C4	-3.57	104.61	109.77
3	A	485	INN	CA-C4-N1	3.30	121.91	116.21
3	A	485	INN	C12-C11-N2	3.18	116.35	110.38
5	B	485	Z59	O19-C4-C6	3.14	117.39	110.63
5	B	485	Z59	C4-C3-C1	-2.94	105.63	109.48
5	B	485	Z59	C27-C21-C12	2.83	124.51	120.19
3	A	485	INN	C6-C5-N1	-2.71	108.45	111.84
5	B	485	Z59	C12-C7-C5	-2.59	115.85	120.76
3	A	485	INN	O1-C4-N1	2.56	127.67	122.93
5	B	485	Z59	C7-C5-N2	-2.54	108.43	112.99
5	B	485	Z59	O19-C4-C3	-2.24	105.78	110.23
3	A	485	INN	O3-C13-C11	-2.15	115.76	120.52
5	B	485	Z59	C23-C5-N2	2.07	104.32	101.94
3	A	485	INN	C9-C6-C5	2.06	113.88	109.70
3	A	485	INN	C9-C6-C8	-2.06	104.80	108.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	485	INN	N3-C14-C15-N4
3	A	485	INN	N2-C11-C13-N3
3	A	485	INN	N2-C11-C13-O3
3	A	485	INN	C13-C11-N2-C10
3	A	485	INN	C2-C1-CB-CA
5	B	485	Z59	C10-C18-N8-C6

There are no ring outliers.

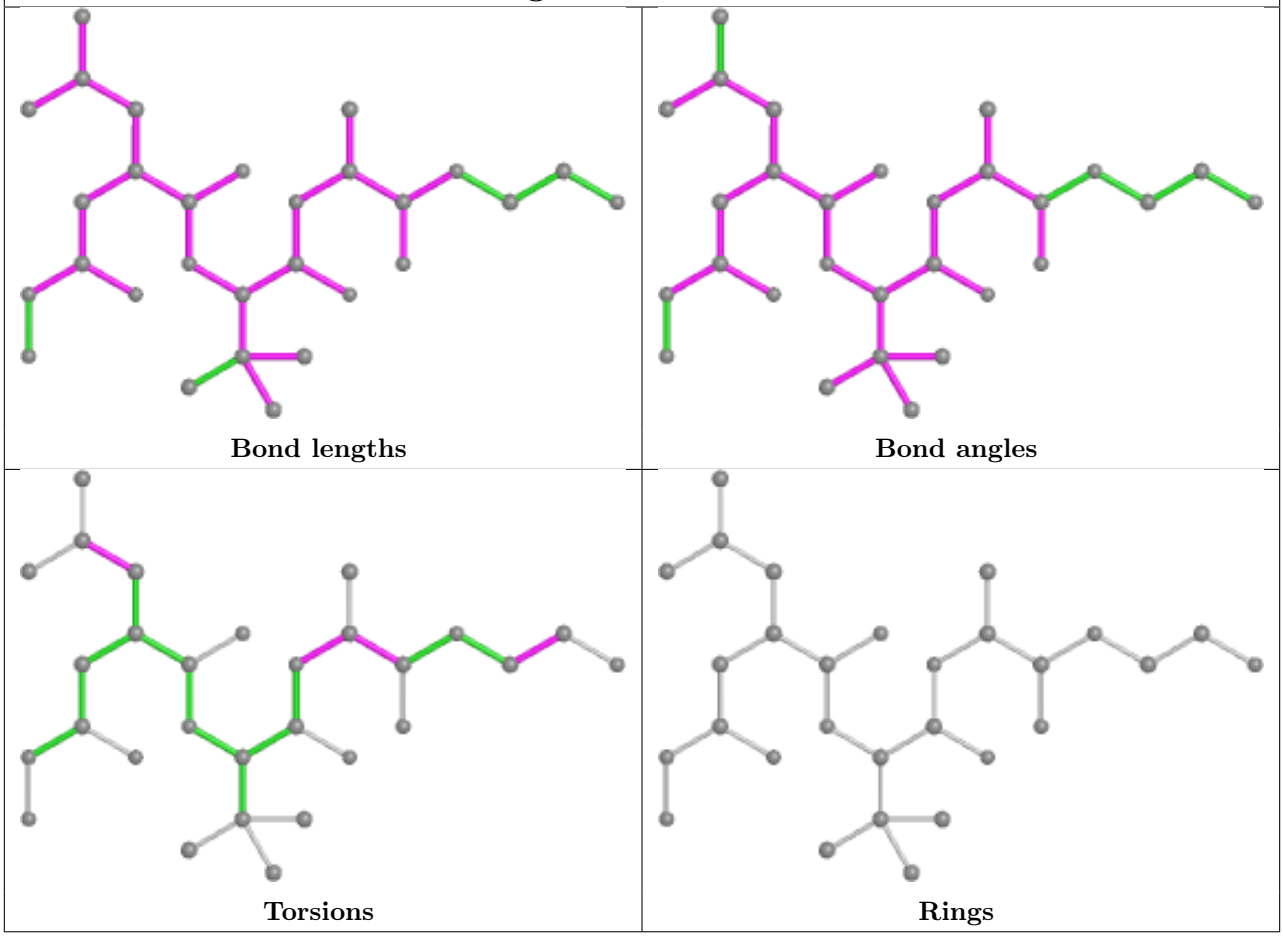
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	485	Z59	1	0

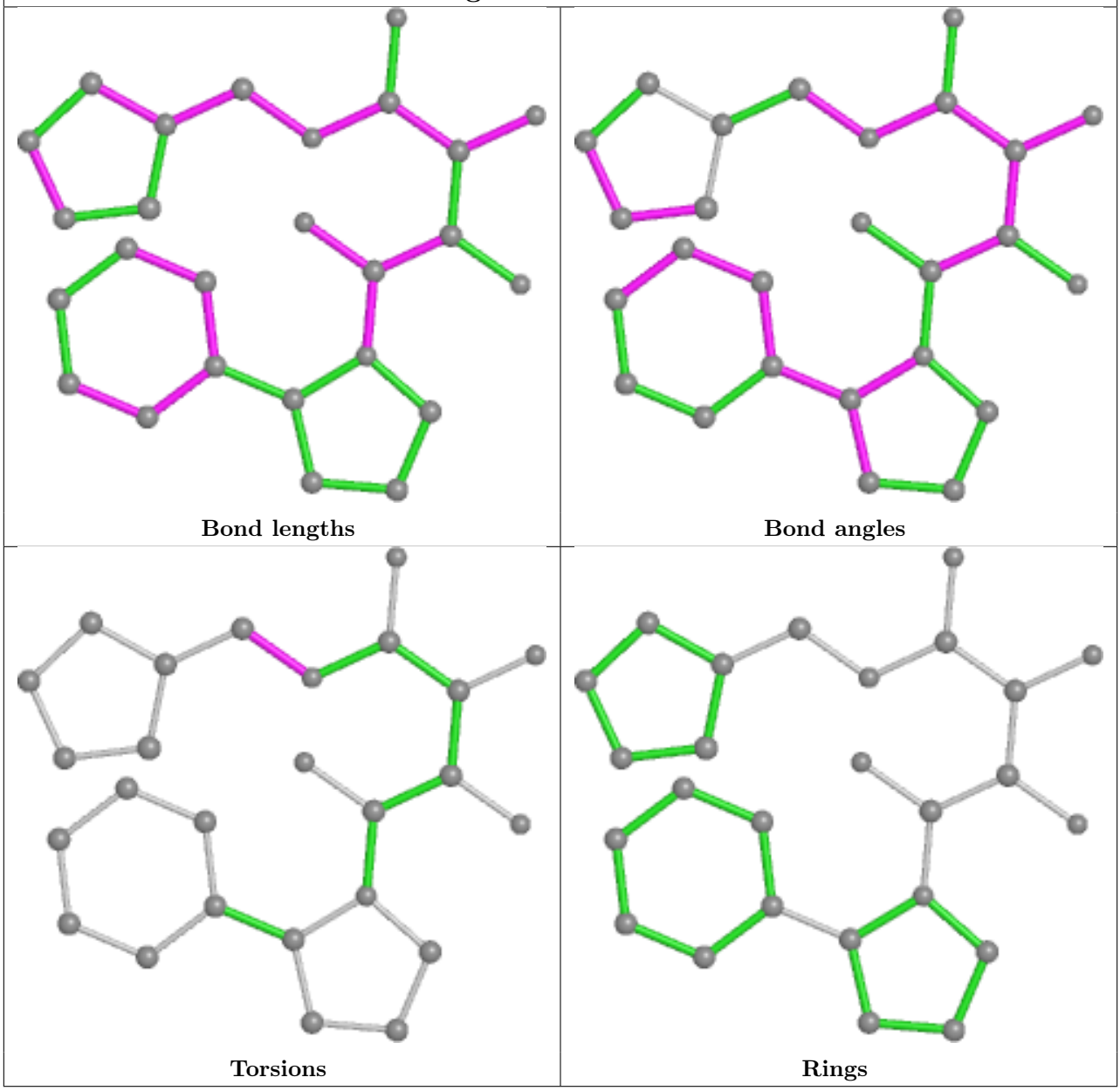
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 INN A 485



Ligand Z59 B 485



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

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	253/270 (93%)	0.27	15 (5%) 22 22	20, 29, 55, 74	0
1	B	254/270 (94%)	0.72	34 (13%) 3 3	22, 39, 61, 79	0
All	All	507/540 (93%)	0.50	49 (9%) 7 7	20, 34, 60, 79	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	440	VAL	5.9
1	B	466	ALA	4.8
1	A	441	SER	4.7
1	B	373	VAL	4.7
1	A	442	GLY	4.4
1	B	459	TYR	4.3
1	B	310	ASP	4.1
1	A	218	PRO	4.0
1	B	293	PRO	4.0
1	A	356	PRO	3.9
1	B	407	LEU	3.9
1	A	221	MET	3.7
1	A	355	SER	3.6
1	A	293	PRO	3.4
1	B	306	ASN	3.2
1	B	345	MET	3.1
1	B	272	PHE	3.1
1	B	361	HIS	3.0
1	B	270	ALA	3.0
1	B	304	TYR	3.0
1	B	391	GLY	3.0
1	B	305	PRO	2.9
1	A	337	LEU	2.9
1	B	294	GLY	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	361	HIS	2.9
1	B	336	HIS	2.7
1	B	464	SER	2.7
1	B	337	LEU	2.7
1	B	291	VAL	2.7
1	A	229	VAL	2.6
1	A	304	TYR	2.6
1	B	467	GLN	2.6
1	B	236	TYR	2.6
1	B	375	LYS	2.5
1	A	220	PRO	2.5
1	B	334	LEU	2.5
1	B	390	TYR	2.5
1	B	463	GLU	2.4
1	B	275	TYR	2.4
1	A	228	LEU	2.2
1	B	318	LEU	2.2
1	B	372	PRO	2.2
1	B	351	ALA	2.2
1	A	407	LEU	2.1
1	B	220	PRO	2.1
1	B	383	GLY	2.1
1	B	358	ALA	2.1
1	B	271	GLY	2.1
1	B	359	ASN	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

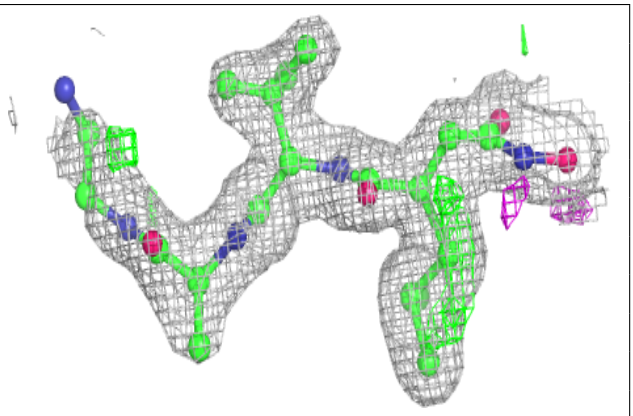
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

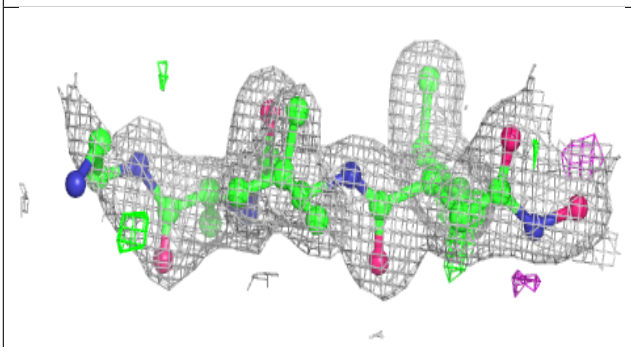
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	INN	A	485	29/29	0.89	0.14	24,32,55,59	0
5	Z59	B	485	26/26	0.89	0.14	28,34,44,44	0
4	IPA	A	7	4/4	0.96	0.13	27,31,31,32	0
2	ZN	B	2	1/1	0.99	0.06	30,30,30,30	0
2	ZN	A	1	1/1	1.00	0.06	30,30,30,30	0

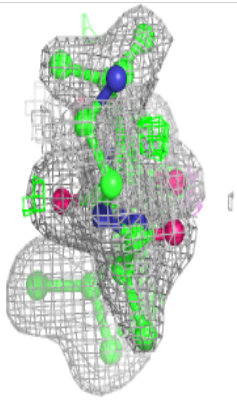
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around INN A 485:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

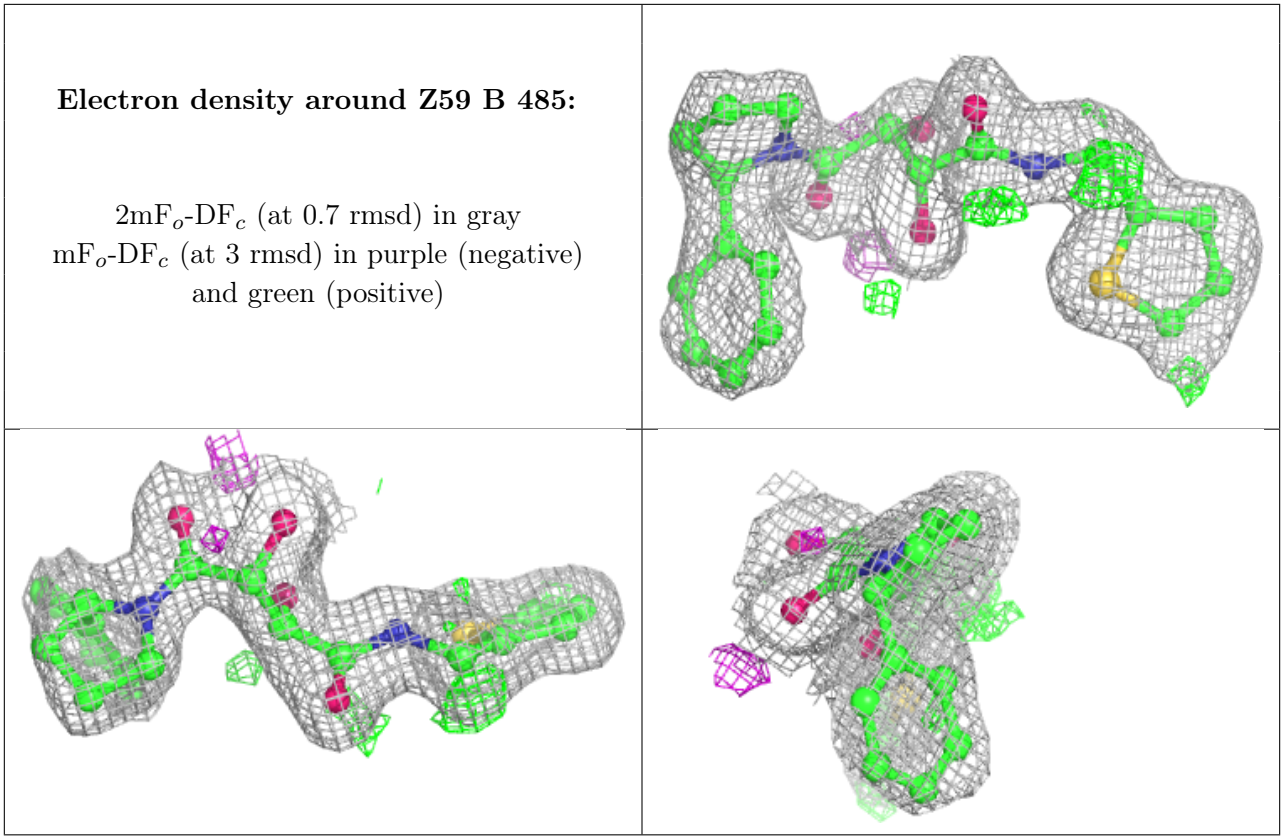






Electron density around Z59 B 485:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.