Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 01:46 am BST

PDB ID	:	4WHN
Title	:	Structure of toxin-activating acyltransferase (TAAT)
Authors	:	Crow, A.; Greene, N.P.; Hughes, C.; Koronakis, V.
Deposited on	:	2014-09-23
Resolution	:	2.15 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 following versions of software and data (see references ⓘ) were used in the production of this report:

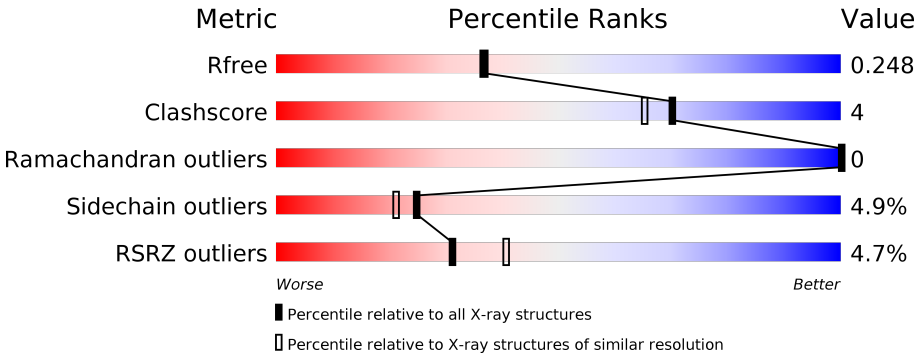
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 on 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	183	8% 84% 7% • 7%
1	B	183	5% 80% 11% •• 8%
1	C	183	3% 81% 9% • 8%
1	D	183	% 84% 6% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5868 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 ApxC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	3	0
			1417	921	242	251	3			
1	B	169	Total	C	N	O	S	0	5	0
			1424	924	242	255	3			
1	C	168	Total	C	N	O	S	0	3	0
			1406	913	240	250	3			
1	D	168	Total	C	N	O	S	0	1	0
			1389	904	237	245	3			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP P55132
A	-9	ARG	-	expression tag	UNP P55132
A	-8	GLY	-	expression tag	UNP P55132
A	-7	SER	-	expression tag	UNP P55132
A	-6	HIS	-	expression tag	UNP P55132
A	-5	HIS	-	expression tag	UNP P55132
A	-4	HIS	-	expression tag	UNP P55132
A	-3	HIS	-	expression tag	UNP P55132
A	-2	HIS	-	expression tag	UNP P55132
A	-1	HIS	-	expression tag	UNP P55132
A	0	GLY	-	expression tag	UNP P55132
A	1	SER	-	expression tag	UNP P55132
B	-10	MET	-	initiating methionine	UNP P55132
B	-9	ARG	-	expression tag	UNP P55132
B	-8	GLY	-	expression tag	UNP P55132
B	-7	SER	-	expression tag	UNP P55132
B	-6	HIS	-	expression tag	UNP P55132
B	-5	HIS	-	expression tag	UNP P55132
B	-4	HIS	-	expression tag	UNP P55132
B	-3	HIS	-	expression tag	UNP P55132
B	-2	HIS	-	expression tag	UNP P55132

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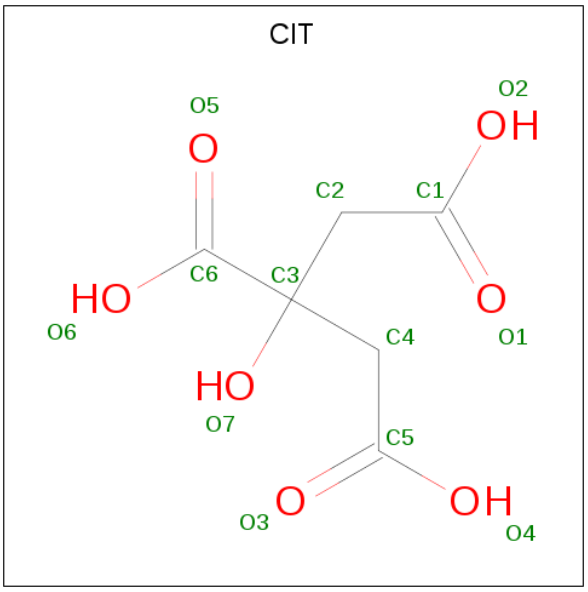
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	HIS	-	expression tag	UNP P55132
B	0	GLY	-	expression tag	UNP P55132
B	1	SER	-	expression tag	UNP P55132
C	-10	MET	-	initiating methionine	UNP P55132
C	-9	ARG	-	expression tag	UNP P55132
C	-8	GLY	-	expression tag	UNP P55132
C	-7	SER	-	expression tag	UNP P55132
C	-6	HIS	-	expression tag	UNP P55132
C	-5	HIS	-	expression tag	UNP P55132
C	-4	HIS	-	expression tag	UNP P55132
C	-3	HIS	-	expression tag	UNP P55132
C	-2	HIS	-	expression tag	UNP P55132
C	-1	HIS	-	expression tag	UNP P55132
C	0	GLY	-	expression tag	UNP P55132
C	1	SER	-	expression tag	UNP P55132
D	-10	MET	-	initiating methionine	UNP P55132
D	-9	ARG	-	expression tag	UNP P55132
D	-8	GLY	-	expression tag	UNP P55132
D	-7	SER	-	expression tag	UNP P55132
D	-6	HIS	-	expression tag	UNP P55132
D	-5	HIS	-	expression tag	UNP P55132
D	-4	HIS	-	expression tag	UNP P55132
D	-3	HIS	-	expression tag	UNP P55132
D	-2	HIS	-	expression tag	UNP P55132
D	-1	HIS	-	expression tag	UNP P55132
D	0	GLY	-	expression tag	UNP P55132
D	1	SER	-	expression tag	UNP P55132

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 13 6 7	0	0

- Molecule 3 is water.

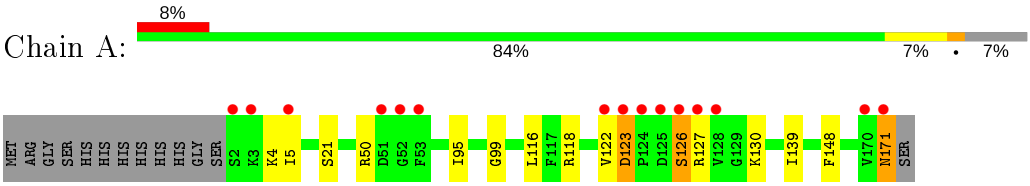
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	52	Total O 52 52	0	0
3	B	53	Total O 53 53	0	0
3	C	49	Total O 49 49	0	0
3	D	65	Total O 65 65	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

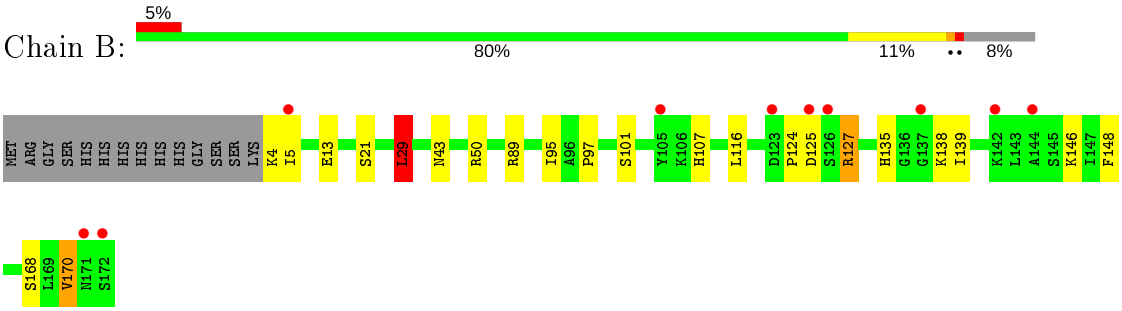
- Molecule 1: ApxC

Chain A:



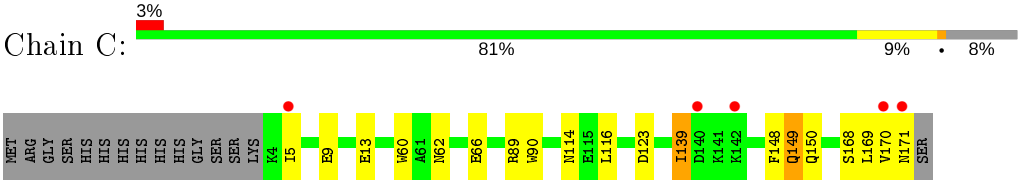
- Molecule 1: ApxC

Chain B:



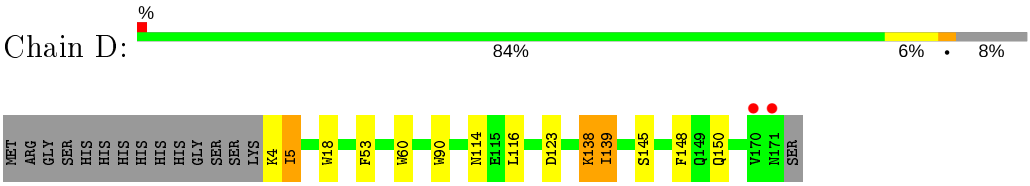
- Molecule 1: ApxC

Chain C:



- Molecule 1: ApxC

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	82.45Å 86.37Å 131.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.29 – 2.15 54.29 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (54.29-2.15) 100.0 (54.29-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	2.39 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.200 , 0.242 0.208 , 0.248	Depositor DCC
R_{free} test set	2629 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	31.9	Xtriage
Anisotropy	0.514	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 39.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.021 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5868	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: CIT

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	0.84	0/1457	0.89	2/1972 (0.1%)
1	B	0.83	0/1464	0.92	3/1983 (0.2%)
1	C	0.81	0/1446	0.85	2/1958 (0.1%)
1	D	0.86	0/1429	0.87	1/1935 (0.1%)
All	All	0.84	0/5796	0.88	8/7848 (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	A	0	1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	29	LEU	CA-CB-CG	-7.69	97.62	115.30
1	B	50	ARG	CG-CD-NE	6.05	124.50	111.80
1	D	123	ASP	CB-CG-OD1	5.89	123.60	118.30
1	C	123	ASP	CB-CG-OD1	5.56	123.31	118.30
1	C	66	GLU	OE1-CD-OE2	-5.47	116.73	123.30
1	B	89	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	123	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	118	ARG	NE-CZ-NH2	-5.09	117.75	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	122	VAL	Peptide

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	1417	0	1395	12	0
1	B	1424	0	1394	15	0
1	C	1406	0	1375	8	0
1	D	1389	0	1365	9	0
2	B	13	0	5	2	0
3	A	52	0	0	2	0
3	B	53	0	0	2	0
3	C	49	0	0	0	0
3	D	65	0	0	0	0
All	All	5868	0	5534	40	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 4.

All (40) 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:127:ARG:HD2	1:B:127:ARG:N	1.96	0.80
1:B:21[B]:SER:OG	2:B:201:CIT:O6	2.06	0.73
1:B:21[A]:SER:OG	1:B:95:ILE:HD11	1.91	0.70
1:A:21:SER:OG	1:A:95[A]:ILE:HD11	1.98	0.63
1:A:171:ASN:OD1	1:A:171:ASN:C	2.37	0.61
1:B:107:HIS:ND1	3:B:353:HOH:O	2.31	0.60
1:B:21[B]:SER:OG	2:B:201:CIT:C6	2.51	0.58
1:C:116:LEU:HD23	1:C:148:PHE:CE2	2.39	0.57
1:A:116:LEU:HD23	1:A:148:PHE:CE2	2.41	0.56
1:A:99:GLY:C	3:A:236:HOH:O	2.44	0.56
1:B:116:LEU:HD12	1:B:135:HIS:HB3	1.89	0.55
1:D:116:LEU:HD23	1:D:148:PHE:CE2	2.42	0.54
1:A:116:LEU:HD23	1:A:148:PHE:CZ	2.44	0.53
1:A:130:LYS:HE3	1:B:170:VAL:HG22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:PRO:HA	1:B:127:ARG:NH1	2.24	0.52
1:A:123:ASP:HB3	1:A:126:SER:O	2.12	0.49
1:A:50:ARG:HB3	3:A:234:HOH:O	2.11	0.49
1:C:149[B]:GLN:CA	1:C:149[B]:GLN:OE1	2.60	0.49
1:C:149[B]:GLN:OE1	1:C:149[B]:GLN:HA	2.11	0.49
1:B:124:PRO:HA	1:B:127:ARG:HH12	1.78	0.49
1:B:95:ILE:HG12	1:B:97:PRO:HD3	1.94	0.49
1:B:13:GLU:OE1	3:B:352:HOH:O	2.20	0.47
1:A:123:ASP:CB	1:A:126:SER:HB3	2.44	0.46
1:A:171:ASN:HA	1:B:148:PHE:HE2	1.80	0.46
1:D:116:LEU:HD23	1:D:148:PHE:CZ	2.51	0.46
1:C:116:LEU:HD23	1:C:148:PHE:CZ	2.51	0.45
1:C:114:ASN:HA	1:C:139:ILE:HB	1.99	0.44
1:B:21[A]:SER:HG	1:B:95:ILE:HD11	1.81	0.43
1:A:4:LYS:O	1:A:4:LYS:HD2	2.19	0.43
1:B:29:LEU:HD13	1:D:18:TRP:HE3	1.84	0.43
1:D:138:LYS:HB3	1:D:138:LYS:HE2	1.76	0.43
1:B:4:LYS:HD2	1:D:53:PHE:CE1	2.54	0.42
1:D:114:ASN:HA	1:D:139:ILE:HB	2.01	0.42
1:C:9:GLU:OE2	1:C:13:GLU:OE1	2.38	0.42
1:D:5:ILE:HG22	1:D:5:ILE:O	2.19	0.41
1:C:60:TRP:HA	1:C:90:TRP:O	2.20	0.41
1:A:95[B]:ILE:HD12	1:A:95[B]:ILE:HG21	1.69	0.41
1:D:60:TRP:HA	1:D:90:TRP:O	2.20	0.41
1:C:62:ASN:OD1	1:C:89:ARG:HG2	2.21	0.41
1:D:150[B]:GLN:O	1:D:150[B]:GLN:HG2	2.21	0.40

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	171/183 (93%)	169 (99%)	2 (1%)	0	100	100
1	B	172/183 (94%)	172 (100%)	0	0	100	100
1	C	169/183 (92%)	169 (100%)	0	0	100	100
1	D	167/183 (91%)	166 (99%)	1 (1%)	0	100	100
All	All	679/732 (93%)	676 (100%)	3 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	152/160 (95%)	147 (97%)	5 (3%)	38	37
1	B	153/160 (96%)	142 (93%)	11 (7%)	14	9
1	C	150/160 (94%)	141 (94%)	9 (6%)	19	14
1	D	148/160 (92%)	143 (97%)	5 (3%)	37	35
All	All	603/640 (94%)	573 (95%)	30 (5%)	25	21

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	126	SER
1	A	127	ARG
1	A	139	ILE
1	A	171	ASN
1	B	5	ILE
1	B	29	LEU
1	B	43	ASN
1	B	101	SER
1	B	125	ASP
1	B	127	ARG
1	B	138	LYS
1	B	139	ILE

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Mol	Chain	Res	Type
1	B	146	LYS
1	B	168	SER
1	B	170	VAL
1	C	5	ILE
1	C	139	ILE
1	C	149[A]	GLN
1	C	149[B]	GLN
1	C	150	GLN
1	C	168	SER
1	C	169	LEU
1	C	170	VAL
1	C	171	ASN
1	D	4	LYS
1	D	5	ILE
1	D	138	LYS
1	D	139	ILE
1	D	145	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	152	HIS
1	B	35	ASN
1	B	107	HIS
1	B	149	GLN
1	C	107	HIS
1	C	150	GLN
1	C	163	GLN
1	C	171	ASN
1	D	111	ASN
1	D	171	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	$\#\|Z\| > 2$
2	CIT	B	201	-	3,12,12	0.94	0	3,17,17	1.80	1 (33%)

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
2	CIT	B	201	-	-	6/6/16/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	201	CIT	C3-C4-C5	-3.04	110.12	114.98

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	201	CIT	C1-C2-C3-O7
2	B	201	CIT	C1-C2-C3-C4
2	B	201	CIT	C1-C2-C3-C6
2	B	201	CIT	C2-C3-C4-C5
2	B	201	CIT	O7-C3-C4-C5

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Mol	Chain	Res	Type	Atoms
2	B	201	CIT	C6-C3-C4-C5

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	201	CIT	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	170/183 (92%)	0.16	15 (8%)	10	14	24, 34, 88, 125	0
1	B	169/183 (92%)	0.14	10 (5%)	22	30	22, 34, 79, 103	0
1	C	168/183 (91%)	-0.08	5 (2%)	50	59	24, 35, 68, 87	0
1	D	168/183 (91%)	0.01	2 (1%)	79	83	19, 32, 66, 105	0
All	All	675/732 (92%)	0.06	32 (4%)	31	41	19, 34, 74, 125	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	PRO	9.4
1	A	2	SER	7.3
1	A	5	ILE	5.5
1	A	126	SER	5.1
1	B	172	SER	4.6
1	A	127	ARG	4.4
1	D	171	ASN	4.2
1	A	122	VAL	3.9
1	B	123	ASP	3.9
1	A	128	VAL	3.6
1	A	52	GLY	3.5
1	A	170	VAL	3.5
1	B	125	ASP	3.5
1	A	3	LYS	3.5
1	B	142	LYS	3.4
1	C	140	ASP	3.2
1	B	105	TYR	3.2
1	A	125	ASP	3.2
1	A	51	ASP	3.1
1	A	123	ASP	3.1
1	B	171	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	170	VAL	2.9
1	A	171	ASN	2.9
1	B	144	ALA	2.8
1	B	5	ILE	2.5
1	C	142	LYS	2.4
1	C	5	ILE	2.3
1	A	53	PHE	2.2
1	B	126	SER	2.2
1	C	170	VAL	2.2
1	B	137	GLY	2.2
1	C	171	ASN	2.1

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 carbohydrates 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
2	CIT	B	201	13/13	0.75	0.24	46,64,73,79	0

6.5 Other polymers (i)

There are no such residues in this entry.