



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 06:13 am BST

PDB ID : 4GYX
Title : Crystal structure of human O-GlcNAc Transferase with UDP-5SGlcNAc and a peptide substrate
Authors : Lazarus, M.B.; Jiang, J.; Gloster, T.M.; Zandberg, W.F.; Vocadlo, D.J.; Walker, S.
Deposited on : 2012-09-05
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 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
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) : 2.11

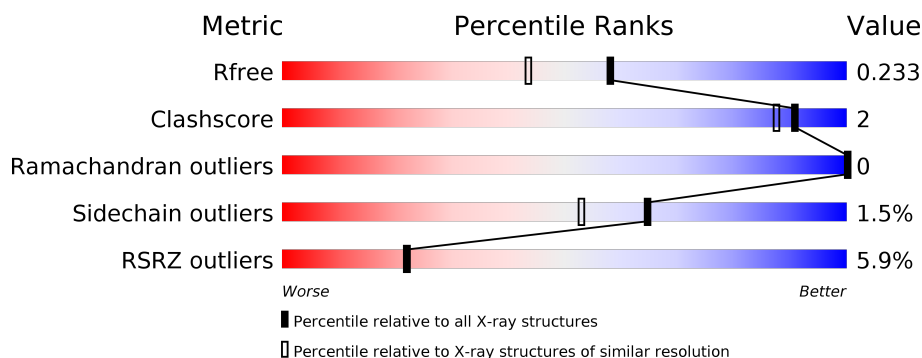
1 Overall quality at a glance

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 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 $\leq 5\%$. 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	723	<div> <div>6%</div> <div>90%</div> <div>6%</div> <div>.</div> </div>
1	C	723	<div> <div>6%</div> <div>89%</div> <div>7%</div> <div>.</div> </div>
2	B	14	<div> <div>86%</div> <div>14%</div> </div>
2	D	14	<div> <div>86%</div> <div>14%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11974 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 UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	693	Total	C	N	O	S	0	10	0
			5525	3507	964	1017	37			
1	C	671	Total	C	N	O	S	0	6	0
			5332	3394	926	975	37			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	309	GLY	-	EXPRESSION TAG	UNP O15294
A	310	PRO	-	EXPRESSION TAG	UNP O15294
A	311	GLY	-	EXPRESSION TAG	UNP O15294
A	312	SER	-	EXPRESSION TAG	UNP O15294
C	309	GLY	-	EXPRESSION TAG	UNP O15294
C	310	PRO	-	EXPRESSION TAG	UNP O15294
C	311	GLY	-	EXPRESSION TAG	UNP O15294
C	312	SER	-	EXPRESSION TAG	UNP O15294

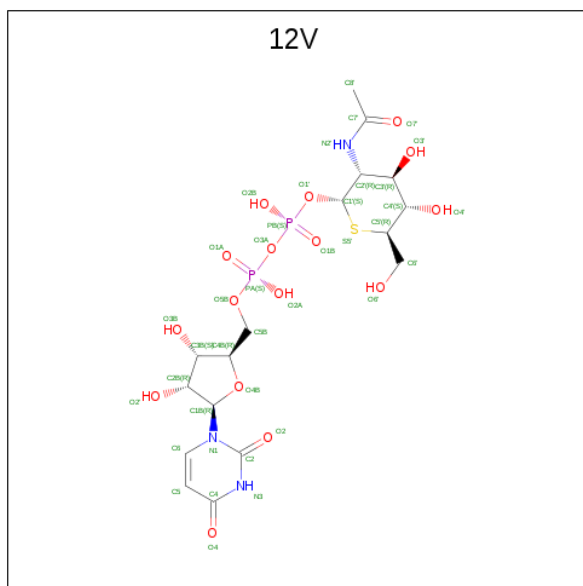
- Molecule 2 is a protein called Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	S	0	0	0
			94	58	15	19	2			
2	D	14	Total	C	N	O	S	0	0	0
			94	58	15	19	2			

There are 2 discrepancies between the modelled and reference sequences:

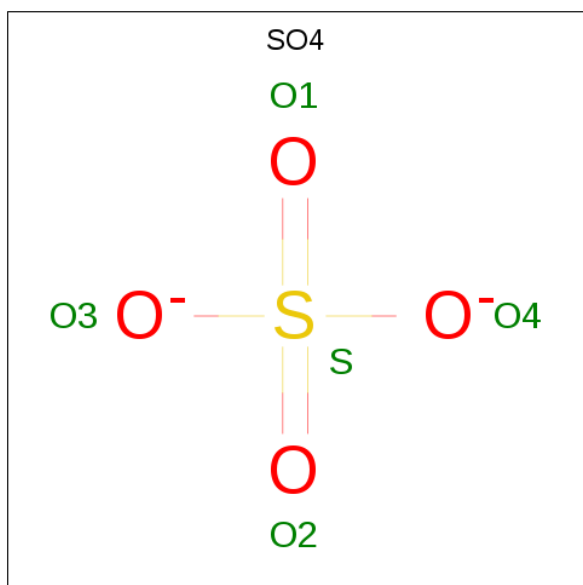
Chain	Residue	Modelled	Actual	Comment	Reference
B	13	TYR	-	EXPRESSION TAG	UNP P68400
D	13	TYR	-	EXPRESSION TAG	UNP P68400

- Molecule 3 is (2S,3R,4R,5S,6R)-3-(acetylamino)-4,5-dihydroxy-6-(hydroxymethyl)tetrahydro-2H-thiopyran-2-yl [(2R,3S,4R,5R)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-3,4-dihydroxytetrahydrofuran-2-yl]methyl dihydrogen diphosphate (three-letter code: 12V) (formula: $C_{17}H_{27}N_3O_{16}P_2S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			39	17	3	16	2	1		
3	C	1	Total	C	N	O	P	S	0	0
			39	17	3	16	2	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

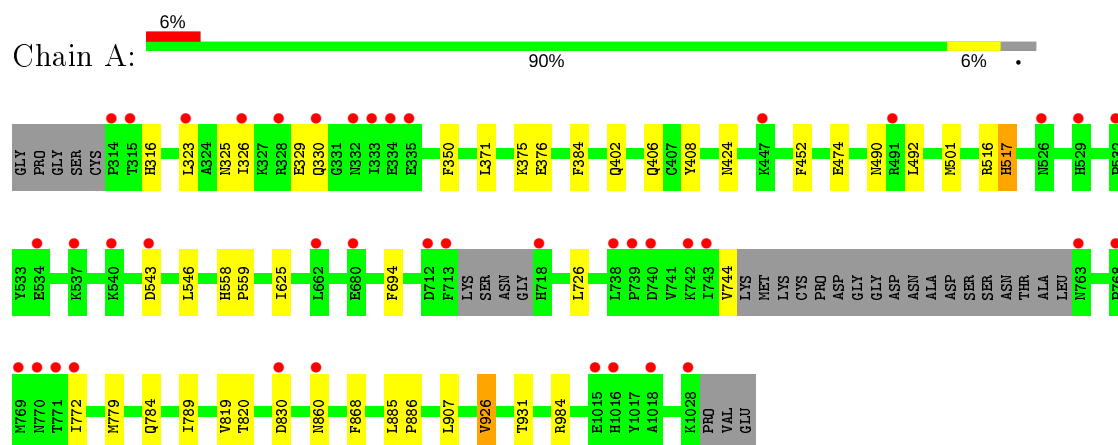
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	410	Total O 410 410	0	0
5	B	10	Total O 10 10	0	0
5	C	403	Total O 403 403	0	0
5	D	13	Total O 13 13	0	0

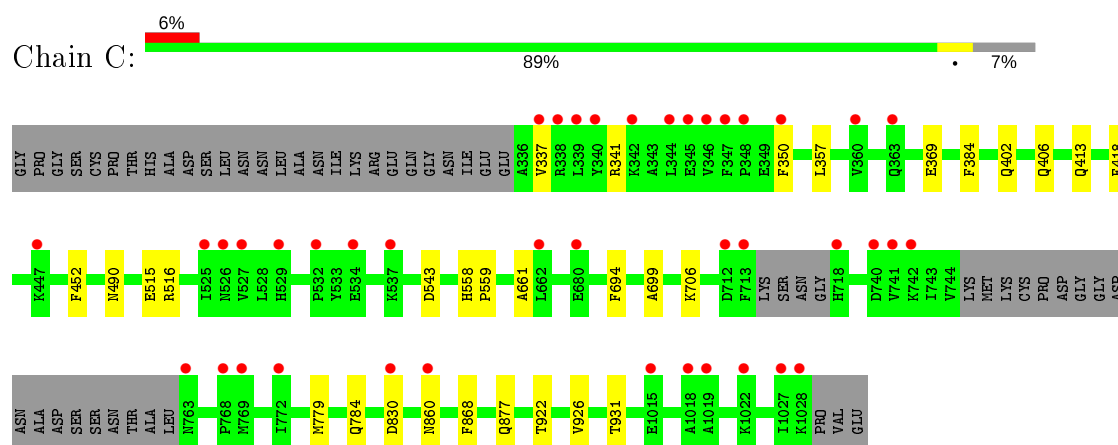
3 Residue-property plots [i](#)

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.

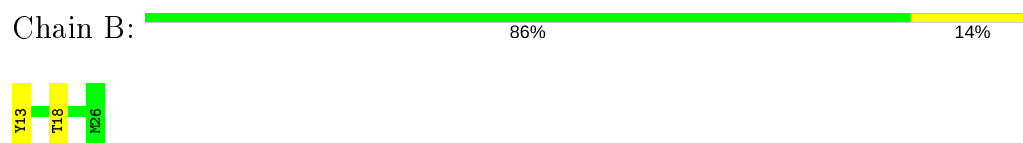
- Molecule 1: UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit




- Molecule 1: UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit



- Molecule 2: Casein kinase II subunit alpha



- Molecule 2: Casein kinase II subunit alpha

Chain D:  86% 14%



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	98.52Å 136.48Å 152.77Å 90.00° 103.51° 90.00°	Depositor
Resolution (Å)	59.95 – 1.85 59.95 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.5 (59.95-1.85) 99.5 (59.95-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 1.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.218 , 0.237 0.213 , 0.233	Depositor DCC
R_{free} test set	8351 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11974	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.10 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.1069e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, 12V

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	0.25	0/5680	0.43	0/7706
1	C	0.25	0/5476	0.43	0/7429
2	B	0.29	0/96	0.44	0/130
2	D	0.27	0/96	0.44	0/130
All	All	0.25	0/11348	0.43	0/15395

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 [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	5525	0	5508	21	0
1	C	5332	0	5320	15	0
2	B	94	0	85	1	0
2	D	94	0	85	1	0
3	A	39	0	25	1	0
3	C	39	0	25	1	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	D	5	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	410	0	0	2	0
5	B	10	0	0	0	0
5	C	403	0	0	5	0
5	D	13	0	0	0	0
All	All	11974	0	11048	38	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 (38) 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:B:13:TYR:N	2:B:18:THR:HG1	1.87	0.71
1:C:661:ALA:O	5:C:1809:HOH:O	2.13	0.67
2:D:13:TYR:N	2:D:18:THR:HG1	1.91	0.67
1:C:515[B]:GLU:OE1	5:C:1897:HOH:O	2.15	0.64
1:C:490:ASN:OD1	1:C:516:ARG:NH1	2.32	0.61
1:A:490:ASN:OD1	1:A:516:ARG:NH1	2.33	0.60
1:C:830:ASP:O	1:C:860:ASN:ND2	2.34	0.60
1:A:830:ASP:O	1:A:860:ASN:ND2	2.37	0.58
1:C:926:VAL:HG22	1:C:931:THR:HB	1.86	0.58
1:C:341:ARG:NH2	1:C:369:GLU:OE2	2.36	0.55
1:A:931[B]:THR:HG22	1:A:984:ARG:HH12	1.75	0.51
1:C:413:GLN:NE2	5:C:1899:HOH:O	2.45	0.50
1:A:474:GLU:HG3	5:A:1931:HOH:O	2.12	0.50
1:C:337:VAL:HG13	1:C:357:LEU:HD11	1.94	0.49
1:C:877:GLN:NE2	5:C:1954:HOH:O	2.38	0.49
1:A:779:MET:HG3	1:A:784:GLN:HB2	1.93	0.49
1:A:492:LEU:HD11	1:A:517:HIS:ND1	2.29	0.47
1:A:323:LEU:HD23	1:A:326:ILE:HD12	1.96	0.47
1:A:820:THR:HG22	1:A:907:LEU:HD11	1.97	0.46
1:A:376:GLU:HG2	5:A:1819:HOH:O	2.17	0.45
1:C:699:ALA:O	1:C:706:LYS:NZ	2.50	0.45
1:C:922[B]:THR:HG21	5:C:1636:HOH:O	2.17	0.43
1:A:546:LEU:HD21	1:A:625:ILE:HD12	1.99	0.43
1:C:558:HIS:CG	1:C:559:PRO:HD2	2.53	0.43
1:C:779:MET:HG3	1:C:784:GLN:HB2	1.98	0.43
1:A:325:ASN:O	1:A:329:GLU:HG2	2.19	0.42
1:A:371:LEU:HG	1:A:375:LYS:HE3	2.01	0.42
1:C:559:PRO:HB2	3:C:1501:12V:H6'A	2.01	0.42
1:C:402:GLN:O	1:C:406:GLN:HG2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:GLN:O	1:A:406:GLN:HG2	2.20	0.42
1:A:726:LEU:CD2	1:A:819:VAL:HG22	2.50	0.41
1:A:559:PRO:HB2	3:A:1501:12V:H6'A	2.02	0.41
1:A:326:ILE:HG22	1:A:330:GLN:HE21	1.85	0.41
1:A:885:LEU:HA	1:A:886:PRO:HD2	1.97	0.41
1:A:558:HIS:CG	1:A:559:PRO:HD2	2.55	0.40
1:A:772:ILE:HG23	1:A:789:ILE:HD13	2.02	0.40
1:A:408:TYR:CZ	1:A:424:ASN:HB3	2.57	0.40
1:A:926:VAL:HG22	1:A:931[B]:THR:OG1	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	697/723 (96%)	681 (98%)	16 (2%)	0	100	100
1	C	671/723 (93%)	660 (98%)	11 (2%)	0	100	100
2	B	12/14 (86%)	12 (100%)	0	0	100	100
2	D	12/14 (86%)	12 (100%)	0	0	100	100
All	All	1392/1474 (94%)	1365 (98%)	27 (2%)	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	605/618 (98%)	594 (98%)	11 (2%)	59	45
1	C	582/618 (94%)	575 (99%)	7 (1%)	71	62
2	B	10/11 (91%)	10 (100%)	0	100	100
2	D	10/11 (91%)	10 (100%)	0	100	100
All	All	1207/1258 (96%)	1189 (98%)	18 (2%)	65	53

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	316	HIS
1	A	350	PHE
1	A	384	PHE
1	A	452	PHE
1	A	501	MET
1	A	517	HIS
1	A	543	ASP
1	A	694	PHE
1	A	744	VAL
1	A	868	PHE
1	A	926	VAL
1	C	350	PHE
1	C	384	PHE
1	C	418	PHE
1	C	452	PHE
1	C	543	ASP
1	C	694	PHE
1	C	868	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

5 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	12V	A	1501	-	32,41,41	1.85	6 (18%)	38,62,62	1.41	6 (15%)
4	SO4	D	101	-	4,4,4	0.17	0	6,6,6	0.15	0
3	12V	C	1501	-	32,41,41	1.77	6 (18%)	38,62,62	1.39	6 (15%)
4	SO4	A	1502	-	4,4,4	0.15	0	6,6,6	0.05	0
4	SO4	B	101	-	4,4,4	0.14	0	6,6,6	0.12	0

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	12V	A	1501	-	-	4/23/63/63	0/3/3/3
3	12V	C	1501	-	-	4/23/63/63	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1501	12V	PB-O1'	6.54	1.77	1.60
3	C	1501	12V	PB-O1'	6.17	1.76	1.60
3	A	1501	12V	O4-C4	4.31	1.35	1.24
3	C	1501	12V	O4-C4	4.12	1.34	1.24
3	C	1501	12V	PA-O5B	3.27	1.72	1.59
3	A	1501	12V	PA-O5B	3.26	1.72	1.59
3	A	1501	12V	C6'-C5'	3.02	1.54	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1501	12V	C6-N1	2.99	1.39	1.35
3	C	1501	12V	C6'-C5'	2.73	1.54	1.52
3	A	1501	12V	C6-N1	2.34	1.38	1.35
3	A	1501	12V	O5B-C5B	-2.18	1.36	1.44
3	C	1501	12V	O5B-C5B	-2.16	1.36	1.44

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1501	12V	O1'-C1'-C2'	4.72	114.61	107.47
3	C	1501	12V	O1'-C1'-C2'	4.32	114.00	107.47
3	C	1501	12V	O2A-PA-O1A	3.31	128.59	112.24
3	A	1501	12V	O2A-PA-O1A	3.28	128.47	112.24
3	A	1501	12V	O2B-PB-O1B	2.85	126.32	112.24
3	C	1501	12V	O2B-PB-O1B	2.76	125.89	112.24
3	A	1501	12V	C4'-C3'-C2'	2.57	114.11	110.34
3	C	1501	12V	C4'-C3'-C2'	2.47	113.96	110.34
3	C	1501	12V	O4'-C4'-C3'	-2.21	105.23	110.35
3	C	1501	12V	O3'-C3'-C4'	-2.17	105.32	110.35
3	A	1501	12V	O3'-C3'-C4'	-2.01	105.70	110.35
3	A	1501	12V	O4'-C4'-C3'	-2.01	105.71	110.35

There are no chirality outliers.

All (8) torsion outliers are listed below:

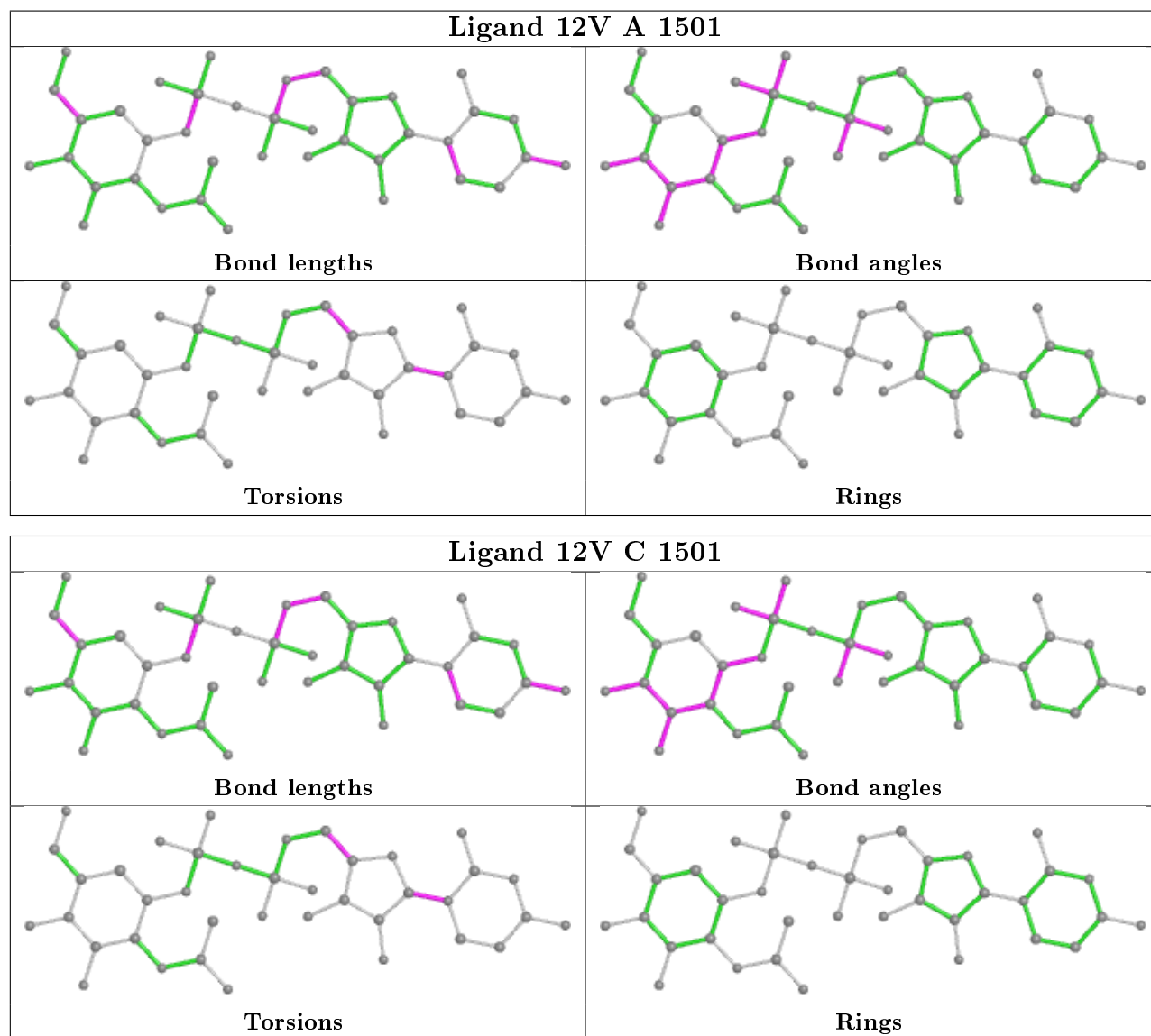
Mol	Chain	Res	Type	Atoms
3	A	1501	12V	C2B-C1B-N1-C6
3	A	1501	12V	O4B-C1B-N1-C6
3	A	1501	12V	O4B-C4B-C5B-O5B
3	C	1501	12V	C2B-C1B-N1-C6
3	C	1501	12V	O4B-C1B-N1-C6
3	C	1501	12V	O4B-C4B-C5B-O5B
3	A	1501	12V	C3B-C4B-C5B-O5B
3	C	1501	12V	C3B-C4B-C5B-O5B

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1501	12V	1	0
3	C	1501	12V	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 than 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.



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, 95th 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	693/723 (95%)	0.27	41 (5%) 22 22	13, 25, 52, 94	0
1	C	671/723 (92%)	0.29	41 (6%) 21 20	13, 24, 52, 96	0
2	B	14/14 (100%)	0.45	0 100 100	15, 22, 46, 48	0
2	D	14/14 (100%)	0.52	0 100 100	14, 20, 42, 43	0
All	All	1392/1474 (94%)	0.28	82 (5%) 22 22	13, 24, 52, 96	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	713	PHE	11.9
1	A	713	PHE	9.2
1	A	769	MET	7.7
1	C	338	ARG	6.3
1	A	740	ASP	6.2
1	C	339	LEU	6.2
1	C	769	MET	6.1
1	A	718	HIS	6.1
1	A	314	PRO	5.7
1	C	718	HIS	5.6
1	C	860	ASN	5.5
1	C	348	PRO	5.4
1	A	772	ILE	5.3
1	C	772	ILE	5.3
1	C	740	ASP	5.1
1	C	526	ASN	4.9
1	A	860	ASN	4.8
1	A	326	ILE	4.6
1	C	337	VAL	4.6
1	C	532	PRO	4.5
1	A	526	ASN	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	1028	LYS	4.4
1	C	347	PHE	4.4
1	C	344	LEU	4.3
1	C	346	VAL	4.2
1	A	333	ILE	4.1
1	A	315	THR	3.5
1	C	742	LYS	3.3
1	C	340	TYR	3.2
1	A	447	LYS	3.1
1	A	491	ARG	3.1
1	C	525	ILE	3.0
1	C	1019	ALA	3.0
1	A	742	LYS	3.0
1	A	534	GLU	2.9
1	C	527	VAL	2.9
1	C	447	LYS	2.8
1	A	830	ASP	2.8
1	C	712	ASP	2.8
1	C	534	GLU	2.8
1	C	363	GLN	2.8
1	A	768	PRO	2.8
1	A	328	ARG	2.8
1	A	540	LYS	2.7
1	C	342	LYS	2.7
1	A	537	LYS	2.7
1	A	330	GLN	2.7
1	A	335	GLU	2.7
1	A	763	ASN	2.7
1	C	529	HIS	2.7
1	A	332	ASN	2.6
1	A	529	HIS	2.6
1	A	739	PRO	2.6
1	A	771	THR	2.5
1	A	680	GLU	2.5
1	C	768	PRO	2.5
1	A	1018	ALA	2.5
1	C	662	LEU	2.4
1	A	532	PRO	2.4
1	C	350	PHE	2.4
1	C	345	GLU	2.4
1	C	830	ASP	2.3
1	A	1016	HIS	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	543	ASP	2.3
1	C	1022	LYS	2.3
1	A	712	ASP	2.2
1	A	738	LEU	2.2
1	A	1028	LYS	2.2
1	C	537	LYS	2.2
1	C	741	VAL	2.2
1	A	323	LEU	2.2
1	A	662	LEU	2.2
1	C	763	ASN	2.2
1	A	334	GLU	2.2
1	C	1015	GLU	2.2
1	C	360	VAL	2.2
1	C	1018	ALA	2.1
1	C	680	GLU	2.1
1	A	770	ASN	2.1
1	A	1015	GLU	2.1
1	A	743	ILE	2.0
1	C	1027	ILE	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 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, 95th 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.

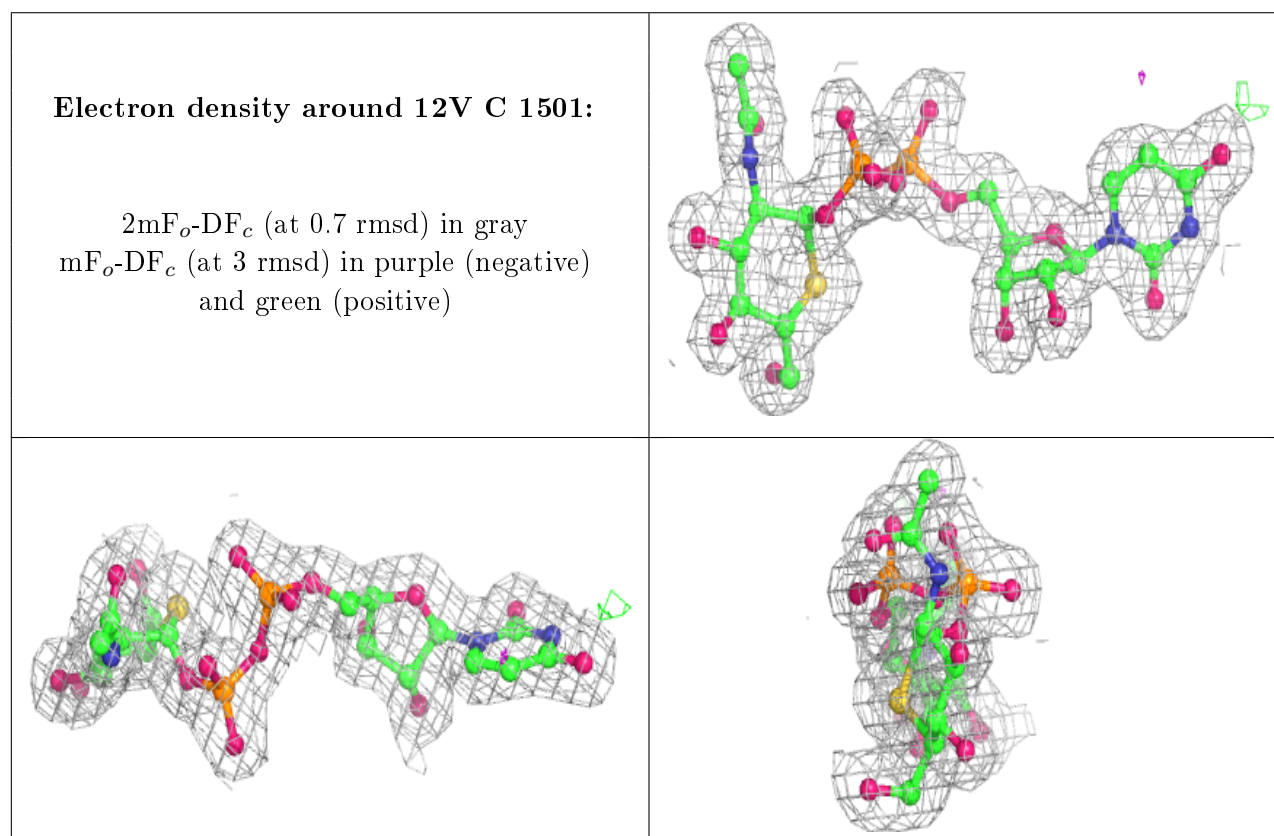
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	A	1502	5/5	0.94	0.17	63,64,65,65	0
3	12V	C	1501	39/39	0.97	0.12	8,14,18,23	0
3	12V	A	1501	39/39	0.97	0.11	10,14,19,22	0
4	SO4	D	101	5/5	0.98	0.12	33,33,35,37	0

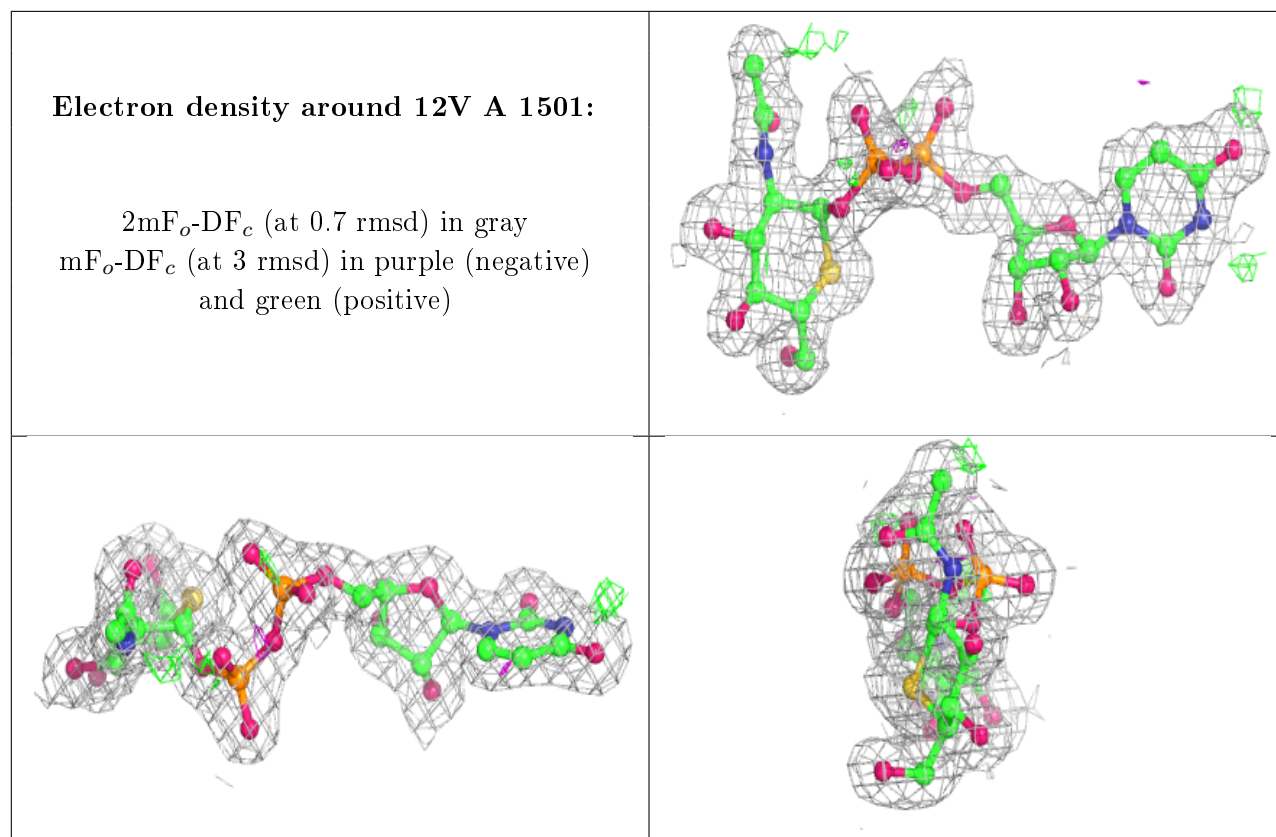
Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	B	101	5/5	0.98	0.10	32,34,37,38	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.