Full wwPDB X-ray Structure Validation Report (i)

Mar 23, 2024 – 05:11 PM EDT

PDB ID	:	3V2Y
Title	:	Crystal Structure of a Lipid G protein-Coupled Receptor at 2.80A
Authors	:	Hanson, M.A.; Roth, C.B.; Jo, E.; Griffith, M.T.; Scott, F.L.; Reinhart, G.; Desale, H.; Clemons, B.; Cahalan, S.M.; Schuerer, S.C.; Sanna, M.G.; Han, G.W.; Kuhn, P.; Rosen, H.; Stevens, R.C.; GPCR Network (GPCR)
Deposited on	:	2011-12-12
Resolution	:	2.80 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 (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 (i)) were used in the production of this report:

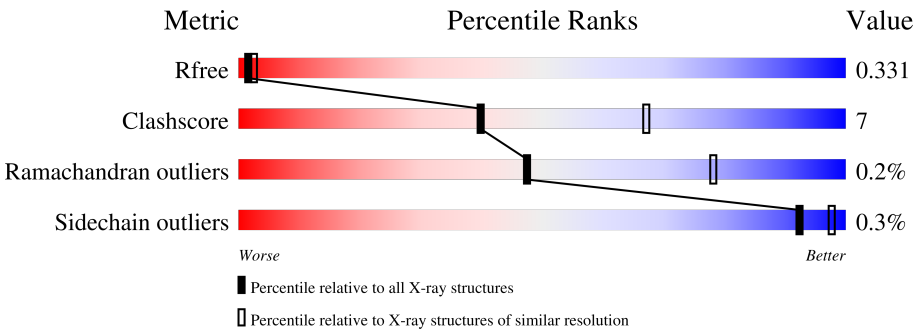
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.1

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 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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%

Mol	Chain	Length	Quality of chain
1	A	520	77% 10% 12%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3523 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 Sphingosine 1-phosphate receptor 1, Lysozyme chimera (E.C.3.2.1.17).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	455	3475	2278	564	613	20	0	0	0

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	expression tag	UNP P21453
A	-16	LYS	-	expression tag	UNP P21453
A	-15	THR	-	expression tag	UNP P21453
A	-14	ILE	-	expression tag	UNP P21453
A	-13	ILE	-	expression tag	UNP P21453
A	-12	ALA	-	expression tag	UNP P21453
A	-11	LEU	-	expression tag	UNP P21453
A	-10	SER	-	expression tag	UNP P21453
A	-9	TYR	-	expression tag	UNP P21453
A	-8	ILE	-	expression tag	UNP P21453
A	-7	PHE	-	expression tag	UNP P21453
A	-6	CYS	-	expression tag	UNP P21453
A	-5	LEU	-	expression tag	UNP P21453
A	-4	VAL	-	expression tag	UNP P21453
A	-3	PHE	-	expression tag	UNP P21453
A	-2	ALA	-	expression tag	UNP P21453
A	-1	GLY	-	expression tag	UNP P21453
A	0	ALA	-	expression tag	UNP P21453
A	1	PRO	-	expression tag	UNP P21453
A	1012	GLY	ARG	conflict	UNP P00720
A	1054	THR	CYS	engineered mutation	UNP P00720
A	1097	ALA	CYS	engineered mutation	UNP P00720
A	1137	ARG	ILE	conflict	UNP P00720
A	?	-	LYS	deletion	UNP P21453
A	251	ASN	SER	see remark 999	UNP P21453
A	252	VAL	LEU	see remark 999	UNP P21453
A	327	GLY	-	expression tag	UNP P21453

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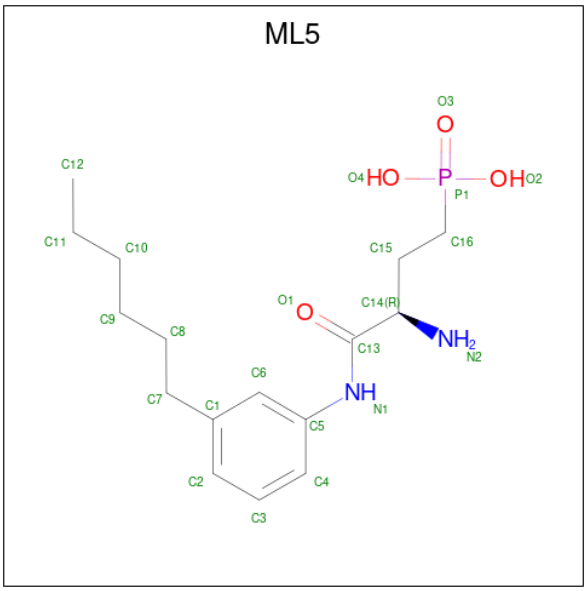
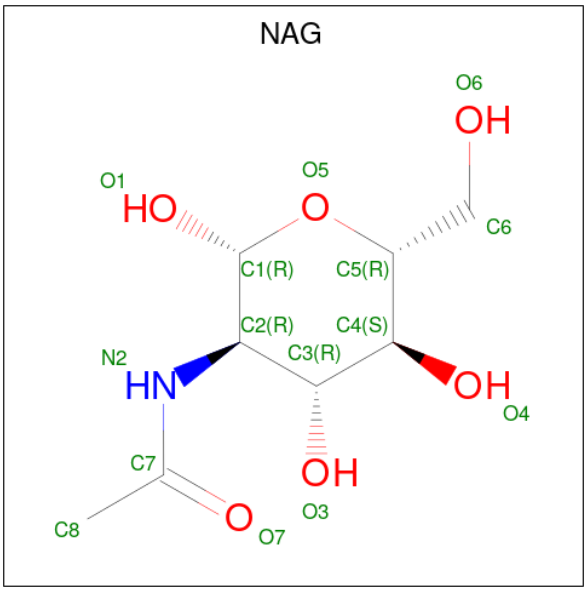
Chain	Residue	Modelled	Actual	Comment	Reference
A	328	ARG	-	expression tag	UNP P21453
A	329	PRO	-	expression tag	UNP P21453
A	330	LEU	-	expression tag	UNP P21453
A	331	GLU	-	expression tag	UNP P21453
A	332	VAL	-	expression tag	UNP P21453
A	333	LEU	-	expression tag	UNP P21453
A	334	PHE	-	expression tag	UNP P21453
A	335	GLN	-	expression tag	UNP P21453
A	336	GLY	-	expression tag	UNP P21453
A	337	PRO	-	expression tag	UNP P21453
A	338	HIS	-	expression tag	UNP P21453
A	339	HIS	-	expression tag	UNP P21453
A	340	HIS	-	expression tag	UNP P21453
A	341	HIS	-	expression tag	UNP P21453
A	342	HIS	-	expression tag	UNP P21453
A	343	HIS	-	expression tag	UNP P21453
A	344	HIS	-	expression tag	UNP P21453
A	345	HIS	-	expression tag	UNP P21453
A	346	HIS	-	expression tag	UNP P21453
A	347	HIS	-	expression tag	UNP P21453
A	348	ASP	-	expression tag	UNP P21453
A	349	TYR	-	expression tag	UNP P21453
A	350	LYS	-	expression tag	UNP P21453
A	351	ASP	-	expression tag	UNP P21453
A	352	ASP	-	expression tag	UNP P21453
A	353	ASP	-	expression tag	UNP P21453
A	354	ASP	-	expression tag	UNP P21453
A	355	LYS	-	expression tag	UNP P21453

- Molecule 2 is {(3R)-3-amino-4-[(3-hexylphenyl)amino]-4-oxobutyl}phosphonic acid (three-letter code: ML5) (formula: $C_{16}H_{27}N_2O_4P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	23	16	2	4	1	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	14	8	1	5	0	0

- Molecule 4 is water.

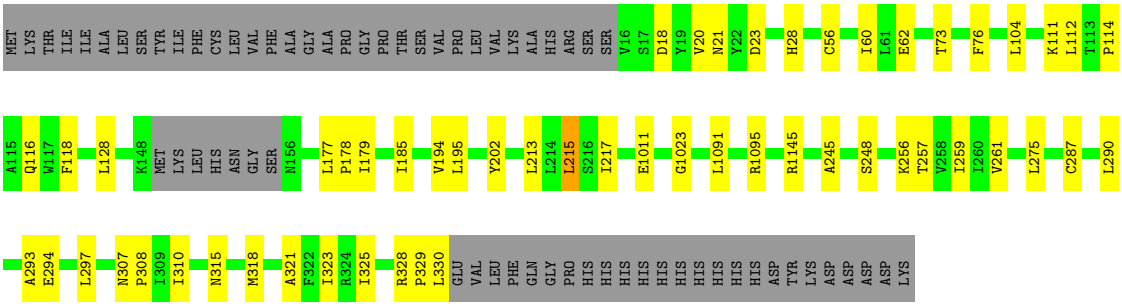
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	11	11	11	0	0

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.

- Molecule 1: Sphingosine 1-phosphate receptor 1, Lysozyme chimera (E.C.3.2.1.17)

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	107.94Å 69.70Å 81.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.52 – 2.80 19.52 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (19.52-2.80) 97.1 (19.52-2.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.70 (at 2.79Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.229 , 0.272 0.272 , 0.331	Depositor DCC
R_{free} test set	742 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	52.0	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 50.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.39$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3523	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.46% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ML5, NAG

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	0.49	0/3545	0.38	0/4837

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	3475	0	3486	50	0
2	A	23	0	27	3	0
3	A	14	0	13	0	0
4	A	11	0	0	0	0
All	All	3523	0	3526	51	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 7.

All (51) 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:A:325:ILE:O	1:A:325:ILE:HG22	1.67	0.91
1:A:1011:GLU:HG2	1:A:1145:ARG:HH12	1.44	0.82
1:A:1011:GLU:CG	1:A:1145:ARG:HH12	1.93	0.81
1:A:328:ARG:CB	1:A:329:PRO:CD	2.67	0.72
1:A:1011:GLU:HG2	1:A:1145:ARG:NH1	2.07	0.67
1:A:328:ARG:CB	1:A:329:PRO:HD3	2.28	0.64
1:A:325:ILE:O	1:A:325:ILE:CG2	2.40	0.64
1:A:1011:GLU:CG	1:A:1145:ARG:NH1	2.62	0.62
1:A:177:LEU:HD21	1:A:202:TYR:HE1	1.63	0.62
1:A:321:ALA:O	1:A:325:ILE:HG12	2.00	0.61
1:A:118:PHE:HB3	1:A:179:ILE:HG12	1.83	0.60
1:A:177:LEU:N	1:A:178:PRO:HD2	2.19	0.58
1:A:215:LEU:O	1:A:215:LEU:HD12	2.07	0.54
1:A:294:GLU:HA	1:A:297:LEU:HD12	1.90	0.54
1:A:28:HIS:CE1	1:A:185:ILE:HA	2.44	0.53
1:A:297:LEU:HD13	2:A:1201:ML5:H6	1.92	0.51
1:A:261:VAL:HG22	1:A:310:ILE:HG21	1.93	0.50
1:A:323:ILE:C	1:A:325:ILE:H	2.13	0.50
1:A:73:THR:HB	1:A:76:PHE:HB2	1.92	0.50
2:A:1201:ML5:H12	2:A:1201:ML5:O1	2.11	0.50
1:A:104:LEU:HD22	1:A:112:LEU:HD21	1.93	0.50
1:A:307:ASN:O	1:A:310:ILE:HG22	2.13	0.49
1:A:275:LEU:HD21	1:A:293:ALA:HB1	1.95	0.49
1:A:287:CYS:HB2	1:A:290:LEU:HD12	1.95	0.49
1:A:18:ASP:C	1:A:20:VAL:H	2.16	0.48
1:A:177:LEU:HD21	1:A:202:TYR:CE1	2.47	0.47
1:A:76:PHE:HZ	1:A:318:MET:HA	1.79	0.47
1:A:104:LEU:HB3	1:A:112:LEU:HD11	1.97	0.47
1:A:62:GLU:HB3	1:A:308:PRO:HG2	1.98	0.46
1:A:112:LEU:HD22	1:A:116:GLN:HB3	1.98	0.46
1:A:20:VAL:O	1:A:20:VAL:HG12	2.16	0.46
1:A:245:ALA:HB1	1:A:248:SER:HB2	1.98	0.45
1:A:257:THR:HG21	1:A:315:ASN:HD22	1.79	0.45
1:A:128:LEU:CD2	2:A:1201:ML5:H25	2.47	0.45
1:A:323:ILE:C	1:A:325:ILE:N	2.71	0.45
1:A:330:LEU:HD13	1:A:330:LEU:HA	1.86	0.44
1:A:177:LEU:N	1:A:178:PRO:CD	2.80	0.44
1:A:213:LEU:O	1:A:217:ILE:HG12	2.19	0.43
1:A:21:ASN:HD22	1:A:23:ASP:HB3	1.82	0.43
1:A:329:PRO:O	1:A:330:LEU:C	2.56	0.43
1:A:20:VAL:HA	1:A:114:PRO:HD2	2.01	0.43
1:A:328:ARG:CB	1:A:329:PRO:HD2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:ASN:ND2	1:A:23:ASP:HB3	2.36	0.41
1:A:28:HIS:HE1	1:A:185:ILE:HA	1.84	0.41
1:A:111:LYS:HD2	1:A:111:LYS:HA	1.91	0.41
1:A:56:CYS:O	1:A:60:ILE:HG12	2.21	0.40
1:A:194:VAL:HG13	1:A:195:LEU:HD12	2.04	0.40
1:A:307:ASN:HB2	1:A:308:PRO:HD3	2.03	0.40
1:A:256:LYS:HA	1:A:259:ILE:HD12	2.02	0.40
1:A:321:ALA:O	1:A:325:ILE:CG1	2.70	0.40
1:A:1091:LEU:HD22	1:A:1095:ARG:HB3	2.02	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	451/520 (87%)	430 (95%)	20 (4%)	1 (0%)	47 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1023	GLY

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	362/454 (80%)	361 (100%)	1 (0%)	92 98

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

Mol	Chain	Res	Type
1	A	215	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	199	HIS

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)

2 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	NAG	A	1202	1	14,14,15	1.60	2 (14%)	17,19,21	0.94	0
2	ML5	A	1201	-	23,23,23	0.99	2 (8%)	28,30,30	1.27	2 (7%)

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	NAG	A	1202	1	-	0/6/23/26	0/1/1/1
2	ML5	A	1201	-	-	5/20/20/20	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1202	NAG	C1-C2	4.14	1.58	1.52
2	A	1201	ML5	P1-C16	3.18	1.82	1.78
2	A	1201	ML5	C5-N1	-2.16	1.37	1.41
3	A	1202	NAG	C3-C2	2.05	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1201	ML5	O3-P1-C16	-4.00	103.99	111.40
2	A	1201	ML5	P1-C16-C15	-3.90	110.10	114.98

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	ML5	N2-C14-C15-C16
2	A	1201	ML5	C11-C10-C9-C8
2	A	1201	ML5	C7-C8-C9-C10
2	A	1201	ML5	C9-C10-C11-C12
2	A	1201	ML5	C13-C14-C15-C16

There are no ring outliers.

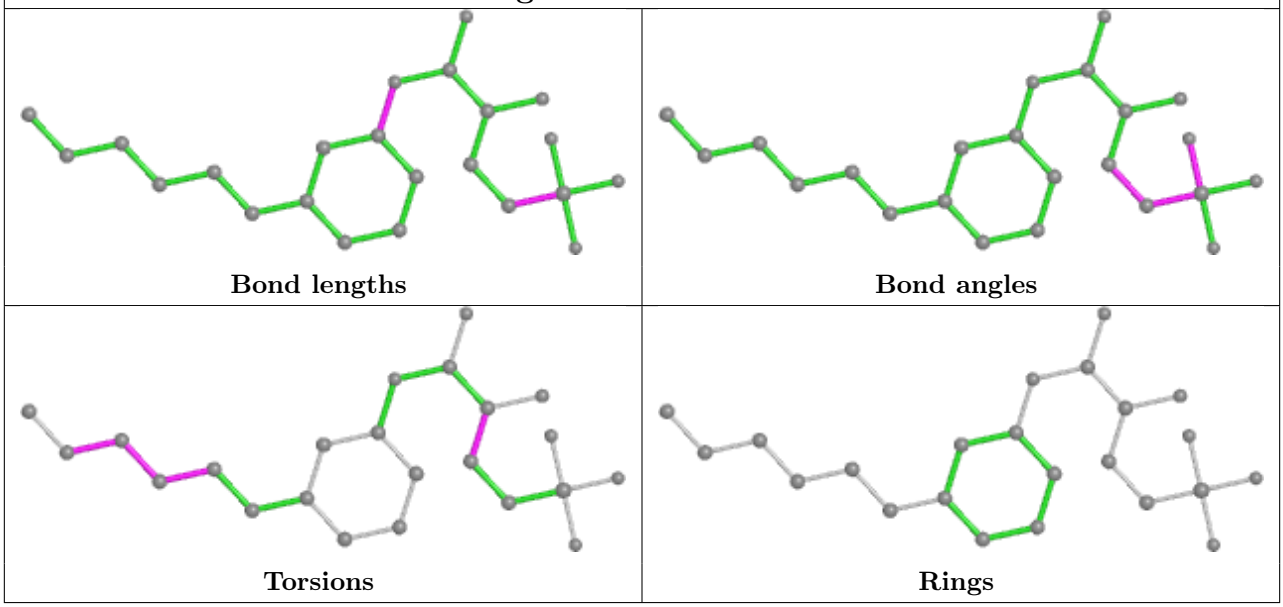
1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	ML5	3	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 ML5 A 1201



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 (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

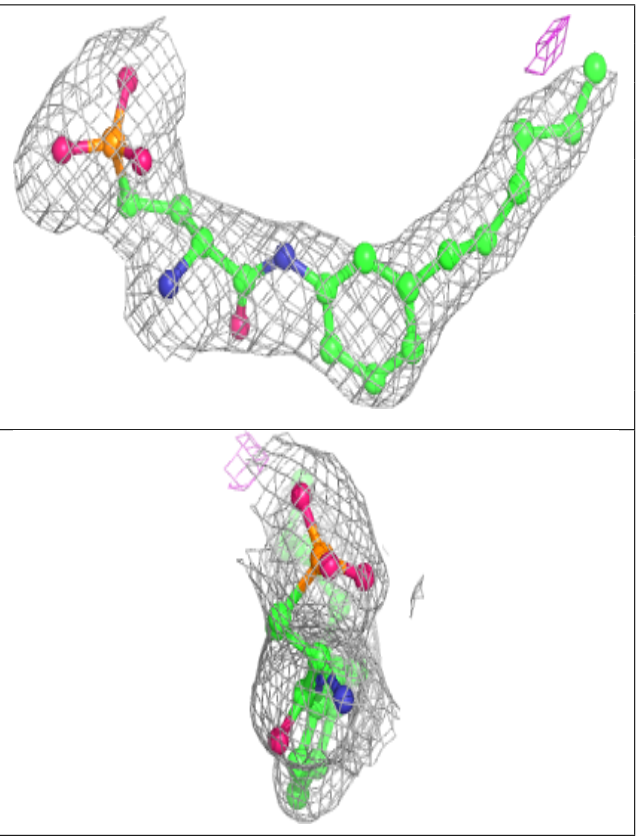
6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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 ML5 A 1201:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.