Full wwPDB X-ray Structure Validation Report (i)

Mar 3, 2024 – 01:39 AM EST

PDB ID	:	6B72
Title	:	A novel HIV-1 Nef dimer interface induced by a single octyl-glucoside molecule
Authors	:	Wu, M.; Augelli-Szafran, C.E.; Ptak, R.G.; Smithgall, T.E.
Deposited on	:	2017-10-03
Resolution	:	3.20 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:

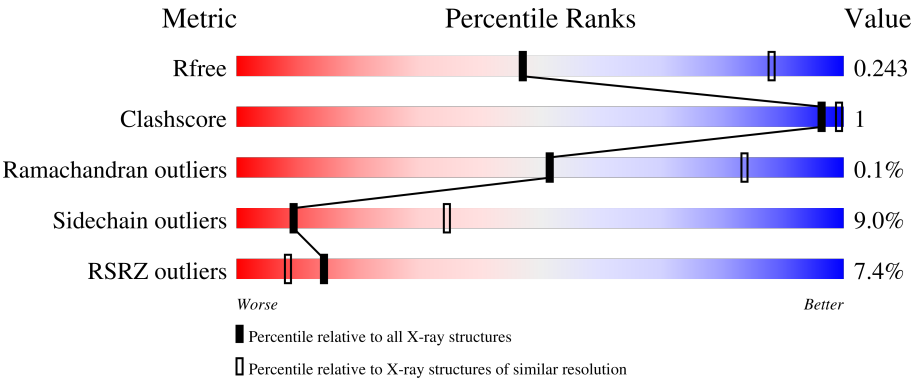
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	151	5% 73% 9% • 18%
1	B	151	7% 72% 7% • 20%
1	C	151	3% 73% 7% • 19%
1	D	151	5% 74% 7% • 19%
1	E	151	9% 70% 9% 21%

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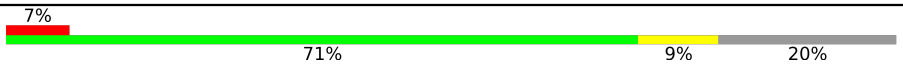
Mol	Chain	Length	Quality of chain
1	F	151	

2 Entry composition

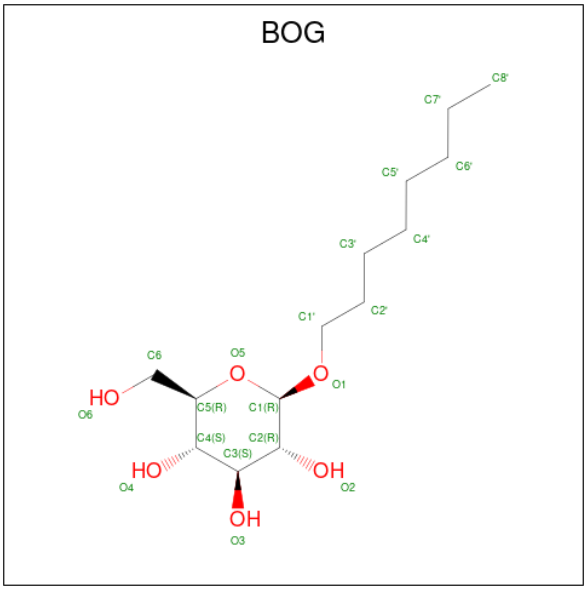
There are 2 unique types of molecules in this entry. The entry contains 6243 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Protein Nef.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	124	Total	C	N	O	S	0	0	0
			1049	690	174	181	4			
1	B	121	Total	C	N	O	S	0	0	0
			1027	678	171	174	4			
1	C	122	Total	C	N	O	S	0	0	0
			1036	683	172	177	4			
1	D	122	Total	C	N	O	S	0	0	0
			1036	683	172	177	4			
1	E	119	Total	C	N	O	S	0	0	0
			1009	667	168	170	4			
1	F	121	Total	C	N	O	S	0	0	0
			1026	677	171	174	4			

- Molecule 2 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula: $C_{14}H_{28}O_6$).



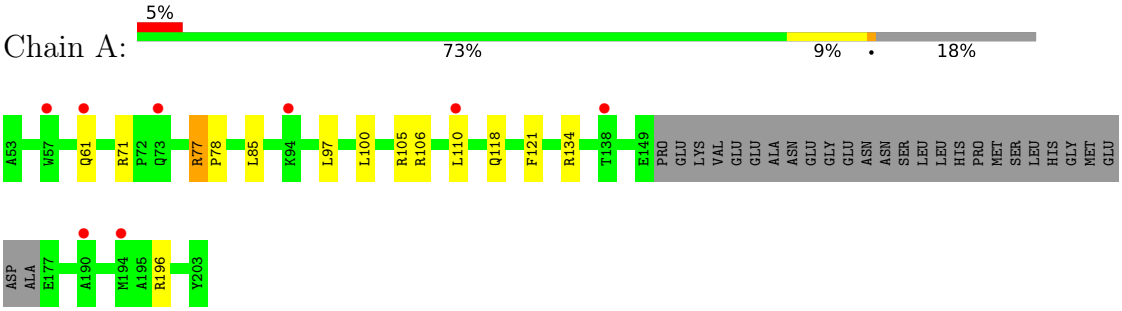
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			20	14	6		
2	C	1	Total	C	O	0	0
			20	14	6		
2	F	1	Total	C	O	0	0
			20	14	6		

3 Residue-property plots

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.

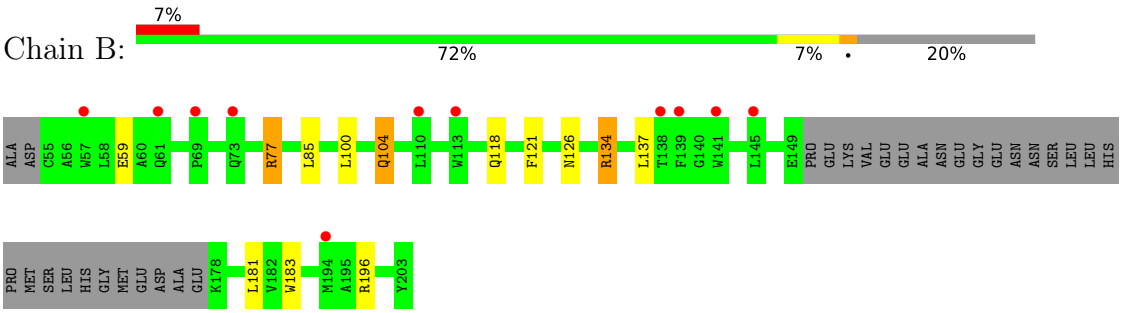
• Molecule 1: Protein Nef

Chain A:



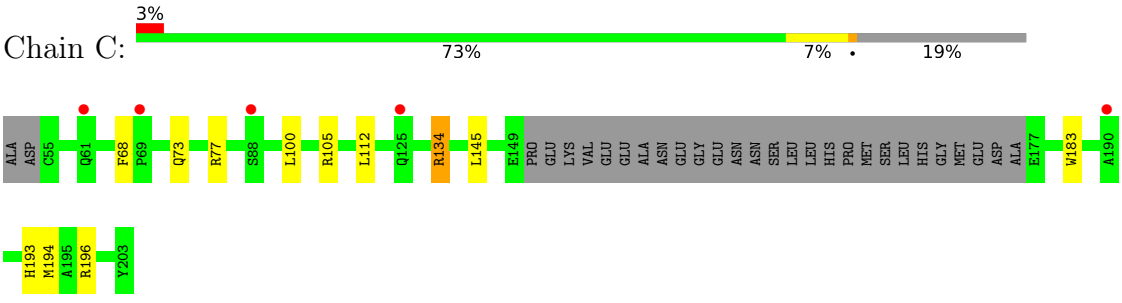
• Molecule 1: Protein Nef

Chain B:



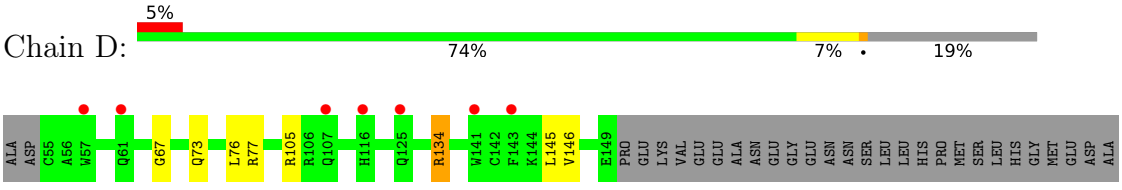
• Molecule 1: Protein Nef

Chain C:

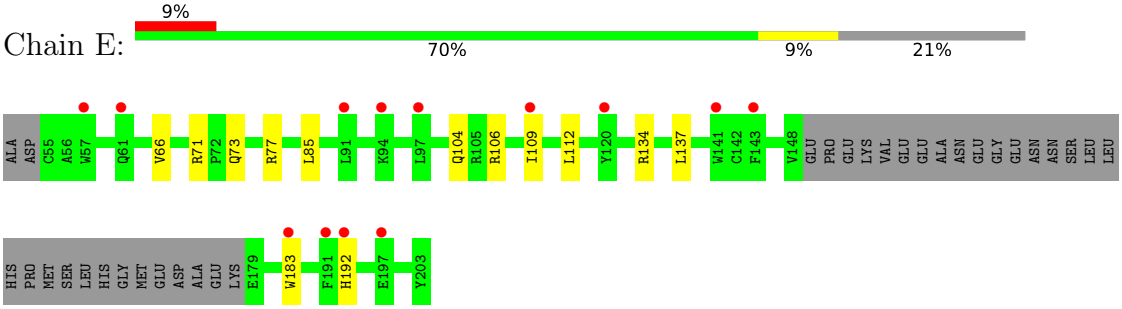


• Molecule 1: Protein Nef

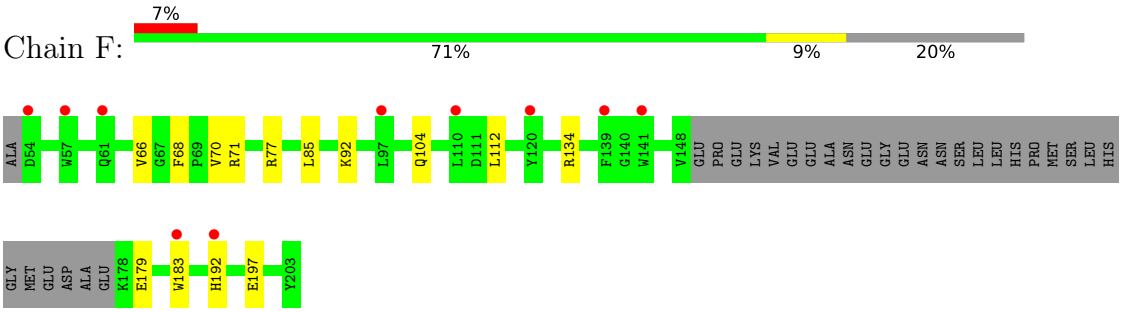
Chain D:



• Molecule 1: Protein Nef



• Molecule 1: Protein Nef



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	109.58Å 109.58Å 247.04Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	94.90 – 3.20 88.59 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (94.90-3.20) 100.0 (88.59-3.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.00 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.233 , 0.251 0.233 , 0.243	Depositor DCC
R_{free} test set	1494 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	109.6	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 85.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.53$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6243	wwPDB-VP
Average B, all atoms (Å^2)	120.0	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 40.74 % 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 2.6149e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: BOG

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	0.39	0/1088	0.60	0/1480
1	B	0.39	0/1066	0.59	0/1450
1	C	0.38	0/1075	0.60	0/1462
1	D	0.39	0/1075	0.59	0/1462
1	E	0.40	0/1048	0.60	0/1427
1	F	0.38	0/1065	0.64	0/1449
All	All	0.39	0/6417	0.60	0/8730

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
1	F	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	67	GLY	Peptide
1	F	66	VAL	Peptide

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	1049	0	1001	3	0
1	B	1027	0	986	3	0
1	C	1036	0	992	3	0
1	D	1036	0	992	2	0
1	E	1009	0	967	2	0
1	F	1026	0	984	0	0
2	A	20	0	28	0	0
2	C	20	0	28	0	0
2	F	20	0	28	0	0
All	All	6243	0	6006	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 1.

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:77:ARG:NH1	1:B:118:GLN:O	2.36	0.59
1:A:97:LEU:HD21	1:A:110:LEU:HD22	1.90	0.53
1:D:134:ARG:HB2	1:D:145:LEU:HB2	1.91	0.52
1:B:134:ARG:NH2	1:B:181:LEU:HD21	2.27	0.48
1:D:193:HIS:ND1	1:D:196:ARG:HB2	2.30	0.46
1:B:104:GLN:HE21	1:B:104:GLN:HA	1.83	0.43
1:A:77:ARG:NH1	1:A:118:GLN:O	2.49	0.43
1:C:193:HIS:ND1	1:C:196:ARG:HB2	2.33	0.43
1:C:134:ARG:HB2	1:C:145:LEU:HB2	2.01	0.42
1:A:100:LEU:HD22	1:A:106:ARG:NH1	2.36	0.41
1:C:112:LEU:CD1	1:E:109:ILE:HD12	2.51	0.41
1:E:66:VAL:O	1:E:66:VAL:HG23	2.22	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	120/151 (80%)	109 (91%)	10 (8%)	1 (1%)	19 58
1	B	117/151 (78%)	110 (94%)	7 (6%)	0	100 100
1	C	118/151 (78%)	112 (95%)	6 (5%)	0	100 100
1	D	118/151 (78%)	113 (96%)	5 (4%)	0	100 100
1	E	115/151 (76%)	105 (91%)	10 (9%)	0	100 100
1	F	117/151 (78%)	109 (93%)	8 (7%)	0	100 100
All	All	705/906 (78%)	658 (93%)	46 (6%)	1 (0%)	51 83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	78	PRO

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	109/132 (83%)	101 (93%)	8 (7%)	14 46
1	B	107/132 (81%)	96 (90%)	11 (10%)	7 29
1	C	108/132 (82%)	100 (93%)	8 (7%)	13 46
1	D	108/132 (82%)	101 (94%)	7 (6%)	17 51
1	E	105/132 (80%)	94 (90%)	11 (10%)	7 28
1	F	107/132 (81%)	94 (88%)	13 (12%)	5 22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	644/792 (81%)	586 (91%)	58 (9%)	9 34

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	71	ARG
1	A	77	ARG
1	A	85	LEU
1	A	105	ARG
1	A	121	PHE
1	A	134	ARG
1	A	196	ARG
1	B	59	GLU
1	B	77	ARG
1	B	85	LEU
1	B	100	LEU
1	B	104	GLN
1	B	121	PHE
1	B	126	ASN
1	B	134	ARG
1	B	137	LEU
1	B	183	TRP
1	B	196	ARG
1	C	68	PHE
1	C	73	GLN
1	C	77	ARG
1	C	100	LEU
1	C	105	ARG
1	C	134	ARG
1	C	183	TRP
1	C	194	MET
1	D	73	GLN
1	D	76	LEU
1	D	77	ARG
1	D	105	ARG
1	D	134	ARG
1	D	146	VAL
1	D	183	TRP
1	E	71	ARG
1	E	73	GLN
1	E	77	ARG

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Mol	Chain	Res	Type
1	E	85	LEU
1	E	104	GLN
1	E	106	ARG
1	E	112	LEU
1	E	134	ARG
1	E	137	LEU
1	E	183	TRP
1	E	192	HIS
1	F	68	PHE
1	F	70	VAL
1	F	71	ARG
1	F	77	ARG
1	F	85	LEU
1	F	92	LYS
1	F	104	GLN
1	F	112	LEU
1	F	134	ARG
1	F	179	GLU
1	F	183	TRP
1	F	192	HIS
1	F	197	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	B	104	GLN
1	C	61	GLN
1	C	73	GLN
1	D	73	GLN
1	E	73	GLN
1	E	104	GLN
1	F	61	GLN

5.3.3 RNA

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)

3 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	$\#\|Z\| > 2$
2	BOG	C	301	-	20,20,20	0.54	0	25,25,25	0.59	0
2	BOG	A	601	-	20,20,20	0.60	1 (5%)	25,25,25	0.46	0
2	BOG	F	301	-	20,20,20	0.55	0	25,25,25	0.57	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
2	BOG	C	301	-	-	1/11/31/31	0/1/1/1
2	BOG	A	601	-	-	3/11/31/31	0/1/1/1
2	BOG	F	301	-	-	2/11/31/31	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	BOG	O1-C1	2.07	1.43	1.40

There are no bond angle outliers.

There are no chirality outliers.

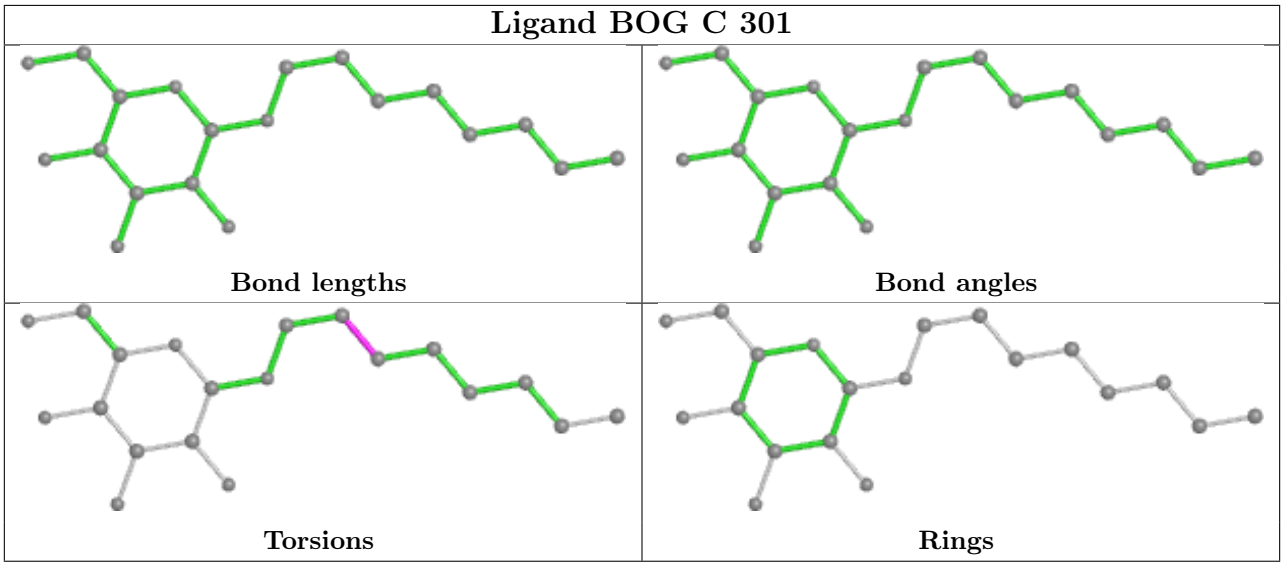
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	BOG	O5-C1-O1-C1'
2	F	301	BOG	C1'-C2'-C3'-C4'
2	A	601	BOG	C1'-C2'-C3'-C4'
2	A	601	BOG	O1-C1'-C2'-C3'
2	C	301	BOG	C1'-C2'-C3'-C4'
2	F	301	BOG	C2'-C3'-C4'-C5'

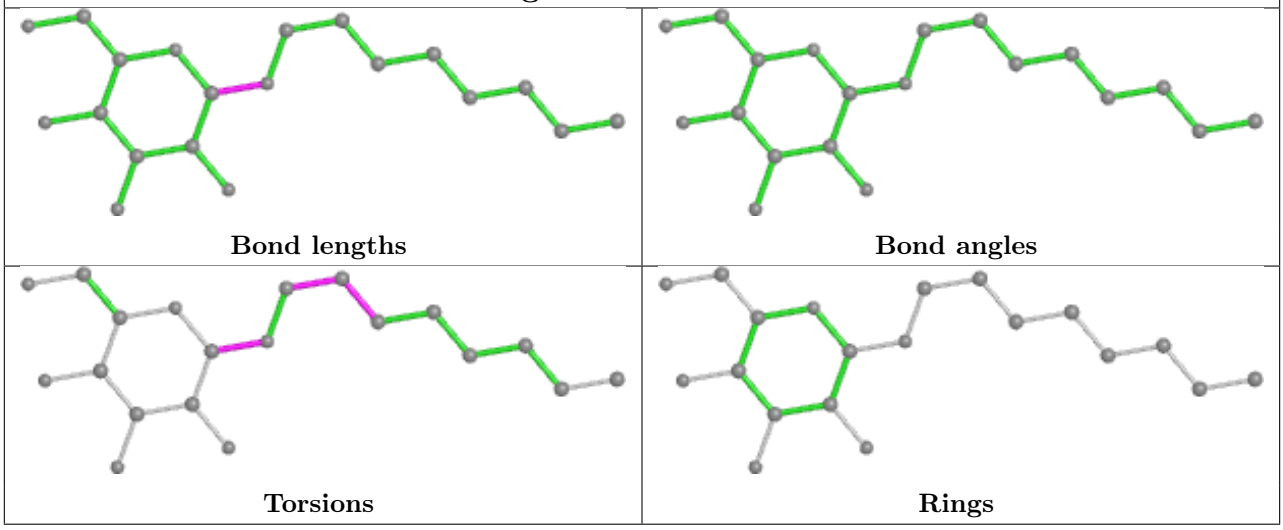
There are no ring outliers.

No monomer is involved in short contacts.

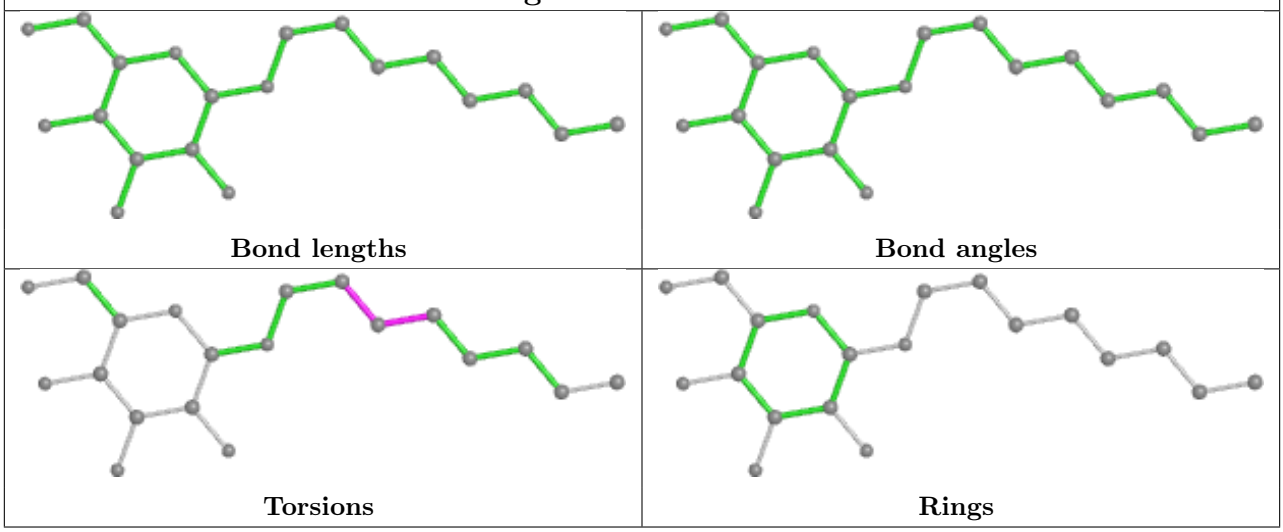
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 BOG A 601



Ligand BOG F 301



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	124/151 (82%)	0.73	8 (6%) 18 11	91, 114, 159, 177	0
1	B	121/151 (80%)	0.80	11 (9%) 9 5	92, 110, 150, 186	0
1	C	122/151 (80%)	0.77	5 (4%) 37 24	97, 115, 181, 208	0
1	D	122/151 (80%)	0.75	7 (5%) 23 13	91, 111, 153, 197	0
1	E	119/151 (78%)	0.80	13 (10%) 5 3	98, 119, 161, 195	0
1	F	121/151 (80%)	0.81	10 (8%) 11 6	96, 119, 162, 197	0
All	All	729/906 (80%)	0.78	54 (7%) 14 8	91, 115, 167, 208	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	192	HIS	5.1
1	A	57	TRP	4.8
1	F	61	GLN	4.6
1	D	57	TRP	4.4
1	B	57	TRP	4.1
1	C	61	GLN	4.0
1	E	192	HIS	4.0
1	B	61	GLN	3.7
1	F	54	ASP	3.6
1	E	61	GLN	3.4
1	B	73	GLN	3.3
1	E	57	TRP	3.2
1	E	183	TRP	3.2
1	F	57	TRP	3.1
1	A	73	GLN	2.9
1	D	61	GLN	2.9
1	E	120	TYR	2.9
1	F	141	TRP	2.9
1	D	107	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	94	LYS	2.8
1	C	69	PRO	2.7
1	B	194	MET	2.7
1	E	143	PHE	2.7
1	E	141	TRP	2.7
1	A	194	MET	2.6
1	E	97	LEU	2.6
1	F	110	LEU	2.6
1	A	110	LEU	2.5
1	B	110	LEU	2.5
1	B	141	TRP	2.5
1	D	143	PHE	2.5
1	A	94	LYS	2.4
1	F	97	LEU	2.4
1	F	183	TRP	2.4
1	F	139	PHE	2.3
1	A	138	THR	2.3
1	D	116	HIS	2.3
1	E	109	ILE	2.3
1	F	120	TYR	2.3
1	B	69	PRO	2.2
1	E	197	GLU	2.2
1	D	141	TRP	2.2
1	E	191	PHE	2.2
1	A	61	GLN	2.2
1	B	145	LEU	2.2
1	B	138	THR	2.2
1	C	190	ALA	2.1
1	C	88	SER	2.1
1	C	125	GLN	2.1
1	B	113	TRP	2.1
1	D	125	GLN	2.0
1	A	190	ALA	2.0
1	B	139	PHE	2.0
1	E	91	LEU	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)

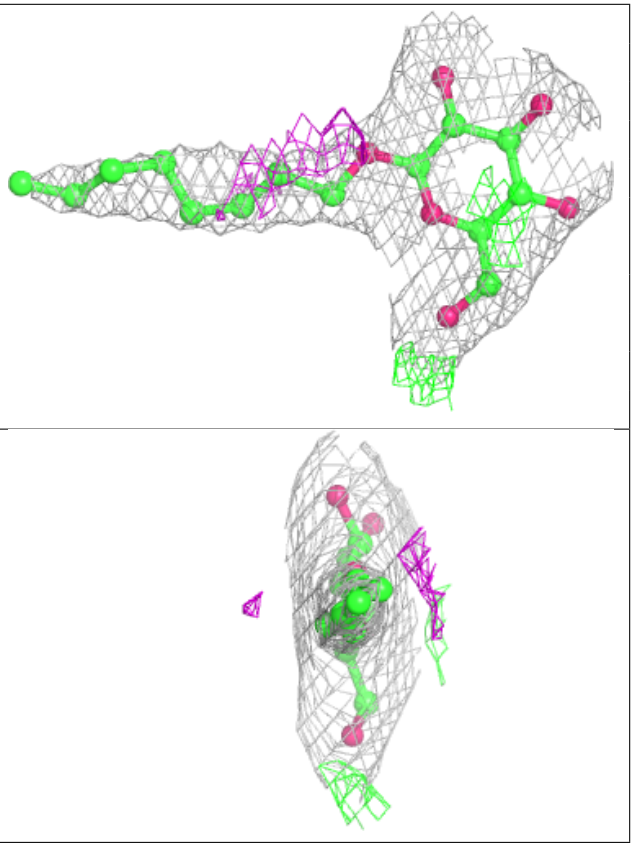
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
2	BOG	A	601	20/20	0.81	0.36	89,109,121,125	0
2	BOG	F	301	20/20	0.84	0.59	115,126,131,133	0
2	BOG	C	301	20/20	0.85	0.54	124,127,133,133	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.

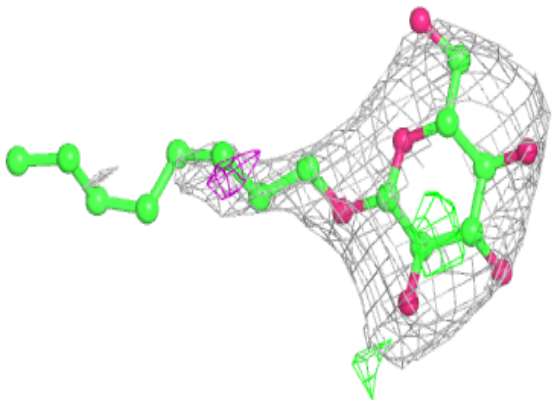
Electron density around BOG A 601:

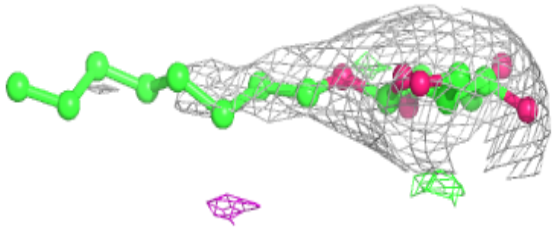
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

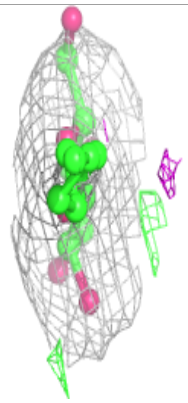


Electron density around BOG F 301:

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

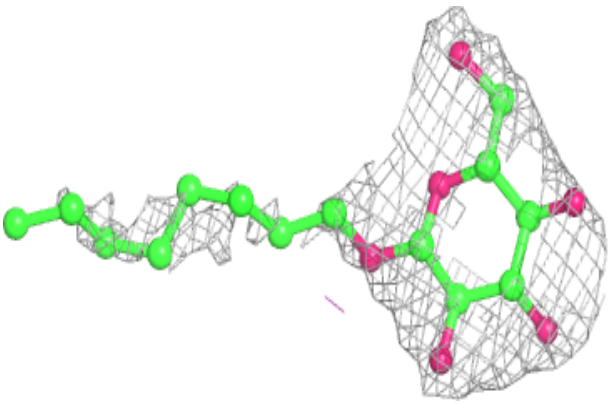


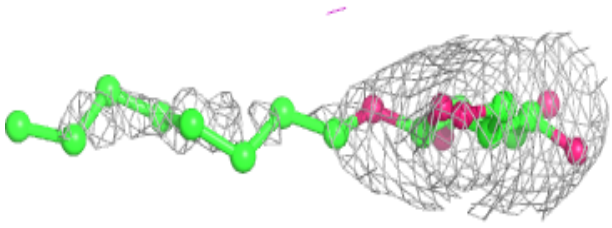


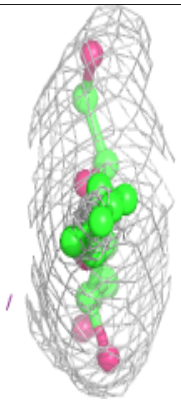


Electron density around BOG C 301:

$2mF_o$-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.