



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2022 – 02:02 PM EDT

PDB ID : 7MHX
Title : KcsA E71V closed gate with Ba²⁺
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Deposited on : 2021-04-15
Resolution : 2.85 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 : 2.27
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) : 2.27

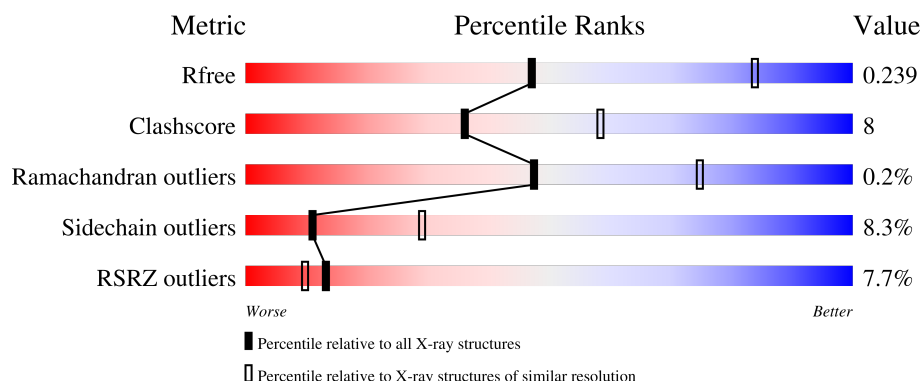
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 $\leq 5\%$. 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	219	<div> <div>10%</div> <div>72%</div> <div>27%</div> <div>.</div> </div>
2	B	212	<div> <div>6%</div> <div>75%</div> <div>25%</div> <div>.</div> </div>
3	C	124	<div> <div>6%</div> <div>70%</div> <div>12%</div> <div>.</div> <div>17%</div> </div>

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
5	DGA	C	202	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4072 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 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1606	1020	268	312	6			

- Molecule 2 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	0	0
			1646	1022	282	337	5			

- Molecule 3 is a protein called pH-gated potassium channel KcsA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	103	Total	C	N	O	S	0	0	0
			768	504	132	130	2			

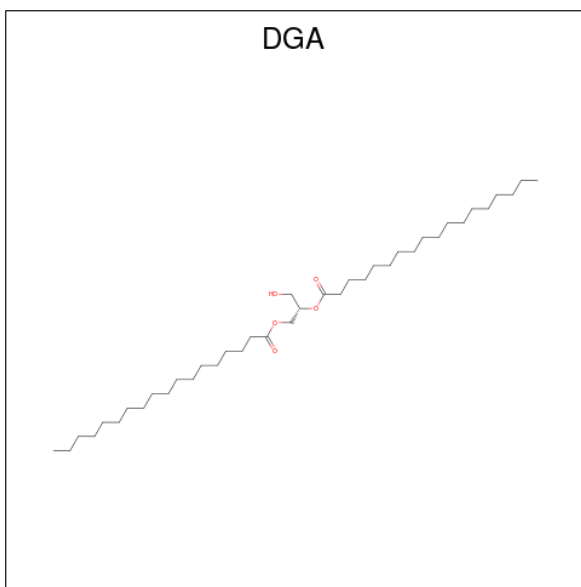
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	initiating methionine	UNP P0A334
C	2	ALA	PRO	engineered mutation	UNP P0A334
C	71	VAL	GLU	engineered mutation	UNP P0A334
C	90	CYS	LEU	engineered mutation	UNP P0A334

- Molecule 4 is BARIUM ION (three-letter code: BA) (formula: Ba) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Ba	0	0
			1	1		

- Molecule 5 is DIACYL GLYCEROL (three-letter code: DGA) (formula: C₃₉H₇₆O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			31	26	5		

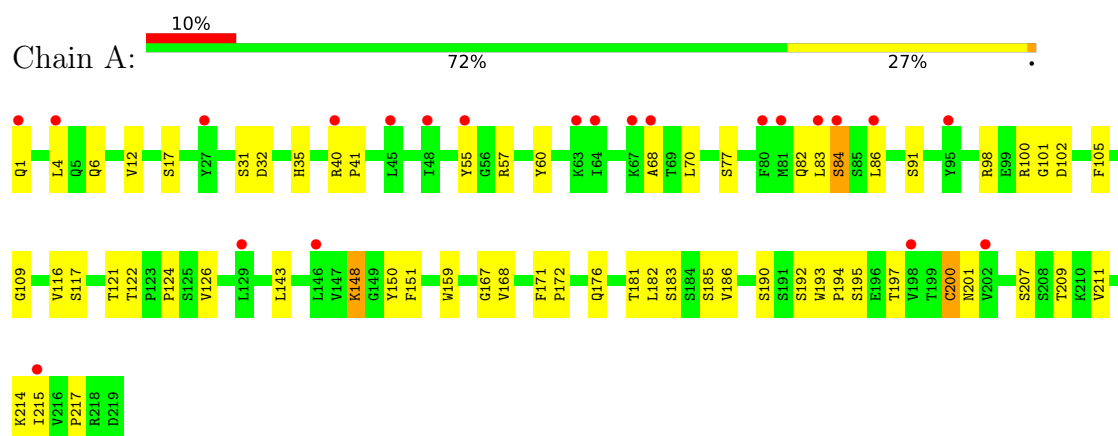
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	6	Total	O	0	0
			6	6		
6	B	5	Total	O	0	0
			5	5		
6	C	9	Total	O	0	0
			9	9		

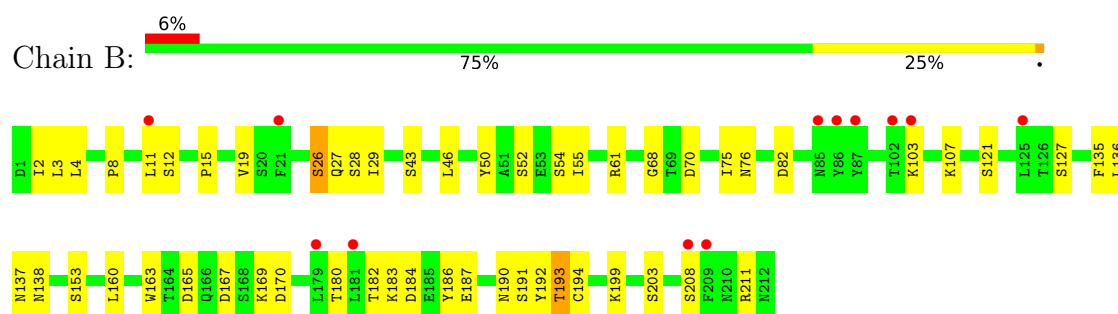
3 Residue-property plots [i](#)

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.

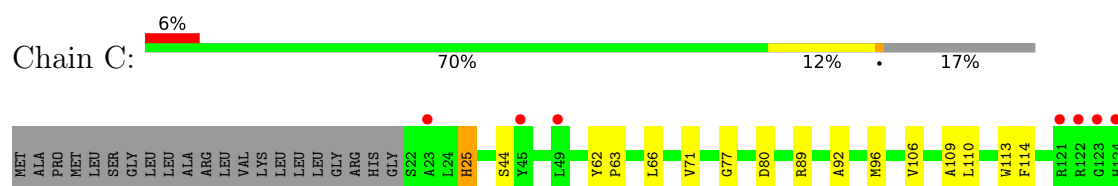
- Molecule 1: Fab heavy chain



- Molecule 2: Fab light chain



- Molecule 3: pH-gated potassium channel KcsA



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	155.17Å 155.17Å 75.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.01 – 2.85 77.58 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.01-2.85) 99.8 (77.58-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.202 , 0.244 0.214 , 0.239	Depositor DCC
R_{free} test set	1043 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	89.5	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 71.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.032 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4072	wwPDB-VP
Average B, all atoms (Å ²)	106.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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

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	0.77	0/1650	1.02	1/2263 (0.0%)
2	B	0.77	0/1683	0.99	1/2283 (0.0%)
3	C	0.87	0/788	1.07	2/1083 (0.2%)
All	All	0.79	0/4121	1.02	4/5629 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	89	ARG	NE-CZ-NH2	-9.41	115.60	120.30
2	B	76	ASN	CB-CA-C	-6.99	96.42	110.40
3	C	80	ASP	CB-CA-C	5.28	120.95	110.40
1	A	57	ARG	NE-CZ-NH1	5.10	122.85	120.30

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	1606	0	1534	35	0
2	B	1646	0	1572	24	0
3	C	768	0	779	10	0
4	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	31	0	44	0	0
6	A	6	0	0	0	0
6	B	5	0	0	0	0
6	C	9	0	0	0	0
All	All	4072	0	3929	64	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 8.

All (64) 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:102:ASP:O	2:B:50:TYR:OH	2.02	0.76
1:A:17:SER:HB2	1:A:84:SER:HA	1.78	0.64
2:B:8:PRO:HG2	2:B:11:LEU:HD13	1.80	0.63
3:C:44:SER:OG	3:C:66:LEU:HA	1.98	0.62
1:A:60:TYR:CE2	1:A:70:LEU:HG	2.34	0.62
1:A:35:HIS:CD2	1:A:105:PHE:HE1	2.20	0.60
1:A:35:HIS:CG	1:A:105:PHE:HE1	2.20	0.58
1:A:194:PRO:HG3	1:A:217:PRO:HG3	1.86	0.57
1:A:60:TYR:HE2	1:A:70:LEU:HG	1.72	0.54
2:B:46:LEU:HG	2:B:55:ILE:HG13	1.90	0.53
1:A:143:LEU:HB3	1:A:215:ILE:HG21	1.90	0.53
1:A:197:THR:OG1	1:A:214:LYS:HE3	2.09	0.52
1:A:126:VAL:HG21	1:A:211:VAL:CG2	2.40	0.52
2:B:2:ILE:HD13	2:B:29:ILE:HG22	1.92	0.51
2:B:19:VAL:HG12	2:B:75:ILE:HB	1.93	0.51
2:B:27:GLN:O	2:B:29:ILE:HG23	2.11	0.51
2:B:2:ILE:HD13	2:B:29:ILE:CG2	2.41	0.51
1:A:17:SER:CB	1:A:84:SER:HA	2.41	0.51
1:A:31:SER:HB2	3:C:62:TYR:CE2	2.45	0.51
1:A:159:TRP:CZ3	1:A:200:CYS:HB3	2.46	0.50
1:A:168:VAL:HA	1:A:185:SER:O	2.11	0.50
2:B:186:TYR:CE1	2:B:192:TYR:CE2	2.99	0.50
2:B:193:THR:HB	2:B:208:SER:OG	2.11	0.49
3:C:113:TRP:CZ3	3:C:114:PHE:HE1	2.30	0.49
1:A:185:SER:HB2	2:B:135:PHE:CE2	2.47	0.49
3:C:113:TRP:CE3	3:C:114:PHE:CE1	3.01	0.48
2:B:61:ARG:HG2	2:B:75:ILE:HG23	1.95	0.48
1:A:6:GLN:HE21	1:A:109:GLY:HA3	1.79	0.48
2:B:15:PRO:HD3	2:B:107:LYS:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:HIS:CG	1:A:105:PHE:CE1	3.01	0.47
1:A:101:GLY:HA3	3:C:62:TYR:CE2	2.49	0.47
2:B:8:PRO:CG	2:B:11:LEU:HD13	2.44	0.47
3:C:71:VAL:HG12	3:C:77:GLY:H	1.80	0.47
1:A:148:LYS:HB3	1:A:181:THR:HG23	1.98	0.46
2:B:3:LEU:HB3	2:B:26:SER:HB3	1.98	0.46
3:C:25:HIS:HB2	3:C:109:ALA:HA	1.97	0.46
2:B:187:GLU:HA	2:B:187:GLU:OE2	2.16	0.46
1:A:12:VAL:O	1:A:116:VAL:HA	2.17	0.45
2:B:61:ARG:NH1	2:B:82:ASP:OD1	2.49	0.45
1:A:98:ARG:HD3	1:A:100:ARG:CZ	2.47	0.45
3:C:92:ALA:O	3:C:96:MET:HG3	2.17	0.44
1:A:32:ASP:OD2	1:A:100:ARG:NH1	2.51	0.44
2:B:167:ASP:OD2	2:B:169:LYS:HB2	2.18	0.44
2:B:28:SER:HA	2:B:68:GLY:O	2.18	0.43
1:A:40:ARG:HB3	1:A:41:PRO:HD2	2.00	0.43
1:A:148:LYS:HA	1:A:181:THR:HA	2.01	0.43
3:C:62:TYR:N	3:C:63:PRO:CD	2.81	0.43
1:A:167:GLY:O	1:A:186:VAL:HA	2.19	0.42
1:A:121:THR:HA	1:A:151:PHE:O	2.19	0.42
2:B:186:TYR:HA	2:B:192:TYR:OH	2.19	0.42
2:B:136:LEU:HD22	2:B:136:LEU:N	2.33	0.42
1:A:83:LEU:HB3	1:A:86:LEU:HD21	2.00	0.42
1:A:55:TYR:CD1	1:A:55:TYR:O	2.73	0.42
1:A:68:ALA:HA	1:A:82:GLN:O	2.19	0.42
1:A:207:SER:O	1:A:209:THR:HG23	2.20	0.42
2:B:211:ARG:HB3	2:B:211:ARG:CZ	2.50	0.41
2:B:137:ASN:HB3	2:B:138:ASN:HD22	1.85	0.41
3:C:106:VAL:O	3:C:110:LEU:HG	2.20	0.41
1:A:176:GLN:CD	2:B:160:LEU:HD11	2.40	0.41
1:A:124:PRO:CA	1:A:150:TYR:HB3	2.51	0.41
2:B:182:THR:O	2:B:183:LYS:C	2.59	0.41
1:A:182:LEU:C	1:A:182:LEU:HD12	2.41	0.40
1:A:171:PHE:HA	1:A:172:PRO:HD3	1.96	0.40
1:A:193:TRP:CD1	1:A:194:PRO:HA	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	217/219 (99%)	202 (93%)	14 (6%)	1 (0%)	29	57
2	B	210/212 (99%)	195 (93%)	15 (7%)	0	100	100
3	C	101/124 (82%)	90 (89%)	11 (11%)	0	100	100
All	All	528/555 (95%)	487 (92%)	40 (8%)	1 (0%)	47	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	192	SER

5.3.2 Protein sidechains

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	171/185 (92%)	158 (92%)	13 (8%)	13	33
2	B	189/190 (100%)	167 (88%)	22 (12%)	5	14
3	C	73/91 (80%)	72 (99%)	1 (1%)	67	86
All	All	433/466 (93%)	397 (92%)	36 (8%)	11	29

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLN
1	A	4	LEU

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Mol	Chain	Res	Type
1	A	77	SER
1	A	84	SER
1	A	91	SER
1	A	117	SER
1	A	122	THR
1	A	148	LYS
1	A	183	SER
1	A	190	SER
1	A	195	SER
1	A	200	CYS
1	A	201	ASN
2	B	4	LEU
2	B	12	SER
2	B	26	SER
2	B	43	SER
2	B	52	SER
2	B	54	SER
2	B	70	ASP
2	B	103	LYS
2	B	121	SER
2	B	127	SER
2	B	153	SER
2	B	163	TRP
2	B	165	ASP
2	B	170	ASP
2	B	180	THR
2	B	184	ASP
2	B	190	ASN
2	B	191	SER
2	B	193	THR
2	B	194	CYS
2	B	199	LYS
2	B	203	SER
3	C	25	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	6	GLN
2	B	138	ASN
2	B	190	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
5	DGA	C	202	-	30,30,43	0.49	0	32,32,45	0.87	1 (3%)

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
5	DGA	C	202	-	-	14/32/32/45	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	C	202	DGA	OG2-CB1-CB2	2.99	117.94	111.50

There are no chirality outliers.

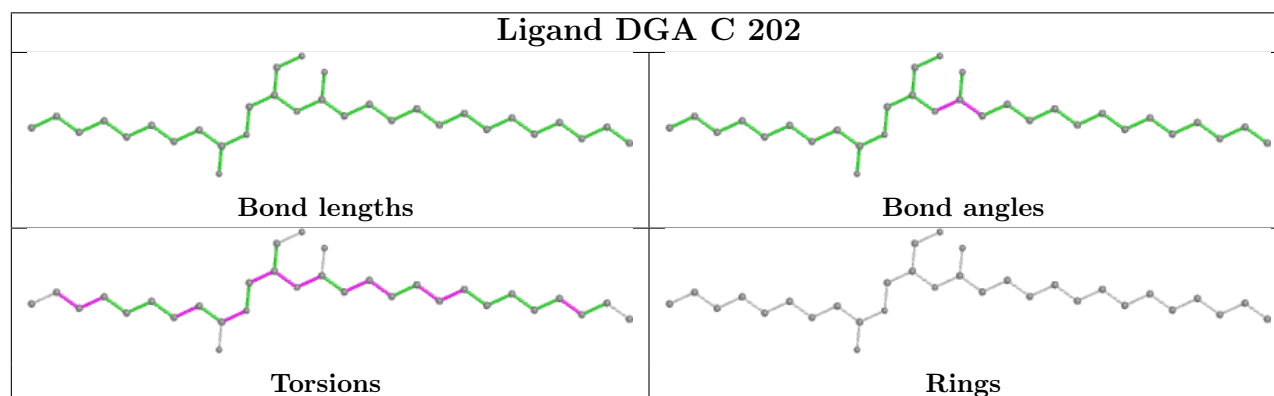
All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	202	DGA	CB2-CB1-OG2-CG2
5	C	202	DGA	OB1-CB1-OG2-CG2
5	C	202	DGA	CA2-CA1-OG1-CG1
5	C	202	DGA	CB4-CB5-CB6-CB7
5	C	202	DGA	OA1-CA1-OG1-CG1
5	C	202	DGA	CA1-CA2-CA3-CA4
5	C	202	DGA	CB1-CB2-CB3-CB4
5	C	202	DGA	CG1-CG2-OG2-CB1
5	C	202	DGA	CAB-CBB-CCB-CDB
5	C	202	DGA	CB2-CB3-CB4-CB5
5	C	202	DGA	OG1-CG1-CG2-OG2
5	C	202	DGA	CA6-CA7-CA8-CA9
5	C	202	DGA	CB5-CB6-CB7-CB8
5	C	202	DGA	CA5-CA6-CA7-CA8

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 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 [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, 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	219/219 (100%)	0.54	22 (10%) 7 5	67, 112, 151, 163	0
2	B	212/212 (100%)	0.45	12 (5%) 23 19	62, 106, 155, 169	0
3	C	103/124 (83%)	0.91	7 (6%) 17 13	54, 72, 143, 164	0
All	All	534/555 (96%)	0.57	41 (7%) 13 10	54, 106, 154, 169	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	124	HIS	5.1
3	C	123	GLY	4.9
1	A	83	LEU	4.7
3	C	122	ARG	4.6
1	A	198	VAL	4.6
3	C	121	ARG	4.4
1	A	215	ILE	3.9
1	A	67	LYS	3.4
2	B	209	PHE	3.4
3	C	45	TYR	3.3
1	A	45	LEU	3.3
2	B	181	LEU	3.3
1	A	129	LEU	3.2
1	A	1	GLN	3.2
1	A	48	ILE	3.0
2	B	103	LYS	2.8
1	A	80	PHE	2.8
3	C	49	LEU	2.8
1	A	86	LEU	2.7
2	B	87	TYR	2.7
1	A	4	LEU	2.7
1	A	95	TYR	2.5
1	A	84	SER	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	11	LEU	2.5
1	A	27	TYR	2.4
2	B	102	THR	2.4
2	B	21	PHE	2.4
1	A	81	MET	2.4
1	A	146	LEU	2.3
1	A	63	LYS	2.3
2	B	179	LEU	2.3
1	A	64	ILE	2.2
3	C	23	ALA	2.2
2	B	86	TYR	2.2
2	B	208	SER	2.2
1	A	202	VAL	2.2
2	B	125	LEU	2.1
2	B	85	ASN	2.1
1	A	40	ARG	2.1
1	A	68	ALA	2.0
1	A	55	TYR	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.

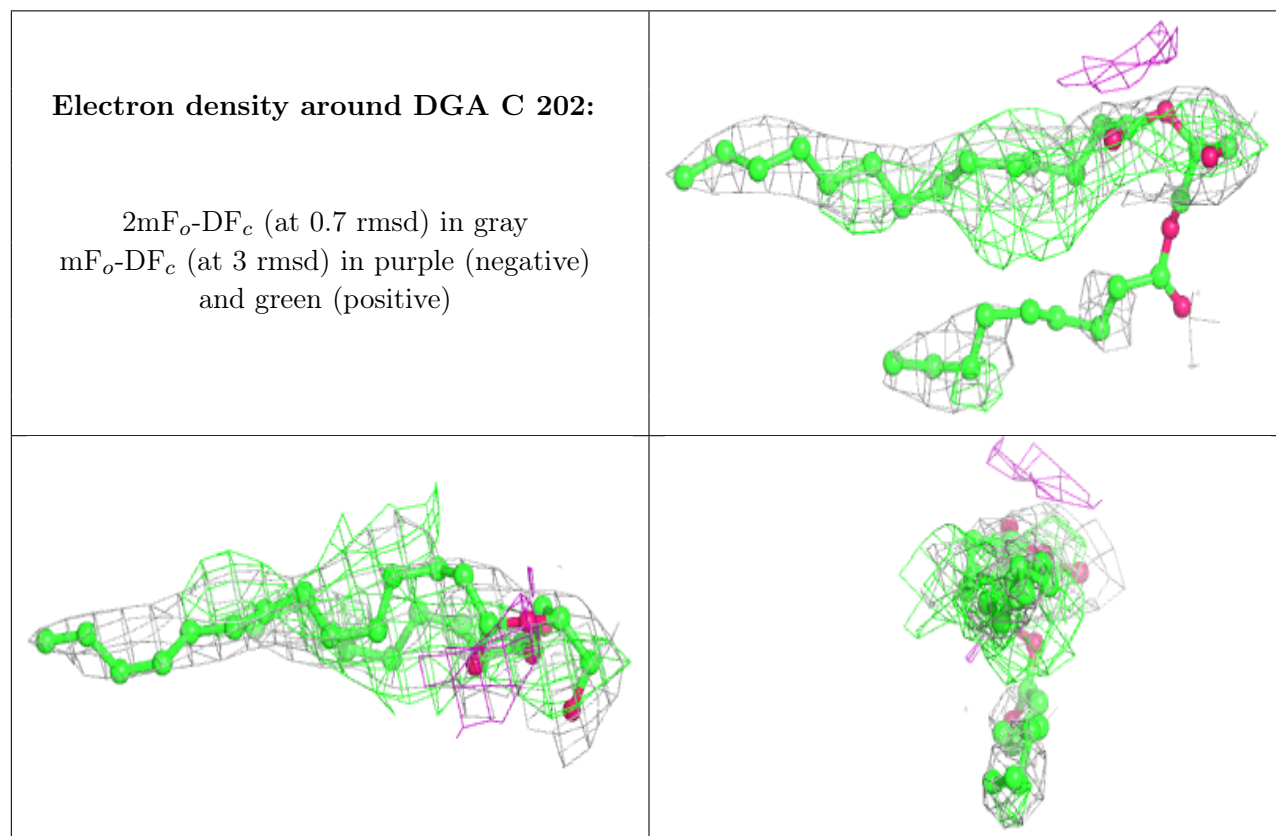
6.4 Ligands [i](#)

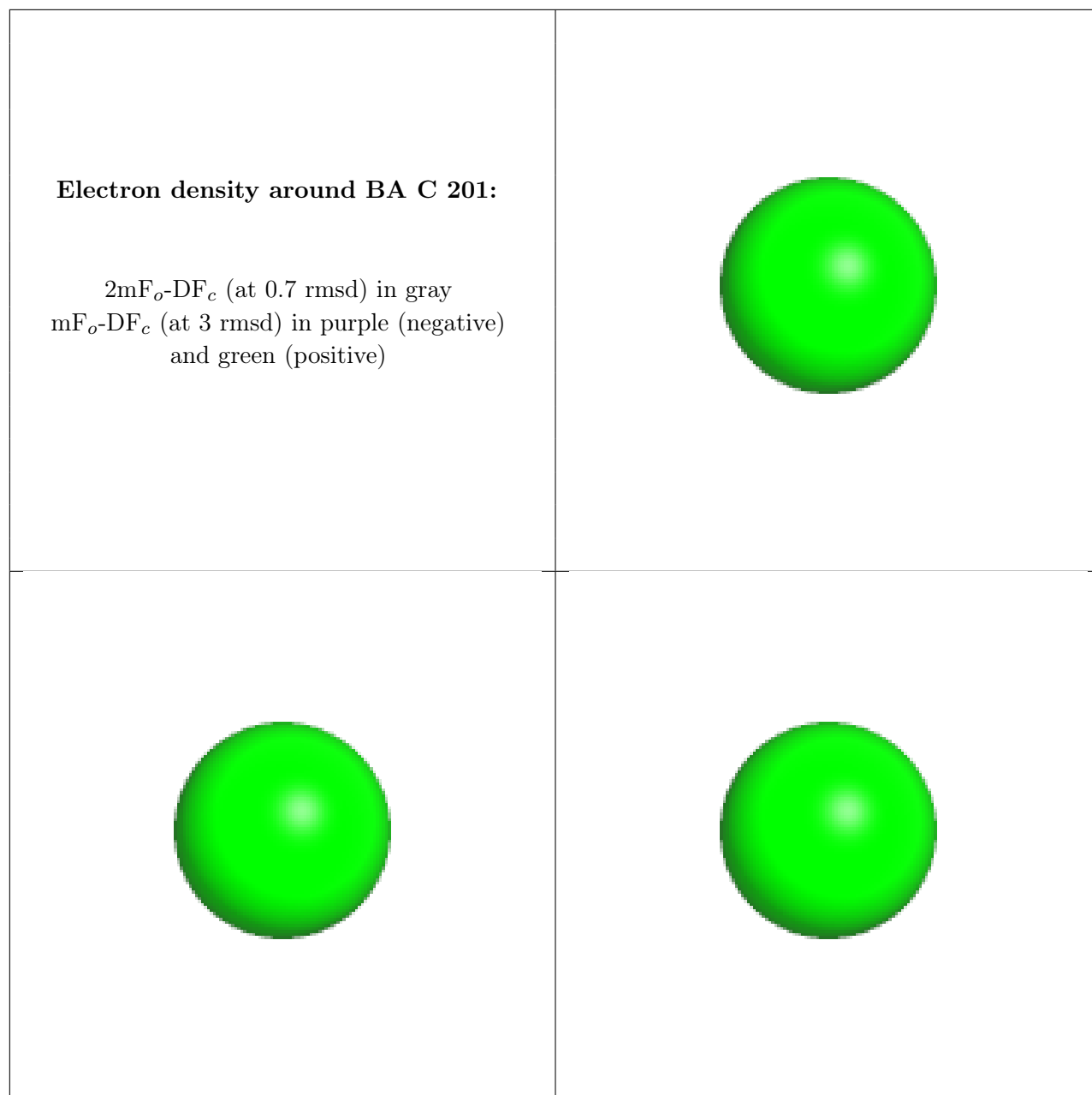
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	DGA	C	202	31/44	0.58	0.56	66,155,236,260	0
4	BA	C	201	1/1	1.00	0.30	73,73,73,73	1

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.