wwPDB X-ray Structure Validation Summary Report (i)

Nov 1, 2026 – 12:09 PM EST

PDB ID	:	9Z5G / pdb_00009z5g
Title	:	Crystal structure of MPXV-B6-SCR4 in complex with antibody B6-Ab9
Authors	:	Zhang, D.; Wilson, I.A.
Deposited on	:	2025-11-11
Resolution	:	2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

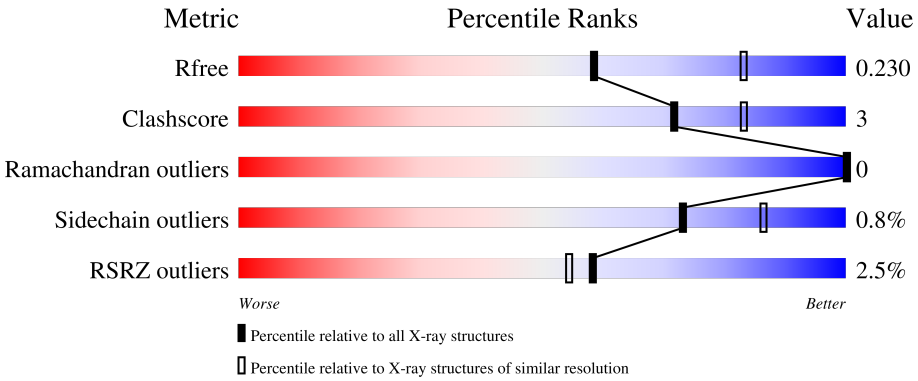
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 2.40 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.



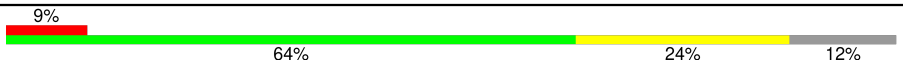
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	221	3% 91% 6% ·
1	H	221	89% 10% ·
2	B	215	% 93% 7%
2	L	215	% 95% 5%
3	C	67	10% 75% 13% 12%

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Mol	Chain	Length	Quality of chain
3	D	67	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7752 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 antibody B6-Ab9 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1621	1021	279	313	8			
1	H	219	Total	C	N	O	S	0	0	0
			1649	1037	284	320	8			

- Molecule 2 is a protein called antibody B6-Ab9 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	0	0
			1643	1025	279	334	5			
2	L	214	Total	C	N	O	S	0	0	0
			1637	1022	278	333	4			

- Molecule 3 is a protein called Protein OPG190.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	59	Total	C	N	O	S	0	0	0
			425	264	73	84	4			
3	D	59	Total	C	N	O	S	0	0	0
			425	264	73	84	4			

There are 16 discrepancies between the modelled and reference sequences:

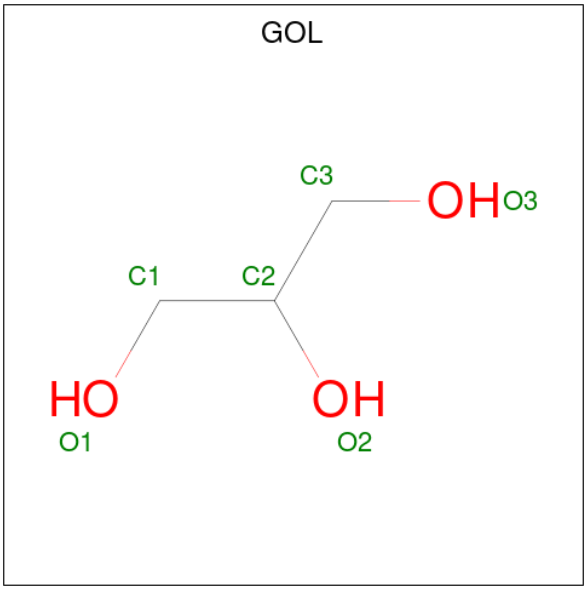
Chain	Residue	Modelled	Actual	Comment	Reference
C	225	GLY	-	expression tag	UNP P0DTN2
C	226	SER	-	expression tag	UNP P0DTN2
C	227	HIS	-	expression tag	UNP P0DTN2
C	228	HIS	-	expression tag	UNP P0DTN2
C	229	HIS	-	expression tag	UNP P0DTN2
C	230	HIS	-	expression tag	UNP P0DTN2
C	231	HIS	-	expression tag	UNP P0DTN2
C	232	HIS	-	expression tag	UNP P0DTN2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	225	GLY	-	expression tag	UNP P0DTN2
D	226	SER	-	expression tag	UNP P0DTN2
D	227	HIS	-	expression tag	UNP P0DTN2
D	228	HIS	-	expression tag	UNP P0DTN2
D	229	HIS	-	expression tag	UNP P0DTN2
D	230	HIS	-	expression tag	UNP P0DTN2
D	231	HIS	-	expression tag	UNP P0DTN2
D	232	HIS	-	expression tag	UNP P0DTN2

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	H	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0

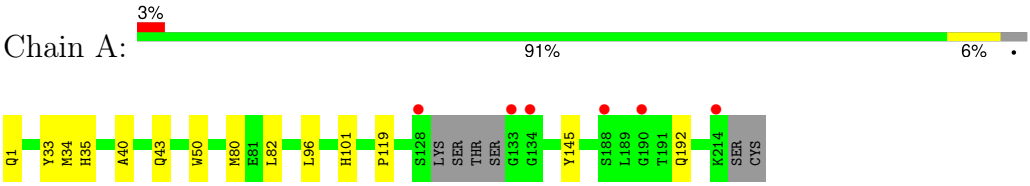
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	88	Total O 88 88	0	0
5	B	63	Total O 63 63	0	0
5	C	5	Total O 5 5	0	0
5	H	90	Total O 90 90	0	0
5	L	62	Total O 62 62	0	0
5	D	8	Total O 8 8	0	0

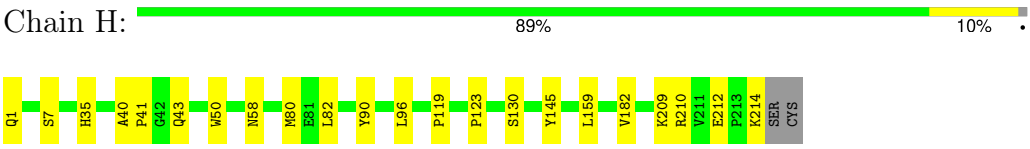
3 Residue-property plots (i)

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 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.

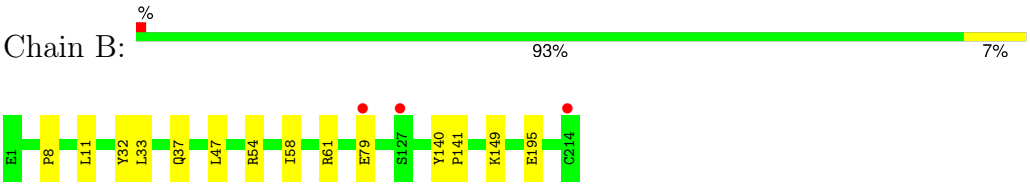
• Molecule 1: antibody B6-Ab9 heavy chain



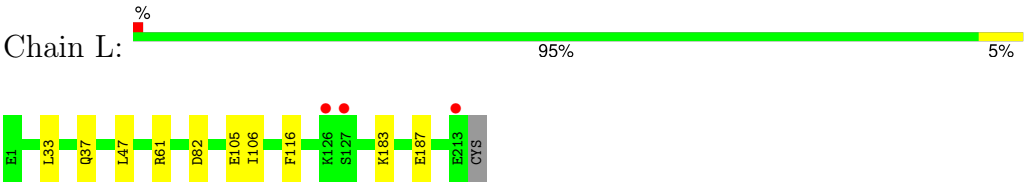
• Molecule 1: antibody B6-Ab9 heavy chain



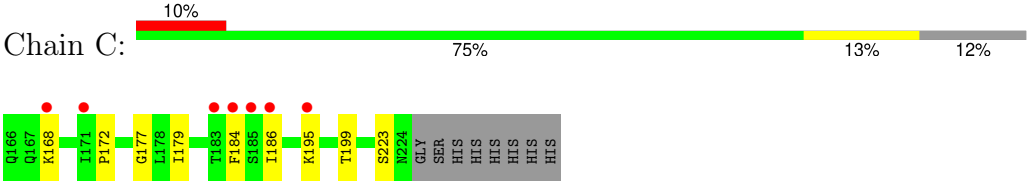
• Molecule 2: antibody B6-Ab9 light chain



• Molecule 2: antibody B6-Ab9 light chain

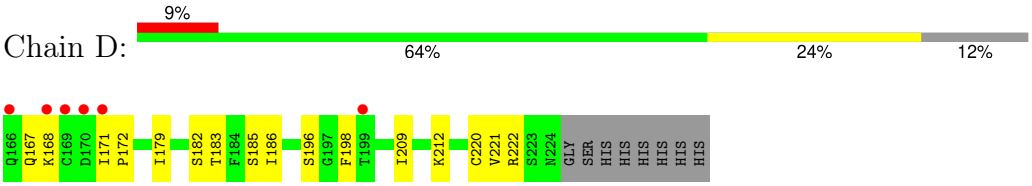


• Molecule 3: Protein OPG190



• Molecule 3: Protein OPG190

Chain D:


9%
64%
24%
12%
Q166
Q167
K168
C169
D170
I171
P172
I179
S182
T183
F184
S185
I186
S196
G197
F198
T199
I209
K212
C220
V221
R222
S223
N224
GLY
SER
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	72.03Å 110.11Å 136.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.70 – 2.40 32.70 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.7 (32.70-2.40) 95.7 (32.70-2.40)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.25 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.188 , 0.230 0.188 , 0.230	Depositor DCC
R_{free} test set	2000 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å^2)	28.9	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 46.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7752	wwPDB-VP
Average B, all atoms (Å^2)	35.0	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 46.54 % 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 1.1291e-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: GOL

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	0.22	0/1665	0.40	0/2269
1	H	0.26	0/1694	0.42	0/2309
2	B	0.20	0/1678	0.41	0/2279
2	L	0.25	0/1672	0.47	0/2271
3	C	0.74	0/433	1.00	0/587
3	D	0.52	0/433	0.70	0/587
All	All	0.31	0/7575	0.50	0/10302

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

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	1621	0	1566	9	1
1	H	1649	0	1597	15	0
2	B	1643	0	1595	8	0
2	L	1637	0	1590	4	0
3	C	425	0	422	4	1
3	D	425	0	422	11	2
4	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	8	0	0
4	H	6	0	8	0	0
4	L	18	0	24	0	0
5	A	88	0	0	2	0
5	B	63	0	0	0	0
5	C	5	0	0	0	0
5	D	8	0	0	1	0
5	H	90	0	0	3	0
5	L	62	0	0	0	0
All	All	7752	0	7240	48	2

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 3.

The worst 5 of 48 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)
3:D:212:LYS:NZ	5:D:301:HOH:O	2.20	0.71
1:H:1:GLN:N	5:H:403:HOH:O	2.28	0.66
1:H:58:ASN:ND2	5:H:404:HOH:O	2.30	0.65
1:A:1:GLN:N	5:A:403:HOH:O	2.22	0.64
1:H:7:SER:OG	5:H:401:HOH:O	2.09	0.64

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:GLN:OE1	3:D:196:SER:OG[2_554]	1.63	0.57
3:C:177:GLY:O	3:D:182:SER:OG[2_454]	2.14	0.06

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	211/221 (96%)	209 (99%)	2 (1%)	0	100	100
1	H	217/221 (98%)	215 (99%)	2 (1%)	0	100	100
2	B	213/215 (99%)	207 (97%)	6 (3%)	0	100	100
2	L	212/215 (99%)	206 (97%)	6 (3%)	0	100	100
3	C	57/67 (85%)	56 (98%)	1 (2%)	0	100	100
3	D	57/67 (85%)	56 (98%)	1 (2%)	0	100	100
All	All	967/1006 (96%)	949 (98%)	18 (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	178/184 (97%)	178 (100%)	0	100	100
1	H	182/184 (99%)	181 (100%)	1 (0%)	81	91
2	B	185/185 (100%)	184 (100%)	1 (0%)	81	91
2	L	184/185 (100%)	181 (98%)	3 (2%)	55	76
3	C	52/59 (88%)	51 (98%)	1 (2%)	50	71
3	D	52/59 (88%)	51 (98%)	1 (2%)	50	71
All	All	833/856 (97%)	826 (99%)	7 (1%)	73	86

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	33	LEU
2	L	105	GLU
3	D	183	THR
2	L	106	ILE
1	H	96	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	147	GLN
2	L	152	ASN
2	L	160	GLN
2	B	210	ASN
1	H	5	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	$\#\|Z\| > 2$
4	GOL	A	301	-	5,5,5	0.34	0	5,5,5	0.44	0
4	GOL	H	301	-	5,5,5	0.35	0	5,5,5	0.52	0
4	GOL	B	301	-	5,5,5	0.32	0	5,5,5	0.41	0
4	GOL	L	301	-	5,5,5	0.32	0	5,5,5	0.42	0
4	GOL	L	303	-	5,5,5	0.07	0	5,5,5	0.33	0
4	GOL	L	302	-	5,5,5	0.08	0	5,5,5	0.30	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
4	GOL	A	301	-	-	1/4/4/4	-
4	GOL	H	301	-	-	0/4/4/4	-
4	GOL	B	301	-	-	0/4/4/4	-
4	GOL	L	301	-	-	0/4/4/4	-
4	GOL	L	303	-	-	2/4/4/4	-
4	GOL	L	302	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

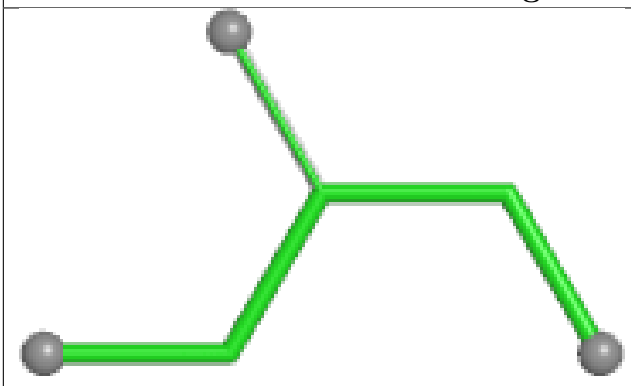
Mol	Chain	Res	Type	Atoms
4	L	303	GOL	C1-C2-C3-O3
4	L	302	GOL	C1-C2-C3-O3
4	L	303	GOL	O2-C2-C3-O3
4	L	302	GOL	O2-C2-C3-O3
4	A	301	GOL	O2-C2-C3-O3

There are no ring outliers.

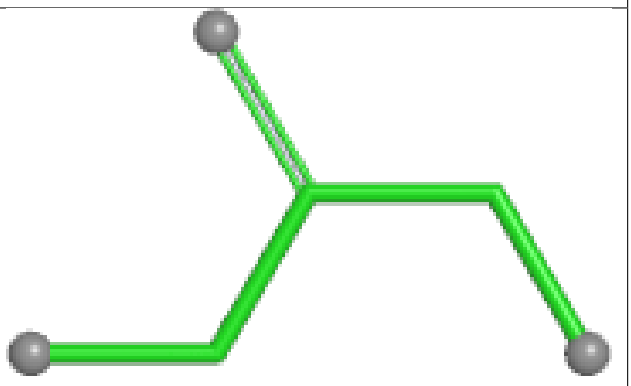
No monomer is involved in short contacts.

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.

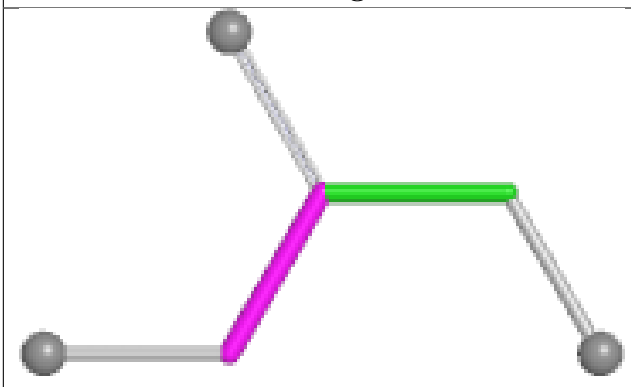
Ligand GOL A 301



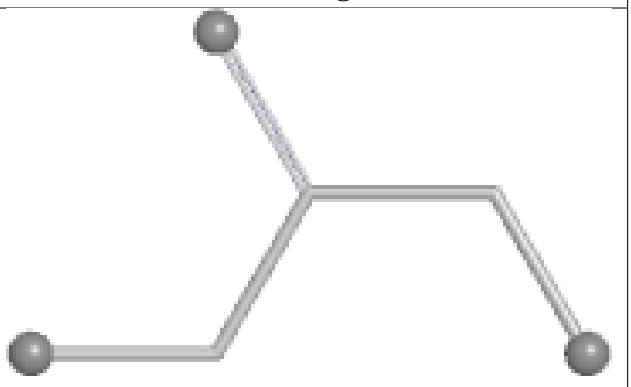
Bond lengths



Bond angles

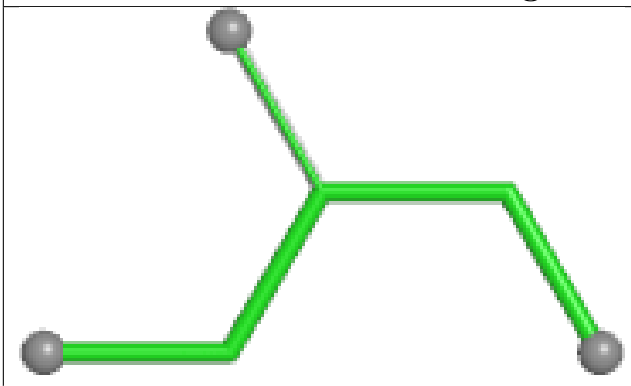


Torsions

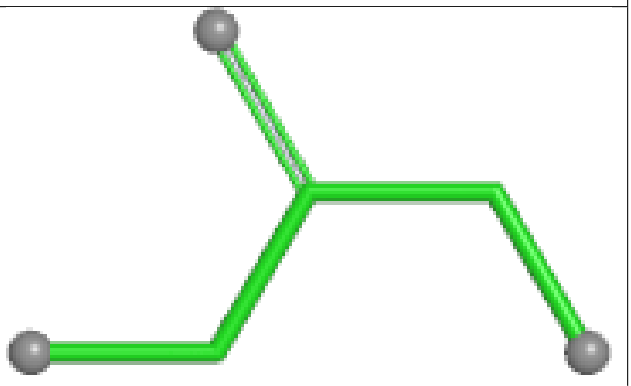


Rings

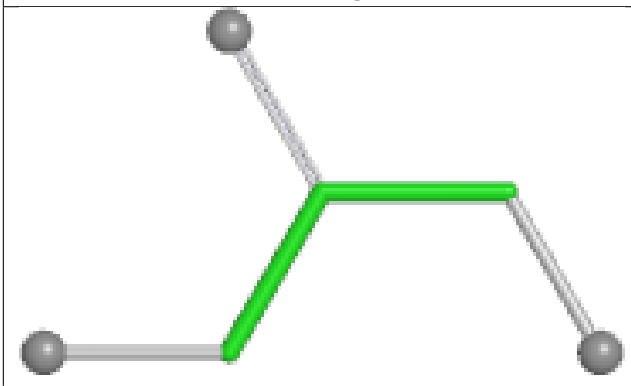
Ligand GOL H 301



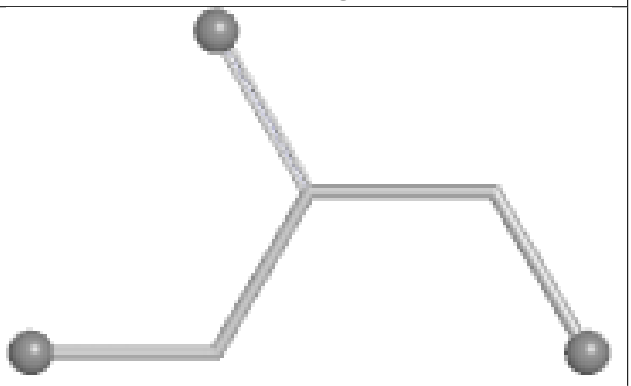
Bond lengths



Bond angles

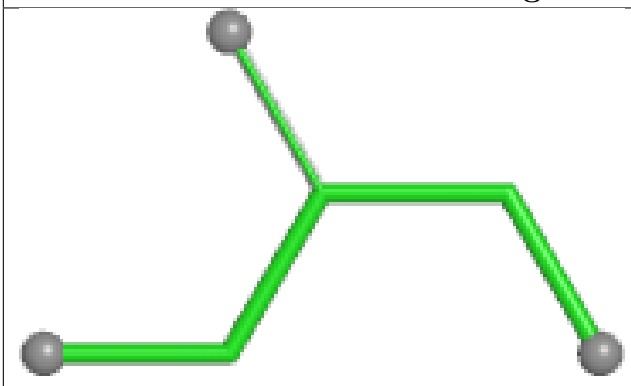


Torsions

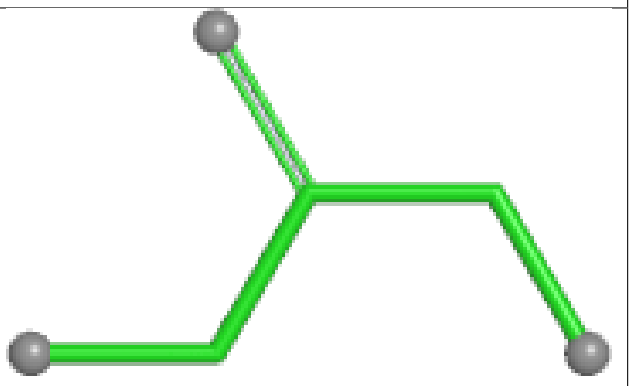


Rings

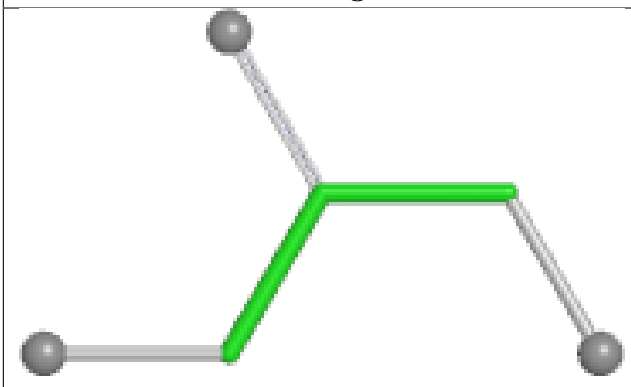
Ligand GOL B 301



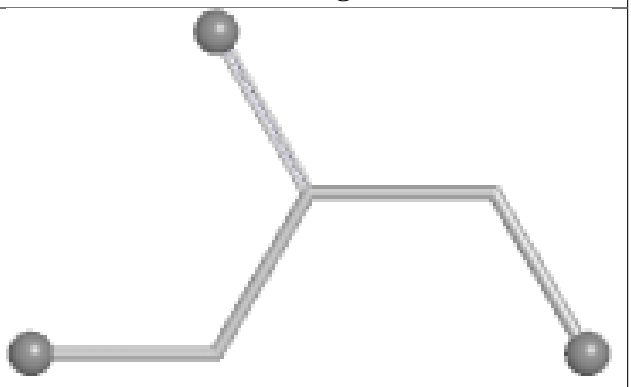
Bond lengths



Bond angles

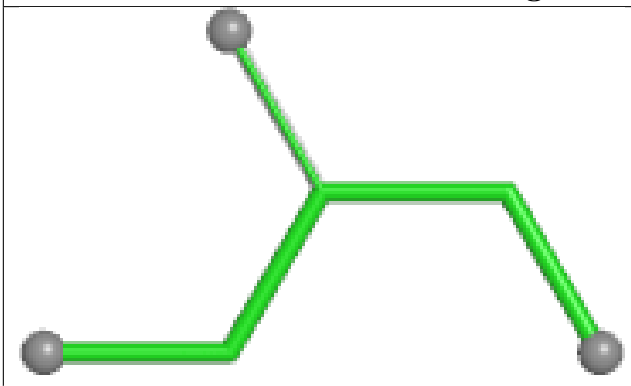


Torsions

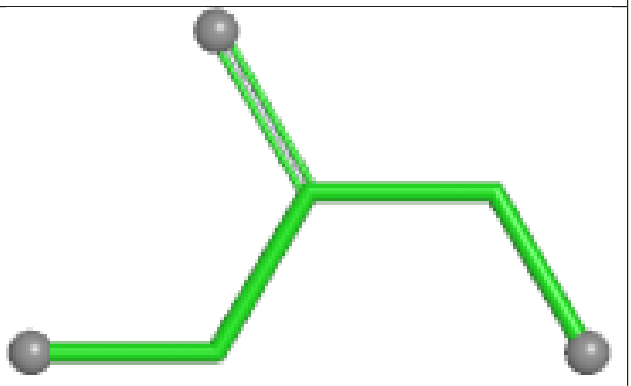


Rings

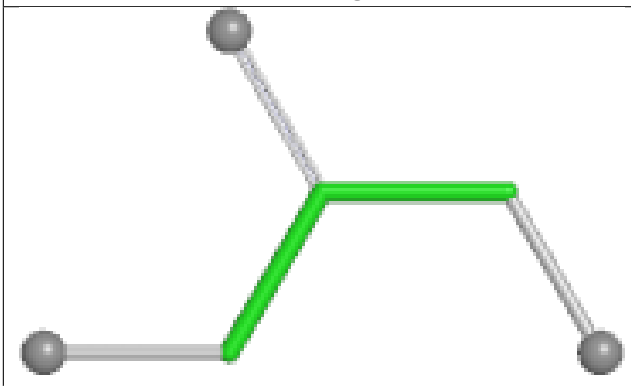
Ligand GOL L 301



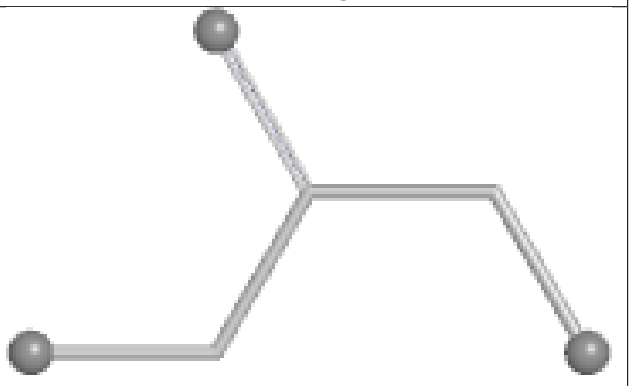
Bond lengths



Bond angles

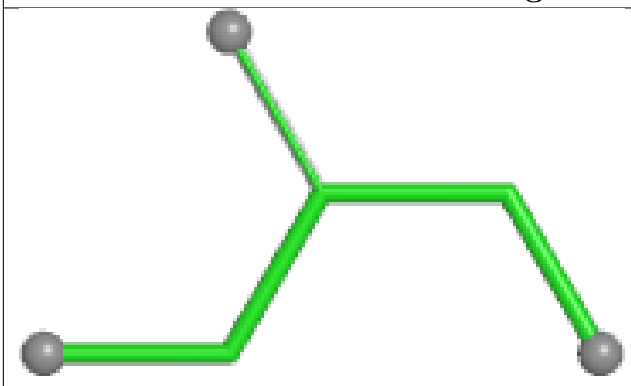


Torsions

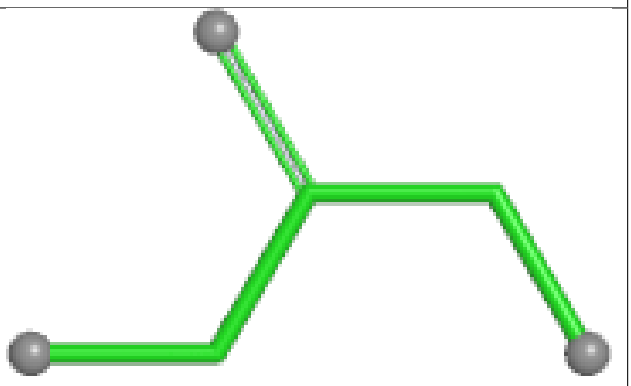


Rings

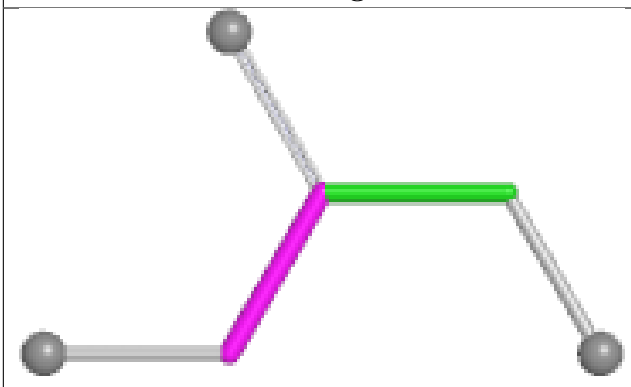
Ligand GOL L 303



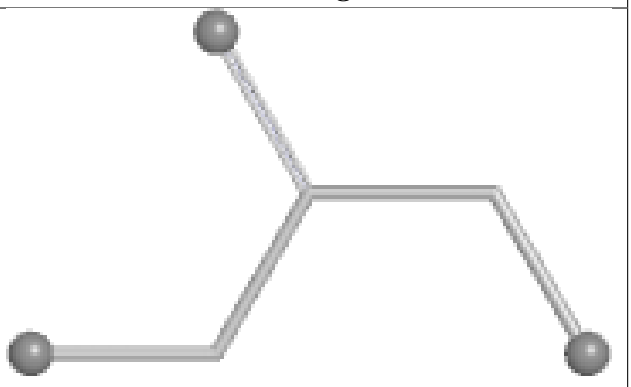
Bond lengths



Bond angles

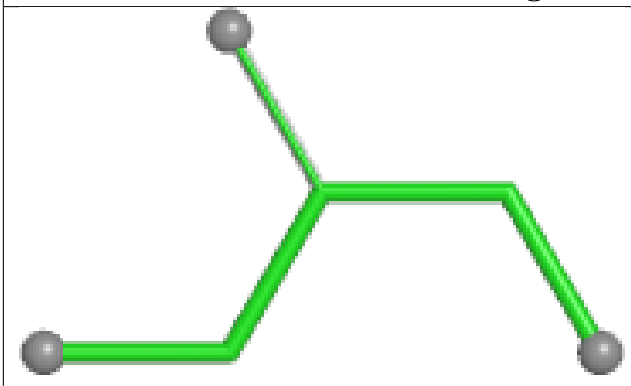


Torsions

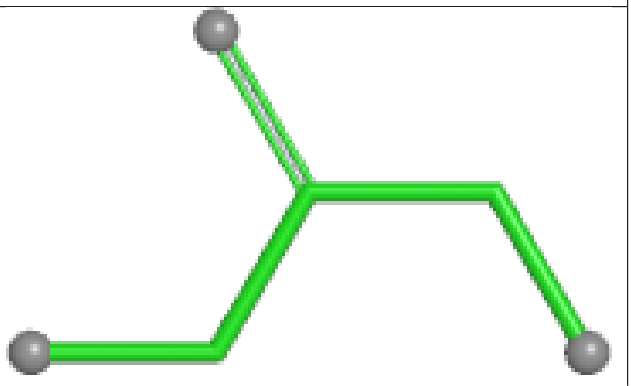


Rings

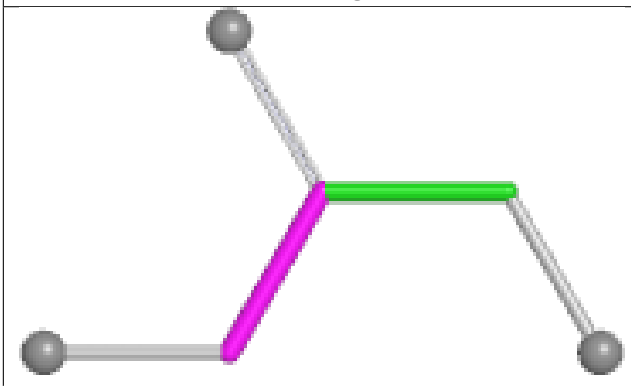
Ligand GOL L 302



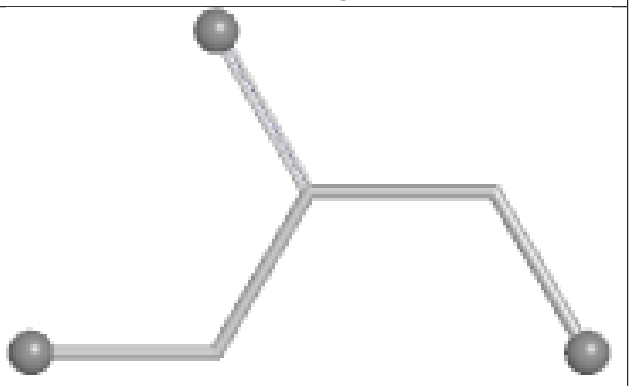
Bond lengths



Bond angles



Torsions



Rings

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	215/221 (97%)	-0.34	6 (2%) 55 51	17, 27, 52, 85	0
1	H	219/221 (99%)	-0.35	0 100 100	18, 29, 47, 58	0
2	B	215/215 (100%)	-0.22	3 (1%) 73 69	20, 31, 50, 86	0
2	L	214/215 (99%)	-0.17	3 (1%) 73 69	21, 34, 51, 73	0
3	C	59/67 (88%)	0.97	7 (11%) 9 6	37, 56, 80, 82	0
3	D	59/67 (88%)	0.75	6 (10%) 12 9	33, 55, 81, 97	0
All	All	981/1006 (97%)	-0.13	25 (2%) 58 54	17, 32, 60, 97	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	171	ILE	3.3
1	A	128	SER	3.2
3	C	185	SER	3.2
3	C	186	ILE	3.1
2	B	79	GLU	3.1

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands (i)

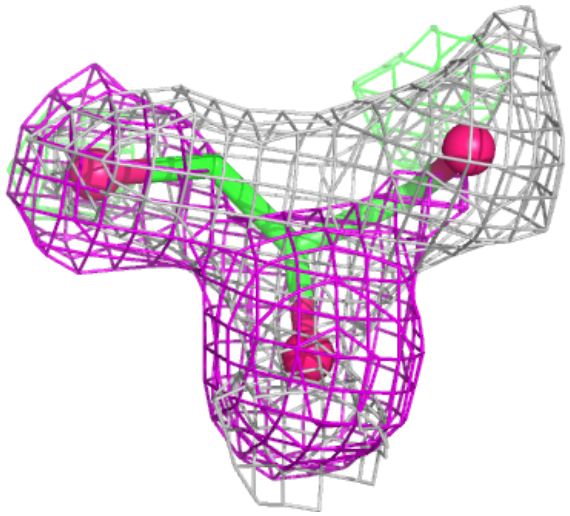
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

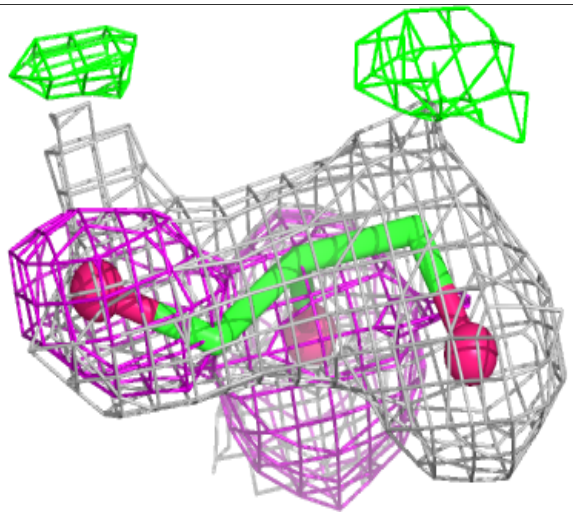
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	L	303	6/6	0.72	0.24	20,20,20,20	0
4	GOL	L	302	6/6	0.82	0.18	53,58,82,87	0
4	GOL	H	301	6/6	0.82	0.13	44,52,58,58	0
4	GOL	A	301	6/6	0.83	0.14	40,43,55,59	0
4	GOL	B	301	6/6	0.94	0.10	23,29,36,37	0
4	GOL	L	301	6/6	0.95	0.08	24,32,37,37	0

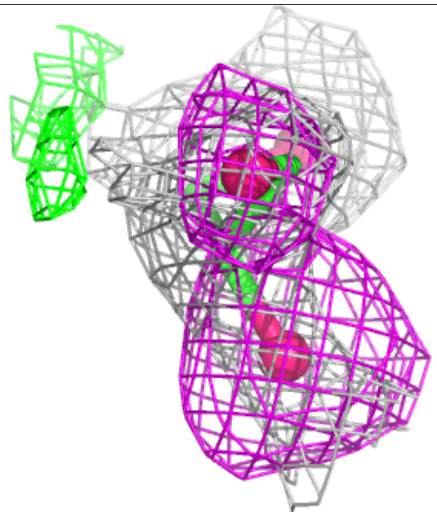
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around GOL L 303:

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

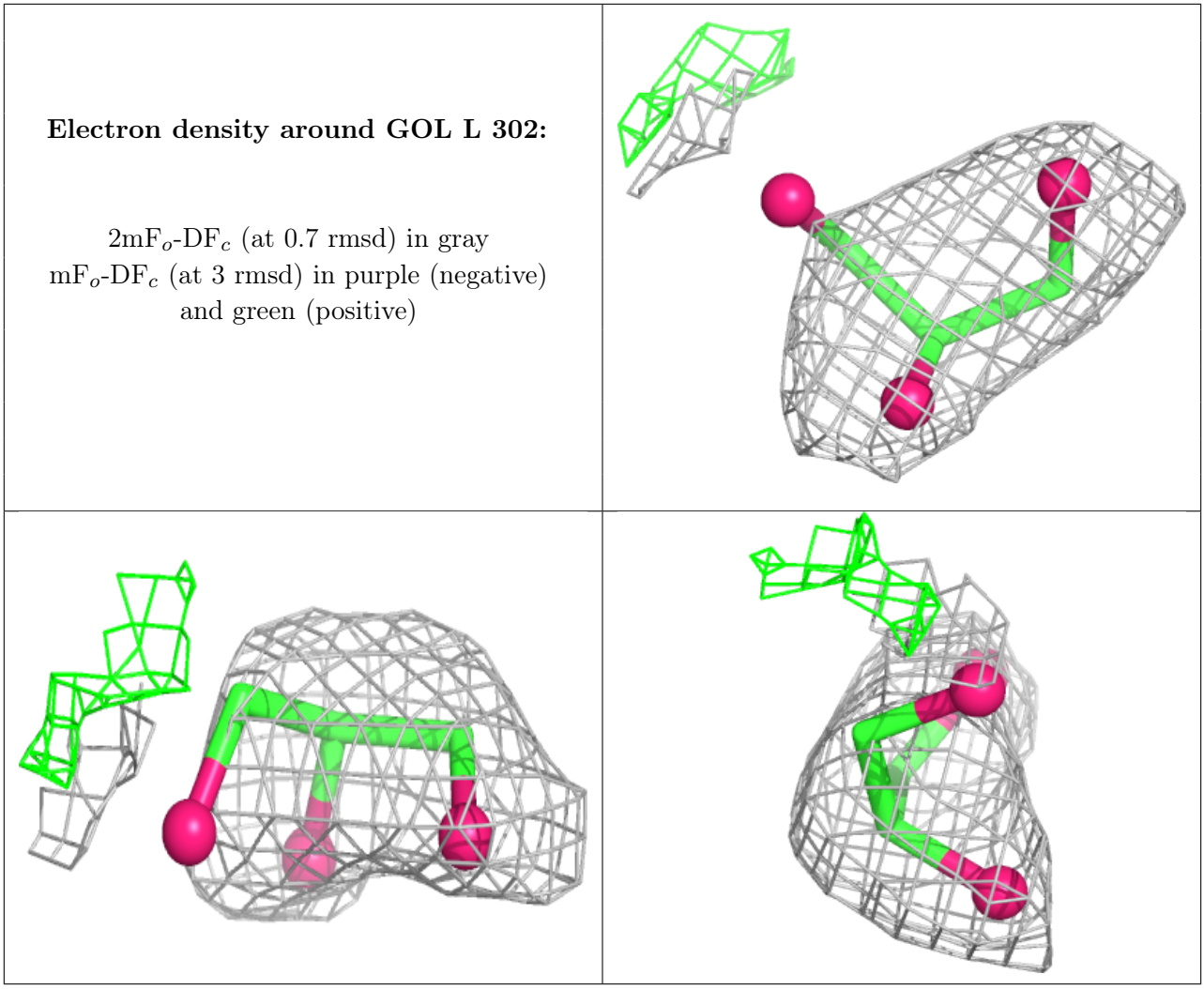






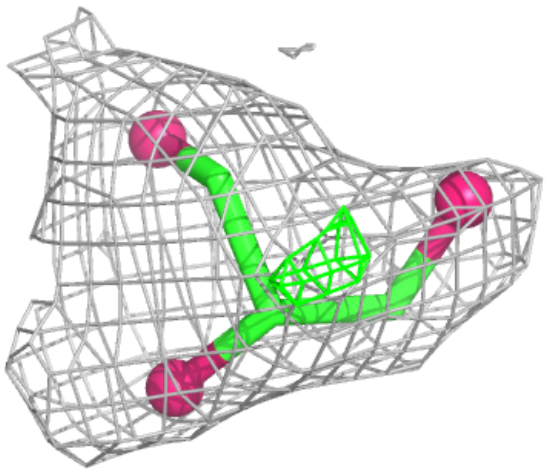
Electron density around GOL L 302:

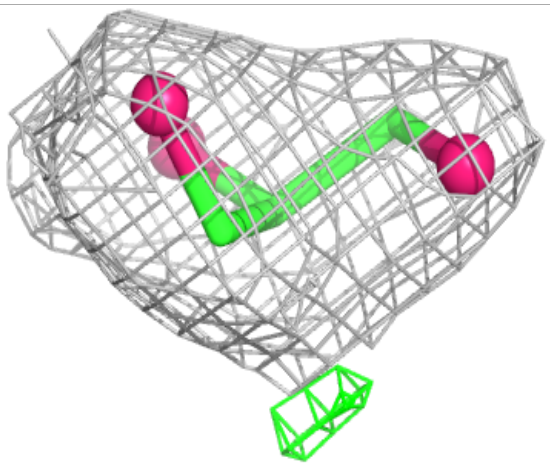
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

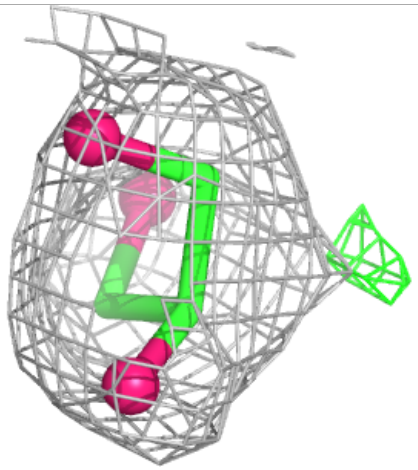


Electron density around GOL H 301:

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

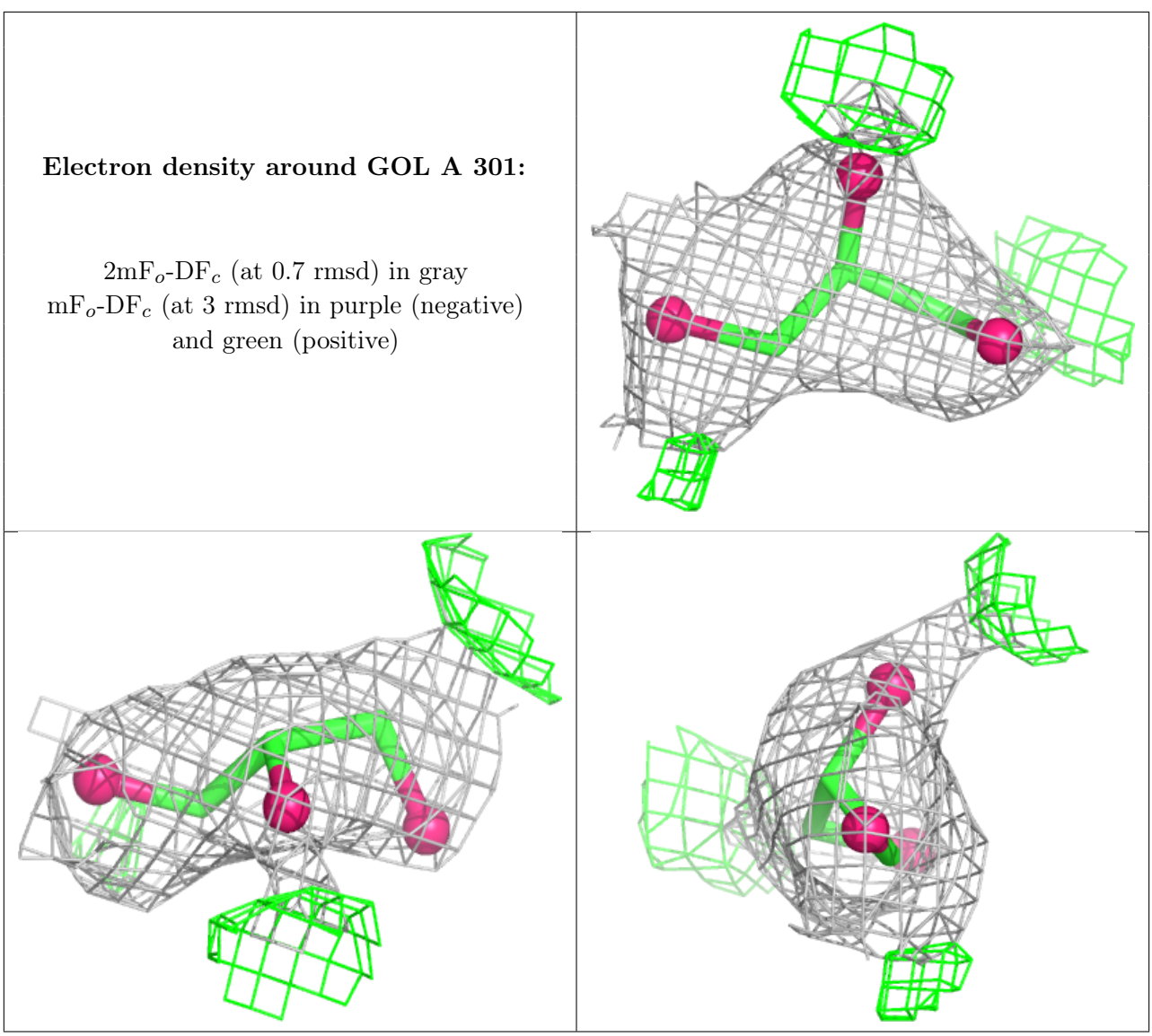






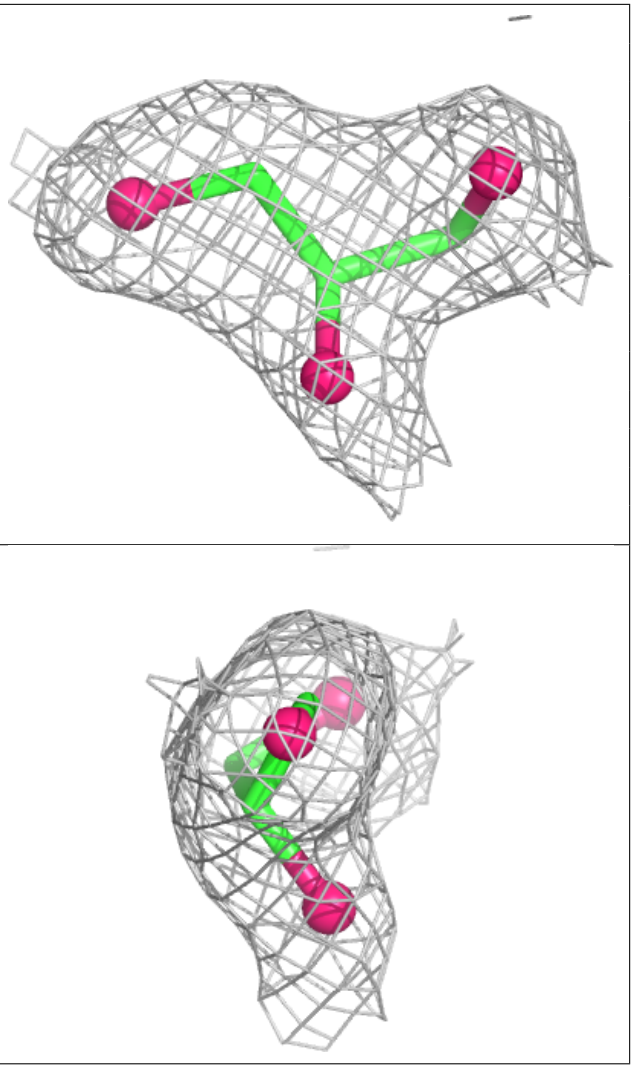
Electron density around GOL A 301:

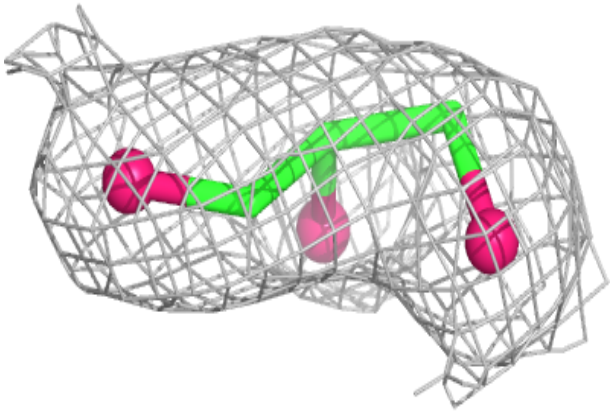
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around GOL B 301:

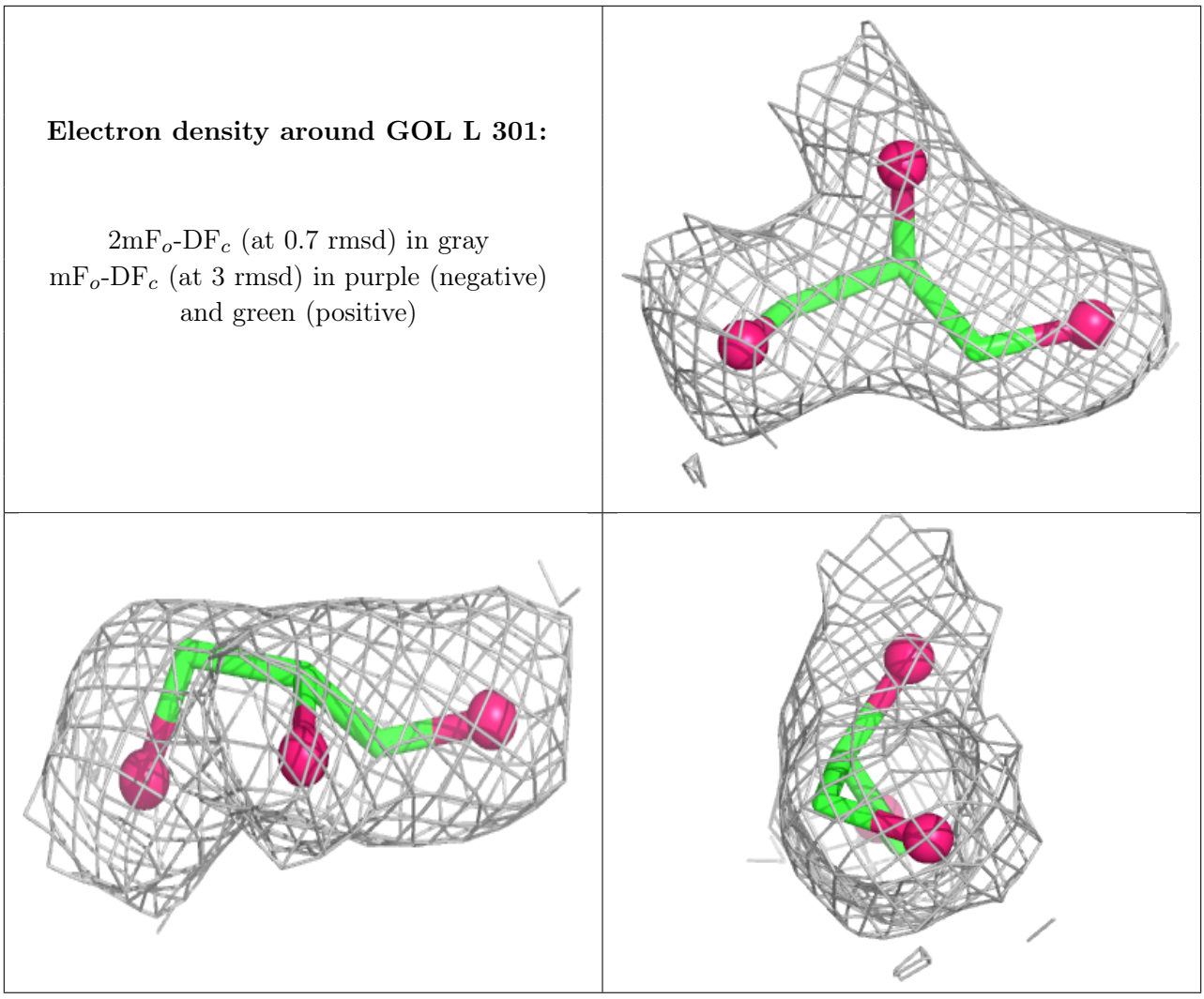
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around GOL L 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

There are no such residues in this entry.