



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:08 AM UTC

PDB ID : 9GIZ / pdb_00009giz
Title : UMG-SP-1, a promiscuous hydrolase
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Deposited on : 2024-08-20
Resolution : 1.89 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
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	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

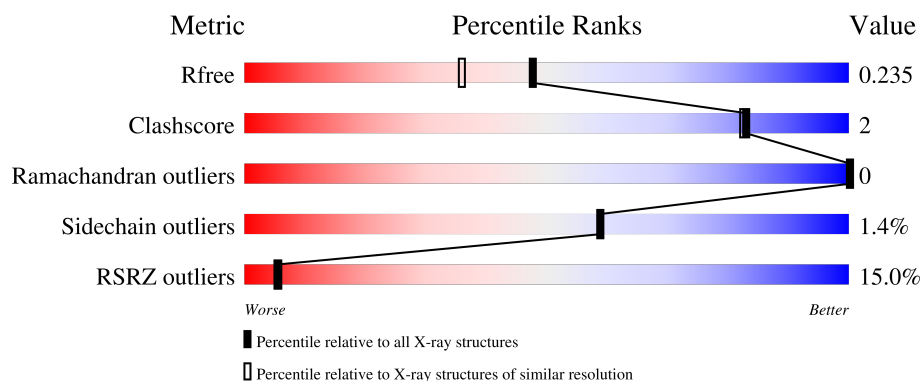
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	438	<div> <div>6%</div> <div>87%</div> <div>5%</div> <div>8%</div> </div>
1	B	438	<div> <div>21%</div> <div>79%</div> <div>6%</div> <div>14%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6045 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 UMG-SP-1.

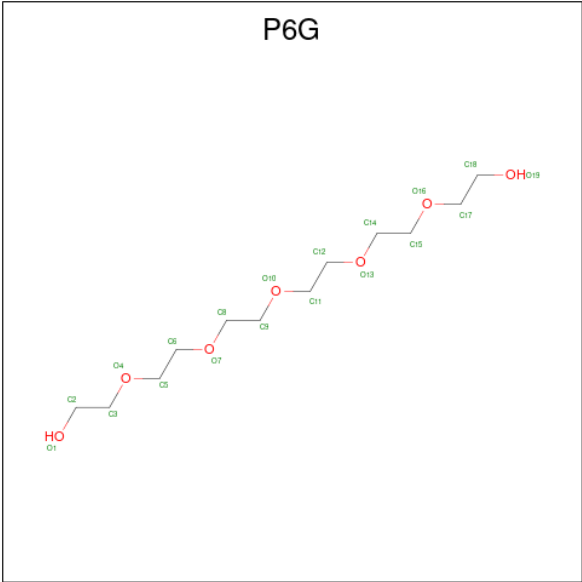
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	0	0	0
			2939	1844	538	549	8			
1	B	376	Total	C	N	O	S	0	0	0
			2743	1720	502	513	8			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).

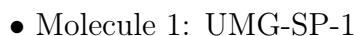


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			19	12	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	217	Total	O	0	0
			217	217		
4	B	121	Total	O	0	0
			121	121		

- Molecule 1: UMG-SP-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.87Å 108.33Å 114.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	78.60 – 1.89 78.60 – 1.89	Depositor EDS
% Data completeness (in resolution range)	78.7 (78.60-1.89) 79.1 (78.60-1.89)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.193 , 0.232 0.204 , 0.235	Depositor DCC
R_{free} test set	2707 reflections (3.84%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.009	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6045	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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: GOL, P6G

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	0.67	3/3005 (0.1%)	1.02	8/4112 (0.2%)
1	B	0.65	1/2797 (0.0%)	1.04	1/3824 (0.0%)
All	All	0.66	4/5802 (0.1%)	1.03	9/7936 (0.1%)

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	A	0	1
1	B	0	2
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	ARG	C-N	9.35	1.46	1.33
1	A	91	PHE	C-N	7.38	1.43	1.33
1	B	39	ILE	C-O	-5.60	1.18	1.24
1	A	216	ILE	CB-CG1	-5.35	1.42	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	369	LEU	N-CA-CB	-6.99	99.48	110.46
1	A	402	THR	CA-CB-OG1	-6.41	99.98	109.60
1	A	91	PHE	O-C-N	5.73	129.88	122.89
1	A	92	ARG	CA-C-N	5.70	131.54	122.59
1	A	92	ARG	C-N-CA	5.70	131.54	122.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	290	ASP	CA-CB-CG	5.48	118.08	112.60
1	A	190	LYS	CG-CD-CE	5.31	123.52	111.30
1	A	20	THR	CA-CB-OG1	-5.13	101.91	109.60
1	A	357	PHE	CA-CB-CG	5.09	118.89	113.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	202	ARG	Sidechain
1	B	247	ARG	Sidechain
1	B	49	ARG	Sidechain

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	2939	0	2919	8	0
1	B	2743	0	2744	18	0
2	A	6	0	8	1	0
3	B	19	0	26	0	0
4	A	217	0	0	1	0
4	B	121	0	0	1	0
All	All	6045	0	5697	27	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:501:GOL:H2	4:A:663:HOH:O	1.58	1.04
1:B:381:HIS:HB2	4:B:602:HOH:O	1.88	0.71
1:A:167:LEU:HD22	1:A:229:MET:SD	2.38	0.64
1:B:71:GLY:HA2	1:B:115:ILE:HD11	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:GLU:HA	1:B:119:LYS:HE3	1.81	0.61
1:A:3:ARG:HA	1:A:3:ARG:NH2	2.18	0.59
1:B:167:LEU:HD22	1:B:229:MET:SD	2.43	0.58
1:B:211:THR:HG23	1:B:214:GLY:H	1.69	0.57
1:B:36:ASP:OD1	1:B:164:MET:HE1	2.04	0.56
1:B:36:ASP:HA	1:B:39:ILE:O	2.06	0.56
1:B:7:ALA:HB2	1:B:167:LEU:HG	1.88	0.56
1:A:89:TRP:CE3	1:A:96:GLY:O	2.61	0.54
1:A:89:TRP:HE3	1:A:96:GLY:O	1.92	0.53
1:A:3:ARG:HA	1:A:3:ARG:HH21	1.74	0.50
1:A:212:PRO:HB2	1:A:301:MET:HE1	1.97	0.47
1:B:313:LEU:N	1:B:313:LEU:CD1	2.78	0.47
1:B:76:VAL:O	1:B:119:LYS:HA	2.14	0.47
1:B:311:PRO:HA	1:B:314:HIS:CD2	2.50	0.46
1:B:32:ILE:O	1:B:36:ASP:HB2	2.16	0.46
1:B:313:LEU:N	1:B:313:LEU:HD12	2.33	0.44
1:A:41:ALA:O	1:A:120:THR:HA	2.18	0.44
1:A:76:VAL:O	1:A:119:LYS:HA	2.18	0.43
1:B:154:GLY:HA3	1:B:180:PRO:HB3	2.01	0.43
1:B:78:GLU:HA	1:B:119:LYS:HB3	2.00	0.43
1:B:268:ASP:O	1:B:272:GLU:HG3	2.20	0.42
1:B:115:ILE:HD12	1:B:115:ILE:N	2.36	0.41
1:B:312:THR:OG1	1:B:313:LEU:CD1	2.69	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	397/438 (91%)	389 (98%)	8 (2%)	0	100	100
1	B	364/438 (83%)	356 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	761/876 (87%)	745 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	289/317 (91%)	285 (99%)	4 (1%)	59	59
1	B	272/317 (86%)	268 (98%)	4 (2%)	57	56
All	All	561/634 (88%)	553 (99%)	8 (1%)	59	59

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ILE
1	A	216	ILE
1	A	285	THR
1	A	434	GLU
1	B	216	ILE
1	B	285	THR
1	B	313	LEU
1	B	368	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	296	HIS
1	A	327	GLN
1	A	333	ASN
1	A	404	ASN
1	A	411	GLN
1	B	40	ASN

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Mol	Chain	Res	Type
1	B	296	HIS
1	B	333	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
2	GOL	A	501	-	5,5,5	0.21	0	5,5,5	0.62	0
3	P6G	B	501	-	18,18,18	0.35	0	17,17,17	0.27	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	GOL	A	501	-	-	2/4/4/4	-
3	P6G	B	501	-	-	9/16/16/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

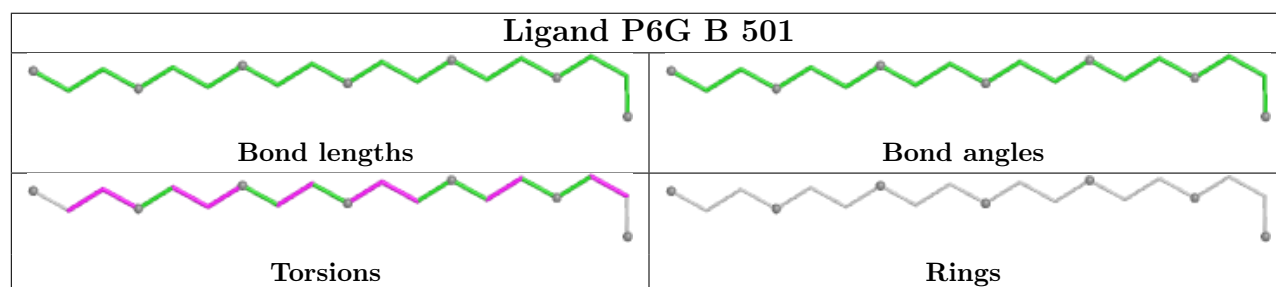
Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-C3
3	B	501	P6G	O4-C5-C6-O7
3	B	501	P6G	C18-C17-O16-C15
3	B	501	P6G	O1-C2-C3-O4
3	B	501	P6G	O16-C17-C18-O19
3	B	501	P6G	C15-C14-O13-C12
3	B	501	P6G	O13-C14-C15-O16
2	A	501	GOL	O1-C1-C2-O2
3	B	501	P6G	O7-C8-C9-O10
3	B	501	P6G	O10-C11-C12-O13
3	B	501	P6G	C8-C9-O10-C11

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [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	403/438 (92%)	0.16	27 (6%) 24 25	17, 27, 53, 82	0
1	B	376/438 (85%)	1.04	90 (23%) 2 1	19, 36, 69, 90	0
All	All	779/876 (88%)	0.58	117 (15%) 5 5	17, 30, 62, 90	0

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	92	ARG	6.6
1	A	89	TRP	6.0
1	B	154	GLY	5.6
1	B	61	ILE	5.3
1	A	126	LEU	5.3
1	B	35	LEU	4.6
1	B	66	THR	4.5
1	B	371	ILE	4.5
1	B	34	ALA	4.3
1	B	37	GLY	4.2
1	B	377	PRO	4.2
1	B	174	GLY	4.0
1	B	276	GLY	4.0
1	A	88	HIS	4.0
1	B	368	THR	3.9
1	B	173	ILE	3.9
1	B	43	VAL	3.7
1	B	59	ALA	3.7
1	B	23	ALA	3.7
1	B	122	VAL	3.6
1	A	357	PHE	3.6
1	B	306	PHE	3.6
1	B	30	ALA	3.6
1	B	49	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	29	ILE	3.6
1	B	27	ALA	3.5
1	B	14	ILE	3.5
1	B	39	ILE	3.5
1	B	209	ALA	3.5
1	B	207	ASN	3.5
1	A	369	LEU	3.5
1	A	375	ALA	3.5
1	B	51	LEU	3.4
1	A	38	ALA	3.4
1	B	5	PRO	3.3
1	A	202	ARG	3.3
1	A	91	PHE	3.3
1	B	357	PHE	3.3
1	B	16	SER	3.3
1	B	12	ALA	3.2
1	B	32	ILE	3.1
1	A	93	GLN	3.1
1	B	62	GLN	3.1
1	B	63	ALA	3.1
1	B	123	PRO	3.1
1	A	95	ALA	3.1
1	B	376	SER	3.0
1	B	21	ALA	3.0
1	B	40	ASN	3.0
1	B	65	ASP	3.0
1	B	11	ALA	2.9
1	B	202	ARG	2.9
1	B	18	ALA	2.9
1	B	67	ALA	2.9
1	A	94	HIS	2.8
1	B	42	VAL	2.8
1	A	87	THR	2.8
1	B	47	PHE	2.8
1	B	70	LEU	2.8
1	A	37	GLY	2.7
1	B	378	TYR	2.7
1	A	149	PRO	2.7
1	B	3	ARG	2.7
1	B	17	GLY	2.6
1	B	208	GLY	2.6
1	B	85	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	232	LEU	2.6
1	B	434	GLU	2.6
1	B	52	ALA	2.6
1	B	433	THR	2.6
1	B	381	HIS	2.5
1	A	39	ILE	2.5
1	B	213	LEU	2.5
1	A	3	ARG	2.5
1	A	148	THR	2.5
1	B	72	VAL	2.5
1	B	98	ILE	2.5
1	A	129	TRP	2.5
1	B	13	ALA	2.5
1	B	315	ALA	2.5
1	B	246	ARG	2.4
1	B	117	LEU	2.4
1	B	84	GLY	2.4
1	B	26	GLU	2.4
1	B	99	ALA	2.4
1	B	68	PRO	2.4
1	A	90	GLY	2.3
1	B	247	ARG	2.3
1	B	88	HIS	2.3
1	B	56	ALA	2.3
1	A	128	ASP	2.3
1	B	309	SER	2.3
1	B	8	LEU	2.3
1	B	258	ARG	2.2
1	B	9	ALA	2.2
1	B	370	ASP	2.2
1	B	97	ASN	2.2
1	A	127	GLY	2.2
1	B	36	ASP	2.2
1	A	40	ASN	2.2
1	B	82	VAL	2.2
1	B	402	THR	2.2
1	A	309	SER	2.2
1	B	38	ALA	2.2
1	B	15	ARG	2.2
1	A	151	GLY	2.2
1	B	57	ALA	2.2
1	B	278	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	60	ARG	2.1
1	B	28	ALA	2.1
1	B	33	GLU	2.1
1	B	275	ALA	2.1
1	A	124	LYS	2.1
1	B	10	THR	2.1
1	B	400	VAL	2.1
1	B	172	ASP	2.0
1	B	284	SER	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

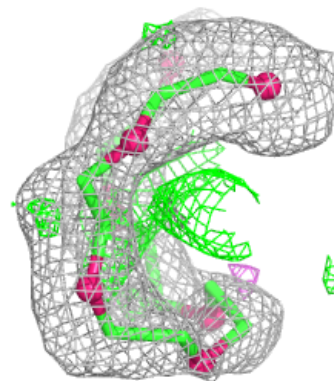
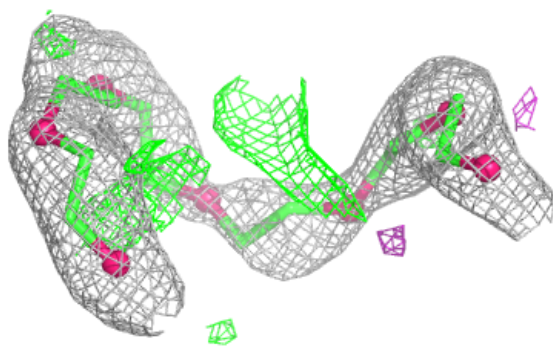
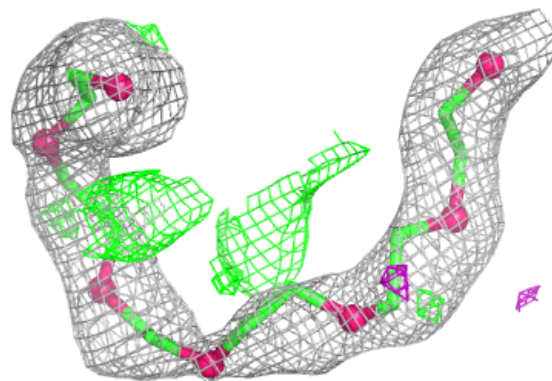
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GOL	A	501	6/6	0.79	0.17	44,50,51,53	0
3	P6G	B	501	19/19	0.79	0.20	41,55,72,75	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 P6G B 501:

$2mF_o-DF_c$ (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.