



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:45 AM UTC

PDB ID : 2EXL / pdb_00002exl
Title : GRP94 N-terminal Domain bound to geldanamycin
Authors : Reardon, P.N.; Immormino, R.M.; Gewirth, D.T.
Deposited on : 2005-11-08
Resolution : 2.35 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

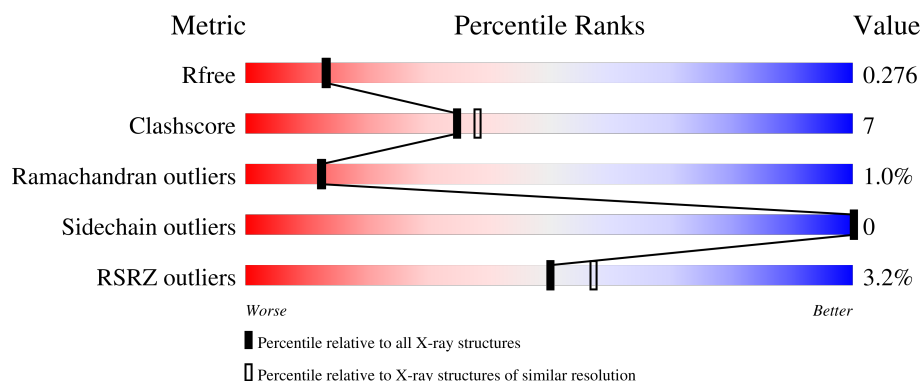
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

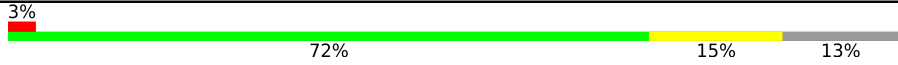
The reported resolution of this entry is 2.35 Å.

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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	236	
1	B	236	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3679 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.

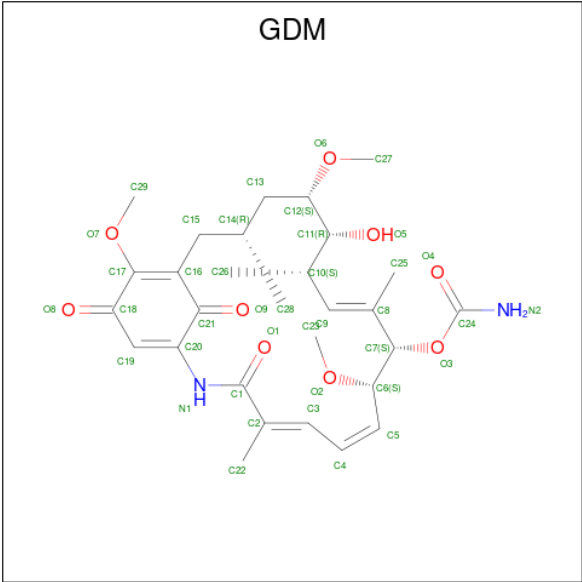
- Molecule 1 is a protein called Endoplasmin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1635	1038	271	321	5			
1	B	204	Total	C	N	O	S	0	0	0
			1614	1024	268	317	5			

There are 16 discrepancies between the modelled and reference sequences:

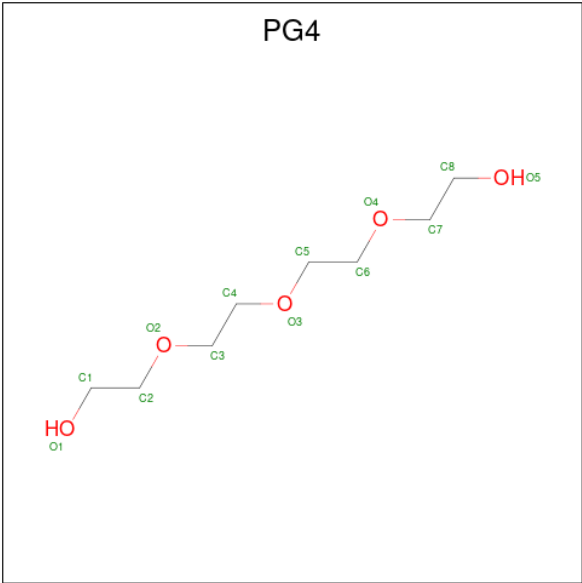
Chain	Residue	Modelled	Actual	Comment	Reference
A	65	GLY	-	cloning artifact	UNP P41148
A	66	SER	-	cloning artifact	UNP P41148
A	67	HIS	-	cloning artifact	UNP P41148
A	68	MET	-	cloning artifact	UNP P41148
A	324	GLY	-	SEE REMARK 999	UNP P41148
A	325	GLY	-	SEE REMARK 999	UNP P41148
A	326	GLY	-	SEE REMARK 999	UNP P41148
A	327	GLY	-	SEE REMARK 999	UNP P41148
B	65	GLY	-	cloning artifact	UNP P41148
B	66	SER	-	cloning artifact	UNP P41148
B	67	HIS	-	cloning artifact	UNP P41148
B	68	MET	-	cloning artifact	UNP P41148
B	324	GLY	-	SEE REMARK 999	UNP P41148
B	325	GLY	-	SEE REMARK 999	UNP P41148
B	326	GLY	-	SEE REMARK 999	UNP P41148
B	327	GLY	-	SEE REMARK 999	UNP P41148

- Molecule 2 is GELDANAMYCIN (CCD ID: GDM) (formula: C₂₉H₄₀N₂O₉).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			40	29	2	9		
2	B	1	Total	C	N	O	0	0
			40	29	2	9		

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



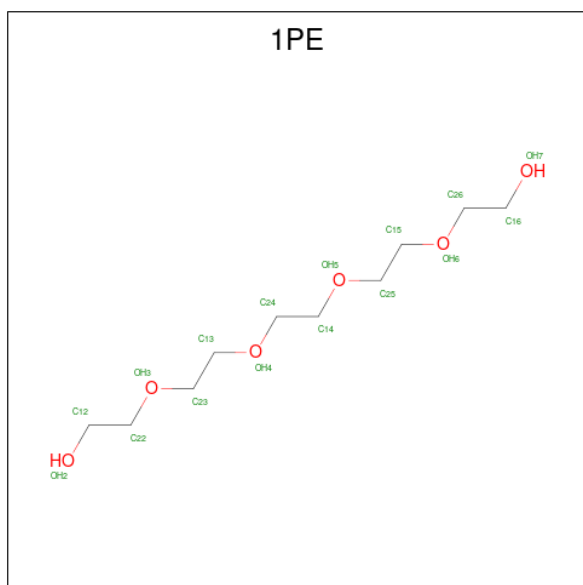
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	8	5		
3	A	1	Total	C	O	0	0
			13	8	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			13	8	5		
3	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			16	10	6		

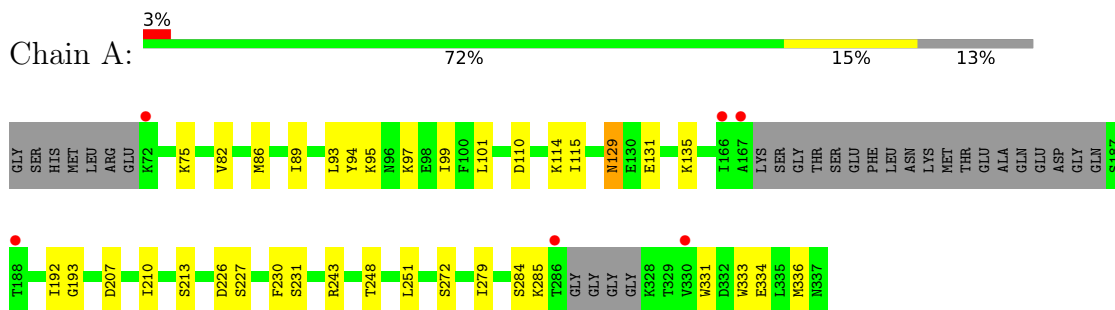
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	134	Total	O	0	0
			134	134		
5	B	148	Total	O	0	0
			148	148		

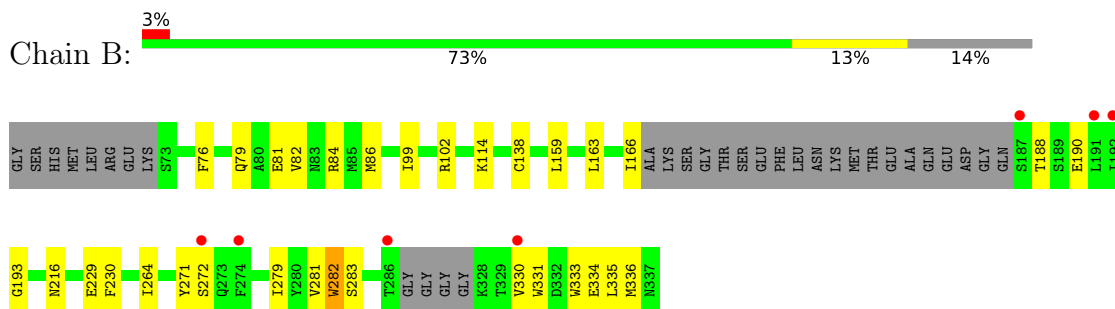
3 Residue-property plots [i](#)

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: Endoplasmic



• Molecule 1: Endoplasmic



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.82Å 84.36Å 95.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.61 – 2.35 45.61 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.7 (45.61-2.35) 98.8 (45.61-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.34Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.221 , 0.276 0.221 , 0.276	Depositor DCC
R_{free} test set	2270 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtrriage
Anisotropy	0.272	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3679	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.76 % 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 4.0858e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: PG4, GDM, 1PE

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	0.41	0/1658	0.89	3/2236 (0.1%)
1	B	0.42	0/1637	0.90	2/2209 (0.1%)
All	All	0.41	0/3295	0.89	5/4445 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	LEU	N-CA-C	7.13	120.05	110.35
1	B	193	GLY	N-CA-C	-5.34	105.93	112.77
1	A	207	ASP	N-CA-C	-5.22	106.91	113.28
1	B	188	THR	N-CA-C	-5.17	106.75	113.16
1	A	213	SER	N-CA-C	5.06	117.67	109.06

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	1635	0	1639	22	0
1	B	1614	0	1608	25	0
2	A	40	0	39	1	0
2	B	40	0	39	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	26	0	36	1	0
3	B	26	0	36	1	0
4	A	16	0	22	0	0
5	A	134	0	0	2	0
5	B	148	0	0	3	0
All	All	3679	0	3419	51	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (51) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:VAL:HG12	1:B:86:MET:HE2	1.74	0.69
1:A:82:VAL:HG12	1:A:86:MET:HE2	1.77	0.67
1:B:335:LEU:O	1:B:336:MET:HE2	1.99	0.62
1:A:334:GLU:OE2	1:A:336:MET:HE1	2.03	0.58
1:B:283:SER:OG	1:B:334:GLU:HB2	2.03	0.58
1:B:159:LEU:O	1:B:163:LEU:HB2	2.03	0.57
2:A:301:GDM:H233	2:A:301:GDM:C4	2.35	0.56
1:B:99:ILE:HD11	1:B:102:ARG:HH21	1.70	0.56
2:B:302:GDM:C4	2:B:302:GDM:H233	2.35	0.56
1:A:129:ASN:OD1	1:A:131:GLU:HG2	2.06	0.55
1:A:93:LEU:HD13	1:A:99:ILE:HD11	1.88	0.55
1:B:99:ILE:HD11	1:B:102:ARG:NH2	2.21	0.55
1:B:190:GLU:HA	5:B:587:HOH:O	2.08	0.54
1:A:89:ILE:HG23	1:A:93:LEU:HD12	1.89	0.53
1:B:99:ILE:CD1	1:B:102:ARG:NH2	2.71	0.53
1:B:99:ILE:HG13	1:B:102:ARG:NH2	2.24	0.53
1:A:284:SER:HB3	1:A:331:TRP:CZ2	2.44	0.52
1:A:135:LYS:HD3	1:A:333:TRP:CZ2	2.47	0.49
1:B:272:SER:HB3	1:B:279:ILE:HG13	1.94	0.49
3:A:501:PG4:H42	5:A:507:HOH:O	2.12	0.49
1:A:135:LYS:HD3	1:A:333:TRP:CE2	2.48	0.48
1:A:129:ASN:O	1:A:243:ARG:NH2	2.44	0.48
1:A:94:TYR:CE1	1:A:95:LYS:HG3	2.49	0.48
1:B:76:PHE:HB2	1:B:230:PHE:CZ	2.49	0.48
1:B:79:GLN:HG2	1:B:81:GLU:OE2	2.15	0.47
1:B:330:VAL:HG12	1:B:331:TRP:N	2.30	0.47
1:B:281:VAL:O	1:B:283:SER:N	2.49	0.46
1:B:282:TRP:CZ2	3:B:406:PG4:H81	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:TYR:O	1:A:97:LYS:HE2	2.16	0.46
1:A:230:PHE:C	1:A:230:PHE:CD1	2.95	0.45
1:A:210:ILE:HB	1:A:248:THR:HB	2.00	0.44
1:B:114:LYS:HD2	2:B:302:GDM:H261	2.00	0.44
2:B:302:GDM:H232	5:B:513:HOH:O	2.16	0.44
1:A:110:ASP:O	1:A:114:LYS:HG3	2.18	0.44
1:A:272:SER:OG	1:A:279:ILE:HD12	2.18	0.44
1:A:75:LYS:HD3	1:A:231:SER:HB3	1.99	0.43
1:B:334:GLU:OE2	1:B:336:MET:HE1	2.18	0.43
1:B:102:ARG:HB2	1:B:271:TYR:CD2	2.54	0.42
1:B:138:CYS:SG	1:B:264:ILE:HG13	2.59	0.42
1:B:282:TRP:HB2	1:B:333:TRP:CZ3	2.54	0.42
1:A:192:ILE:HG13	1:A:193:GLY:N	2.34	0.42
1:B:76:PHE:N	1:B:76:PHE:CD1	2.88	0.42
1:A:135:LYS:HB3	1:A:333:TRP:CH2	2.55	0.42
1:A:285:LYS:HD3	1:A:285:LYS:HA	1.73	0.42
5:A:620:HOH:O	1:B:84:ARG:NH2	2.53	0.41
1:A:115:ILE:HD12	1:A:115:ILE:HA	1.88	0.41
1:B:166:ILE:CB	5:B:518:HOH:O	2.68	0.41
1:A:226:ASP:O	1:A:227:SER:CB	2.69	0.41
1:A:101:LEU:HD12	1:A:101:LEU:HA	1.84	0.40
1:B:99:ILE:CG1	1:B:102:ARG:NH2	2.84	0.40
1:B:81:GLU:OE2	1:B:81:GLU:N	2.47	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	200/236 (85%)	190 (95%)	9 (4%)	1 (0%)	24	27
1	B	198/236 (84%)	183 (92%)	12 (6%)	3 (2%)	8	7

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	398/472 (84%)	373 (94%)	21 (5%)	4 (1%)	12	12

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	282	TRP
1	B	216	ASN
1	A	129	ASN
1	B	229	GLU

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	183/207 (88%)	183 (100%)	0	100	100
1	B	180/207 (87%)	180 (100%)	0	100	100
All	All	363/414 (88%)	363 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	A	266	ASN
1	A	273	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	PG4	A	502	-	12,12,12	0.71	0	11,11,11	0.80	0
3	PG4	A	501	-	12,12,12	0.72	0	11,11,11	0.77	0
2	GDM	B	302	-	41,41,41	1.52	5 (12%)	56,57,57	2.01	17 (30%)
3	PG4	B	406	-	12,12,12	0.77	0	11,11,11	0.68	0
4	1PE	A	409	-	15,15,15	0.65	0	14,14,14	0.89	0
2	GDM	A	301	-	41,41,41	1.52	5 (12%)	56,57,57	1.97	13 (23%)
3	PG4	B	508	-	12,12,12	0.70	0	11,11,11	0.75	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
3	PG4	A	502	-	-	1/10/10/10	-
3	PG4	A	501	-	-	2/10/10/10	-
2	GDM	B	302	-	-	8/52/72/72	1/2/2/2
3	PG4	B	406	-	-	0/10/10/10	-
4	1PE	A	409	-	-	3/13/13/13	-
2	GDM	A	301	-	-	8/52/72/72	1/2/2/2
3	PG4	B	508	-	-	0/10/10/10	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	GDM	C4-C5	5.46	1.53	1.33
2	B	302	GDM	C4-C5	5.45	1.53	1.33
2	B	302	GDM	C17-C18	-3.16	1.39	1.46
2	A	301	GDM	C17-C18	-3.11	1.39	1.46
2	A	301	GDM	C20-N1	-2.85	1.33	1.41
2	B	302	GDM	C20-N1	-2.79	1.33	1.41
2	A	301	GDM	C9-C8	2.78	1.39	1.33
2	B	302	GDM	C9-C8	2.70	1.39	1.33
2	A	301	GDM	C16-C21	-2.43	1.39	1.46
2	B	302	GDM	C16-C21	-2.37	1.39	1.46

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	GDM	C6-C5-C4	-6.09	113.55	125.88
2	B	302	GDM	C6-C5-C4	-5.70	114.33	125.88
2	B	302	GDM	C28-C14-C13	4.99	126.09	110.84
2	A	301	GDM	C28-C14-C13	4.92	125.89	110.84
2	B	302	GDM	C3-C4-C5	-4.75	113.42	124.43
2	A	301	GDM	C3-C4-C5	-4.74	113.43	124.43
2	B	302	GDM	O3-C24-N2	4.43	117.78	110.92
2	A	301	GDM	O3-C24-N2	4.40	117.74	110.92
2	B	302	GDM	C19-C20-N1	-4.27	119.61	126.91
2	A	301	GDM	C19-C20-N1	-4.26	119.62	126.91
2	B	302	GDM	C13-C12-C11	-3.10	109.22	113.98
2	A	301	GDM	C13-C12-C11	-3.07	109.27	113.98
2	B	302	GDM	C2-C1-N1	2.91	120.50	115.01
2	A	301	GDM	C2-C1-N1	2.75	120.19	115.01
2	B	302	GDM	C21-C20-N1	2.72	122.54	111.12
2	B	302	GDM	C14-C13-C12	-2.66	111.82	115.93
2	A	301	GDM	C21-C20-N1	2.63	122.16	111.12
2	B	302	GDM	C10-C9-C8	-2.57	122.06	128.00
2	A	301	GDM	C10-C9-C8	-2.56	122.08	128.00
2	B	302	GDM	C7-C6-C5	-2.39	109.08	112.91
2	B	302	GDM	C7-O3-C24	-2.28	113.07	116.14
2	A	301	GDM	C19-C18-C17	2.28	122.02	115.39
2	A	301	GDM	C14-C13-C12	-2.22	112.50	115.93
2	A	301	GDM	O3-C24-O4	-2.21	119.68	123.06
2	B	302	GDM	O3-C24-O4	-2.20	119.69	123.06
2	B	302	GDM	C19-C18-C17	2.20	121.80	115.39
2	B	302	GDM	C25-C8-C7	2.14	120.19	115.96
2	B	302	GDM	O1-C1-C2	-2.07	117.68	121.49

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	GDM	C25-C8-C7	2.05	120.00	115.96
2	B	302	GDM	O8-C18-C17	-2.02	118.56	121.66

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	GDM	O1-C1-N1-C20
2	A	301	GDM	C2-C1-N1-C20
2	A	301	GDM	C19-C20-N1-C1
2	A	301	GDM	C21-C20-N1-C1
2	A	301	GDM	C3-C4-C5-C6
2	A	301	GDM	C4-C5-C6-O2
2	A	301	GDM	C4-C5-C6-C7
2	A	301	GDM	C12-C13-C14-C28
2	B	302	GDM	O1-C1-N1-C20
2	B	302	GDM	C2-C1-N1-C20
2	B	302	GDM	C19-C20-N1-C1
2	B	302	GDM	C21-C20-N1-C1
2	B	302	GDM	C3-C4-C5-C6
2	B	302	GDM	C4-C5-C6-O2
2	B	302	GDM	C4-C5-C6-C7
2	B	302	GDM	C12-C13-C14-C28
4	A	409	1PE	OH2-C12-C22-OH3
3	A	501	PG4	O3-C5-C6-O4
4	A	409	1PE	OH7-C16-C26-OH6
4	A	409	1PE	OH6-C15-C25-OH5
3	A	502	PG4	O2-C3-C4-O3
3	A	501	PG4	O4-C7-C8-O5

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	GDM	C1-C10-C11-C12-C13-C14-C15-C16-C2-C20-C21-C3-C4-C5-C6-C7-C8-C9-N
2	B	302	GDM	C1-C10-C11-C12-C13-C14-C15-C16-C2-C20-C21-C3-C4-C5-C6-C7-C8-C9-N

4 monomers are involved in 6 short contacts:

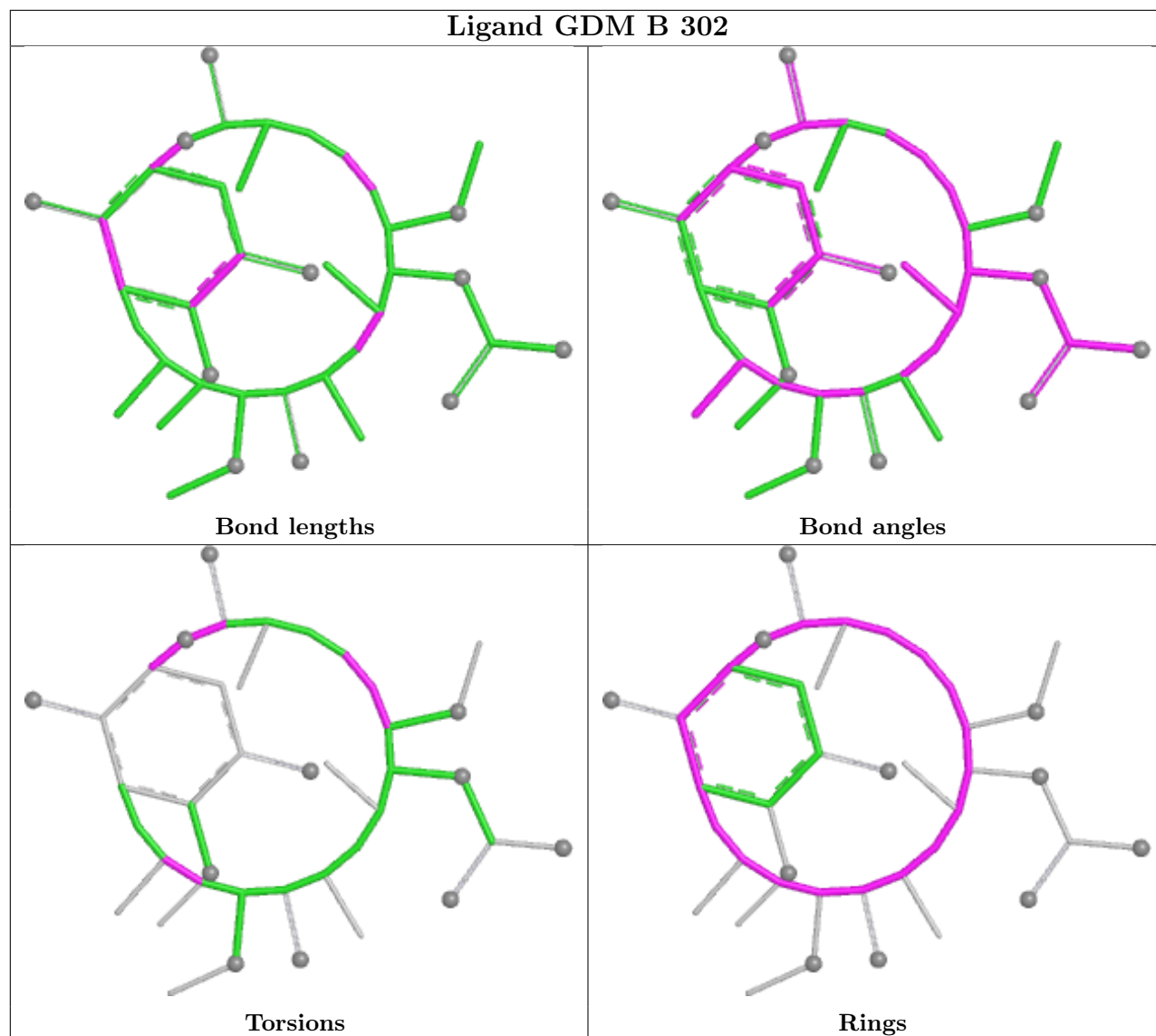
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	PG4	1	0
2	B	302	GDM	3	0

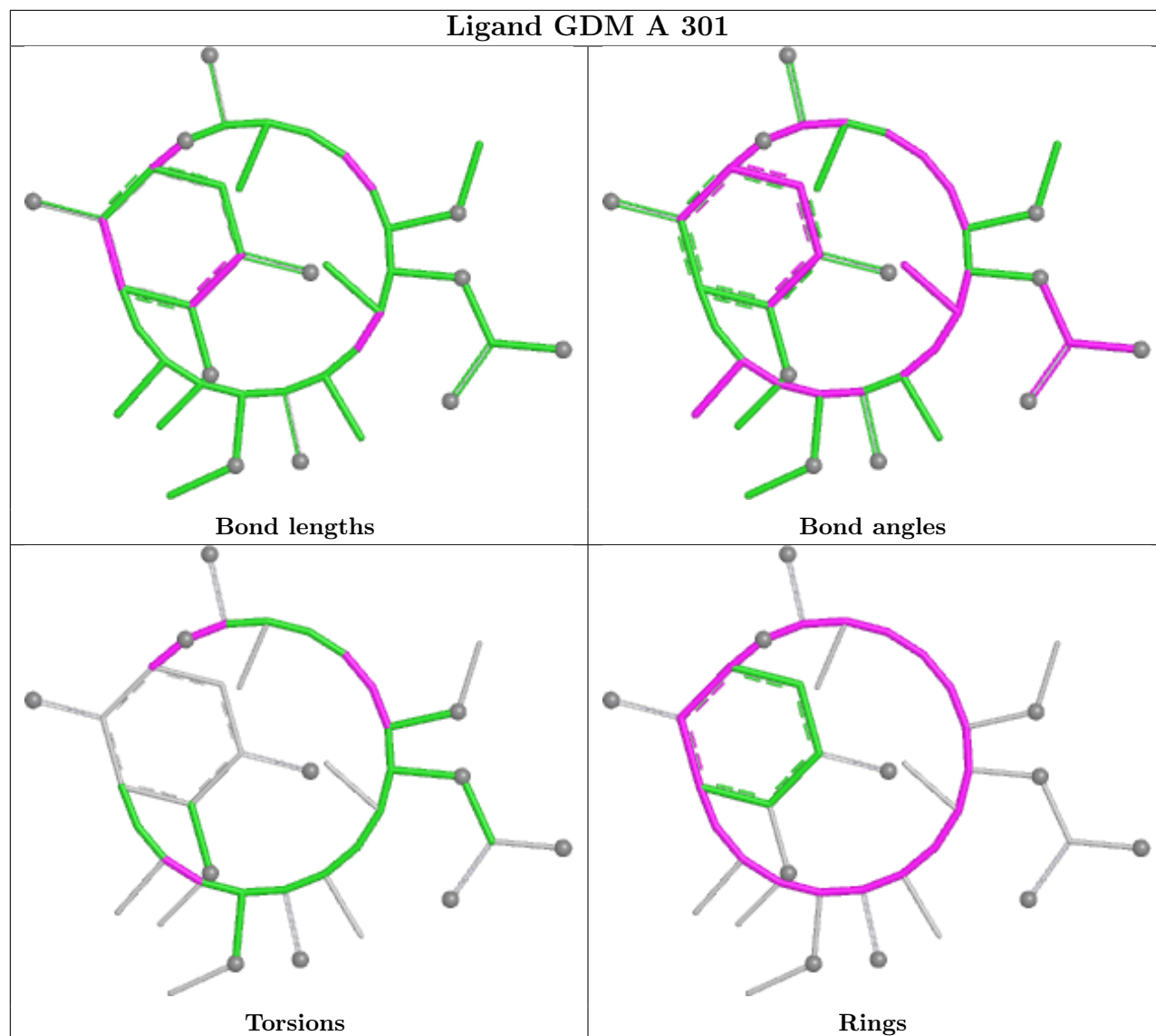
Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	406	PG4	1	0
2	A	301	GDM	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	206/236 (87%)	-0.03	6 (2%)	53	60	12, 25, 57, 80	0
1	B	204/236 (86%)	0.02	7 (3%)	48	55	11, 25, 61, 80	0
All	All	410/472 (86%)	-0.01	13 (3%)	50	57	11, 25, 60, 80	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	272	SER	3.8
1	A	167	ALA	3.0
1	B	286	THR	2.7
1	A	286	THR	2.7
1	B	274	PHE	2.6
1	A	166	ILE	2.5
1	B	330	VAL	2.4
1	A	72	LYS	2.4
1	B	187	SER	2.3
1	A	330	VAL	2.2
1	B	191	LEU	2.2
1	A	188	THR	2.2
1	B	192	ILE	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

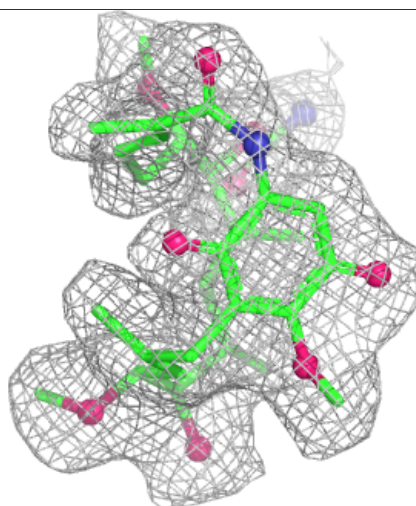
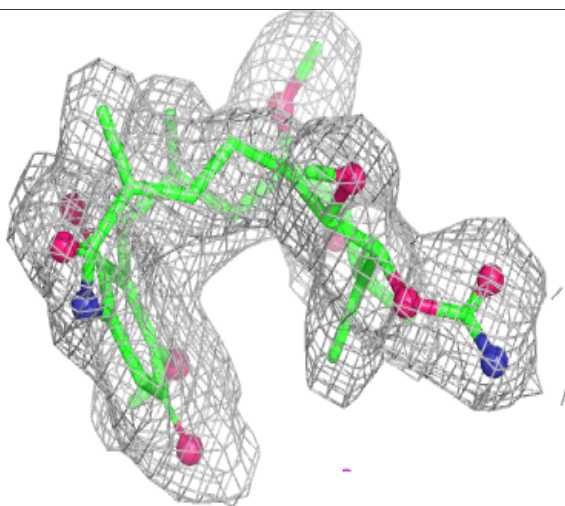
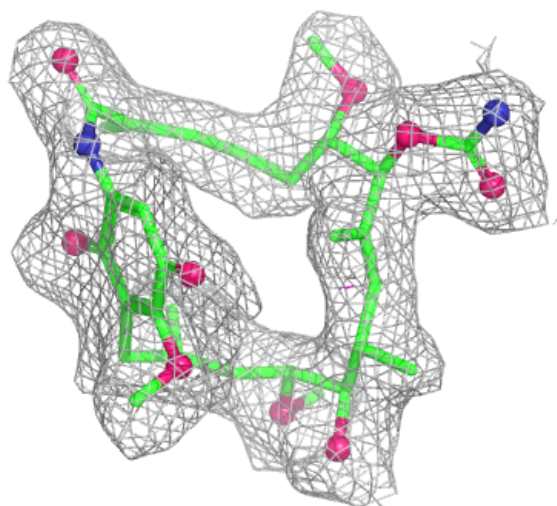
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PG4	B	406	13/13	0.84	0.17	48,57,63,63	0
3	PG4	A	502	13/13	0.90	0.14	59,61,63,63	0
4	1PE	A	409	16/16	0.90	0.14	32,36,39,43	0
3	PG4	A	501	13/13	0.91	0.13	43,45,49,49	0
3	PG4	B	508	13/13	0.93	0.10	27,30,49,49	0
2	GDM	A	301	40/40	0.94	0.07	10,20,28,30	0
2	GDM	B	302	40/40	0.95	0.07	12,22,26,27	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.

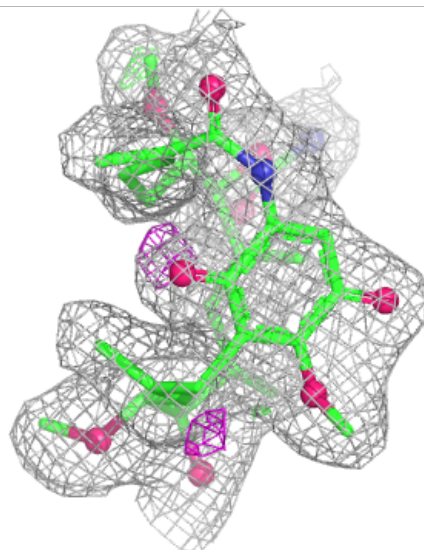
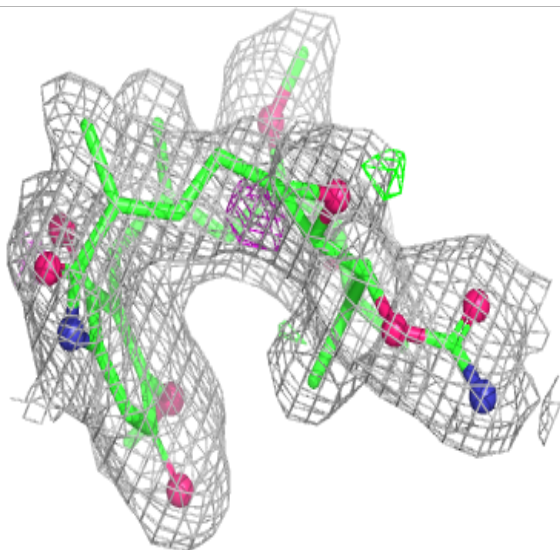
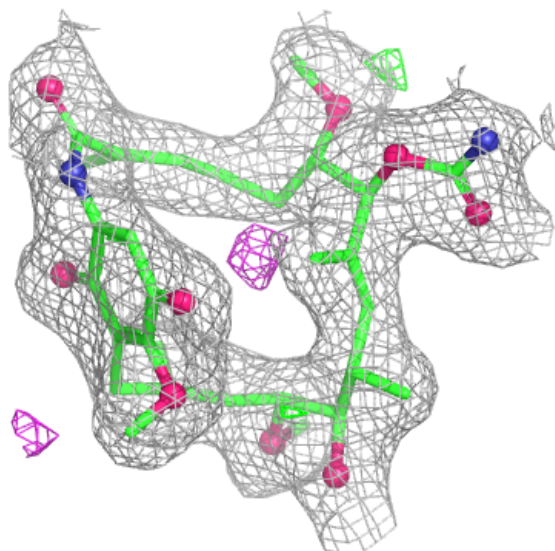
Electron density around GDM A 301:

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



Electron density around GDM B 302:

$2mF_o-DF_c$ (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.