Full wwPDB X-ray Structure Validation Report (i)

Nov 3, 2026 – 12:11 pm GMT

PDB ID	:	9RZW / pdb_00009rzw
Title	:	Crystal structure of PNGase A from Bifidobacterium bifidum LMG13195
Authors	:	Caulton, S.G.; Crouch, L.I.; Lovering, A.L.; Ojuri, T.O.
Deposited on	:	2025-07-16
Resolution	:	1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

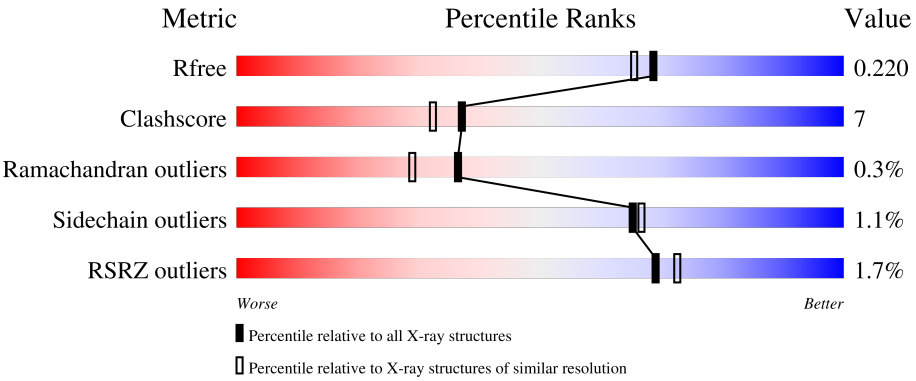
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 1.90 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 <=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	568	2% 84% 10% • 5%
1	B	568	% 81% 13% • 5%

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
4	PEG	A	604	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 9454 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 PNGase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	539	Total	C	N	O	S	0	18	0
			4160	2585	704	860	11			
1	B	539	Total	C	N	O	S	0	13	0
			4125	2566	696	851	12			

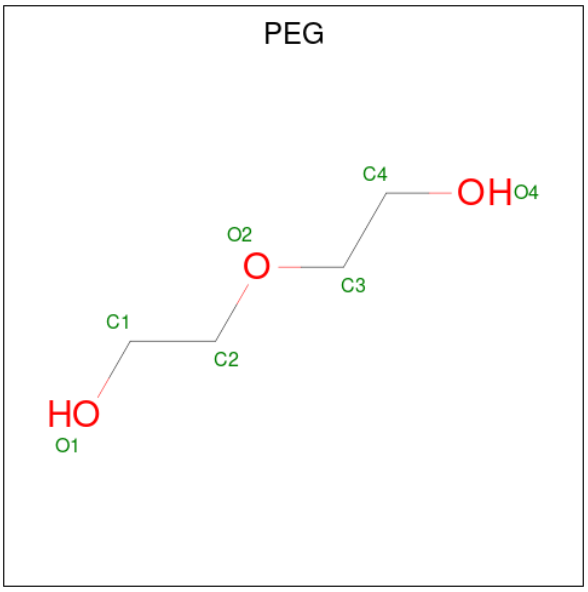
- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	B	2	Total	Cl	0	0
			2	2		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

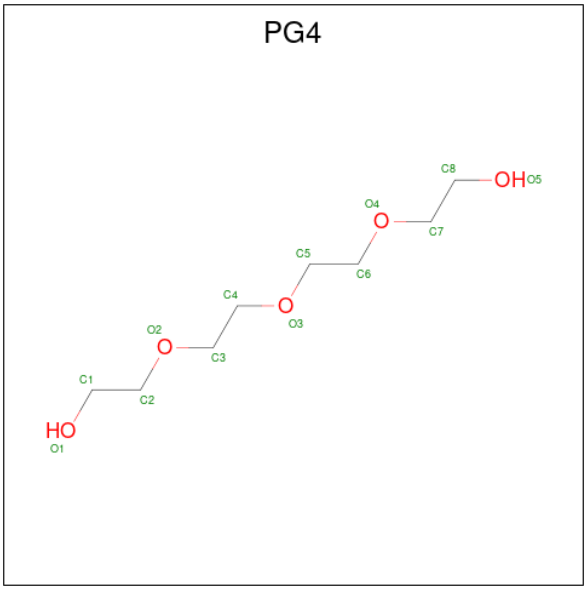
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



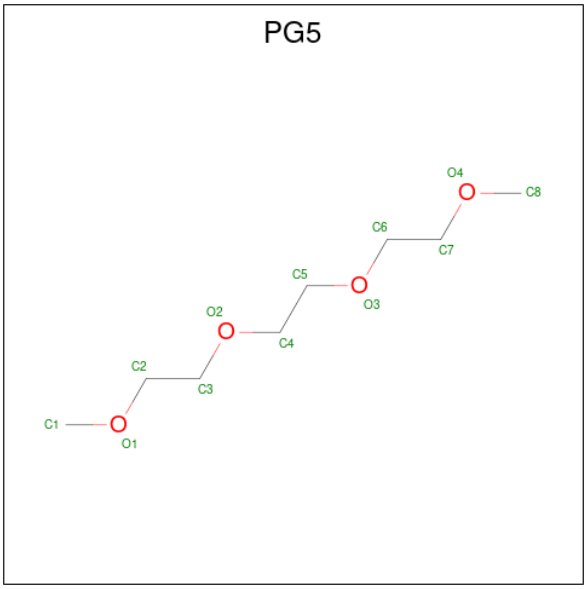
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0

- Molecule 5 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



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

- Molecule 6 is 1-METHOXY-2-[2-(2-METHOXY-ETHOXY]-ETHANE (CCD ID: PG5) (formula: $C_8H_{18}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 12 8 4	0	0

- Molecule 7 is water.

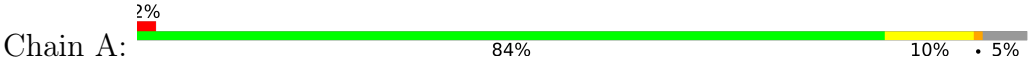
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	564	Total O 564 564	0	0
7	B	548	Total O 548 548	0	0

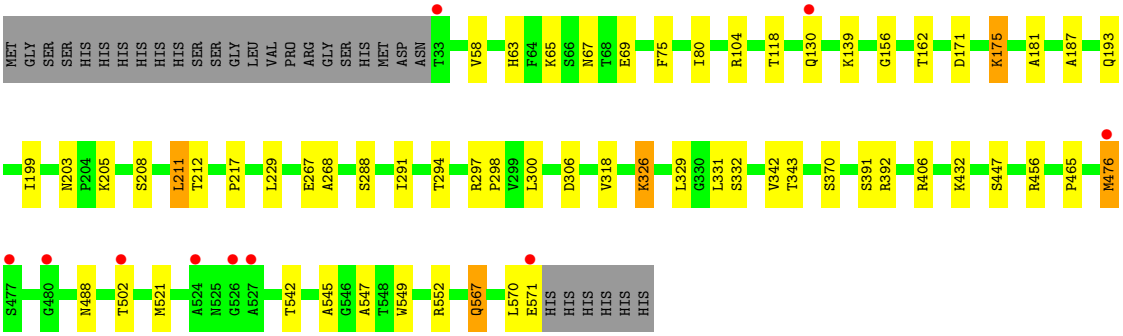
3 Residue-property plots (i)

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: PNGase A

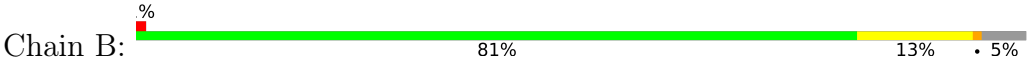
Chain A:

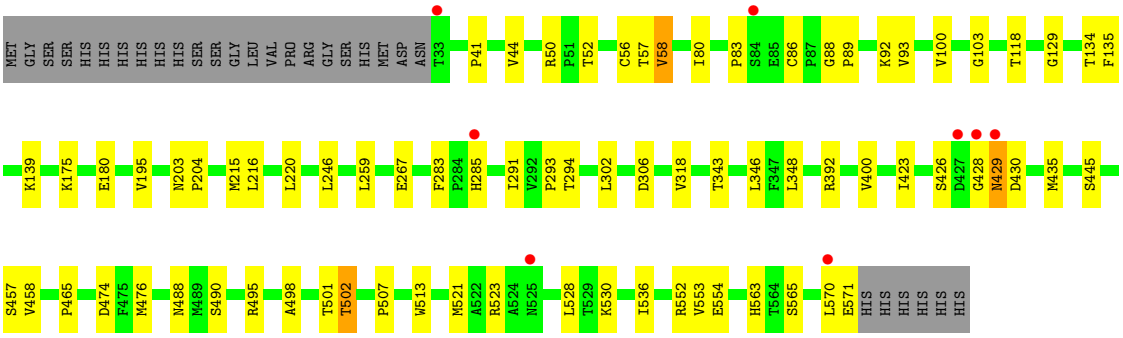




• Molecule 1: PNGase A

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	161.98Å 81.04Å 124.64Å 90.00° 127.83° 90.00°	Depositor
Resolution (Å)	68.46 – 1.90 68.46 – 1.90	Depositor EDS
% Data completeness (in resolution range)	84.6 (68.46-1.90) 84.6 (68.46-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.77 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.21.1.5286	Depositor
R, R_{free}	0.184 , 0.220 0.184 , 0.220	Depositor DCC
R_{free} test set	4124 reflections (2.83%)	wwPDB-VP
Wilson B-factor (Å^2)	24.4	Xtriage
Anisotropy	0.688	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 41.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.003 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9454	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.47% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: PG5, CL, MG, PG4, PEG

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	0.62	0/4286	0.83	0/5857
1	B	0.66	0/4244	0.80	0/5803
All	All	0.64	0/8530	0.81	0/11660

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	4160	0	4010	51	0
1	B	4125	0	3979	61	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	14	0	20	7	0
5	B	26	0	36	6	0
6	B	12	0	18	5	0
7	A	564	0	0	12	0
7	B	548	0	0	12	0
All	All	9454	0	8063	116	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 (116) 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:205:LYS:HE2	7:A:1122:HOH:O	1.77	0.84
1:B:565:SER:HB2	7:B:1123:HOH:O	1.83	0.77
1:A:465:PRO:HB2	4:A:604:PEG:H21	1.71	0.72
1:A:69:GLU:H	1:A:69:GLU:CD	1.99	0.71
1:B:429:ASN:HD22	1:B:476:MET:HB2	1.54	0.71
1:A:203:ASN:HD21	1:A:205:LYS:HB2	1.55	0.71
1:B:57:THR:HG21	5:B:605:PG4:H22	1.72	0.71
1:A:268:ALA:HB1	1:A:331:LEU:HD11	1.72	0.69
1:A:567:GLN:HE22	1:A:570:LEU:HD13	1.57	0.68
1:A:175:LYS:HE3	4:A:603:PEG:H31	1.76	0.66
1:A:118[B]:THR:HG23	1:A:343:THR:HG23	1.80	0.64
1:A:432:LYS:HG2	7:A:753:HOH:O	1.96	0.64
1:B:400:VAL:HG21	7:B:813:HOH:O	1.97	0.63
1:B:283:PHE:HB3	1:B:285:HIS:CE1	2.33	0.63
4:A:604:PEG:H22	7:A:1067:HOH:O	1.99	0.62
1:A:205:LYS:CE	7:A:1122:HOH:O	2.42	0.61
1:B:502:THR:HG23	7:B:1004:HOH:O	2.00	0.61
1:A:406:ARG:NH2	7:A:705:HOH:O	2.35	0.60
1:B:118[B]:THR:HG21	7:B:848:HOH:O	2.00	0.60
1:B:536:ILE:HG21	1:B:552:ARG:NH2	2.16	0.60
1:A:545:ALA:O	1:A:571:GLU:HG2	2.01	0.59
1:A:203:ASN:HD22	1:A:205:LYS:H	1.49	0.59
1:B:259:LEU:HD21	1:B:423:ILE:HD12	1.84	0.59
1:A:294:THR:HG23	1:A:521:MET:HE2	1.84	0.59
1:B:495:ARG:HD2	1:B:507:PRO:O	2.03	0.59
1:A:67[B]:ASN:OD1	1:A:162:THR:HG23	2.04	0.58
1:A:488:ASN:OD1	4:A:604:PEG:H42	2.04	0.58
1:B:56[B]:CYS:SG	1:B:83:PRO:HB3	2.43	0.57
1:B:195[B]:VAL:HG23	1:B:346:LEU:HB2	1.86	0.57
1:B:570:LEU:HG	1:B:571:GLU:H	1.69	0.57
1:B:294:THR:HG23	1:B:521:MET:HE2	1.86	0.57
1:A:447:SER:HB2	1:A:456:ARG:HG2	1.87	0.57
1:B:175:LYS:HD2	5:B:605:PG4:H32	1.87	0.56
1:B:86[B]:CYS:SG	1:B:180:GLU:HG2	2.45	0.56
1:A:570:LEU:O	1:A:571:GLU:HB3	2.05	0.55
4:A:604:PEG:C2	7:A:1067:HOH:O	2.53	0.55
1:B:293:PRO:HB2	1:B:521:MET:HE1	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:VAL:HG22	1:B:134[B]:THR:HG22	1.88	0.54
1:B:445:SER:HB3	1:B:458[B]:VAL:HG22	1.89	0.54
1:B:267:GLU:OE1	1:B:392:ARG:HD2	2.07	0.54
1:A:208:SER:HB3	1:A:332:SER:HB3	1.89	0.54
1:B:52:THR:HG22	7:B:1163:HOH:O	2.05	0.54
1:A:203:ASN:ND2	1:A:205:LYS:HB2	2.22	0.53
1:B:553[B]:VAL:HG12	1:B:563:HIS:CG	2.44	0.53
1:A:502:THR:HG21	7:A:1097:HOH:O	2.09	0.53
1:B:139:LYS:NZ	7:B:705:HOH:O	2.42	0.53
1:B:563:HIS:HE1	7:B:1051:HOH:O	1.92	0.53
1:A:104[A]:ARG:NE	7:A:707:HOH:O	2.42	0.53
1:A:118[B]:THR:CG2	1:A:343:THR:HG23	2.39	0.52
1:B:175:LYS:HZ3	5:B:605:PG4:C3	2.21	0.52
1:B:129:GLY:HA2	6:B:606:PG5:H83	1.92	0.51
1:B:563:HIS:HD2	7:B:1156:HOH:O	1.94	0.51
1:B:458[B]:VAL:HG12	1:B:501:THR:HG21	1.93	0.51
1:B:246:LEU:C	1:B:246:LEU:HD23	2.35	0.51
1:B:44:VAL:HG12	1:B:553[A]:VAL:HG23	1.92	0.50
1:B:57:THR:HG21	5:B:605:PG4:C2	2.40	0.50
1:B:58[A]:VAL:HG11	1:B:80:ILE:HD11	1.93	0.50
1:B:41:PRO:HG2	1:B:135:PHE:HB3	1.92	0.50
1:B:44:VAL:CG1	1:B:553[A]:VAL:HG23	2.42	0.50
1:A:306:ASP:HB3	7:A:721:HOH:O	2.11	0.50
1:A:211:LEU:HD12	1:A:329:LEU:O	2.12	0.50
1:B:215:MET:HG3	1:B:216:LEU:N	2.27	0.49
1:A:75:PHE:HB3	1:A:156:GLY:O	2.13	0.49
1:A:567:GLN:HE22	1:A:570:LEU:CD1	2.23	0.49
1:A:139:LYS:HE3	1:A:306:ASP:OD1	2.13	0.48
1:A:549:TRP:CZ3	1:A:567:GLN:HB3	2.48	0.48
1:B:50:ARG:NH1	7:B:707:HOH:O	2.45	0.48
1:A:63:HIS:HA	1:A:171:ASP:OD1	2.14	0.48
1:A:199:ILE:HD12	1:A:331:LEU:HD23	1.96	0.48
1:B:294:THR:HG23	1:B:521:MET:CE	2.44	0.48
1:A:175:LYS:NZ	7:A:711:HOH:O	2.45	0.48
1:A:229:LEU:HD11	1:A:268:ALA:HB2	1.96	0.47
1:B:195[B]:VAL:CG2	1:B:346:LEU:HB2	2.44	0.47
1:B:343:THR:HG23	7:B:968:HOH:O	2.14	0.47
1:B:428:GLY:O	1:B:429:ASN:C	2.58	0.47
1:B:465:PRO:HG2	1:B:490:SER:HB2	1.97	0.47
1:B:488:ASN:OD1	5:B:604:PG4:H52	2.14	0.47
1:B:220:LEU:HD21	1:B:348:LEU:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:SER:HB3	1:B:498:ALA:HB3	1.97	0.46
1:A:331:LEU:HD21	1:A:342:VAL:HG11	1.97	0.46
1:B:203:ASN:HB2	1:B:204:PRO:CD	2.44	0.46
1:B:429:ASN:OD1	1:B:474:ASP:HA	2.16	0.46
1:B:103:GLY:HA2	6:B:606:PG5:C6	2.46	0.46
1:B:302:LEU:HD22	1:B:513:TRP:CE2	2.51	0.46
1:B:134[B]:THR:HG21	7:B:1045:HOH:O	2.16	0.45
1:A:58[A]:VAL:HG21	1:A:80:ILE:HD11	1.98	0.45
1:B:488:ASN:CG	5:B:604:PG4:H52	2.41	0.45
6:B:606:PG5:H32	6:B:606:PG5:H12	1.61	0.45
1:B:103:GLY:HA2	6:B:606:PG5:H61	1.98	0.45
1:A:476:MET:HA	1:A:476:MET:HE2	1.99	0.44
1:A:326:LYS:HB3	1:A:326:LYS:HE2	1.40	0.44
1:A:552:ARG:NH1	7:A:716:HOH:O	2.49	0.44
1:A:212:THR:HG23	7:A:873:HOH:O	2.18	0.44
1:B:521:MET:HE3	1:B:521:MET:HB2	1.88	0.44
1:B:139:LYS:HE3	1:B:306:ASP:OD1	2.17	0.43
1:A:181:ALA:HB2	1:A:187:ALA:HB2	2.01	0.43
1:A:175:LYS:HE3	4:A:603:PEG:C3	2.46	0.43
1:A:65:LYS:HE3	1:A:171:ASP:OD2	2.18	0.42
1:B:523:ARG:HG2	1:B:528:LEU:HA	2.00	0.42
1:A:268:ALA:HB1	1:A:331:LEU:CD1	2.45	0.42
1:A:193:GLN:HE22	1:A:217:PRO:HG3	1.85	0.42
1:B:536:ILE:HG12	1:B:554:GLU:HG2	2.00	0.42
1:B:92:LYS:HG3	1:B:93:VAL:N	2.35	0.42
1:B:458[A]:VAL:HG22	1:B:501:THR:HG21	2.01	0.42
1:B:88:GLY:CA	1:B:89:PRO:C	2.93	0.42
1:A:69:GLU:CD	1:A:69:GLU:N	2.74	0.41
1:A:175:LYS:HE3	4:A:603:PEG:O4	2.20	0.41
1:A:267:GLU:OE1	1:A:392:ARG:HD2	2.19	0.41
1:A:370[A]:SER:OG	1:A:391:SER:HB2	2.20	0.41
6:B:606:PG5:H41	6:B:606:PG5:H62	1.75	0.41
1:A:542:THR:HA	1:A:547:ALA:O	2.20	0.41
1:A:288[A]:SER:HB3	1:A:300:LEU:HD23	2.03	0.40
1:A:297:ARG:HA	1:A:298:PRO:HA	1.87	0.40
1:B:435:MET:C	1:B:435:MET:SD	3.04	0.40
1:B:530:LYS:HD2	7:B:1085:HOH:O	2.21	0.40
1:B:426:SER:OG	1:B:430:ASP:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	555/568 (98%)	541 (98%)	13 (2%)	1 (0%)	43	36
1	B	550/568 (97%)	529 (96%)	19 (4%)	2 (0%)	30	22
All	All	1105/1136 (97%)	1070 (97%)	32 (3%)	3 (0%)	36	29

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	291	ILE
1	B	429	ASN
1	A	291	ILE

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	465/473 (98%)	458 (98%)	7 (2%)	57	56
1	B	460/473 (97%)	456 (99%)	4 (1%)	70	73
All	All	925/946 (98%)	914 (99%)	11 (1%)	65	63

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	175	LYS
1	A	211	LEU

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Mol	Chain	Res	Type
1	A	318	VAL
1	A	326	LYS
1	A	476	MET
1	A	567	GLN
1	B	58[A]	VAL
1	B	58[B]	VAL
1	B	318	VAL
1	B	502	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	193	GLN
1	A	203	ASN
1	A	249	HIS
1	A	393	ASN
1	A	514	ASN
1	A	567	GLN
1	B	193	GLN
1	B	249	HIS
1	B	363	GLN
1	B	419	GLN
1	B	459	ASN
1	B	479	ASN
1	B	563	HIS

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 (i)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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	$\#\|Z\| > 2$
6	PG5	B	606	-	11,11,11	0.14	0	10,10,10	0.19	0
4	PEG	A	603	-	6,6,6	0.10	0	5,5,5	0.08	0
5	PG4	B	604	-	12,12,12	0.15	0	11,11,11	0.17	0
4	PEG	A	604	-	6,6,6	0.11	0	5,5,5	0.07	0
5	PG4	B	605	-	12,12,12	0.14	0	11,11,11	0.46	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
6	PG5	B	606	-	-	6/9/9/9	-
4	PEG	A	603	-	-	2/4/4/4	-
5	PG4	B	604	-	-	3/10/10/10	-
4	PEG	A	604	-	-	2/4/4/4	-
5	PG4	B	605	-	-	5/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	606	PG5	C4-C5-O3-C6
5	B	605	PG4	O2-C3-C4-O3
5	B	604	PG4	O3-C5-C6-O4
6	B	606	PG5	O1-C2-C3-O2
4	A	604	PEG	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
6	B	606	PG5	O3-C6-C7-O4
6	B	606	PG5	C3-C2-O1-C1
4	A	604	PEG	O2-C3-C4-O4
5	B	605	PG4	O4-C7-C8-O5
5	B	604	PG4	C5-C6-O4-C7
6	B	606	PG5	C6-C7-O4-C8
5	B	605	PG4	C1-C2-O2-C3
4	A	603	PEG	O1-C1-C2-O2
4	A	603	PEG	C1-C2-O2-C3
5	B	605	PG4	C5-C6-O4-C7
5	B	605	PG4	C6-C5-O3-C4
6	B	606	PG5	O2-C4-C5-O3
5	B	604	PG4	O4-C7-C8-O5

There are no ring outliers.

5 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	606	PG5	5	0
4	A	603	PEG	3	0
5	B	604	PG4	2	0
4	A	604	PEG	4	0
5	B	605	PG4	4	0

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	539/568 (94%)	0.20	10 (1%) 66 70	13, 29, 46, 90	18 (3%)
1	B	539/568 (94%)	0.23	8 (1%) 72 75	15, 28, 48, 110	13 (2%)
All	All	1078/1136 (94%)	0.21	18 (1%) 69 72	13, 29, 47, 110	31 (2%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	428	GLY	5.9
1	B	429	ASN	4.1
1	A	33	THR	3.5
1	B	33	THR	3.2
1	B	570	LEU	3.2
1	A	526	GLY	3.2
1	B	427	ASP	3.2
1	A	476	MET	3.0
1	A	527	ALA	2.5
1	A	571	GLU	2.4
1	A	524	ALA	2.4
1	A	480	GLY	2.4
1	A	502	THR	2.3
1	B	84	SER	2.2
1	B	525	ASN	2.1
1	B	285	HIS	2.1
1	A	130	GLN	2.0
1	A	477	SER	2.0

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 (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

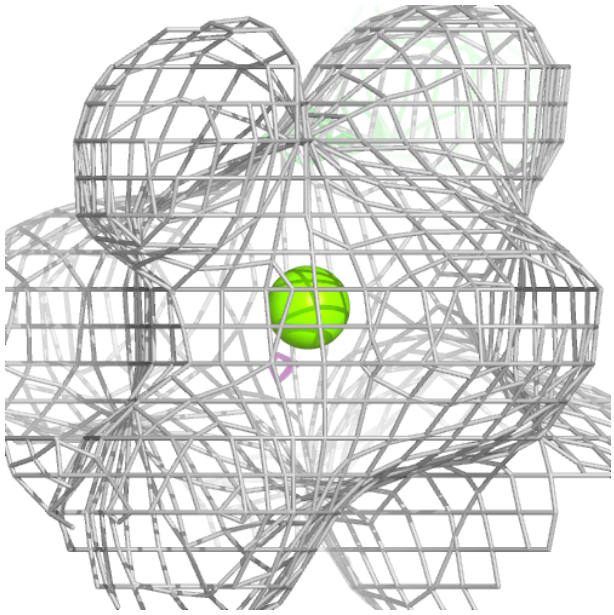
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

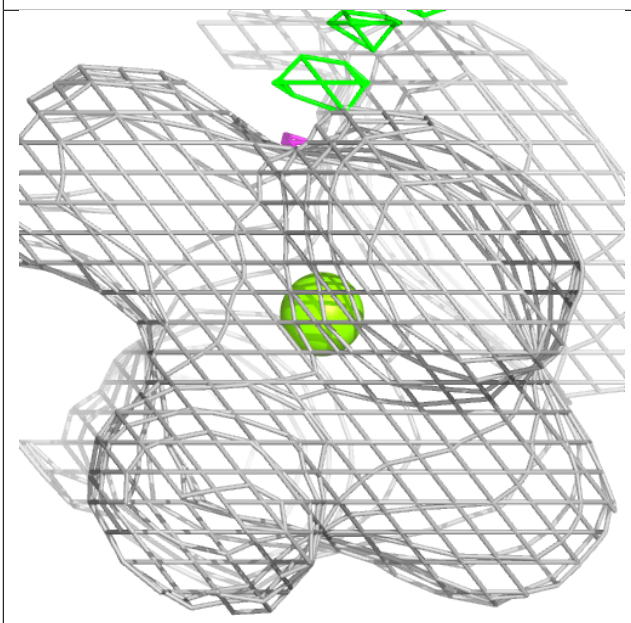
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	PG5	B	606	12/12	0.72	0.22	58,67,72,76	0
4	PEG	A	603	7/7	0.75	0.20	59,62,66,71	0
5	PG4	B	605	13/13	0.83	0.16	49,54,60,61	0
4	PEG	A	604	7/7	0.85	0.12	40,40,48,55	0
5	PG4	B	604	13/13	0.91	0.09	36,40,59,64	0
2	CL	B	602	1/1	0.97	0.06	37,37,37,37	0
3	MG	B	603	1/1	0.98	0.03	34,34,34,34	0
2	CL	B	601	1/1	0.98	0.10	30,30,30,30	0
3	MG	A	602	1/1	0.98	0.05	29,29,29,29	0
2	CL	A	601	1/1	0.99	0.04	25,25,25,25	0

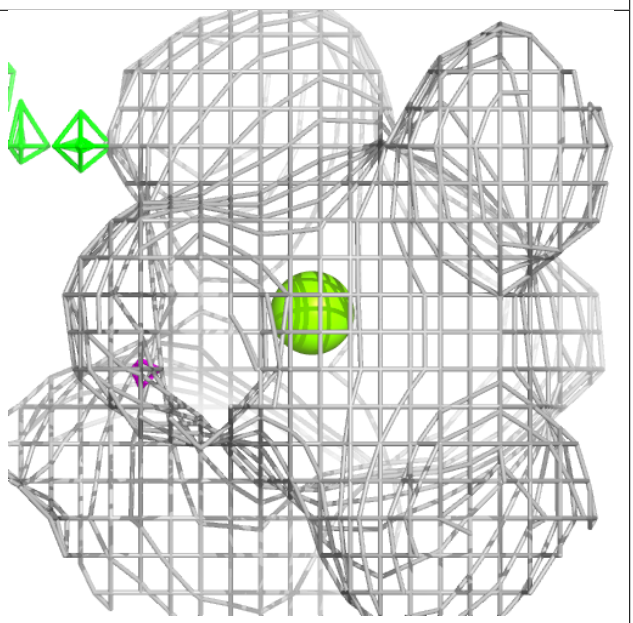
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MG B 603:

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

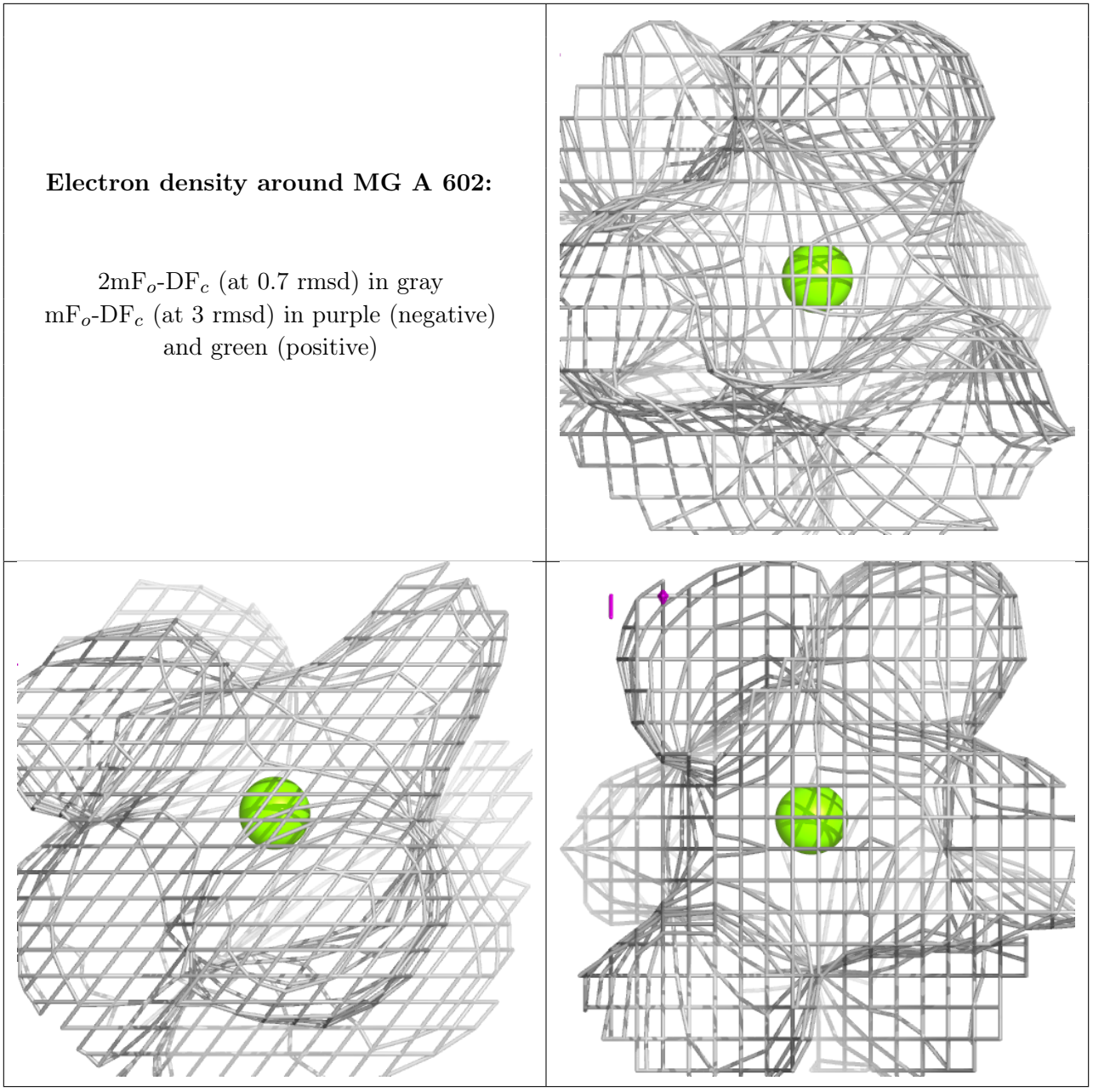






Electron density around MG A 602:

$2mF_o$-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.