Full wwPDB X-ray Structure Validation Report ⓘ

Mar 28, 2024 – 12:05 PM EDT

PDB ID	:	8UQZ
Title	:	Round 18 Arylesterase Variant of Phosphotriesterase Bound to Gadolinium(III) Measured at 9.5 keV
Authors	:	Breeze, C.W.; Frkic, R.L.; Campbell, E.C.; Jackson, C.J.
Deposited on	:	2023-10-25
Resolution	:	1.61 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:

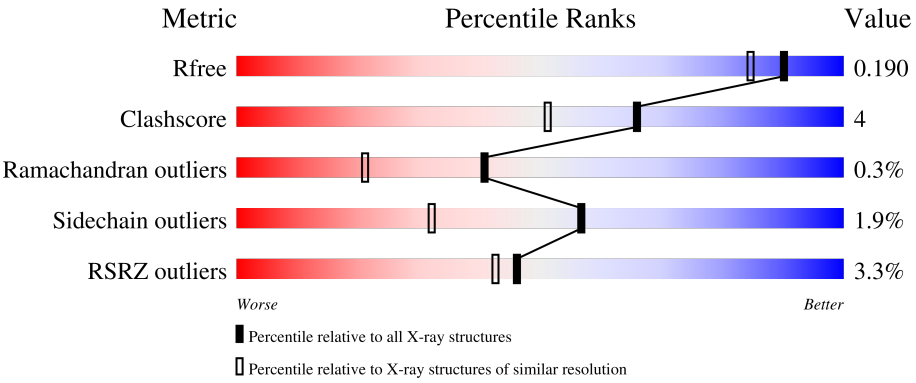
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.1

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 1.61 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4693 (1.64-1.60)
Clashscore	141614	5002 (1.64-1.60)
Ramachandran outliers	138981	4888 (1.64-1.60)
Sidechain outliers	138945	4887 (1.64-1.60)
RSRZ outliers	127900	4609 (1.64-1.60)

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	333	4% 84% 10% • 5%
1	B	333	3% 91% 7% ••

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	CL	A	404	-	-	X	-

2 Entry composition

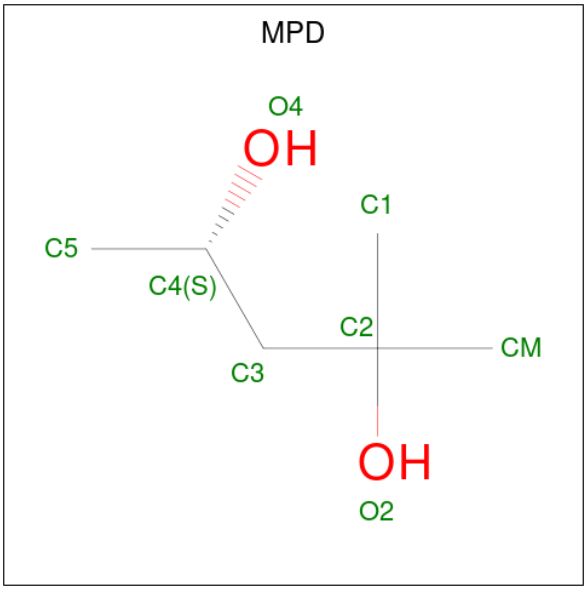
There are 5 unique types of molecules in this entry. The entry contains 10405 atoms, of which 5083 are hydrogens and 0 are deuteriums.

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 Phosphotriesterase variant PTE-R18.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	316	Total	C	H	N	O	S	0	2	0
			4925	1547	2484	439	448	7			
1	B	328	Total	C	H	N	O	S	0	0	0
			5055	1591	2543	447	466	8			

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			22	6	14	2		
2	A	1	Total	C	H	O	0	0
			22	6	14	2		
2	B	1	Total	C	H	O	0	0
			22	6	14	2		
2	B	1	Total	C	H	O	0	0
			22	6	14	2		

- Molecule 3 is GADOLINIUM ION (three-letter code: GD3) (formula: Gd) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Gd 1 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

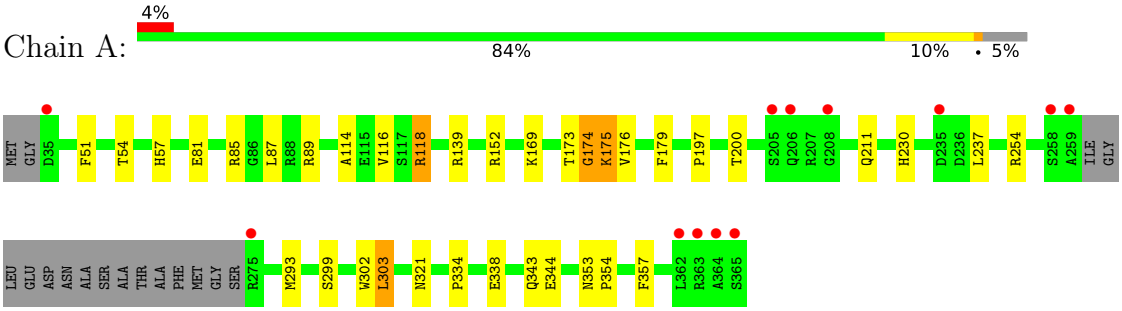
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	179	Total O 179 179	0	0
5	B	155	Total O 155 155	0	0

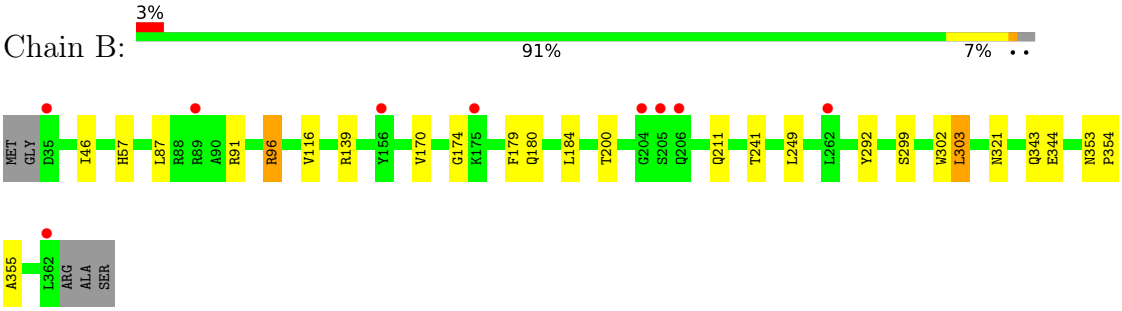
3 Residue-property plots (i)

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: Phosphotriesterase variant PTE-R18



• Molecule 1: Phosphotriesterase variant PTE-R18



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	85.71Å 86.14Å 89.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.86 – 1.61 44.62 – 1.61	Depositor EDS
% Data completeness (in resolution range)	98.1 (42.86-1.61) 98.1 (44.62-1.61)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.86 (at 1.61Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.170 , 0.195 0.167 , 0.190	Depositor DCC
R_{free} test set	3960 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å^2)	25.1	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 45.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.003 for -l,-k,-h 0.003 for k,h,-l 0.000 for k,l,h 0.000 for l,h,k	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	10405	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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: GD3, CL, MPD

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	0.45	0/2493	0.68	0/3382
1	B	0.43	0/2559	0.66	1/3474 (0.0%)
All	All	0.44	0/5052	0.67	1/6856 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	249	LEU	CA-CB-CG	-5.73	102.12	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2441	2484	2474	25	0
1	B	2512	2543	2542	13	1
2	A	16	28	28	3	0
2	B	16	28	28	1	0
3	A	1	0	0	0	0
4	A	1	0	0	2	0
4	B	1	0	0	0	0
5	A	179	0	0	3	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	155	0	0	0	0
All	All	5322	5083	5072	40	1

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 4.

All (40) 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:169[B]:LYS:NZ	4:A:404:CL:CL	2.18	1.13
1:B:170:VAL:HG11	1:B:184:LEU:HD12	1.55	0.88
1:A:87:LEU:HD12	1:A:116:VAL:HG12	1.73	0.69
1:A:54:THR:HG23	5:A:540:HOH:O	1.98	0.64
1:B:343:GLN:OE1	2:B:401:MPD:H11	1.98	0.64
1:B:170:VAL:HG11	1:B:184:LEU:CD1	2.29	0.62
1:A:175:LYS:O	1:A:175:LYS:HD2	2.05	0.56
1:A:176:VAL:HG23	1:A:211:GLN:OE1	2.07	0.55
1:A:169[A]:LYS:HE2	4:A:404:CL:CL	2.44	0.54
2:A:402:MPD:H53	2:A:402:MPD:HM1	1.90	0.53
1:B:46:ILE:HG23	1:B:355:ALA:HB1	1.91	0.53
1:A:87:LEU:HD12	1:A:116:VAL:CG1	2.38	0.53
2:A:401:MPD:O4	2:A:401:MPD:H13	2.09	0.53
1:A:114:ALA:O	1:A:118:ARG:HD2	2.10	0.52
1:A:302:TRP:CH2	1:A:321:ASN:HB3	2.48	0.48
1:B:241:THR:HG23	1:B:292:TYR:CE2	2.48	0.48
1:A:353:ASN:HB2	1:A:354:PRO:HD3	1.96	0.48
1:A:343:GLN:OE1	2:A:401:MPD:H11	2.14	0.47
1:B:139:ARG:HA	1:B:179:PHE:CE1	2.51	0.46
1:B:170:VAL:O	1:B:200:THR:HA	2.16	0.46
1:A:344:GLU:CD	1:A:344:GLU:H	2.19	0.45
1:A:118:ARG:HH11	1:A:118:ARG:HG2	1.82	0.45
1:A:89:ARG:NH1	5:A:501:HOH:O	2.47	0.45
1:A:237:LEU:HD12	1:A:237:LEU:O	2.16	0.45
1:B:87:LEU:HD12	1:B:116:VAL:HG12	1.99	0.45
1:B:91:ARG:O	1:B:96:ARG:NH1	2.48	0.45
1:B:302:TRP:CH2	1:B:321:ASN:HB3	2.52	0.44
1:B:353:ASN:HB2	1:B:354:PRO:HD3	1.99	0.43
1:A:230:HIS:CE1	1:A:254:ARG:HD2	2.53	0.43
1:A:81:GLU:CD	1:A:85:ARG:HE	2.22	0.43
1:A:57:HIS:HB2	1:A:303:LEU:HB3	2.00	0.42
1:B:180:GLN:O	1:B:184:LEU:HD13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:HIS:O	1:B:303:LEU:HA	2.19	0.42
1:A:334:PRO:O	1:A:338:GLU:HG3	2.20	0.42
1:A:173:THR:O	1:A:174:GLY:C	2.58	0.42
1:A:293:MET:HB2	5:A:660:HOH:O	2.21	0.41
1:A:139:ARG:HA	1:A:179:PHE:CE1	2.56	0.40
1:A:57:HIS:O	1:A:303:LEU:HA	2.22	0.40
1:A:197:PRO:HB2	1:A:357:PHE:CZ	2.56	0.40

All (1) 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:B:344:GLU:OE1	5:A:580:HOH:O[1_556]	1.84	0.36

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	314/333 (94%)	302 (96%)	11 (4%)	1 (0%)	41	21
1	B	326/333 (98%)	317 (97%)	8 (2%)	1 (0%)	41	21
All	All	640/666 (96%)	619 (97%)	19 (3%)	2 (0%)	41	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	174	GLY
1	B	174	GLY

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	260/269 (97%)	254 (98%)	6 (2%)	50 24
1	B	266/269 (99%)	262 (98%)	4 (2%)	65 43
All	All	526/538 (98%)	516 (98%)	10 (2%)	57 32

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	PHE
1	A	118	ARG
1	A	152	ARG
1	A	175	LYS
1	A	299	SER
1	A	303	LEU
1	B	96	ARG
1	B	211	GLN
1	B	299	SER
1	B	303	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	HIS
1	A	230	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
2	MPD	A	401	-	7,7,7	0.29	0	9,10,10	0.18	0
2	MPD	A	402	-	7,7,7	0.29	0	9,10,10	0.63	0
2	MPD	B	401	-	7,7,7	0.27	0	9,10,10	0.40	0
2	MPD	B	403	-	7,7,7	0.29	0	9,10,10	0.36	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	MPD	A	401	-	-	0/5/5/5	-
2	MPD	A	402	-	-	1/5/5/5	-
2	MPD	B	401	-	-	2/5/5/5	-
2	MPD	B	403	-	-	0/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	402	MPD	O2-C2-C3-C4
2	B	401	MPD	C2-C3-C4-C5
2	B	401	MPD	C2-C3-C4-O4

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	MPD	2	0
2	A	402	MPD	1	0
2	B	401	MPD	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	316/333 (94%)	0.06	12 (3%) 40 37	16, 27, 57, 95	0
1	B	328/333 (98%)	0.12	9 (2%) 54 51	20, 36, 59, 101	0
All	All	644/666 (96%)	0.09	21 (3%) 46 42	16, 32, 59, 101	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	365	SER	8.8
1	B	362	LEU	6.1
1	B	206	GLN	5.9
1	A	35	ASP	5.7
1	A	362	LEU	5.1
1	B	35	ASP	5.1
1	A	259	ALA	4.6
1	A	363	ARG	4.5
1	A	235	ASP	3.8
1	A	208	GLY	3.6
1	A	275	ARG	3.4
1	A	364	ALA	3.3
1	B	205	SER	2.8
1	A	206	GLN	2.8
1	B	89	ARG	2.7
1	B	262	LEU	2.7
1	B	204	GLY	2.5
1	B	175	LYS	2.5
1	A	205	SER	2.1
1	A	258	SER	2.0
1	B	156	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

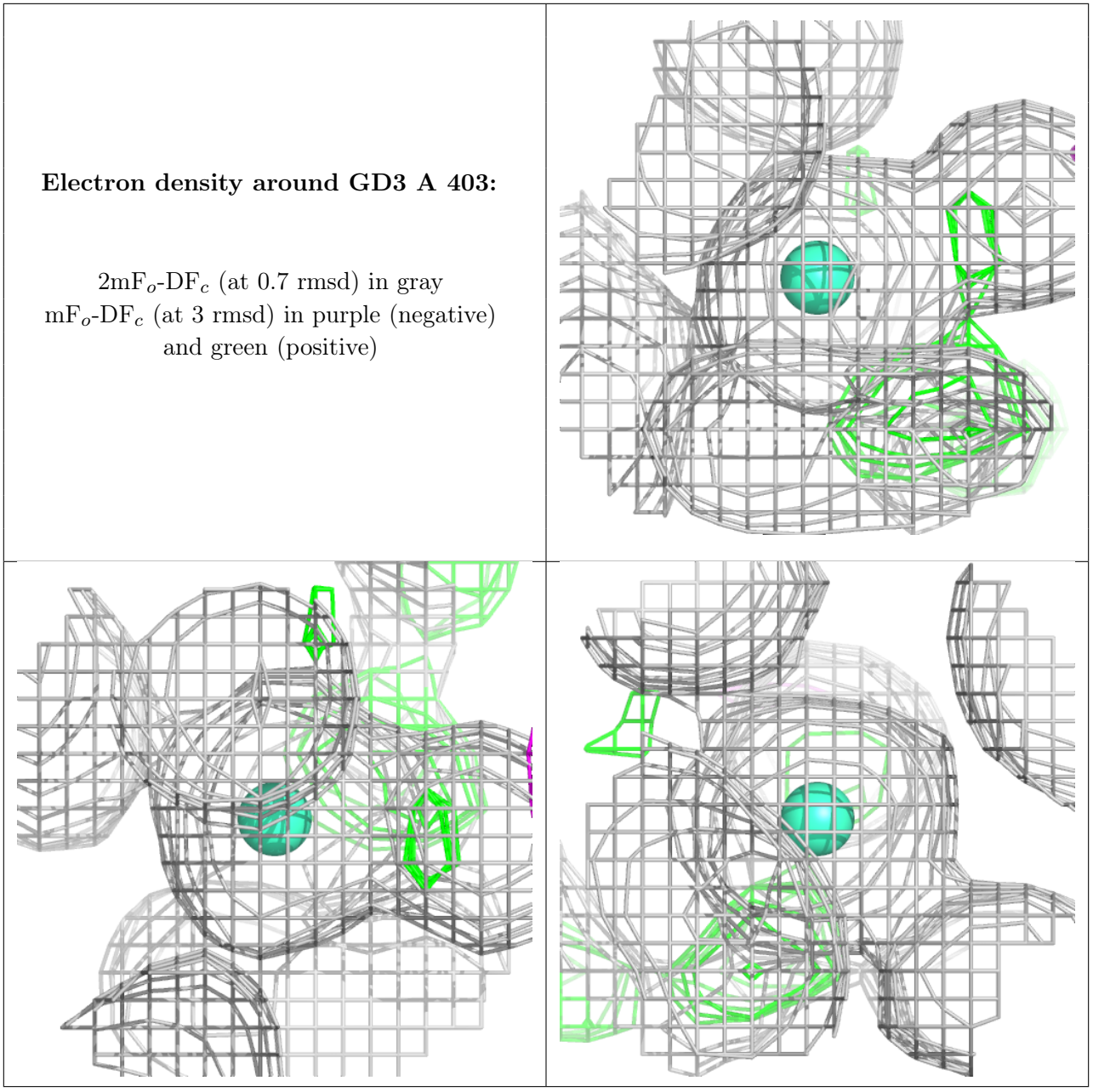
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
2	MPD	A	402	8/8	0.80	0.23	40,55,67,72	0
2	MPD	B	401	8/8	0.81	0.25	66,85,101,123	0
2	MPD	B	403	8/8	0.81	0.33	46,60,68,72	0
2	MPD	A	401	8/8	0.84	0.24	51,64,74,89	0
4	CL	B	402	1/1	0.95	0.09	34,34,34,34	1
4	CL	A	404	1/1	0.98	0.09	31,31,31,31	1
3	GD3	A	403	1/1	0.99	0.07	26,26,26,26	1

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

Electron density around GD3 A 403:

$2mF_o$-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.