



wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 03:59 am BST

PDB ID : 5OPQ
Title : A 3,6-anhydro-D-galactosidase produced by *Zobellia galactanivorans*. This is an exo-lytic enzyme that hydrolyzes terminal 3,6-anhydro-D-galactose from the non-reducing end of carrageenan oligosaccharides.
Authors : Ficko-Blean, E.; Michel, G.; Czjzek, M.
Deposited on : 2017-08-10
Resolution : 1.70 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 ⓘ symbol.

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 : 2.11
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) : 2.11

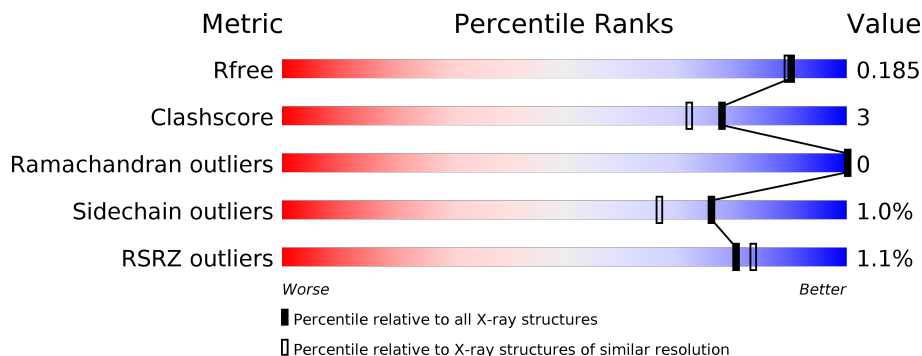
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 on 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	693	 2% 86% 9% 5%
1	B	693	 2% 85% 9% 5%
1	C	693	 86% 8% 5%
1	D	693	 2% 88% 7% 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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MPD	A	702	-	X	X	-
2	MPD	B	701	-	X	X	-
2	MPD	D	701	-	X	X	-
3	TRS	A	703[A]	-	X	-	-
3	TRS	A	703[B]	-	X	-	-
3	TRS	B	702[A]	-	X	-	-
3	TRS	C	702[A]	-	X	-	-
3	TRS	C	703	-	X	-	-
3	TRS	D	702[A]	-	X	-	-

2 Entry composition [i](#)

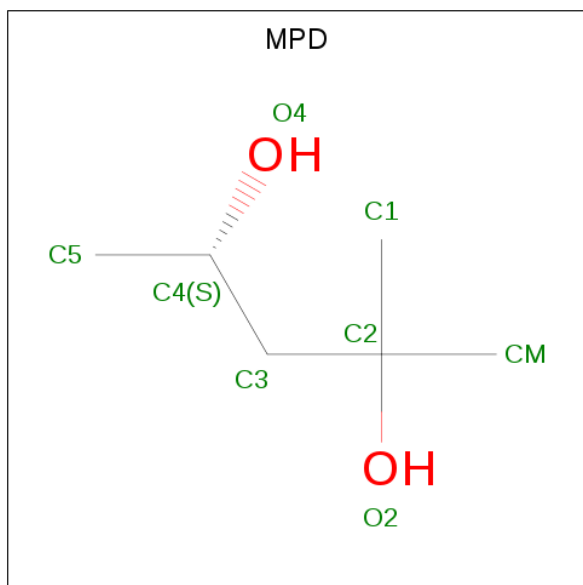
There are 5 unique types of molecules in this entry. The entry contains 23909 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 3,6-anhydro-D-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	659	Total 5244	C 3345	N 884	O 991	S 24	0	6	0
1	B	659	Total 5256	C 3356	N 892	O 984	S 24	0	4	0
1	C	659	Total 5224	C 3333	N 883	O 984	S 24	0	3	0
1	D	658	Total 5228	C 3337	N 884	O 983	S 24	0	3	0

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C₆H₁₄O₂).



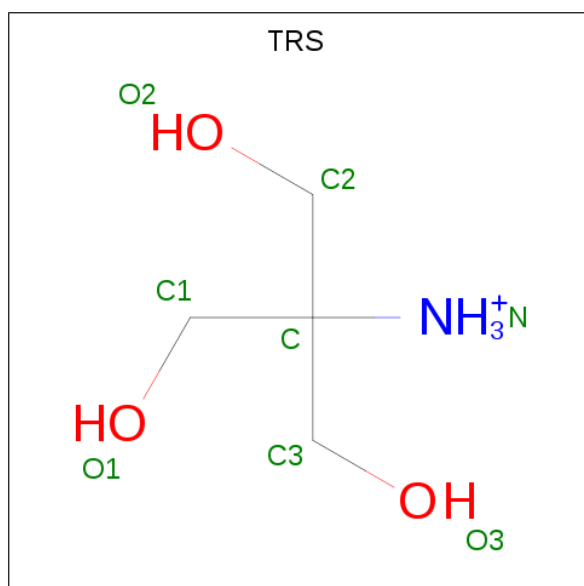
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total 8	C 6	O 2	0	0
2	A	1	Total 8	C 6	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	1
			16	8	2	6		
3	B	1	Total	C	N	O	0	1
			16	8	2	6		
3	C	1	Total	C	N	O	0	1
			16	8	2	6		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	D	1	Total	C	N	O	0	1
			16	8	2	6		

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

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

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

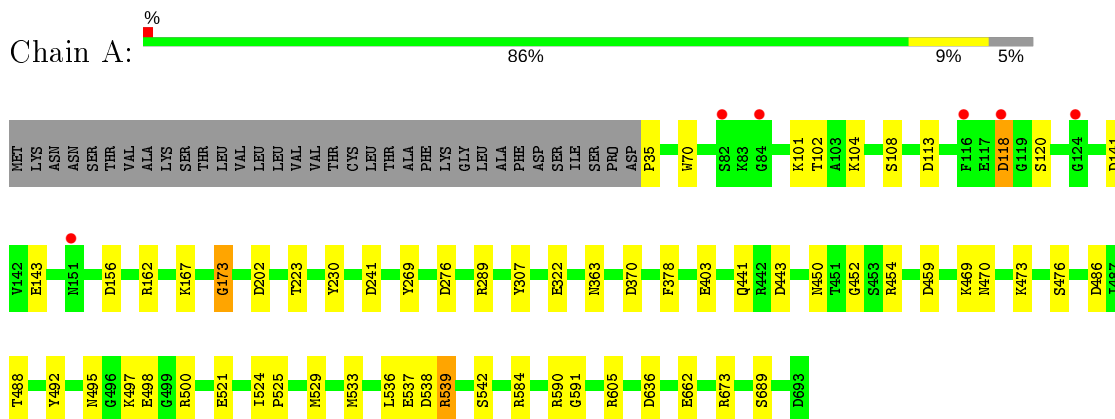
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	706	Total O 718 718	0	12
5	B	686	Total O 695 695	0	9
5	C	733	Total O 745 745	0	11
5	D	669	Total O 683 683	0	14

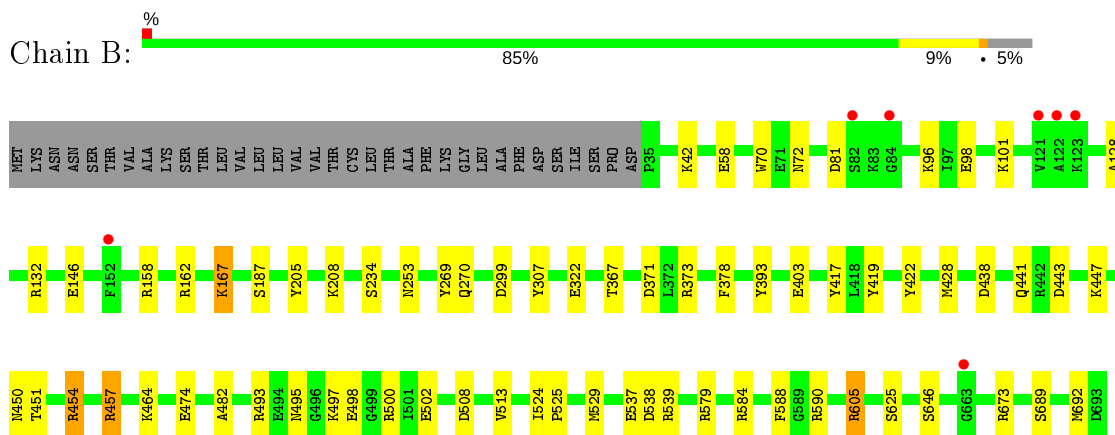
3 Residue-property plots i

These plots are drawn for all protein, RNA and DNA 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.

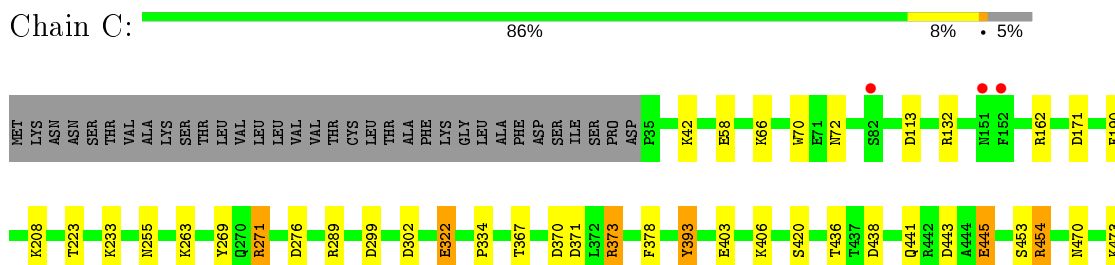
- Molecule 1: 3,6-anhydro-D-galactosidase



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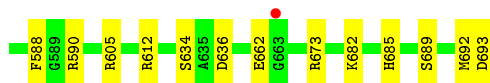
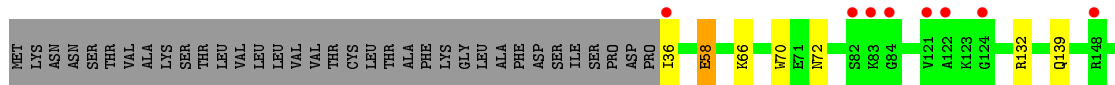
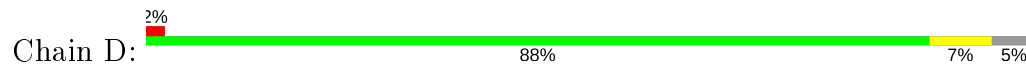


- Molecule 1: 3,6-anhydro-D-galactosidase





● Molecule 1: 3,6-anhydro-D-galactosidase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	222.00Å 107.50Å 165.80Å 90.00° 114.00° 90.00°	Depositor
Resolution (Å)	46.70 – 1.70 46.66 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.70-1.70) 99.6 (46.66-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 1.70Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.146 , 0.176 0.158 , 0.185	Depositor DCC
R_{free} test set	19548 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	18.9	Xtrriage
Anisotropy	0.048	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	23909	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, MPD, CL

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	1.22	11/5381 (0.2%)	1.21	29/7285 (0.4%)
1	B	1.22	9/5393 (0.2%)	1.20	29/7292 (0.4%)
1	C	1.23	9/5361 (0.2%)	1.18	33/7258 (0.5%)
1	D	1.21	10/5361 (0.2%)	1.17	26/7254 (0.4%)
All	All	1.22	39/21496 (0.2%)	1.19	117/29089 (0.4%)

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	B	0	1

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	322	GLU	CD-OE2	12.32	1.39	1.25
1	D	322	GLU	CD-OE1	11.02	1.37	1.25
1	C	322	GLU	CD-OE1	10.04	1.36	1.25
1	B	403	GLU	CD-OE1	8.92	1.35	1.25
1	C	403	GLU	CD-OE1	8.25	1.34	1.25

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	289	ARG	NE-CZ-NH2	-19.88	110.36	120.30
1	A	289	ARG	NE-CZ-NH1	18.23	129.41	120.30
1	D	289	ARG	NE-CZ-NH2	-18.02	111.29	120.30
1	D	289	ARG	NE-CZ-NH1	13.57	127.08	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	457[A]	ARG	NE-CZ-NH1	-12.65	113.97	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	205	TYR	Mainchain

5.2 Too-close contacts [i](#)

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	5244	0	5064	28	0
1	B	5256	0	5129	34	0
1	C	5224	0	5055	29	0
1	D	5228	0	5070	20	0
2	A	16	0	27	7	0
2	B	8	0	12	7	0
2	C	8	0	14	0	0
2	D	8	0	12	8	0
3	A	16	0	23	0	0
3	B	16	0	24	3	0
3	C	24	0	36	2	0
3	D	16	0	24	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	718	0	0	13	1
5	B	695	0	0	9	0
5	C	745	0	0	17	1
5	D	683	0	0	6	0
All	All	23909	0	20490	121	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 3.

The worst 5 of 121 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:C:406:LYS:HE2	5:C:1079:HOH:O	1.37	1.24
2:B:701:MPD:H51	5:B:1334:HOH:O	1.49	1.13
2:D:701:MPD:H52	2:D:701:MPD:H12	1.21	1.10
1:C:498:GLU:OE1	5:C:801:HOH:O	1.71	1.09
1:C:233:LYS:HE2	5:C:1349:HOH:O	1.51	1.08

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)
5:A:1240:HOH:O	5:C:806:HOH:O[2_556]	2.02	0.18

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	663/693 (96%)	637 (96%)	26 (4%)	0	100	100
1	B	661/693 (95%)	637 (96%)	24 (4%)	0	100	100
1	C	660/693 (95%)	639 (97%)	21 (3%)	0	100	100
1	D	659/693 (95%)	631 (96%)	28 (4%)	0	100	100
All	All	2643/2772 (95%)	2544 (96%)	99 (4%)	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	558/592 (94%)	555 (100%)	3 (0%)	88	83
1	B	562/592 (95%)	557 (99%)	5 (1%)	78	70
1	C	556/592 (94%)	550 (99%)	6 (1%)	73	63
1	D	556/592 (94%)	547 (98%)	9 (2%)	62	48
All	All	2232/2368 (94%)	2209 (99%)	23 (1%)	76	67

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	378	PHE
1	C	454	ARG
1	D	529	MET
1	C	445	GLU
1	C	529	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	387	ASN
1	C	151	ASN
1	D	387	ASN
1	C	87	GLN
1	C	283	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 18 ligands modelled in this entry, 4 are monoatomic - leaving 14 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	701	-	7,7,7	0.93	0	9,10,10	0.90	0
3	TRS	D	702[A]	-	7,7,7	1.01	1 (14%)	9,9,9	1.83	3 (33%)
3	TRS	B	702[A]	-	7,7,7	1.11	0	9,9,9	2.69	5 (55%)
2	MPD	C	701	-	7,7,7	0.81	0	9,10,10	1.07	0
3	TRS	A	703[A]	-	7,7,7	0.71	0	9,9,9	2.36	4 (44%)
3	TRS	C	703	-	7,7,7	2.29	2 (28%)	9,9,9	5.28	7 (77%)
3	TRS	A	703[B]	-	7,7,7	2.41	3 (42%)	9,9,9	4.13	6 (66%)
2	MPD	D	701	-	7,7,7	2.22	5 (71%)	9,10,10	3.07	5 (55%)
2	MPD	B	701	-	7,7,7	2.51	2 (28%)	9,10,10	7.79	6 (66%)
3	TRS	C	702[A]	-	7,7,7	1.86	3 (42%)	9,9,9	2.45	5 (55%)
3	TRS	D	702[B]	-	7,7,7	0.85	0	9,9,9	1.52	2 (22%)
2	MPD	A	702	-	7,7,7	3.27	5 (71%)	9,10,10	3.80	7 (77%)
3	TRS	C	702[B]	-	7,7,7	0.88	0	9,9,9	3.08	4 (44%)
3	TRS	B	702[B]	-	7,7,7	0.96	0	9,9,9	1.60	3 (33%)

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	701	-	-	0/5/5/5	-
3	TRS	D	702[A]	-	-	6/9/9/9	-
3	TRS	B	702[A]	-	-	8/9/9/9	-
2	MPD	C	701	-	-	0/5/5/5	-
3	TRS	A	703[A]	-	-	6/9/9/9	-
3	TRS	C	703	-	-	4/9/9/9	-
3	TRS	A	703[B]	-	-	7/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MPD	D	701	-	-	3/5/5/5	-
2	MPD	B	701	-	-	3/5/5/5	-
3	TRS	C	702[A]	-	-	5/9/9/9	-
3	TRS	D	702[B]	-	-	0/9/9/9	-
2	MPD	A	702	-	-	2/5/5/5	-
3	TRS	C	702[B]	-	-	5/9/9/9	-
3	TRS	B	702[B]	-	-	3/9/9/9	-

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	702	MPD	C3-C2	-5.91	1.37	1.53
2	B	701	MPD	O2-C2	5.39	1.58	1.44
3	C	703	TRS	C3-C	4.86	1.68	1.53
3	A	703[B]	TRS	O2-C2	4.10	1.55	1.42
2	A	702	MPD	C5-C4	-3.64	1.35	1.51

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	MPD	CM-C2-C1	16.76	145.50	110.57
2	B	701	MPD	O2-C2-C1	-14.13	62.73	108.08
3	C	703	TRS	C2-C-C1	-8.92	83.14	110.81
3	C	703	TRS	C1-C-N	-8.44	82.78	107.98
3	A	703[B]	TRS	C3-C-C1	-8.29	85.12	110.81

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	702[A]	TRS	C1-C-C2-O2
3	D	702[A]	TRS	C3-C-C2-O2
3	D	702[A]	TRS	N-C-C2-O2
3	B	702[A]	TRS	C2-C-C1-O1
3	B	702[A]	TRS	C3-C-C1-O1

There are no ring outliers.

6 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	703	TRS	1	0
2	D	701	MPD	8	0
2	B	701	MPD	7	0
3	C	702[A]	TRS	1	0
2	A	702	MPD	7	0
3	B	702[B]	TRS	3	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 [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	659/693 (95%)	-0.36	6 (0%) 84 87	11, 17, 36, 60	0
1	B	659/693 (95%)	-0.44	7 (1%) 80 83	11, 18, 37, 57	0
1	C	659/693 (95%)	-0.41	3 (0%) 91 92	12, 18, 36, 56	0
1	D	658/693 (94%)	-0.37	12 (1%) 68 72	11, 19, 37, 57	0
All	All	2635/2772 (95%)	-0.40	28 (1%) 80 83	11, 18, 37, 60	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	82	SER	4.0
1	C	82	SER	3.4
1	B	82	SER	3.1
1	A	84	GLY	3.1
1	B	663	GLY	2.8

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 carbohydrates 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(\AA^2)	Q<0.9
3	TRS	C	703	8/8	0.77	0.19	21,28,30,40	0
2	MPD	D	701	8/8	0.81	0.21	21,25,31,32	0
2	MPD	A	702	8/8	0.81	0.19	14,24,31,31	0
2	MPD	B	701	8/8	0.83	0.19	14,21,30,34	0
3	TRS	C	702[A]	8/8	0.86	0.20	9,17,19,24	8
3	TRS	C	702[B]	8/8	0.86	0.20	16,22,23,28	8
3	TRS	D	702[B]	8/8	0.88	0.20	13,16,19,28	8
2	MPD	A	701	8/8	0.88	0.13	30,35,38,38	0
3	TRS	D	702[A]	8/8	0.88	0.20	15,25,27,30	8
3	TRS	B	702[A]	8/8	0.92	0.17	10,17,18,20	8
3	TRS	B	702[B]	8/8	0.92	0.17	13,24,31,35	8
2	MPD	C	701	8/8	0.93	0.11	29,35,39,40	0
3	TRS	A	703[B]	8/8	0.93	0.14	12,15,18,19	8
3	TRS	A	703[A]	8/8	0.93	0.14	19,21,23,25	8
4	CL	D	703	1/1	0.98	0.06	24,24,24,24	0
4	CL	B	703	1/1	0.99	0.07	23,23,23,23	0
4	CL	C	704	1/1	0.99	0.07	24,24,24,24	0
4	CL	A	704	1/1	0.99	0.05	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.