



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:01 PM UTC

PDB ID : 7QI3 / pdb_00007qi3
Title : Structure of Fusarium verticillioides NAT1 (FDB2) N-malonyltransferase
Authors : Lowe, E.D.; Kotomina, E.; Karagianni, E.; Boukouvala, S.
Deposited on : 2021-12-14
Resolution : 1.80 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
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

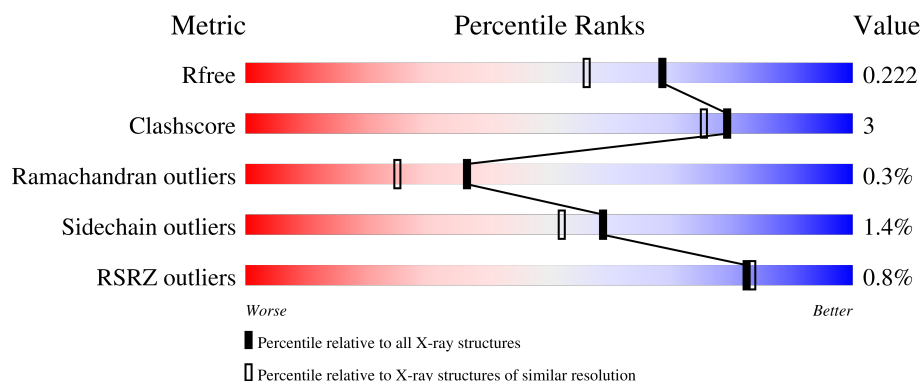
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	344	% 92% 6%
1	B	344	% 90% 8%
1	C	344	% 92% 7%
1	D	344	% 93% 6%

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
2	PEG	B	405	-	-	X	-

2 Entry composition [i](#)

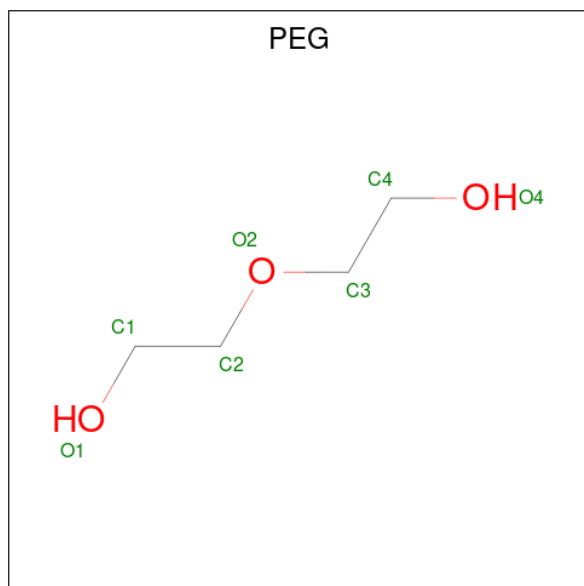
There are 6 unique types of molecules in this entry. The entry contains 12925 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Arylamine N-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	15	0
			2867	1810	492	548	17			
1	B	340	Total	C	N	O	S	0	13	0
			2847	1804	485	541	17			
1	C	340	Total	C	N	O	S	0	15	0
			2867	1816	488	546	17			
1	D	340	Total	C	N	O	S	0	13	0
			2847	1798	486	546	17			

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



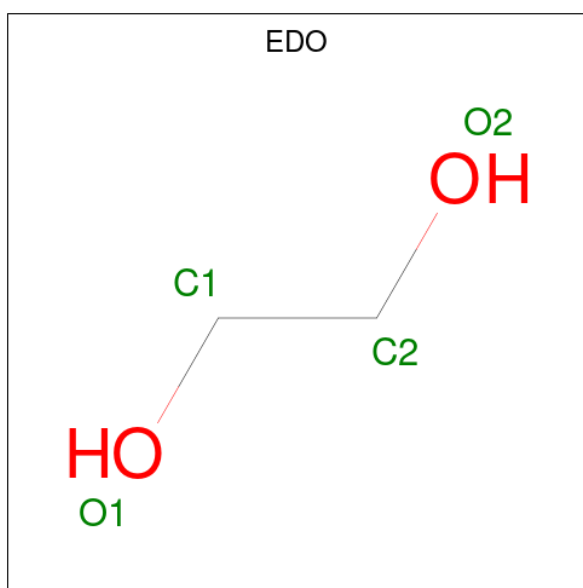
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			7	4	3		
2	A	1	Total	C	O	0	0
			7	4	3		

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

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		

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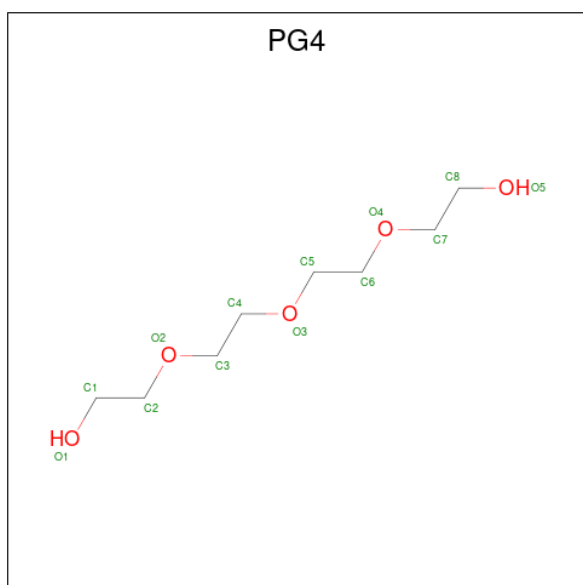
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



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

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



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	357	Total	O	0	2
			359	359		
6	B	341	Total	O	0	3
			344	344		
6	C	350	Total	O	0	1
			351	351		
6	D	342	Total	O	0	1
			343	343		

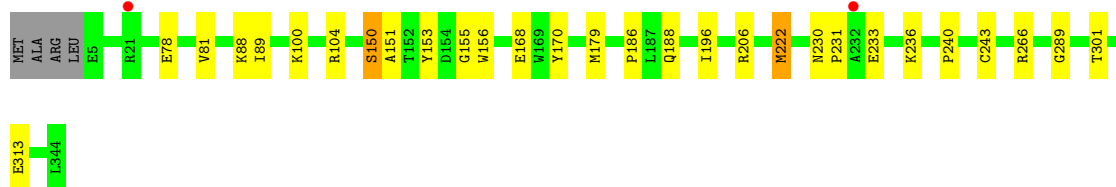
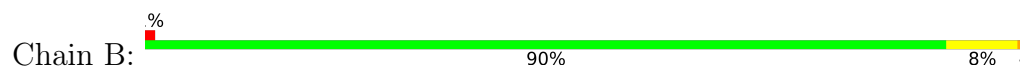
3 Residue-property plots [i](#)

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: Arylamine N-acetyltransferase



- Molecule 1: Arylamine N-acetyltransferase



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- Molecule 1: Arylamine N-acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	72.58Å 76.88Å 92.54Å 76.22° 73.06° 72.49°	Depositor
Resolution (Å)	87.32 – 1.80 87.31 – 1.80	Depositor EDS
% Data completeness (in resolution range)	95.1 (87.32-1.80) 95.1 (87.31-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.20rc4_4425	Depositor
R, R_{free}	0.178 , 0.222 0.179 , 0.222	Depositor DCC
R_{free} test set	7764 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12925	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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: PGE, PEG, PG4, EDO

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	0.28	0/2932	0.48	0/3971
1	B	0.28	0/2914	0.48	0/3949
1	C	0.30	0/2932	0.48	0/3971
1	D	0.28	0/2912	0.46	0/3944
All	All	0.28	0/11690	0.48	0/15835

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 [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	2867	0	2800	12	0
1	B	2847	0	2773	21	0
1	C	2867	0	2823	12	0
1	D	2847	0	2761	15	0
2	A	14	0	20	0	0
2	B	28	0	40	11	0
2	C	7	0	10	0	0
3	A	8	0	12	1	0
3	B	8	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	8	0	12	0	0
3	D	4	0	6	1	0
4	D	10	0	14	4	0
5	D	13	0	18	2	0
6	A	359	0	0	3	1
6	B	344	0	0	5	0
6	C	351	0	0	1	0
6	D	343	0	0	2	1
All	All	12925	0	11301	62	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.

All (62) 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:240:PRO:HG3	2:B:405:PEG:H22	1.73	0.71
2:B:405:PEG:O2	6:B:501:HOH:O	2.09	0.71
1:D:222[B]:MET:HG2	1:D:245:THR:HG22	1.73	0.71
1:D:251:PRO:HG3	4:D:401:PGE:H4	1.78	0.66
1:B:151:ALA:HA	2:B:405:PEG:H21	1.79	0.63
1:B:153:TYR:CZ	2:B:405:PEG:H11	2.36	0.61
1:D:115:ILE:HG23	4:D:401:PGE:H6	1.85	0.58
1:C:333[B]:GLU:HG2	1:C:334:GLU:N	2.21	0.56
1:D:29:ASP:OD1	6:D:502:HOH:O	2.18	0.56
1:A:186:PRO:HD3	3:A:402:EDO:H22	1.87	0.55
1:B:179:MET:HE1	2:B:401:PEG:H22	1.89	0.54
1:A:301:THR:HG22	1:A:306:ARG:HG3	1.89	0.53
1:B:104:ARG:HA	3:B:403:EDO:H11	1.91	0.53
1:B:266:ARG:NH1	6:B:508:HOH:O	2.36	0.51
1:B:206:ARG:HH21	2:B:405:PEG:C3	2.25	0.50
1:B:230[A]:ASN:ND2	1:B:233:GLU:HG3	2.27	0.50
1:A:38[B]:GLN:NE2	1:A:42:ASP:OD1	2.45	0.49
1:D:115:ILE:HG23	4:D:401:PGE:C6	2.43	0.48
1:A:218:HIS:ND1	6:A:505:HOH:O	2.35	0.48
1:C:13[B]:LEU:HD12	1:C:14:PRO:HD2	1.95	0.48
1:B:168:GLU:HG3	1:B:170:TYR:CE1	2.50	0.47
1:A:18:ALA:O	6:A:501:HOH:O	2.20	0.47
1:B:150:SER:HB3	2:B:404:PEG:H32	1.96	0.47
1:B:100[A]:LYS:NZ	6:B:503:HOH:O	2.28	0.46
1:A:81:VAL:O	1:A:88:LYS:HA	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:268:PHE:CE2	5:D:403:PG4:H61	2.50	0.46
1:D:81:VAL:O	1:D:88:LYS:HA	2.17	0.45
1:C:316:GLU:H	1:C:316:GLU:CD	2.23	0.45
1:D:251:PRO:HB3	4:D:401:PGE:O2	2.16	0.45
1:D:100[A]:LYS:HG3	1:D:106:ARG:HB2	1.98	0.45
1:D:266[A]:ARG:NH1	6:D:523:HOH:O	2.48	0.45
1:B:222[A]:MET:HB3	1:B:222[A]:MET:HE3	1.80	0.45
1:D:315:GLU:OE2	1:D:318:ARG:NH2	2.49	0.44
1:C:201:ILE:HG22	1:C:227:VAL:HG12	1.98	0.44
1:D:155:GLY:O	1:D:156:TRP:C	2.60	0.44
1:B:240:PRO:CG	2:B:405:PEG:H22	2.43	0.44
1:A:266:ARG:NH1	6:A:522:HOH:O	2.50	0.44
2:B:402:PEG:H22	2:B:402:PEG:H41	1.75	0.43
1:A:171:GLY:HA3	1:A:185:PHE:CZ	2.54	0.43
1:D:222[B]:MET:HE3	1:D:222[B]:MET:HB2	1.68	0.43
1:C:45:ASN:OD1	6:C:501:HOH:O	2.21	0.43
1:A:7:PRO:HD2	1:C:142:TYR:CZ	2.54	0.43
1:C:155:GLY:O	1:C:156:TRP:C	2.62	0.43
1:C:81:VAL:O	1:C:88[B]:LYS:HA	2.20	0.42
1:B:240:PRO:HG3	2:B:405:PEG:C2	2.47	0.42
1:B:206:ARG:HH21	2:B:405:PEG:C4	2.32	0.42
6:B:505:HOH:O	1:D:271:ARG:NH1	2.49	0.42
1:B:81:VAL:O	1:B:88:LYS:HA	2.20	0.42
1:C:171:GLY:HA3	1:C:185:PHE:CZ	2.55	0.42
1:C:86:PRO:HG3	1:C:333[B]:GLU:HG3	2.01	0.41
1:A:230[A]:ASN:ND2	1:A:233:GLU:HG3	2.36	0.41
1:B:231:PRO:HB3	1:B:236:LYS:HE2	2.02	0.41
1:B:186:PRO:HB2	1:B:188[B]:GLN:CG	2.51	0.41
1:C:81:VAL:O	1:C:88[A]:LYS:HA	2.20	0.41
1:A:155:GLY:O	1:A:156:TRP:C	2.63	0.41
1:B:155:GLY:O	1:B:156:TRP:C	2.63	0.41
1:B:222[A]:MET:HE2	1:B:243:CYS:SG	2.61	0.41
1:C:289:GLY:HA3	1:C:301:THR:O	2.20	0.41
1:D:268:PHE:HE2	5:D:403:PG4:H71	1.86	0.41
6:B:724:HOH:O	3:D:402:EDO:H21	2.20	0.41
1:A:21:ARG:NH1	1:A:22:TYR:O	2.55	0.40
1:B:289:GLY:HA3	1:B:301:THR:O	2.21	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)
6:A:710:HOH:O	6:D:759:HOH:O[1_564]	2.14	0.06

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	353/344 (103%)	346 (98%)	6 (2%)	1 (0%)	36	25
1	B	351/344 (102%)	342 (97%)	8 (2%)	1 (0%)	36	25
1	C	353/344 (103%)	344 (98%)	8 (2%)	1 (0%)	36	25
1	D	351/344 (102%)	343 (98%)	7 (2%)	1 (0%)	36	25
All	All	1408/1376 (102%)	1375 (98%)	29 (2%)	4 (0%)	36	25

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	ILE
1	B	196	ILE
1	C	196	ILE
1	D	196	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	321/312 (103%)	317 (99%)	4 (1%)	63	57
1	B	317/312 (102%)	311 (98%)	6 (2%)	50	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	323/312 (104%)	317 (98%)	6 (2%)	50	41
1	D	316/312 (101%)	313 (99%)	3 (1%)	70	67
All	All	1277/1248 (102%)	1258 (98%)	19 (2%)	59	49

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	GLU
1	A	301	THR
1	A	307	LYS
1	A	313	GLU
1	B	78	GLU
1	B	89	ILE
1	B	150	SER
1	B	222[A]	MET
1	B	222[B]	MET
1	B	313	GLU
1	C	78	GLU
1	C	205	LYS
1	C	230[A]	ASN
1	C	230[B]	ASN
1	C	307	LYS
1	C	313	GLU
1	D	36	PHE
1	D	78	GLU
1	D	313	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	ASN
1	A	336	ASN
1	C	148	ASN
1	D	28	GLN
1	D	113	ASN
1	D	182	ASN

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](#)

16 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	PEG	A	403	-	6,6,6	0.20	0	5,5,5	0.15	0
2	PEG	B	401	-	6,6,6	0.18	0	5,5,5	0.15	0
2	PEG	C	401	-	6,6,6	0.21	0	5,5,5	0.13	0
2	PEG	B	404	-	6,6,6	0.20	0	5,5,5	0.05	0
3	EDO	C	402	-	3,3,3	0.46	0	2,2,2	0.42	0
3	EDO	C	403	-	3,3,3	0.44	0	2,2,2	0.32	0
2	PEG	B	405	-	6,6,6	0.23	0	5,5,5	0.35	0
3	EDO	D	402	-	3,3,3	0.45	0	2,2,2	0.20	0
3	EDO	B	406	-	3,3,3	0.48	0	2,2,2	0.35	0
3	EDO	A	402	-	3,3,3	0.48	0	2,2,2	0.30	0
5	PG4	D	403	-	12,12,12	0.16	0	11,11,11	0.63	0
3	EDO	A	404	-	3,3,3	0.47	0	2,2,2	0.33	0
2	PEG	A	401	-	6,6,6	0.13	0	5,5,5	0.08	0
4	PGE	D	401	-	9,9,9	0.36	0	8,8,8	0.55	0
3	EDO	B	403	-	3,3,3	0.48	0	2,2,2	0.26	0
2	PEG	B	402	-	6,6,6	0.13	0	5,5,5	0.12	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	PEG	A	403	-	-	1/4/4/4	-
2	PEG	B	401	-	-	2/4/4/4	-
2	PEG	C	401	-	-	2/4/4/4	-
2	PEG	B	404	-	-	4/4/4/4	-
3	EDO	C	402	-	-	1/1/1/1	-
3	EDO	C	403	-	-	0/1/1/1	-
2	PEG	B	405	-	-	2/4/4/4	-
3	EDO	D	402	-	-	0/1/1/1	-
3	EDO	B	406	-	-	0/1/1/1	-
3	EDO	A	402	-	-	0/1/1/1	-
5	PG4	D	403	-	-	6/10/10/10	-
3	EDO	A	404	-	-	1/1/1/1	-
2	PEG	A	401	-	-	4/4/4/4	-
4	PGE	D	401	-	-	3/7/7/7	-
3	EDO	B	403	-	-	1/1/1/1	-
2	PEG	B	402	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	403	PEG	C1-C2-O2-C3
2	B	404	PEG	O2-C3-C4-O4
5	D	403	PG4	O2-C3-C4-O3
2	A	401	PEG	O1-C1-C2-O2
2	B	402	PEG	O1-C1-C2-O2
2	B	402	PEG	O2-C3-C4-O4
2	B	405	PEG	O2-C3-C4-O4
2	C	401	PEG	O1-C1-C2-O2
2	A	401	PEG	O2-C3-C4-O4
2	B	401	PEG	O1-C1-C2-O2
5	D	403	PG4	O4-C7-C8-O5
2	B	402	PEG	C4-C3-O2-C2
4	D	401	PGE	O2-C3-C4-O3
2	B	404	PEG	C1-C2-O2-C3
2	A	401	PEG	C1-C2-O2-C3
5	D	403	PG4	C4-C3-O2-C2
2	B	405	PEG	C1-C2-O2-C3

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Mol	Chain	Res	Type	Atoms
2	B	404	PEG	O1-C1-C2-O2
4	D	401	PGE	C1-C2-O2-C3
2	B	401	PEG	C1-C2-O2-C3
2	C	401	PEG	C1-C2-O2-C3
4	D	401	PGE	O3-C5-C6-O4
5	D	403	PG4	C8-C7-O4-C6
3	B	403	EDO	O1-C1-C2-O2
3	C	402	EDO	O1-C1-C2-O2
5	D	403	PG4	C3-C4-O3-C5
3	A	404	EDO	O1-C1-C2-O2
2	A	401	PEG	C4-C3-O2-C2
2	B	404	PEG	C4-C3-O2-C2
5	D	403	PG4	O3-C5-C6-O4

There are no ring outliers.

9 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	PEG	1	0
2	B	404	PEG	1	0
2	B	405	PEG	8	0
3	D	402	EDO	1	0
3	A	402	EDO	1	0
5	D	403	PG4	2	0
4	D	401	PGE	4	0
3	B	403	EDO	1	0
2	B	402	PEG	1	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	340/344 (98%)	-0.03	2 (0%) 85 86	11, 27, 47, 65	15 (4%)
1	B	340/344 (98%)	0.05	2 (0%) 85 86	10, 30, 51, 82	13 (3%)
1	C	340/344 (98%)	-0.04	3 (0%) 81 81	10, 26, 48, 65	15 (4%)
1	D	340/344 (98%)	0.01	4 (1%) 76 77	12, 28, 51, 65	13 (3%)
All	All	1360/1376 (98%)	-0.00	11 (0%) 82 83	10, 28, 49, 82	56 (4%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	310[A]	LYS	3.1
1	D	294	PHE	2.8
1	C	89[A]	ILE	2.8
1	A	232	ALA	2.5
1	B	232	ALA	2.5
1	D	344	LEU	2.2
1	D	266[A]	ARG	2.2
1	C	232	ALA	2.1
1	C	234	SER	2.1
1	B	21	ARG	2.0
1	A	294	PHE	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	EDO	B	406	4/4	0.72	0.20	56,57,66,69	0
3	EDO	A	402	4/4	0.76	0.13	47,48,55,57	0
2	PEG	A	403	7/7	0.79	0.15	44,48,57,62	0
3	EDO	B	403	4/4	0.80	0.15	39,41,47,50	4
3	EDO	C	402	4/4	0.80	0.18	52,55,56,62	0
2	PEG	A	401	7/7	0.81	0.14	38,48,56,58	0
2	PEG	B	404	7/7	0.81	0.17	45,47,57,61	0
3	EDO	C	403	4/4	0.81	0.14	61,62,63,63	0
5	PG4	D	403	13/13	0.81	0.18	37,45,51,57	13
2	PEG	B	402	7/7	0.82	0.13	32,36,44,44	7
3	EDO	A	404	4/4	0.83	0.18	54,59,60,64	0
2	PEG	B	405	7/7	0.84	0.18	19,29,38,39	7
2	PEG	C	401	7/7	0.85	0.13	41,46,52,52	0
3	EDO	D	402	4/4	0.86	0.14	21,34,43,48	0
2	PEG	B	401	7/7	0.86	0.14	34,40,42,49	7
4	PGE	D	401	10/10	0.89	0.13	18,24,28,30	10

6.5 Other polymers ⓘ

There are no such residues in this entry.