



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:10 PM UTC

PDB ID : 4J0C / pdb_00004j0c
Title : tannin acyl hydrolase from *Lactobacillus plantarum* (native structure)
Authors : Wu, M.; Wang, Q.; Peng, X.; Wen, H.; Chen, Q.; McKinstry, W.J.
Deposited on : 2013-01-30
Resolution : 1.65 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

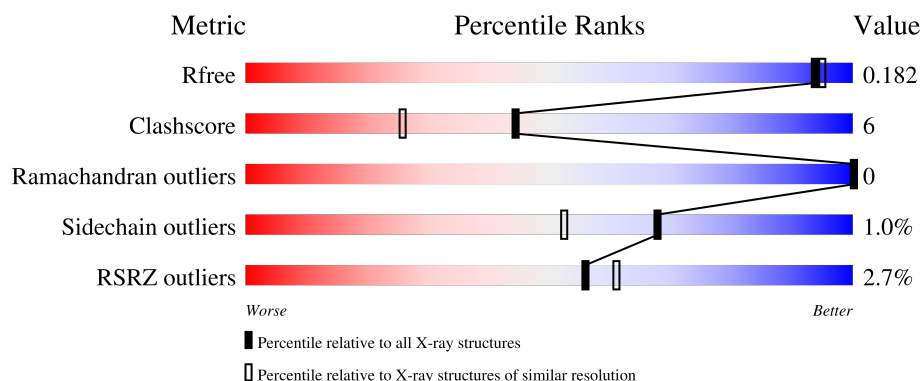
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	491	4% 81% 11% 8%
1	B	491	% 87% 7% 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
2	PEG	A	501	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7737 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 Tannase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	5	0
			3479	2203	604	662	10			
1	B	458	Total	C	N	O	S	0	5	0
			3528	2235	611	673	9			

There are 44 discrepancies between the modelled and reference sequences:

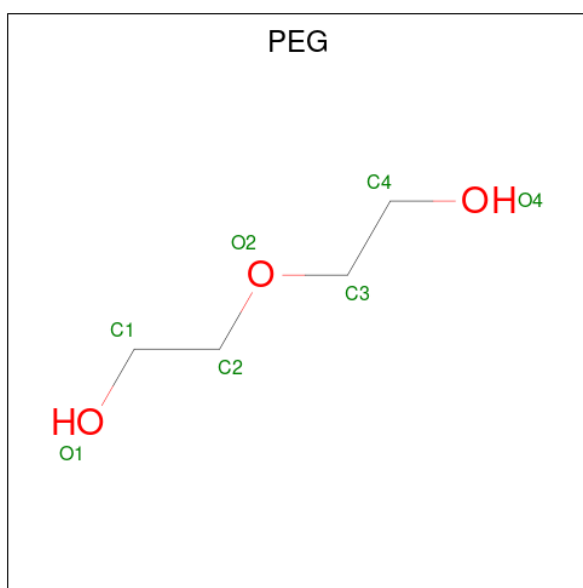
Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	expression tag	UNP B3Y018
A	-20	HIS	-	expression tag	UNP B3Y018
A	-19	HIS	-	expression tag	UNP B3Y018
A	-18	HIS	-	expression tag	UNP B3Y018
A	-17	HIS	-	expression tag	UNP B3Y018
A	-16	HIS	-	expression tag	UNP B3Y018
A	-15	HIS	-	expression tag	UNP B3Y018
A	-14	SER	-	expression tag	UNP B3Y018
A	-13	SER	-	expression tag	UNP B3Y018
A	-12	GLY	-	expression tag	UNP B3Y018
A	-11	VAL	-	expression tag	UNP B3Y018
A	-10	ASP	-	expression tag	UNP B3Y018
A	-9	LEU	-	expression tag	UNP B3Y018
A	-8	GLY	-	expression tag	UNP B3Y018
A	-7	THR	-	expression tag	UNP B3Y018
A	-6	GLU	-	expression tag	UNP B3Y018
A	-5	ASN	-	expression tag	UNP B3Y018
A	-4	LEU	-	expression tag	UNP B3Y018
A	-3	TYR	-	expression tag	UNP B3Y018
A	-2	PHE	-	expression tag	UNP B3Y018
A	-1	GLN	-	expression tag	UNP B3Y018
A	0	SER	-	expression tag	UNP B3Y018
B	-21	MET	-	expression tag	UNP B3Y018
B	-20	HIS	-	expression tag	UNP B3Y018
B	-19	HIS	-	expression tag	UNP B3Y018

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	HIS	-	expression tag	UNP B3Y018
B	-17	HIS	-	expression tag	UNP B3Y018
B	-16	HIS	-	expression tag	UNP B3Y018
B	-15	HIS	-	expression tag	UNP B3Y018
B	-14	SER	-	expression tag	UNP B3Y018
B	-13	SER	-	expression tag	UNP B3Y018
B	-12	GLY	-	expression tag	UNP B3Y018
B	-11	VAL	-	expression tag	UNP B3Y018
B	-10	ASP	-	expression tag	UNP B3Y018
B	-9	LEU	-	expression tag	UNP B3Y018
B	-8	GLY	-	expression tag	UNP B3Y018
B	-7	THR	-	expression tag	UNP B3Y018
B	-6	GLU	-	expression tag	UNP B3Y018
B	-5	ASN	-	expression tag	UNP B3Y018
B	-4	LEU	-	expression tag	UNP B3Y018
B	-3	TYR	-	expression tag	UNP B3Y018
B	-2	PHE	-	expression tag	UNP B3Y018
B	-1	GLN	-	expression tag	UNP B3Y018
B	0	SER	-	expression tag	UNP B3Y018

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



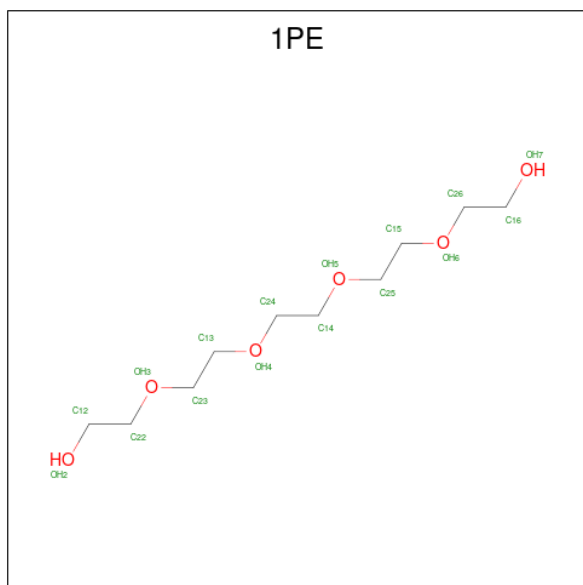
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			7	4	3		
2	A	1	Total	C	O	0	0
			7	4	3		

Continued on next page...

Continued from previous page...

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		

- Molecule 3 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			16	10	6		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	300	Total	O	0	0
			300	300		
4	B	379	Total	O	0	0
			379	379		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.46Å 62.79Å 83.80Å 70.39° 86.01° 79.41°	Depositor
Resolution (Å)	19.68 – 1.65 19.68 – 1.65	Depositor EDS
% Data completeness (in resolution range)	95.7 (19.68-1.65) 95.7 (19.68-1.65)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 1.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7 _650)	Depositor
R, R_{free}	0.165 , 0.192 (Not available) , 0.182	Depositor DCC
R_{free} test set	5039 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	14.6	Xtriage
Anisotropy	0.854	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.009 for -h,-k,-k+1	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7737	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1PE, 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	0.50	0/3566	0.75	0/4863
1	B	0.55	0/3618	0.75	0/4938
All	All	0.53	0/7184	0.75	0/9801

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	3479	0	3409	57	0
1	B	3528	0	3452	25	0
2	A	14	0	20	15	0
2	B	21	0	30	2	0
3	B	16	0	22	0	0
4	A	300	0	0	10	0
4	B	379	0	0	8	1
All	All	7737	0	6933	84	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 6.

All (84) 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:326:GLN:HE21	1:B:328:THR:HG22	1.08	1.05
1:B:14:PRO:HB2	2:B:503:PEG:H32	1.47	0.96
1:B:342:MET:HE1	1:B:421[B]:ASP:OD1	1.64	0.95
1:B:326:GLN:NE2	1:B:328:THR:HG22	1.81	0.94
1:A:414:ARG:HH21	2:A:501:PEG:H32	1.33	0.90
1:B:374:LEU:HG	4:B:926:HOH:O	1.74	0.86
1:A:404:SER:OG	1:A:406:GLN:OE1	1.93	0.85
1:A:412:ARG:HE	2:A:501:PEG:H11	1.41	0.84
1:A:176:GLY:O	1:A:406:GLN:HG3	1.81	0.80
1:B:271:GLN:HG3	4:B:700:HOH:O	1.82	0.80
1:A:269[B]:LEU:HD21	1:A:292:PHE:CG	2.19	0.78
1:B:267:THR:O	1:B:271:GLN:HG2	1.83	0.78
1:A:412:ARG:HH21	2:A:501:PEG:H11	1.49	0.76
1:B:244:GLU:N	4:B:929:HOH:O	2.20	0.74
1:A:278:ASP:OD1	1:A:280:THR:HG23	1.89	0.73
1:A:412:ARG:NE	2:A:501:PEG:H11	2.08	0.68
2:A:501:PEG:H41	4:A:636:HOH:O	1.94	0.68
1:B:326:GLN:HE21	1:B:328:THR:CG2	1.96	0.68
1:A:412:ARG:HE	2:A:501:PEG:C1	2.06	0.68
1:A:336:LEU:HD12	2:A:502:PEG:H41	1.79	0.65
1:A:412:ARG:NH2	2:A:501:PEG:H11	2.12	0.64
1:A:414:ARG:HH21	2:A:501:PEG:C3	2.09	0.63
1:B:342:MET:HE1	1:B:421[B]:ASP:CG	2.24	0.63
1:A:217:GLU:OE2	1:A:341:ARG:NH2	2.32	0.61
1:A:414:ARG:NH2	2:A:501:PEG:H32	2.12	0.59
2:A:501:PEG:H12	4:A:779:HOH:O	2.02	0.59
1:A:406:GLN:NE2	4:A:856:HOH:O	2.37	0.57
1:A:158:ILE:HG12	1:A:199:ALA:HB3	1.88	0.55
1:A:64:ARG:NH1	4:A:898:HOH:O	2.40	0.55
1:A:278:ASP:CG	1:A:280:THR:HG23	2.32	0.54
1:A:217:GLU:CD	1:A:341:ARG:HH22	2.15	0.54
1:A:294:ASP:OD2	1:A:298:GLN:NE2	2.41	0.53
1:A:64:ARG:HH11	1:A:64:ARG:HG2	1.74	0.52
1:B:149:ARG:NH1	4:B:764:HOH:O	2.43	0.52
1:A:20:ALA:N	4:A:860:HOH:O	2.42	0.52
1:A:269[B]:LEU:HD21	1:A:292:PHE:CD2	2.45	0.52
1:A:269[B]:LEU:HD23	1:A:284:LEU:HG	1.91	0.52
1:A:403:THR:HG23	1:A:403:THR:O	2.11	0.51
1:B:254:GLU:OE2	1:B:344:ALA:HB1	2.09	0.51
1:A:85:ASP:HB3	1:A:88:ARG:HB2	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:ARG:CZ	2:A:501:PEG:H11	2.41	0.50
1:B:85:ASP:HB3	1:B:88:ARG:HB2	1.92	0.50
1:B:25:GLN:OE1	2:B:503:PEG:H42	2.12	0.49
1:B:326:GLN:NE2	1:B:328:THR:CG2	2.66	0.49
1:A:400:LEU:C	1:A:402:THR:H	2.20	0.49
1:A:442:ASP:OD2	2:A:501:PEG:O1	2.30	0.49
1:B:342:MET:CE	4:B:915:HOH:O	2.60	0.48
1:A:180:TYR:CE1	1:A:389:GLU:HG2	2.49	0.47
1:A:336:LEU:CD1	2:A:502:PEG:H41	2.43	0.47
1:A:350[A]:GLN:OE1	1:A:354:THR:OG1	2.26	0.47
1:A:406:GLN:CD	4:A:861:HOH:O	2.59	0.46
1:B:244:GLU:HB2	4:B:699:HOH:O	2.15	0.46
1:A:400:LEU:C	1:A:402:THR:N	2.74	0.45
1:A:12:LEU:HB3	1:A:27:TYR:HB3	1.98	0.45
1:A:269[B]:LEU:HD23	1:A:284:LEU:CD1	2.46	0.45
1:A:294:ASP:O	1:A:298:GLN:HG3	2.16	0.45
1:B:415:HIS:O	1:B:445:LEU:HA	2.18	0.44
1:A:19:VAL:HB	1:A:24:ILE:CG1	2.47	0.44
1:B:230:GLN:HB2	1:B:231:PRO:HD2	1.99	0.44
1:A:94:ASN:OD1	4:A:794:HOH:O	2.21	0.44
1:A:339:LEU:HD11	1:A:418:ALA:HA	2.00	0.43
1:A:402:THR:HA	1:A:437:HIS:CD2	2.53	0.43
1:A:406:GLN:NE2	4:A:861:HOH:O	2.50	0.43
1:A:330:LEU:HD11	1:A:335:TYR:HB2	2.00	0.43
1:B:1:MET:HE3	4:B:751:HOH:O	2.19	0.42
1:A:27:TYR:CG	1:A:54[B]:LEU:HD12	2.55	0.42
1:A:268:TYR:O	1:A:271:GLN:HG2	2.19	0.42
1:A:1:MET:HE2	1:A:1:MET:HB3	1.81	0.42
1:A:415:HIS:O	1:A:445:LEU:HA	2.20	0.42
1:A:120:ASP:HB2	4:A:832:HOH:O	2.19	0.41
1:B:94:ASN:HB2	4:B:883:HOH:O	2.19	0.41
1:B:115:GLY:O	1:B:127:GLY:HA3	2.20	0.41
1:B:294:ASP:O	1:B:298:GLN:HG2	2.20	0.41
1:A:341:ARG:NH2	1:A:345:VAL:HG22	2.36	0.41
1:A:218:TRP:HA	1:A:262:LYS:HG3	2.02	0.41
1:B:226:TRP:CZ2	1:B:248:GLY:HA3	2.56	0.41
1:A:19:VAL:CG2	1:A:24:ILE:HG13	2.51	0.41
1:B:257:LEU:HD11	1:B:378:ARG:HD3	2.03	0.40
1:A:269[B]:LEU:CD2	1:A:292:PHE:CD2	3.05	0.40
1:A:412:ARG:HH21	2:A:501:PEG:C1	2.29	0.40
1:A:121:LYS:H	1:A:121:LYS:HG3	1.59	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:ARG:C	4:A:899:HOH:O	2.65	0.40
1:A:433:MET:HE3	1:A:433:MET:HB2	1.87	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)
4:B:840:HOH:O	4:B:857:HOH:O[1_565]	2.13	0.07

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	453/491 (92%)	443 (98%)	10 (2%)	0	100	100
1	B	459/491 (94%)	450 (98%)	9 (2%)	0	100	100
All	All	912/982 (93%)	893 (98%)	19 (2%)	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	360/389 (92%)	356 (99%)	4 (1%)	65	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	366/389 (94%)	363 (99%)	3 (1%)	73	60
All	All	726/778 (93%)	719 (99%)	7 (1%)	68	52

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	LYS
1	A	332	LEU
1	A	402	THR
1	A	420	ARG
1	B	17	VAL
1	B	121	LYS
1	B	420	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	94	ASN
1	B	100	GLN
1	B	221	ASN
1	B	326	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	B	502	-	6,6,6	0.73	0	5,5,5	1.09	0
2	PEG	B	503	-	6,6,6	0.57	0	5,5,5	1.60	1 (20%)
3	1PE	B	501	-	15,15,15	0.71	0	14,14,14	1.23	0
2	PEG	A	502	-	6,6,6	0.67	0	5,5,5	1.36	0
2	PEG	A	501	-	6,6,6	0.73	0	5,5,5	1.34	0
2	PEG	B	504	-	6,6,6	0.53	0	5,5,5	1.18	1 (20%)

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	B	502	-	-	1/4/4/4	-
2	PEG	B	503	-	-	2/4/4/4	-
3	1PE	B	501	-	-	2/13/13/13	-
2	PEG	A	502	-	-	3/4/4/4	-
2	PEG	A	501	-	-	3/4/4/4	-
2	PEG	B	504	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	503	PEG	O2-C3-C4	2.41	120.74	110.11
2	B	504	PEG	C3-O2-C2	2.23	123.03	113.26

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	503	PEG	C1-C2-O2-C3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	B	502	PEG	O1-C1-C2-O2
2	B	503	PEG	O1-C1-C2-O2
2	A	501	PEG	O1-C1-C2-O2
3	B	501	1PE	OH5-C14-C24-OH4
2	A	502	PEG	C4-C3-O2-C2
2	A	502	PEG	O2-C3-C4-O4
2	A	501	PEG	C1-C2-O2-C3
2	A	502	PEG	C1-C2-O2-C3
3	B	501	1PE	OH4-C13-C23-OH3
2	B	504	PEG	C4-C3-O2-C2
2	A	501	PEG	O2-C3-C4-O4
2	B	504	PEG	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	503	PEG	2	0
2	A	502	PEG	2	0
2	A	501	PEG	13	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, 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	452/491 (92%)	-0.26	20 (4%) 39 42	8, 18, 40, 84	5 (1%)
1	B	458/491 (93%)	-0.41	5 (1%) 78 83	7, 15, 33, 53	5 (1%)
All	All	910/982 (92%)	-0.33	25 (2%) 56 61	7, 17, 37, 84	10 (1%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	402	THR	4.2
1	A	403	THR	3.4
1	A	401	THR	3.4
1	A	404	SER	3.2
1	A	91	TRP	2.7
1	A	19	VAL	2.7
1	A	226	TRP	2.7
1	A	405	SER	2.7
1	A	247	SER	2.6
1	B	229	TYR	2.6
1	B	91	TRP	2.6
1	A	122	SER	2.6
1	A	20	ALA	2.6
1	A	18	GLN	2.5
1	A	400	LEU	2.5
1	A	89	VAL	2.3
1	B	231	PRO	2.3
1	A	21	GLY	2.3
1	A	271	GLN	2.2
1	B	402	THR	2.1
1	A	406	GLN	2.1
1	A	252	VAL	2.1
1	B	55	HIS	2.1
1	A	248	GLY	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	365	THR	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 [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(Å ²)	Q<0.9
2	PEG	A	501	7/7	0.76	0.15	29,31,44,47	0
2	PEG	B	503	7/7	0.77	0.16	44,45,46,48	0
2	PEG	B	504	7/7	0.84	0.10	24,25,28,28	0
2	PEG	B	502	7/7	0.90	0.10	32,33,35,37	0
3	1PE	B	501	16/16	0.91	0.09	17,26,30,31	0
2	PEG	A	502	7/7	0.92	0.10	34,37,41,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.