



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 23, 2022 – 12:12 pm GMT

PDB ID : 7Q6Y
Title : The X-ray crystal structure of CbTan2, a tannase enzyme from *Clostridium butyricum*
Authors : Coleman, T.; Mazurkewich, S.; Larsbrink, J.
Deposited on : 2021-11-09
Resolution : 2.22 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.26
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

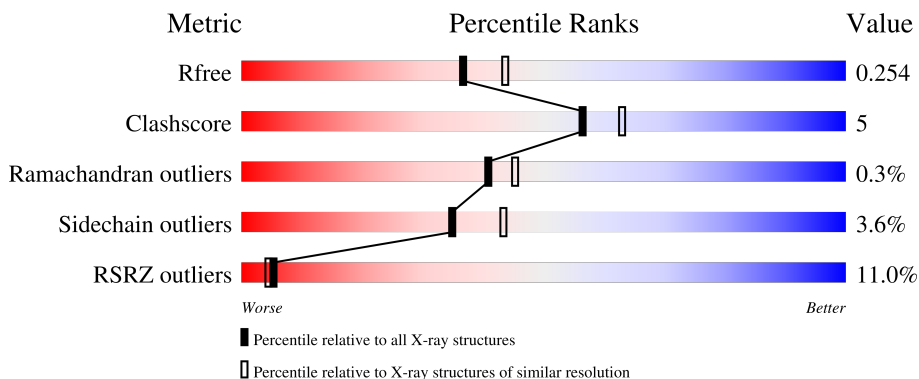
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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	490	 7% 82% 13%
1	B	490	 14% 78% 16% 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
3	EDO	B	502	-	-	-	X

2 Entry composition [i](#)

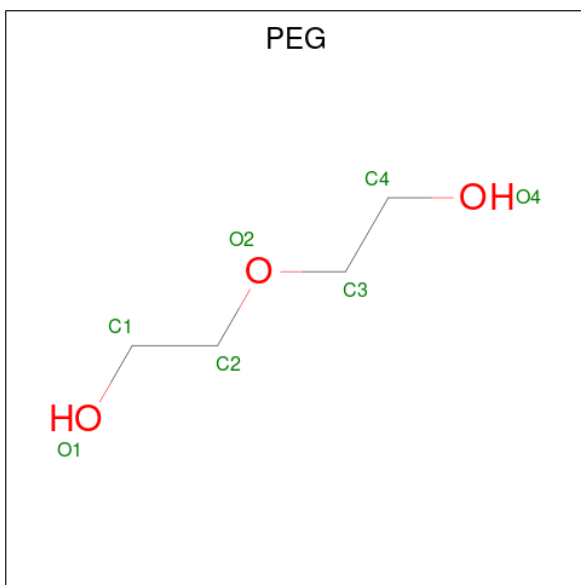
There are 4 unique types of molecules in this entry. The entry contains 7678 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alpha/beta hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	470	Total 3730	C 2372	N 620	O 721	S 17	0	2	0
1	B	459	Total 3641	C 2316	N 606	O 703	S 16	0	1	0

- Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



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

Continued on next page...

Continued from previous page...

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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

Continued on next page...

Continued from previous page...

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

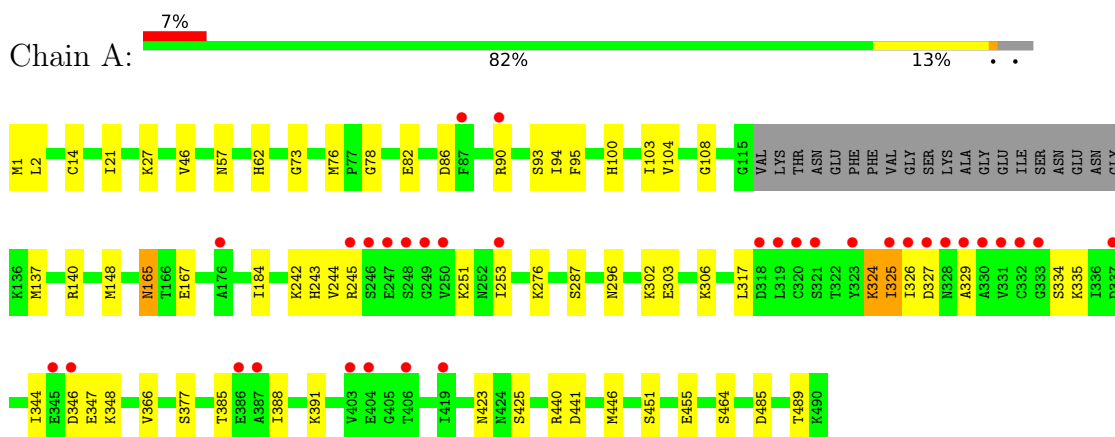
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	156	Total	O	0	0
			156	156		
4	B	72	Total	O	0	0
			72	72		

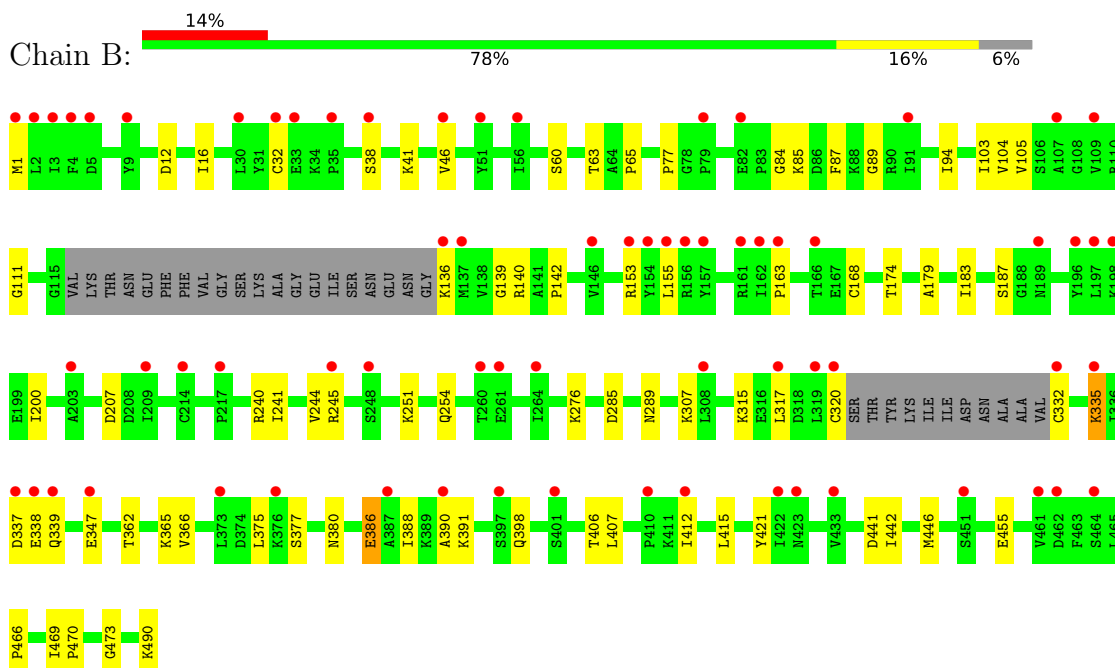
3 Residue-property plots [i](#)

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: Alpha/beta hydrolase



- Molecule 1: Alpha/beta hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.67Å 95.00Å 131.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.45 – 2.22 46.45 – 2.22	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.45-2.22) 99.9 (46.45-2.22)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.22Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.200 , 0.257 0.200 , 0.254	Depositor DCC
R_{free} test set	1993 reflections (3.51%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtrriage
Anisotropy	0.546	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.016 for k,h,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7678	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% 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: EDO, 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	0.45	0/3809	0.62	0/5148
1	B	0.40	0/3718	0.58	0/5022
All	All	0.43	0/7527	0.60	0/10170

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	3730	0	3663	34	0
1	B	3641	0	3573	39	0
2	A	28	0	40	4	0
2	B	7	0	10	2	0
3	A	28	0	42	3	0
3	B	16	0	24	1	0
4	A	156	0	0	4	0
4	B	72	0	0	2	0
All	All	7678	0	7352	74	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 5.

All (74) 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:14:CYS:SG	4:A:753:HOH:O	2.39	0.80
1:A:325:ILE:HG22	1:A:326:ILE:HD12	1.74	0.69
1:B:94:ILE:HG23	1:B:104:VAL:HG11	1.77	0.66
1:B:241:ILE:HD12	1:B:254:GLN:HG2	1.78	0.66
1:B:412:ILE:HA	1:B:415:LEU:HD12	1.81	0.63
1:B:174:THR:HG21	1:B:473:GLY:HA3	1.83	0.60
1:A:388:ILE:HD12	1:A:391:LYS:HE2	1.85	0.59
1:A:366:VAL:H	2:A:501:PEG:H31	1.67	0.58
1:B:244:VAL:HB	1:B:251:LYS:HB3	1.86	0.57
1:B:398:GLN:HB2	1:B:407:LEU:HD13	1.88	0.56
1:B:307:LYS:NZ	4:B:603:HOH:O	2.35	0.55
1:A:165:ASN:ND2	1:A:167:GLU:H	2.05	0.54
1:A:276:LYS:HD2	1:A:276:LYS:C	2.27	0.54
1:B:60:SER:H	1:B:63:THR:HB	1.72	0.53
1:B:38:SER:O	1:B:41:LYS:HE3	2.08	0.52
1:A:303:GLU:HG3	3:A:508:EDO:O2	2.09	0.52
1:B:136:LYS:HG2	1:B:386:GLU:HB2	1.92	0.52
1:A:385:THR:HG23	1:A:391:LYS:HE3	1.92	0.51
1:B:105:VAL:HG11	1:B:155:LEU:HD11	1.92	0.51
1:B:365:LYS:HB3	2:B:503:PEG:H22	1.93	0.51
1:B:315:LYS:HD2	4:B:646:HOH:O	2.11	0.50
1:A:62:HIS:HD2	4:A:627:HOH:O	1.93	0.50
1:B:16:ILE:HD11	1:B:84:GLY:HA2	1.93	0.50
1:A:27:LYS:NZ	1:A:82:GLU:OE1	2.45	0.49
1:A:334:SER:O	1:A:335:LYS:C	2.51	0.49
1:B:179:ALA:O	1:B:183:ILE:HD12	2.13	0.49
2:A:507:PEG:H41	4:A:608:HOH:O	2.12	0.48
1:B:240:ARG:C	1:B:241:ILE:HD13	2.34	0.48
1:A:1:MET:HG3	1:A:2:LEU:N	2.29	0.48
1:A:366:VAL:HG22	2:A:501:PEG:H21	1.95	0.48
1:B:388:ILE:HD12	1:B:391:LYS:HE2	1.96	0.48
1:B:240:ARG:O	1:B:241:ILE:HD13	2.13	0.48
1:B:187:SER:HB3	1:B:421:TYR:CG	2.49	0.47
1:A:244:VAL:HG13	1:A:251:LYS:HB3	1.96	0.47
1:B:289:ASN:HA	3:B:505:EDO:H12	1.95	0.47
1:B:377:SER:HB3	1:B:380:ASN:OD1	2.15	0.47
1:A:73:GLY:O	1:A:76:MET:HB2	2.15	0.47
1:A:306:LYS:NZ	3:A:510:EDO:H12	2.30	0.47
1:B:317:LEU:HD21	1:B:347:GLU:HB3	1.97	0.47
1:B:375:LEU:HD13	1:B:390:ALA:HB3	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:PRO:HG3	1:B:415:LEU:HD13	1.97	0.46
1:A:137:MET:SD	1:A:140:ARG:NH2	2.88	0.46
1:A:242:LYS:HB2	1:A:253:ILE:HB	1.98	0.46
1:A:324:LYS:O	1:A:325:ILE:C	2.55	0.45
1:A:243:HIS:O	1:A:245:ARG:HG3	2.17	0.45
1:A:306:LYS:HZ1	3:A:510:EDO:H12	1.82	0.45
1:B:46:VAL:HG21	1:B:163:PRO:HG2	1.99	0.45
1:B:65:PRO:HB3	1:B:168:CYS:SG	2.57	0.44
1:A:78:GLY:O	1:A:108:GLY:HA2	2.18	0.43
1:A:46:VAL:HG13	1:A:103:ILE:HD12	2.00	0.43
1:A:366:VAL:HG22	2:A:501:PEG:C2	2.48	0.43
1:B:85:LYS:HE2	1:B:89:GLY:O	2.18	0.43
1:B:335:LYS:O	1:B:339:GLN:HG2	2.19	0.43
1:B:466:PRO:HB2	1:B:469:ILE:HG12	2.00	0.43
1:A:148:MET:HB3	1:A:184:ILE:HD11	2.00	0.43
1:B:391:LYS:HD3	1:B:406:THR:HG23	1.99	0.43
1:B:442:ILE:HG12	1:B:446:MET:HG2	2.01	0.42
1:A:21:ILE:HG12	1:A:95:PHE:CE2	2.55	0.42
1:B:77:PRO:N	1:B:111:GLY:HA3	2.35	0.42
1:A:485:ASP:O	1:A:489:THR:HG23	2.20	0.42
1:A:287:SER:HB3	4:A:618:HOH:O	2.19	0.42
1:B:111:GLY:O	1:B:139:GLY:HA3	2.19	0.42
1:B:276:LYS:HD2	1:B:276:LYS:HA	1.88	0.42
1:A:94:ILE:HG12	1:A:104:VAL:HG11	2.02	0.41
1:B:366:VAL:HG22	2:B:503:PEG:H12	2.03	0.41
1:B:32:CYS:HB2	1:B:200:ILE:O	2.21	0.41
1:B:46:VAL:HG13	1:B:103:ILE:HD12	2.03	0.41
1:B:153:ARG:HE	1:B:207:ASP:HB3	1.85	0.41
1:A:327:ASP:C	1:A:329:ALA:H	2.24	0.41
1:A:451:SER:O	1:A:455:GLU:HG3	2.21	0.41
1:B:285:ASP:OD2	1:B:289:ASN:HB2	2.21	0.41
1:A:317:LEU:HD22	1:A:344:ILE:HD13	2.02	0.40
1:A:57:ASN:ND2	1:A:100:HIS:O	2.50	0.40
1:A:86:ASP:OD2	1:A:90:ARG:NE	2.50	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	468/490 (96%)	442 (94%)	25 (5%)	1 (0%)	47	54
1	B	454/490 (93%)	432 (95%)	20 (4%)	2 (0%)	34	37
All	All	922/980 (94%)	874 (95%)	45 (5%)	3 (0%)	41	45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	423	ASN
1	B	362	THR
1	B	470	PRO

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	405/419 (97%)	389 (96%)	16 (4%)	31	38
1	B	395/419 (94%)	381 (96%)	14 (4%)	36	44
All	All	800/838 (96%)	770 (96%)	30 (4%)	35	41

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	93[A]	SER
1	A	93[B]	SER
1	A	165	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	296	ASN
1	A	302	LYS
1	A	324	LYS
1	A	325	ILE
1	A	346	ASP
1	A	347	GLU
1	A	348	LYS
1	A	377	SER
1	A	425	SER
1	A	440	ARG
1	A	441	ASP
1	A	446	MET
1	A	464	SER
1	B	1	MET
1	B	12	ASP
1	B	87	PHE
1	B	140	ARG
1	B	245	ARG
1	B	320	CYS
1	B	332	CYS
1	B	335	LYS
1	B	337	ASP
1	B	338	GLU
1	B	386	GLU
1	B	441	ASP
1	B	455	GLU
1	B	490	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	328	ASN

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](#)

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	$\# Z > 2$
3	EDO	A	510	-	3,3,3	0.53	0	2,2,2	0.26	0
2	PEG	B	503	-	6,6,6	0.30	0	5,5,5	0.23	0
2	PEG	A	507	-	6,6,6	0.23	0	5,5,5	0.12	0
3	EDO	B	504	-	3,3,3	0.55	0	2,2,2	0.34	0
3	EDO	B	502	-	3,3,3	0.55	0	2,2,2	0.38	0
2	PEG	A	501	-	6,6,6	0.16	0	5,5,5	0.22	0
3	EDO	A	503	-	3,3,3	0.64	0	2,2,2	0.36	0
3	EDO	A	504	-	3,3,3	0.54	0	2,2,2	0.04	0
3	EDO	A	508	-	3,3,3	0.54	0	2,2,2	0.30	0
3	EDO	A	509	-	3,3,3	0.47	0	2,2,2	0.38	0
2	PEG	A	506	-	6,6,6	0.17	0	5,5,5	0.12	0
3	EDO	A	502	-	3,3,3	0.58	0	2,2,2	0.35	0
3	EDO	B	505	-	3,3,3	0.53	0	2,2,2	0.12	0
3	EDO	A	505	-	3,3,3	0.44	0	2,2,2	0.54	0
3	EDO	B	501	-	3,3,3	0.55	0	2,2,2	0.27	0
2	PEG	A	511	-	6,6,6	0.15	0	5,5,5	0.06	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	510	-	-	0/1/1/1	-
2	PEG	B	503	-	-	3/4/4/4	-
2	PEG	A	507	-	-	1/4/4/4	-
3	EDO	B	504	-	-	0/1/1/1	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	502	-	-	0/1/1/1	-
2	PEG	A	501	-	-	0/4/4/4	-
3	EDO	A	503	-	-	0/1/1/1	-
3	EDO	A	504	-	-	0/1/1/1	-
3	EDO	A	508	-	-	0/1/1/1	-
3	EDO	A	509	-	-	0/1/1/1	-
2	PEG	A	506	-	-	0/4/4/4	-
3	EDO	A	502	-	-	1/1/1/1	-
3	EDO	B	505	-	-	0/1/1/1	-
3	EDO	A	505	-	-	1/1/1/1	-
3	EDO	B	501	-	-	0/1/1/1	-
2	PEG	A	511	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	503	PEG	O1-C1-C2-O2
3	A	502	EDO	O1-C1-C2-O2
2	B	503	PEG	O2-C3-C4-O4
2	B	503	PEG	C4-C3-O2-C2
2	A	511	PEG	O2-C3-C4-O4
3	A	505	EDO	O1-C1-C2-O2
2	A	507	PEG	C4-C3-O2-C2

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	510	EDO	2	0
2	B	503	PEG	2	0
2	A	507	PEG	1	0
2	A	501	PEG	3	0
3	A	508	EDO	1	0
3	B	505	EDO	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

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	470/490 (95%)	0.78	33 (7%) 16 15	32, 44, 79, 110	0
1	B	459/490 (93%)	1.04	69 (15%) 2 1	41, 58, 83, 97	0
All	All	929/980 (94%)	0.91	102 (10%) 5 4	32, 51, 82, 110	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	323	TYR	9.9
1	B	155	LEU	8.8
1	A	328	ASN	8.1
1	B	2	LEU	8.0
1	A	329	ALA	7.4
1	B	157	TYR	7.0
1	B	337	ASP	6.9
1	A	330	ALA	6.7
1	A	331	VAL	6.7
1	B	1	MET	6.5
1	A	321	SER	6.3
1	A	246	SER	6.2
1	A	346	ASP	6.1
1	A	325	ILE	5.6
1	A	327	ASP	5.4
1	B	387	ALA	5.2
1	B	410	PRO	5.1
1	B	3	ILE	5.1
1	B	197	LEU	5.0
1	A	326	ILE	4.7
1	A	247	GLU	4.6
1	A	406	THR	4.4
1	B	332	CYS	4.4
1	B	412	ILE	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	333	GLY	4.3
1	B	51	TYR	4.2
1	B	32	CYS	4.1
1	A	248	SER	4.1
1	B	136	LYS	4.0
1	B	30	LEU	4.0
1	A	318	ASP	3.9
1	B	423	ASN	3.8
1	B	203	ALA	3.8
1	A	87	PHE	3.6
1	A	337	ASP	3.5
1	B	146	VAL	3.4
1	B	397	SER	3.4
1	B	161	ARG	3.3
1	A	249	GLY	3.3
1	A	404	GLU	3.3
1	B	248	SER	3.3
1	B	245	ARG	3.3
1	B	209	ILE	3.2
1	B	162	ILE	3.1
1	B	109	VAL	3.1
1	B	153	ARG	3.1
1	A	320	CYS	3.1
1	B	433	VAL	3.0
1	B	319	LEU	3.0
1	B	335	LYS	3.0
1	B	214	CYS	2.9
1	A	253	ILE	2.9
1	B	339	GLN	2.8
1	B	320	CYS	2.8
1	B	264	ILE	2.8
1	A	245	ARG	2.8
1	B	46	VAL	2.8
1	B	91	ILE	2.8
1	B	373	LEU	2.7
1	A	319	LEU	2.7
1	B	464	SER	2.6
1	B	154	TYR	2.6
1	B	317	LEU	2.6
1	B	260	THR	2.6
1	B	261	GLU	2.5
1	A	419	ILE	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	338	GLU	2.5
1	B	9	TYR	2.4
1	A	386	GLU	2.4
1	B	5	ASP	2.4
1	B	56	ILE	2.3
1	A	345	GLU	2.3
1	A	332	CYS	2.3
1	A	403	VAL	2.3
1	B	79	PRO	2.3
1	B	347	GLU	2.2
1	B	217	PRO	2.2
1	B	390	ALA	2.2
1	B	196	TYR	2.2
1	B	198	LYS	2.2
1	B	166	THR	2.2
1	A	250	VAL	2.2
1	B	38	SER	2.2
1	B	4	PHE	2.2
1	B	33	GLU	2.2
1	B	376	LYS	2.2
1	B	163	PRO	2.2
1	B	107	ALA	2.2
1	B	35	PRO	2.2
1	B	82	GLU	2.1
1	B	401	SER	2.1
1	A	176	ALA	2.1
1	A	90	ARG	2.1
1	B	461	VAL	2.1
1	B	422	ILE	2.1
1	B	156	ARG	2.0
1	B	137	MET	2.0
1	A	387	ALA	2.0
1	B	451	SER	2.0
1	B	462	ASP	2.0
1	B	308	LEU	2.0
1	B	189	ASN	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 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, 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	B	503	7/7	0.35	0.28	53,60,66,70	0
2	PEG	A	511	7/7	0.42	0.25	69,76,81,83	0
2	PEG	A	506	7/7	0.46	0.27	65,67,71,77	0
3	EDO	A	502	4/4	0.49	0.40	57,60,67,68	0
2	PEG	A	501	7/7	0.52	0.31	51,53,56,58	0
2	PEG	A	507	7/7	0.59	0.28	52,55,57,61	0
3	EDO	A	508	4/4	0.59	0.23	62,67,69,69	0
3	EDO	A	510	4/4	0.67	0.20	64,69,69,70	0
3	EDO	A	505	4/4	0.70	0.20	63,63,63,72	0
3	EDO	B	502	4/4	0.77	0.44	52,55,58,61	0
3	EDO	B	505	4/4	0.78	0.18	59,63,63,67	0
3	EDO	B	504	4/4	0.81	0.47	67,70,73,74	0
3	EDO	B	501	4/4	0.83	0.17	51,52,58,58	0
3	EDO	A	503	4/4	0.87	0.31	41,44,45,46	0
3	EDO	A	504	4/4	0.89	0.24	55,58,63,65	0
3	EDO	A	509	4/4	0.90	0.21	54,57,59,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.