



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 16, 2020 – 10:20 AM JST

PDB ID : 6LD7
Title : Native Structure of cystathionine gamma synthase (XometB) from Xanthomonas oryzae pv. oryzae
Authors : Ngo, H.P.T.; Nguyen, T.D.Q.; Kang, L.W.
Deposited on : 2019-11-20
Resolution : 2.10 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 : 2.14.6
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) : 2.14.6

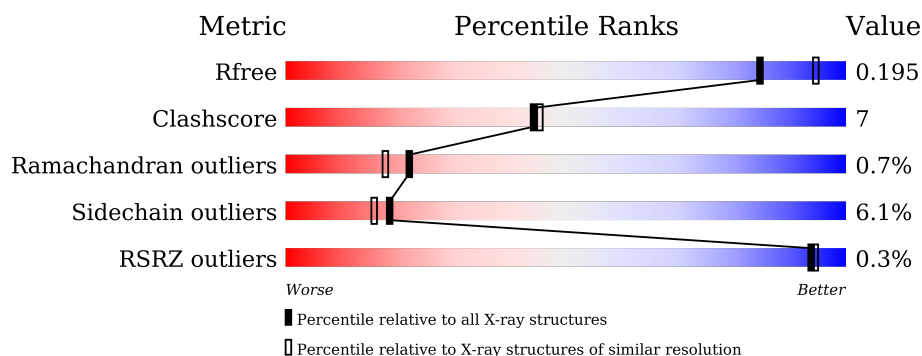
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	408	<div> <div style="width: 82%;"></div> <div style="width: 9%;"></div> <div style="width: 5%;"></div> <div style="width: 5%;"></div> </div> <div>82% 9% . . 5%</div>
1	B	408	<div> <div style="width: 80%;"></div> <div style="width: 10%;"></div> <div style="width: 5%;"></div> <div style="width: 5%;"></div> </div> <div>80% 10% . . 5%</div>
1	C	408	<div> <div style="width: 79%;"></div> <div style="width: 13%;"></div> <div style="width: 5%;"></div> <div style="width: 5%;"></div> </div> <div>79% 13% . . 5%</div>
1	D	408	<div> <div style="width: 79%;"></div> <div style="width: 11%;"></div> <div style="width: 5%;"></div> <div style="width: 5%;"></div> </div> <div>79% 11% . . 5%</div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12288 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 Cystathionine gamma-synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	P	S	0	2	0
			2891	1826	507	550	1	7			
1	B	386	Total	C	N	O	P	S	0	1	0
			2878	1819	506	545	1	7			
1	C	388	Total	C	N	O	P	S	0	1	0
			2892	1826	508	550	1	7			
1	D	386	Total	C	N	O	P	S	0	2	0
			2884	1822	506	548	1	7			

There are 16 discrepancies between the modelled and reference sequences:

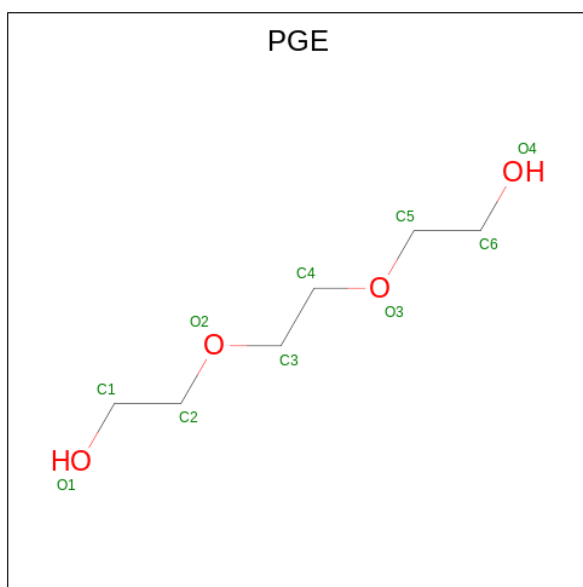
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q5H1U9
A	-1	SER	-	expression tag	UNP Q5H1U9
A	0	HIS	-	expression tag	UNP Q5H1U9
A	134	VAL	ASP	engineered mutation	UNP Q5H1U9
B	-2	GLY	-	expression tag	UNP Q5H1U9
B	-1	SER	-	expression tag	UNP Q5H1U9
B	0	HIS	-	expression tag	UNP Q5H1U9
B	134	VAL	ASP	engineered mutation	UNP Q5H1U9
C	-2	GLY	-	expression tag	UNP Q5H1U9
C	-1	SER	-	expression tag	UNP Q5H1U9
C	0	HIS	-	expression tag	UNP Q5H1U9
C	134	VAL	ASP	engineered mutation	UNP Q5H1U9
D	-2	GLY	-	expression tag	UNP Q5H1U9
D	-1	SER	-	expression tag	UNP Q5H1U9
D	0	HIS	-	expression tag	UNP Q5H1U9
D	134	VAL	ASP	engineered mutation	UNP Q5H1U9

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



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

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



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

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

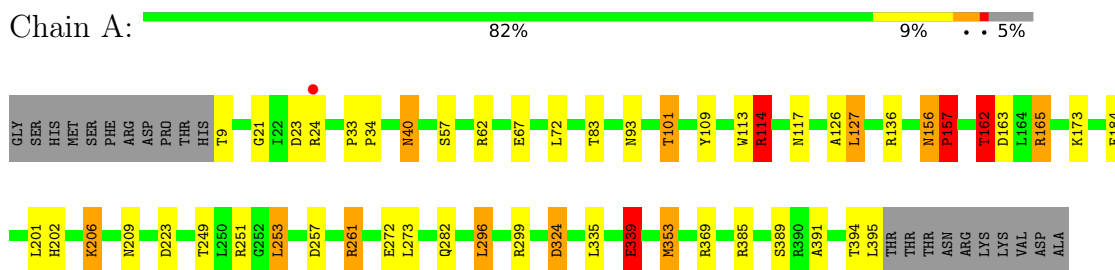
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	146	Total	O	0	0
			146	146		
4	B	187	Total	O	0	0
			187	187		
4	C	176	Total	O	0	0
			176	176		
4	D	163	Total	O	0	0
			163	163		

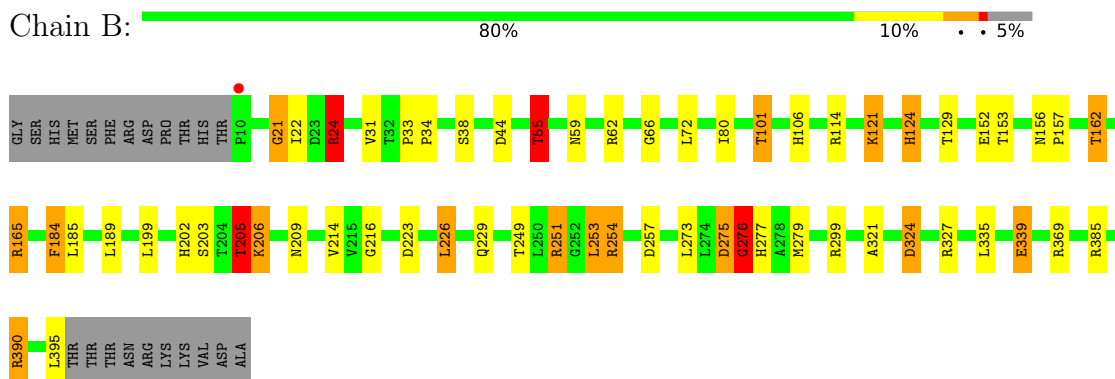
3 Residue-property plots

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.

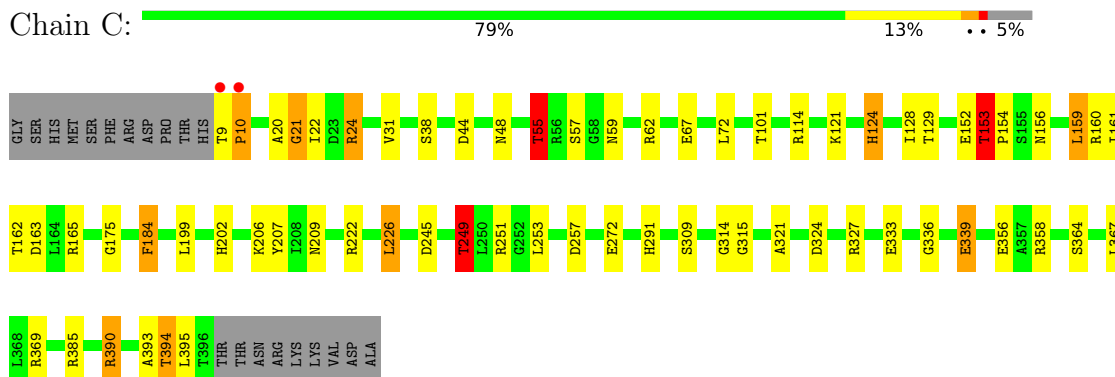
- Molecule 1: Cystathionine gamma-synthase



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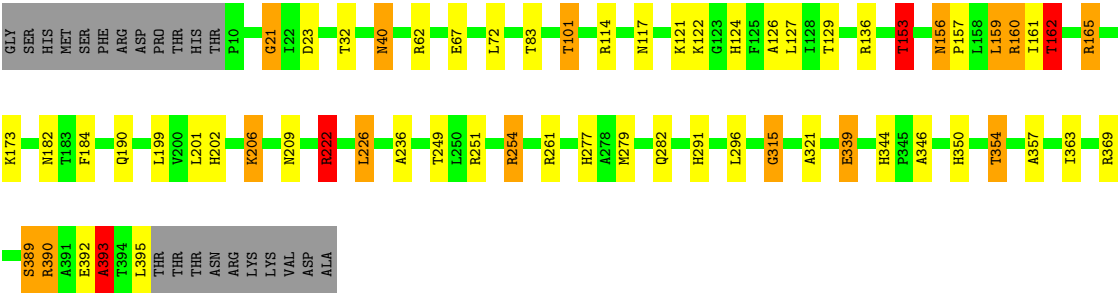
- Molecule 1: Cystathionine gamma-synthase

Chain D:

79%

11%

• • 5%



4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	165.42Å 165.42Å 241.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.80 – 2.10 48.80 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.80-2.10) 99.9 (48.80-2.10)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.162 , 0.190 0.169 , 0.195	Depositor DCC
R_{free} test set	9421 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	33.1	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 27.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.004 for -1/2*h-1/2*k+1/2*l,-1/2*h-1/2*k-1/2*l,h-k 0.004 for -1/2*h-1/2*k-1/2*l,-1/2*h-1/2*k+1/2*l,-h+k 0.000 for -1/2*h+1/2*k+1/2*l,1/2*h-1/2*k+1/2*l,h+k 0.002 for -1/2*h+1/2*k-1/2*l,1/2*h-1/2*k-1/2*l,-h-k 0.487 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12288	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: LLP, PEG, PGE

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	1.08	7/2926 (0.2%)	1.21	19/3982 (0.5%)
1	B	1.10	5/2910 (0.2%)	1.34	23/3959 (0.6%)
1	C	1.11	10/2924 (0.3%)	1.43	32/3979 (0.8%)
1	D	1.09	5/2919 (0.2%)	1.30	24/3971 (0.6%)
All	All	1.09	27/11679 (0.2%)	1.32	98/15891 (0.6%)

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	A	0	1
1	B	0	4
1	C	0	2
1	D	0	3
All	All	0	10

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	339	GLU	CD-OE2	14.11	1.41	1.25
1	B	339	GLU	CD-OE2	11.44	1.38	1.25
1	A	339	GLU	CD-OE2	10.30	1.36	1.25
1	C	339	GLU	CD-OE2	8.61	1.35	1.25
1	C	152	GLU	CD-OE2	8.28	1.34	1.25

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	390	ARG	NE-CZ-NH2	-21.95	109.32	120.30
1	C	114	ARG	NE-CZ-NH1	21.40	131.00	120.30
1	C	390	ARG	NE-CZ-NH2	-19.76	110.42	120.30
1	C	114	ARG	NE-CZ-NH2	-19.41	110.60	120.30
1	D	390	ARG	NE-CZ-NH1	18.40	129.50	120.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	202	HIS	Peptide
1	B	202	HIS	Peptide
1	B	21	GLY	Peptide
1	B	276	GLY	Peptide
1	B	44	ASP	Peptide

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	2891	0	2886	35	0
1	B	2878	0	2873	49	0
1	C	2892	0	2879	32	0
1	D	2884	0	2880	47	0
2	A	7	0	10	1	0
2	D	14	0	20	0	0
3	B	30	0	42	6	0
3	C	10	0	14	0	0
3	D	10	0	14	0	0
4	A	146	0	0	7	0
4	B	187	0	0	11	0
4	C	176	0	0	1	0
4	D	163	0	0	7	0
All	All	12288	0	11618	153	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 7.

The worst 5 of 153 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:223:ASP:HB2	4:A:724:HOH:O	1.60	1.01
1:D:153:THR:HG23	1:D:162:THR:H	1.36	0.90
1:D:277:HIS:HD2	1:D:279:MET:H	1.20	0.89
1:D:315:GLY:HA3	4:D:747:HOH:O	1.72	0.88
1:C:153:THR:HG23	1:C:162:THR:H	1.38	0.86

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	386/408 (95%)	374 (97%)	10 (3%)	2 (0%)	29	26
1	B	384/408 (94%)	375 (98%)	7 (2%)	2 (0%)	29	26
1	C	386/408 (95%)	374 (97%)	7 (2%)	5 (1%)	12	7
1	D	385/408 (94%)	375 (97%)	9 (2%)	1 (0%)	41	41
All	All	1541/1632 (94%)	1498 (97%)	33 (2%)	10 (1%)	22	21

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	10	PRO
1	C	394	THR
1	D	393	ALA
1	A	324	ASP
1	A	353	MET

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	292/309 (94%)	273 (94%)	19 (6%)	17	14
1	B	289/309 (94%)	272 (94%)	17 (6%)	19	17
1	C	291/309 (94%)	275 (94%)	16 (6%)	21	19
1	D	291/309 (94%)	272 (94%)	19 (6%)	17	14
All	All	1163/1236 (94%)	1092 (94%)	71 (6%)	18	16

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	253	LEU
1	C	72	LEU
1	D	222	ARG
1	B	273	LEU
1	C	24	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	51	GLN
1	C	190	GLN
1	D	209	ASN
1	C	124	HIS
1	C	156	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](#)

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	LLP	B	206	1	23,24,25	1.78	5 (21%)	25,32,34	1.60	4 (16%)
1	LLP	D	206	1	23,24,25	1.35	3 (13%)	25,32,34	1.48	5 (20%)
1	LLP	A	206	1	23,24,25	1.32	2 (8%)	25,32,34	1.34	3 (12%)
1	LLP	C	206	1	23,24,25	1.43	3 (13%)	25,32,34	1.19	2 (8%)

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
1	LLP	B	206	1	-	5/16/17/19	0/1/1/1
1	LLP	D	206	1	-	3/16/17/19	0/1/1/1
1	LLP	A	206	1	-	6/16/17/19	0/1/1/1
1	LLP	C	206	1	-	4/16/17/19	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	206	LLP	C4'-NZ	5.36	1.45	1.27
1	A	206	LLP	C4'-NZ	4.50	1.42	1.27
1	C	206	LLP	C3-C2	-3.76	1.37	1.40
1	D	206	LLP	C4'-NZ	3.71	1.39	1.27
1	B	206	LLP	CD-CE	3.43	1.63	1.51

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	206	LLP	C3-C4-C5	-3.62	115.48	118.26
1	B	206	LLP	C5-C4-C4'	3.49	127.30	121.56
1	B	206	LLP	C4-C3-C2	3.27	122.21	120.19
1	A	206	LLP	C5-C4-C4'	3.08	126.62	121.56
1	D	206	LLP	C4-C3-C2	2.91	121.99	120.19

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	206	LLP	O-C-CA-CB
1	D	206	LLP	O-C-CA-CB
1	A	206	LLP	O-C-CA-CB
1	C	206	LLP	C4-C4'-NZ-CE
1	C	206	LLP	O-C-CA-CB

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	206	LLP	3	0
1	D	206	LLP	1	0
1	A	206	LLP	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	501	-	6,6,6	0.50	0	5,5,5	0.48	0
3	PGE	C	501	-	9,9,9	0.45	0	8,8,8	0.29	0
3	PGE	B	501	-	9,9,9	0.64	0	8,8,8	0.41	0
2	PEG	D	502	-	6,6,6	0.29	0	5,5,5	0.19	0
2	PEG	D	501	-	6,6,6	0.52	0	5,5,5	0.52	0
3	PGE	B	503	-	9,9,9	0.57	0	8,8,8	0.47	0
3	PGE	D	503	-	9,9,9	0.28	0	8,8,8	0.13	0
3	PGE	B	502	-	9,9,9	0.38	0	8,8,8	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	PEG	A	501	-	-	1/4/4/4	-
3	PGE	C	501	-	-	3/7/7/7	-
3	PGE	B	501	-	-	4/7/7/7	-
2	PEG	D	502	-	-	3/4/4/4	-
2	PEG	D	501	-	-	2/4/4/4	-
3	PGE	B	503	-	-	6/7/7/7	-
3	PGE	D	503	-	-	4/7/7/7	-
3	PGE	B	502	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	502	PGE	C4-C3-O2-C2
3	B	503	PGE	O2-C3-C4-O3
2	D	501	PEG	C1-C2-O2-C3
3	D	503	PGE	O2-C3-C4-O3
3	B	501	PGE	O2-C3-C4-O3

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	PEG	1	0
3	B	501	PGE	2	0
3	B	503	PGE	1	0
3	B	502	PGE	3	0

5.7 Other polymers [i](#)

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 [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	386/408 (94%)	-0.02	1 (0%) 94 94	24, 35, 59, 91	0
1	B	385/408 (94%)	-0.03	1 (0%) 94 94	23, 32, 52, 97	0
1	C	387/408 (94%)	-0.02	2 (0%) 91 92	23, 32, 54, 123	0
1	D	385/408 (94%)	-0.04	0 100 100	23, 35, 59, 86	0
All	All	1543/1632 (94%)	-0.03	4 (0%) 94 94	23, 34, 56, 123	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	9	THR	9.3
1	C	10	PRO	4.0
1	B	10	PRO	3.1
1	A	24	ARG	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LLP	A	206	24/25	0.96	0.13	26,35,40,46	0
1	LLP	D	206	24/25	0.97	0.14	28,36,45,47	0
1	LLP	B	206	24/25	0.97	0.13	27,33,38,46	0
1	LLP	C	206	24/25	0.97	0.12	25,35,43,52	0

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(\AA^2)	Q<0.9
2	PEG	D	502	7/7	0.74	0.15	68,71,79,79	0
3	PGE	C	501	10/10	0.80	0.29	39,83,90,90	0
3	PGE	B	503	10/10	0.80	0.18	52,62,69,72	0
3	PGE	B	501	10/10	0.81	0.26	40,83,98,99	0
3	PGE	B	502	10/10	0.81	0.18	56,75,83,85	0
2	PEG	D	501	7/7	0.84	0.12	44,61,81,81	0
3	PGE	D	503	10/10	0.89	0.19	53,74,77,79	0
2	PEG	A	501	7/7	0.92	0.12	41,54,69,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.