



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 12, 2014 – 01:58 AM EDT

PDB ID : 4POV
Title : ThiT with LMG135 bound
Authors : Swier, L.J.Y.M.; Guskov, A.; Slotboom, D.J.
Deposited on : 2014-02-26
Resolution : 2.20 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

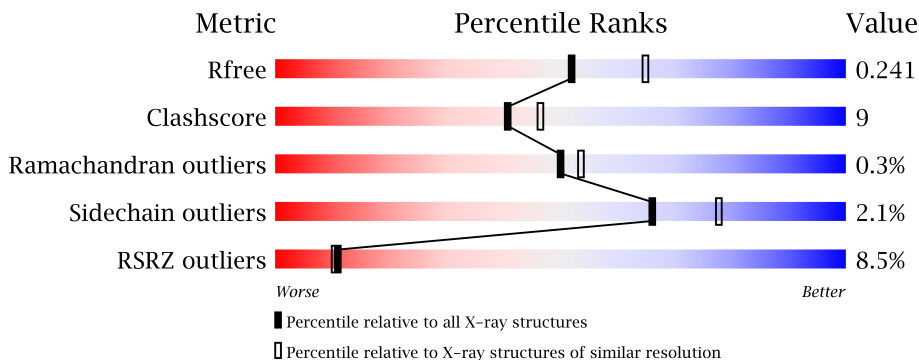
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	192	
1	B	192	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
10	CL	B	217	-	X
4	PG4	A	205	-	X
4	PG4	A	206	-	X
4	PG4	A	207	-	X
4	PG4	B	203	-	X
4	PG4	B	204	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
5	BNG	A	208	-	X
5	BNG	A	209	-	X
5	BNG	A	210	-	X
5	BNG	B	207	-	X
5	BNG	B	209	-	X
6	PEG	A	211	-	X
6	PEG	A	213	-	X
6	PEG	A	214	-	X
6	PEG	A	215	-	X
6	PEG	B	214	-	X
7	1PE	B	215	-	X
8	PGE	A	217	-	X
8	PGE	A	218	-	X
8	PGE	A	219	-	X
9	P6G	A	220	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 3276 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

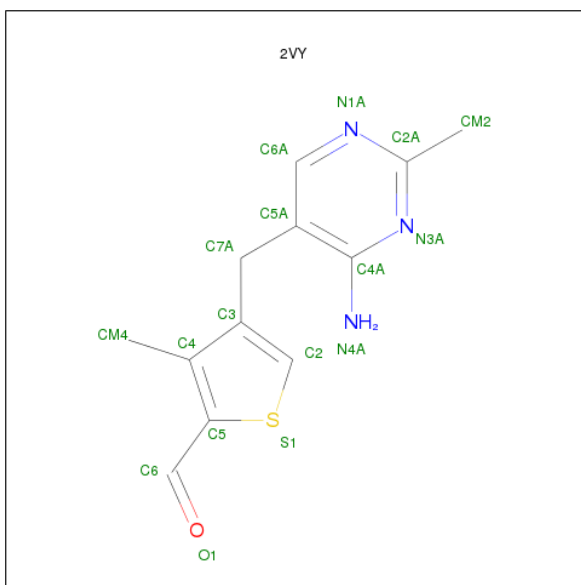
- Molecule 1 is a protein called Thiamine transporter ThiT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1386	951	216	216	3			
1	B	176	Total	C	N	O	S	0	0	0
			1366	936	213	214	3			

There are 20 discrepancies between the modelled and reference sequences:

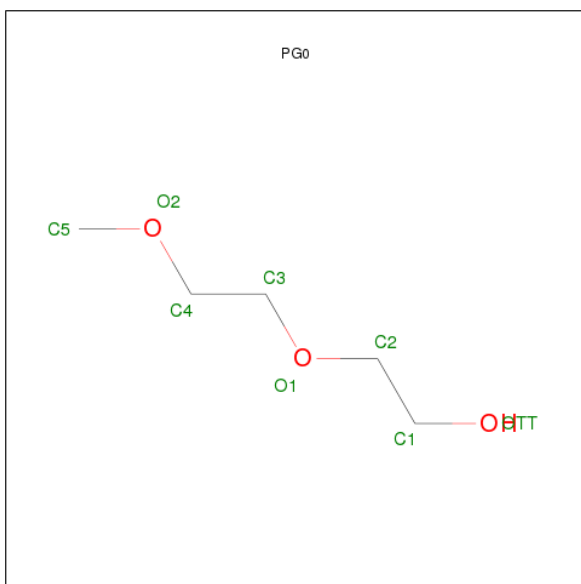
Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	INITIATING METHIONINE	UNP A2RI47
A	-8	HIS	-	EXPRESSION TAG	UNP A2RI47
A	-7	HIS	-	EXPRESSION TAG	UNP A2RI47
A	-6	HIS	-	EXPRESSION TAG	UNP A2RI47
A	-5	HIS	-	EXPRESSION TAG	UNP A2RI47
A	-4	HIS	-	EXPRESSION TAG	UNP A2RI47
A	-3	HIS	-	EXPRESSION TAG	UNP A2RI47
A	-2	HIS	-	EXPRESSION TAG	UNP A2RI47
A	-1	HIS	-	EXPRESSION TAG	UNP A2RI47
A	0	ALA	-	EXPRESSION TAG	UNP A2RI47
B	-9	MET	-	INITIATING METHIONINE	UNP A2RI47
B	-8	HIS	-	EXPRESSION TAG	UNP A2RI47
B	-7	HIS	-	EXPRESSION TAG	UNP A2RI47
B	-6	HIS	-	EXPRESSION TAG	UNP A2RI47
B	-5	HIS	-	EXPRESSION TAG	UNP A2RI47
B	-4	HIS	-	EXPRESSION TAG	UNP A2RI47
B	-3	HIS	-	EXPRESSION TAG	UNP A2RI47
B	-2	HIS	-	EXPRESSION TAG	UNP A2RI47
B	-1	HIS	-	EXPRESSION TAG	UNP A2RI47
B	0	ALA	-	EXPRESSION TAG	UNP A2RI47

- Molecule 2 is 4-[(4-AMINO-2-METHYLPYRIMIDIN-5-YL)METHYL]-3-METHYLTHIOPHENE-2-CARBALDEHYDE (three-letter code: 2VY) (formula: C₁₂H₁₃N₃OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			17	12	3	1	1		
2	B	1	Total	C	N	O	S	0	0
			17	12	3	1	1		

- Molecule 3 is 2-(2-METHOXYETHOXY)ETHANOL (three-letter code: PG0) (formula: $C_5H_{12}O_3$).



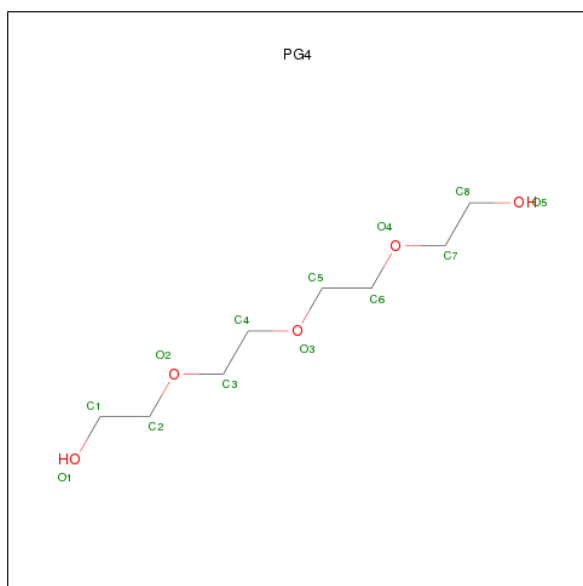
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	5	3		

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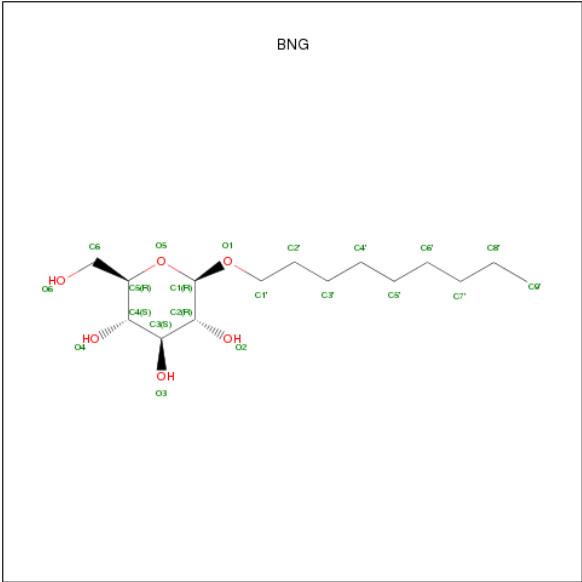
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			8	5	3		

- Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



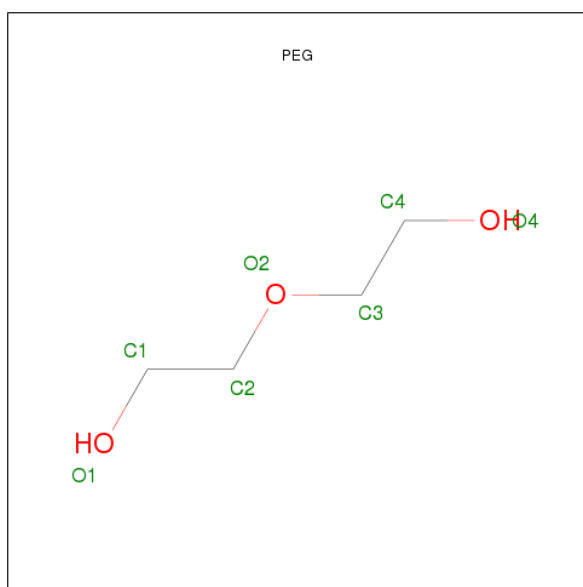
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is SUGAR (B-NONYLGLUCOSIDE) (three-letter code: BNG) (formula: $C_{15}H_{30}O_6$).



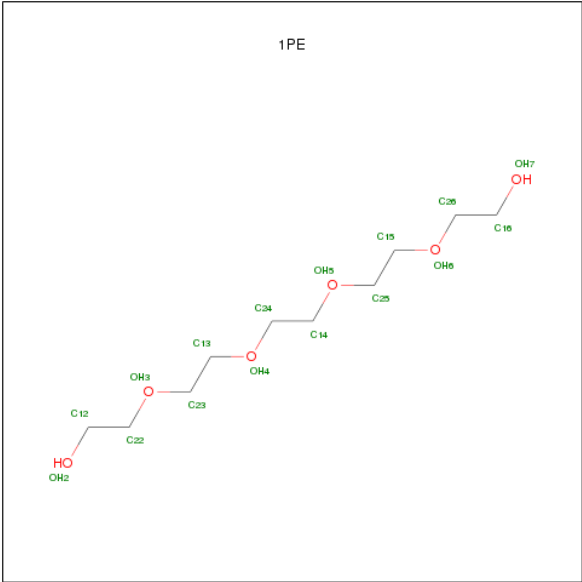
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			21	15	6		
5	A	1	Total	C	O	0	0
			21	15	6		
5	A	1	Total	C	O	0	0
			21	15	6		
5	B	1	Total	C	O	0	0
			21	15	6		
5	B	1	Total	C	O	0	0
			21	15	6		
5	B	1	Total	C	O	0	0
			21	15	6		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



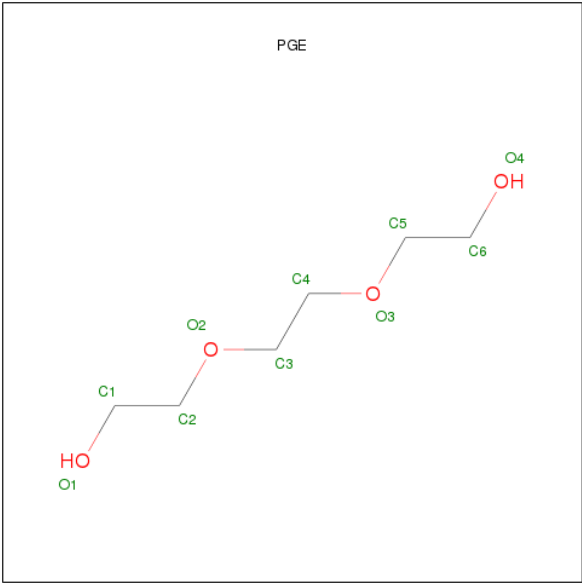
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total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

- Molecule 7 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



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

- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



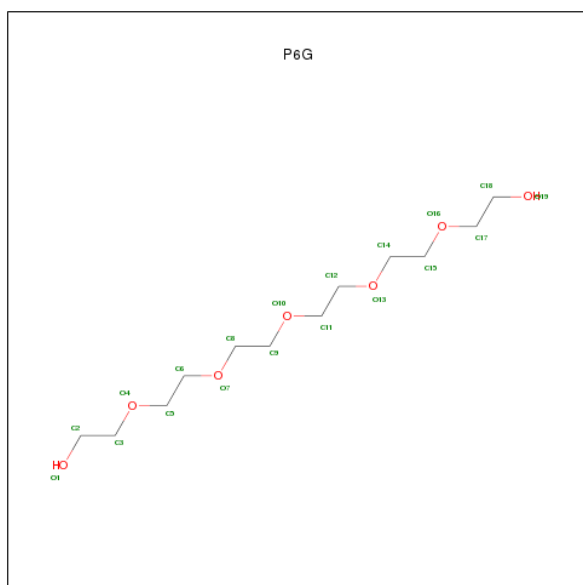
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			10	6	4		

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

- Molecule 9 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			19	12	7		

- Molecule 10 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 11 is water.

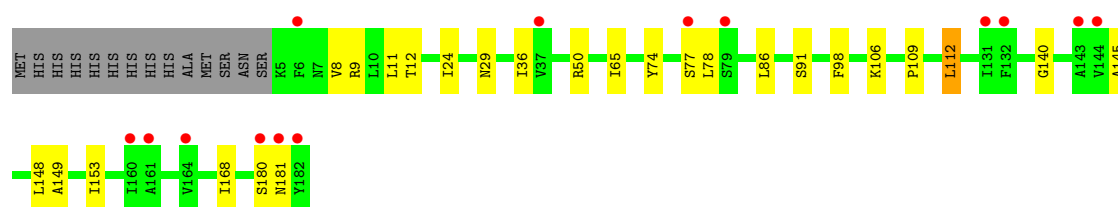
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	33	Total	O	0	0
			33	33		
11	B	30	Total	O	0	0
			30	30		

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 errors 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.

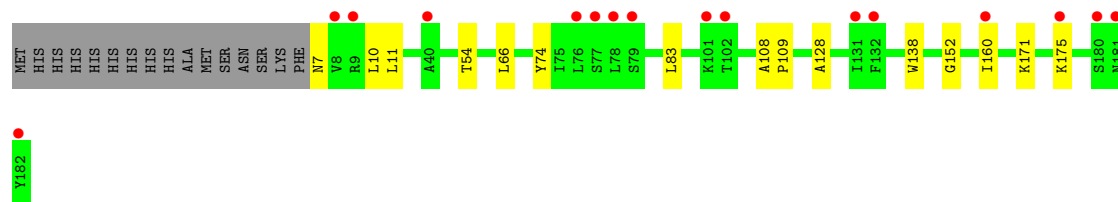
- Molecule 1: Thiamine transporter ThiT

Chain A:



- Molecule 1: Thiamine transporter ThiT

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	62.72Å 84.35Å 127.25Å 90.00° 96.08° 90.00°	Depositor
Resolution (Å)	48.04 – 2.20 48.04 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (48.04-2.20) 99.4 (48.04-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.185 , 0.237 0.190 , 0.241	Depositor DCC
R_{free} test set	1667 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 70.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 33360 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3276	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, P6G, CL, 1PE, PG4, PG0, 2VY, PEG, BNG

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	0.67	0/1425	0.63	0/1941
1	B	0.62	0/1404	0.62	0/1914
All	All	0.64	0/2829	0.62	0/3855

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1386	0	1484	27	0
1	B	1366	0	1462	11	0
2	A	17	0	0	0	0
2	B	17	0	0	0	0
3	A	8	0	12	1	0
3	B	8	0	12	2	0
4	A	65	0	90	11	0
4	B	52	0	72	12	0
5	A	63	0	90	12	0
5	B	63	0	90	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	35	0	46	6	0
6	B	35	0	45	5	0
7	A	16	0	22	4	0
7	B	32	0	44	0	0
8	A	30	0	42	3	0
9	A	19	0	26	3	0
10	B	1	0	0	0	0
11	A	33	0	0	1	0
11	B	30	0	0	2	0
All	All	3276	0	3537	63	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (63) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:A:220:P6G:H32	9:A:220:P6G:H82	1.35	1.09
4:B:206:PG4:H51	5:B:209:BNG:H3'1	1.52	0.88
7:A:216:1PE:H252	4:B:204:PG4:H22	1.58	0.85
5:A:208:BNG:H9'3	5:A:208:BNG:H5'1	1.61	0.81
1:B:160:ILE:HG22	6:B:210:PEG:H12	1.65	0.79
9:A:220:P6G:C3	9:A:220:P6G:H82	2.12	0.76
4:B:206:PG4:C5	5:B:209:BNG:H3'1	2.15	0.76
1:A:109:PRO:HG3	8:A:217:PGE:H5	1.68	0.75
1:A:74:TYR:CE2	4:A:207:PG4:H22	2.22	0.74
4:A:204:PG4:H31	4:B:206:PG4:H52	1.71	0.72
4:B:206:PG4:H51	5:B:209:BNG:C3'	2.21	0.70
1:A:78:LEU:CD2	5:A:209:BNG:H4'2	2.24	0.67
1:A:98:PHE:HA	8:A:219:PGE:H52	1.78	0.64
5:B:207:BNG:H2'2	5:B:207:BNG:O5	1.99	0.63
4:A:204:PG4:C3	4:B:206:PG4:H52	2.33	0.58
1:A:77:SER:HA	5:A:209:BNG:H61	1.87	0.57
1:A:112:LEU:HD12	8:A:217:PGE:H12	1.85	0.56
1:B:160:ILE:CG2	6:B:210:PEG:H12	2.33	0.56
1:A:153:ILE:HD13	6:B:211:PEG:H11	1.88	0.55
1:A:78:LEU:HD22	5:A:209:BNG:H4'2	1.87	0.55
1:B:175:LYS:HB2	6:B:214:PEG:H32	1.88	0.55
1:B:74:TYR:CE2	3:B:202:PG0:H42	2.41	0.55
4:B:203:PG4:H62	11:B:311:HOH:O	2.08	0.54
1:A:65:ILE:HG23	5:A:210:BNG:H9'3	1.89	0.53
1:A:168:ILE:HG12	6:A:212:PEG:H21	1.91	0.53
1:A:140:GLY:H	3:A:202:PG0:H21	1.73	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:B:206:PG4:H51	5:B:209:BNG:C2'	2.38	0.53
1:A:36:ILE:HG21	4:A:207:PG4:H62	1.92	0.52
5:A:208:BNG:H1'1	5:A:208:BNG:O2	2.10	0.52
1:A:149:ALA:HA	7:A:216:1PE:H131	1.92	0.51
1:A:24:ILE:CD1	4:A:203:PG4:H61	2.40	0.51
1:A:106:LYS:HB3	6:A:215:PEG:H21	1.92	0.50
1:A:78:LEU:HD23	5:A:209:BNG:H4'2	1.93	0.49
3:B:202:PG0:H12	11:B:305:HOH:O	2.12	0.49
4:A:206:PG4:H71	4:A:206:PG4:H51	1.66	0.47
1:A:153:ILE:HG21	6:B:211:PEG:H11	1.96	0.47
4:A:207:PG4:H82	11:A:311:HOH:O	2.15	0.47
1:A:91:SER:HA	4:A:205:PG4:H22	1.97	0.47
1:A:148:LEU:HD23	7:A:216:1PE:H222	1.97	0.47
1:B:83:LEU:HD23	1:B:128:ALA:HB2	1.95	0.47
1:B:152:GLY:HA2	4:B:204:PG4:H52	1.98	0.46
1:B:10:LEU:HD21	4:B:203:PG4:H61	1.98	0.46
1:A:86:LEU:HD12	5:A:209:BNG:H7'1	1.97	0.45
1:A:8:VAL:O	1:A:12:THR:HG23	2.16	0.45
5:A:208:BNG:H6'2	5:A:208:BNG:H3'2	1.71	0.45
7:A:216:1PE:H241	7:A:216:1PE:H232	1.71	0.44
1:B:66:LEU:HD11	5:B:207:BNG:H1'1	1.99	0.44
6:A:215:PEG:H12	6:A:215:PEG:C4	2.39	0.44
4:B:204:PG4:H62	4:B:204:PG4:H41	1.65	0.44
9:A:220:P6G:H181	9:A:220:P6G:H142	2.01	0.43
5:A:210:BNG:H9'2	5:A:210:BNG:H6'2	1.66	0.42
1:A:24:ILE:HD13	4:A:203:PG4:H61	2.01	0.42
1:A:36:ILE:CG2	4:A:207:PG4:H62	2.49	0.42
5:A:208:BNG:H5'1	5:A:208:BNG:C9'	2.30	0.42
1:A:50:ARG:NH2	6:A:213:PEG:H32	2.35	0.41
1:A:29:ASN:HA	4:A:204:PG4:H71	2.01	0.41
6:A:215:PEG:H32	6:A:215:PEG:H12	1.36	0.41
1:B:54:THR:HB	4:B:203:PG4:H72	2.02	0.41
6:A:215:PEG:H42	6:A:215:PEG:H12	2.03	0.41
1:B:108:ALA:CB	5:B:209:BNG:H2'2	2.51	0.41
1:A:145:ALA:HB2	5:A:208:BNG:H3	2.03	0.41
1:A:180:SER:OG	1:A:181:ASN:O	2.37	0.41
1:B:108:ALA:HB3	1:B:109:PRO:HD3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	176/192 (92%)	173 (98%)	3 (2%)	0	100	100
1	B	174/192 (91%)	170 (98%)	3 (2%)	1 (1%)	33	32
All	All	350/384 (91%)	343 (98%)	6 (2%)	1 (0%)	50	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	138	TRP

5.3.2 Protein sidechains ⓘ

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	142/155 (92%)	139 (98%)	3 (2%)	66	78
1	B	140/155 (90%)	137 (98%)	3 (2%)	66	78
All	All	282/310 (91%)	276 (98%)	6 (2%)	66	78

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	11	LEU
1	A	112	LEU
1	B	7	ASN
1	B	11	LEU
1	B	171	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 37 ligands modelled in this entry, 1 is monoatomic - leaving 36 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	2VY	A	201	-	18,18,18	3.75	6 (33%)	25,25,25	3.27	10 (40%)
3	PG0	A	202	-	7,7,7	0.39	0	6,6,6	0.96	1 (16%)
4	PG4	A	203	-	12,12,12	0.73	0	11,11,11	0.38	0
4	PG4	A	204	-	12,12,12	0.82	0	11,11,11	0.24	0
4	PG4	A	205	-	12,12,12	0.79	0	11,11,11	0.41	0
4	PG4	A	206	-	12,12,12	0.74	0	11,11,11	0.44	0
4	PG4	A	207	-	12,12,12	0.84	0	11,11,11	0.53	0
5	BNG	A	208	-	21,21,21	1.11	2 (9%)	26,26,26	1.14	1 (3%)
5	BNG	A	209	-	21,21,21	1.13	3 (14%)	26,26,26	1.03	1 (3%)
5	BNG	A	210	-	21,21,21	1.10	2 (9%)	26,26,26	0.77	0
6	PEG	A	211	-	6,6,6	0.61	0	5,5,5	0.31	0
6	PEG	A	212	-	6,6,6	0.56	0	5,5,5	0.24	0
6	PEG	A	213	-	6,6,6	0.56	0	5,5,5	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	PEG	A	214	-	6,6,6	0.57	0	5,5,5	0.33	0
6	PEG	A	215	-	6,6,6	0.69	0	5,5,5	0.42	0
7	1PE	A	216	-	15,15,15	0.81	0	14,14,14	0.41	0
8	PGE	A	217	-	9,9,9	0.37	0	8,8,8	0.29	0
8	PGE	A	218	-	9,9,9	0.30	0	8,8,8	0.34	0
8	PGE	A	219	-	9,9,9	0.33	0	8,8,8	0.38	0
9	P6G	A	220	-	18,18,18	0.86	0	17,17,17	0.36	0
2	2VY	B	201	-	18,18,18	3.52	5 (27%)	25,25,25	2.72	11 (44%)
3	PG0	B	202	-	7,7,7	0.25	0	6,6,6	0.67	0
4	PG4	B	203	-	12,12,12	0.72	0	11,11,11	0.33	0
4	PG4	B	204	-	12,12,12	0.77	0	11,11,11	0.34	0
4	PG4	B	205	-	12,12,12	0.72	0	11,11,11	0.42	0
4	PG4	B	206	-	12,12,12	0.78	0	11,11,11	0.50	0
5	BNG	B	207	-	21,21,21	1.09	1 (4%)	26,26,26	0.90	0
5	BNG	B	208	-	21,21,21	1.02	1 (4%)	26,26,26	1.12	2 (7%)
5	BNG	B	209	-	21,21,21	1.16	2 (9%)	26,26,26	1.44	3 (11%)
6	PEG	B	210	-	6,6,6	0.59	0	5,5,5	0.48	0
6	PEG	B	211	-	6,6,6	0.56	0	5,5,5	0.42	0
6	PEG	B	212	-	6,6,6	0.56	0	5,5,5	0.29	0
6	PEG	B	213	-	6,6,6	0.56	0	5,5,5	0.31	0
6	PEG	B	214	-	6,6,6	0.57	0	5,5,5	0.22	0
7	1PE	B	215	-	15,15,15	0.78	0	14,14,14	0.38	0
7	1PE	B	216	-	15,15,15	0.78	0	14,14,14	0.35	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	2VY	A	201	-	-	0/4/6/6	0/2/2/2
3	PG0	A	202	-	-	0/5/5/5	0/0/0/0
4	PG4	A	203	-	-	0/10/10/10	0/0/0/0
4	PG4	A	204	-	-	0/10/10/10	0/0/0/0
4	PG4	A	205	-	-	0/10/10/10	0/0/0/0
4	PG4	A	206	-	-	0/10/10/10	0/0/0/0
4	PG4	A	207	-	-	0/10/10/10	0/0/0/0
5	BNG	A	208	-	-	0/12/32/32	0/1/1/1
5	BNG	A	209	-	-	0/12/32/32	0/1/1/1
5	BNG	A	210	-	-	0/12/32/32	0/1/1/1
6	PEG	A	211	-	-	0/4/4/4	0/0/0/0
6	PEG	A	212	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	PEG	A	213	-	-	0/4/4/4	0/0/0/0
6	PEG	A	214	-	-	0/4/4/4	0/0/0/0
6	PEG	A	215	-	-	0/4/4/4	0/0/0/0
7	1PE	A	216	-	-	0/13/13/13	0/0/0/0
8	PGE	A	217	-	-	0/7/7/7	0/0/0/0
8	PGE	A	218	-	-	0/7/7/7	0/0/0/0
8	PGE	A	219	-	-	0/7/7/7	0/0/0/0
9	P6G	A	220	-	-	0/16/16/16	0/0/0/0
2	2VY	B	201	-	-	0/4/6/6	0/2/2/2
3	PG0	B	202	-	-	0/5/5/5	0/0/0/0
4	PG4	B	203	-	-	0/10/10/10	0/0/0/0
4	PG4	B	204	-	-	0/10/10/10	0/0/0/0
4	PG4	B	205	-	-	0/10/10/10	0/0/0/0
4	PG4	B	206	-	-	0/10/10/10	0/0/0/0
5	BNG	B	207	-	-	0/12/32/32	0/1/1/1
5	BNG	B	208	-	-	0/12/32/32	0/1/1/1
5	BNG	B	209	-	-	0/12/32/32	0/1/1/1
6	PEG	B	210	-	-	0/4/4/4	0/0/0/0
6	PEG	B	211	-	-	0/4/4/4	0/0/0/0
6	PEG	B	212	-	-	0/4/4/4	0/0/0/0
6	PEG	B	213	-	-	0/4/4/4	0/0/0/0
6	PEG	B	214	-	-	0/4/4/4	0/0/0/0
7	1PE	B	215	-	-	0/13/13/13	0/0/0/0
7	1PE	B	216	-	-	0/13/13/13	0/0/0/0

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	2VY	C2-C3	11.32	1.44	1.37
2	A	201	2VY	C2-C3	10.77	1.43	1.37
2	A	201	2VY	C5-S1	-8.91	1.66	1.73
2	B	201	2VY	O1-C6	5.76	1.40	1.21
2	A	201	2VY	O1-C6	5.41	1.38	1.21
2	B	201	2VY	C5-S1	-4.65	1.69	1.73
2	B	201	2VY	C5-C6	4.30	1.53	1.48
2	A	201	2VY	C5-C6	3.34	1.52	1.48
5	B	209	BNG	O5-C1	3.12	1.49	1.41
2	B	201	2VY	C4A-N4A	3.03	1.41	1.34
5	A	209	BNG	O5-C1	3.01	1.49	1.41
5	A	208	BNG	O5-C1	2.99	1.49	1.41
5	A	210	BNG	O5-C1	2.93	1.49	1.41
2	A	201	2VY	C4A-N4A	2.83	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	208	BNG	O5-C1	2.65	1.48	1.41
5	B	207	BNG	O5-C1	2.59	1.48	1.41
5	B	209	BNG	O1-C1	2.56	1.44	1.40
5	A	210	BNG	O1-C1	2.26	1.44	1.40
2	A	201	2VY	C6A-C5A	2.18	1.42	1.37
5	A	209	BNG	O1-C1	2.11	1.43	1.40
5	A	208	BNG	O5-C5	2.10	1.49	1.44
5	A	209	BNG	O5-C5	2.09	1.49	1.44

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	2VY	O1-C6-C5	-8.61	106.90	125.27
2	B	201	2VY	C5-C4-C3	7.62	115.15	106.69
2	A	201	2VY	C5-C4-C3	6.45	113.84	106.69
2	A	201	2VY	C2-S1-C5	6.18	99.61	91.16
2	B	201	2VY	O1-C6-C5	-5.83	112.83	125.27
2	A	201	2VY	C3-C2-S1	-5.00	106.93	112.26
2	A	201	2VY	C4-C5-S1	-4.40	107.31	110.96
2	B	201	2VY	C5A-C6A-N1A	-3.65	117.29	123.88
5	B	209	BNG	O5-C1-C2	3.65	117.77	110.30
2	B	201	2VY	C6A-N1A-C2A	3.62	122.03	115.68
2	A	201	2VY	C6A-N1A-C2A	3.58	121.97	115.68
2	B	201	2VY	C2-S1-C5	3.55	96.01	91.16
2	A	201	2VY	C5A-C6A-N1A	-3.43	117.70	123.88
5	A	208	BNG	O5-C5-C4	3.06	115.42	109.73
2	B	201	2VY	C4-C5-S1	-2.99	108.48	110.96
5	B	209	BNG	C1-O5-C5	2.92	119.38	113.73
2	B	201	2VY	CM4-C4-C3	-2.88	119.51	124.94
5	B	209	BNG	C1-C2-C3	2.82	115.44	109.99
2	A	201	2VY	CM4-C4-C3	-2.48	120.27	124.94
2	A	201	2VY	C6A-C5A-C4A	2.46	119.15	115.69
2	A	201	2VY	C7A-C5A-C6A	-2.46	118.60	121.82
2	B	201	2VY	CM2-C2A-N1A	2.45	119.93	117.02
5	A	209	BNG	C6-C5-C4	-2.42	107.13	113.04
2	B	201	2VY	C7A-C3-C4	-2.37	121.84	126.85
2	B	201	2VY	N1A-C2A-N3A	-2.15	121.77	125.65
5	B	208	BNG	C1-C2-C3	2.08	114.02	109.99
2	B	201	2VY	C6A-C5A-C4A	2.07	118.61	115.69
5	B	208	BNG	O5-C1-C2	2.05	114.49	110.30
3	A	202	PG0	OTT-C1-C2	-2.04	99.43	112.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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 ⓘ

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	178/192 (92%)	0.36	14 (7%) 13 12	34, 48, 78, 111	0
1	B	176/192 (91%)	0.40	16 (9%) 9 9	35, 52, 83, 140	0
All	All	354/384 (92%)	0.38	30 (8%) 11 10	34, 50, 82, 140	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	182	TYR	8.6
1	B	182	TYR	8.2
1	B	180	SER	5.3
1	B	9	ARG	5.2
1	A	181	ASN	5.1
1	A	131	ILE	4.1
1	A	6	PHE	4.0
1	A	132	PHE	4.0
1	A	180	SER	4.0
1	B	79	SER	3.4
1	A	79	SER	3.3
1	B	181	ASN	3.1
1	A	160	ILE	3.1
1	B	160	ILE	3.1
1	B	132	PHE	3.0
1	B	131	ILE	2.9
1	A	77	SER	2.8
1	B	8	VAL	2.8
1	B	77	SER	2.7
1	B	78	LEU	2.6
1	B	76	LEU	2.5
1	A	144	VAL	2.5
1	A	143	ALA	2.5
1	B	101	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	102	THR	2.3
1	A	164	VAL	2.2
1	B	175	LYS	2.2
1	A	161	ALA	2.1
1	A	37	VAL	2.1
1	B	40	ALA	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 ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	PEG	A	213	7/7	0.70	56.26	71,100,116,123	0
4	PG4	A	205	13/13	0.26	12.07	73,91,102,103	0
4	PG4	A	206	13/13	0.29	10.66	53,93,117,119	0
7	1PE	B	215	16/16	0.34	7.51	62,95,104,105	0
5	BNG	A	210	21/21	0.24	7.19	58,126,137,164	0
6	PEG	A	214	7/7	0.23	5.80	70,89,96,104	0
9	P6G	A	220	19/19	0.25	5.55	63,97,140,142	19
5	BNG	B	207	21/21	0.24	5.02	64,110,154,163	0
6	PEG	B	214	7/7	0.47	4.29	75,90,99,104	0
8	PGE	A	218	10/10	0.26	3.59	76,92,108,114	0
5	BNG	B	209	21/21	0.19	3.38	70,102,126,149	0
8	PGE	A	219	10/10	0.23	3.27	71,93,104,107	0
4	PG4	B	203	13/13	0.22	3.21	88,102,121,128	0
6	PEG	A	211	7/7	0.17	3.08	66,79,93,100	0
10	CL	B	217	1/1	0.26	2.80	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	PEG	A	215	7/7	0.17	2.78	47,54,80,101	0
5	BNG	A	209	21/21	0.36	2.68	60,114,150,169	0
8	PGE	A	217	10/10	0.19	2.64	66,81,87,91	0
5	BNG	A	208	21/21	0.29	2.45	84,117,148,166	0
4	PG4	B	204	13/13	0.25	2.41	60,72,168,171	0
4	PG4	A	207	13/13	0.21	2.34	65,81,107,124	0
7	1PE	B	216	16/16	0.21	1.83	85,104,123,128	0
3	PG0	A	202	8/8	0.24	1.74	32,62,79,81	0
6	PEG	B	211	7/7	0.22	1.65	79,87,102,114	0
4	PG4	B	205	13/13	0.15	1.28	75,97,110,119	0
4	PG4	B	206	13/13	0.18	0.73	68,81,115,120	0
3	PG0	B	202	8/8	0.17	0.71	53,59,76,80	0
4	PG4	A	204	13/13	0.20	0.62	69,97,117,117	0
6	PEG	B	210	7/7	0.22	0.60	65,80,89,98	0
7	1PE	A	216	16/16	0.17	0.57	59,71,82,95	0
5	BNG	B	208	21/21	0.20	0.55	53,65,118,128	0
6	PEG	B	213	7/7	0.20	0.34	80,90,94,98	0
6	PEG	A	212	7/7	0.19	0.31	69,81,96,98	0
4	PG4	A	203	13/13	0.15	-0.12	71,86,98,107	0
6	PEG	B	212	7/7	0.13	-0.18	69,74,89,91	0
2	2VY	B	201	17/17	0.12	-0.28	32,39,57,61	0
2	2VY	A	201	17/17	0.10	-0.75	34,40,49,51	0

6.5 Other polymers ⓘ

There are no such residues in this entry.