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wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 25, 2024 – 02:33 AM EST

PDB ID	:	5D09
Title	:	Neisseria meningitidis 3 deoxy-D-arabino-heptulosonate 7-phosphate synthase Phe211Ala variant
Authors	:	Heyes, L.C.; Parker, E.J.
Deposited on	:	2015-08-02
Resolution	:	2.35 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 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:

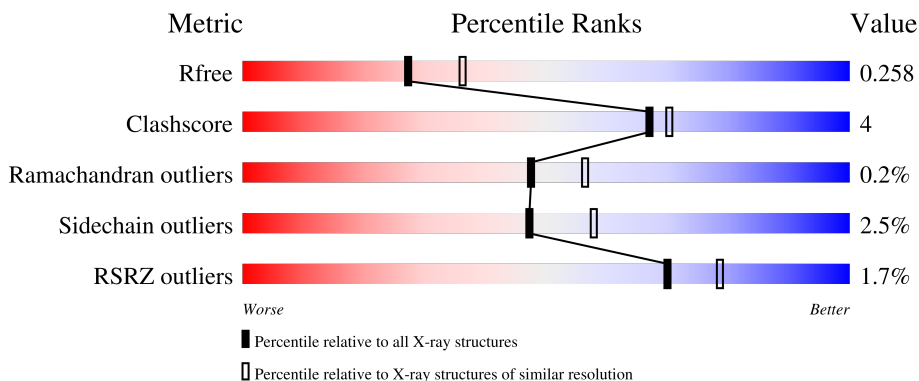|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.35 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	Percentile Ranks	Value
Rfree		0.258
Clashscore		4
Ramachandran outliers		0.2%
Sidechain outliers		2.5%
RSRZ outliers		1.7%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 <=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	351	3% 84% 10% · 5%
1	B	351	.% 87% 8% 5%
1	C	351	.% 88% 6% 5%
1	D	351	2% 85% 8% · 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
6	EDO	C	403	-	-	X	-

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 10453 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 Phospho-2-dehydro-3-deoxyheptonate aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	3	0
			2546	1585	461	486	14			
1	B	334	Total	C	N	O	S	0	1	0
			2518	1572	455	477	14			
1	C	333	Total	C	N	O	S	0	0	0
			2518	1572	456	476	14			
1	D	329	Total	C	N	O	S	0	2	0
			2497	1561	449	473	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	211	ALA	PHE	engineered mutation	UNP Q9K169
B	211	ALA	PHE	engineered mutation	UNP Q9K169
C	211	ALA	PHE	engineered mutation	UNP Q9K169
D	211	ALA	PHE	engineered mutation	UNP Q9K169

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		

- Molecule 3 is PHOSPHOENOLPYRUVATE (three-letter code: PEP) (formula: $C_3H_5O_6P$).

PEP
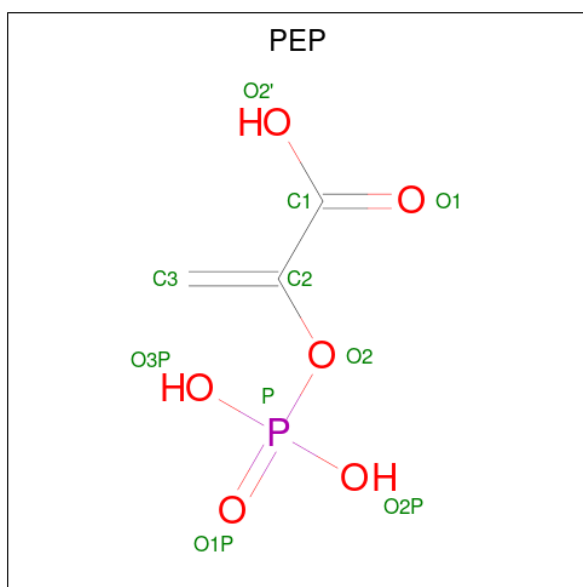
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
3	A	1	10	3	6	1	0	0

- Molecule 4 is trimethylamine oxide (three-letter code: TMO) (formula: C_3H_9NO).

TMO
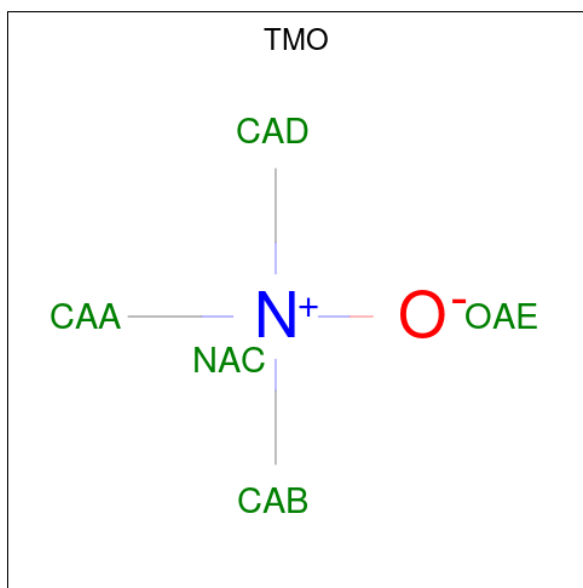
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	5	3	1	1	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).

PEG

C4

OH O4

O2

O

C3

C1

HO

O1

C2

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

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

EDO

O2

OH

C1

C2

HO

O1

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

• Molecule 7 is water.

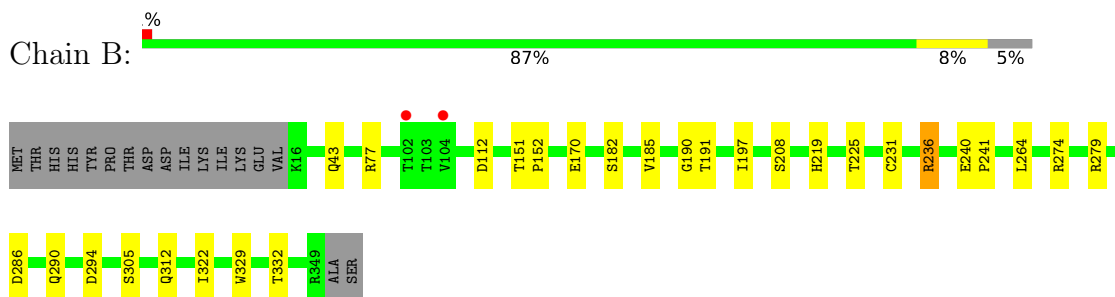| Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	92	Total O 92 92	0	0
7	B	84	Total O 84 84	0	0
7	C	93	Total O 93 93	0	0
7	D	64	Total O 64 64	0	0

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.
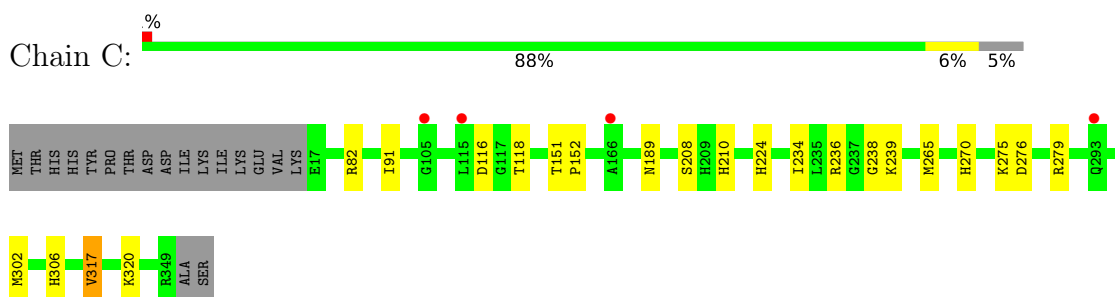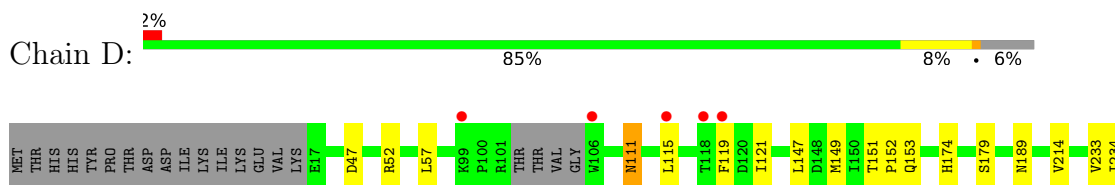
- Molecule 1: Phospho-2-dehydro-3-deoxyheptonate aldolase
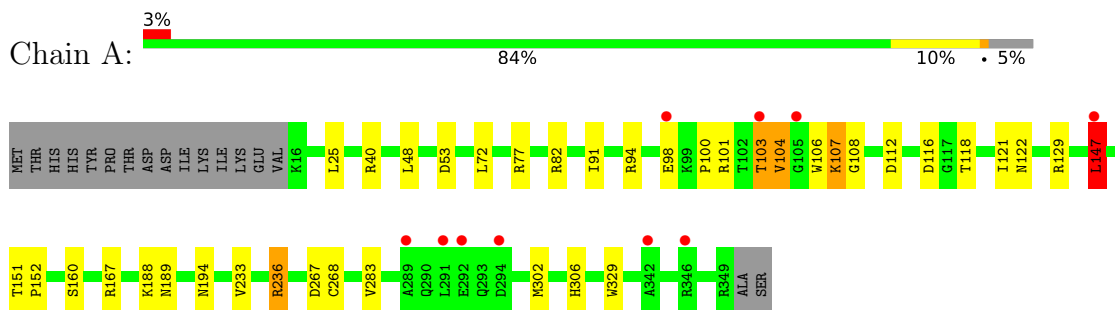
Chain A:

- Molecule 1: Phospho-2-dehydro-3-deoxyheptonate aldolase
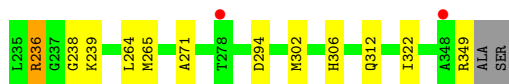
Chain B:

- Molecule 1: Phospho-2-dehydro-3-deoxyheptonate aldolase

Chain C:

- Molecule 1: Phospho-2-dehydro-3-deoxyheptonate aldolase

Chain D:

L235 R236 G237 G238 K239 L264 M265 A271 T278 D294 M302 H306 Q312 I322 A348 R349 ALA SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	78.67Å 135.73Å 149.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.45 – 2.35 48.59 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.3 (100.45-2.35) 99.4 (48.59-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.51 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.210 , 0.259 0.216 , 0.258	Depositor DCC
R_{free} test set	4109 reflections (6.14%)	wwPDB-VP
Wilson B-factor (Å^2)	42.1	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 28.9	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	10453	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: PEG, PEP, TMO, MN, EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$ >5	RMSZ	#$|Z|$ >5
1	A	0.61	0/2592	0.76	2/3514 (0.1%)
1	B	0.62	0/2565	0.75	1/3480 (0.0%)
1	C	0.58	0/2565	0.71	0/3476
1	D	0.57	0/2544	0.72	0/3451
All	All	0.59	0/10266	0.73	3/13921 (0.0%)

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	2
1	D	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	104	VAL	N-CA-C	6.37	128.21	111.00
1	B	112	ASP	CB-CG-OD1	5.57	123.31	118.30
1	A	94	ARG	NE-CZ-NH1	5.08	122.84	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	103	THR	Peptide

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Mol	Chain	Res	Type	Group
1	A	147	LEU	Peptide
1	D	147	LEU	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	2546	0	2480	25	0
1	B	2518	0	2446	22	0
1	C	2518	0	2470	16	0
1	D	2497	0	2420	16	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	10	0	2	0	0
4	A	5	0	9	0	0
5	B	7	0	10	0	0
5	C	7	0	10	0	0
6	B	4	0	6	0	0
6	C	4	0	6	4	0
7	A	92	0	0	3	0
7	B	84	0	0	3	0
7	C	93	0	0	0	0
7	D	64	0	0	0	0
All	All	10453	0	9859	77	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 4.

The worst 5 of 77 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:112:ASP:OD1	1:A:118:THR:O	1.77	1.03
1:B:274:ARG:HH21	1:B:274:ARG:HG3	1.32	0.92
1:A:40[B]:ARG:HG3	1:A:40[B]:ARG:HH21	1.41	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:238:GLY:HA3	1:D:239:LYS:CB	2.11	0.80
1:B:274:ARG:HD2	1:B:279:ARG:NH2	1.96	0.79

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	335/351 (95%)	324 (97%)	10 (3%)	1 (0%)	41	47
1	B	333/351 (95%)	322 (97%)	10 (3%)	1 (0%)	41	47
1	C	331/351 (94%)	317 (96%)	14 (4%)	0	100	100
1	D	327/351 (93%)	313 (96%)	13 (4%)	1 (0%)	41	47
All	All	1326/1404 (94%)	1276 (96%)	47 (4%)	3 (0%)	47	56

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	VAL
1	B	294	ASP
1	D	294	ASP

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	262/288 (91%)	254 (97%)	8 (3%)	40	48
1	B	257/288 (89%)	254 (99%)	3 (1%)	71	82
1	C	260/288 (90%)	254 (98%)	6 (2%)	50	61
1	D	256/288 (89%)	247 (96%)	9 (4%)	36	44
All	All	1035/1152 (90%)	1009 (98%)	26 (2%)	47	58

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	236	ARG
1	D	111	ASN
1	D	306	HIS
1	C	317	VAL
1	D	115	LEU

Sometimes 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 molecules 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 monosaccharides in this entry.

5.6   Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	#$|Z| > 2$
5	PEG	C	402	-	6,6,6	0.76	0	5,5,5	0.85	0
6	EDO	C	403	-	3,3,3	0.65	0	2,2,2	0.55	0
4	TMO	A	403	-	4,4,4	6.30	1 (25%)	6,6,6	0.17	0
6	EDO	B	403	-	3,3,3	0.87	0	2,2,2	0.42	0
5	PEG	B	402	-	6,6,6	0.72	0	5,5,5	0.42	0
3	PEP	A	402	-	9,9,9	1.56	2 (22%)	11,13,13	1.67	3 (27%)

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
5	PEG	C	402	-	-	2/4/4/4	-
6	EDO	C	403	-	-	1/1/1/1	-
6	EDO	B	403	-	-	1/1/1/1	-
5	PEG	B	402	-	-	3/4/4/4	-
3	PEP	A	402	-	-	4/9/9/9	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	403	TMO	OAE-NAC	-12.60	1.25	1.42
3	A	402	PEP	O2-C2	2.92	1.47	1.39
3	A	402	PEP	P-O2	2.04	1.62	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	402	PEP	O2'-C1-C2	3.29	119.53	113.91
3	A	402	PEP	O2P-P-O2	-2.18	98.62	105.25
3	A	402	PEP	O2'-C1-O1	-2.10	118.80	123.61

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	PEP	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
3	A	402	PEP	O1-C1-C2-O2
3	A	402	PEP	O2'-C1-C2-C3
3	A	402	PEP	O2'-C1-C2-O2
5	B	402	PEG	O2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	403	EDO	4	0

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(Å²)	Q<0.9
1	A	334/351 (95%)	-0.07	10 (2%)	50	61	28, 40, 60, 100	0
1	B	334/351 (95%)	-0.24	2 (0%)	89	93	27, 40, 63, 107	0
1	C	333/351 (94%)	-0.03	4 (1%)	79	86	29, 43, 64, 100	0
1	D	329/351 (93%)	-0.06	7 (2%)	63	74	30, 48, 69, 97	0
All	All	1330/1404 (94%)	-0.10	23 (1%)	70	78	27, 42, 66, 107	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	105	GLY	4.7
1	A	289	ALA	3.2
1	C	115	LEU	3.0
1	D	106	TRP	3.0
1	C	166	ALA	2.8

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 monosaccharides in this entry.

6.4   Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PEG	B	402	7/7	0.53	0.30	65,74,79,79	0
5	PEG	C	402	7/7	0.63	0.31	59,64,68,71	0
6	EDO	C	403	4/4	0.78	0.25	52,57,58,58	0
4	TMO	A	403	5/5	0.82	0.22	80,81,86,89	0
6	EDO	B	403	4/4	0.84	0.33	50,52,55,55	0
3	PEP	A	402	10/10	0.87	0.21	56,61,70,70	0
2	MN	D	401	1/1	0.94	0.10	57,57,57,57	0
2	MN	C	401	1/1	0.99	0.12	41,41,41,41	0
2	MN	A	401	1/1	0.99	0.09	37,37,37,37	0
2	MN	B	401	1/1	1.00	0.07	38,38,38,38	0

6.5   Other polymers ⓘ

There are no such residues in this entry.