



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:27 AM UTC

PDB ID : 5VNX / pdb_00005vnx
Title : Crystal structure of an 8-amino-7-oxononanoate synthase from Burkholderia multivorans with a potential glycine-PLP-Lys242 cyclized intermediate or byproduct
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2017-05-01
Resolution : 1.65 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

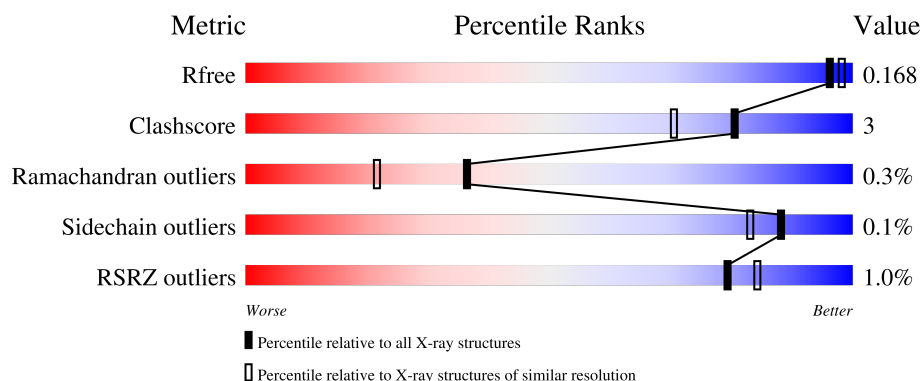
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	393	95% 5%
1	B	393	93% 6%
1	C	393	94% 5%

2 Entry composition [i](#)

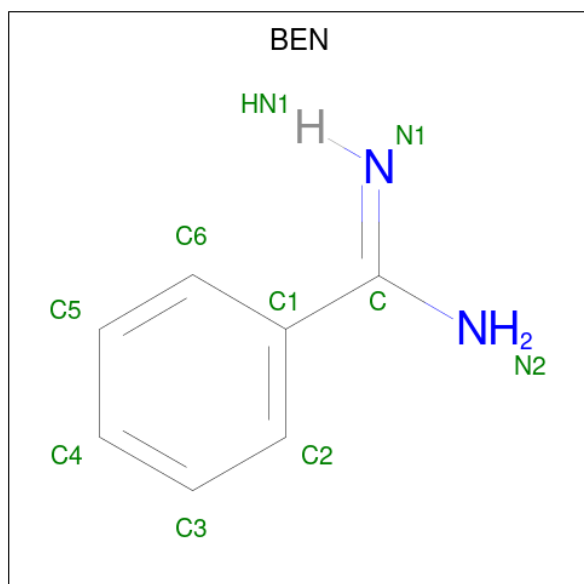
There are 5 unique types of molecules in this entry. The entry contains 10651 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 8-amino-7-oxononanoate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	P	S	0	22	0
			3009	1894	540	566	1	8			
1	B	392	Total	C	N	O	P	S	0	25	0
			3041	1911	550	572	1	7			
1	C	392	Total	C	N	O	P	S	0	28	0
			3064	1923	556	577	1	7			

- Molecule 2 is BENZAMIDINE (CCD ID: BEN) (formula: C₇H₈N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			9	7	2		
2	A	1	Total	C	N	0	0
			9	7	2		
2	B	1	Total	C	N	0	0
			9	7	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	N	0	0
			9	7	2		
2	C	1	Total	C	N	0	0
			9	7	2		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

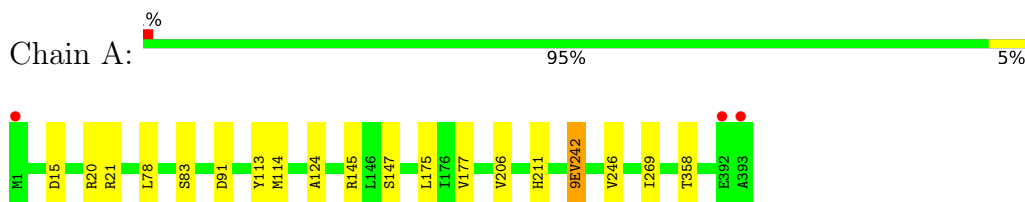
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	485	Total	O	0	18
			501	501		
5	B	494	Total	O	0	15
			505	505		
5	C	434	Total	O	0	9
			439	439		

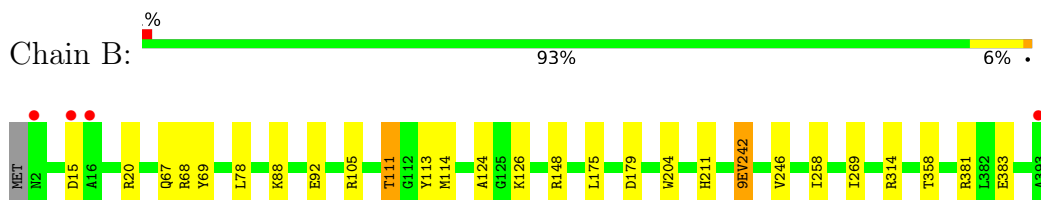
3 Residue-property plots

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.

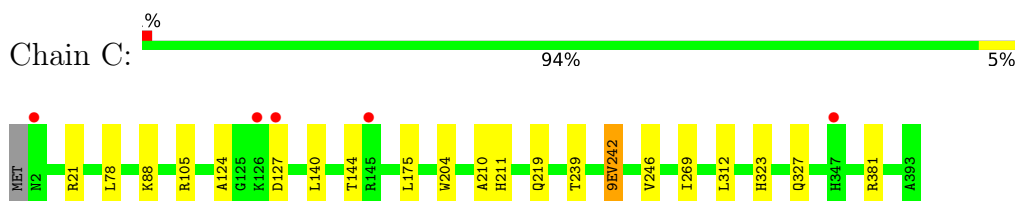
- Molecule 1: 8-amino-7-oxononanoate synthase



- Molecule 1: 8-amino-7-oxononanoate synthase



- Molecule 1: 8-amino-7-oxononanoate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	177.53Å 262.09Å 65.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.38 – 1.65 44.38 – 1.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.38-1.65) 100.0 (44.38-1.65)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.46 (at 1.65Å)	Xtriage
Refinement program	PHENIX dev_2733	Depositor
R, R_{free}	0.146 , 0.167 0.147 , 0.168	Depositor DCC
R_{free} test set	2011 reflections (1.10%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.274	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10651	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 9EV, BEN, EDO, SO4

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	0.51	0/3084	0.67	2/4202 (0.0%)
1	B	0.49	0/3110	0.65	1/4235 (0.0%)
1	C	0.44	0/3126	0.61	0/4257
All	All	0.48	0/9320	0.65	3/12694 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	147	SER	CA-C-N	-5.46	111.38	122.31
1	A	147	SER	C-N-CA	-5.46	111.38	122.31
1	B	179	ASP	CA-CB-CG	5.00	117.60	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3009	0	2978	15	0
1	B	3041	0	3005	19	0
1	C	3064	0	3032	14	0
2	A	18	0	14	2	0
2	B	18	0	14	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	9	0	7	1	0
3	A	12	0	18	0	0
3	B	8	0	12	1	0
3	C	12	0	18	0	0
4	A	5	0	0	0	0
4	C	10	0	0	0	0
5	A	501	0	0	3	0
5	B	505	0	0	7	0
5	C	439	0	0	6	1
All	All	10651	0	9098	47	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 47 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:175[B]:LEU:HD21	1:A:177[B]:VAL:HG13	1.64	0.80
1:B:314[B]:ARG:NH1	1:B:383:GLU:OE2	2.21	0.74
1:C:127[A]:ASP:OD2	5:C:701:HOH:O	2.10	0.69
1:B:15:ASP:OD2	5:B:701[A]:HOH:O	2.13	0.66
1:B:78[A]:LEU:HD22	1:B:269:ILE:HG12	1.76	0.66

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:986:HOH:O	5:C:1003:HOH:O[4_556]	2.07	0.13

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	412/393 (105%)	404 (98%)	7 (2%)	1 (0%)	43	27
1	B	414/393 (105%)	401 (97%)	12 (3%)	1 (0%)	43	27
1	C	417/393 (106%)	409 (98%)	7 (2%)	1 (0%)	43	27
All	All	1243/1179 (105%)	1214 (98%)	26 (2%)	3 (0%)	36	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	246	VAL
1	B	246	VAL
1	C	246	VAL

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	295/283 (104%)	295 (100%)	0	100	100
1	B	298/283 (105%)	296 (99%)	2 (1%)	76	64
1	C	302/283 (107%)	302 (100%)	0	100	100
All	All	895/849 (105%)	893 (100%)	2 (0%)	88	83

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	111[A]	THR
1	B	111[B]	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	B	47	ASN
1	C	47	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	9EV	B	242	1	26,29,30	1.83	4 (15%)	28,41,43	3.85	8 (28%)
1	9EV	C	242	1	26,29,30	1.69	5 (19%)	28,41,43	3.51	8 (28%)
1	9EV	A	242	1	26,29,30	1.73	2 (7%)	28,41,43	4.03	6 (21%)

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	9EV	B	242	1	-	4/18/31/33	0/2/2/2
1	9EV	C	242	1	-	5/18/31/33	0/2/2/2
1	9EV	A	242	1	-	3/18/31/33	0/2/2/2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	242	9EV	O14-C15	6.15	1.46	1.35
1	A	242	9EV	O14-C15	5.60	1.45	1.35
1	C	242	9EV	O14-C15	5.03	1.44	1.35
1	B	242	9EV	C01-C02	3.62	1.56	1.50
1	A	242	9EV	C01-C02	3.60	1.56	1.50

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	242	9EV	O14-C13-N18	13.12	112.24	103.26
1	A	242	9EV	O14-C13-N18	12.21	111.62	103.26
1	A	242	9EV	C13-O14-C15	-11.98	101.03	111.88
1	B	242	9EV	C13-O14-C15	-11.75	101.23	111.88
1	C	242	9EV	C13-O14-C15	-11.38	101.57	111.88

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	242	9EV	O-C-CA-C22
1	B	242	9EV	C12-C05-C06-O07
1	B	242	9EV	O-C-CA-C22
1	C	242	9EV	O-C-CA-C22
1	A	242	9EV	N18-C19-C20-C21

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	242	9EV	1	0
1	C	242	9EV	1	0
1	A	242	9EV	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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
2	BEN	B	601	-	9,9,9	1.28	1 (11%)	7,11,11	1.28	1 (14%)
2	BEN	A	601	-	9,9,9	1.25	1 (11%)	7,11,11	0.74	0
3	EDO	C	606	-	3,3,3	0.37	0	2,2,2	0.40	0
4	SO4	A	605	-	4,4,4	0.23	0	6,6,6	0.14	0
4	SO4	C	602	-	4,4,4	0.23	0	6,6,6	0.16	0
3	EDO	A	604	-	3,3,3	0.46	0	2,2,2	0.58	0
3	EDO	C	605	-	3,3,3	0.38	0	2,2,2	0.49	0
3	EDO	B	604	-	3,3,3	0.50	0	2,2,2	0.17	0
4	SO4	C	603	-	4,4,4	0.24	0	6,6,6	0.05	0
2	BEN	C	601	-	9,9,9	1.21	1 (11%)	7,11,11	1.25	1 (14%)
3	EDO	C	604	-	3,3,3	0.49	0	2,2,2	0.38	0
3	EDO	B	603	-	3,3,3	0.41	0	2,2,2	0.31	0
2	BEN	B	602	-	9,9,9	1.40	1 (11%)	7,11,11	1.04	1 (14%)
3	EDO	A	606	-	3,3,3	0.46	0	2,2,2	0.46	0
3	EDO	A	603	-	3,3,3	0.39	0	2,2,2	0.21	0
2	BEN	A	602	-	9,9,9	1.30	1 (11%)	7,11,11	1.35	1 (14%)

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	BEN	B	601	-	-	1/4/4/4	0/1/1/1
2	BEN	A	601	-	-	0/4/4/4	0/1/1/1
3	EDO	C	606	-	-	0/1/1/1	-
3	EDO	A	604	-	-	0/1/1/1	-
3	EDO	C	605	-	-	1/1/1/1	-
3	EDO	B	604	-	-	1/1/1/1	-
2	BEN	C	601	-	-	1/4/4/4	0/1/1/1
3	EDO	C	604	-	-	1/1/1/1	-
3	EDO	B	603	-	-	0/1/1/1	-
2	BEN	B	602	-	-	4/4/4/4	0/1/1/1
3	EDO	A	606	-	-	1/1/1/1	-
3	EDO	A	603	-	-	0/1/1/1	-
2	BEN	A	602	-	-	4/4/4/4	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	602	BEN	C1-C	-3.71	1.40	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	602	BEN	C1-C	-3.51	1.40	1.47
2	A	601	BEN	C1-C	-3.19	1.41	1.47
2	B	601	BEN	C1-C	-3.14	1.41	1.47
2	C	601	BEN	C1-C	-2.94	1.41	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	BEN	C1-C-N2	2.53	121.85	118.01
2	A	602	BEN	C1-C-N2	2.47	121.76	118.01
2	B	601	BEN	C1-C-N2	2.41	121.67	118.01
2	B	602	BEN	C1-C-N2	2.33	121.55	118.01

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	604	EDO	O1-C1-C2-O2
3	C	604	EDO	O1-C1-C2-O2
3	A	606	EDO	O1-C1-C2-O2
2	A	602	BEN	N2-C-C1-C2
2	A	602	BEN	N2-C-C1-C6

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	BEN	2	0
2	A	601	BEN	2	0
3	B	604	EDO	1	0
2	C	601	BEN	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 [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	392/393 (99%)	-0.53	3 (0%) 82 87	8, 17, 33, 73	22 (5%)
1	B	391/393 (99%)	-0.42	4 (1%) 79 84	8, 18, 34, 61	25 (6%)
1	C	391/393 (99%)	-0.31	5 (1%) 75 80	8, 20, 36, 63	28 (7%)
All	All	1174/1179 (99%)	-0.42	12 (1%) 79 84	8, 18, 35, 73	75 (6%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	4.5
1	C	127[A]	ASP	3.5
1	C	145[A]	ARG	2.9
1	B	15	ASP	2.8
1	A	393	ALA	2.6

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	9EV	B	242	28/29	0.96	0.09	14,19,26,28	0
1	9EV	C	242	28/29	0.96	0.10	13,22,31,32	0
1	9EV	A	242	28/29	0.97	0.09	12,18,24,27	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	A	605	5/5	0.68	0.21	102,105,107,114	0
4	SO4	C	602	5/5	0.75	0.18	113,113,115,116	0
4	SO4	C	603	5/5	0.75	0.15	106,106,108,110	0
3	EDO	C	605	4/4	0.79	0.17	54,55,55,58	0
3	EDO	A	606	4/4	0.79	0.19	47,51,52,55	0
2	BEN	A	602	9/9	0.81	0.13	34,40,54,59	0
3	EDO	C	604	4/4	0.81	0.17	35,48,49,56	0
2	BEN	B	602	9/9	0.84	0.15	33,44,51,57	0
3	EDO	B	603	4/4	0.85	0.20	49,54,56,59	0
3	EDO	A	604	4/4	0.87	0.16	40,47,48,57	0
3	EDO	C	606	4/4	0.89	0.16	45,54,57,59	0
3	EDO	A	603	4/4	0.90	0.13	33,37,40,43	0
3	EDO	B	604	4/4	0.93	0.11	31,34,38,43	0
2	BEN	C	601	9/9	0.97	0.05	18,19,22,22	0
2	BEN	B	601	9/9	0.97	0.06	17,22,25,26	0
2	BEN	A	601	9/9	0.97	0.05	14,16,19,19	0

6.5 Other polymers

There are no such residues in this entry.