



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 08:46 AM UTC

PDB ID : 2FEF / pdb_00002fef
Title : The Crystal Structure of Protein PA2201 from Pseudomonas aeruginosa
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Midwest Center for Structural Genomics (MCSG)
Deposited on : 2005-12-15
Resolution : 1.90 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 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)
Xtrriage (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

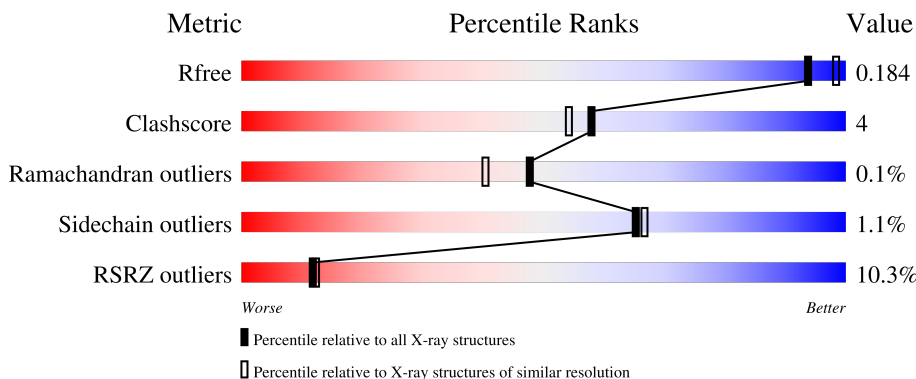
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	294	 16% 88% 7% . .
1	B	294	 5% 90% 6% .
1	C	294	 9% 88% 7% .

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
2	EDO	C	603	-	X	X	-

2 Entry composition [i](#)

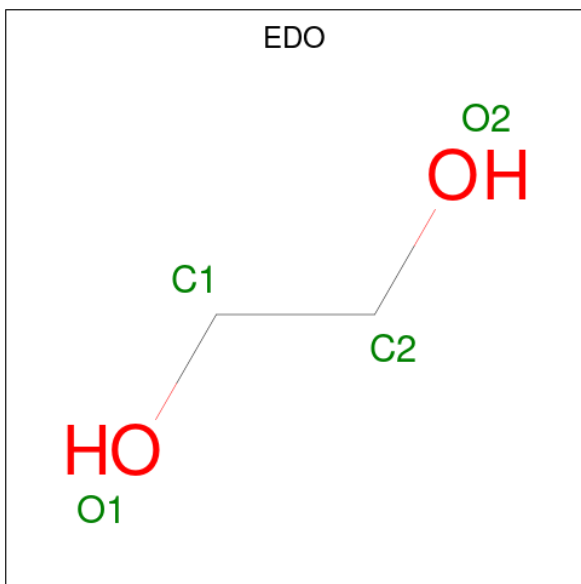
There are 3 unique types of molecules in this entry. The entry contains 7187 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 hypothetical protein PA2201.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	282	Total 2217	C 1424	N 394	O 397	Se 2	0	4	1
1	B	284	Total 2255	C 1444	N 405	O 404	Se 2	0	5	0
1	C	281	Total 2223	C 1427	N 396	O 398	Se 2	0	5	1

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



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

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

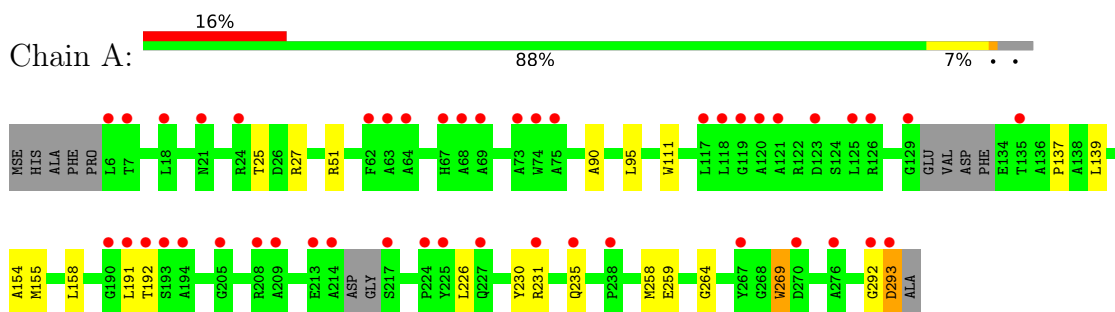
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	142	Total	O	0	0
			142	142		
3	B	162	Total	O	0	0
			162	162		
3	C	172	Total	O	0	0
			172	172		

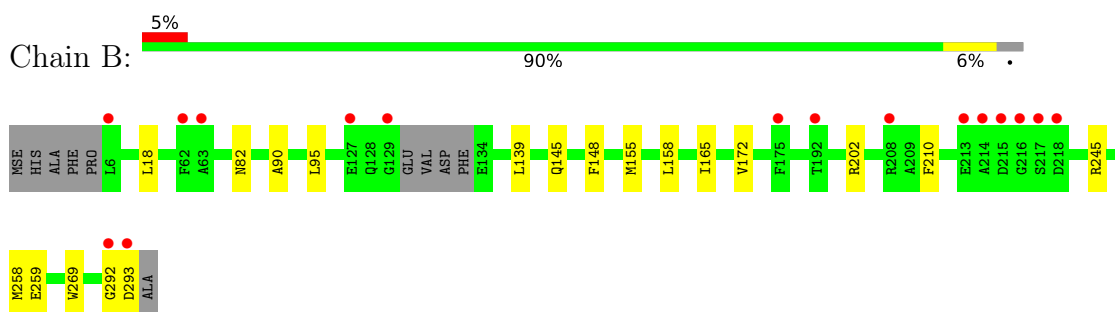
3 Residue-property plots [i](#)

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.

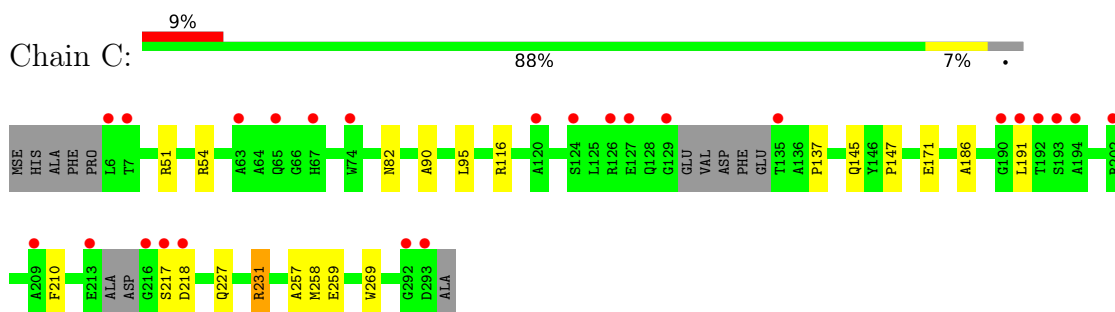
- Molecule 1: hypothetical protein PA2201



- Molecule 1: hypothetical protein PA2201



- Molecule 1: hypothetical protein PA2201



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	118.59Å 118.59Å 144.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.83 – 1.90 45.83 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (45.83-1.90) 98.8 (45.83-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.70 (at 1.89Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.186 , 0.222 0.188 , 0.184	Depositor DCC
R_{free} test set	4070 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtrriage
Anisotropy	0.138	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7187	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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: 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	0.80	0/2283	0.91	0/3101
1	B	0.85	1/2322 (0.0%)	0.87	0/3155
1	C	0.89	1/2293 (0.0%)	0.89	1/3116 (0.0%)
All	All	0.85	2/6898 (0.0%)	0.89	1/9372 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	ILE	CA-CB	6.17	1.58	1.53
1	C	257	ALA	CA-CB	5.09	1.59	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	258	MSE	CG-SE-CE	-5.85	86.06	98.92

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	2217	0	2141	18	0
1	B	2255	0	2195	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2223	0	2158	22	0
2	B	8	0	12	0	0
2	C	8	0	12	4	0
3	A	142	0	0	3	0
3	B	162	0	0	0	0
3	C	172	0	0	4	0
All	All	7187	0	6518	59	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.

All (59) 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:C:147:PRO:HB2	2:C:603:EDO:H12	1.22	1.16
1:A:155:MSE:HE1	1:A:158:LEU:HD12	1.41	1.02
1:A:155:MSE:CE	1:A:158:LEU:HD12	1.92	0.98
1:A:51[B]:ARG:HH12	1:C:82:ASN:HD21	1.24	0.84
1:A:155:MSE:HE1	1:A:158:LEU:CD1	2.08	0.84
1:C:147:PRO:HB2	2:C:603:EDO:C1	2.10	0.76
1:B:155:MSE:HE3	1:B:258:MSE:SE	2.40	0.72
1:C:147:PRO:CB	2:C:603:EDO:H12	2.12	0.72
1:B:82:ASN:HD21	1:C:51[B]:ARG:HH12	1.37	0.70
1:A:292:GLY:O	1:A:293:ASP:HB2	1.91	0.69
1:C:210:PHE:CE1	1:C:269[A]:TRP:CH2	2.81	0.69
1:C:210:PHE:HE1	1:C:269[A]:TRP:CZ3	2.11	0.69
1:A:155:MSE:HE2	1:A:158:LEU:HD12	1.75	0.67
1:B:245:ARG:HH11	1:B:245:ARG:HG2	1.60	0.67
1:B:155:MSE:CE	1:B:158:LEU:HD12	2.27	0.65
1:A:231:ARG:O	1:A:235:GLN:HG3	1.98	0.64
1:B:155:MSE:HE3	1:B:258:MSE:CG	2.27	0.64
1:A:137:PRO:HG3	3:A:304:HOH:O	2.00	0.62
1:C:116:ARG:NH2	1:C:171:GLU:OE1	2.22	0.62
1:C:210:PHE:CE1	1:C:269[A]:TRP:CZ3	2.88	0.61
1:A:137:PRO:CG	3:A:304:HOH:O	2.48	0.61
1:B:155:MSE:HE1	1:B:158:LEU:HD12	1.81	0.60
1:C:137:PRO:HG3	3:C:610:HOH:O	2.01	0.60
1:A:90:ALA:HB1	1:A:95:LEU:HD12	1.86	0.57
1:B:202:ARG:HG2	1:B:245:ARG:HG3	1.87	0.57
1:C:210:PHE:CE1	1:C:269[A]:TRP:HH2	2.27	0.53
1:B:18:LEU:HD12	1:B:18:LEU:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:90:ALA:HB1	1:C:95:LEU:HD12	1.90	0.52
1:A:264:GLY:HA2	1:A:269:TRP:CZ3	2.48	0.49
1:C:186:ALA:HA	1:C:191:LEU:HB2	1.95	0.49
1:C:116:ARG:NE	1:C:171:GLU:OE2	2.42	0.48
1:B:145[B]:GLN:HE22	1:C:54:ARG:HH22	1.62	0.48
1:A:226:LEU:O	1:A:230:TYR:HB2	2.14	0.48
1:C:210:PHE:HE1	1:C:269[A]:TRP:CH2	2.27	0.48
1:B:155:MSE:HE3	1:B:258:MSE:HB3	1.95	0.47
1:C:210:PHE:CZ	1:C:269[A]:TRP:HH2	2.33	0.47
1:B:155:MSE:HE1	1:B:158:LEU:CD1	2.46	0.46
1:B:90:ALA:HB1	1:B:95:LEU:HD12	1.96	0.46
1:A:154:ALA:C	1:A:155:MSE:HE2	2.41	0.46
1:C:210:PHE:CZ	1:C:269[A]:TRP:CH2	3.04	0.45
2:C:603:EDO:C2	3:C:729:HOH:O	2.65	0.45
1:A:25:THR:OG1	1:A:27:ARG:HG2	2.17	0.45
1:B:292:GLY:O	1:B:293:ASP:HB2	2.16	0.44
1:A:155:MSE:CE	1:A:258:MSE:HG2	2.48	0.44
1:C:227:GLN:OE1	1:C:231[B]:ARG:HD3	2.18	0.43
1:B:18:LEU:HD12	1:B:18:LEU:H	1.82	0.43
1:B:245:ARG:HG2	1:B:245:ARG:NH1	2.30	0.43
1:A:111:TRP:CZ3	1:A:139:LEU:HD13	2.54	0.43
1:C:218:ASP:HA	3:C:684:HOH:O	2.19	0.43
1:B:155:MSE:CE	1:B:258:MSE:HG2	2.49	0.43
1:B:210:PHE:HE1	1:B:269:TRP:CZ3	2.35	0.43
1:B:139[A]:LEU:HD11	1:B:148:PHE:HB2	2.01	0.42
1:C:217:SER:HB3	1:C:218:ASP:H	1.65	0.42
1:A:111:TRP:CH2	1:A:139:LEU:HD13	2.55	0.42
1:B:155:MSE:HE3	1:B:258:MSE:CB	2.49	0.42
1:B:155:MSE:CE	1:B:258:MSE:HB3	2.50	0.42
1:C:145:GLN:HG2	3:C:761:HOH:O	2.20	0.41
1:A:137:PRO:HG2	3:A:304:HOH:O	2.18	0.40
1:B:139[B]:LEU:HB2	1:B:172:VAL:HG12	2.02	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	280/294 (95%)	271 (97%)	8 (3%)	1 (0%)	30	22
1	B	285/294 (97%)	279 (98%)	6 (2%)	0	100	100
1	C	280/294 (95%)	270 (96%)	10 (4%)	0	100	100
All	All	845/882 (96%)	820 (97%)	24 (3%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	192	THR

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	207/222 (93%)	203 (98%)	4 (2%)	50	47
1	B	213/222 (96%)	212 (100%)	1 (0%)	81	84
1	C	210/222 (95%)	207 (99%)	3 (1%)	59	59
All	All	630/666 (95%)	622 (99%)	8 (1%)	65	61

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	191	LEU
1	A	259	GLU
1	A	269	TRP
1	A	293	ASP
1	B	259	GLU
1	C	231[A]	ARG
1	C	231[B]	ARG
1	C	259	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	235	GLN
1	B	82	ASN
1	C	65	GLN
1	C	82	ASN
1	C	128	GLN
1	C	206	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	EDO	C	603	-	3,3,3	0.18	0	2,2,2	2.36	2 (100%)
2	EDO	C	602	-	3,3,3	0.37	0	2,2,2	0.67	0
2	EDO	B	601	-	3,3,3	0.52	0	2,2,2	0.32	0
2	EDO	B	604	-	3,3,3	0.39	0	2,2,2	0.64	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	EDO	C	603	-	-	1/1/1/1	-
2	EDO	C	602	-	-	1/1/1/1	-
2	EDO	B	601	-	-	0/1/1/1	-
2	EDO	B	604	-	-	1/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	603	EDO	O1-C1-C2	-2.36	94.40	112.39
2	C	603	EDO	O2-C2-C1	-2.35	94.48	112.39

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	602	EDO	O1-C1-C2-O2
2	C	603	EDO	O1-C1-C2-O2
2	B	604	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	603	EDO	4	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	280/294 (95%)	0.98	46 (16%) 4 4	14, 28, 44, 55	4 (1%)
1	B	282/294 (95%)	0.46	16 (5%) 29 31	14, 28, 42, 52	5 (1%)
1	C	279/294 (94%)	0.47	25 (8%) 15 16	13, 27, 44, 53	5 (1%)
All	All	841/882 (95%)	0.64	87 (10%) 12 12	13, 28, 44, 55	14 (1%)

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	129	GLY	7.1
1	C	216	GLY	6.7
1	C	6	LEU	6.2
1	B	293	ASP	5.4
1	A	214	ALA	5.3
1	B	6	LEU	5.1
1	B	214	ALA	5.1
1	A	129	GLY	5.0
1	B	215	ASP	4.4
1	A	193	SER	4.2
1	C	209	ALA	4.2
1	C	193	SER	3.9
1	A	68	ALA	3.8
1	C	293	ASP	3.8
1	A	194	ALA	3.8
1	A	190	GLY	3.7
1	C	191	LEU	3.6
1	A	63	ALA	3.6
1	A	293	ASP	3.5
1	A	235	GLN	3.5
1	C	135	THR	3.4
1	B	216	GLY	3.4
1	A	276	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	126	ARG	3.4
1	A	231	ARG	3.3
1	C	218	ASP	3.3
1	A	7	THR	3.2
1	A	62	PHE	3.2
1	A	135	THR	3.2
1	B	217	SER	3.2
1	C	292	GLY	3.2
1	A	209	ALA	3.1
1	A	67[A]	HIS	3.1
1	C	192	THR	3.1
1	C	67	HIS	3.0
1	A	6	LEU	2.9
1	A	192	THR	2.9
1	C	7	THR	2.9
1	A	217	SER	2.9
1	A	119	GLY	2.8
1	C	63	ALA	2.8
1	A	292	GLY	2.8
1	A	18	LEU	2.8
1	A	191	LEU	2.8
1	B	63	ALA	2.7
1	A	64	ALA	2.7
1	C	202	ARG	2.6
1	B	175	PHE	2.6
1	C	127	GLU	2.6
1	C	190	GLY	2.6
1	B	218	ASP	2.6
1	C	65	GLN	2.6
1	B	62	PHE	2.6
1	C	120	ALA	2.6
1	B	192	THR	2.5
1	B	213	GLU	2.5
1	C	74	TRP	2.5
1	A	21	ASN	2.5
1	A	75	ALA	2.5
1	A	73	ALA	2.4
1	A	224	PRO	2.4
1	C	213	GLU	2.4
1	A	208	ARG	2.4
1	A	227	GLN	2.4
1	A	24	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	208	ARG	2.3
1	C	194	ALA	2.3
1	A	270	ASP	2.3
1	A	213	GLU	2.3
1	A	74	TRP	2.2
1	B	127	GLU	2.2
1	A	125	LEU	2.2
1	A	267	TYR	2.2
1	A	205	GLY	2.2
1	A	121	ALA	2.2
1	C	217	SER	2.1
1	A	120	ALA	2.1
1	A	225	TYR	2.1
1	A	123	ASP	2.1
1	B	129	GLY	2.1
1	A	118	LEU	2.1
1	A	238	PRO	2.1
1	A	69	ALA	2.1
1	C	124	SER	2.0
1	B	292	GLY	2.0
1	A	117	LEU	2.0
1	A	126	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

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

6.3 Carbohydrates [\(i\)](#)

There are no oligosaccharides 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	EDO	C	602	4/4	0.82	0.18	58,59,60,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	B	604	4/4	0.84	0.16	57,57,58,59	0
2	EDO	B	601	4/4	0.93	0.10	32,35,38,45	0
2	EDO	C	603	4/4	0.95	0.17	28,31,32,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.