



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 8DQO / pdb_00008dqo
Title : Crystal structure of Arabidopsis thaliana COSY
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Deposited on : 2022-07-19
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)
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

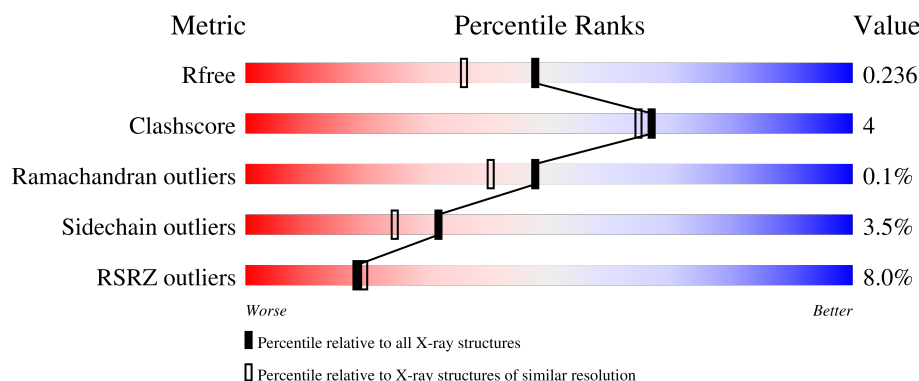
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	451	6% 88% 8% ..
1	B	451	9% 84% 11% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7232 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 Coumarin Synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	436	Total	C	N	O	S	0	2	0
			3421	2181	580	644	16			
1	B	437	Total	C	N	O	S	0	1	0
			3414	2177	578	642	17			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

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



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

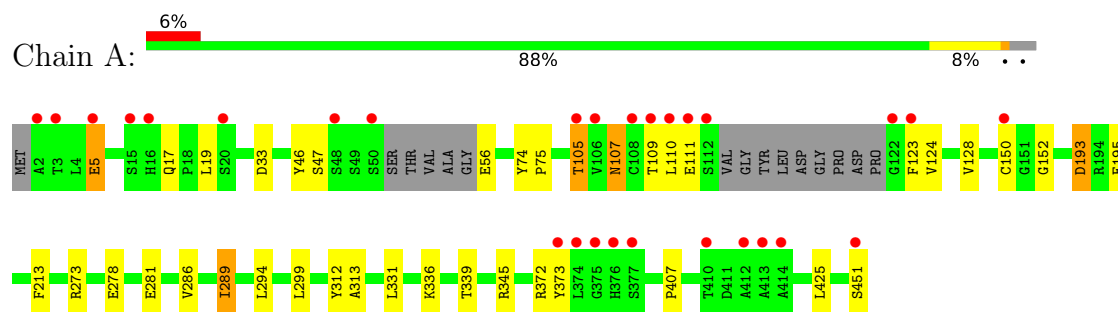
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	228	Total O 228 228	0	0
4	B	123	Total O 123 123	0	0

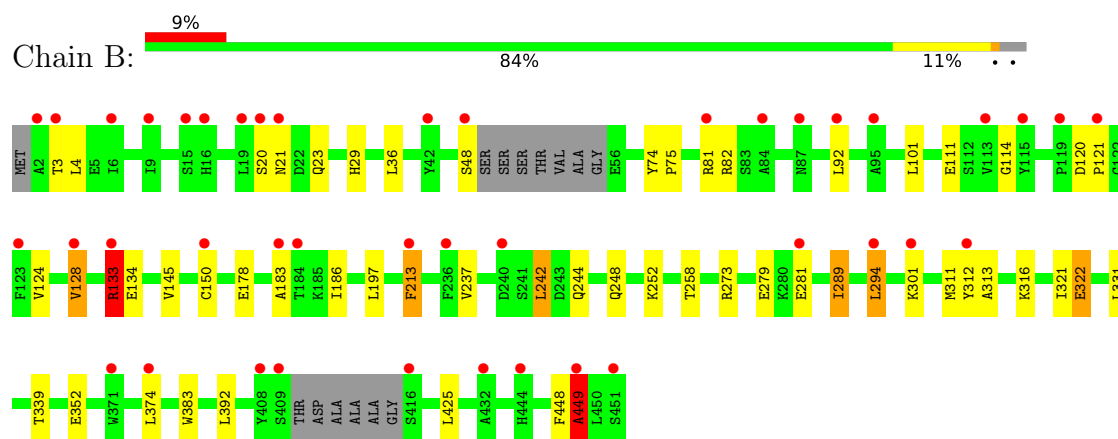
3 Residue-property plots [i](#)

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: Coumarin Synthase



• Molecule 1: Coumarin Synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.41Å 57.90Å 270.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.76 – 1.90 48.76 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.76-1.90) 98.6 (48.76-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.190 , 0.230 0.199 , 0.236	Depositor DCC
R_{free} test set	3653 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	25.2	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7232	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, CA

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	0.88	3/3504 (0.1%)	0.97	6/4750 (0.1%)
1	B	0.83	5/3498 (0.1%)	0.97	3/4747 (0.1%)
All	All	0.85	8/7002 (0.1%)	0.97	9/9497 (0.1%)

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	B	0	3
All	All	0	5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	449	ALA	C-O	12.23	1.39	1.24
1	A	105	THR	C-O	-10.23	1.12	1.23
1	B	322	GLU	CG-CD	8.09	1.72	1.52
1	A	5	GLU	C-O	7.50	1.32	1.24
1	B	316	LYS	C-O	-7.25	1.15	1.23
1	B	279	GLU	CD-OE1	-6.82	1.12	1.25
1	B	183	ALA	C-O	6.36	1.31	1.23
1	A	5	GLU	CD-OE2	-5.18	1.15	1.25

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	213	PHE	CA-CB-CG	8.19	121.99	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	322	GLU	CB-CG-CD	6.91	124.35	112.60
1	A	33	ASP	CA-CB-CG	6.44	119.04	112.60
1	A	193	ASP	CA-CB-CG	-6.12	106.48	112.60
1	A	111	GLU	N-CA-C	-5.81	106.73	113.88
1	B	281	GLU	CB-CA-C	5.43	118.59	109.89
1	A	373	TYR	CB-CA-C	5.37	119.94	111.72
1	A	46	TYR	CA-C-N	5.31	127.66	120.44
1	A	46	TYR	C-N-CA	5.31	127.66	120.44

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	105	THR	Mainchain
1	A	273	ARG	Sidechain
1	B	114	GLY	Peptide
1	B	133	ARG	Sidechain
1	B	273	ARG	Sidechain

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	3421	0	3351	26	0
1	B	3414	0	3332	27	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	36	0	54	2	0
3	B	8	0	12	0	0
4	A	228	0	0	1	0
4	B	123	0	0	0	0
All	All	7232	0	6749	51	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 (51) 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:286:VAL:HG22	1:A:312[B]:TYR:CD1	2.01	0.94
1:B:48:SER:HG	1:B:383:TRP:CD1	1.89	0.89
1:A:286:VAL:CG2	1:A:312[B]:TYR:CD1	2.75	0.67
1:A:345:ARG:HH22	3:A:509:EDO:C2	2.12	0.62
1:B:294:LEU:CD2	1:B:339:THR:HG22	2.31	0.61
1:B:29:HIS:HE1	1:B:352:GLU:OE1	1.83	0.60
1:A:286:VAL:HG21	1:A:312[B]:TYR:CE1	2.37	0.59
1:A:286:VAL:CG2	1:A:312[B]:TYR:CE1	2.87	0.58
1:B:48:SER:OG	1:B:383:TRP:CD1	2.56	0.57
1:A:213[A]:PHE:HB2	1:A:312[A]:TYR:CE1	2.40	0.56
1:B:120:ASP:OD1	1:B:124:VAL:HG23	2.06	0.56
1:B:4:LEU:C	1:B:4:LEU:HD23	2.32	0.54
1:B:425:LEU:C	1:B:425:LEU:HD23	2.34	0.52
1:B:101:LEU:HD11	1:B:145:VAL:HG23	1.91	0.52
1:B:178:GLU:OE1	1:B:186:ILE:HA	2.10	0.52
1:B:81:ARG:NH2	1:B:92:LEU:HD22	2.27	0.50
1:B:321:ILE:HG13	1:B:322:GLU:HG2	1.93	0.50
1:B:128:VAL:CG1	1:B:392:LEU:HD12	2.42	0.49
1:A:345:ARG:HH22	3:A:509:EDO:H21	1.78	0.49
1:A:110:LEU:HD11	1:A:152:GLY:HA3	1.94	0.49
1:B:23:GLN:NE2	1:B:74:TYR:OH	2.45	0.49
1:B:237:VAL:HG12	1:B:242:LEU:CD2	2.43	0.48
1:A:195:GLU:HB3	4:A:607:HOH:O	2.12	0.48
1:B:294:LEU:HD22	1:B:339:THR:HG22	1.95	0.48
1:A:107:ASN:O	1:A:107:ASN:ND2	2.46	0.47
1:A:56:GLU:N	1:A:56:GLU:OE1	2.48	0.47
1:B:448:PHE:O	1:B:449:ALA:C	2.59	0.46
1:A:109:THR:HA	1:A:150:CYS:HB2	1.97	0.46
1:A:17:GLN:HE21	1:A:19:LEU:H	1.63	0.46
1:A:289:ILE:CD1	1:A:339:THR:HG23	2.45	0.46
1:A:425:LEU:C	1:A:425:LEU:HD23	2.40	0.46
1:B:82:ARG:NH2	1:B:133:ARG:HH22	2.14	0.45
1:B:82:ARG:HH21	1:B:133:ARG:HH22	1.65	0.44
1:A:278:GLU:HB2	1:A:281:GLU:HG3	2.00	0.44
1:B:313:ALA:HB1	1:B:331:LEU:HG	2.00	0.44
1:B:29:HIS:CE1	1:B:352:GLU:OE1	2.69	0.43
1:B:289:ILE:HG13	1:B:311:MET:HG2	1.99	0.43
1:A:278:GLU:HB2	1:A:281:GLU:CG	2.49	0.42
1:A:289:ILE:HD11	1:A:339:THR:HG23	2.01	0.41
1:A:372:ARG:HA	1:A:407:PRO:HA	2.01	0.41
1:A:294:LEU:HD22	1:A:339:THR:HG22	2.03	0.41
1:A:313:ALA:HB1	1:A:331:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ILE:HD13	1:A:339:THR:CG2	2.50	0.41
1:A:5:GLU:CD	1:B:258:THR:HA	2.46	0.41
1:B:74:TYR:N	1:B:75:PRO:CD	2.84	0.41
1:B:121:PRO:HD2	1:B:124:VAL:HG23	2.03	0.41
1:B:213:PHE:HB2	1:B:312:TYR:CE1	2.55	0.41
1:A:5:GLU:OE1	1:B:258:THR:HA	2.21	0.41
1:B:244:GLN:HE21	1:B:248:GLN:HE21	1.69	0.41
1:A:74:TYR:N	1:A:75:PRO:CD	2.85	0.40
1:A:107:ASN:HD22	1:A:107:ASN:C	2.29	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	432/451 (96%)	423 (98%)	9 (2%)	0	100	100
1	B	432/451 (96%)	423 (98%)	8 (2%)	1 (0%)	43	36
All	All	864/902 (96%)	846 (98%)	17 (2%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	449	ALA

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	371/380 (98%)	361 (97%)	10 (3%)	39	34
1	B	370/380 (97%)	354 (96%)	16 (4%)	26	18
All	All	741/760 (98%)	715 (96%)	26 (4%)	32	24

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	SER
1	A	107	ASN
1	A	123	PHE
1	A	124	VAL
1	A	128	VAL
1	A	193	ASP
1	A	289	ILE
1	A	299	LEU
1	A	336	LYS
1	A	451	SER
1	B	3	THR
1	B	20	SER
1	B	21	ASN
1	B	36	LEU
1	B	111	GLU
1	B	128	VAL
1	B	133	ARG
1	B	134	GLU
1	B	150	CYS
1	B	197	LEU
1	B	242	LEU
1	B	252	LYS
1	B	289	ILE
1	B	294	LEU
1	B	301	LYS
1	B	374	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	17	GLN

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Mol	Chain	Res	Type
1	A	23	GLN
1	A	107	ASN
1	A	139	ASN
1	A	174	ASN
1	A	225	GLN
1	A	355	HIS
1	B	21	ASN
1	B	23	GLN
1	B	29	HIS
1	B	149	GLN
1	B	244	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](#)

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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	$\# Z > 2$
3	EDO	A	507	-	3,3,3	0.43	0	2,2,2	0.30	0
3	EDO	B	503	-	3,3,3	0.37	0	2,2,2	0.33	0
3	EDO	A	504	-	3,3,3	0.37	0	2,2,2	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	502	-	3,3,3	0.37	0	2,2,2	0.47	0
3	EDO	A	502	-	3,3,3	0.35	0	2,2,2	0.45	0
3	EDO	A	506	-	3,3,3	0.37	0	2,2,2	0.40	0
3	EDO	A	503	-	3,3,3	0.32	0	2,2,2	0.73	0
3	EDO	A	505	-	3,3,3	0.36	0	2,2,2	0.55	0
3	EDO	A	509	-	3,3,3	0.41	0	2,2,2	0.50	0
3	EDO	A	508	-	3,3,3	0.39	0	2,2,2	0.57	0
3	EDO	A	510	-	3,3,3	0.49	0	2,2,2	0.48	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
3	EDO	A	507	-	-	0/1/1/1	-
3	EDO	B	503	-	-	1/1/1/1	-
3	EDO	A	504	-	-	1/1/1/1	-
3	EDO	B	502	-	-	1/1/1/1	-
3	EDO	A	502	-	-	0/1/1/1	-
3	EDO	A	506	-	-	0/1/1/1	-
3	EDO	A	503	-	-	1/1/1/1	-
3	EDO	A	505	-	-	0/1/1/1	-
3	EDO	A	509	-	-	1/1/1/1	-
3	EDO	A	508	-	-	0/1/1/1	-
3	EDO	A	510	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	504	EDO	O1-C1-C2-O2
3	A	503	EDO	O1-C1-C2-O2
3	A	510	EDO	O1-C1-C2-O2
3	B	502	EDO	O1-C1-C2-O2
3	A	509	EDO	O1-C1-C2-O2
3	B	503	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	509	EDO	2	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	436/451 (96%)	0.17	28 (6%) 25 27	9, 24, 49, 76	2 (0%)
1	B	437/451 (96%)	0.80	42 (9%) 13 14	15, 39, 64, 73	1 (0%)
All	All	873/902 (96%)	0.49	70 (8%) 18 19	9, 32, 61, 76	3 (0%)

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	408	TYR	4.2
1	A	376	HIS	4.2
1	B	409	SER	4.1
1	A	374	LEU	4.0
1	A	375	GLY	3.9
1	B	84	ALA	3.8
1	B	150	CYS	3.7
1	B	113	VAL	3.6
1	B	20	SER	3.5
1	A	110	LEU	3.5
1	A	112	SER	3.4
1	B	294	LEU	3.3
1	A	150	CYS	3.3
1	A	122	GLY	3.2
1	A	48	SER	3.1
1	A	2	ALA	3.0
1	A	16	HIS	3.0
1	A	377	SER	3.0
1	B	16	HIS	2.9
1	A	20	SER	2.9
1	B	21	ASN	2.9
1	B	48	SER	2.8
1	A	50	SER	2.8
1	A	413	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	123	PHE	2.8
1	B	184	THR	2.7
1	B	371	TRP	2.7
1	A	373	TYR	2.7
1	B	9	ILE	2.7
1	B	81	ARG	2.7
1	B	2	ALA	2.7
1	B	451	SER	2.7
1	B	133	ARG	2.6
1	A	3	THR	2.6
1	B	236	PHE	2.6
1	B	374	LEU	2.6
1	B	42	TYR	2.6
1	B	115	TYR	2.6
1	B	432	ALA	2.6
1	A	109	THR	2.6
1	B	416	SER	2.6
1	B	449	ALA	2.6
1	B	312	TYR	2.5
1	B	92	LEU	2.4
1	A	414	ALA	2.4
1	B	121	PRO	2.4
1	B	213	PHE	2.4
1	B	6	ILE	2.4
1	B	95	ALA	2.4
1	A	108	CYS	2.3
1	A	105	THR	2.3
1	B	301	LYS	2.3
1	B	15	SER	2.3
1	B	444	HIS	2.3
1	A	5	GLU	2.2
1	A	15	SER	2.2
1	A	451	SER	2.2
1	A	106	VAL	2.2
1	B	123	PHE	2.2
1	A	412	ALA	2.2
1	A	410	THR	2.1
1	B	3	THR	2.1
1	B	19	LEU	2.1
1	B	119	PRO	2.1
1	B	183	ALA	2.1
1	B	87	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	240	ASP	2.1
1	B	281	GLU	2.0
1	B	128	VAL	2.0
1	A	111	GLU	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
3	EDO	A	503	4/4	0.73	0.27	38,40,41,46	0
3	EDO	A	509	4/4	0.79	0.23	55,57,57,59	0
3	EDO	B	502	4/4	0.79	0.20	41,45,46,49	0
3	EDO	B	503	4/4	0.79	0.17	50,50,50,55	0
3	EDO	A	502	4/4	0.81	0.19	29,35,37,44	0
3	EDO	A	510	4/4	0.81	0.16	29,37,38,43	0
3	EDO	A	504	4/4	0.82	0.15	31,36,39,46	0
3	EDO	A	505	4/4	0.84	0.14	39,39,42,45	0
3	EDO	A	506	4/4	0.90	0.12	30,31,33,36	0
3	EDO	A	508	4/4	0.90	0.15	36,40,41,41	0
3	EDO	A	507	4/4	0.91	0.11	35,37,38,40	0
2	CA	B	501	1/1	0.96	0.06	28,28,28,28	0
2	CA	A	501	1/1	0.99	0.04	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.