



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:49 AM UTC

PDB ID : 7QK7 / pdb_00007qk7
Title : Crystal structure of the APO form of ALDH1A3
Authors : Castellvi, A.; Farres, J.
Deposited on : 2021-12-17
Resolution : 2.29 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

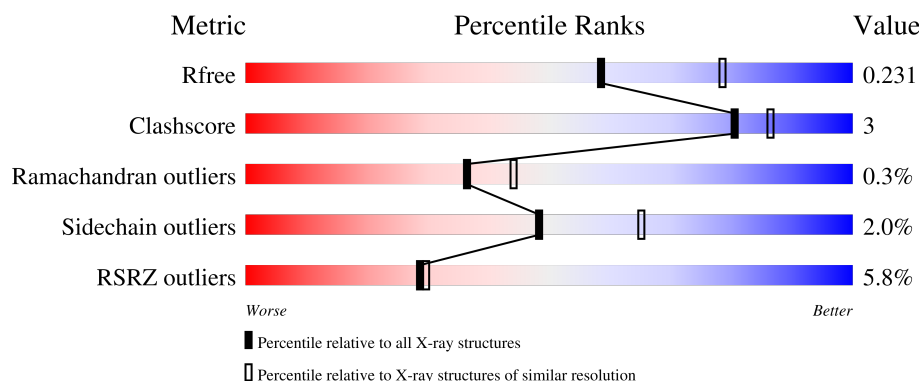
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	529	3% 85% 8% 8%
1	B	529	8% 85% 8% 8%

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	PEG	A	603	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7811 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 Aldehyde dehydrogenase family 1 member A3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	489	Total	C	N	O	S	0	2	0
			3711	2369	635	686	21			
1	B	489	Total	C	N	O	S	0	3	0
			3688	2358	621	687	22			

There are 34 discrepancies between the modelled and reference sequences:

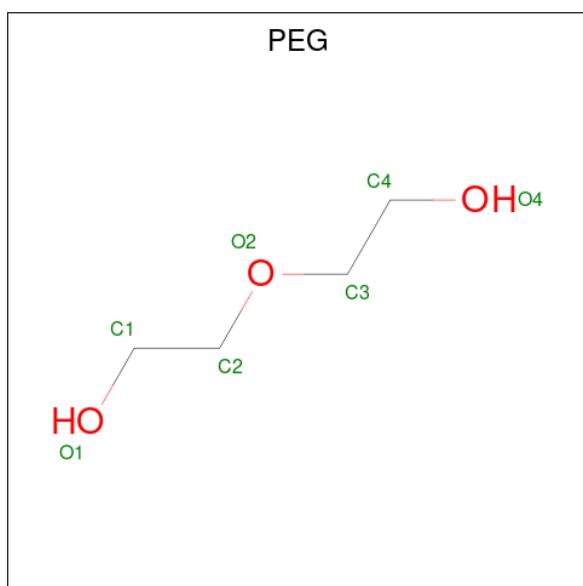
Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	HIS	-	expression tag	UNP P47895
A	-15	HIS	-	expression tag	UNP P47895
A	-14	HIS	-	expression tag	UNP P47895
A	-13	HIS	-	expression tag	UNP P47895
A	-12	HIS	-	expression tag	UNP P47895
A	-11	HIS	-	expression tag	UNP P47895
A	-10	LEU	-	expression tag	UNP P47895
A	-9	GLU	-	expression tag	UNP P47895
A	-8	SER	-	expression tag	UNP P47895
A	-7	THR	-	expression tag	UNP P47895
A	-6	SER	-	expression tag	UNP P47895
A	-5	LEU	-	expression tag	UNP P47895
A	-4	TYR	-	expression tag	UNP P47895
A	-3	LYS	-	expression tag	UNP P47895
A	-2	LYS	-	expression tag	UNP P47895
A	-1	ALA	-	expression tag	UNP P47895
A	0	GLY	-	expression tag	UNP P47895
B	-16	HIS	-	expression tag	UNP P47895
B	-15	HIS	-	expression tag	UNP P47895
B	-14	HIS	-	expression tag	UNP P47895
B	-13	HIS	-	expression tag	UNP P47895
B	-12	HIS	-	expression tag	UNP P47895
B	-11	HIS	-	expression tag	UNP P47895
B	-10	LEU	-	expression tag	UNP P47895
B	-9	GLU	-	expression tag	UNP P47895

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	SER	-	expression tag	UNP P47895
B	-7	THR	-	expression tag	UNP P47895
B	-6	SER	-	expression tag	UNP P47895
B	-5	LEU	-	expression tag	UNP P47895
B	-4	TYR	-	expression tag	UNP P47895
B	-3	LYS	-	expression tag	UNP P47895
B	-2	LYS	-	expression tag	UNP P47895
B	-1	ALA	-	expression tag	UNP P47895
B	0	GLY	-	expression tag	UNP P47895

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

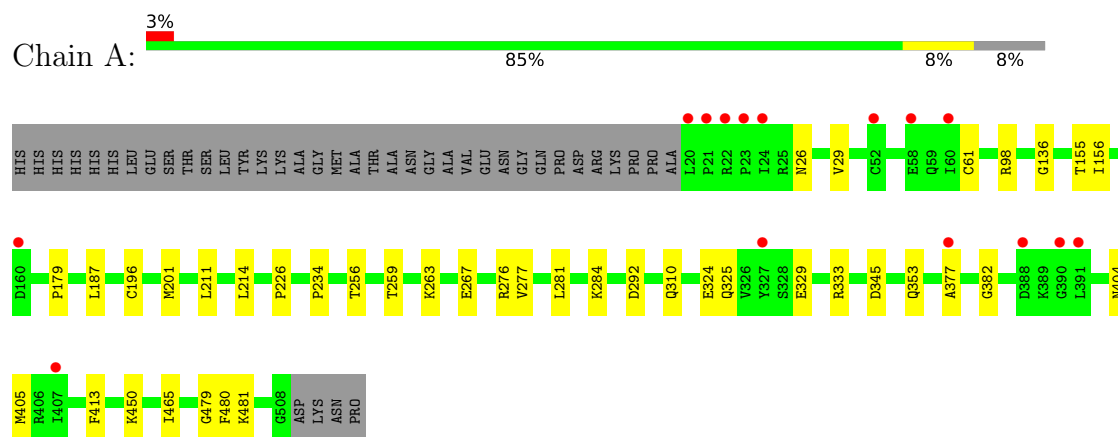
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	175	Total	O	0	0
			175	175		
4	B	182	Total	O	0	1
			183	183		

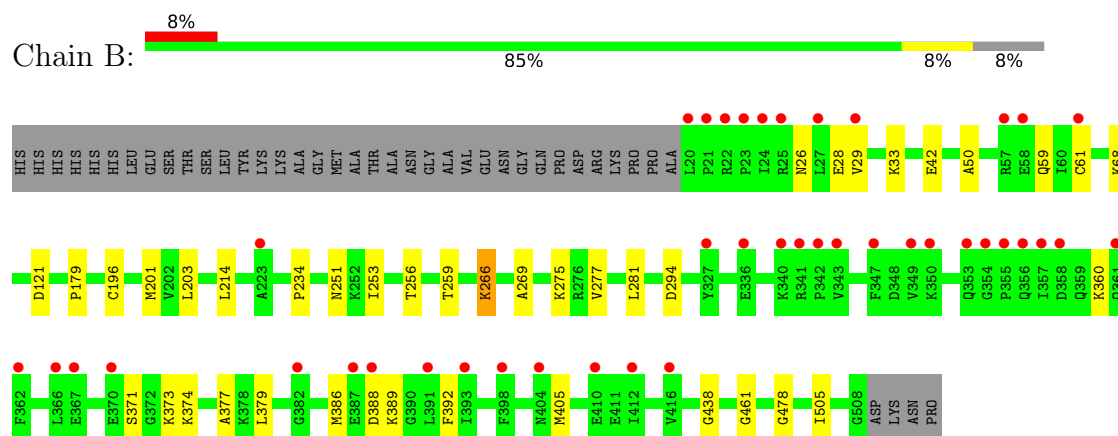
3 Residue-property plots [i](#)

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: Aldehyde dehydrogenase family 1 member A3



- Molecule 1: Aldehyde dehydrogenase family 1 member A3



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	82.96Å 90.13Å 159.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.44 – 2.29 48.44 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.7 (48.44-2.29) 98.7 (48.44-2.29)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.10.3 (18-SEP-2020)	Depositor
R, R_{free}	0.190 , 0.227 0.194 , 0.231	Depositor DCC
R_{free} test set	2559 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	44.0	Xtriage
Anisotropy	0.799	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 55.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7811	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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: PEG, GOL

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	0.73	2/3789 (0.1%)	1.05	7/5145 (0.1%)
1	B	0.77	0/3765	1.06	3/5113 (0.1%)
All	All	0.75	2/7554 (0.0%)	1.06	10/10258 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	201	MET	SD-CE	5.86	1.94	1.79
1	A	226	PRO	CA-C	5.45	1.54	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	479	GLY	N-CA-C	5.92	122.30	111.12
1	B	294	ASP	N-CA-C	-5.72	98.39	108.23
1	A	480	PHE	CA-CB-CG	5.44	119.24	113.80
1	A	211	LEU	N-CA-C	5.42	116.87	111.07
1	B	392	PHE	CA-CB-CG	5.38	119.18	113.80
1	A	156	ILE	N-CA-C	5.37	113.85	107.73
1	A	284	LYS	N-CA-C	-5.19	101.22	108.54
1	B	201	MET	N-CA-C	5.13	117.18	109.23
1	A	345	ASP	CA-CB-CG	5.02	117.62	112.60
1	A	480	PHE	N-CA-C	-5.00	103.11	110.52

There are no chirality outliers.

There are no planarity outliers.

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	3711	0	3659	20	0
1	B	3688	0	3624	19	0
2	A	21	0	30	7	0
2	B	21	0	30	2	0
3	A	12	0	16	1	0
4	A	175	0	0	0	0
4	B	183	0	0	0	0
All	All	7811	0	7359	38	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 3.

All (38) 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)
2:A:603:PEG:H21	1:B:266:LYS:HZ3	1.34	0.92
2:A:603:PEG:H21	1:B:266:LYS:NZ	1.89	0.88
1:B:377:ALA:HB2	1:B:405:MET:HE1	1.57	0.87
1:A:377:ALA:HB2	1:A:405:MET:HE1	1.64	0.78
1:B:371:SER:HA	1:B:374:LYS:HE2	1.67	0.75
1:B:377:ALA:HB2	1:B:405:MET:CE	2.31	0.59
1:B:29:VAL:HG21	1:B:61:CYS:SG	2.45	0.57
1:B:371:SER:HA	1:B:374:LYS:CE	2.33	0.57
1:B:269:ALA:HB1	1:B:275:LYS:HG3	1.87	0.56
1:B:373:LYS:HE2	1:B:379:LEU:HD22	1.88	0.56
1:A:136:GLY:HA2	2:A:601:PEG:H22	1.87	0.55
1:A:481:LYS:H	2:B:603:PEG:H31	1.71	0.55
1:A:325:GLN:NE2	1:A:325:GLN:H	2.05	0.55
1:A:277:VAL:H	2:A:603:PEG:H31	1.73	0.53
1:A:259:THR:HA	1:A:281:LEU:HD13	1.90	0.53
1:B:251:ASN:HB3	2:B:603:PEG:H41	1.91	0.51
1:A:276:ARG:HA	2:A:603:PEG:H31	1.91	0.50
1:B:33:LYS:NZ	1:B:42:GLU:HG3	2.26	0.50
1:A:382:GLY:H	3:A:604:GOL:H2	1.77	0.48
1:A:263:LYS:O	1:A:267:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:ALA:HB2	1:A:405:MET:CE	2.41	0.45
1:B:50:ALA:HB1	1:B:59:GLN:HG3	1.98	0.45
1:A:155:THR:HB	2:A:605:PEG:H32	2.00	0.44
1:B:179:PRO:HD3	1:B:256:THR:HB	2.00	0.44
1:A:292:ASP:CG	1:A:450:LYS:HZ1	2.27	0.43
1:A:214:LEU:HD21	1:A:234:PRO:HG3	1.99	0.43
1:A:179:PRO:HD3	1:A:256:THR:HB	2.00	0.43
1:A:187:LEU:HD23	1:A:187:LEU:C	2.44	0.43
1:A:465:ILE:HD12	1:B:505:ILE:HG12	1.99	0.43
2:A:603:PEG:H21	1:B:266:LYS:HZ1	1.78	0.43
1:B:214:LEU:HD21	1:B:234:PRO:HG3	2.01	0.43
1:B:461:GLY:HA3	1:B:478:GLY:O	2.19	0.42
1:B:253:ILE:HG23	1:B:277:VAL:HG13	2.01	0.42
1:A:29:VAL:HG21	1:A:61:CYS:SG	2.60	0.41
1:A:310:GLN:HG3	1:A:353:GLN:HG3	2.01	0.41
1:B:259:THR:HA	1:B:281:LEU:HD13	2.01	0.41
1:A:329:GLU:HG3	1:A:333:ARG:HE	1.85	0.41
1:A:276:ARG:N	1:A:276:ARG:HD2	2.35	0.41

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	489/529 (92%)	467 (96%)	22 (4%)	0	100	100
1	B	490/529 (93%)	466 (95%)	21 (4%)	3 (1%)	21	25
All	All	979/1058 (92%)	933 (95%)	43 (4%)	3 (0%)	36	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	388	ASP
1	B	389	LYS
1	B	438	GLY

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	383/437 (88%)	377 (98%)	6 (2%)	55	71
1	B	379/437 (87%)	370 (98%)	9 (2%)	43	59
All	All	762/874 (87%)	747 (98%)	15 (2%)	48	65

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	98	ARG
1	A	196	CYS
1	A	324	GLU
1	A	404	ASN
1	A	413	PHE
1	B	26	ASN
1	B	28	GLU
1	B	68	LYS
1	B	121	ASP
1	B	196	CYS
1	B	203	LEU
1	B	266	LYS
1	B	360	LYS
1	B	386	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN

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Mol	Chain	Res	Type
1	A	310	GLN
1	A	325	GLN
1	A	356	GLN
1	B	37	ASN
1	B	83	GLN
1	B	304	GLN
1	B	310	GLN
1	B	325	GLN
1	B	417	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](#)

8 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	$\# Z > 2$
3	GOL	A	602	-	5,5,5	0.10	0	5,5,5	0.31	0
2	PEG	B	601	-	6,6,6	0.19	0	5,5,5	0.08	0
2	PEG	B	603	-	6,6,6	0.10	0	5,5,5	0.12	0
2	PEG	A	601	-	6,6,6	0.17	0	5,5,5	0.13	0
2	PEG	A	603	-	6,6,6	0.31	0	5,5,5	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PEG	B	602	-	6,6,6	0.16	0	5,5,5	0.17	0
3	GOL	A	604	-	5,5,5	0.10	0	5,5,5	0.21	0
2	PEG	A	605	-	6,6,6	0.19	0	5,5,5	0.15	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	GOL	A	602	-	-	0/4/4/4	-
2	PEG	B	601	-	-	1/4/4/4	-
2	PEG	B	603	-	-	0/4/4/4	-
2	PEG	A	601	-	-	1/4/4/4	-
2	PEG	A	603	-	-	2/4/4/4	-
2	PEG	B	602	-	-	2/4/4/4	-
3	GOL	A	604	-	-	0/4/4/4	-
2	PEG	A	605	-	-	0/4/4/4	-

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
2	A	603	PEG	O2-C3-C4-O4
2	B	602	PEG	O1-C1-C2-O2
2	A	603	PEG	O1-C1-C2-O2
2	B	601	PEG	C1-C2-O2-C3
2	A	601	PEG	C4-C3-O2-C2
2	B	602	PEG	C4-C3-O2-C2

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	603	PEG	2	0
2	A	601	PEG	1	0
2	A	603	PEG	5	0
3	A	604	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	605	PEG	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

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	489/529 (92%)	0.38	15 (3%)	51	53	25, 53, 81, 108	2 (0%)
1	B	489/529 (92%)	0.48	42 (8%)	16	17	23, 53, 93, 108	3 (0%)
All	All	978/1058 (92%)	0.43	57 (5%)	29	30	23, 53, 90, 108	5 (0%)

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	22	ARG	4.9
1	A	388	ASP	4.5
1	B	349	VAL	4.4
1	B	24	ILE	4.3
1	B	347	PHE	4.3
1	A	24	ILE	4.3
1	B	388	ASP	4.0
1	B	356	GLN	3.9
1	A	23	PRO	3.6
1	B	357	ILE	3.6
1	A	21	PRO	3.6
1	B	393	ILE	3.4
1	B	382	GLY	3.4
1	B	23	PRO	3.3
1	B	387	GLU	3.2
1	B	354	GLY	3.2
1	B	358	ASP	3.2
1	B	27	LEU	3.1
1	B	25	ARG	2.9
1	B	361	GLN	2.7
1	B	410	GLU	2.7
1	B	340	LYS	2.7
1	B	404	ASN	2.7
1	B	342	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	366	LEU	2.6
1	B	22	ARG	2.5
1	B	343	VAL	2.5
1	B	341	ARG	2.5
1	A	20	LEU	2.5
1	B	336	GLU	2.5
1	B	223	ALA	2.5
1	B	416	VAL	2.4
1	B	58	GLU	2.4
1	A	407	ILE	2.3
1	B	57	ARG	2.3
1	A	327	TYR	2.3
1	B	412	ILE	2.3
1	A	391	LEU	2.3
1	B	367	GLU	2.3
1	B	327	TYR	2.2
1	B	20	LEU	2.2
1	B	391	LEU	2.2
1	B	61	CYS	2.2
1	B	21	PRO	2.2
1	B	350	LYS	2.1
1	B	355	PRO	2.1
1	A	390	GLY	2.1
1	A	377	ALA	2.1
1	B	370	GLU	2.1
1	B	398	PHE	2.1
1	A	52	CYS	2.0
1	A	60	ILE	2.0
1	B	29	VAL	2.0
1	B	362	PHE	2.0
1	A	58	GLU	2.0
1	B	353	GLN	2.0
1	A	160	ASP	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	PEG	A	605	7/7	0.82	0.22	69,69,69,69	0
2	PEG	B	603	7/7	0.83	0.25	86,87,87,87	0
2	PEG	A	603	7/7	0.85	0.17	58,59,61,62	0
3	GOL	A	604	6/6	0.87	0.14	88,88,88,88	0
2	PEG	B	602	7/7	0.91	0.16	68,69,70,70	0
2	PEG	B	601	7/7	0.92	0.16	71,72,73,73	0
3	GOL	A	602	6/6	0.94	0.11	68,69,69,69	0
2	PEG	A	601	7/7	0.94	0.12	67,67,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.