



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2020 – 09:26 pm BST

PDB ID : 5MZ5
Title : Crystal structure of aldehyde dehydrogenase 21 (ALDH21) from *Physcomitrella patens* in its apoform
Authors : Kopecny, D.; Koncitikova, R.; Briozzo, P.; Morera, S.
Deposited on : 2017-01-30
Resolution : 2.15 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 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 : 2.11
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) : 2.11

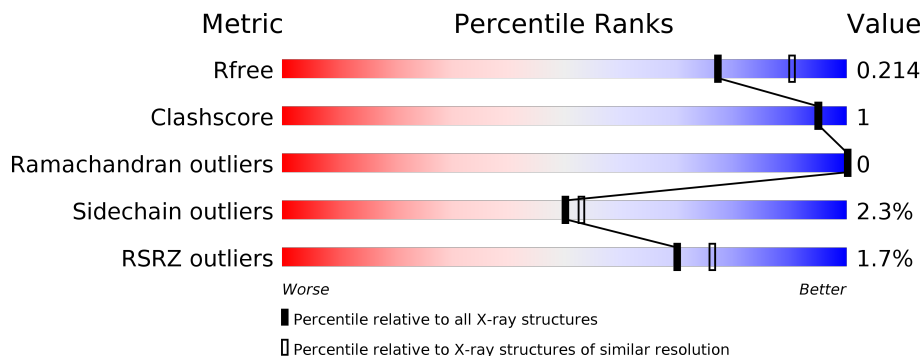
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 on 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	515	 2% 88% 5% 7%
1	B	515	 % 88% 5% 7%
1	C	515	 2% 89% 5% 7%
1	D	515	 2% 90% 5% 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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	B	505	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 15896 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 ALDH21).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	481	3720	2379	627	696	18	0	0	0
1	B	480	3713	2374	626	695	18	0	0	0
1	C	481	3720	2379	627	696	18	0	0	0
1	D	480	3713	2374	626	695	18	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP A9SS48
A	-16	GLY	-	expression tag	UNP A9SS48
A	-15	SER	-	expression tag	UNP A9SS48
A	-14	SER	-	expression tag	UNP A9SS48
A	-13	HIS	-	expression tag	UNP A9SS48
A	-12	HIS	-	expression tag	UNP A9SS48
A	-11	HIS	-	expression tag	UNP A9SS48
A	-10	HIS	-	expression tag	UNP A9SS48
A	-9	HIS	-	expression tag	UNP A9SS48
A	-8	HIS	-	expression tag	UNP A9SS48
A	-7	SER	-	expression tag	UNP A9SS48
A	-6	GLN	-	expression tag	UNP A9SS48
A	-5	ASP	-	expression tag	UNP A9SS48
A	-4	PRO	-	expression tag	UNP A9SS48
A	-3	ASN	-	expression tag	UNP A9SS48
A	-2	SER	-	expression tag	UNP A9SS48
A	-1	SER	-	expression tag	UNP A9SS48
A	0	SER	-	expression tag	UNP A9SS48
B	-17	MET	-	initiating methionine	UNP A9SS48
B	-16	GLY	-	expression tag	UNP A9SS48
B	-15	SER	-	expression tag	UNP A9SS48

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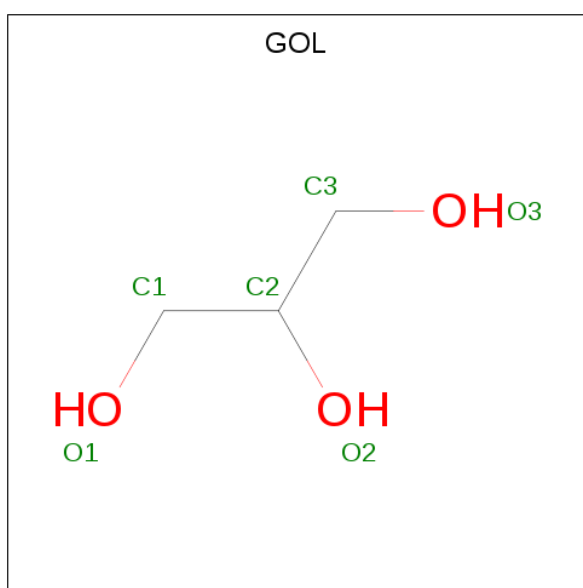
Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	SER	-	expression tag	UNP A9SS48
B	-13	HIS	-	expression tag	UNP A9SS48
B	-12	HIS	-	expression tag	UNP A9SS48
B	-11	HIS	-	expression tag	UNP A9SS48
B	-10	HIS	-	expression tag	UNP A9SS48
B	-9	HIS	-	expression tag	UNP A9SS48
B	-8	HIS	-	expression tag	UNP A9SS48
B	-7	SER	-	expression tag	UNP A9SS48
B	-6	GLN	-	expression tag	UNP A9SS48
B	-5	ASP	-	expression tag	UNP A9SS48
B	-4	PRO	-	expression tag	UNP A9SS48
B	-3	ASN	-	expression tag	UNP A9SS48
B	-2	SER	-	expression tag	UNP A9SS48
B	-1	SER	-	expression tag	UNP A9SS48
B	0	SER	-	expression tag	UNP A9SS48
C	-17	MET	-	initiating methionine	UNP A9SS48
C	-16	GLY	-	expression tag	UNP A9SS48
C	-15	SER	-	expression tag	UNP A9SS48
C	-14	SER	-	expression tag	UNP A9SS48
C	-13	HIS	-	expression tag	UNP A9SS48
C	-12	HIS	-	expression tag	UNP A9SS48
C	-11	HIS	-	expression tag	UNP A9SS48
C	-10	HIS	-	expression tag	UNP A9SS48
C	-9	HIS	-	expression tag	UNP A9SS48
C	-8	HIS	-	expression tag	UNP A9SS48
C	-7	SER	-	expression tag	UNP A9SS48
C	-6	GLN	-	expression tag	UNP A9SS48
C	-5	ASP	-	expression tag	UNP A9SS48
C	-4	PRO	-	expression tag	UNP A9SS48
C	-3	ASN	-	expression tag	UNP A9SS48
C	-2	SER	-	expression tag	UNP A9SS48
C	-1	SER	-	expression tag	UNP A9SS48
C	0	SER	-	expression tag	UNP A9SS48
D	-17	MET	-	initiating methionine	UNP A9SS48
D	-16	GLY	-	expression tag	UNP A9SS48
D	-15	SER	-	expression tag	UNP A9SS48
D	-14	SER	-	expression tag	UNP A9SS48
D	-13	HIS	-	expression tag	UNP A9SS48
D	-12	HIS	-	expression tag	UNP A9SS48
D	-11	HIS	-	expression tag	UNP A9SS48
D	-10	HIS	-	expression tag	UNP A9SS48
D	-9	HIS	-	expression tag	UNP A9SS48

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	HIS	-	expression tag	UNP A9SS48
D	-7	SER	-	expression tag	UNP A9SS48
D	-6	GLN	-	expression tag	UNP A9SS48
D	-5	ASP	-	expression tag	UNP A9SS48
D	-4	PRO	-	expression tag	UNP A9SS48
D	-3	ASN	-	expression tag	UNP A9SS48
D	-2	SER	-	expression tag	UNP A9SS48
D	-1	SER	-	expression tag	UNP A9SS48
D	0	SER	-	expression tag	UNP A9SS48

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



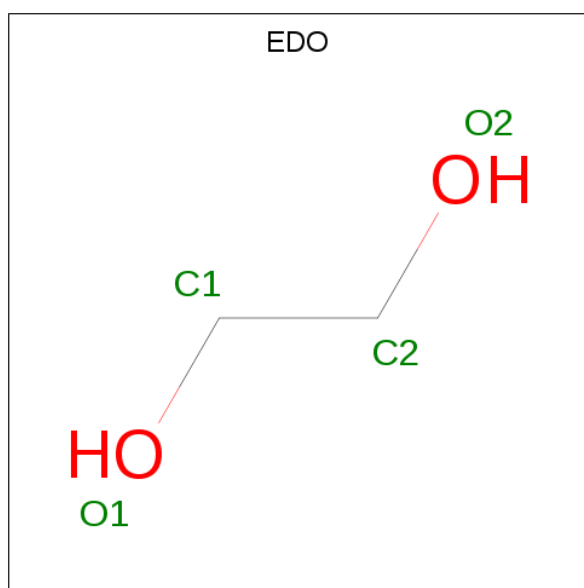
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



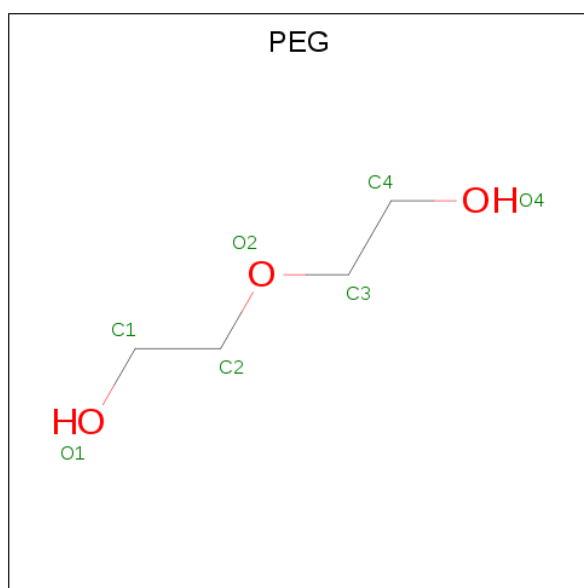
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	220	Total O 220 220	0	0
5	B	238	Total O 238 238	0	0

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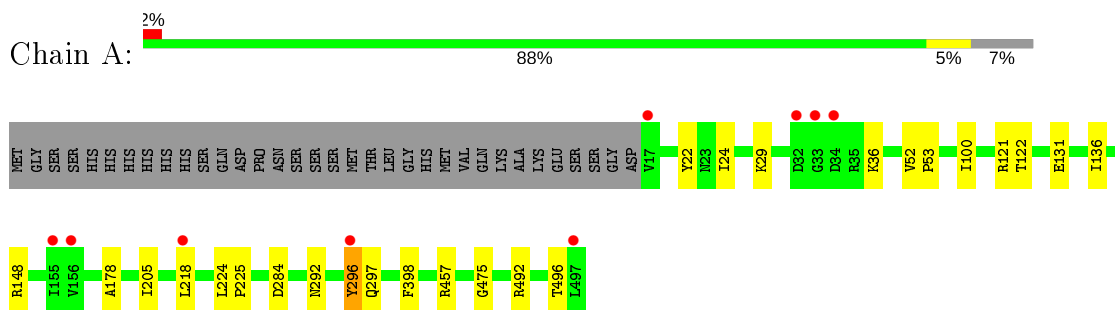
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	235	Total 235	O 235	0	0
5	D	207	Total 207	O 207	0	0

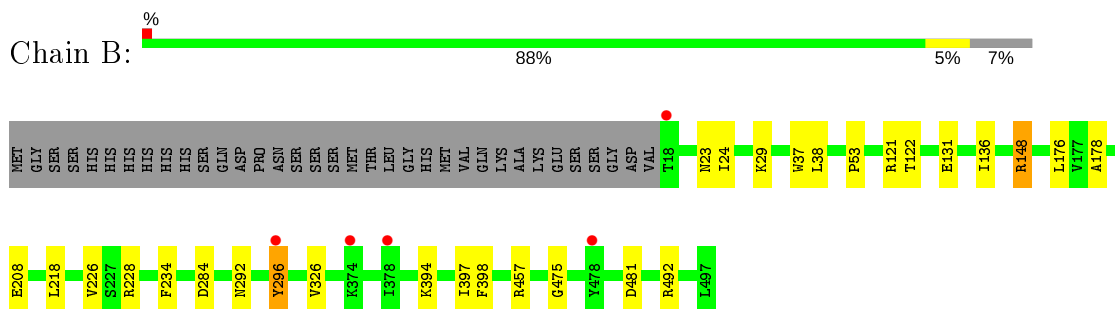
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

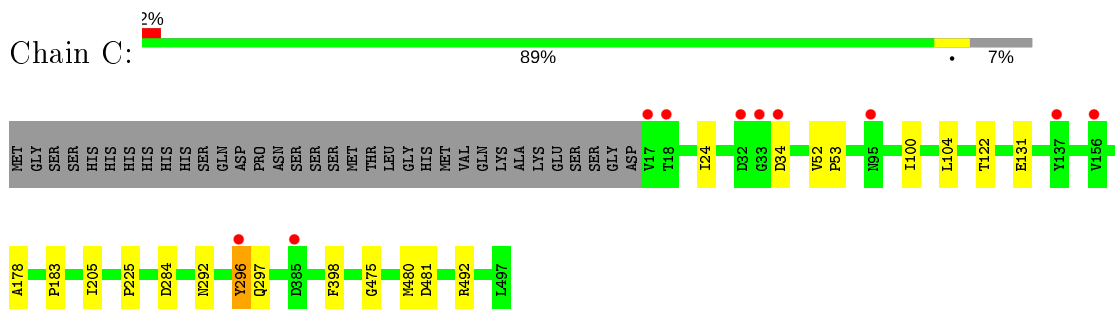
- Molecule 1: ALDH21)



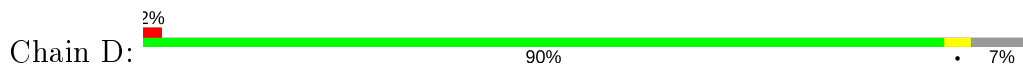
- Molecule 1: ALDH21)

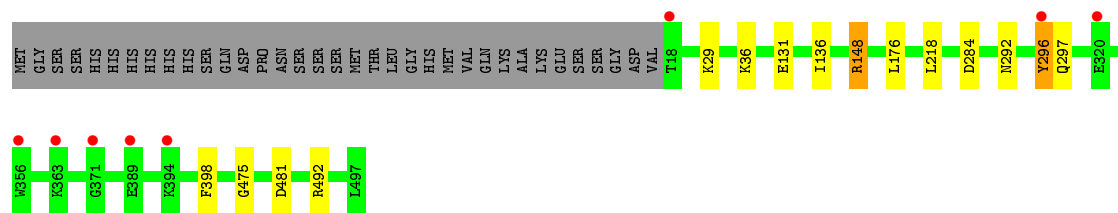


- Molecule 1: ALDH21)



- Molecule 1: ALDH21)





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.80Å 151.79Å 158.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.20 – 2.15 47.06 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.20-2.15) 99.2 (47.06-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.16Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.184 , 0.210 0.189 , 0.214	Depositor DCC
R_{free} test set	5992 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtrriage
Anisotropy	0.417	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.000 for -h,l,k	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15896	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.47 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3158e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: GOL, PEG, 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	0.50	0/3796	0.67	1/5133 (0.0%)
1	B	0.51	0/3789	0.67	1/5123 (0.0%)
1	C	0.50	0/3796	0.67	1/5133 (0.0%)
1	D	0.50	0/3789	0.66	1/5123 (0.0%)
All	All	0.50	0/15170	0.67	4/20512 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	475	GLY	N-CA-C	-6.63	96.52	113.10
1	D	475	GLY	N-CA-C	-6.08	97.90	113.10
1	A	475	GLY	N-CA-C	-5.98	98.15	113.10
1	C	475	GLY	N-CA-C	-5.79	98.62	113.10

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	3720	0	3765	12	0
1	B	3713	0	3756	14	0
1	C	3720	0	3765	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3713	0	3756	6	0
2	A	18	0	24	3	0
2	B	18	0	24	2	0
2	C	18	0	24	0	0
2	D	18	0	24	2	0
3	A	12	0	18	1	0
3	B	16	0	24	4	0
3	C	12	0	18	0	0
3	D	4	0	6	0	0
4	A	7	0	10	0	0
4	B	7	0	10	0	0
5	A	220	0	0	0	0
5	B	238	0	0	1	0
5	C	235	0	0	0	0
5	D	207	0	0	1	0
All	All	15896	0	15224	37	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 1.

All (37) 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:131:GLU:HG2	1:C:131:GLU:HG2	1.71	0.73
1:C:292:ASN:O	1:C:296:TYR:HB3	1.95	0.64
1:D:292:ASN:O	1:D:296:TYR:HB3	1.98	0.63
1:B:208:GLU:HG2	3:B:505:EDO:H22	1.81	0.62
1:B:292:ASN:O	1:B:296:TYR:HB3	2.02	0.59
1:B:131:GLU:HG2	1:D:131:GLU:HG2	1.84	0.59
1:B:148:ARG:HG2	5:B:811:HOH:O	2.03	0.59
1:A:52:VAL:HG11	1:A:225:PRO:HG2	1.88	0.54
1:D:176:LEU:HD21	2:D:502:GOL:H31	1.90	0.54
1:A:136:ILE:HA	2:A:503:GOL:H31	1.90	0.54
1:A:121:ARG:HH22	2:A:501:GOL:H11	1.73	0.53
1:B:23:ASN:HB2	3:B:505:EDO:H21	1.91	0.51
1:D:29:LYS:HE2	1:D:218:LEU:HD11	1.93	0.51
1:B:29:LYS:HE2	1:B:218:LEU:HD11	1.93	0.50
1:A:29:LYS:HE2	1:A:218:LEU:HD11	1.92	0.50
1:B:136:ILE:HA	2:B:503:GOL:H12	1.94	0.49
1:C:24:ILE:HG23	1:C:53:PRO:HD2	1.93	0.49
1:D:148:ARG:HG2	5:D:784:HOH:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:VAL:HG21	1:C:225:PRO:HG2	1.98	0.46
1:B:208:GLU:CG	3:B:505:EDO:H22	2.45	0.46
1:A:24:ILE:HG23	1:A:53:PRO:HD2	1.97	0.45
1:A:496:THR:HB	3:A:507:EDO:H11	1.98	0.44
1:D:136:ILE:HA	2:D:503:GOL:H12	2.00	0.44
1:B:176:LEU:HD21	2:B:502:GOL:H12	2.00	0.44
1:A:292:ASN:O	1:A:296:TYR:HB3	2.18	0.43
1:B:23:ASN:H	3:B:505:EDO:H12	1.84	0.42
1:B:24:ILE:HG23	1:B:53:PRO:HD2	2.01	0.42
1:C:122:THR:HG23	1:C:178:ALA:HB2	2.02	0.42
1:B:121:ARG:HH22	1:B:457:ARG:HD3	1.85	0.42
1:A:122:THR:HG23	1:A:178:ALA:HB2	2.02	0.41
1:A:22:TYR:O	1:A:53:PRO:HD3	2.21	0.41
1:B:226:VAL:HG21	1:B:234:PHE:HE1	1.85	0.41
1:C:183:PRO:HB3	1:C:480:MET:HG3	2.03	0.41
1:A:100:ILE:HG12	1:A:205:ILE:HG21	2.03	0.40
1:B:122:THR:HG23	1:B:178:ALA:HB2	2.03	0.40
1:A:457:ARG:HH11	2:A:501:GOL:H12	1.86	0.40
1:C:100:ILE:HG12	1:C:205:ILE:HG21	2.03	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	479/515 (93%)	468 (98%)	11 (2%)	0	100	100
1	B	478/515 (93%)	467 (98%)	11 (2%)	0	100	100
1	C	479/515 (93%)	468 (98%)	11 (2%)	0	100	100
1	D	478/515 (93%)	466 (98%)	12 (2%)	0	100	100
All	All	1914/2060 (93%)	1869 (98%)	45 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	395/425 (93%)	387 (98%)	8 (2%)	55 59
1	B	394/425 (93%)	382 (97%)	12 (3%)	41 40
1	C	395/425 (93%)	387 (98%)	8 (2%)	55 59
1	D	394/425 (93%)	386 (98%)	8 (2%)	55 59
All	All	1578/1700 (93%)	1542 (98%)	36 (2%)	50 53

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	LYS
1	A	148	ARG
1	A	224	LEU
1	A	284	ASP
1	A	296	TYR
1	A	297	GLN
1	A	398	PHE
1	A	492	ARG
1	B	37	TRP
1	B	38	LEU
1	B	148	ARG
1	B	228	ARG
1	B	284	ASP
1	B	296	TYR
1	B	326	VAL
1	B	394	LYS
1	B	397	ILE
1	B	398	PHE
1	B	481	ASP
1	B	492	ARG
1	C	34	ASP
1	C	104	LEU

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Mol	Chain	Res	Type
1	C	284	ASP
1	C	296	TYR
1	C	297	GLN
1	C	398	PHE
1	C	481	ASP
1	C	492	ARG
1	D	36	LYS
1	D	148	ARG
1	D	284	ASP
1	D	296	TYR
1	D	297	GLN
1	D	398	PHE
1	D	481	ASP
1	D	492	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

25 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
4	PEG	B	508	-	6,6,6	0.23	0	5,5,5	0.10	0
3	EDO	C	506	-	3,3,3	0.55	0	2,2,2	0.39	0
2	GOL	A	503	-	5,5,5	0.27	0	5,5,5	0.42	0
3	EDO	A	507	-	3,3,3	0.71	0	2,2,2	0.13	0
2	GOL	A	501	-	5,5,5	0.05	0	5,5,5	0.25	0
2	GOL	D	503	-	5,5,5	0.19	0	5,5,5	0.42	0
3	EDO	B	505	-	3,3,3	0.64	0	2,2,2	0.35	0
2	GOL	B	502	-	5,5,5	0.04	0	5,5,5	0.25	0
2	GOL	D	501	-	5,5,5	0.11	0	5,5,5	0.43	0
3	EDO	A	504	-	3,3,3	0.66	0	2,2,2	0.05	0
2	GOL	A	502	-	5,5,5	0.11	0	5,5,5	0.33	0
2	GOL	C	502	-	5,5,5	0.08	0	5,5,5	0.47	0
3	EDO	D	504	-	3,3,3	0.56	0	2,2,2	0.47	0
2	GOL	B	501	-	5,5,5	0.10	0	5,5,5	0.28	0
2	GOL	C	501	-	5,5,5	0.07	0	5,5,5	0.21	0
3	EDO	B	507	-	3,3,3	0.68	0	2,2,2	0.10	0
3	EDO	C	505	-	3,3,3	0.75	0	2,2,2	0.11	0
3	EDO	B	506	-	3,3,3	0.46	0	2,2,2	0.36	0
4	PEG	A	506	-	6,6,6	0.15	0	5,5,5	0.12	0
2	GOL	B	503	-	5,5,5	0.25	0	5,5,5	0.46	0
2	GOL	C	503	-	5,5,5	0.09	0	5,5,5	0.15	0
2	GOL	D	502	-	5,5,5	0.07	0	5,5,5	0.22	0
3	EDO	C	504	-	3,3,3	0.60	0	2,2,2	0.26	0
3	EDO	B	504	-	3,3,3	0.47	0	2,2,2	0.41	0
3	EDO	A	505	-	3,3,3	0.75	0	2,2,2	0.13	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
4	PEG	B	508	-	-	3/4/4/4	-
3	EDO	C	506	-	-	1/1/1/1	-
2	GOL	A	503	-	-	4/4/4/4	-
3	EDO	A	507	-	-	0/1/1/1	-
2	GOL	A	501	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	D	503	-	-	0/4/4/4	-
3	EDO	B	505	-	-	0/1/1/1	-
2	GOL	B	502	-	-	0/4/4/4	-
2	GOL	D	501	-	-	2/4/4/4	-
3	EDO	A	504	-	-	0/1/1/1	-
2	GOL	A	502	-	-	2/4/4/4	-
2	GOL	C	502	-	-	0/4/4/4	-
3	EDO	D	504	-	-	1/1/1/1	-
2	GOL	B	501	-	-	2/4/4/4	-
2	GOL	C	501	-	-	2/4/4/4	-
3	EDO	B	507	-	-	0/1/1/1	-
3	EDO	C	505	-	-	0/1/1/1	-
3	EDO	B	506	-	-	0/1/1/1	-
4	PEG	A	506	-	-	1/4/4/4	-
2	GOL	B	503	-	-	0/4/4/4	-
2	GOL	C	503	-	-	2/4/4/4	-
2	GOL	D	502	-	-	0/4/4/4	-
3	EDO	C	504	-	-	0/1/1/1	-
3	EDO	B	504	-	-	0/1/1/1	-
3	EDO	A	505	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	503	GOL	C1-C2-C3-O3
2	A	501	GOL	O1-C1-C2-C3
2	C	503	GOL	O1-C1-C2-C3
2	B	501	GOL	O2-C2-C3-O3
2	A	503	GOL	O1-C1-C2-C3
2	A	502	GOL	C1-C2-C3-O3
2	B	501	GOL	C1-C2-C3-O3
2	C	501	GOL	O1-C1-C2-C3
2	A	501	GOL	O1-C1-C2-O2
2	C	501	GOL	O1-C1-C2-O2
2	C	503	GOL	O1-C1-C2-O2
3	C	506	EDO	O1-C1-C2-O2
2	A	503	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	A	503	GOL	O2-C2-C3-O3
2	D	501	GOL	O1-C1-C2-O2
2	A	502	GOL	O2-C2-C3-O3
4	A	506	PEG	C1-C2-O2-C3
4	B	508	PEG	C1-C2-O2-C3
4	B	508	PEG	O2-C3-C4-O4
3	D	504	EDO	O1-C1-C2-O2
4	B	508	PEG	C4-C3-O2-C2
2	D	501	GOL	O1-C1-C2-C3

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	503	GOL	1	0
3	A	507	EDO	1	0
2	A	501	GOL	2	0
2	D	503	GOL	1	0
3	B	505	EDO	4	0
2	B	502	GOL	1	0
2	B	503	GOL	1	0
2	D	502	GOL	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	481/515 (93%)	0.07	9 (1%) 66 74	20, 32, 52, 69	0
1	B	480/515 (93%)	0.12	5 (1%) 82 86	21, 31, 47, 63	0
1	C	481/515 (93%)	0.11	10 (2%) 63 71	21, 31, 51, 74	0
1	D	480/515 (93%)	0.17	8 (1%) 70 76	21, 33, 54, 73	0
All	All	1922/2060 (93%)	0.12	32 (1%) 70 76	20, 32, 52, 74	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	296	TYR	6.9
1	C	17	VAL	6.8
1	C	34	ASP	5.8
1	C	296	TYR	5.4
1	B	18	THR	4.5
1	A	34	ASP	4.4
1	A	296	TYR	4.2
1	B	296	TYR	3.5
1	C	33	GLY	3.5
1	A	33	GLY	3.2
1	C	18	THR	3.1
1	D	356	TRP	2.8
1	B	374	LYS	2.8
1	D	363	LYS	2.8
1	A	17	VAL	2.7
1	C	156	VAL	2.7
1	D	320	GLU	2.6
1	A	156	VAL	2.5
1	C	137	TYR	2.5
1	A	155	ILE	2.4
1	A	32	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	18	THR	2.4
1	C	95	ASN	2.4
1	B	378	ILE	2.3
1	A	497	LEU	2.3
1	D	389	GLU	2.3
1	D	371	GLY	2.3
1	A	218	LEU	2.2
1	C	385	ASP	2.2
1	B	478	TYR	2.0
1	C	32	ASP	2.0
1	D	394	LYS	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 carbohydrates 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	B	507	4/4	0.78	0.27	49,52,53,54	0
2	GOL	A	503	6/6	0.79	0.38	41,51,54,56	0
3	EDO	A	505	4/4	0.79	0.30	37,41,42,44	0
3	EDO	C	505	4/4	0.81	0.41	53,55,56,56	0
3	EDO	A	507	4/4	0.83	0.36	46,48,50,52	0
3	EDO	C	506	4/4	0.84	0.26	64,65,65,67	0
2	GOL	D	503	6/6	0.84	0.32	42,46,47,51	0
2	GOL	B	503	6/6	0.84	0.32	37,41,45,47	0
3	EDO	A	504	4/4	0.84	0.20	60,60,61,61	0
2	GOL	B	501	6/6	0.86	0.19	36,46,47,50	0
3	EDO	B	504	4/4	0.87	0.35	45,48,48,52	0
2	GOL	B	502	6/6	0.87	0.22	56,57,58,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	B	506	4/4	0.88	0.61	50,53,55,59	0
2	GOL	C	501	6/6	0.88	0.24	39,45,48,48	0
2	GOL	A	502	6/6	0.89	0.18	50,55,56,58	0
4	PEG	B	508	7/7	0.89	0.16	43,43,45,46	0
4	PEG	A	506	7/7	0.89	0.18	52,53,56,58	0
3	EDO	C	504	4/4	0.90	0.10	53,54,54,55	0
2	GOL	A	501	6/6	0.91	0.17	47,50,51,52	0
2	GOL	D	502	6/6	0.92	0.19	52,56,57,57	0
2	GOL	D	501	6/6	0.92	0.23	49,52,54,57	0
3	EDO	B	505	4/4	0.92	0.18	42,43,44,44	0
2	GOL	C	503	6/6	0.92	0.14	49,51,51,52	0
2	GOL	C	502	6/6	0.94	0.20	43,49,54,59	0
3	EDO	D	504	4/4	0.96	0.13	44,45,47,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.