



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 02:33 PM UTC

PDB ID : 3ITK / pdb_00003itk
Title : Crystal structure of human UDP-glucose dehydrogenase Thr131Ala, apo form.
Authors : Chaikuad, A.; Egger, S.; Yue, W.W.; Sethi, R.; Filippakopoulos, P.; Muniz, J.R.C.; von Delft, F.; Bountra, C.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.M.; Kavanagh, K.L.; Nidetzky, B.; Oppermann, U.; Structural Genomics Consortium (SGC)
Deposited on : 2009-08-28
Resolution : 2.40 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

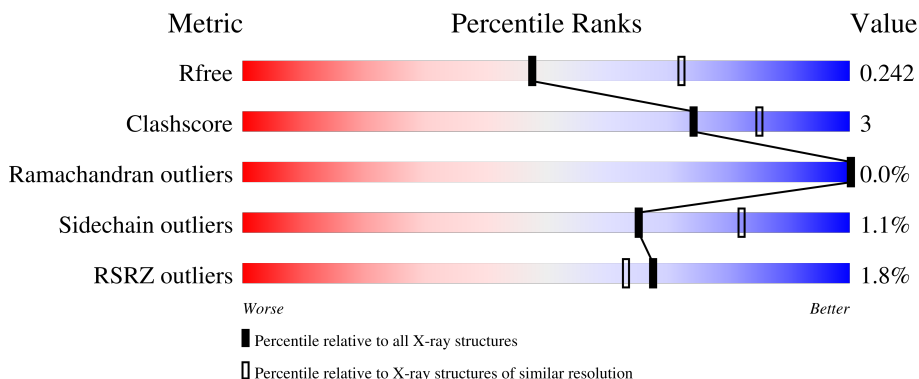
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

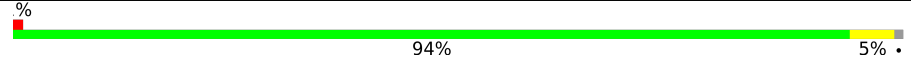
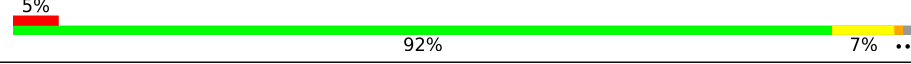
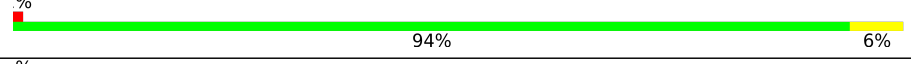
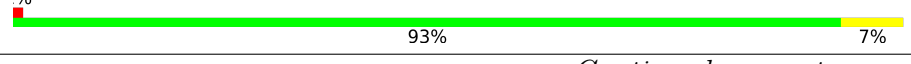
The reported resolution of this entry is 2.40 Å.

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.



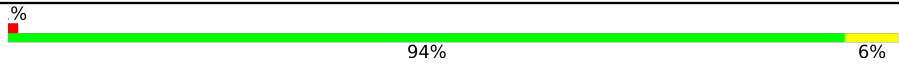
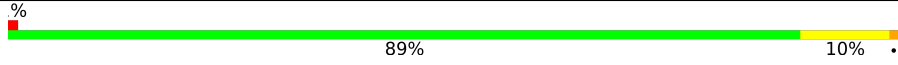
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	467	 94% 5%
1	B	467	 92% 7%
1	C	467	 94% 6%
1	D	467	 93% 7%

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Mol	Chain	Length	Quality of chain
1	E	467	 <p>% 94% 6%</p>
1	F	467	 <p>% 89% 10%</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 22977 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 UDP-glucose 6-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	464	3591	2277	615	680	19	0	0	0
1	B	462	3586	2270	615	681	20	0	2	0
1	C	467	3629	2297	625	688	19	0	1	0
1	D	467	3622	2295	622	685	20	0	0	0
1	E	466	3604	2284	619	682	19	0	2	0
1	F	467	3624	2290	625	690	19	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

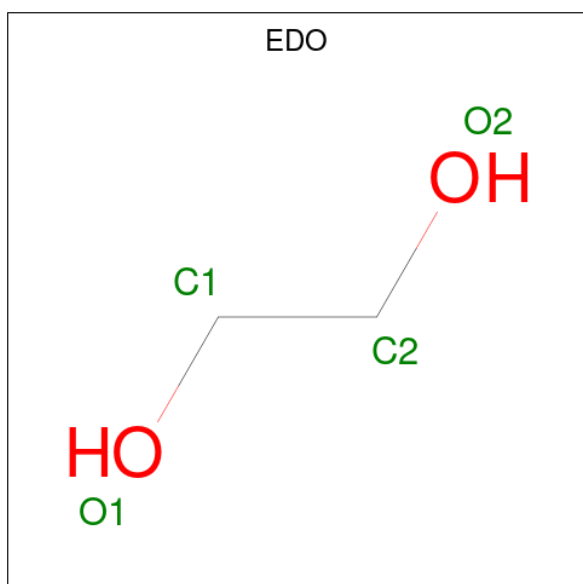
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O60701
A	131	ALA	THR	engineered mutation	UNP O60701
B	0	SER	-	expression tag	UNP O60701
B	131	ALA	THR	engineered mutation	UNP O60701
C	0	SER	-	expression tag	UNP O60701
C	131	ALA	THR	engineered mutation	UNP O60701
D	0	SER	-	expression tag	UNP O60701
D	131	ALA	THR	engineered mutation	UNP O60701
E	0	SER	-	expression tag	UNP O60701
E	131	ALA	THR	engineered mutation	UNP O60701
F	0	SER	-	expression tag	UNP O60701
F	131	ALA	THR	engineered mutation	UNP O60701

- Molecule 2 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 8 5	0	0
2	C	1	Total C O 13 8 5	0	0
2	C	1	Total C O 13 8 5	0	0
2	D	1	Total C O 13 8 5	0	0
2	F	1	Total C O 13 8 5	0	0

- 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	B	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
3	B	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
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	211	Total O 211 211	0	0
4	B	171	Total O 171 171	0	0
4	C	215	Total O 215 215	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	202	Total 202	O 202	0	0
4	E	174	Total 174	O 174	0	0
4	F	215	Total 215	O 215	0	0

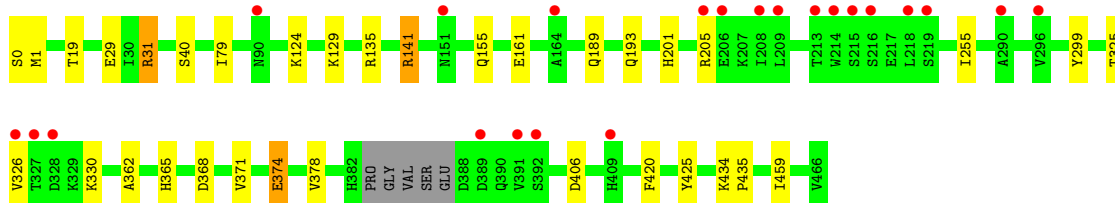
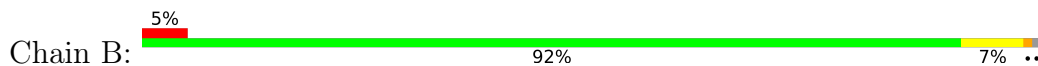
3 Residue-property plots [i](#)

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: UDP-glucose 6-dehydrogenase



- Molecule 1: UDP-glucose 6-dehydrogenase



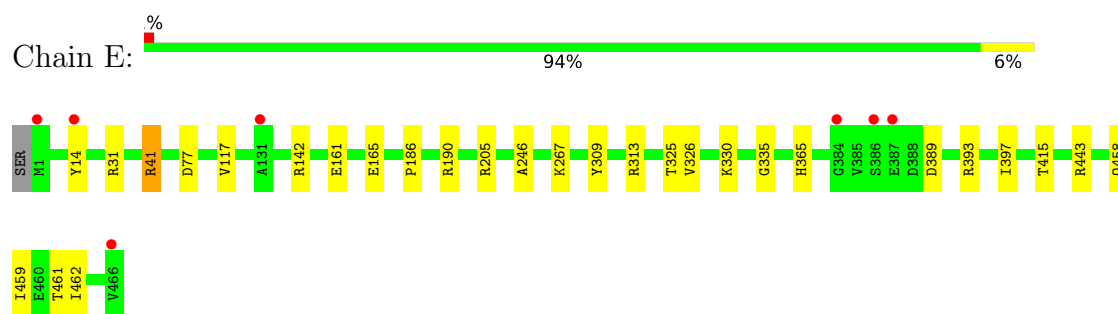
- Molecule 1: UDP-glucose 6-dehydrogenase



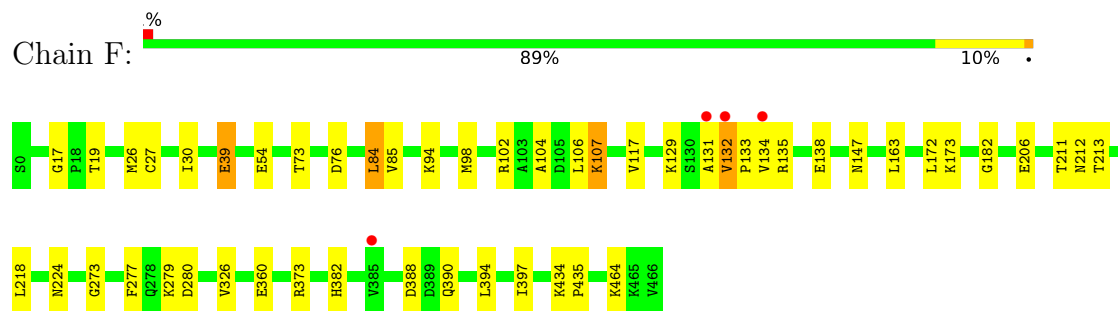
- Molecule 1: UDP-glucose 6-dehydrogenase



- Molecule 1: UDP-glucose 6-dehydrogenase



- Molecule 1: UDP-glucose 6-dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.06Å 106.61Å 349.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.90 – 2.40 52.90 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (52.90-2.40) 99.7 (52.90-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.5.0089	Depositor
R, R_{free}	0.198 , 0.241 0.199 , 0.242	Depositor DCC
R_{free} test set	2134 reflections (1.64%)	wwPDB-VP
Wilson B-factor (Å ²)	32.0	Xtrriage
Anisotropy	0.110	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 29.2	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	0.93	EDS
Total number of atoms	22977	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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: PG4, 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	0.90	2/3657 (0.1%)	0.89	4/4956 (0.1%)
1	B	0.90	1/3656 (0.0%)	1.00	8/4953 (0.2%)
1	C	0.91	2/3699 (0.1%)	0.89	3/5012 (0.1%)
1	D	0.92	3/3689 (0.1%)	0.93	4/4998 (0.1%)
1	E	0.87	1/3676 (0.0%)	0.88	5/4984 (0.1%)
1	F	0.92	0/3691	0.96	4/5003 (0.1%)
All	All	0.90	9/22068 (0.0%)	0.93	28/29906 (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	B	0	1
1	D	0	1
1	E	0	1
All	All	0	3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	31	ARG	CZ-NH1	-11.40	1.16	1.32
1	D	121	ASN	CG-ND2	-8.54	1.15	1.33
1	C	240	LEU	C-O	-7.28	1.15	1.24
1	D	121	ASN	CG-OD1	-7.03	1.10	1.23
1	C	31	ARG	CZ-NH1	-6.11	1.24	1.32

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	31	ARG	NE-CZ-NH2	23.40	140.26	119.20
1	B	31	ARG	NE-CZ-NH1	-18.16	103.33	121.50
1	D	205	ARG	CD-NE-CZ	13.42	143.18	124.40
1	D	205	ARG	NE-CZ-NH2	-11.04	109.26	119.20
1	E	41	ARG	CD-NE-CZ	9.06	137.09	124.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	31	ARG	Sidechain
1	D	205	ARG	Sidechain
1	E	41	ARG	Sidechain

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	3591	0	3566	14	0
1	B	3586	0	3562	21	1
1	C	3629	0	3611	12	1
1	D	3622	0	3613	22	0
1	E	3604	0	3576	14	0
1	F	3624	0	3595	43	0
2	A	13	0	18	4	0
2	C	26	0	36	4	0
2	D	13	0	18	2	0
2	F	13	0	18	5	0
3	A	4	0	6	0	0
3	B	16	0	24	0	0
3	C	4	0	6	0	0
3	D	20	0	30	0	0
3	E	12	0	18	0	0
3	F	12	0	18	0	0
4	A	211	0	0	6	0
4	B	171	0	0	4	0
4	C	215	0	0	2	0
4	D	202	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	174	0	0	3	0
4	F	215	0	0	3	0
All	All	22977	0	21715	134	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 134 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:D:467:PG4:O3	2:D:467:PG4:H72	1.65	0.93
1:B:326:VAL:HG11	1:B:362:ALA:HB2	1.53	0.90
1:B:326:VAL:CG1	1:B:362:ALA:HB2	2.10	0.81
1:B:374:GLU:O	1:B:378:VAL:HG23	1.81	0.80
1:F:326:VAL:CG1	1:F:360:GLU:HB3	2.11	0.80

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)
1:B:40:SER:OG	1:C:77:ASP:OD1[1_455]	1.82	0.38

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	460/467 (98%)	449 (98%)	11 (2%)	0	100	100
1	B	460/467 (98%)	447 (97%)	13 (3%)	0	100	100
1	C	466/467 (100%)	453 (97%)	13 (3%)	0	100	100
1	D	465/467 (100%)	455 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	466/467 (100%)	454 (97%)	12 (3%)	0	100	100
1	F	465/467 (100%)	446 (96%)	18 (4%)	1 (0%)	43	58
All	All	2782/2802 (99%)	2704 (97%)	77 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	132	VAL

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	385/400 (96%)	380 (99%)	5 (1%)	61	80
1	B	386/400 (96%)	381 (99%)	5 (1%)	61	80
1	C	391/400 (98%)	387 (99%)	4 (1%)	68	84
1	D	391/400 (98%)	388 (99%)	3 (1%)	73	86
1	E	385/400 (96%)	380 (99%)	5 (1%)	61	80
1	F	391/400 (98%)	387 (99%)	4 (1%)	68	84
All	All	2329/2400 (97%)	2303 (99%)	26 (1%)	65	82

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	161	GLU
1	E	117	VAL
1	F	107	LYS
1	D	462	ILE
1	E	161	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	155	GLN
1	E	302	GLN
1	F	390	GLN
1	F	292	ASN
1	B	302	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](#)

22 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	EDO	D	470	-	3,3,3	0.52	0	2,2,2	0.69	0
3	EDO	C	469	-	3,3,3	0.60	0	2,2,2	0.15	0
3	EDO	D	471	-	3,3,3	0.57	0	2,2,2	0.19	0
3	EDO	F	470	-	3,3,3	0.55	0	2,2,2	0.36	0
3	EDO	F	468	-	3,3,3	0.50	0	2,2,2	0.21	0
3	EDO	B	467	-	3,3,3	0.56	0	2,2,2	0.20	0
2	PG4	C	468	-	12,12,12	0.48	0	11,11,11	0.45	0
2	PG4	C	467	-	12,12,12	0.62	0	11,11,11	0.87	0
3	EDO	D	468	-	3,3,3	0.69	0	2,2,2	0.22	0
3	EDO	D	469	-	3,3,3	0.51	0	2,2,2	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	468	-	3,3,3	0.61	0	2,2,2	0.13	0
3	EDO	F	469	-	3,3,3	0.63	0	2,2,2	0.25	0
3	EDO	E	467	-	3,3,3	0.65	0	2,2,2	0.04	0
2	PG4	F	467	-	12,12,12	0.67	0	11,11,11	0.84	0
3	EDO	B	469	-	3,3,3	0.44	0	2,2,2	0.54	0
2	PG4	A	467	-	12,12,12	0.53	0	11,11,11	0.58	0
3	EDO	E	469	-	3,3,3	0.55	0	2,2,2	0.19	0
3	EDO	B	470	-	3,3,3	0.53	0	2,2,2	0.16	0
3	EDO	E	468	-	3,3,3	0.67	0	2,2,2	0.13	0
2	PG4	D	467	-	12,12,12	0.83	0	11,11,11	1.05	0
3	EDO	B	468	-	3,3,3	0.49	0	2,2,2	0.31	0
3	EDO	D	472	-	3,3,3	0.50	0	2,2,2	0.26	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	D	470	-	-	0/1/1/1	-
3	EDO	C	469	-	-	0/1/1/1	-
3	EDO	D	471	-	-	1/1/1/1	-
3	EDO	F	470	-	-	0/1/1/1	-
3	EDO	F	468	-	-	1/1/1/1	-
3	EDO	B	467	-	-	1/1/1/1	-
2	PG4	C	468	-	-	6/10/10/10	-
2	PG4	C	467	-	-	7/10/10/10	-
3	EDO	D	468	-	-	1/1/1/1	-
3	EDO	D	469	-	-	0/1/1/1	-
3	EDO	A	468	-	-	1/1/1/1	-
3	EDO	F	469	-	-	1/1/1/1	-
3	EDO	E	467	-	-	1/1/1/1	-
2	PG4	F	467	-	-	6/10/10/10	-
3	EDO	B	469	-	-	0/1/1/1	-
2	PG4	A	467	-	-	7/10/10/10	-
3	EDO	E	469	-	-	0/1/1/1	-
3	EDO	B	470	-	-	1/1/1/1	-
3	EDO	E	468	-	-	1/1/1/1	-
2	PG4	D	467	-	-	7/10/10/10	-
3	EDO	B	468	-	-	1/1/1/1	-
3	EDO	D	472	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	467	PG4	C5-C6-O4-C7
2	F	467	PG4	C3-C4-O3-C5
2	C	467	PG4	C1-C2-O2-C3
2	D	467	PG4	C1-C2-O2-C3
2	F	467	PG4	O3-C5-C6-O4

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	467	PG4	4	0
2	F	467	PG4	5	0
2	A	467	PG4	4	0
2	D	467	PG4	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 [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	464/467 (99%)	-0.52	6 (1%) 75 71	2, 13, 32, 52	0
1	B	462/467 (98%)	0.09	22 (4%) 35 32	3, 13, 32, 58	2 (0%)
1	C	467/467 (100%)	-0.52	5 (1%) 78 74	2, 13, 32, 68	1 (0%)
1	D	467/467 (100%)	-0.43	6 (1%) 75 71	3, 13, 32, 65	0
1	E	466/467 (99%)	-0.32	7 (1%) 72 68	2, 13, 32, 64	2 (0%)
1	F	467/467 (100%)	-0.52	4 (0%) 81 78	3, 13, 32, 64	0
All	All	2793/2802 (99%)	-0.37	50 (1%) 67 63	2, 13, 32, 68	5 (0%)

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	0	SER	4.7
1	B	213	THR	4.2
1	C	1	MET	4.2
1	A	1	MET	3.8
1	B	389	ASP	3.8

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	D	470	4/4	0.56	0.25	43,56,58,63	0
3	EDO	B	467	4/4	0.68	0.24	58,59,59,65	0
3	EDO	F	470	4/4	0.73	0.18	52,53,55,60	0
3	EDO	C	469	4/4	0.75	0.18	55,63,65,67	0
3	EDO	E	468	4/4	0.77	0.25	49,54,55,61	0
2	PG4	F	467	13/13	0.79	0.17	30,47,61,67	0
3	EDO	D	472	4/4	0.81	0.24	62,64,66,70	0
3	EDO	B	469	4/4	0.81	0.20	29,51,56,60	0
3	EDO	D	469	4/4	0.81	0.17	60,63,69,69	0
3	EDO	B	468	4/4	0.82	0.23	52,59,63,64	0
2	PG4	D	467	13/13	0.82	0.18	27,44,51,55	0
3	EDO	F	468	4/4	0.83	0.22	36,47,55,57	0
3	EDO	D	471	4/4	0.84	0.17	39,49,49,53	0
3	EDO	F	469	4/4	0.86	0.15	39,45,49,51	0
3	EDO	E	469	4/4	0.88	0.15	49,50,54,56	0
3	EDO	B	470	4/4	0.88	0.21	38,54,55,57	0
2	PG4	C	468	13/13	0.89	0.12	23,49,59,64	0
3	EDO	A	468	4/4	0.89	0.15	32,39,44,48	0
3	EDO	E	467	4/4	0.90	0.19	32,37,37,38	0
2	PG4	C	467	13/13	0.90	0.15	26,42,49,49	0
3	EDO	D	468	4/4	0.90	0.12	38,39,41,42	0
2	PG4	A	467	13/13	0.92	0.11	17,36,51,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.