



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:34 PM GMT

PDB ID : 3U2X
Title : Crystal Structure of Human Glycogenin-1 (GYG1) complexed with manganese, UDP and 1'-deoxyglucose
Authors : Chaikuad, A.; Froese, D.S.; Kryzstofinska, E.; von Delft, F.; Weigelt, J.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Oppermann, U.; Yue, W.W.; Structural Genomics Consortium (SGC)
Deposited on : 2011-10-04
Resolution : 1.77 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

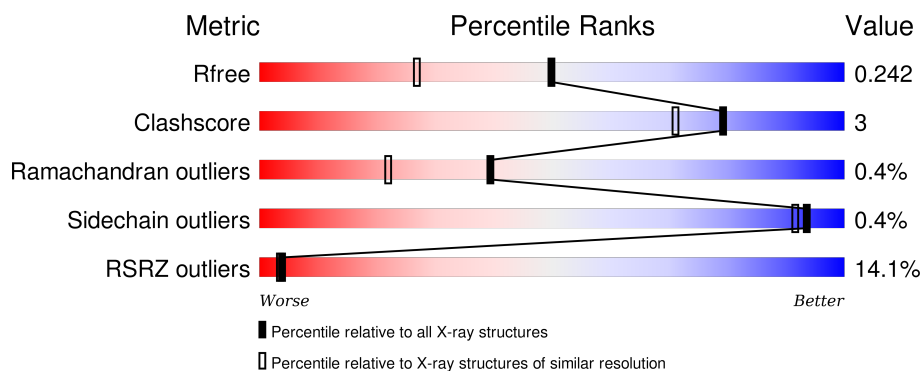
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 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}	91344	6655 (1.80-1.76)
Clashscore	102246	7658 (1.80-1.76)
Ramachandran outliers	100387	7570 (1.80-1.76)
Sidechain outliers	100360	7569 (1.80-1.76)
RSRZ outliers	91569	6671 (1.80-1.76)

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. 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	263	
1	B	263	

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
4	ASO	A	265[A]	-	-	-	X
4	ASO	A	265[B]	-	-	-	X
4	ASO	B	265[A]	-	-	-	X
4	ASO	B	265[B]	-	-	-	X
5	EDO	A	266	-	-	-	X
5	EDO	A	268	-	-	-	X
5	EDO	A	270[A]	-	-	-	X
5	EDO	A	270[B]	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4764 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 Glycogenin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	4	0
			2101	1354	343	396	8			
1	B	263	Total	C	N	O	S	0	2	0
			2098	1353	345	392	8			

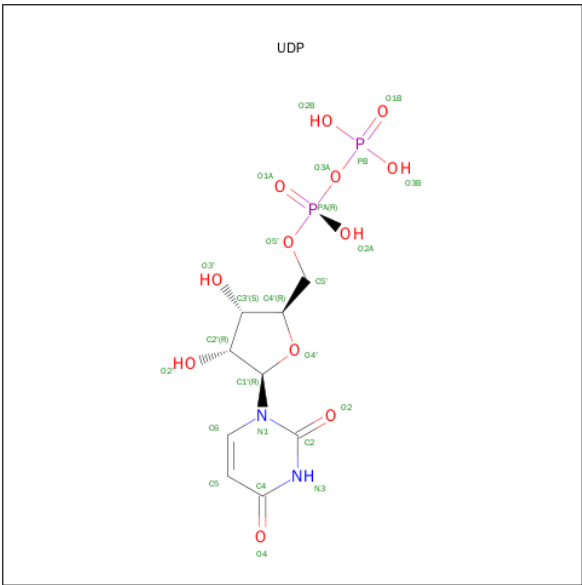
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP P46976
B	0	SER	-	EXPRESSION TAG	UNP P46976

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

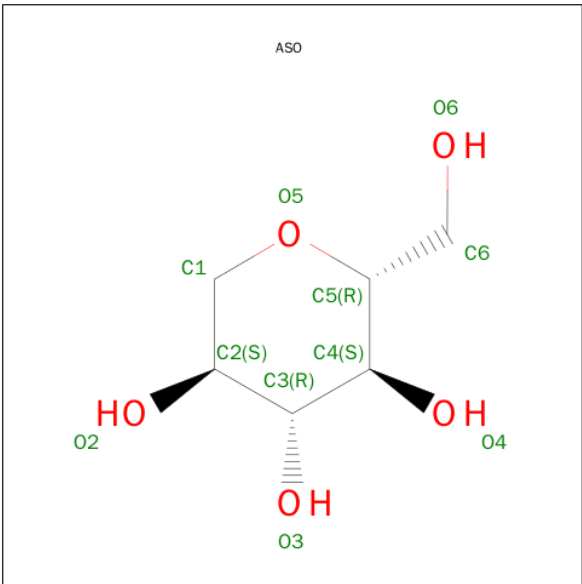
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mn	0	0
			1	1		
2	A	1	Total	Mn	0	0
			1	1		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C₉H₁₄N₂O₁₂P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 4 is SUGAR (1,5-ANHYDROSORBITOL) (three-letter code: ASO) (formula: $C_6H_{12}O_5$).



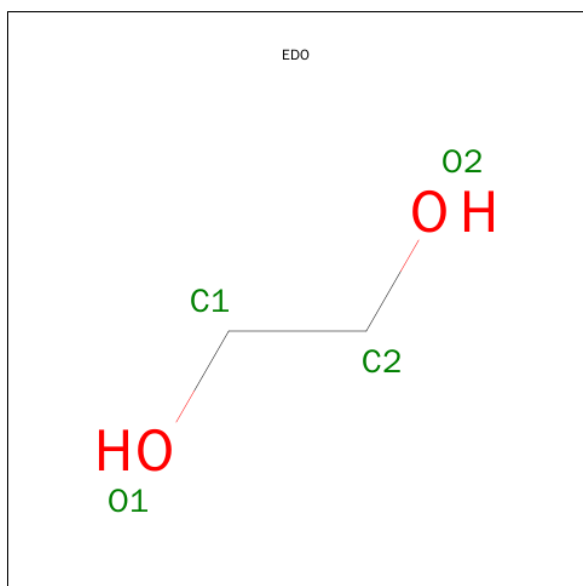
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	1
			22	12	10		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	1
			22	12	10		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	1
			8	4	4		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

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

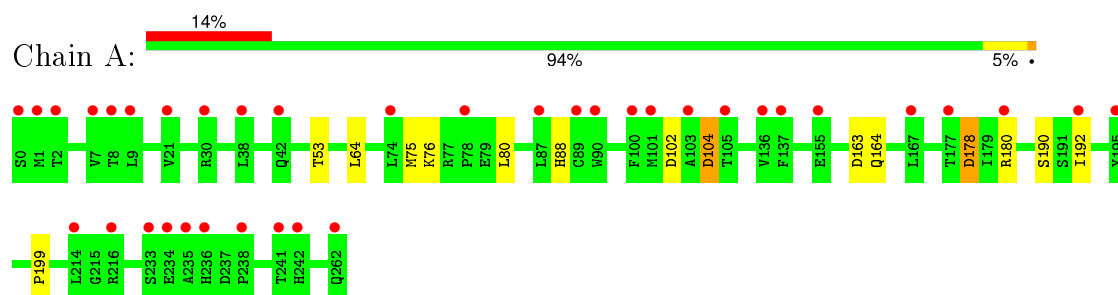
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	213	Total	O	0	0
			213	213		
6	B	208	Total	O	0	0
			208	208		

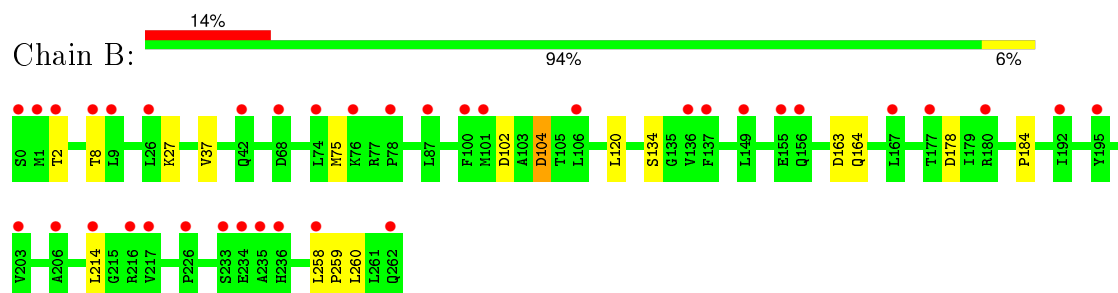
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: Glycogenin-1



• Molecule 1: Glycogenin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.70 Å 46.86 Å 69.70 Å 79.57° 88.96° 77.25°	Depositor
Resolution (Å)	30.00 – 1.77 30.46 – 1.77	Depositor EDS
% Data completeness (in resolution range)	91.1 (30.00-1.77) 85.5 (30.46-1.77)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 1.77 Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.198 , 0.247 0.197 , 0.242	Depositor DCC
R_{free} test set	2540 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	25.0	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 50332 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4764	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.81% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: UDP, MN, ASO, 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	0.68	0/2168	0.73	1/2956 (0.0%)
1	B	0.69	0/2160	0.75	4/2944 (0.1%)
All	All	0.68	0/4328	0.74	5/5900 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	104	ASP	CB-CG-OD2	7.59	125.13	118.30
1	B	104	ASP	CB-CG-OD1	7.44	124.99	118.30
1	B	104	ASP	OD1-CG-OD2	-7.10	109.81	123.30
1	A	104	ASP	CB-CG-OD1	6.54	124.18	118.30
1	B	214	LEU	CA-CB-CG	5.08	126.99	115.30

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	2101	0	2073	13	0
1	B	2098	0	2068	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	25	0	11	3	0
3	B	25	0	11	2	0
4	A	22	0	24	6	0
4	B	22	0	24	6	0
5	A	36	0	54	1	0
5	B	12	0	18	1	0
6	A	213	0	0	2	0
6	B	208	0	0	1	0
All	All	4764	0	4283	30	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 (30) 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)
3:B:264:UDP:O1B	4:B:265[B]:ASO:H11	1.61	0.99
3:A:264:UDP:O2B	4:A:265[A]:ASO:H11	1.78	0.83
3:B:264:UDP:O1B	4:B:265[B]:ASO:C1	2.39	0.70
1:B:164:GLN:HB2	4:B:265[B]:ASO:H4	1.76	0.67
1:B:102:ASP:HB3	1:B:104:ASP:OD1	1.96	0.65
1:A:164:GLN:HB2	4:A:265[B]:ASO:H4	1.82	0.62
4:A:265[B]:ASO:H11	6:A:482:HOH:O	2.04	0.58
1:A:64:LEU:CD1	1:A:88:HIS:NE2	2.67	0.58
1:B:164:GLN:OE1	4:B:265[A]:ASO:H12	2.08	0.52
5:A:271:EDO:H12	5:A:272:EDO:H22	1.90	0.52
1:A:64:LEU:HD11	1:A:88:HIS:NE2	2.24	0.52
1:B:134:SER:HG	4:B:265[A]:ASO:H2	1.75	0.51
1:A:64:LEU:HD13	1:A:88:HIS:NE2	2.26	0.51
1:B:184:PRO:HD3	5:B:268:EDO:H11	1.93	0.50
1:A:190[B]:SER:OG	1:A:192:ILE:HG22	2.13	0.49
1:B:2:THR:HG22	1:B:2:THR:O	2.13	0.49
1:A:64:LEU:HD11	1:A:88:HIS:CE1	2.50	0.47
1:A:102:ASP:HB3	1:A:104:ASP:OD1	2.15	0.47
1:A:199:PRO:HG2	1:B:75:MET:HG3	1.98	0.46
1:B:163:ASP:OD1	4:B:265[B]:ASO:O4	2.30	0.45
3:A:264:UDP:O2B	4:A:265[B]:ASO:H11	2.17	0.45
3:A:264:UDP:PB	4:A:265[A]:ASO:H11	2.57	0.44
1:A:163:ASP:OD1	4:A:265[B]:ASO:O4	2.32	0.43
1:A:53:THR:HG21	6:A:441:HOH:O	2.18	0.43
1:A:75:MET:O	1:A:76:LYS:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:THR:HG23	1:B:37:VAL:HG23	2.01	0.42
1:A:178:ASP:OD1	1:A:180:ARG:HB2	2.20	0.42
1:A:80:LEU:HD23	1:A:80:LEU:HA	1.86	0.41
1:B:27:LYS:NZ	6:B:282:HOH:O	2.53	0.41
1:B:258:LEU:N	1:B:259:PRO:CD	2.84	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	265/263 (101%)	257 (97%)	7 (3%)	1 (0%)	39	22
1	B	263/263 (100%)	256 (97%)	6 (2%)	1 (0%)	39	22
All	All	528/526 (100%)	513 (97%)	13 (2%)	2 (0%)	39	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	ASP
1	B	178	ASP

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	237/235 (101%)	237 (100%)	0	100	100
1	B	235/235 (100%)	233 (99%)	2 (1%)	84	78
All	All	472/470 (100%)	470 (100%)	2 (0%)	93	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	120	LEU
1	B	260	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

Of 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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	UDP	A	264	2	18,26,26	1.42	2 (11%)	26,40,40	1.72	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ASO	A	265[A]	-	11,11,11	0.62	0	14,15,15	1.71	4 (28%)
4	ASO	A	265[B]	-	11,11,11	1.06	0	14,15,15	1.88	4 (28%)
5	EDO	A	266	-	3,3,3	0.59	0	2,2,2	0.20	0
5	EDO	A	267	-	3,3,3	0.48	0	2,2,2	0.71	0
5	EDO	A	268	-	3,3,3	0.50	0	2,2,2	0.34	0
5	EDO	A	269	-	3,3,3	0.48	0	2,2,2	0.29	0
5	EDO	A	270[A]	-	3,3,3	0.53	0	2,2,2	0.26	0
5	EDO	A	270[B]	-	3,3,3	0.57	0	2,2,2	0.16	0
5	EDO	A	271	-	3,3,3	0.34	0	2,2,2	0.45	0
5	EDO	A	272	-	3,3,3	0.53	0	2,2,2	0.22	0
5	EDO	A	273	-	3,3,3	0.46	0	2,2,2	0.27	0
3	UDP	B	264	2	18,26,26	1.07	3 (16%)	26,40,40	2.05	4 (15%)
4	ASO	B	265[A]	-	11,11,11	0.58	0	14,15,15	1.41	3 (21%)
4	ASO	B	265[B]	-	11,11,11	0.73	0	14,15,15	1.53	4 (28%)
5	EDO	B	266	-	3,3,3	0.45	0	2,2,2	0.24	0
5	EDO	B	267	-	3,3,3	0.39	0	2,2,2	0.25	0
5	EDO	B	268	-	3,3,3	0.45	0	2,2,2	0.53	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	UDP	A	264	2	-	0/12/32/32	0/2/2/2
4	ASO	A	265[A]	-	-	0/2/19/19	0/1/1/1
4	ASO	A	265[B]	-	-	0/2/19/19	0/1/1/1
5	EDO	A	266	-	-	0/1/1/1	0/0/0/0
5	EDO	A	267	-	-	0/1/1/1	0/0/0/0
5	EDO	A	268	-	-	0/1/1/1	0/0/0/0
5	EDO	A	269	-	-	0/1/1/1	0/0/0/0
5	EDO	A	270[A]	-	-	0/1/1/1	0/0/0/0
5	EDO	A	270[B]	-	-	0/1/1/1	0/0/0/0
5	EDO	A	271	-	-	0/1/1/1	0/0/0/0
5	EDO	A	272	-	-	0/1/1/1	0/0/0/0
5	EDO	A	273	-	-	0/1/1/1	0/0/0/0
3	UDP	B	264	2	-	0/12/32/32	0/2/2/2
4	ASO	B	265[A]	-	-	0/2/19/19	0/1/1/1
4	ASO	B	265[B]	-	-	0/2/19/19	0/1/1/1
5	EDO	B	266	-	-	0/1/1/1	0/0/0/0
5	EDO	B	267	-	-	0/1/1/1	0/0/0/0
5	EDO	B	268	-	-	0/1/1/1	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	264	UDP	PB-O3B	-2.56	1.45	1.54
3	B	264	UDP	PB-O2B	-2.01	1.47	1.54
3	B	264	UDP	C6-N1	2.06	1.38	1.35
3	B	264	UDP	C4-N3	2.35	1.37	1.33
3	A	264	UDP	C4-N3	3.09	1.38	1.33

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	265[A]	ASO	O2-C2-C3	-3.44	103.21	110.12
4	B	265[B]	ASO	C1-O5-C5	-2.97	108.48	112.25
4	B	265[A]	ASO	O2-C2-C3	-2.83	104.42	110.12
3	B	264	UDP	PA-O3A-PB	-2.78	123.36	132.67
3	B	264	UDP	C4'-O4'-C1'	-2.44	107.04	109.72
3	A	264	UDP	PA-O3A-PB	-2.37	124.70	132.67
4	A	265[B]	ASO	O2-C2-C3	-2.35	105.39	110.12
4	B	265[B]	ASO	O3-C3-C4	-2.18	105.42	110.34
4	A	265[B]	ASO	C6-C5-C4	-2.11	107.80	113.02
4	A	265[A]	ASO	O3-C3-C4	2.00	114.85	110.34
4	B	265[A]	ASO	O3-C3-C4	2.13	115.13	110.34
4	B	265[B]	ASO	O4-C4-C5	2.20	115.07	109.24
4	B	265[A]	ASO	C1-C2-C3	2.28	112.24	109.54
4	A	265[A]	ASO	O2-C2-C1	2.35	113.91	109.21
4	B	265[B]	ASO	C3-C4-C5	2.47	114.50	110.20
3	A	264	UDP	O2B-PB-O1B	2.55	118.79	110.58
3	B	264	UDP	O3B-PB-O1B	2.60	118.94	110.58
4	A	265[B]	ASO	C1-O5-C5	2.85	115.87	112.25
4	A	265[A]	ASO	C1-O5-C5	3.02	116.08	112.25
4	A	265[B]	ASO	C1-C2-C3	4.20	114.51	109.54
3	A	264	UDP	C4-N3-C2	6.46	120.54	114.14
3	B	264	UDP	C4-N3-C2	8.12	122.18	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	264	UDP	3	0
4	A	265[A]	ASO	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	265[B]	ASO	4	0
5	A	271	EDO	1	0
5	A	272	EDO	1	0
3	B	264	UDP	2	0
4	B	265[A]	ASO	2	0
4	B	265[B]	ASO	4	0
5	B	268	EDO	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	263/263 (100%)	0.81	37 (14%) 4 3	14, 24, 42, 66	0
1	B	263/263 (100%)	0.78	37 (14%) 4 3	14, 23, 43, 71	0
All	All	526/526 (100%)	0.80	74 (14%) 4 3	14, 24, 43, 71	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	THR	7.4
1	B	236	HIS	6.7
1	B	235	ALA	6.4
1	A	1	MET	6.0
1	A	0	SER	6.0
1	A	233	SER	5.9
1	B	233	SER	5.9
1	A	136	VAL	4.9
1	A	236	HIS	4.7
1	B	1	MET	4.5
1	B	136	VAL	4.5
1	A	100	PHE	4.2
1	A	137	PHE	4.1
1	A	235	ALA	4.0
1	B	262	GLN	3.9
1	A	2	THR	3.9
1	B	180[A]	ARG	3.7
1	B	234	GLU	3.6
1	A	9	LEU	3.6
1	B	137	PHE	3.5
1	A	216	ARG	3.4
1	B	216	ARG	3.3
1	B	74	LEU	3.3
1	B	100	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	87	LEU	3.2
1	B	0	SER	3.1
1	A	234	GLU	3.1
1	A	7	VAL	3.1
1	A	8	THR	3.1
1	B	192	ILE	3.0
1	B	76	LYS	3.0
1	B	258	LEU	3.0
1	A	238	PRO	3.0
1	A	195	TYR	2.9
1	B	206	ALA	2.8
1	A	155	GLU	2.8
1	A	214	LEU	2.8
1	A	74	LEU	2.7
1	A	180	ARG	2.7
1	A	87	LEU	2.6
1	B	156	GLN	2.6
1	B	155	GLU	2.5
1	B	106	LEU	2.5
1	A	103	ALA	2.5
1	B	217	VAL	2.5
1	A	177[A]	THR	2.4
1	A	241	THR	2.4
1	A	242	HIS	2.4
1	A	262	GLN	2.3
1	A	101	MET	2.3
1	A	78	PRO	2.3
1	B	78	PRO	2.3
1	A	89	CYS	2.3
1	A	192	ILE	2.3
1	B	195	TYR	2.2
1	B	167	LEU	2.2
1	B	203	VAL	2.2
1	A	167	LEU	2.2
1	B	9	LEU	2.2
1	B	177	THR	2.2
1	B	68	ASP	2.2
1	B	101	MET	2.2
1	A	38	LEU	2.1
1	B	149	LEU	2.1
1	A	105	THR	2.1
1	A	42[A]	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	90	TRP	2.1
1	A	30	ARG	2.1
1	B	42	GLN	2.1
1	B	26	LEU	2.1
1	B	214	LEU	2.1
1	B	8	THR	2.0
1	A	21	VAL	2.0
1	B	226	PRO	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	EDO	A	270[B]	4/4	0.90	0.30	6.24	23,24,24,25	4
5	EDO	A	270[A]	4/4	0.90	0.30	5.93	28,30,30,33	4
4	ASO	B	265[A]	11/11	0.80	0.30	5.53	28,38,39,40	11
4	ASO	B	265[B]	11/11	0.80	0.30	5.50	3,15,19,19	11
4	ASO	A	265[B]	11/11	0.78	0.28	3.60	2,17,21,21	11
4	ASO	A	265[A]	11/11	0.78	0.28	3.56	24,32,35,35	11
5	EDO	A	268	4/4	0.83	0.15	2.19	63,63,64,64	0
5	EDO	A	266	4/4	0.93	0.20	2.09	33,35,35,36	0
5	EDO	A	269	4/4	0.79	0.14	1.27	46,48,48,50	0
5	EDO	B	267	4/4	0.92	0.19	0.92	35,39,40,42	0
5	EDO	B	266	4/4	0.94	0.14	0.79	29,32,33,33	0
5	EDO	A	271	4/4	0.95	0.10	0.41	28,29,30,30	0
5	EDO	A	273	4/4	0.80	0.15	-0.29	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	EDO	B	268	4/4	0.81	0.14	-0.41	42,43,43,43	0
3	UDP	B	264	25/25	0.96	0.09	-1.11	13,17,19,21	0
3	UDP	A	264	25/25	0.96	0.10	-1.15	13,17,20,21	0
5	EDO	A	272	4/4	0.80	0.15	-	40,42,44,45	0
2	MN	A	263	1/1	1.00	0.05	-	15,15,15,15	0
2	MN	B	263	1/1	1.00	0.05	-	14,14,14,14	0
5	EDO	A	267	4/4	0.64	0.41	-	56,56,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.