



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 5, 2025 – 02:14 PM EDT

PDB ID : 9O4U / pdb\_00009o4u  
Title : Apo-structure of a beta-D-glucuronate dehydratase  
Authors : Alvarez, B.; Hettle, A.; Boraston, A.B.  
Deposited on : 2025-04-08  
Resolution : 2.19 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](mailto: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 Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

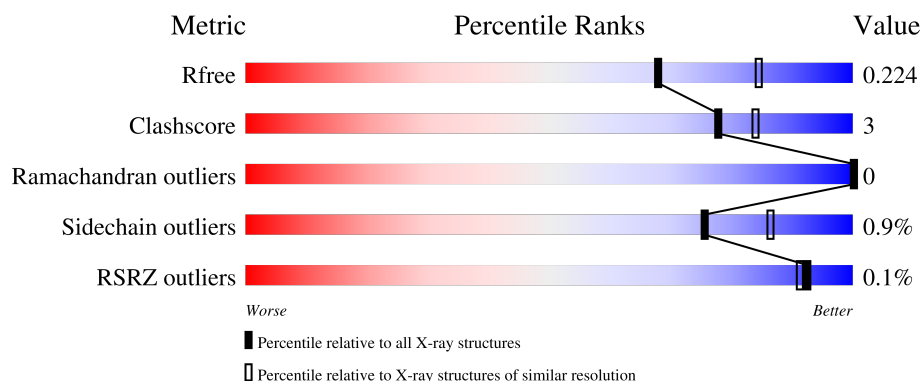
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*





The reported resolution of this entry is 2.19 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))
$R_{free}$	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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  $\geq 3$ , 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	400	
1	B	400	
1	C	400	
1	D	400	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13276 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 Beta-D-glucuronic acid dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	S	0	0	0
			3070	1961	530	563	16			
1	B	386	Total	C	N	O	S	0	0	0
			3058	1955	524	563	16			
1	C	384	Total	C	N	O	S	0	0	0
			3072	1962	531	563	16			
1	D	385	Total	C	N	O	S	0	0	0
			3070	1962	529	563	16			

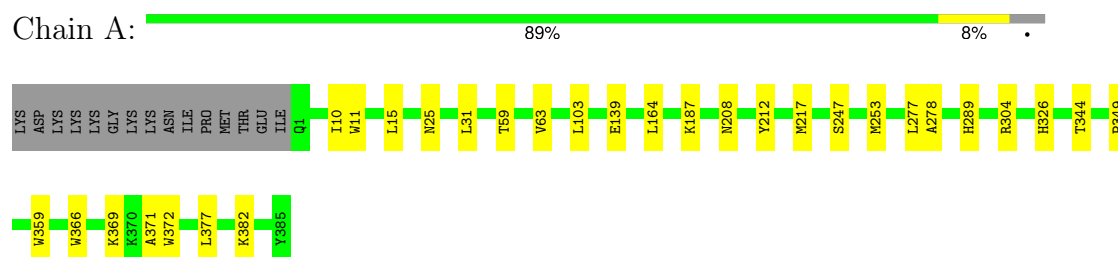
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	265	Total	O	0	0
			265	265		
2	B	254	Total	O	0	0
			254	254		
2	C	252	Total	O	0	0
			252	252		
2	D	235	Total	O	0	0
			235	235		

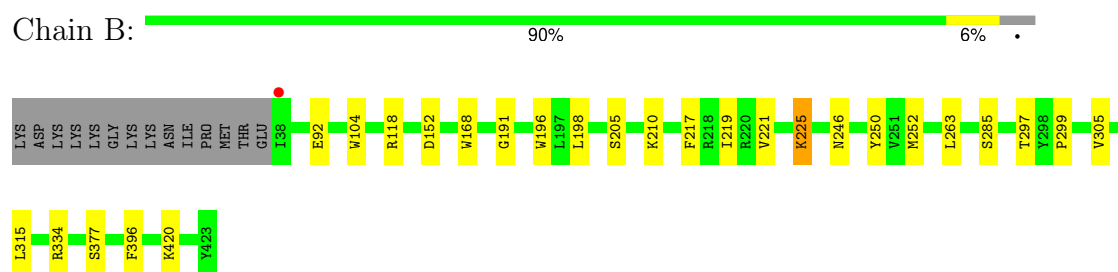
### 3 Residue-property plots [i](#)

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.

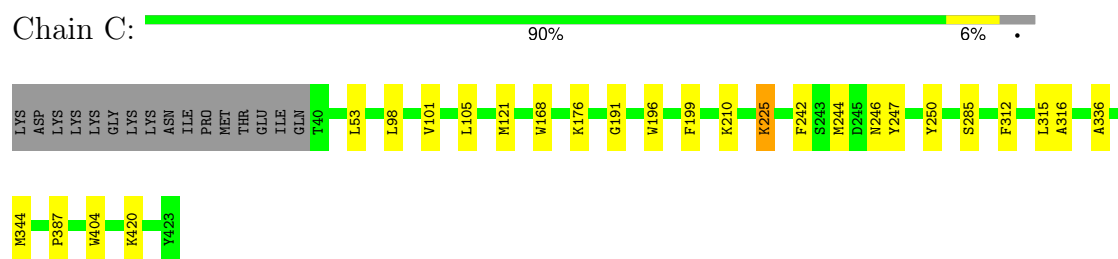
- Molecule 1: Beta-D-glucuronic acid dehydratase



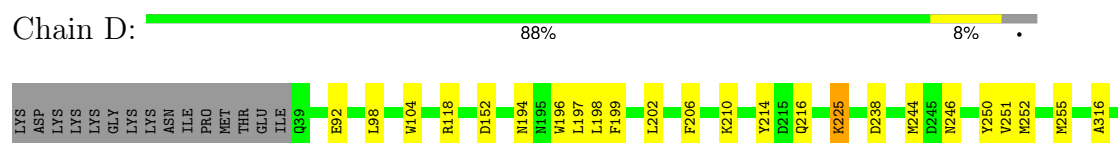
- Molecule 1: Beta-D-glucuronic acid dehydratase



- Molecule 1: Beta-D-glucuronic acid dehydratase



- Molecule 1: Beta-D-glucuronic acid dehydratase



S329	
Q332	
A336	
I337	
T338	
A339	
V340	
H341	
R342	
S377	
P387	
W410	
K420	
Y423	

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.52Å 161.37Å 88.61Å 90.00° 95.70° 90.00°	Depositor
Resolution (Å)	19.84 – 2.19 19.84 – 2.19	Depositor EDS
% Data completeness (in resolution range)	91.9 (19.84-2.19) 91.9 (19.84-2.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.84 (at 2.19Å)	Xtriage
Refinement program	REFMAC 9.0.005, PHENIX 1.21.2_5419	Depositor
R, $R_{free}$	0.163 , 0.216 0.174 , 0.224	Depositor DCC
$R_{free}$ test set	3865 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.1	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 28.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13276	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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](#)

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	0.29	0/3156	0.48	0/4286
1	B	0.29	0/3144	0.47	0/4276
1	C	0.29	0/3158	0.47	0/4286
1	D	0.28	0/3156	0.46	0/4287
All	All	0.29	0/12614	0.47	0/17135

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	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	251	VAL	Peptide

### 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	3070	0	2970	18	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3058	0	2928	16	0
1	C	3072	0	2983	19	0
1	D	3070	0	2963	19	0
2	A	265	0	0	2	0
2	B	254	0	0	0	0
2	C	252	0	0	1	0
2	D	235	0	0	0	0
All	All	13276	0	11844	66	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 (66) 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:187:LYS:HD3	1:C:225:LYS:HD3	1.74	0.70
1:D:244:MET:HA	1:D:244:MET:HE2	1.74	0.69
1:B:225:LYS:HD3	1:D:225:LYS:HD3	1.79	0.64
1:B:219:ILE:HD12	1:B:263:LEU:HD21	1.79	0.64
1:B:191:GLY:HA3	1:B:196:TRP:CE3	2.37	0.59
1:C:191:GLY:HA3	1:C:196:TRP:CE3	2.42	0.54
1:C:316:ALA:HB1	1:C:387:PRO:HD3	1.91	0.52
1:A:15:LEU:HD11	1:A:63:VAL:HG12	1.93	0.51
1:A:371:ALA:HB2	1:A:377:LEU:HD13	1.92	0.50
1:C:168:TRP:NE1	1:C:210:LYS:HE3	2.26	0.50
1:B:168:TRP:NE1	1:B:210:LYS:HE3	2.26	0.50
1:C:246:ASN:HB2	1:C:250:TYR:CZ	2.47	0.49
1:C:53:LEU:HD11	1:C:101:VAL:HG12	1.94	0.49
1:A:289:HIS:HE1	2:A:641:HOH:O	1.96	0.48
1:C:98:LEU:HA	1:C:101:VAL:HG22	1.95	0.48
1:B:92:GLU:HG2	1:B:152:ASP:OD2	2.14	0.47
1:B:285:SER:HB2	1:B:315:LEU:HA	1.97	0.47
1:A:59:THR:HA	1:A:344:THR:HG21	1.96	0.47
1:D:196:TRP:HA	1:D:199:PHE:CD2	2.50	0.46
1:D:214:TYR:CE2	1:D:216:GLN:HG2	2.51	0.46
1:A:278:ALA:HB1	1:A:349:PRO:HD3	1.98	0.46
1:C:196:TRP:HA	1:C:199:PHE:CD2	2.51	0.46
1:A:247:SER:HB2	1:A:277:LEU:HA	1.98	0.46
1:D:104:TRP:CE2	1:D:118:ARG:HG2	2.51	0.46
1:B:334:ARG:HD3	1:B:396:PHE:O	2.16	0.46
1:D:202:LEU:HD22	1:D:255:MET:HG2	1.98	0.45

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:SER:N	1:B:219:ILE:HD11	2.31	0.45
1:A:103:LEU:HA	1:A:103:LEU:HD23	1.75	0.45
1:D:225:LYS:HD2	1:D:225:LYS:HA	1.65	0.45
1:B:198:LEU:CD1	1:B:252:MET:HA	2.47	0.45
1:C:225:LYS:HA	1:C:225:LYS:HD2	1.53	0.45
1:A:10:ILE:HD13	1:A:304:ARG:HD2	1.99	0.44
1:A:11:TRP:CD2	1:A:359:TRP:HH2	2.35	0.44
1:C:336:ALA:HB2	1:C:404:TRP:HB3	1.98	0.44
1:C:242:PHE:CZ	1:C:244:MET:HE2	2.52	0.44
1:C:344:MET:HE3	1:D:410:TRP:CH2	2.53	0.44
1:D:98:LEU:HD23	1:D:98:LEU:HA	1.77	0.44
1:A:208:ASN:HB2	1:A:212:TYR:CZ	2.52	0.44
1:B:225:LYS:HD2	1:B:225:LYS:HA	1.69	0.44
1:C:168:TRP:O	1:C:176:LYS:HE3	2.18	0.44
1:D:316:ALA:HB1	1:D:387:PRO:HD3	2.00	0.44
1:C:168:TRP:CD1	1:C:210:LYS:HE3	2.53	0.43
1:A:366:TRP:CZ2	1:A:369:LYS:HD2	2.53	0.43
1:D:92:GLU:HG2	1:D:152:ASP:CG	2.44	0.43
1:D:329:SER:O	1:D:332:GLN:HG2	2.19	0.43
1:A:187:LYS:HA	1:A:187:LYS:HD2	1.79	0.43
1:A:139:GLU:HB3	2:A:569:HOH:O	2.18	0.42
1:A:372:TRP:CE2	1:B:297:THR:HB	2.54	0.42
1:C:312:PHE:HA	2:C:560:HOH:O	2.19	0.42
1:B:217:PHE:HE1	1:D:197:LEU:HD22	1.83	0.42
1:B:246:ASN:HB2	1:B:250:TYR:CZ	2.55	0.42
1:A:253:MET:HA	1:B:299:PRO:HB3	2.02	0.42
1:D:194:ASN:HB2	1:D:238:ASP:OD1	2.19	0.42
1:B:217:PHE:O	1:B:221:VAL:HG22	2.19	0.42
1:C:242:PHE:CE2	1:C:244:MET:HE2	2.55	0.41
1:D:246:ASN:HB2	1:D:250:TYR:CZ	2.55	0.41
1:C:285:SER:HB2	1:C:315:LEU:HA	2.01	0.41
1:D:198:LEU:CD1	1:D:252:MET:HA	2.50	0.41
1:D:338:THR:O	1:D:342:ARG:HG3	2.20	0.41
1:C:247:TYR:HA	1:C:250:TYR:HB2	2.03	0.41
1:A:164:LEU:HD22	1:A:217:MET:HG2	2.01	0.41
1:D:206:PHE:CE2	1:D:210:LYS:HE2	2.56	0.41
1:B:104:TRP:CE2	1:B:118:ARG:HG2	2.56	0.41
1:C:105:LEU:HD11	1:C:121:MET:HG2	2.03	0.41
1:D:336:ALA:O	1:D:340:VAL:HG23	2.21	0.40
1:A:25:ASN:HB3	1:A:31:LEU:HA	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	383/400 (96%)	374 (98%)	9 (2%)	0	100	100
1	B	384/400 (96%)	374 (97%)	10 (3%)	0	100	100
1	C	382/400 (96%)	371 (97%)	11 (3%)	0	100	100
1	D	383/400 (96%)	375 (98%)	8 (2%)	0	100	100
All	All	1532/1600 (96%)	1494 (98%)	38 (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	318/338 (94%)	316 (99%)	2 (1%)	84	91
1	B	313/338 (93%)	309 (99%)	4 (1%)	65	78
1	C	320/338 (95%)	318 (99%)	2 (1%)	84	91
1	D	317/338 (94%)	314 (99%)	3 (1%)	75	86
All	All	1268/1352 (94%)	1257 (99%)	11 (1%)	75	86

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	326	HIS
1	A	382	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	225	LYS
1	B	305	VAL
1	B	377	SER
1	B	420	LYS
1	C	225	LYS
1	C	420	LYS
1	D	225	LYS
1	D	377	SER
1	D	420	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	GLN
1	A	208	ASN
1	B	71	GLN
1	B	120	GLN
1	C	71	GLN
1	C	120	GLN
1	C	216	GLN
1	D	71	GLN
1	D	246	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	385/400 (96%)	-0.60	0 100 100	23, 30, 38, 51	0
1	B	386/400 (96%)	-0.59	1 (0%) 90 89	25, 30, 41, 53	0
1	C	384/400 (96%)	-0.56	0 100 100	26, 31, 41, 48	0
1	D	385/400 (96%)	-0.54	0 100 100	25, 32, 41, 51	0
All	All	1540/1600 (96%)	-0.57	1 (0%) 92 91	23, 31, 41, 53	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	38	ILE	2.3

### 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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.