



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 23, 2023 – 02:25 AM JST

PDB ID : 7YF5
Title : Crystal Structure of the UDPGA Binding Domain of the Human Phase II Metabolizing Enzyme UDP-Glucuronosyltransferase 2B10
Authors : Yin, X.L.; Tong, J.S.
Deposited on : 2022-07-07
Resolution : 1.53 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

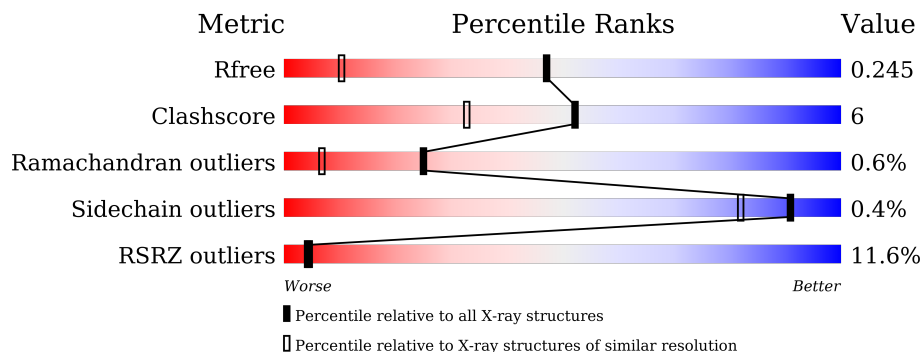
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.53 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	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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	174	
1	B	174	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2778 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-glucuronosyltransferase 2B10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	163	1266	808	219	232	7	0	0	0
1	A	174	1342	854	234	246	8	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	276	GLY	-	expression tag	UNP P36537
B	277	SER	-	expression tag	UNP P36537
B	278	ALA	-	expression tag	UNP P36537
B	279	MET	-	expression tag	UNP P36537
B	280	GLY	-	expression tag	UNP P36537
B	281	SER	-	expression tag	UNP P36537
A	276	GLY	-	expression tag	UNP P36537
A	277	SER	-	expression tag	UNP P36537
A	278	ALA	-	expression tag	UNP P36537
A	279	MET	-	expression tag	UNP P36537
A	280	GLY	-	expression tag	UNP P36537
A	281	SER	-	expression tag	UNP P36537

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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


- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	86	Total	O	0	0
			86	86		
3	A	79	Total	O	0	0
			79	79		

3 Residue-property plots [i](#)

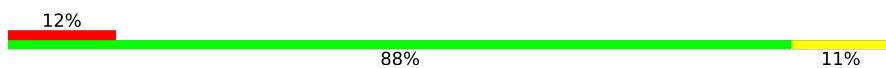
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

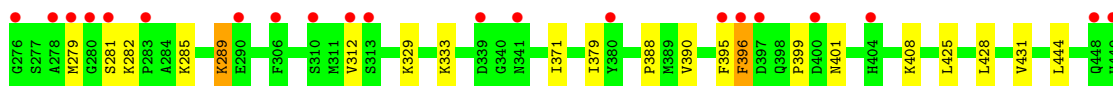
- Molecule 1: UDP-glucuronosyltransferase 2B10

Chain B: 



- Molecule 1: UDP-glucuronosyltransferase 2B10

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	85.91Å 58.39Å 68.87Å 90.00° 98.14° 90.00°	Depositor
Resolution (Å)	34.09 – 1.53 34.09 – 1.53	Depositor EDS
% Data completeness (in resolution range)	93.9 (34.09-1.53) 93.9 (34.09-1.53)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 1.53Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.215 , 0.245 0.215 , 0.245	Depositor DCC
R_{free} test set	2406 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.5	Xtrriage
Anisotropy	0.156	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2778	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.06% 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: SO4

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	0.40	1/1372 (0.1%)	0.55	0/1856
1	B	0.38	0/1294	0.56	0/1752
All	All	0.39	1/2666 (0.0%)	0.56	0/3608

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	289	LYS	CD-CE	-5.18	1.38	1.51

There are no bond angle outliers.

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	1342	0	1354	18	0
1	B	1266	0	1278	11	0
2	B	5	0	0	0	0
3	A	79	0	0	1	0
3	B	86	0	0	0	0
All	All	2778	0	2632	29	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 6.

All (29) 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:B:285:LYS:HZ2	1:B:287:LEU:H	1.15	0.89
1:B:395:PHE:HB3	1:B:396:PHE:CD2	2.27	0.69
1:A:289:LYS:N	1:A:289:LYS:HD3	2.15	0.60
1:A:395:PHE:HB3	1:A:396:PHE:CE1	2.37	0.60
1:B:371:ILE:HD11	1:B:428:LEU:HD21	1.84	0.59
1:B:408:LYS:HA	1:B:408:LYS:HE2	1.88	0.55
1:A:379:ILE:HD12	1:A:401:ASN:HB3	1.88	0.55
1:A:388:PRO:HB2	1:A:431:VAL:HG13	1.91	0.52
1:A:329:LYS:HD3	1:A:425:LEU:HD22	1.90	0.52
1:B:445:SER:O	1:B:446:ARG:HG2	2.09	0.52
1:B:285:LYS:HD2	1:B:286:PRO:HD2	1.93	0.51
1:B:395:PHE:HB3	1:B:396:PHE:CE2	2.46	0.51
1:A:371:ILE:HD11	1:A:428:LEU:HD21	1.92	0.51
1:A:395:PHE:HB3	1:A:396:PHE:CD1	2.46	0.51
1:B:446:ARG:NE	1:B:446:ARG:HA	2.27	0.50
1:A:312:VAL:HG12	1:A:312:VAL:O	2.13	0.48
1:A:396:PHE:CD1	1:A:396:PHE:N	2.81	0.46
1:A:285:LYS:HA	1:A:285:LYS:HD2	1.79	0.46
1:A:333:LYS:NZ	3:A:504:HOH:O	2.49	0.46
1:A:371:ILE:HD12	1:A:371:ILE:N	2.32	0.44
1:A:408:LYS:HD2	1:A:444:LEU:HD21	2.01	0.43
1:A:371:ILE:HG13	1:A:390:VAL:HB	2.01	0.42
1:A:396:PHE:O	1:A:399:PRO:HD2	2.19	0.42
1:B:303:VAL:HG12	1:B:333:LYS:HB2	2.02	0.41
1:B:443:LYS:HE3	1:B:443:LYS:HB3	1.76	0.41
1:A:279:MET:H	1:A:279:MET:HG2	1.68	0.41
1:B:396:PHE:CD2	1:B:396:PHE:N	2.87	0.41
1:A:281:SER:C	1:A:282:LYS:HD3	2.41	0.41
1:A:289:LYS:N	1:A:289:LYS:CD	2.82	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	172/174 (99%)	168 (98%)	3 (2%)	1 (1%)	25	7
1	B	161/174 (92%)	157 (98%)	3 (2%)	1 (1%)	25	7
All	All	333/348 (96%)	325 (98%)	6 (2%)	2 (1%)	25	7

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	396	PHE
1	A	396	PHE

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	145/145 (100%)	145 (100%)	0	100	100
1	B	137/145 (94%)	136 (99%)	1 (1%)	84	69
All	All	282/290 (97%)	281 (100%)	1 (0%)	91	82

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	354	LYS

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
2	SO4	B	501	-	4,4,4	0.24	0	6,6,6	0.37	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	174/174 (100%)	0.62	21 (12%) 4 4	18, 29, 49, 55	0
1	B	163/174 (93%)	0.53	18 (11%) 5 5	17, 26, 47, 66	0
All	All	337/348 (96%)	0.58	39 (11%) 4 4	17, 28, 49, 66	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	284	ALA	9.4
1	A	396	PHE	7.9
1	B	446	ARG	6.8
1	A	313	SER	6.6
1	A	276	GLY	5.3
1	B	285	LYS	5.1
1	A	395	PHE	4.9
1	B	396	PHE	4.9
1	A	278	ALA	4.7
1	A	448	GLN	4.3
1	B	289	LYS	4.1
1	B	287	LEU	3.9
1	A	449	HIS	3.8
1	B	286	PRO	3.6
1	A	380	TYR	3.5
1	B	445	SER	3.4
1	A	312	VAL	3.3
1	A	400	ASP	3.2
1	A	310	SER	3.1
1	B	339	ASP	3.1
1	A	339	ASP	3.1
1	B	313	SER	3.0
1	A	290	GLU	2.9
1	B	290	GLU	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	279	MET	2.8
1	A	397	ASP	2.7
1	B	314	ASN	2.5
1	A	281	SER	2.5
1	B	322	VAL	2.4
1	B	293	GLU	2.4
1	B	312	VAL	2.3
1	B	395	PHE	2.3
1	A	283	PRO	2.3
1	A	341	ASN	2.2
1	A	404	HIS	2.2
1	B	355	TRP	2.2
1	A	280	GLY	2.1
1	A	306	PHE	2.1
1	B	348	LEU	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 monosaccharides 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	SO4	B	501	5/5	0.96	0.13	29,30,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.