Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2023 – 06:52 PM EDT

PDB ID	:	5CMH
Title	:	GTA mutant with mercury - E303D
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Deposited on	:	2015-07-16
Resolution	:	1.61 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:

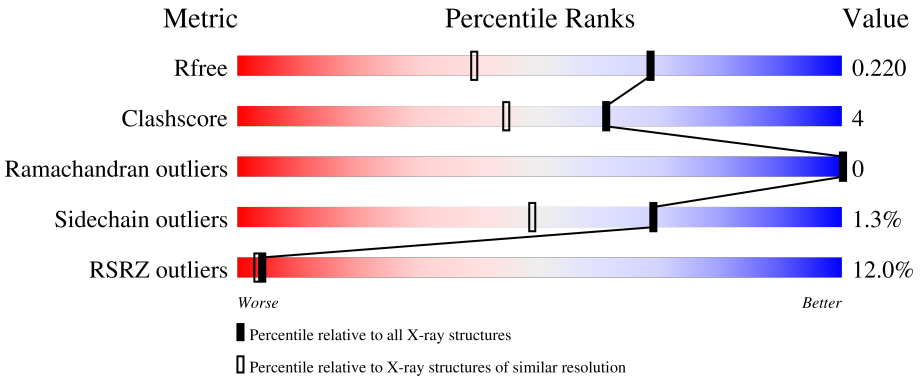
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.61 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	4693 (1.64-1.60)
Clashscore	141614	5002 (1.64-1.60)
Ramachandran outliers	138981	4888 (1.64-1.60)
Sidechain outliers	138945	4887 (1.64-1.60)
RSRZ outliers	127900	4609 (1.64-1.60)

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 <=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	295	11% 79% 8% 12%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2326 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 Histo-blood group ABO system transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	4	0
			2131	1390	360	371	10			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	GLU	-	expression tag	UNP P16442
A	62	PHE	-	expression tag	UNP P16442
A	63	MET	-	expression tag	UNP P16442
A	303	ASP	GLU	engineered mutation	UNP P16442
A	355	GLU	-	expression tag	UNP P16442

- Molecule 2 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Hg	0	0
			4	4		

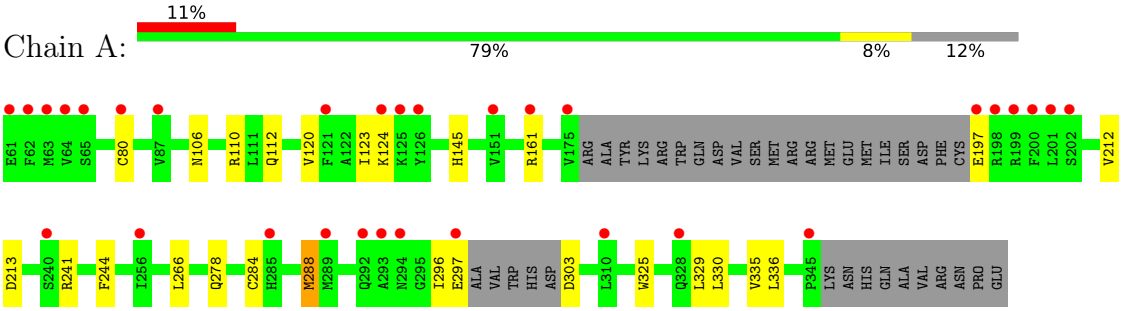
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	191	Total	O	0	0
			191	191		

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: Histo-blood group ABO system transferase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	52.77Å 148.83Å 79.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.33 – 1.61 19.84 – 1.61	Depositor EDS
% Data completeness (in resolution range)	98.8 (74.33-1.61) 98.9 (19.84-1.61)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 1.61Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.187 , 0.210 0.198 , 0.220	Depositor DCC
R_{free} test set	2026 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	24.9	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 45.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2326	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 5.27% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: HG

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	0.65	0/2201	0.87	9/2990 (0.3%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	288	MET	CG-SD-CE	9.22	114.95	100.20
1	A	241	ARG	NE-CZ-NH1	7.17	123.88	120.30
1	A	110	ARG	NE-CZ-NH2	6.59	123.60	120.30
1	A	241	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	A	161	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	A	244	PHE	CB-CG-CD1	5.37	124.56	120.80
1	A	244	PHE	CB-CG-CD2	-5.31	117.08	120.80
1	A	161	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	A	213	ASP	CB-CG-OD1	5.09	122.88	118.30

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	2131	0	2125	19	0
2	A	4	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	191	0	0	5	0
All	All	2326	0	2125	19	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 4.

All (19) 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:266:LEU:HD12	1:A:303:ASP:OD2	1.70	0.91
1:A:80:CYS:SG	2:A:403:HG:HG	2.08	0.71
1:A:329:LEU:O	3:A:501:HOH:O	2.09	0.71
1:A:123:ILE:HG22	1:A:124:LYS:HG3	1.74	0.67
1:A:284[B]:CYS:O	1:A:288:MET:HG3	1.99	0.63
1:A:284[A]:CYS:SG	1:A:288:MET:CE	2.88	0.62
1:A:325:TRP:CZ3	1:A:336[B]:LEU:HD11	2.38	0.58
1:A:330:LEU:HD23	3:A:501:HOH:O	2.07	0.54
1:A:120:VAL:HG22	1:A:212:VAL:HB	1.89	0.54
1:A:106:ASN:OD1	1:A:145:HIS:HE1	1.94	0.51
1:A:112:GLN:NE2	3:A:502:HOH:O	2.30	0.50
1:A:325:TRP:CE3	1:A:336[B]:LEU:HD11	2.49	0.48
1:A:284[A]:CYS:SG	1:A:288:MET:HE1	2.54	0.47
1:A:284[A]:CYS:SG	1:A:288:MET:HE2	2.56	0.45
1:A:120:VAL:CG2	1:A:212:VAL:HB	2.47	0.45
1:A:145:HIS:HD2	3:A:550:HOH:O	1.98	0.45
1:A:278:GLN:NE2	3:A:505:HOH:O	2.47	0.41
1:A:335:VAL:HG13	1:A:336[A]:LEU:HD22	2.03	0.41
1:A:325:TRP:CH2	1:A:336[B]:LEU:HD11	2.55	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	257/295 (87%)	254 (99%)	3 (1%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	234/263 (89%)	231 (99%)	3 (1%)	69 49

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	GLU
1	A	296	ILE
1	A	297	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	145	HIS
1	A	155	GLN
1	A	278	GLN
1	A	294	ASN
1	A	305	HIS

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 (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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, 95^{th} 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	259/295 (87%)	0.73	31 (11%) 4 3	15, 23, 42, 64	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	61	GLU	6.7
1	A	201	LEU	4.7
1	A	199	ARG	4.2
1	A	63	MET	4.2
1	A	64	VAL	4.2
1	A	197	GLU	4.1
1	A	200	PHE	4.0
1	A	297	GLU	4.0
1	A	293	ALA	3.9
1	A	202	SER	3.6
1	A	121	PHE	3.5
1	A	292	GLN	3.4
1	A	62	PHE	3.4
1	A	345	PRO	3.4
1	A	198	ARG	3.4
1	A	161	ARG	3.4
1	A	289	MET	3.0
1	A	310	LEU	2.9
1	A	285	HIS	2.8
1	A	65	SER	2.8
1	A	126	TYR	2.7
1	A	294	ASN	2.7
1	A	256	ILE	2.5
1	A	124	LYS	2.5
1	A	151	VAL	2.5
1	A	80	CYS	2.4
1	A	240	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	87[A]	VAL	2.2
1	A	328	GLN	2.1
1	A	175	VAL	2.0
1	A	125	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 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, 95^{th} 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	HG	A	402	1/1	0.95	0.07	27,27,27,27	1
2	HG	A	403	1/1	0.97	0.06	27,27,27,27	1
2	HG	A	401	1/1	0.98	0.04	33,33,33,33	1
2	HG	A	404	1/1	0.98	0.06	24,24,24,24	1

6.5 Other polymers (i)

There are no such residues in this entry.