

Full wwPDB X-ray Structure Validation Report (i)

Jul 9, 2024 – 08:02 PM EDT

PDB ID	:	8UAN
Title	:	The crystal structure of cobalt-bound human ADO C18S C239S variant at
		1.99 Angstrom
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Deposited on	:	2023-09-21
Resolution	:	1.99 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 (i) 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 (1)) were used in the production of this report:

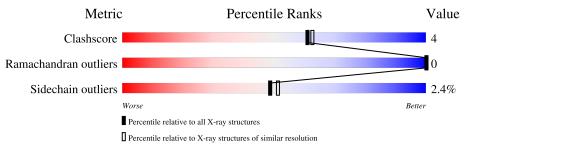
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.99 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 $(\#Entries)$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
	(#Entries)	(#Entries, resolution range(A))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain			
1	А	274	77%	10%	•	13%



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2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1993 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 2-aminoethanethiol dioxygenase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	239	Total 1888	C 1198	N 332	O 348	S 10	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

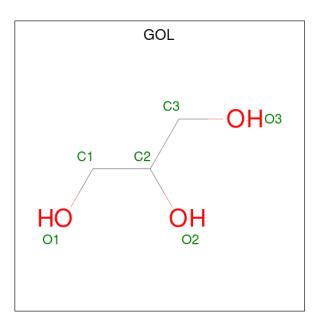
Chain	Residue	Modelled	Actual	Comment	Reference
А	-3	GLY	-	expression tag	UNP Q96SZ5
А	-2	HIS	-	expression tag	UNP Q96SZ5
А	-1	MET	-	expression tag	UNP Q96SZ5
А	0	ALA	-	expression tag	UNP Q96SZ5
А	1	SER	-	expression tag	UNP Q96SZ5
А	18	SER	CYS	engineered mutation	UNP Q96SZ5
А	239	SER	CYS	engineered mutation	UNP Q96SZ5

• Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co) (labeled as "Ligand of Interest" by depositor).

\mathbb{N}	ſol	Chain	Residues	Atoms	ZeroOcc	AltConf
	2	А	1	Total Co 1 1	0	0

• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	80	Total O 80 80	0	0

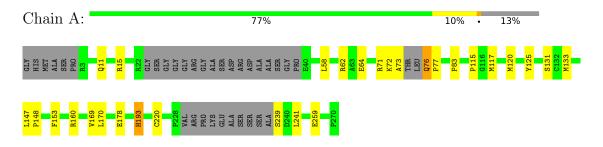


3 Residue-property plots (i)

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. 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. 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.

Note EDS failed to run properly.

• Molecule 1: 2-aminoethanethiol dioxygenase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	54.86Å 95.92 Å 118.16 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.62 - 1.99	Depositor
% Data completeness	98.9 (47.62-1.99)	Depositor
(in resolution range)		-
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.71 (at 1.98 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.198 , 0.235	Depositor
Wilson B-factor $(Å^2)$	37.6	Xtriage
Anisotropy	0.579	Xtriage
L-test for twinning ²	$< L > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.028 for $1/2$ *h- $1/2$ *k,- $3/2$ *h- $1/2$ *k,-l	Xtriage
Estimated twinning fraction	0.037 for $1/2$ *h+ $1/2$ *k, $3/2$ *h- $1/2$ *k,-l	Aurage
Total number of atoms	1993	wwPDB-VP
Average B, all atoms $(Å^2)$	47.0	wwPDB-VP

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.04% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: GOL, CO

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	А	0.40	0/1942	0.64	0/2643	

There are no bond length outliers.

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	А	1888	0	1851	17	0
2	А	1	0	0	0	0
3	А	24	0	32	1	0
4	А	80	0	0	0	0
All	All	1993	0	1883	17	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 (17) 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:76:GLN:HA	1:A:77:PRO:C	2.17	0.64
1:A:220:CYS:SG	3:A:302:GOL:H31	2.39	0.62
1:A:147:LEU:HD21	1:A:153:PHE:HE1	1.68	0.58
1:A:58:LEU:HD12	1:A:120:MET:HG2	1.87	0.56
1:A:72:LYS:O	1:A:73:ALA:HB2	2.11	0.51
1:A:83:PRO:HG3	1:A:259:GLU:HG2	1.94	0.50
1:A:170:LEU:HG	1:A:241:LEU:HD23	1.94	0.48
1:A:62:ARG:HH21	1:A:64:GLU:CD	2.18	0.45
1:A:11:GLN:O	1:A:15:ARG:HG3	2.17	0.44
1:A:115:PRO:O	1:A:117:MET:HG3	2.17	0.44
1:A:71:ARG:HG3	1:A:125:TYR:OH	2.19	0.42
1:A:133:MET:HB3	1:A:169:VAL:O	2.19	0.42
1:A:131:SER:O	1:A:193:HIS:HA	2.19	0.42
1:A:147:LEU:HD21	1:A:153:PHE:CE1	2.51	0.42
1:A:71:ARG:C	1:A:72:LYS:HG2	2.40	0.41
1:A:58:LEU:HA	1:A:58:LEU:HD23	1.87	0.41
1:A:147:LEU:HD12	1:A:148:PRO:HD2	2.02	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	А	231/274 (84%)	229~(99%)	2(1%)	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 Outlier		Outliers	Percentiles
1	А	206/228~(90%)	201~(98%)	5(2%)	49 51

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	76	GLN
1	А	160	ARG
1	А	178	GLU
1	А	193	HIS
1	А	239	SER

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)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	B	ond leng	gths	B	Bond ang	gles
10101	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	GOL	А	302	-	5,5,5	0.99	0	$5,\!5,\!5$	0.94	0
3	GOL	А	304	-	5,5,5	1.02	0	$5,\!5,\!5$	1.00	0
3	GOL	А	303	-	5,5,5	1.40	1 (20%)	$5,\!5,\!5$	0.72	0
3	GOL	А	305	-	$5,\!5,\!5$	0.95	0	$5,\!5,\!5$	1.09	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	GOL	А	302	-	-	1/4/4/4	-
3	GOL	А	304	-	-	1/4/4/4	-
3	GOL	А	303	-	-	1/4/4/4	-
3	GOL	А	305	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	303	GOL	C3-C2	2.05	1.60	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	305	GOL	O1-C1-C2-C3
3	А	305	GOL	O1-C1-C2-O2
3	А	303	GOL	C1-C2-C3-O3
3	А	305	GOL	C1-C2-C3-O3
3	А	305	GOL	O2-C2-C3-O3
3	А	302	GOL	C1-C2-C3-O3
3	А	304	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	302	GOL	1	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)

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

6.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

