

# wwPDB X-ray Structure Validation Summary Report (i)

May 26, 2020 – 10:31 am BST

PDB ID	:	50M8
$\operatorname{Title}$	:	Crystal form 2 of Alpha1-antichymotrypsin variant DBS-II-allo: an allosteri-
		cally modulated drug-binding serpin for doxorubicin
Authors	:	Schmidt, K.; Muller, Y.A.
Deposited on		
$\operatorname{Resolution}$	:	2.20  Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see references (1)) were used in the production of this report:

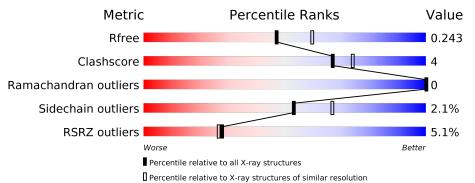
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
CCP4	:	7.0.044   (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 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 2.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	4898 (2.20-2.20)
Clashscore	141614	5594(2.20-2.20)
Ramachandran outliers	138981	5503(2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 on 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	А	369	80%	10%	• 9%
2	В	40	75%	8%	18%



## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3102 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 Alpha-1-antichymotrypsin.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	336	Total 2669	C 1705	N 437	O 516	S 11	0	0	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	-8	MET	-	initiating methionine	UNP P01011
А	-7	LYS	_	expression tag	UNP P01011
А	-6	HIS	-	expression tag	UNP P01011
А	-5	HIS	-	expression tag	UNP P01011
А	-4	HIS	-	expression tag	UNP P01011
А	-3	HIS	-	expression tag	UNP P01011
А	-2	HIS	-	expression tag	UNP P01011
А	-1	HIS	-	expression tag	UNP P01011
А	0	MET	-	expression tag	UNP P01011
А	1	LYS	_	expression tag	UNP P01011
A	2	GLN	_	expression tag	UNP P01011
А	24	ARG	LEU	engineered mutation	UNP P01011
А	194	$\mathbf{P}\mathbf{H}\mathbf{E}$	TRP	engineered mutation	UNP P01011
A	215	TYR	TRP	engineered mutation	UNP P01011
А	242	GLN	GLU	engineered mutation	UNP P01011
A	244	ASN	LYS	engineered mutation	UNP P01011
A	269	$\operatorname{SER}$	LEU	engineered mutation	UNP P01011
A	270	GLN	PRO	engineered mutation	UNP P01011
A	274	$\operatorname{SER}$	LYS	engineered mutation	UNP P01011
A	276	PHE	TRP	engineered mutation	UNP P01011
A	277	$\mathbf{P}\mathbf{H}\mathbf{E}$	ARG	engineered mutation	UNP P01011
A	278	GLU	ASP	engineered mutation	UNP P01011
А	349	ARG	ALA	engineered mutation	UNP P01011
А	355	LEU	VAL	engineered mutation	UNP P01011
А	356	GLU	LYS	engineered mutation	UNP P01011
А	357	VAL	ILE	engineered mutation	UNP P01011
A	358	LEU	THR	engineered mutation	UNP P01011

There are 29 discrepancies between the modelled and reference sequences:

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Chain	Residue	Modelled	Actual	Comment	Reference
A	359	PHE	LEU	engineered mutation	UNP P01011
A	360	GLN	LEU	engineered mutation	UNP P01011

• Molecule 2 is a protein called Alpha-1-antichymotrypsin.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace			
2	В	33	Total	C 187	N 46	O 44	S 2	0	0	0
2	В	33	279	187	46	44	$\frac{1}{2}$	0	(	)

There are 7 discrepancies between the modelled and reference sequences:

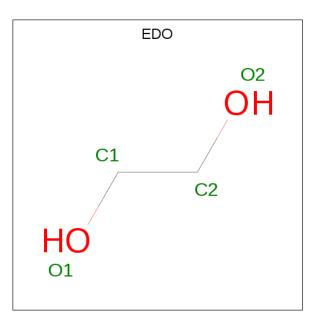
Chain	Residue	Modelled	Actual	Comment	Reference
В	361	GLY	SER	engineered mutation	UNP P01011
В	362	PRO	ALA	engineered mutation	UNP P01011
В	382	ASP	PRO	engineered mutation	UNP P01011
В	383	ASN	THR	engineered mutation	UNP P01011
В	384	PHE	ASP	engineered mutation	UNP P01011
В	386	TRP	GLN	engineered mutation	UNP P01011
В	387	SER	ASN	engineered mutation	UNP P01011

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Cl 1 1	0	0

• Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	А	1	Total 4	${ m C} 2$	O 2	0	0

• Molecule 5 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

$\mathbb{N}$	[o]	Chain	Residues	Atoms	ZeroOcc	AltConf
	5	А	1	Total Ni 1 1	0	0

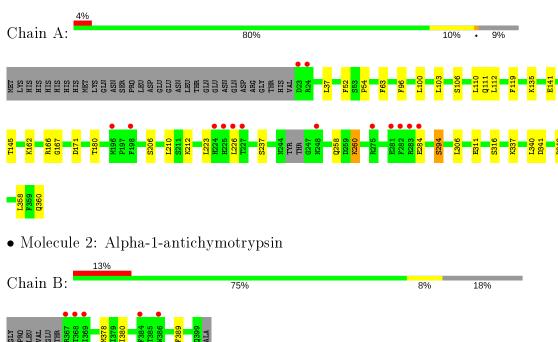
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	141	Total O 141 141	0	0
6	В	7	Total O 7 7	0	0



## 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 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: Alpha-1-antichymotrypsin



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	84.54Å $84.54$ Å $97.52$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	40.58 - 2.20	Depositor
Resolution (A)	40.58 - 2.15	EDS
% Data completeness	99.8 (40.58-2.20)	Depositor
(in resolution range)	99.7(40.58 - 2.15)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.06 (at 2.14 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
D D .	0.185 , $0.242$	Depositor
$R, R_{free}$	0.185 , $0.243$	DCC
$R_{free}$ test set	1120 reflections $(5.00\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	32.6	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.34 , $43.7$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3102	wwPDB-VP
Average B, all atoms $(Å^2)$	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.76% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: NI, EDO, CL

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		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.41	0/2715	0.58	0/3662	
2	В	0.47	0/287	0.57	0/388	
All	All	0.42	0/3002	0.58	0/4050	

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	2669	0	2661	23	0
2	В	279	0	283	3	0
3	А	1	0	0	0	0
4	А	4	0	6	0	0
5	А	1	0	0	0	0
6	А	141	0	0	1	0
6	В	7	0	0	0	0
All	All	3102	0	2950	23	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.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:LYS:HE2	1:A:258:GLN:HG2	1.10	1.09
1:A:212:LYS:HE2	1:A:258:GLN:CG	1.86	1.06
1:A:103:LEU:HD13	1:A:112:LEU:HD23	1.68	0.74
1:A:212:LYS:CE	1:A:258:GLN:HG2	2.06	0.66
1:A:96:PHE:O	1:A:100:LEU:HG	1.97	0.64

The worst 5 of 23 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	Perce	$\mathbf{ntiles}$
1	А	332/369~(90%)	329~(99%)	3~(1%)	0	100	100
2	В	31/40~(78%)	30~(97%)	1 (3%)	0	100	100
All	All	363/409~(89%)	359~(99%)	4 (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	Outliers	Percentiles	
1	А	296/328~(90%)	289~(98%)	7(2%)	49 62	

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Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
2	В	32/38~(84%)	32~(100%)	0	100	100
All	All	328/366~(90%)	321~(98%)	7 (2%)	53	67

5 of 7 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	А	210	LEU
1	А	294	SER
1	А	260	LYS
1	А	63	PHE
1	А	284	GLU

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 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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 Lin		Link	B	Bond lengths			Bond angles		
	Type	Cham	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
4	EDO	А	502	-	3,3,3	0.49	0	$^{2,2,2}$	0.38	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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
4	EDO	А	502	-	-	0/1/1/1	-

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 (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 $>2$	$OWAB(Å^2)$	Q<0.9
1	А	336/369~(91%)	-0.01	14 (4%) 36 34	18, 31, 54, 69	0
2	В	33/40~(82%)	0.34	5(15%) 2 2	22, 28, 56, 68	0
All	All	369/409 (90%)	0.02	19 (5%) 28 26	18, 31, 54, 69	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	284	GLU	5.2
2	В	384	PHE	4.7
1	А	226	LEU	4.5
1	А	282	PHE	4.4
1	А	225	HIS	4.2

### 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. 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	$\mathbf{Res}$	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{\AA}^2)$	Q<0.9
4	EDO	А	502	4/4	0.91	0.14	$39,\!41,\!43,\!51$	0
3	CL	А	501	1/1	0.98	0.09	32,32,32,32	0
5	NI	А	503	1/1	0.99	0.13	32,32,32,32	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

