

wwPDB X-ray Structure Validation Summary Report (i)

Oct 25, 2022 – 09:03 PM EDT

PDB ID : 7FLW

Title: PanDDA analysis group deposition – Aar2/RNaseH in complex with fragment

P05G07 from the F2X-Universal Library

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Deposited on : 2022-08-26

Resolution : 1.55 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 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 : 2.31.2

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

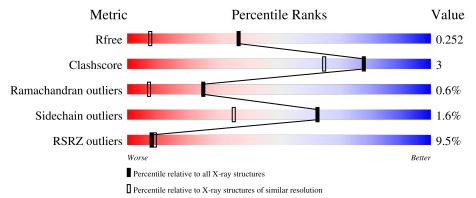
Validation Pipeline (wwPDB-VP) : 2.31.2

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 1.55 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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	258	8%	• • 8%		
2	В	308	87%	9% • •		



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9171 atoms, of which 4510 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	237	Total 4068	C 1287	H 2060	N 336	O 373	S 12	0	21	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1833	GLY	-	expression tag	UNP P33334
A	1834	ALA	-	expression tag	UNP P33334
A	1835	MET	-	expression tag	UNP P33334

• Molecule 2 is a protein called A1 cistron-splicing factor AAR2.

	Mol	Chain	Residues			Atom	S			ZeroOcc	AltConf	Trace
Ī	2	В	300	Total 5013	C 1645	H 2450	N 417	O 481	S 20	0	15	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-3	GLY	=	expression tag	UNP P32357
В	-2	ALA	-	expression tag	UNP P32357
В	-1	MET	-	expression tag	UNP P32357
В	0	ALA	-	expression tag	UNP P32357
В	166	SER	LEU	$\operatorname{conflict}$	UNP P32357
В	167	SER	LYS	$\operatorname{conflict}$	UNP P32357
В	?	-	LEU	deletion	UNP P32357
В	?	-	GLN	deletion	UNP P32357
В	?	-	LYS	deletion	UNP P32357
В	?	-	ALA	deletion	UNP P32357
В	?	-	GLY	deletion	UNP P32357
В	?	-	SER	deletion	UNP P32357
В	?	-	LYS	deletion	UNP P32357

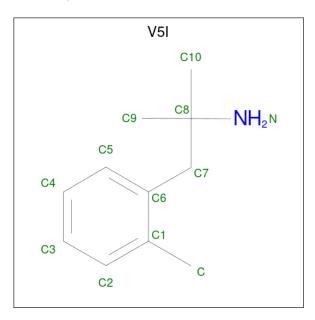
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Chain	Residue	Modelled	Actual	Comment	Reference
В	?	-	MET	deletion	UNP P32357
В	?	-	GLU	deletion	UNP P32357
В	?	-	ALA	deletion	UNP P32357
В	?	-	LYS	deletion	UNP P32357
В	?	-	ASN	deletion	UNP P32357
В	?	-	GLU	deletion	UNP P32357
В	170	SER	ASP	conflict	UNP P32357

 \bullet Molecule 3 is 2-methyl-1-(2-methylphenyl) propan-2-amine (three-letter code: V5I) (formula: $C_{11}H_{17}N).$



Mol	Chain	Residues	At	oms		ZeroOcc	AltConf
3	В	1	Total 12	C 11	N 1	0	0

• Molecule 4 is water.

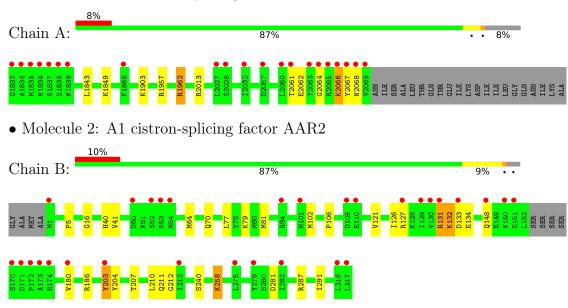
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	37	Total O 37 37	0	0
4	В	41	Total O 41 41	0	0



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 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: Pre-mRNA-splicing factor 8





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	87.65Å 82.00Å 93.84Å	Depositor
a, b, c, α , β , γ	90.00° 107.87° 90.00°	Depositor
Resolution (Å)	44.71 - 1.55	Depositor
resolution (A)	44.71 - 1.55	EDS
% Data completeness	99.5 (44.71-1.55)	Depositor
(in resolution range)	99.6 (44.71-1.55)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	0.96 (at 1.55Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
P.P.	0.220 , 0.255	Depositor
R, R_{free}	0.229 , 0.252	DCC
R_{free} test set	2099 reflections (2.30%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.344	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.41, 50.7	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	9171	wwPDB-VP
Average B, all atoms $(Å^2)$	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.00% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: V5I

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	Bo	nd lengths	Bond angles	
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5
1	A	0.52	0/2149	0.63	0/2911
2	В	0.70	8/2722 (0.3%)	0.81	9/3676 (0.2%)
All	All	0.63	8/4871 (0.2%)	0.74	9/6587 (0.1%)

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
2	В	0	2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
2	В	203[A]	TYR	C-N	-5.88	1.20	1.34
2	В	203[B]	TYR	C-N	-5.88	1.20	1.34
2	В	203[C]	TYR	C-N	-5.88	1.20	1.34
2	В	240	SER	C-O	-5.72	1.12	1.23
2	В	211[A]	GLN	C-N	5.28	1.42	1.33

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
2	В	127	ARG	NE-CZ-NH1	-8.14	116.23	120.30
2	В	211[A]	GLN	C-N-CA	-6.70	108.22	122.30
2	В	211[B]	GLN	C-N-CA	-6.70	108.22	122.30
2	В	203[A]	TYR	O-C-N	-6.59	112.15	122.70
2	В	203[B]	TYR	O-C-N	-6.59	112.15	122.70



There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	В	210	LEU	Mainchain

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	2008	2060	1974	8	0
2	В	2563	2450	2384	18	0
3	В	12	0	0	0	0
4	A	37	0	0	1	0
4	В	41	0	0	1	0
All	All	4661	4510	4358	26	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.

The worst 5 of 26 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} & (ext{Å}) \end{aligned}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:A:2061:THR:O	1:A:2064:GLY:N	2.08	0.87
2:B:132:LYS:O	2:B:134:GLU:N	2.28	0.67
2:B:70:GLN:HB3	2:B:81:MET:HE2	1.81	0.62
2:B:70:GLN:HB3	2:B:81:MET:CE	2.33	0.59
2:B:77:LEU:HD21	2:B:79:LYS:HE3	1.87	0.57

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	258/258 (100%)	247 (96%)	10 (4%)	1 (0%)	34 14
2	В	313/308 (102%)	297 (95%)	14 (4%)	2 (1%)	25 7
All	All	571/566 (101%)	544 (95%)	24 (4%)	3 (0%)	25 9

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	133	ASP
1	A	2068	ASN
2	В	106	PRO

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	$237/233\ (102\%)$	234 (99%)	3 (1%)	69 44		
2	В	292/284~(103%)	285 (98%)	7 (2%)	49 20		
All	All	529/517 (102%)	519 (98%)	10 (2%)	62 28		

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	204[C]	TYR
2	В	258	LYS
2	В	281	ASP
2	В	131	ARG
2	В	132	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	tes Link Bond lengths		Bond angles				
MOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts $ RMSZ \# Z > 2$		
3	V5I	В	501	-	8,12,12	2.28	4 (50%)	12,17,17	1.55	2 (16%)

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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	V5I	В	501	-	-	0/5/5/5	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
3	В	501	V5I	C-C1	-4.64	1.41	1.51
3	В	501	V5I	C7-C6	-2.34	1.48	1.51
3	В	501	V5I	C6-C1	-2.33	1.36	1.40
3	В	501	V5I	C2-C1	-2.19	1.35	1.39



All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
3	В	501	V5I	C9-C8-C7	2.92	113.79	109.95
3	В	501	V5I	C-C1-C2	-2.66	115.12	120.31

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^{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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	237/258 (91%)	0.65	21 (8%) 9 11	35, 47, 87, 116	0
2	В	300/308 (97%)	0.82	30 (10%) 7 8	35, 49, 88, 129	0
All	All	537/566 (94%)	0.74	51 (9%) 8 9	35, 48, 88, 129	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2069	VAL	10.7
2	В	53	SER	8.7
2	В	170	SER	7.6
1	A	1833	GLY	7.2
1	A	2060	LEU	6.8

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.



\mathbf{N}	lol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
	3	V5I	В	501	12/12	0.90	0.16	20,20,20,20	12

6.5 Other polymers (i)

There are no such residues in this entry.

