

Full wwPDB X-ray Structure Validation Report (i)

Aug 10, 2020 – 05:33 AM BST

PDB ID : 5QZJ

Title: PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for

ground state model 34

Authors: Weiss, M.S.; Wollenhaupt, J.; Metz, A.; Barthel, T.; Lima, G.M.A.; Heine, A.;

Mueller, U.; Klebe, G.

Deposited on : 2020-02-12

Resolution : 1.51 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 following versions of software and data (see references (1)) were used in the production of this report:

 $\begin{array}{ccc} Mol Probity & : & 4.02b\text{-}467 \\ Xtriage & (Phenix) & : & 1.13 \end{array}$

EDS : 2.13.1

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)

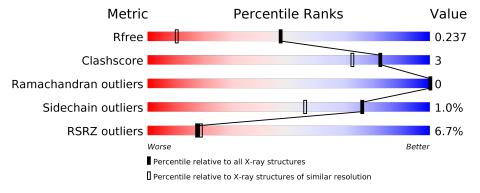
Validation Pipeline (wwPDB-VP) : 2.13.1

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 1.51 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$egin{aligned} ext{Similar resolution} \ (\# ext{Entries}, ext{resolution range}(ext{Å})) \end{aligned}$
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 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	A	258	88%	• 8%
2	В	308	7% 91%	6% • •



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4725 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Λ	237	Total	С	N	О	S	0	1.0	0
1	A	∠31	2002	1283	335	372	12	0	12	

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		At	oms			ZeroOcc	AltConf	Trace
9	D	300	Total	С	N	О	S	0	0	0
2	Б	300	2580	1654	421	485	20	U	9	U

There are 9 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	-	linker	UNP P32357
В	167	SER	-	linker	UNP P32357
В	168	SER	-	linker	UNP P32357
В	169	SER	_	linker	UNP P32357
В	170	SER	-	linker	UNP P32357

• Molecule 3 is water.



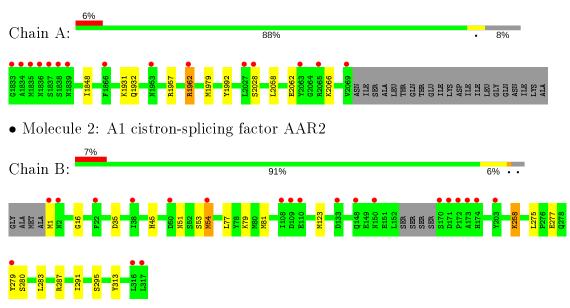
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	73	Total O 73 73	0	0
3	В	70	Total O 70 70	0	0



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	88.88Å 81.85Å 93.78Å	Depositor
a, b, c, α , β , γ	90.00° 108.61° 90.00°	Depositor
Resolution (Å)	44.67 - 1.51	Depositor
Resolution (A)	44.63 - 1.51	EDS
% Data completeness	98.2 (44.67-1.51)	Depositor
(in resolution range)	98.3 (44.63-1.51)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	0.95 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0238, PHENIX 1.16.3549	Depositor
D D.	0.221 , 0.223	Depositor
R, R_{free}	0.233 , 0.237	DCC
R_{free} test set	4836 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.169	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35, 38.0	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	4725	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.57% 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)

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	Mol Chain		lengths	Bond angles		
WIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	Α	0.74	0/2049	0.80	1/2775~(0.0%)	
2	В	0.71	0/2651	0.78	1/3581 (0.0%)	
All	All	0.72	0/4700	0.79	$2/6356 \ (0.0\%)$	

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	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
2	В	123	MET	CG-SD-CE	7.93	112.89	100.20
1	A	1992	TYR	CB-CG-CD1	5.31	124.19	121.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	В	54[A]	MET	Peptide

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	2002	0	2029	7	0
2	В	2580	0	2450	16	0
3	A	73	0	0	0	0
3	В	70	0	0	5	0
All	All	4725	0	4479	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 3.

All (23) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash	
Atom-1	Atom-2	${f distance} \; ({f \AA})$	$overlap (\AA)$	
2:B:54[B]:MET:SD	3:B:461:HOH:O	2.02	1.17	
2:B:54[A]:MET:HE2	3:B:469:HOH:O	1.81	0.81	
2:B:1:MET:SD	3:B:459:HOH:O	2.41	0.77	
2:B:54[A]:MET:CE	3:B:469:HOH:O	2.44	0.62	
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.20	0.62	
2:B:287:ARG:O	2:B:291:ILE:HD13	2.00	0.60	
1:A:1962:ARG:H	1:A:1962:ARG:HD3	1.72	0.55	
2:B:275:LEU:CD2	2:B:283:LEU:HD13	2.36	0.55	
2:B:280:SER:HB3	2:B:313:TYR:CE1	2.42	0.55	
2:B:51:ASN:HD21	2:B:53:SER:HB2	1.72	0.55	
2:B:1:MET:HB3	2:B:35:ASP:HA	1.90	0.53	
2:B:275:LEU:HD22	2:B:283:LEU:HD13	1.91	0.53	
2:B:258:LYS:HD2	2:B:258:LYS:H	1.77	0.48	
2:B:16:GLY:HA3	2:B:45:HIS:CE1	2.49	0.47	
1:A:2062:GLU:O	1:A:2066:LYS:HG2	2.15	0.47	
2:B:54[A]:MET:HG3	3:B:461:HOH:O	2.15	0.46	
1:A:1932:GLN:OE1	1:A:1957:ARG:NH1	2.45	0.43	
2:B:277:GLU:CD	2:B:277:GLU:H	2.22	0.43	
2:B:279:TYR:HB3	2:B:283:LEU:HD12	2.00	0.43	
2:B:77:LEU:HD21	2:B:79:LYS:HE3	2.01	0.42	
1:A:2062:GLU:HB3	1:A:2066:LYS:HE3	2.00	0.42	
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.67	0.41	

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	A	$248/258 \ (96\%)$	244 (98%)	4 (2%)	0	100	100
2	В	306/308~(99%)	295 (96%)	11 (4%)	0	100	100
All	All	554/566~(98%)	539 (97%)	15 (3%)	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	A	$226/233 \ (97\%)$	222 (98%)	4 (2%)	59 29
2	В	287/284 (101%)	284 (99%)	3 (1%)	76 56
All	All	513/517 (99%)	506 (99%)	7 (1%)	76 41

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1962	ARG
1	A	1979[A]	MET
1	A	1979[B]	MET
1	A	1979[C]	MET
2	В	81	MET
2	В	258	LYS
2	В	295	SER



Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	51	ASN

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)

There are no ligands in this entry.

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	${f Analysed}$	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	237/258 (91%)	0.42	15 (6%) 20 21	21, 28, 51, 80	0
2	В	300/308 (97%)	0.55	21 (7%) 16 17	21, 31, 58, 93	0
All	All	537/566 (94%)	0.49	36 (6%) 17 19	21, 30, 54, 93	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	1	MET	9.7
1	A	1833	GLY	8.7
2	В	170	SER	7.4
2	В	173	ALA	6.8
2	В	172	PRO	6.4
1	A	1838	SER	5.6
1	A	1837	SER	4.8
1	A	2065	ARG	4.4
1	A	1836	ASN	4.4
2	В	109	ASP	4.3
2	В	174	HIS	4.2
1	A	2069	VAL	4.1
1	A	1834	ALA	3.8
2	В	316	LEU	3.6
2	В	22	PHE	3.5
2	В	279	TYR	3.3
2	В	150	ASN	3.3
2	В	171	ASP	3.2
2	В	54[A]	MET	3.1
1	A	1839	ASN	2.8
1	A	2063	TYR	2.8
1	A	1866	PHE	2.7
1	A	1962	ARG	2.7
2	В	133	ASP	2.7

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	В	110	GLU	2.5
1	A	1835	MET	2.5
2	В	108	ILE	2.5
1	A	2028	SER	2.3
2	В	2	ASN	2.3
2	В	38	ILE	2.2
2	В	50	ASP	2.2
2	В	203[A]	TYR	2.1
2	В	148	GLN	2.1
1	A	1953	ASN	2.1
1	A	2027	LEU	2.1
2	В	317	LEU	2.1

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

