



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 5QYU / pdb_00005qyu
Title : PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for ground state model 10
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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 ⓘ 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

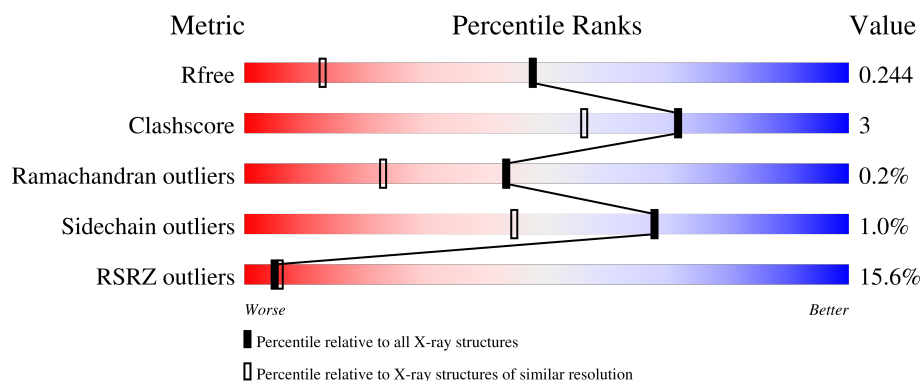
1 Overall quality at a glance

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (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 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 $\leq 5\%$. 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	15% 87% 8%
2	B	308	15% 88% 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4697 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	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	237	2002	1283	335	372	12	0	12	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	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	300	2580	1654	421	485	20	0	9	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P32357
B	-2	ALA	-	expression tag	UNP P32357
B	-1	MET	-	expression tag	UNP P32357
B	0	ALA	-	expression tag	UNP P32357
B	166	SER	-	linker	UNP P32357
B	167	SER	-	linker	UNP P32357
B	168	SER	-	linker	UNP P32357
B	169	SER	-	linker	UNP P32357
B	170	SER	-	linker	UNP P32357

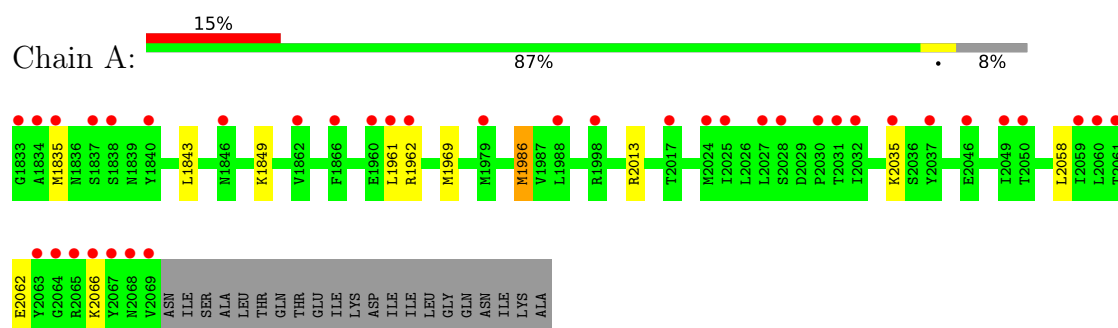
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	57	Total 57	O 57	0	0
3	B	58	Total 58	O 58	0	0

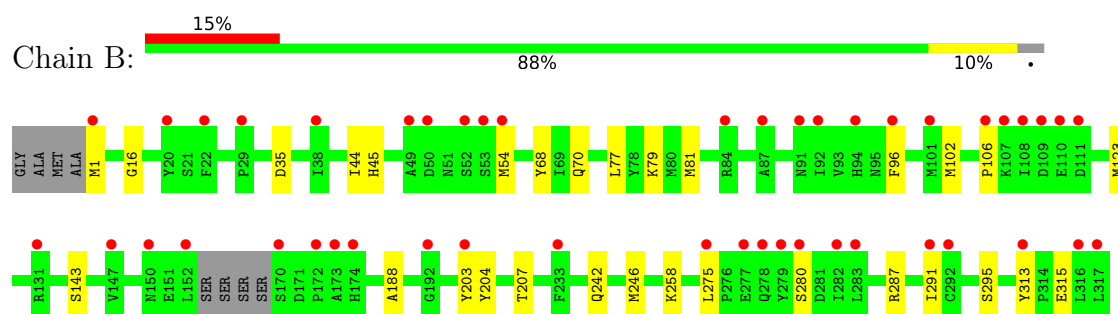
3 Residue-property plots

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



• Molecule 2: A1 cistron-splicing factor AAR2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	89.75Å 81.38Å 92.81Å 90.00° 108.78° 90.00°	Depositor
Resolution (Å)	44.53 – 1.51 44.53 – 1.51	Depositor EDS
% Data completeness (in resolution range)	99.1 (44.53-1.51) 99.9 (44.53-1.51)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.94 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0238, PHENIX 1.16.3549	Depositor
R, R_{free}	0.226 , 0.227 0.240 , 0.244	Depositor DCC
R_{free} test set	4776 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4697	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.05	0/2049	1.23	0/2775
2	B	1.00	0/2651	1.22	0/3581
All	All	1.02	0/4700	1.22	0/6356

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	A	2002	0	2029	9	0
2	B	2580	0	2450	21	0
3	A	57	0	0	0	0
3	B	58	0	0	1	0
All	All	4697	0	4479	30	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 (30) 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)
2:B:70:GLN:HB3	2:B:81:MET:HE2	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1835:MET:HE1	1:A:1961:LEU:HD12	1.73	0.71
2:B:280:SER:HB3	2:B:313:TYR:CE1	2.28	0.68
2:B:70:GLN:HB3	2:B:81:MET:CE	2.25	0.65
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.78	0.64
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.32	0.62
2:B:68:TYR:CE2	2:B:81:MET:HE3	2.37	0.60
2:B:287:ARG:O	2:B:291:ILE:HD13	2.04	0.58
1:A:2062:GLU:O	1:A:2066:LYS:HG2	2.04	0.57
2:B:1:MET:HB3	2:B:35:ASP:HA	1.89	0.53
1:A:1969:MET:HA	1:A:1969:MET:HE2	1.90	0.52
2:B:77:LEU:HD21	2:B:79:LYS:HE3	1.92	0.52
2:B:258:LYS:HD2	2:B:258:LYS:H	1.76	0.51
2:B:1:MET:N	3:B:402:HOH:O	2.45	0.50
2:B:96:PHE:CB	2:B:102:MET:HE3	2.42	0.49
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.38	0.48
2:B:280:SER:CB	2:B:313:TYR:CE1	2.95	0.48
2:B:16:GLY:HA3	2:B:45:HIS:CE1	2.49	0.48
1:A:2062:GLU:HB3	1:A:2066:LYS:HE3	1.98	0.46
2:B:275:LEU:HD23	2:B:275:LEU:HA	1.83	0.45
1:A:1835:MET:HE3	1:A:1835:MET:HB3	1.91	0.45
2:B:280:SER:HB3	2:B:313:TYR:CZ	2.54	0.43
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	2.00	0.43
2:B:54[B]:MET:HE1	2:B:143:SER:HB3	2.00	0.43
2:B:203[A]:TYR:CZ	2:B:207:THR:HG21	2.55	0.42
1:A:1986:MET:HE2	1:A:1986:MET:HB2	1.84	0.42
2:B:242:GLN:O	2:B:246:MET:HG3	2.19	0.42
2:B:44[A]:ILE:O	2:B:44[A]:ILE:HG23	2.19	0.41
2:B:188:ALA:HA	2:B:204:TYR:CD1	2.55	0.41
2:B:258:LYS:H	2:B:258:LYS:CD	2.33	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	248/258 (96%)	244 (98%)	4 (2%)	0	100	100
2	B	306/308 (99%)	297 (97%)	8 (3%)	1 (0%)	36	18
All	All	554/566 (98%)	541 (98%)	12 (2%)	1 (0%)	43	23

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	106	PRO

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	226/233 (97%)	224 (99%)	2 (1%)	70	49
2	B	287/284 (101%)	284 (99%)	3 (1%)	68	44
All	All	513/517 (99%)	508 (99%)	5 (1%)	68	44

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

Mol	Chain	Res	Type
1	A	1986	MET
1	A	2035	LYS
2	B	123	MET
2	B	295	SER
2	B	315	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1869	ASN
2	B	47	GLN
2	B	136	GLN

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 oligosaccharides 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

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, 95th 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	237/258 (91%)	1.00	38 (16%)	5 5	12, 34, 69, 103	12 (5%)
2	B	300/308 (97%)	0.98	46 (15%)	5 6	12, 36, 77, 101	9 (3%)
All	All	537/566 (94%)	0.99	84 (15%)	5 6	12, 35, 72, 103	21 (3%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1988	LEU	7.6
1	A	1979[A]	MET	6.9
2	B	152	LEU	6.9
1	A	2068	ASN	6.6
2	B	22	PHE	6.5
1	A	2069	VAL	6.4
2	B	279	TYR	5.6
2	B	316	LEU	5.6
2	B	170	SER	5.5
1	A	2064	GLY	5.3
1	A	2067	TYR	5.3
1	A	2060	LEU	5.2
2	B	54[A]	MET	5.2
1	A	2027	LEU	5.0
2	B	174	HIS	4.8
1	A	2063	TYR	4.8
2	B	1	MET	4.8
2	B	101	MET	4.8
1	A	2066	LYS	4.7
2	B	173	ALA	4.5
2	B	108	ILE	4.2
2	B	203[A]	TYR	4.1
1	A	2065	ARG	4.0
2	B	317	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	1833	GLY	3.9
2	B	53	SER	3.8
1	A	2061	THR	3.8
2	B	172	PRO	3.5
1	A	1866	PHE	3.4
2	B	147	VAL	3.3
2	B	277	GLU	3.2
1	A	1835	MET	3.1
1	A	2030	PRO	3.1
1	A	2028	SER	3.0
2	B	87	ALA	3.0
1	A	1840	TYR	3.0
2	B	92	ILE	3.0
2	B	111	ASP	3.0
2	B	283	LEU	3.0
1	A	1834	ALA	2.9
1	A	2025	ILE	2.9
2	B	291	ILE	2.9
1	A	2037	TYR	2.9
2	B	282	ILE	2.9
2	B	110	GLU	2.9
1	A	2017[A]	THR	2.9
2	B	96	PHE	2.8
1	A	2031	THR	2.8
1	A	2032	ILE	2.7
2	B	107	LYS	2.7
1	A	2035	LYS	2.7
2	B	84	ARG	2.7
2	B	94	HIS	2.6
2	B	109	ASP	2.6
1	A	1837	SER	2.6
2	B	38	ILE	2.6
2	B	280	SER	2.6
2	B	91	ASN	2.5
2	B	150	ASN	2.5
1	A	1962	ARG	2.5
2	B	20	TYR	2.5
2	B	278	GLN	2.5
1	A	2049	ILE	2.4
1	A	1961	LEU	2.4
2	B	275	LEU	2.4
1	A	2059	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	49	ALA	2.3
2	B	313	TYR	2.3
1	A	1838	SER	2.3
1	A	1846	ASN	2.2
1	A	1960[A]	GLU	2.2
1	A	1862	VAL	2.2
2	B	50	ASP	2.2
1	A	2024[A]	MET	2.2
1	A	2050	THR	2.2
2	B	233	PHE	2.2
2	B	52	SER	2.1
2	B	131	ARG	2.1
2	B	292	CYS	2.1
2	B	192	GLY	2.1
1	A	2046	GLU	2.1
2	B	29	PRO	2.1
1	A	1998	ARG	2.0
2	B	106	PRO	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 oligosaccharides 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.