



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 01:10 AM BST

PDB ID : 5R04
Title : PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for ground state model 55
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Deposited on : 2020-02-12
Resolution : 1.34 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
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

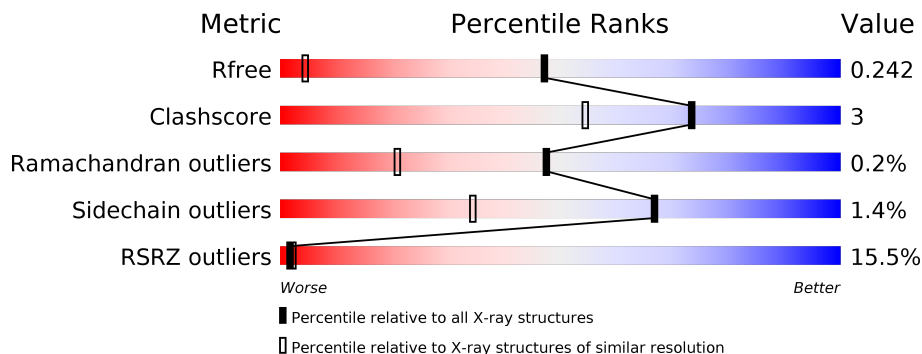
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.34 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}	130704	1385 (1.36-1.32)
Clashscore	141614	1417 (1.36-1.32)
Ramachandran outliers	138981	1397 (1.36-1.32)
Sidechain outliers	138945	1397 (1.36-1.32)
RSRZ outliers	127900	1369 (1.36-1.32)

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 $\leq 5\%$. 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	
2	B	308	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 4787 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

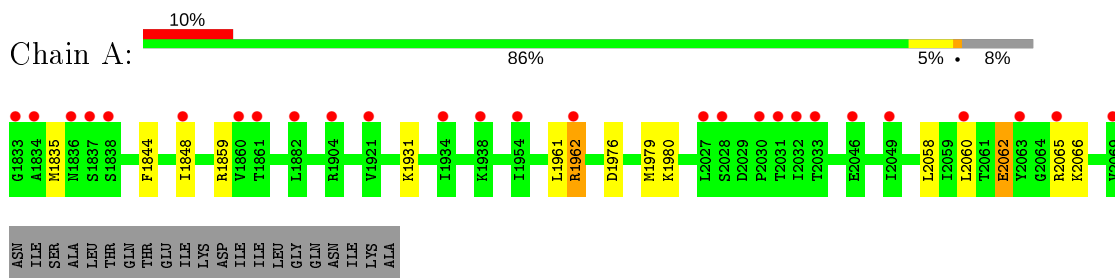
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	112	Total 112	O 112	0	0
3	B	93	Total 93	O 93	0	0

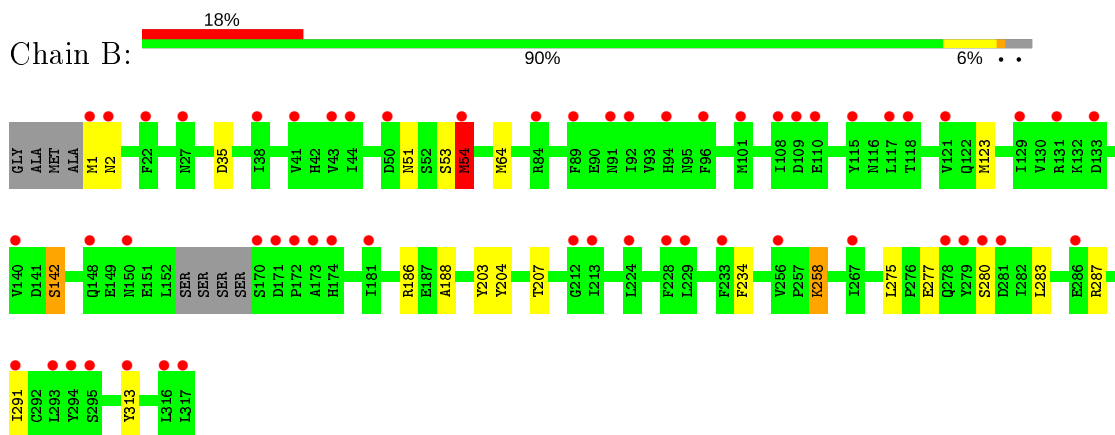
3 Residue-property plots [i](#)

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



- 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	89.08Å 82.03Å 94.30Å 90.00° 108.98° 90.00°	Depositor
Resolution (Å)	42.15 – 1.34 42.12 – 1.34	Depositor EDS
% Data completeness (in resolution range)	96.6 (42.15-1.34) 96.6 (42.12-1.34)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 1.34Å)	Xtriage
Refinement program	REFMAC 5.8.0238, PHENIX 1.16.3549	Depositor
R, R_{free}	0.232 , 0.233 0.241 , 0.242	Depositor DCC
R_{free} test set	6992 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	26.7	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.8	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	4787	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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.

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	0.79	1/2049 (0.0%)	0.90	3/2775 (0.1%)
2	B	0.75	0/2651	0.85	1/3581 (0.0%)
All	All	0.77	1/4700 (0.0%)	0.88	4/6356 (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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2062	GLU	CD-OE1	-5.51	1.19	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1859	ARG	NE-CZ-NH2	8.57	124.58	120.30
1	A	1859	ARG	NE-CZ-NH1	-5.84	117.38	120.30
2	B	186	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	A	1844	PHE	CB-CG-CD2	5.11	124.38	120.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

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

5.2 Too-close contacts

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	12	0
2	B	2580	0	2450	18	0
3	A	112	0	0	6	0
3	B	93	0	0	5	0
All	All	4787	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:54[B]:MET:SD	3:B:401:HOH:O	2.06	1.12
1:A:1976:ASP:HB3	3:A:2116:HOH:O	1.51	1.10
1:A:2062:GLU:O	1:A:2066:LYS:HG2	1.71	0.89
2:B:1:MET:SD	3:B:484:HOH:O	2.34	0.83
2:B:1:MET:HB3	2:B:35:ASP:HA	1.77	0.67
2:B:280:SER:HB3	2:B:313:TYR:CE1	2.32	0.65
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.47	0.62
2:B:142:SER:HB3	2:B:234:PHE:O	2.03	0.59
1:A:1962:ARG:H	1:A:1962:ARG:HD3	1.69	0.57
2:B:258:LYS:HD2	2:B:258:LYS:H	1.74	0.52
2:B:277:GLU:CD	2:B:277:GLU:H	2.14	0.52
2:B:142:SER:CB	3:B:401:HOH:O	2.58	0.51
1:A:2066:LYS:HD3	3:A:2101:HOH:O	2.12	0.48
1:A:1980:LYS:HE2	3:A:2116:HOH:O	2.13	0.48
2:B:51:ASN:OD1	2:B:53:SER:HB2	2.13	0.48
2:B:287:ARG:O	2:B:291:ILE:HD13	2.15	0.46
2:B:275:LEU:CD2	2:B:283:LEU:HD13	2.46	0.46
2:B:54[B]:MET:HA	3:B:401:HOH:O	2.15	0.46
1:A:1962:ARG:CD	1:A:1962:ARG:H	2.29	0.46
1:A:1835:MET:HE1	1:A:1961:LEU:HD12	1.99	0.45
1:A:2066:LYS:HG3	3:A:2131:HOH:O	2.16	0.44
2:B:203[A]:TYR:CZ	2:B:207:THR:HG21	2.53	0.44
2:B:64[A]:MET:SD	2:B:123:MET:HG2	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:ASN:HB2	3:B:423:HOH:O	2.18	0.43
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.40	0.42
1:A:2066:LYS:CE	3:A:2101:HOH:O	2.68	0.41
2:B:275:LEU:HA	2:B:275:LEU:HD23	1.93	0.41
1:A:2066:LYS:CD	3:A:2101:HOH:O	2.67	0.41
2:B:188:ALA:HA	2:B:204:TYR:CD1	2.56	0.40
2:B:280:SER:CB	2:B:313:TYR:CE1	3.04	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	A	248/258 (96%)	246 (99%)	2 (1%)	0	100	100
2	B	306/308 (99%)	297 (97%)	7 (2%)	2 (1%)	22	5
All	All	554/566 (98%)	543 (98%)	9 (2%)	2 (0%)	47	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	54[A]	MET
2	B	54[B]	MET

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%)	220 (97%)	6 (3%)	44	11
2	B	287/284 (101%)	283 (99%)	4 (1%)	67	34
All	All	513/517 (99%)	503 (98%)	10 (2%)	67	22

All (10) 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
1	A	2060	LEU
1	A	2065	ARG
2	B	54[A]	MET
2	B	54[B]	MET
2	B	142	SER
2	B	258	LYS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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%)	1.06	27 (11%) 5 5	16, 23, 41, 57	0
2	B	300/308 (97%)	1.25	56 (18%) 1 1	17, 26, 49, 74	0
All	All	537/566 (94%)	1.17	83 (15%) 2 2	16, 25, 48, 74	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1	MET	13.1
1	A	1833	GLY	9.0
2	B	173	ALA	7.6
1	A	2027	LEU	7.5
2	B	54[A]	MET	7.2
2	B	172	PRO	7.0
1	A	2032	ILE	6.3
2	B	170	SER	6.0
1	A	2028	SER	5.1
1	A	1838	SER	5.1
1	A	1837	SER	4.6
1	A	1836	ASN	4.3
2	B	108	ILE	4.1
2	B	92	ILE	4.0
2	B	229	LEU	4.0
2	B	316	LEU	4.0
1	A	1962	ARG	4.0
2	B	117	LEU	3.8
1	A	2046	GLU	3.8
2	B	279	TYR	3.8
2	B	84	ARG	3.7
2	B	22	PHE	3.7
1	A	2065	ARG	3.7
2	B	110	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
2	B	109	ASP	3.5
2	B	171	ASP	3.5
2	B	91	ASN	3.5
2	B	181	ILE	3.4
2	B	313	TYR	3.4
2	B	43	VAL	3.4
2	B	94	HIS	3.4
2	B	133	ASP	3.3
2	B	174	HIS	3.3
2	B	131	ARG	3.2
1	A	2030	PRO	3.1
2	B	96	PHE	3.0
1	A	1834	ALA	3.0
2	B	317	LEU	3.0
2	B	129	ILE	2.9
2	B	286	GLU	2.9
2	B	228	PHE	2.9
1	A	1954	ILE	2.8
1	A	2033	THR	2.8
2	B	41[A]	VAL	2.8
2	B	294	TYR	2.7
2	B	101	MET	2.7
2	B	2	ASN	2.7
1	A	1934	ILE	2.6
2	B	27	ASN	2.6
2	B	293	LEU	2.6
1	A	1848	ILE	2.6
2	B	267	ILE	2.6
2	B	280	SER	2.6
2	B	295	SER	2.6
2	B	278	GLN	2.5
2	B	44[A]	ILE	2.5
1	A	1860	VAL	2.5
1	A	2069	VAL	2.5
2	B	212	GLY	2.5
2	B	291	ILE	2.5
1	A	2060	LEU	2.4
2	B	50	ASP	2.4
1	A	2063	TYR	2.4
2	B	121	VAL	2.4
1	A	2049	ILE	2.3
2	B	38	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	140	VAL	2.3
2	B	118	THR	2.3
2	B	233	PHE	2.3
2	B	150	ASN	2.3
2	B	213	ILE	2.2
1	A	1904	ARG	2.2
2	B	148	GLN	2.2
1	A	1882	LEU	2.2
1	A	1938	LYS	2.2
2	B	256	VAL	2.2
1	A	2031	THR	2.1
2	B	89	PHE	2.1
2	B	281	ASP	2.1
1	A	1921	VAL	2.1
2	B	224	LEU	2.0
1	A	1861	THR	2.0
2	B	115	TYR	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 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.