



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:01 PM UTC

PDB ID : 5R0V / pdb_00005r0v
Title : PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for ground state model 09, DMSO-free
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Deposited on : 2020-02-12
Resolution : 1.81 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

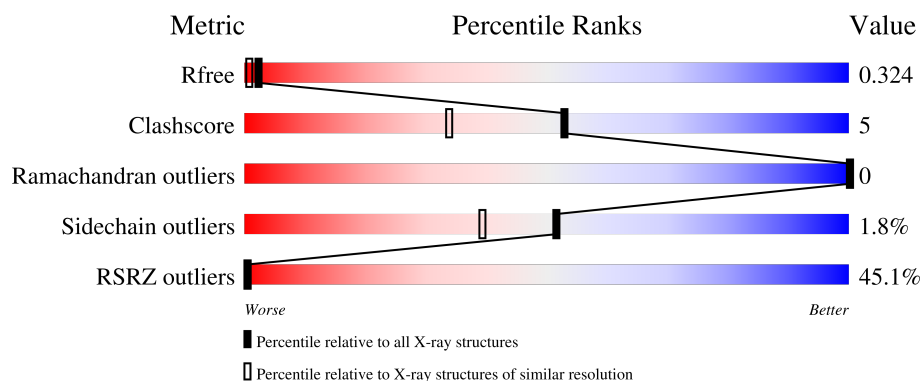
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.81 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	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	45% 79% 12% 8%
2	B	308	41% 84% 13% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4673 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	2568	1645	420	483	20	0	9	0

There are 20 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	LEU	conflict	UNP P32357
B	167	SER	LYS	conflict	UNP P32357
B	170	SER	LEU	conflict	UNP P32357
B	?	-	GLN	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357
B	?	-	ALA	deletion	UNP P32357
B	?	-	GLY	deletion	UNP P32357
B	?	-	SER	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	MET	deletion	UNP P32357
B	?	-	GLU	deletion	UNP P32357
B	?	-	ALA	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357
B	?	-	ASN	deletion	UNP P32357
B	?	-	GLU	deletion	UNP P32357
B	?	-	ASP	deletion	UNP P32357

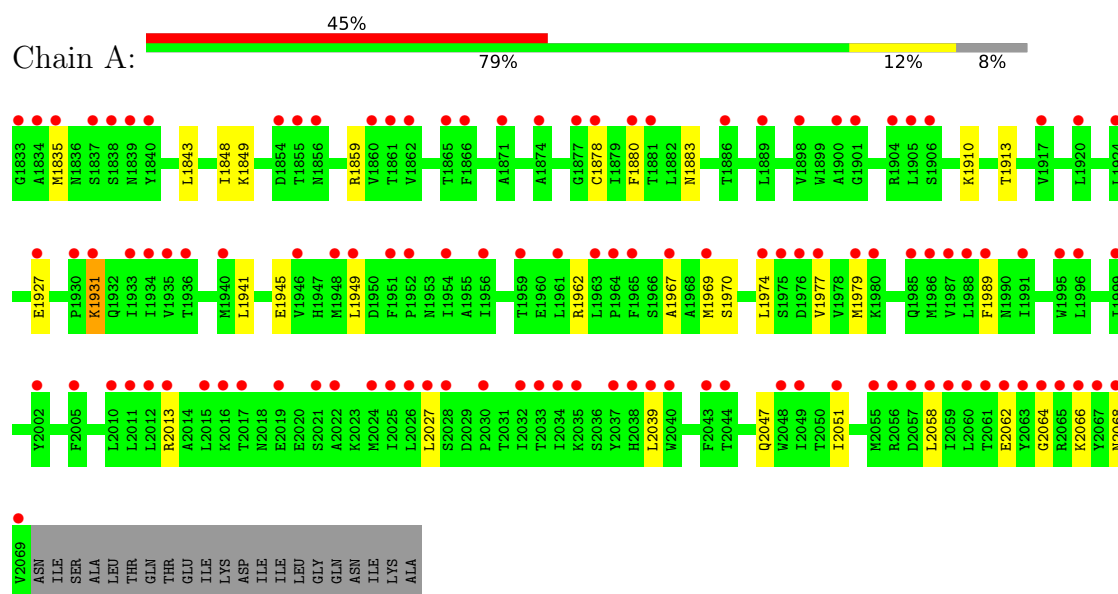
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	63	Total O 63 63	0	0
3	B	40	Total O 40 40	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	88.79Å 82.18Å 92.92Å 90.00° 108.16° 90.00°	Depositor
Resolution (Å)	22.68 – 1.81 22.68 – 1.81	Depositor EDS
% Data completeness (in resolution range)	99.4 (22.68-1.81) 99.9 (22.68-1.81)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 1.81Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.283 , 0.320 0.288 , 0.324	Depositor DCC
R_{free} test set	2100 reflections (3.60%)	wwPDB-VP
Wilson B-factor (Å ²)	43.4	Xtriage
Anisotropy	0.344	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4673	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% 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	0.76	1/2049 (0.0%)	0.88	1/2775 (0.0%)
2	B	0.63	0/2638	0.77	0/3563
All	All	0.69	1/4687 (0.0%)	0.82	1/6338 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1880	PHE	CE2-CZ	-6.25	1.19	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1883	ASN	N-CA-C	-5.36	101.79	109.24

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	18	0
2	B	2568	0	2441	27	0
3	A	63	0	0	0	0
3	B	40	0	0	2	0
All	All	4673	0	4470	45	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 5.

All (45) 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)
1:A:2062:GLU:O	1:A:2066:LYS:HG2	1.92	0.69
2:B:70:GLN:HB3	2:B:81:MET:HE2	1.77	0.65
1:A:2062:GLU:HB3	1:A:2066:LYS:HE3	1.81	0.62
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.33	0.61
1:A:1979[B]:MET:HA	1:A:1979[B]:MET:HE2	1.84	0.60
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.84	0.57
1:A:2047:GLN:O	1:A:2051:ILE:HG12	2.04	0.57
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.53	0.56
2:B:1:MET:N	3:B:401:HOH:O	2.40	0.54
1:A:1989:PHE:CD2	1:A:2039:LEU:HD21	2.44	0.53
2:B:214:PHE:O	2:B:215:LYS:HB2	2.09	0.51
2:B:51:ASN:C	2:B:53:SER:H	2.19	0.51
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.37	0.50
2:B:61:ASP:OD1	2:B:61:ASP:C	2.55	0.50
2:B:16:GLY:HA3	2:B:45:HIS:CE1	2.47	0.49
1:A:1941:LEU:O	1:A:1945:GLU:HB2	2.12	0.49
2:B:190:ARG:HG3	2:B:203[B]:TYR:CZ	2.48	0.49
2:B:1:MET:HB3	2:B:35:ASP:HA	1.95	0.48
2:B:170:SER:HA	3:B:422:HOH:O	2.13	0.47
2:B:237:TYR:CE2	2:B:241:LEU:HD11	2.49	0.47
2:B:258:LYS:HD2	2:B:258:LYS:H	1.78	0.47
2:B:70:GLN:HB3	2:B:81:MET:CE	2.44	0.46
1:A:1859:ARG:NH1	1:A:1979[B]:MET:HE3	2.31	0.46
2:B:251:CYS:O	2:B:296:SER:HB2	2.14	0.46
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.99	0.45
2:B:17:ILE:O	2:B:17:ILE:HG23	2.16	0.45
1:A:1974:LEU:O	1:A:1977:VAL:HG12	2.17	0.45
2:B:70:GLN:OE1	2:B:81:MET:HE1	2.16	0.45
2:B:96:PHE:CB	2:B:102:MET:HE3	2.47	0.45
1:A:1967:ALA:O	1:A:1970:SER:HB2	2.17	0.44
2:B:301:SER:O	2:B:302:LEU:HD23	2.17	0.44
2:B:141:ASP:OD1	2:B:144:MET:HG3	2.18	0.43
2:B:69:ILE:HD13	2:B:80:MET:HA	2.01	0.43
1:A:1927:GLU:OE2	1:A:1927:GLU:N	2.37	0.42
2:B:68:TYR:CE2	2:B:81:MET:HE3	2.54	0.42
1:A:1878:CYS:SG	1:A:1969:MET:HE3	2.59	0.42
1:A:1949:LEU:HA	1:A:1949:LEU:HD23	1.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:70:GLN:CB	2:B:81:MET:HE2	2.46	0.42
2:B:51:ASN:C	2:B:53:SER:N	2.77	0.42
1:A:2064:GLY:O	1:A:2068:ASN:N	2.53	0.42
2:B:260:MET:HE2	2:B:260:MET:HB3	1.93	0.42
1:A:1910:LYS:O	1:A:1913:THR:HB	2.20	0.41
2:B:129:ILE:HA	2:B:177[B]:ASN:HB3	2.01	0.41
2:B:5:PRO:HA	2:B:32:GLY:HA3	2.03	0.41
2:B:242:GLN:O	2:B:246:MET:HG3	2.21	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%)	242 (98%)	6 (2%)	0	100	100
2	B	305/308 (99%)	291 (95%)	14 (5%)	0	100	100
All	All	553/566 (98%)	533 (96%)	20 (4%)	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%)	51	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	286/284 (101%)	280 (98%)	6 (2%)	47	32
All	All	512/517 (99%)	502 (98%)	10 (2%)	51	35

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1835	MET
1	A	1931[A]	LYS
1	A	1931[B]	LYS
1	A	2027	LEU
2	B	17	ILE
2	B	77	LEU
2	B	101	MET
2	B	174	HIS
2	B	282	ILE
2	B	291	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1863	HIS
1	A	2038	HIS
2	B	45	HIS
2	B	47	GLN
2	B	91	ASN
2	B	259	HIS

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

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

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%)	2.23	115 (48%) 0 0	24, 67, 128, 177	12 (5%)
2	B	300/308 (97%)	2.04	127 (42%) 0 0	23, 72, 143, 207	9 (3%)
All	All	537/566 (94%)	2.12	242 (45%) 0 0	23, 70, 138, 207	21 (3%)

All (242) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	189	ILE	8.3
1	A	1964	PRO	7.8
1	A	1878	CYS	7.8
1	A	1979[A]	MET	7.7
1	A	1940	MET	7.3
2	B	22	PHE	7.0
2	B	54[A]	MET	6.7
2	B	96	PHE	6.5
1	A	2061	THR	6.3
2	B	77	LEU	6.2
2	B	313	TYR	6.0
2	B	30	PHE	6.0
2	B	130	VAL	5.9
1	A	1969	MET	5.8
1	A	2060	LEU	5.8
1	A	1840	TYR	5.4
1	A	1934	ILE	5.3
1	A	1963	LEU	5.2
2	B	126	ILE	5.1
1	A	2048	TRP	5.1
1	A	2063	TYR	5.0
1	A	1860	VAL	5.0
1	A	1898[A]	VAL	5.0
1	A	1965	PHE	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	1988	LEU	4.9
2	B	308	ILE	4.9
2	B	283	LEU	4.8
2	B	73	PRO	4.8
2	B	38	ILE	4.6
1	A	2056[A]	ARG	4.6
1	A	1987	VAL	4.6
2	B	52	SER	4.5
2	B	294	TYR	4.5
1	A	2027	LEU	4.5
1	A	1961	LEU	4.5
1	A	1948	MET	4.5
2	B	129	ILE	4.4
2	B	279	TYR	4.4
2	B	108	ILE	4.4
1	A	2055	MET	4.3
2	B	317	LEU	4.3
1	A	2068	ASN	4.3
2	B	295	SER	4.3
2	B	1	MET	4.2
2	B	208	VAL	4.2
2	B	203[A]	TYR	4.2
1	A	2051	ILE	4.2
2	B	291	ILE	4.2
1	A	1855[A]	THR	4.2
2	B	174	HIS	4.2
2	B	170	SER	4.1
1	A	1967	ALA	4.1
1	A	2043	PHE	4.0
2	B	111	ASP	3.9
1	A	1980	LYS	3.9
2	B	196	GLU	3.9
2	B	191	PRO	3.8
2	B	92	ILE	3.8
1	A	1996	LEU	3.8
1	A	2010	LEU	3.8
2	B	316	LEU	3.8
2	B	101	MET	3.7
1	A	2044	THR	3.7
1	A	1866	PHE	3.7
1	A	1877	GLY	3.7
1	A	1889	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
2	B	290	ASN	3.7
2	B	6	PHE	3.7
2	B	89	PHE	3.7
1	A	2016	LYS	3.6
1	A	2039	LEU	3.6
1	A	1954	ILE	3.6
1	A	1834	ALA	3.6
1	A	2065	ARG	3.6
1	A	2025	ILE	3.6
1	A	2015	LEU	3.6
1	A	1881	THR	3.5
2	B	275	LEU	3.5
2	B	121	VAL	3.5
1	A	2058	LEU	3.5
1	A	1835	MET	3.5
2	B	282	ILE	3.5
2	B	146	THR	3.4
2	B	193	HIS	3.4
1	A	1931[A]	LYS	3.4
2	B	258	LYS	3.4
1	A	1946	VAL	3.4
2	B	122[A]	GLN	3.3
2	B	15	ILE	3.3
1	A	1839	ASN	3.3
2	B	53	SER	3.3
1	A	2059	ILE	3.3
2	B	33	ILE	3.3
1	A	1871	ALA	3.3
2	B	284	LEU	3.3
2	B	120	PHE	3.3
1	A	1975	SER	3.3
1	A	2021	SER	3.3
1	A	1959	THR	3.2
1	A	2034	ILE	3.2
1	A	2067	TYR	3.2
1	A	2026	LEU	3.2
1	A	1933	ILE	3.1
2	B	276	PRO	3.1
2	B	69	ILE	3.1
2	B	71	TYR	3.1
1	A	2022	ALA	3.1
2	B	188	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	2038	HIS	3.1
1	A	1917	VAL	3.1
2	B	124	ASP	3.1
2	B	214	PHE	3.1
2	B	172	PRO	3.1
1	A	1833	GLY	3.1
2	B	213	ILE	3.0
2	B	99	ARG	3.0
1	A	1861	THR	3.0
1	A	1901	GLY	3.0
1	A	2066	LYS	3.0
1	A	1920	LEU	3.0
2	B	183	PHE	3.0
2	B	192	GLY	3.0
2	B	314	PRO	3.0
1	A	1856	ASN	3.0
1	A	1956	ILE	3.0
1	A	1906	SER	2.9
2	B	301	SER	2.9
2	B	233	PHE	2.9
2	B	210	LEU	2.9
1	A	2028	SER	2.9
1	A	1977	VAL	2.9
2	B	20	TYR	2.9
1	A	1936	THR	2.9
2	B	47	GLN	2.9
1	A	1924	LEU	2.9
2	B	147	VAL	2.9
1	A	2037	TYR	2.9
2	B	152	LEU	2.9
2	B	302	LEU	2.9
2	B	311	ASN	2.8
1	A	1989	PHE	2.8
1	A	1995	TRP	2.8
2	B	137	PHE	2.8
2	B	84	ARG	2.8
1	A	2019	GLU	2.8
2	B	293	LEU	2.8
2	B	29	PRO	2.8
2	B	150	ASN	2.7
2	B	40	HIS	2.7
1	A	1985	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	2012	LEU	2.7
2	B	131	ARG	2.7
2	B	280	SER	2.7
2	B	289	TRP	2.7
2	B	237	TYR	2.7
1	A	1854	ASP	2.7
1	A	1874	ALA	2.6
1	A	1886	THR	2.6
1	A	1935	VAL	2.6
1	A	2024[A]	MET	2.6
2	B	261	LEU	2.6
1	A	2057[A]	ASP	2.6
1	A	1862	VAL	2.6
1	A	1974	LEU	2.6
2	B	227	ALA	2.6
2	B	2	ASN	2.6
2	B	173	ALA	2.5
2	B	315	GLU	2.5
1	A	2035	LYS	2.5
1	A	2033	THR	2.5
2	B	3	THR	2.5
2	B	139	TYR	2.5
1	A	2005	PHE	2.5
2	B	235	GLY	2.5
1	A	1838	SER	2.5
1	A	2069	VAL	2.5
2	B	41[A]	VAL	2.5
2	B	281	ASP	2.5
2	B	95	ASN	2.4
2	B	198	PHE	2.4
2	B	44[A]	ILE	2.4
2	B	179	THR	2.4
2	B	64[A]	MET	2.4
2	B	220	TYR	2.4
1	A	2049	ILE	2.4
1	A	1952	PRO	2.4
1	A	2030	PRO	2.4
1	A	2064	GLY	2.4
2	B	288	VAL	2.4
2	B	74	LYS	2.4
1	A	1905	LEU	2.3
2	B	241	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	87	ALA	2.3
2	B	221	PHE	2.3
2	B	228	PHE	2.3
2	B	51	ASN	2.3
2	B	231	ALA	2.3
2	B	55	ARG	2.3
2	B	109	ASP	2.3
1	A	1986	MET	2.3
2	B	204	TYR	2.3
2	B	132	LYS	2.3
1	A	1900	ALA	2.3
1	A	1837	SER	2.3
1	A	2013	ARG	2.2
1	A	1951	PHE	2.2
2	B	134	GLU	2.2
2	B	257	PRO	2.2
1	A	1991	ILE	2.2
2	B	250	ILE	2.2
2	B	81	MET	2.2
1	A	1927	GLU	2.2
1	A	1949	LEU	2.2
1	A	1999	ILE	2.2
2	B	312	LYS	2.2
1	A	2062	GLU	2.2
2	B	107	LYS	2.2
1	A	1976	ASP	2.2
1	A	2011	LEU	2.2
2	B	10	PRO	2.2
2	B	299	LYS	2.2
2	B	269	TYR	2.1
2	B	306	GLU	2.1
2	B	19	GLN	2.1
1	A	1865	THR	2.1
2	B	32	GLY	2.1
1	A	1904	ARG	2.1
1	A	1880	PHE	2.1
2	B	114	TRP	2.1
1	A	2032	ILE	2.1
1	A	2040	TRP	2.1
2	B	49	ALA	2.1
2	B	263	LYS	2.0
2	B	307	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	2017[A]	THR	2.0
2	B	206	ASN	2.0
2	B	249	LEU	2.0
2	B	76	GLY	2.0
2	B	86	GLY	2.0
2	B	145	THR	2.0
1	A	2002	TYR	2.0
1	A	1930	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.