



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 5QZK / pdb_00005qzk
Title : PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for ground state model 35
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 : 1.73 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

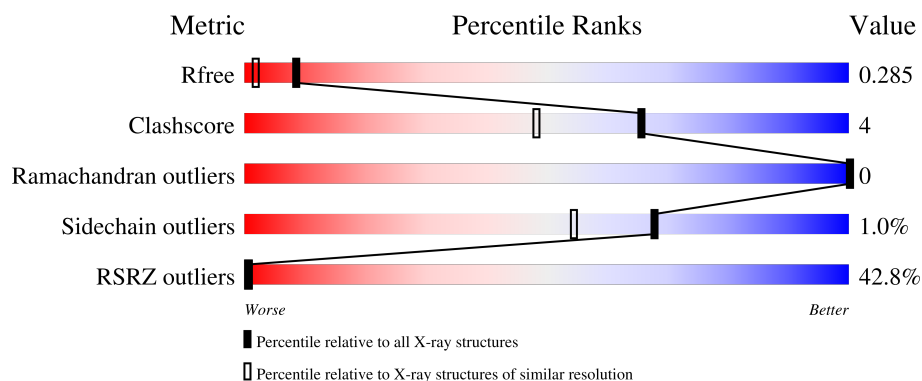
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.73 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	40% 84% 8% 8%
2	B	308	41% 87% 10% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4612 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

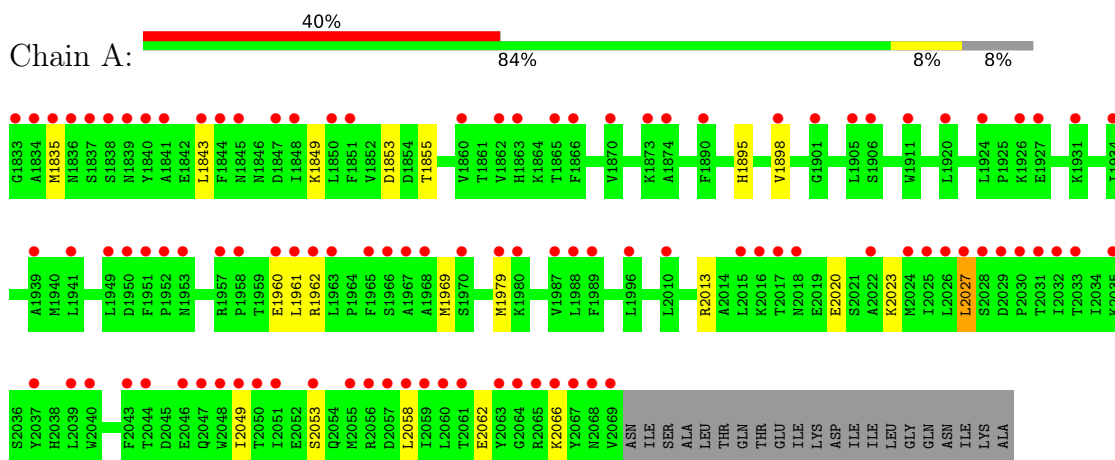
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	17	Total	O	0	0
			17	17		
3	B	13	Total	O	0	0
			13	13		

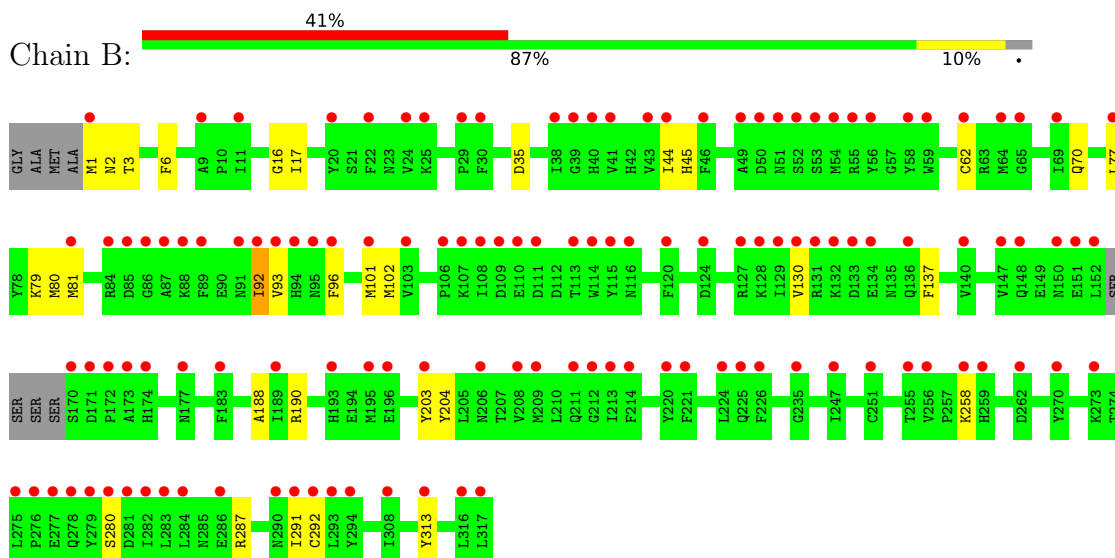
3 Residue-property plots [i](#)

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	88.81Å 81.69Å 93.14Å 90.00° 108.28° 90.00°	Depositor
Resolution (Å)	44.65 – 1.73 44.65 – 1.73	Depositor EDS
% Data completeness (in resolution range)	99.0 (44.65-1.73) 99.1 (44.65-1.73)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.92 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.8.0238, PHENIX 1.16.3549	Depositor
R, R_{free}	0.267 , 0.269 0.272 , 0.285	Depositor DCC
R_{free} test set	3127 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 25.4	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	0.93	EDS
Total number of atoms	4612	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% 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	1.25	0/2775
2	B	1.01	0/2651	1.27	1/3581 (0.0%)
All	All	1.03	0/4700	1.26	1/6356 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6	PHE	CA-CB-CG	5.06	118.86	113.80

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	13	0
2	B	2580	0	2448	21	0
3	A	17	0	0	0	0
3	B	13	0	0	0	0
All	All	4612	0	4477	34	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 4.

All (34) 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	1.89	0.71
2:B:1:MET:HB3	2:B:35:ASP:HA	1.73	0.69
1:A:1979[B]:MET:HA	1:A:1979[B]:MET:HE2	1.78	0.65
2:B:77:LEU:HD21	2:B:79:LYS:HE3	1.80	0.64
2:B:287:ARG:O	2:B:291:ILE:HD13	2.02	0.59
2:B:70:GLN:HB3	2:B:81:MET:HE2	1.87	0.57
2:B:2:ASN:HB3	2:B:62:CYS:SG	2.44	0.56
2:B:2:ASN:CB	2:B:62:CYS:SG	2.94	0.56
2:B:16:GLY:HA3	2:B:45:HIS:CE1	2.41	0.56
2:B:2:ASN:CG	2:B:62:CYS:HB3	2.32	0.55
1:A:1969:MET:HA	1:A:1969:MET:HE2	1.90	0.53
2:B:188:ALA:HA	2:B:204:TYR:CD1	2.45	0.52
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.92	0.52
2:B:80:MET:HG2	2:B:137:PHE:CD2	2.46	0.51
2:B:280:SER:HB3	2:B:313:TYR:CE1	2.46	0.51
1:A:1895:HIS:O	1:A:1898[A]:VAL:HG22	2.11	0.50
2:B:17:ILE:HD13	2:B:44[B]:ILE:HG13	1.94	0.50
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.94	0.49
2:B:17:ILE:HD13	2:B:44[B]:ILE:CG1	2.43	0.48
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.48	0.47
2:B:3:THR:HG21	2:B:93:VAL:HG13	1.96	0.46
1:A:1853:ASP:OD2	1:A:1855[B]:THR:HG23	2.15	0.46
1:A:2023:LYS:O	1:A:2027:LEU:HG	2.16	0.45
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.41	0.45
1:A:1835:MET:HE1	1:A:1961:LEU:HD12	2.01	0.43
2:B:291:ILE:HG22	2:B:292:CYS:N	2.32	0.43
1:A:2049:ILE:O	1:A:2053[A]:SER:OG	2.35	0.43
2:B:190:ARG:HD3	2:B:203[A]:TYR:CE2	2.54	0.42
2:B:258:LYS:HD2	2:B:258:LYS:H	1.85	0.41
1:A:1835:MET:HE2	1:A:1843:LEU:HD21	2.03	0.41
1:A:1960[B]:GLU:HA	1:A:1960[B]:GLU:OE1	2.21	0.40
2:B:92:ILE:HD13	2:B:92:ILE:HA	1.94	0.40
2:B:77:LEU:N	2:B:77:LEU:HD23	2.37	0.40
2:B:80:MET:HG2	2:B:137:PHE:CE2	2.57	0.40

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%)	242 (98%)	6 (2%)	0	100	100
2	B	306/308 (99%)	289 (94%)	17 (6%)	0	100	100
All	All	554/566 (98%)	531 (96%)	23 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	59
2	B	287/284 (101%)	284 (99%)	3 (1%)	68	54
All	All	513/517 (99%)	508 (99%)	5 (1%)	68	54

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

Mol	Chain	Res	Type
1	A	2020	GLU
1	A	2027	LEU
2	B	92	ILE
2	B	101	MET
2	B	130	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1869	ASN
2	B	31	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 [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%)	2.03	103 (43%) 0 1	12, 36, 75, 86	12 (5%)
2	B	300/308 (97%)	2.02	127 (42%) 0 1	12, 39, 76, 125	9 (3%)
All	All	537/566 (94%)	2.03	230 (42%) 0 1	12, 37, 76, 125	21 (3%)

All (230) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1979[A]	MET	10.2
2	B	22	PHE	7.3
2	B	52	SER	7.2
2	B	54[A]	MET	6.9
1	A	2027	LEU	6.7
2	B	1	MET	6.6
2	B	152	LEU	6.3
2	B	108	ILE	6.2
2	B	195	MET	6.2
2	B	275	LEU	5.9
2	B	316	LEU	5.9
1	A	1833	GLY	5.8
1	A	2061	THR	5.6
2	B	279	TYR	5.6
1	A	2060	LEU	5.2
2	B	41[A]	VAL	5.2
2	B	224	LEU	5.1
2	B	317	LEU	5.1
2	B	147	VAL	5.1
1	A	2049	ILE	5.0
1	A	2064	GLY	5.0
2	B	211[A]	GLN	4.9
1	A	2028	SER	4.9
1	A	2032	ILE	4.9

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Mol	Chain	Res	Type	RSRZ
2	B	174	HIS	4.9
2	B	173	ALA	4.8
1	A	2063	TYR	4.8
2	B	87	ALA	4.8
2	B	170	SER	4.7
2	B	292	CYS	4.6
2	B	53	SER	4.6
1	A	1961	LEU	4.5
2	B	136	GLN	4.5
1	A	2059	ILE	4.5
1	A	1834	ALA	4.4
2	B	9	ALA	4.4
2	B	172	PRO	4.3
2	B	283	LEU	4.2
2	B	247	ILE	4.2
2	B	291	ILE	4.2
1	A	1866	PHE	4.1
2	B	89	PHE	4.1
1	A	1840	TYR	4.0
2	B	208	VAL	4.0
1	A	2067	TYR	3.9
2	B	276	PRO	3.9
1	A	1837	SER	3.9
1	A	2030	PRO	3.9
1	A	2066	LYS	3.8
1	A	2069	VAL	3.8
1	A	1835	MET	3.7
1	A	1836	ASN	3.7
1	A	2046	GLU	3.7
2	B	11	ILE	3.7
1	A	1953	ASN	3.7
2	B	213	ILE	3.6
1	A	2017[A]	THR	3.6
1	A	2051	ILE	3.6
2	B	290	ASN	3.6
2	B	280	SER	3.6
1	A	1898[A]	VAL	3.6
2	B	101	MET	3.6
2	B	313	TYR	3.6
2	B	120	PHE	3.5
2	B	106	PRO	3.5
2	B	38	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	2048	TRP	3.5
2	B	282	ILE	3.4
2	B	278	GLN	3.4
2	B	277	GLU	3.4
1	A	1905	LEU	3.4
2	B	124	ASP	3.4
2	B	62	CYS	3.4
1	A	2065	ARG	3.4
2	B	256	VAL	3.4
1	A	2068	ASN	3.4
1	A	2024[A]	MET	3.4
1	A	1920	LEU	3.3
1	A	2026	LEU	3.3
1	A	2058	LEU	3.3
2	B	111	ASP	3.3
1	A	1934	ILE	3.3
1	A	2050	THR	3.3
2	B	189	ILE	3.2
2	B	109	ASP	3.2
2	B	115	TYR	3.2
2	B	129	ILE	3.2
1	A	1874	ALA	3.2
1	A	1962	ARG	3.2
1	A	1950	ASP	3.2
2	B	133	ASP	3.2
1	A	2033	THR	3.2
1	A	2031	THR	3.1
2	B	92	ILE	3.1
2	B	49	ALA	3.1
2	B	128	LYS	3.1
2	B	258	LYS	3.1
1	A	1890	PHE	3.0
1	A	1862	VAL	3.0
2	B	69	ILE	3.0
2	B	96	PHE	3.0
2	B	130	VAL	3.0
2	B	20	TYR	3.0
2	B	114	TRP	3.0
1	A	1939	ALA	3.0
2	B	308	ILE	3.0
1	A	1960[A]	GLU	3.0
2	B	84	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	1850	LEU	2.9
2	B	94	HIS	2.9
1	A	2035	LYS	2.9
2	B	25	LYS	2.9
1	A	1989	PHE	2.9
2	B	293	LEU	2.9
1	A	1848	ILE	2.9
2	B	116	ASN	2.9
1	A	2029	ASP	2.8
2	B	171	ASP	2.8
1	A	1839	ASN	2.8
2	B	203[A]	TYR	2.8
2	B	294	TYR	2.8
1	A	1963	LEU	2.8
2	B	81	MET	2.8
1	A	1970	SER	2.8
1	A	2022	ALA	2.8
1	A	1870	VAL	2.8
2	B	262	ASP	2.8
2	B	40	HIS	2.8
2	B	55	ARG	2.7
2	B	150	ASN	2.7
2	B	51	ASN	2.7
1	A	1931[A]	LYS	2.7
2	B	64[A]	MET	2.7
1	A	2043	PHE	2.7
2	B	226	PHE	2.7
1	A	1863	HIS	2.7
1	A	1996	LEU	2.7
2	B	132	LYS	2.7
1	A	1844	PHE	2.7
2	B	151	GLU	2.7
2	B	93	VAL	2.7
2	B	140	VAL	2.7
1	A	2055	MET	2.7
1	A	1838	SER	2.6
2	B	65	GLY	2.6
1	A	1860	VAL	2.6
2	B	58	TYR	2.6
2	B	220	TYR	2.6
2	B	206	ASN	2.6
1	A	2025	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	113	THR	2.6
1	A	2018	ASN	2.6
2	B	91	ASN	2.6
2	B	85	ASP	2.5
2	B	88	LYS	2.5
1	A	1966	SER	2.5
1	A	1845	ASN	2.5
2	B	110	GLU	2.5
2	B	44[A]	ILE	2.5
1	A	1865	THR	2.5
2	B	284	LEU	2.5
1	A	1958	PRO	2.5
2	B	95	ASN	2.4
2	B	225	GLN	2.4
2	B	134	GLU	2.4
1	A	1911	TRP	2.4
2	B	39	GLY	2.4
1	A	2057[A]	ASP	2.4
1	A	1851	PHE	2.4
2	B	50	ASP	2.4
1	A	2056[A]	ARG	2.4
2	B	86	GLY	2.3
2	B	29	PRO	2.3
1	A	1873	LYS	2.3
2	B	273	LYS	2.3
1	A	2044	THR	2.3
2	B	209	MET	2.3
1	A	1924	LEU	2.3
1	A	1988	LEU	2.3
1	A	2015	LEU	2.3
2	B	177[A]	ASN	2.3
1	A	1957	ARG	2.3
2	B	46	PHE	2.3
2	B	103	VAL	2.3
2	B	196	GLU	2.2
1	A	1967	ALA	2.2
1	A	1949	LEU	2.2
2	B	77	LEU	2.2
2	B	281	ASP	2.2
2	B	30	PHE	2.2
1	A	2037	TYR	2.2
2	B	56	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	107	LYS	2.2
2	B	251	CYS	2.2
1	A	1941	LEU	2.2
2	B	235	GLY	2.2
2	B	131	ARG	2.2
1	A	1952	PRO	2.2
1	A	1926	LYS	2.2
1	A	1841	ALA	2.2
2	B	212	GLY	2.2
2	B	193	HIS	2.2
1	A	1965	PHE	2.2
1	A	1980	LYS	2.2
1	A	2053[A]	SER	2.2
1	A	1987	VAL	2.1
1	A	1968	ALA	2.1
1	A	2039	LEU	2.1
1	A	1906	SER	2.1
1	A	1951	PHE	2.1
2	B	183	PHE	2.1
2	B	43	VAL	2.1
2	B	259	HIS	2.1
1	A	1901	GLY	2.1
1	A	1843	LEU	2.1
1	A	2040	TRP	2.1
2	B	59	TRP	2.1
2	B	270	TYR	2.1
1	A	2016	LYS	2.1
1	A	1927	GLU	2.1
2	B	148	GLN	2.1
1	A	2010	LEU	2.1
2	B	221	PHE	2.1
1	A	2047	GLN	2.0
1	A	1847	ASP	2.0
2	B	127	ARG	2.0
2	B	255	THR	2.0
2	B	286	GLU	2.0
2	B	214	PHE	2.0
2	B	24	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.