



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:46 PM UTC

PDB ID : 5R1K / pdb_00005r1k
Title : PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for ground state model 35, DMSO-free
Authors : Wollenhaupt, J.; Metz, A.; Barthel, T.; Lima, G.M.A.; Heine, A.; Mueller, U.; Klebe, G.; Weiss, M.S.
Deposited on : 2020-02-12
Resolution : 1.99 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

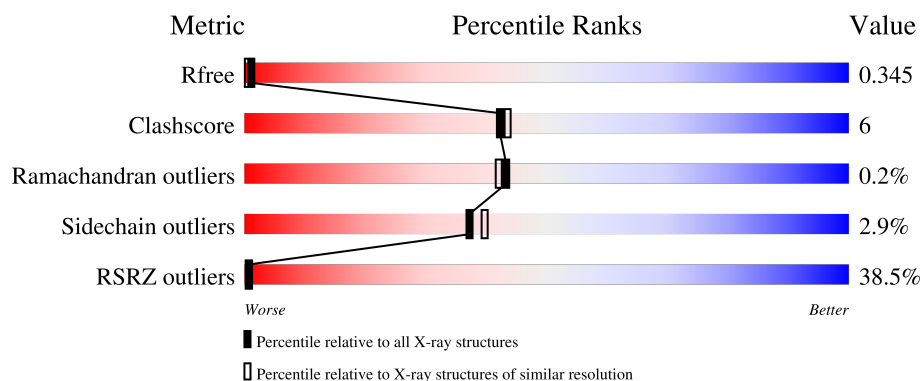
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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% 77% 15% 8%
2	B	308	34% 78% 19% ...

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4605 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

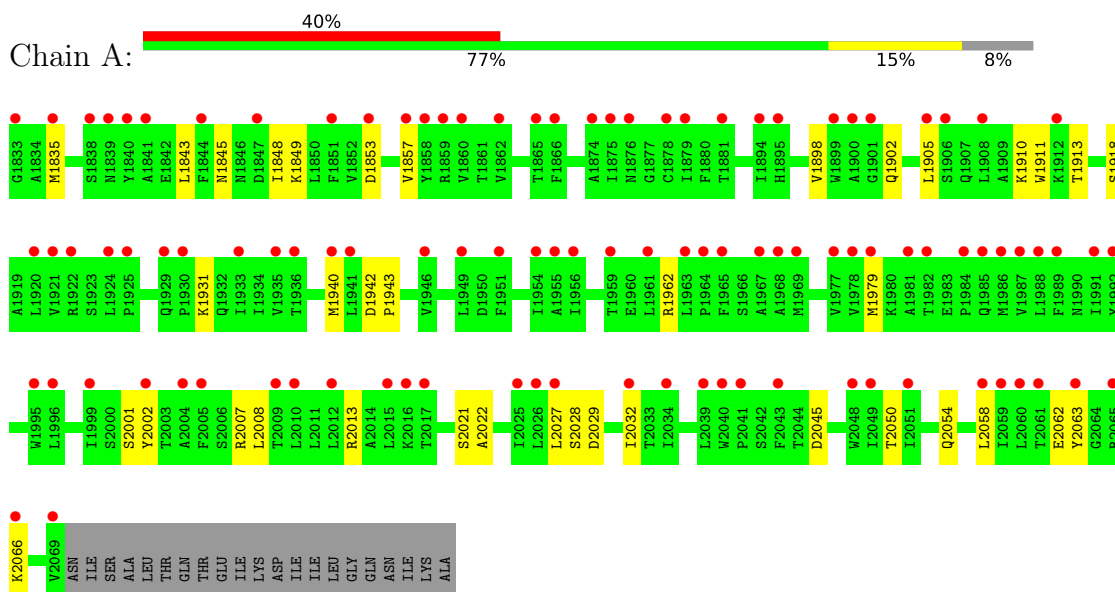
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total	O	0	0
			25	25		
3	B	10	Total	O	0	0
			10	10		

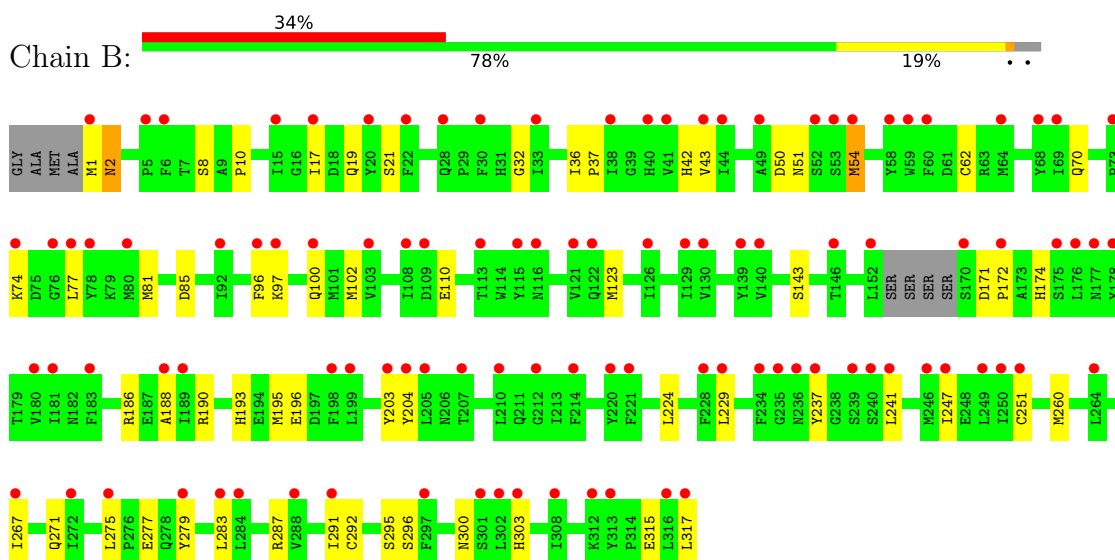
3 Residue-property plots

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	88.89Å 82.66Å 91.95Å 90.00° 107.58° 90.00°	Depositor
Resolution (Å)	21.24 – 1.99 21.24 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.4 (21.24-1.99) 99.3 (21.24-1.99)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.272 , 0.326 0.290 , 0.345	Depositor DCC
R_{free} test set	2100 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	57.8	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 63.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4605	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.29% 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	0.88	1/2049 (0.0%)	1.02	0/2775
2	B	0.73	0/2638	0.92	2/3563 (0.1%)
All	All	0.80	1/4687 (0.0%)	0.96	2/6338 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1853	ASP	CA-C	6.72	1.60	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	229	LEU	CD1-CG-CD2	-6.02	97.56	110.80
2	B	32	GLY	N-CA-C	5.76	118.26	111.63

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	23	0
2	B	2568	0	2439	36	0
3	A	25	0	0	0	0
3	B	10	0	0	2	0
All	All	4605	0	4468	57	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 6.

All (57) 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:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.27	0.83
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.13	0.81
1:A:2062:GLU:O	1:A:2066:LYS:HG2	1.84	0.77
2:B:50:ASP:OD1	2:B:51:ASN:N	2.24	0.70
2:B:287:ARG:O	2:B:291:ILE:HD13	1.92	0.68
2:B:70:GLN:HB3	2:B:81:MET:HE1	1.79	0.65
1:A:1979[B]:MET:HA	1:A:1979[B]:MET:HE2	1.78	0.64
2:B:74:LYS:NZ	3:B:401:HOH:O	2.00	0.62
2:B:1:MET:N	3:B:402:HOH:O	2.35	0.58
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.87	0.56
1:A:1857:VAL:HG21	1:A:1913:THR:OG1	2.06	0.56
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.32	0.55
2:B:70:GLN:HB3	2:B:81:MET:CE	2.38	0.53
2:B:190:ARG:HG3	2:B:203[B]:TYR:CE2	2.43	0.53
2:B:193:HIS:ND1	2:B:196:GLU:OE1	2.32	0.53
2:B:97:LYS:O	2:B:100:GLN:N	2.40	0.53
2:B:224:LEU:C	2:B:224:LEU:HD23	2.34	0.52
2:B:300:ASN:O	2:B:303:HIS:NE2	2.43	0.52
2:B:2:ASN:CG	2:B:62:CYS:HB3	2.35	0.52
2:B:291:ILE:HA	2:B:295:SER:HB2	1.93	0.50
1:A:2050:THR:HG22	1:A:2054:GLN:NE2	2.27	0.50
1:A:1910:LYS:HA	1:A:1940:MET:SD	2.53	0.49
1:A:1848:ILE:H	1:A:1931[A]:LYS:NZ	2.04	0.48
2:B:277:GLU:OE1	2:B:277:GLU:N	2.44	0.47
2:B:43:VAL:HG13	2:B:43:VAL:O	2.14	0.47
2:B:275:LEU:HD22	2:B:283:LEU:HD13	1.97	0.47
2:B:54[B]:MET:HE1	2:B:143:SER:HB3	1.97	0.47
1:A:1911:TRP:CD2	2:B:195:MET:HB2	2.51	0.46
2:B:186:ARG:HA	2:B:186:ARG:HD3	1.75	0.46
1:A:2062:GLU:HB3	1:A:2066:LYS:HE3	1.98	0.45
2:B:237:TYR:CE2	2:B:241:LEU:HD11	2.52	0.45
2:B:251:CYS:O	2:B:296:SER:HB2	2.16	0.45
1:A:1902:GLN:HB2	1:A:1905:LEU:HD21	1.98	0.45
2:B:8:SER:OG	2:B:10:PRO:HD3	2.17	0.44
1:A:2027:LEU:O	1:A:2028:SER:C	2.61	0.43
2:B:171:ASP:HA	2:B:172:PRO:HD3	1.89	0.43
2:B:19:GLN:OE1	2:B:19:GLN:N	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:260:MET:HB3	2:B:260:MET:HE2	1.79	0.42
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	2.00	0.42
1:A:1845:ASN:OD1	1:A:1849:LYS:NZ	2.53	0.42
1:A:2021:SER:O	1:A:2022:ALA:C	2.61	0.42
2:B:37:PRO:O	2:B:42:HIS:NE2	2.52	0.42
2:B:190:ARG:HD3	2:B:203[B]:TYR:CE1	2.55	0.42
1:A:1942:ASP:HB2	1:A:1943:PRO:HD3	2.02	0.41
1:A:2063:TYR:CD1	1:A:2063:TYR:C	2.98	0.41
1:A:2001[A]:SER:O	1:A:2002:TYR:C	2.62	0.41
1:A:2001[B]:SER:O	1:A:2002:TYR:C	2.63	0.41
2:B:85:ASP:C	2:B:85:ASP:OD1	2.64	0.41
2:B:97:LYS:C	2:B:100:GLN:H	2.27	0.41
2:B:188:ALA:HA	2:B:204:TYR:CD1	2.56	0.41
1:A:1911:TRP:CE3	2:B:195:MET:HB2	2.55	0.41
2:B:2:ASN:O	2:B:36:ILE:HB	2.21	0.41
2:B:110:GLU:O	2:B:110:GLU:HG2	2.21	0.41
2:B:247:ILE:HG22	2:B:292:CYS:SG	2.61	0.41
2:B:267:ILE:O	2:B:271:GLN:HG3	2.21	0.41
1:A:2007:ARG:O	1:A:2008:LEU:C	2.64	0.40
1:A:2029:ASP:OD1	1:A:2029:ASP:C	2.63	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%)	240 (97%)	8 (3%)	0	100	100
2	B	305/308 (99%)	285 (93%)	18 (6%)	2 (1%)	18	14
All	All	553/566 (98%)	525 (95%)	26 (5%)	2 (0%)	43	27

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 ⓘ

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%)	219 (97%)	7 (3%)	35	37
2	B	286/284 (101%)	277 (97%)	9 (3%)	35	37
All	All	512/517 (99%)	496 (97%)	16 (3%)	37	37

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1835	MET
1	A	1898[A]	VAL
1	A	1898[B]	VAL
1	A	1918[A]	SER
1	A	1918[B]	SER
1	A	2032	ILE
1	A	2045	ASP
2	B	2	ASN
2	B	17	ILE
2	B	21	SER
2	B	77	LEU
2	B	123	MET
2	B	174	HIS
2	B	279	TYR
2	B	315	GLU
2	B	317	LEU

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

Mol	Chain	Res	Type
1	A	2038	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%)	1.92	103 (43%) 0 1	32, 83, 121, 138	12 (5%)
2	B	300/308 (97%)	1.69	104 (34%) 1 1	33, 95, 137, 191	9 (3%)
All	All	537/566 (94%)	1.79	207 (38%) 1 1	32, 91, 132, 191	21 (3%)

All (207) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1878	CYS	9.4
1	A	1940	MET	7.5
1	A	1879	ILE	5.9
2	B	22	PHE	5.3
1	A	1979[A]	MET	4.8
1	A	1935	VAL	4.8
2	B	54[A]	MET	4.8
1	A	1987	VAL	4.6
1	A	2060	LEU	4.4
1	A	1988	LEU	4.2
1	A	1963	LEU	4.2
1	A	1996	LEU	4.2
1	A	2061	THR	4.2
2	B	203[A]	TYR	4.1
1	A	1894	ILE	4.1
1	A	1969	MET	4.1
1	A	1989	PHE	4.0
2	B	188	ALA	3.9
2	B	41[A]	VAL	3.9
2	B	241	LEU	3.8
2	B	291	ILE	3.8
1	A	1977	VAL	3.8
2	B	96	PHE	3.8
2	B	126	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
2	B	235	GLY	3.7
1	A	2048	TRP	3.7
2	B	53	SER	3.7
1	A	1954	ILE	3.7
1	A	1956	ILE	3.7
2	B	198	PHE	3.7
1	A	1857	VAL	3.6
1	A	1866	PHE	3.6
1	A	1936	THR	3.5
2	B	52	SER	3.5
2	B	100	GLN	3.5
2	B	176	LEU	3.5
2	B	38	ILE	3.5
2	B	130	VAL	3.5
2	B	40	HIS	3.5
2	B	275	LEU	3.5
2	B	183	PHE	3.4
1	A	2040	TRP	3.4
2	B	121	VAL	3.4
2	B	60	PHE	3.4
2	B	313	TYR	3.3
2	B	77	LEU	3.3
2	B	20	TYR	3.3
1	A	2009	THR	3.3
1	A	2039	LEU	3.3
1	A	1841	ALA	3.2
1	A	1922	ARG	3.2
1	A	2065	ARG	3.2
2	B	175	SER	3.2
2	B	139	TYR	3.2
1	A	1986	MET	3.2
1	A	1964	PRO	3.2
2	B	170	SER	3.1
1	A	1900	ALA	3.1
1	A	2063	TYR	3.1
1	A	1955	ALA	3.1
1	A	1858	TYR	3.1
1	A	2012	LEU	3.1
1	A	1951	PHE	3.1
2	B	210	LEU	3.0
2	B	180	VAL	3.0
1	A	1851	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	1991	ILE	3.0
1	A	1946	VAL	3.0
2	B	115	TYR	3.0
2	B	74	LYS	3.0
1	A	1859	ARG	3.0
2	B	204	TYR	2.9
1	A	1968	ALA	2.9
2	B	92	ILE	2.9
2	B	189	ILE	2.9
2	B	264	LEU	2.9
2	B	103	VAL	2.9
1	A	1930	PRO	2.9
2	B	316	LEU	2.9
1	A	1840	TYR	2.8
1	A	1895	HIS	2.8
2	B	279	TYR	2.8
2	B	283	LEU	2.8
2	B	146	THR	2.8
1	A	1984	PRO	2.8
2	B	240	SER	2.8
1	A	2017[A]	THR	2.8
1	A	1862	VAL	2.8
1	A	2066	LYS	2.7
2	B	220	TYR	2.7
1	A	1941	LEU	2.7
2	B	122[A]	GLN	2.7
1	A	1981	ALA	2.7
2	B	76	GLY	2.7
1	A	2041	PRO	2.7
1	A	2059	ILE	2.7
1	A	2005	PHE	2.6
1	A	1924	LEU	2.6
2	B	177[A]	ASN	2.6
2	B	129	ILE	2.6
1	A	2016	LYS	2.6
2	B	249	LEU	2.6
1	A	2049	ILE	2.6
2	B	181	ILE	2.6
1	A	1920	LEU	2.6
2	B	17	ILE	2.6
1	A	1901	GLY	2.6
1	A	1967	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	239	SER	2.6
1	A	1982	THR	2.6
2	B	317	LEU	2.5
1	A	2051	ILE	2.5
1	A	1860	VAL	2.5
2	B	246	MET	2.5
1	A	1999	ILE	2.5
2	B	108	ILE	2.5
2	B	250	ILE	2.5
1	A	2015	LEU	2.5
2	B	199	LEU	2.5
1	A	1925	PRO	2.5
1	A	2027	LEU	2.4
2	B	205	LEU	2.4
2	B	302	LEU	2.4
1	A	2004	ALA	2.4
1	A	1899	TRP	2.4
1	A	1978	VAL	2.4
1	A	1933	ILE	2.4
2	B	113	THR	2.4
2	B	172	PRO	2.4
1	A	2026	LEU	2.4
2	B	178	TYR	2.4
1	A	1965	PHE	2.4
1	A	2043	PHE	2.4
1	A	1985	GLN	2.4
2	B	212	GLY	2.4
1	A	1905	LEU	2.3
2	B	284	LEU	2.3
2	B	228	PHE	2.3
1	A	2034	ILE	2.3
2	B	44[A]	ILE	2.3
2	B	116	ASN	2.3
2	B	5	PRO	2.3
2	B	80	MET	2.3
2	B	312	LYS	2.3
1	A	2010	LEU	2.3
2	B	152	LEU	2.3
2	B	221	PHE	2.3
2	B	234	PHE	2.3
1	A	1874	ALA	2.3
2	B	49	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	1	MET	2.3
1	A	1847	ASP	2.3
2	B	229	LEU	2.3
1	A	1844	PHE	2.3
2	B	58	TYR	2.3
2	B	33	ILE	2.3
2	B	247	ILE	2.3
1	A	1921	VAL	2.3
2	B	288	VAL	2.3
1	A	2058	LEU	2.3
2	B	30	PHE	2.2
2	B	237	TYR	2.2
2	B	69	ILE	2.2
2	B	308	ILE	2.2
2	B	251	CYS	2.2
1	A	1992	TYR	2.2
2	B	78	TYR	2.2
1	A	1875	ILE	2.2
2	B	15	ILE	2.2
2	B	272	ILE	2.2
2	B	64[A]	MET	2.2
1	A	1959	THR	2.2
2	B	301	SER	2.2
2	B	214	PHE	2.2
2	B	297	PHE	2.2
1	A	2025	ILE	2.2
1	A	2032	ILE	2.2
1	A	1876	ASN	2.2
1	A	1929	GLN	2.2
1	A	2069	VAL	2.2
1	A	1881	THR	2.2
1	A	1835	MET	2.1
1	A	1839	ASN	2.1
2	B	267	ILE	2.1
2	B	59	TRP	2.1
1	A	1853	ASP	2.1
1	A	1865	THR	2.1
2	B	97	LYS	2.1
2	B	236	ASN	2.1
1	A	2002	TYR	2.1
1	A	1838	SER	2.1
2	B	207	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1833	GLY	2.1
2	B	43	VAL	2.1
1	A	1961	LEU	2.1
2	B	73	PRO	2.1
2	B	109	ASP	2.1
1	A	1906	SER	2.1
1	A	1912	LYS	2.1
2	B	140	VAL	2.1
1	A	1949	LEU	2.1
2	B	6	PHE	2.0
2	B	303	HIS	2.0
2	B	28	GLN	2.0
1	A	1908	LEU	2.0
1	A	1995	TRP	2.0
2	B	68	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 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.