



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:06 AM UTC

PDB ID : 5R0Y / pdb_00005r0y
Title : PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for ground state model 12, 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 : 1.75 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

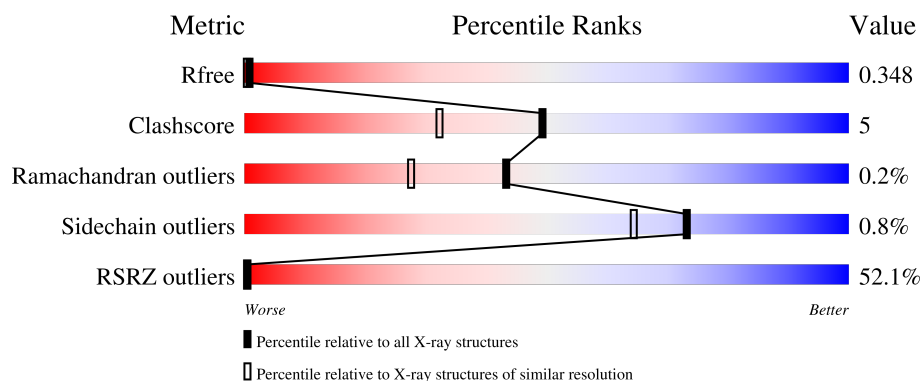
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	53% 81% 11% 8%
2	B	308	47% 82% 14% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4681 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 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

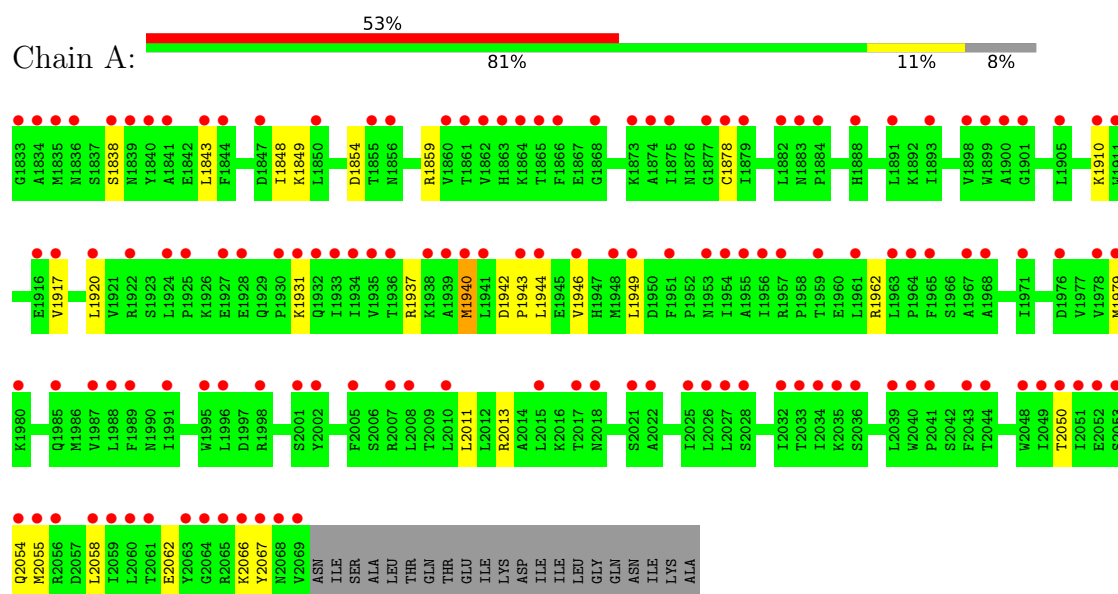
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	61	Total O 61 61	0	0
3	B	38	Total O 38 38	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



E310	E311	E312	Y313	P314	E315	L316	L317
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	88.37Å 82.11Å 92.30Å 90.00° 107.71° 90.00°	Depositor
Resolution (Å)	23.29 – 1.75 23.29 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.6 (23.29-1.75) 99.8 (23.29-1.75)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.286 , 0.342 0.292 , 0.348	Depositor DCC
R_{free} test set	2097 reflections (3.30%)	wwPDB-VP
Wilson B-factor (Å ²)	42.4	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.5	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	4681	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 5.72% 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	0.74	1/2049 (0.0%)	0.96	3/2775 (0.1%)
2	B	0.62	0/2651	0.79	0/3581
All	All	0.67	1/4700 (0.0%)	0.87	3/6356 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1940	MET	SD-CE	-5.75	1.65	1.79

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1859	ARG	NE-CZ-NH1	-5.56	115.94	121.50
1	A	1878	CYS	N-CA-C	5.39	117.28	108.76
1	A	1859	ARG	NE-CZ-NH2	5.06	123.76	119.20

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	16	0
2	B	2580	0	2450	33	0
3	A	61	0	0	0	0
3	B	38	0	0	4	0
All	All	4681	0	4479	49	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 (49) 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	1.69	0.75
1:A:2062:GLU:O	1:A:2066:LYS:HG2	1.87	0.74
2:B:1:MET:N	3:B:401:HOH:O	2.21	0.72
2:B:258:LYS:HD2	2:B:258:LYS:H	1.62	0.64
2:B:68:TYR:CE2	2:B:81:MET:HE3	2.32	0.64
1:A:1979[B]:MET:HA	1:A:1979[B]:MET:HE2	1.83	0.60
2:B:70:GLN:CB	2:B:81:MET:HE2	2.34	0.57
2:B:230[B]:ASN:ND2	2:B:239:SER:OG	2.39	0.56
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.52	0.56
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.87	0.55
2:B:287:ARG:O	2:B:291:ILE:HD13	2.07	0.55
2:B:16:GLY:HA3	2:B:45:HIS:CE1	2.44	0.53
2:B:54[B]:MET:HE1	2:B:143:SER:HB3	1.92	0.52
2:B:1:MET:HB3	2:B:35:ASP:HA	1.91	0.52
2:B:242:GLN:O	2:B:246:MET:HG3	2.12	0.50
1:A:2062:GLU:HB3	1:A:2066:LYS:HE3	1.94	0.49
2:B:214:PHE:O	2:B:215:LYS:HB2	2.13	0.48
2:B:251:CYS:O	2:B:296:SER:HB2	2.13	0.48
1:A:1946:VAL:O	1:A:1949:LEU:HG	2.15	0.47
2:B:6:PHE:CD1	2:B:32:GLY:HA2	2.49	0.47
2:B:6:PHE:CZ	2:B:44[A]:ILE:HD11	2.49	0.47
1:A:1910:LYS:O	1:A:1940:MET:HE1	2.14	0.47
2:B:96:PHE:CB	2:B:102:MET:HE3	2.46	0.46
1:A:2011:LEU:HD23	1:A:2055:MET:HE3	1.98	0.46
2:B:54[B]:MET:N	3:B:402:HOH:O	2.41	0.46
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.44	0.46
2:B:243:TRP:O	2:B:247:ILE:HG13	2.16	0.46
2:B:1:MET:HE3	2:B:35:ASP:O	2.14	0.45
2:B:6:PHE:HZ	2:B:44[A]:ILE:HD11	1.80	0.45
2:B:18:ASP:OD2	2:B:105:TYR:OH	2.31	0.44
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.42	0.44
2:B:114:TRP:CE2	2:B:118:THR:HG21	2.54	0.43
2:B:229:LEU:HD23	2:B:229:LEU:HA	1.89	0.43
1:A:2066:LYS:HB2	1:A:2067:TYR:CD1	2.53	0.43
2:B:114:TRP:CZ2	2:B:118:THR:HG21	2.55	0.42
2:B:244:HIS:CD2	2:B:285:ASN:HB3	2.54	0.42
2:B:188:ALA:HA	2:B:204:TYR:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:51:ASN:C	2:B:53:SER:N	2.78	0.42
2:B:42:HIS:HE1	3:B:429:HOH:O	2.02	0.42
2:B:53:SER:HA	3:B:402:HOH:O	2.20	0.41
2:B:77:LEU:HD21	2:B:79:LYS:HE3	2.03	0.41
1:A:1942:ASP:HB2	1:A:1943:PRO:HD3	2.02	0.41
1:A:1854:ASP:CG	1:A:1937:ARG:HH21	2.29	0.41
1:A:1944:LEU:HD12	1:A:1944:LEU:HA	1.90	0.41
1:A:2050:THR:HG22	1:A:2054:GLN:NE2	2.36	0.41
2:B:134:GLU:OE1	2:B:134:GLU:N	2.47	0.40
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	2.04	0.40
1:A:1917:VAL:O	1:A:1920:LEU:HB3	2.21	0.40
2:B:15:ILE:HD12	2:B:24:VAL:HG21	2.03	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%)	244 (98%)	4 (2%)	0	100	100
2	B	306/308 (99%)	293 (96%)	11 (4%)	2 (1%)	18	7
All	All	554/566 (98%)	537 (97%)	15 (3%)	2 (0%)	43	15

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%)	225 (100%)	1 (0%)	84	80
2	B	287/284 (101%)	284 (99%)	3 (1%)	68	56
All	All	513/517 (99%)	509 (99%)	4 (1%)	73	64

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1838	SER
2	B	77	LEU
2	B	174	HIS
2	B	315	GLU

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	1907	GLN
1	A	2038	HIS
2	B	47	GLN
2	B	91	ASN
2	B	116	ASN
2	B	259	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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%)	2.59	136 (57%) 0 0	27, 69, 119, 192	12 (5%)
2	B	300/308 (97%)	2.26	144 (48%) 0 0	23, 72, 151, 288	9 (3%)
All	All	537/566 (94%)	2.41	280 (52%) 0 0	23, 71, 140, 288	21 (3%)

All (280) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1878	CYS	11.3
1	A	1956	ILE	8.9
1	A	1933	ILE	7.8
2	B	54[A]	MET	7.6
1	A	2048	TRP	7.5
2	B	108	ILE	7.2
1	A	1898[A]	VAL	6.8
1	A	1944	LEU	6.6
1	A	1954	ILE	6.5
1	A	1991	ILE	6.5
1	A	1989	PHE	6.4
2	B	313	TYR	6.4
1	A	1917	VAL	6.3
1	A	1979[A]	MET	6.0
2	B	203[A]	TYR	5.9
2	B	77	LEU	5.8
2	B	96	PHE	5.8
1	A	1963	LEU	5.7
1	A	2034	ILE	5.7
2	B	103	VAL	5.6
2	B	69	ILE	5.6
1	A	1855[A]	THR	5.6
2	B	52	SER	5.5
1	A	1866	PHE	5.5

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Mol	Chain	Res	Type	RSRZ
1	A	1940	MET	5.5
2	B	22	PHE	5.4
1	A	2060	LEU	5.4
2	B	1	MET	5.4
1	A	1905	LEU	5.4
2	B	30	PHE	5.3
2	B	183	PHE	5.3
2	B	28	GLN	5.3
2	B	316	LEU	5.3
1	A	1927	GLU	5.3
1	A	2063	TYR	5.3
1	A	2040	TRP	5.1
2	B	126	ILE	5.1
1	A	1862	VAL	5.1
1	A	2058	LEU	5.0
1	A	1930	PRO	5.0
1	A	1891	LEU	4.9
2	B	20	TYR	4.8
2	B	291	ILE	4.8
2	B	198	PHE	4.8
2	B	129	ILE	4.8
1	A	1834	ALA	4.7
1	A	2017[A]	THR	4.7
2	B	146	THR	4.7
2	B	210	LEU	4.7
2	B	275	LEU	4.6
1	A	2066	LYS	4.6
2	B	279	TYR	4.6
2	B	40	HIS	4.5
1	A	1861	THR	4.5
2	B	152	LEU	4.5
1	A	1935	VAL	4.4
1	A	1980	LYS	4.4
1	A	2008	LEU	4.4
2	B	73	PRO	4.4
1	A	1920	LEU	4.4
1	A	1840	TYR	4.4
1	A	1934	ILE	4.4
2	B	101	MET	4.3
2	B	53	SER	4.3
1	A	1910	LYS	4.3
1	A	1879	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
2	B	303	HIS	4.3
2	B	99	ARG	4.2
2	B	214	PHE	4.2
1	A	2051	ILE	4.2
1	A	2067	TYR	4.1
2	B	261	LEU	4.1
2	B	174	HIS	4.1
1	A	2064	GLY	4.0
1	A	2061	THR	3.9
1	A	1863	HIS	3.9
1	A	1882	LEU	3.9
1	A	2059	ILE	3.9
2	B	19	GLN	3.9
2	B	251	CYS	3.9
2	B	217	SER	3.8
1	A	1998	ARG	3.8
2	B	199	LEU	3.8
2	B	283	LEU	3.8
2	B	288	VAL	3.7
2	B	191	PRO	3.7
2	B	51	ASN	3.7
1	A	1850	LEU	3.7
2	B	181	ILE	3.7
2	B	282	ILE	3.7
2	B	15	ILE	3.6
2	B	137	PHE	3.6
2	B	136	GLN	3.6
1	A	1949	LEU	3.6
1	A	1888	HIS	3.6
1	A	2027	LEU	3.6
2	B	294	TYR	3.6
2	B	150	ASN	3.6
1	A	1951	PHE	3.5
1	A	1971	ILE	3.5
2	B	107	LYS	3.5
1	A	1843	LEU	3.5
1	A	1860	VAL	3.5
2	B	280	SER	3.5
2	B	106	PRO	3.5
2	B	193	HIS	3.5
1	A	2036	SER	3.4
2	B	170	SER	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	284	LEU	3.4
2	B	122[A]	GLN	3.4
2	B	278	GLN	3.4
2	B	24	VAL	3.4
2	B	31	HIS	3.4
1	A	2039	LEU	3.4
2	B	207	THR	3.4
2	B	49	ALA	3.3
1	A	1976	ASP	3.3
1	A	1833	GLY	3.3
2	B	317	LEU	3.3
2	B	257	PRO	3.3
1	A	1968	ALA	3.3
1	A	2049	ILE	3.3
1	A	2068	ASN	3.3
2	B	100	GLN	3.3
1	A	1985	GLN	3.3
1	A	1988	LEU	3.3
1	A	2065	ARG	3.3
2	B	67	PHE	3.2
1	A	1922	ARG	3.2
2	B	289	TRP	3.2
1	A	1941	LEU	3.2
1	A	1948	MET	3.2
1	A	1868	GLY	3.2
1	A	2007	ARG	3.2
2	B	84	ARG	3.1
2	B	281	ASP	3.1
2	B	139	TYR	3.1
1	A	1841	ALA	3.1
1	A	1936	THR	3.1
2	B	310	GLU	3.1
2	B	237	TYR	3.1
1	A	1899	TRP	3.0
2	B	29	PRO	3.0
1	A	1856	ASN	3.0
1	A	1883	ASN	3.0
1	A	2050	THR	3.0
2	B	109	ASP	3.0
1	A	2002	TYR	3.0
2	B	220	TYR	3.0
2	B	262	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	1835	MET	3.0
2	B	89	PHE	3.0
2	B	124	ASP	3.0
2	B	48	HIS	3.0
2	B	147	VAL	2.9
1	A	1838	SER	2.9
1	A	1996	LEU	2.9
2	B	116	ASN	2.9
1	A	2054	GLN	2.9
2	B	38	ILE	2.9
1	A	2021	SER	2.9
2	B	6	PHE	2.9
2	B	228	PHE	2.9
1	A	1967	ALA	2.9
1	A	2005	PHE	2.8
1	A	2044	THR	2.8
1	A	2010	LEU	2.8
1	A	1978	VAL	2.8
1	A	2028	SER	2.8
2	B	17	ILE	2.8
2	B	92	ILE	2.8
1	A	1931[A]	LYS	2.8
2	B	14	THR	2.8
1	A	1911	TRP	2.8
2	B	87	ALA	2.8
2	B	130	VAL	2.8
1	A	1953	ASN	2.7
2	B	311	ASN	2.7
1	A	2055	MET	2.7
1	A	1893	ILE	2.7
1	A	1865	THR	2.7
1	A	1957	ARG	2.7
2	B	176	LEU	2.7
2	B	189	ILE	2.7
2	B	23	ASN	2.7
2	B	233	PHE	2.7
1	A	2069	VAL	2.7
2	B	293	LEU	2.7
2	B	74	LYS	2.7
2	B	299	LYS	2.7
1	A	2056[A]	ARG	2.6
2	B	186	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1884	PRO	2.6
2	B	211[A]	GLN	2.6
1	A	1901	GLY	2.6
2	B	267	ILE	2.6
2	B	173	ALA	2.6
2	B	97	LYS	2.6
2	B	235	GLY	2.6
2	B	297	PHE	2.6
1	A	2052	GLU	2.6
1	A	2043	PHE	2.6
2	B	226	PHE	2.6
2	B	258	LYS	2.6
1	A	2041	PRO	2.6
2	B	10	PRO	2.6
2	B	172	PRO	2.6
1	A	1844	PHE	2.5
1	A	1928	GLU	2.5
1	A	1864	LYS	2.5
1	A	1961	LEU	2.5
2	B	205	LEU	2.5
2	B	134	GLU	2.5
1	A	2053[A]	SER	2.5
2	B	47	GLN	2.5
1	A	1924	LEU	2.4
1	A	1925	PRO	2.4
2	B	276	PRO	2.4
1	A	1946	VAL	2.4
1	A	2032	ILE	2.4
2	B	21	SER	2.4
1	A	1873	LYS	2.4
2	B	260	MET	2.4
2	B	104	SER	2.4
2	B	208	VAL	2.4
2	B	247	ILE	2.4
1	A	1916	GLU	2.4
2	B	259	HIS	2.4
1	A	1836	ASN	2.4
2	B	2	ASN	2.4
1	A	2018	ASN	2.3
1	A	1939	ALA	2.3
2	B	145	THR	2.3
2	B	56	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1987	VAL	2.3
1	A	2033	THR	2.3
1	A	1900	ALA	2.3
1	A	1847	ASP	2.3
1	A	1938	LYS	2.3
1	A	1959	THR	2.3
2	B	55	ARG	2.3
2	B	234	PHE	2.3
2	B	178	TYR	2.3
1	A	1875	ILE	2.3
1	A	2025	ILE	2.3
2	B	314	PRO	2.2
2	B	177[A]	ASN	2.2
2	B	249	LEU	2.2
2	B	301	SER	2.2
2	B	50	ASP	2.2
2	B	149	GLU	2.2
1	A	2035	LYS	2.2
2	B	33	ILE	2.2
2	B	250	ILE	2.2
1	A	2026	LEU	2.2
2	B	94	HIS	2.2
2	B	135	ASN	2.2
1	A	1964	PRO	2.2
2	B	93	VAL	2.1
1	A	2015	LEU	2.1
2	B	128	LYS	2.1
1	A	1877	GLY	2.1
1	A	1839	ASN	2.1
1	A	1965	PHE	2.1
2	B	121	VAL	2.1
2	B	81	MET	2.1
1	A	1995	TRP	2.1
2	B	312	LYS	2.1
1	A	1955	ALA	2.0
1	A	2022	ALA	2.0
2	B	110	GLU	2.0
2	B	206	ASN	2.0
2	B	315	GLU	2.0
2	B	240	SER	2.0
1	A	1943	PRO	2.0
1	A	1932	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	36	ILE	2.0
1	A	1874	ALA	2.0
1	A	2001[A]	SER	2.0
2	B	263	LYS	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.