



Full wwPDB X-ray Structure Validation Report ⓘ

May 7, 2026 – 11:26 AM EDT

PDB ID : 5R1O / pdb_00005r1o
Title : PanDDA analysis group deposition – Auto-refined data of Aar2/RNaseH for ground state model 39, 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 : 1.90 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

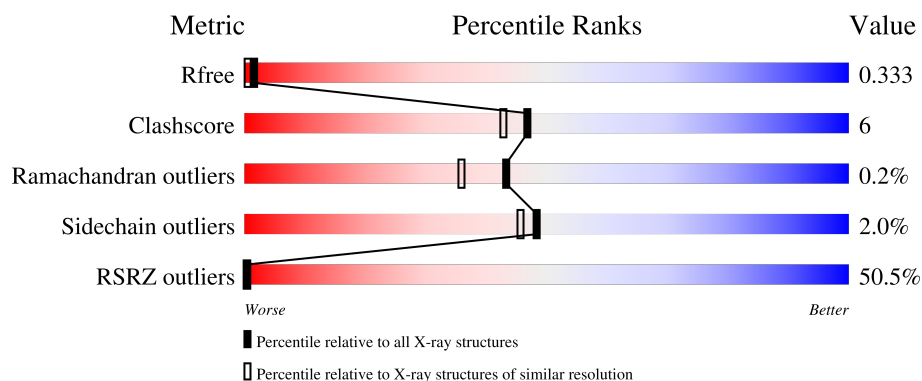
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	41% 81% 10% 8%
2	B	308	54% 80% 18% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4672 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

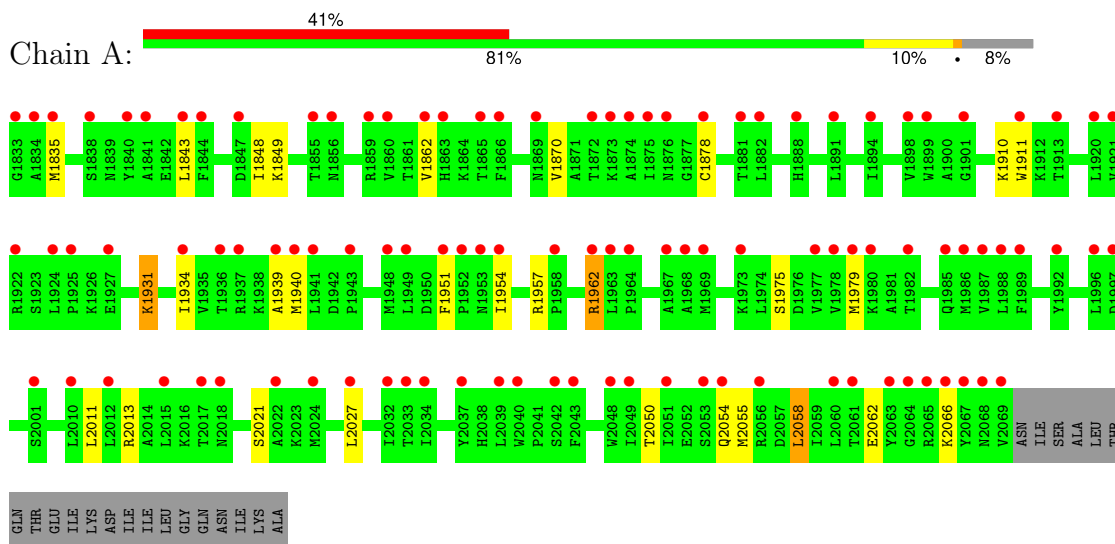
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	55	Total O 55 55	0	0
3	B	35	Total O 35 35	0	0

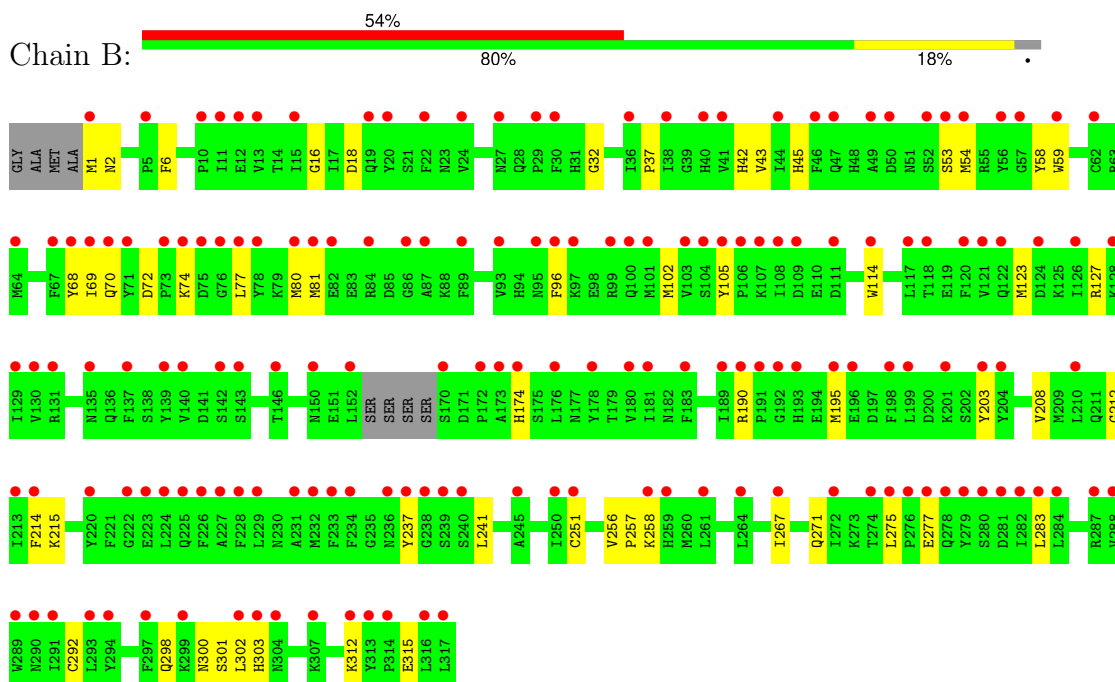
3 Residue-property plots [i](#)

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	88.95Å 82.32Å 92.48Å 90.00° 107.71° 90.00°	Depositor
Resolution (Å)	22.55 – 1.90 22.55 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (22.55-1.90) 99.9 (22.55-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.290 , 0.334 0.295 , 0.333	Depositor DCC
R_{free} test set	2100 reflections (4.18%)	wwPDB-VP
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 64.6	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	0.92	EDS
Total number of atoms	4672	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.75% 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	0.78	1/2049 (0.0%)	0.94	1/2775 (0.0%)
2	B	0.69	0/2651	0.89	0/3581
All	All	0.73	1/4700 (0.0%)	0.91	1/6356 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1878	CYS	CA-C	5.06	1.59	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1878	CYS	N-CA-C	5.19	116.96	108.76

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	2580	0	2450	35	0
3	A	55	0	0	0	0
3	B	35	0	0	3	0
All	All	4672	0	4479	52	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 (52) 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:1:MET:N	3:B:401:HOH:O	1.96	0.98
2:B:70:GLN:HB3	2:B:81:MET:HE2	1.60	0.83
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.29	0.78
1:A:2062:GLU:O	1:A:2066:LYS:HG2	1.87	0.74
2:B:258:LYS:HD2	2:B:258:LYS:H	1.63	0.63
2:B:251:CYS:HG	2:B:292:CYS:HB3	1.63	0.63
1:A:1979[B]:MET:HA	1:A:1979[B]:MET:HE2	1.83	0.61
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.25	0.60
2:B:301:SER:O	2:B:302:LEU:HD23	2.02	0.59
2:B:251:CYS:HG	2:B:292:CYS:CB	2.15	0.58
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.33	0.57
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.86	0.56
1:A:1910:LYS:O	1:A:1940:MET:HE1	2.06	0.56
1:A:2062:GLU:HB3	1:A:2066:LYS:HE3	1.88	0.55
2:B:251:CYS:SG	2:B:292:CYS:SG	3.01	0.55
1:A:1911:TRP:CD1	2:B:195:MET:HE3	2.42	0.54
2:B:42:HIS:O	2:B:59:TRP:HA	2.10	0.52
2:B:300:ASN:O	2:B:303:HIS:NE2	2.42	0.51
2:B:74:LYS:NZ	3:B:402:HOH:O	2.41	0.51
2:B:70:GLN:HB3	2:B:81:MET:CE	2.39	0.49
1:A:1848:ILE:H	1:A:1931[A]:LYS:NZ	2.04	0.49
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.95	0.49
1:A:1848:ILE:N	1:A:1931[A]:LYS:HZ2	2.06	0.49
1:A:2050:THR:HG22	1:A:2054:GLN:NE2	2.29	0.48
1:A:1951:PHE:HB3	1:A:1954:ILE:HD12	1.97	0.46
2:B:251:CYS:SG	2:B:292:CYS:HB3	2.56	0.46
2:B:275:LEU:HD22	2:B:283:LEU:HD13	1.98	0.46
2:B:237:TYR:CE2	2:B:241:LEU:HD11	2.52	0.45
2:B:277:GLU:HG3	2:B:312:LYS:HE2	1.97	0.45
2:B:53:SER:HA	3:B:405:HOH:O	2.18	0.44
2:B:256:VAL:O	2:B:257:PRO:C	2.60	0.44
2:B:267:ILE:O	2:B:271:GLN:HG3	2.18	0.44
2:B:208:VAL:O	2:B:212:GLY:HA3	2.18	0.44
2:B:43:VAL:HA	2:B:58:TYR:O	2.17	0.43
2:B:72:ASP:OD1	2:B:72:ASP:C	2.61	0.43
2:B:277:GLU:CD	2:B:277:GLU:H	2.23	0.43
2:B:298:GLN:HA	2:B:298:GLN:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:37:PRO:HD3	2:B:105:TYR:CD1	2.53	0.42
1:A:1862:VAL:HG13	1:A:1870:VAL:CG1	2.49	0.42
1:A:1910:LYS:HD3	1:A:1939:ALA:HB1	2.00	0.42
1:A:1934:ILE:HA	1:A:1957:ARG:O	2.18	0.42
2:B:6:PHE:CD1	2:B:32:GLY:HA2	2.55	0.42
2:B:18:ASP:HB3	2:B:114:TRP:CE3	2.54	0.42
2:B:68:TYR:CE2	2:B:81:MET:HE3	2.55	0.41
2:B:190:ARG:HG3	2:B:203[B]:TYR:CE2	2.55	0.41
2:B:69:ILE:HD13	2:B:80:MET:HA	2.01	0.41
2:B:123:MET:O	2:B:127:ARG:HG3	2.21	0.41
2:B:16:GLY:HA3	2:B:45:HIS:CE1	2.55	0.41
2:B:275:LEU:CD2	2:B:283:LEU:HD13	2.51	0.41
2:B:214:PHE:O	2:B:215:LYS:HB2	2.20	0.41
1:A:1975:SER:O	1:A:1979[A]:MET:SD	2.79	0.40
1:A:2011:LEU:HD23	1:A:2055:MET:HE3	2.02	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%)	241 (97%)	7 (3%)	0	100	100
2	B	306/308 (99%)	291 (95%)	13 (4%)	2 (1%)	18	10
All	All	554/566 (98%)	532 (96%)	20 (4%)	2 (0%)	43	22

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	29
2	B	287/284 (101%)	283 (99%)	4 (1%)	59	59
All	All	513/517 (99%)	502 (98%)	11 (2%)	48	44

All (11) 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	1962	ARG
1	A	2021	SER
1	A	2027	LEU
1	A	2058	LEU
2	B	2	ASN
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 (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1863	HIS
2	B	259	HIS
2	B	278	GLN

5.3.3 RNA

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%)	2.17	106 (44%) 0 0	22, 73, 122, 198	12 (5%)
2	B	300/308 (97%)	2.28	165 (55%) 0 0	29, 83, 143, 199	9 (3%)
All	All	537/566 (94%)	2.23	271 (50%) 0 0	22, 79, 135, 199	21 (3%)

All (271) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1878	CYS	10.2
1	A	1940	MET	9.4
1	A	2060	LEU	7.3
1	A	1996	LEU	7.1
1	A	1941	LEU	6.9
2	B	54[A]	MET	6.9
2	B	103	VAL	6.8
2	B	73	PRO	6.6
2	B	189	ILE	6.6
1	A	1979[A]	MET	6.5
2	B	203[A]	TYR	6.3
2	B	316	LEU	6.3
2	B	22	PHE	5.7
1	A	1980	LYS	5.6
1	A	1989	PHE	5.5
1	A	1882	LEU	5.4
1	A	1898[A]	VAL	5.2
1	A	1881	THR	5.1
1	A	1888	HIS	5.0
2	B	289	TRP	5.0
2	B	130	VAL	4.9
2	B	117	LEU	4.9
2	B	107	LYS	4.8
1	A	1934	ILE	4.8

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Mol	Chain	Res	Type	RSRZ
2	B	313	TYR	4.7
1	A	2032	ILE	4.7
1	A	2043	PHE	4.6
2	B	20	TYR	4.6
1	A	1968	ALA	4.5
2	B	251	CYS	4.5
1	A	2066	LYS	4.4
1	A	2069	VAL	4.4
2	B	24	VAL	4.4
2	B	40	HIS	4.4
2	B	291	ILE	4.3
2	B	126	ILE	4.3
2	B	71	TYR	4.3
1	A	2017[A]	THR	4.2
1	A	2051	ILE	4.2
1	A	1948	MET	4.2
1	A	2048	TRP	4.2
1	A	1988	LEU	4.2
1	A	1866	PHE	4.2
2	B	80	MET	4.1
2	B	101	MET	4.1
2	B	129	ILE	4.1
2	B	174	HIS	4.1
2	B	275	LEU	4.1
2	B	114	TRP	4.0
2	B	1	MET	4.0
1	A	1954	ILE	4.0
2	B	250	ILE	4.0
2	B	53	SER	4.0
1	A	1891	LEU	3.9
1	A	1860	VAL	3.9
2	B	288	VAL	3.9
2	B	224	LEU	3.8
1	A	1964	PRO	3.8
2	B	64[A]	MET	3.8
1	A	1987	VAL	3.8
1	A	2053[A]	SER	3.8
1	A	2065	ARG	3.7
2	B	191	PRO	3.7
2	B	299	LYS	3.7
2	B	11	ILE	3.7
1	A	1834	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
2	B	74	LYS	3.6
2	B	276	PRO	3.6
2	B	77	LEU	3.6
2	B	139	TYR	3.5
2	B	99	ARG	3.5
2	B	170	SER	3.5
2	B	89	PHE	3.5
1	A	2027	LEU	3.5
2	B	293	LEU	3.5
1	A	1913	THR	3.4
2	B	67	PHE	3.4
1	A	1924	LEU	3.4
2	B	78	TYR	3.3
1	A	2056[A]	ARG	3.3
2	B	210	LEU	3.3
2	B	181	ILE	3.3
2	B	272	ILE	3.3
2	B	152	LEU	3.3
1	A	1951	PHE	3.3
2	B	234	PHE	3.3
2	B	225	GLN	3.3
2	B	193	HIS	3.3
2	B	176	LEU	3.3
1	A	1847	ASP	3.3
2	B	226	PHE	3.3
1	A	2042	SER	3.3
1	A	2034	ILE	3.2
2	B	44[A]	ILE	3.2
1	A	1982	THR	3.2
1	A	2039	LEU	3.2
1	A	2061	THR	3.2
2	B	106	PRO	3.2
2	B	317	LEU	3.2
2	B	104	SER	3.2
1	A	2063	TYR	3.2
2	B	108	ILE	3.2
1	A	2022	ALA	3.2
2	B	173	ALA	3.2
2	B	213	ILE	3.2
2	B	29	PRO	3.2
1	A	2068	ASN	3.2
2	B	59	TRP	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	140	VAL	3.1
1	A	1901	GLY	3.1
2	B	96	PHE	3.1
1	A	1894	ILE	3.1
2	B	5	PRO	3.1
2	B	124	ASP	3.1
2	B	297	PHE	3.1
1	A	1875	ILE	3.1
2	B	279	TYR	3.1
1	A	1876	ASN	3.1
1	A	1872	THR	3.1
1	A	1833	GLY	3.1
2	B	81	MET	3.0
1	A	1963	LEU	3.0
2	B	68	TYR	3.0
2	B	150	ASN	3.0
2	B	237	TYR	3.0
2	B	120	PHE	3.0
2	B	314	PRO	3.0
1	A	1841	ALA	3.0
1	A	1992	TYR	3.0
1	A	1838	SER	3.0
2	B	75	ASP	3.0
2	B	109	ASP	3.0
1	A	1986	MET	3.0
2	B	283	LEU	2.9
2	B	122[A]	GLN	2.9
1	A	1835	MET	2.9
1	A	1953	ASN	2.9
1	A	1874	ALA	2.9
2	B	282	ILE	2.9
2	B	172	PRO	2.9
1	A	2010	LEU	2.9
1	A	1865	THR	2.9
1	A	1863	HIS	2.9
2	B	19	GLN	2.9
2	B	49	ALA	2.9
2	B	128	LYS	2.9
2	B	240	SER	2.9
2	B	204	TYR	2.8
2	B	30	PHE	2.8
1	A	2012	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	264	LEU	2.8
2	B	76	GLY	2.8
2	B	146	THR	2.8
1	A	1977	VAL	2.8
2	B	214	PHE	2.8
2	B	307	LYS	2.8
2	B	195	MET	2.8
1	A	1862	VAL	2.7
1	A	1856	ASN	2.7
1	A	1967	ALA	2.7
2	B	220	TYR	2.7
2	B	231	ALA	2.7
2	B	259	HIS	2.7
1	A	1920	LEU	2.7
2	B	267	ILE	2.7
1	A	2054	GLN	2.7
2	B	190	ARG	2.7
2	B	52	SER	2.7
2	B	41[A]	VAL	2.7
2	B	245	ALA	2.6
2	B	137	PHE	2.6
1	A	1927	GLU	2.6
2	B	278	GLN	2.6
1	A	2040	TRP	2.6
2	B	290	ASN	2.6
2	B	38	ILE	2.6
2	B	12	GLU	2.6
2	B	121	VAL	2.6
2	B	143	SER	2.6
2	B	46	PHE	2.6
2	B	302	LEU	2.6
2	B	238	GLY	2.6
2	B	201	LYS	2.6
2	B	280	SER	2.6
2	B	261	LEU	2.5
2	B	192	GLY	2.5
2	B	95	ASN	2.5
1	A	1921	VAL	2.5
2	B	56	TYR	2.5
2	B	178	TYR	2.5
2	B	294	TYR	2.5
2	B	229	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	2018	ASN	2.5
2	B	93	VAL	2.5
1	A	1958	PRO	2.5
2	B	233	PHE	2.5
2	B	100	GLN	2.5
1	A	2024[A]	MET	2.5
2	B	232	MET	2.5
1	A	2064	GLY	2.4
2	B	84	ARG	2.4
2	B	222	GLY	2.4
1	A	1844	PHE	2.4
2	B	15	ILE	2.4
2	B	281	ASP	2.4
2	B	10	PRO	2.4
1	A	2037	TYR	2.4
2	B	284	LEU	2.4
2	B	198	PHE	2.4
1	A	2033	THR	2.4
1	A	1985	GLN	2.4
1	A	1969	MET	2.4
2	B	258	LYS	2.4
1	A	2049	ILE	2.4
1	A	1859	ARG	2.3
1	A	1937	ARG	2.3
2	B	131	ARG	2.3
2	B	228	PHE	2.3
2	B	69	ILE	2.3
1	A	1869	ASN	2.3
2	B	97	LYS	2.3
2	B	239	SER	2.3
1	A	1962	ARG	2.3
2	B	62	CYS	2.3
1	A	2067	TYR	2.3
2	B	312	LYS	2.3
2	B	142	SER	2.3
2	B	196	GLU	2.3
1	A	1899	TRP	2.3
2	B	199	LEU	2.3
1	A	1840	TYR	2.3
2	B	105	TYR	2.3
1	A	1873	LYS	2.3
1	A	1973	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	86	GLY	2.3
2	B	223	GLU	2.3
2	B	13	VAL	2.3
2	B	57	GLY	2.2
1	A	1943	PRO	2.2
2	B	227	ALA	2.2
1	A	1922	ARG	2.2
1	A	1978	VAL	2.2
2	B	111	ASP	2.2
1	A	1952	PRO	2.2
2	B	183	PHE	2.1
2	B	36	ILE	2.1
1	A	1936	THR	2.1
2	B	50	ASP	2.1
1	A	1925	PRO	2.1
1	A	2015	LEU	2.1
2	B	82	GLU	2.1
1	A	1939	ALA	2.1
2	B	27	ASN	2.1
2	B	304	ASN	2.1
2	B	274	THR	2.1
2	B	303	HIS	2.1
2	B	87	ALA	2.1
1	A	1855[A]	THR	2.1
2	B	118	THR	2.1
1	A	1843	LEU	2.1
1	A	1949	LEU	2.1
1	A	2001[A]	SER	2.0
2	B	47	GLN	2.0
2	B	70	GLN	2.0
1	A	1911	TRP	2.0
1	A	1997	ASP	2.0
2	B	287	ARG	2.0
2	B	277	GLU	2.0
2	B	135	ASN	2.0
2	B	236	ASN	2.0
2	B	180	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.