



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:27 AM UTC

PDB ID : 7XDS / pdb_00007xds
Title : Crystal structure of wheat stem rust effector AvrSr35
Authors : Ouyang, S.Y.; Zhao, Y.B.
Deposited on : 2022-03-28
Resolution : 2.06 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
Mogul : 2022.3.0, CSD as543be (2022)
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

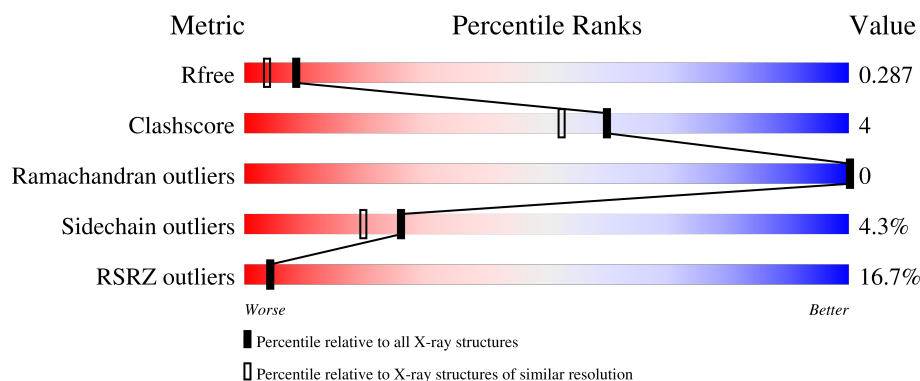
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	575	9% 54% 9% 36%
1	B	575	12% 58% 6% 35%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6188 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 AvrSr35.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	369	Total	C	N	O	S	Se	0	0	0
			3039	1951	496	583	2	7			
1	B	375	Total	C	N	O	S	Se	0	0	0
			3092	1988	506	589	2	7			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	HIS	-	expression tag	UNP A0A5B0N367
A	5	HIS	-	expression tag	UNP A0A5B0N367
A	6	HIS	-	expression tag	UNP A0A5B0N367
A	7	HIS	-	expression tag	UNP A0A5B0N367
A	8	HIS	-	expression tag	UNP A0A5B0N367
A	9	HIS	-	expression tag	UNP A0A5B0N367
A	10	SER	-	expression tag	UNP A0A5B0N367
A	11	SER	-	expression tag	UNP A0A5B0N367
A	12	GLY	-	expression tag	UNP A0A5B0N367
A	13	VAL	-	expression tag	UNP A0A5B0N367
A	14	ASP	-	expression tag	UNP A0A5B0N367
A	15	LEU	-	expression tag	UNP A0A5B0N367
A	16	GLY	-	expression tag	UNP A0A5B0N367
A	17	THR	-	expression tag	UNP A0A5B0N367
A	18	GLU	-	expression tag	UNP A0A5B0N367
A	19	ASN	-	expression tag	UNP A0A5B0N367
A	20	LEU	-	expression tag	UNP A0A5B0N367
A	21	TYR	-	expression tag	UNP A0A5B0N367
A	22	PHE	-	expression tag	UNP A0A5B0N367
A	23	GLN	-	expression tag	UNP A0A5B0N367
A	24	SER	-	expression tag	UNP A0A5B0N367
A	25	ASN	-	expression tag	UNP A0A5B0N367
B	4	HIS	-	expression tag	UNP A0A5B0N367
B	5	HIS	-	expression tag	UNP A0A5B0N367
B	6	HIS	-	expression tag	UNP A0A5B0N367

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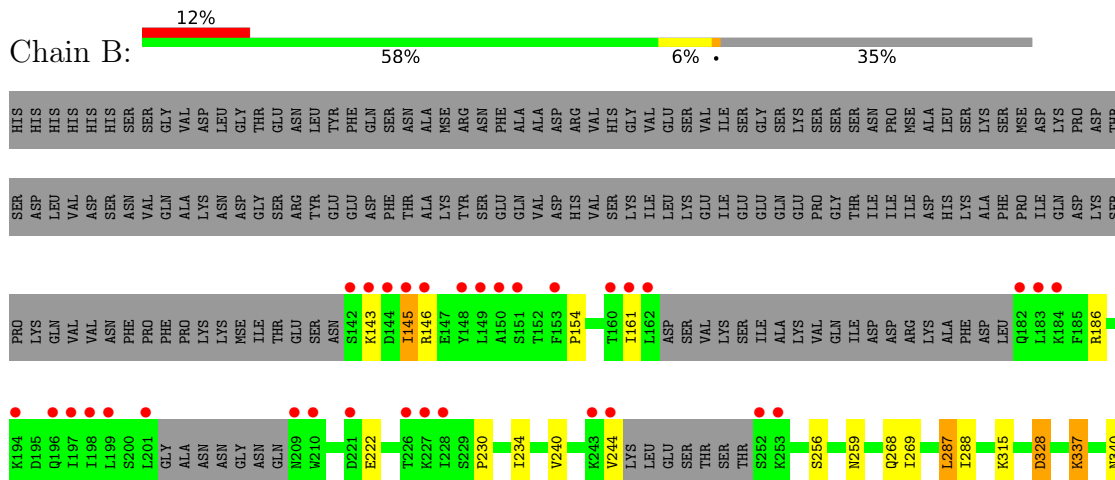
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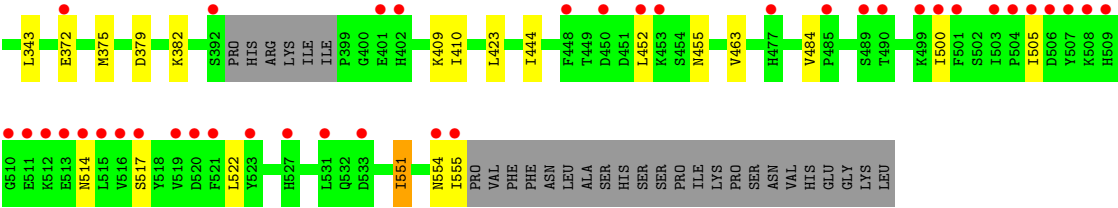
Chain	Residue	Modelled	Actual	Comment	Reference
B	7	HIS	-	expression tag	UNP A0A5B0N367
B	8	HIS	-	expression tag	UNP A0A5B0N367
B	9	HIS	-	expression tag	UNP A0A5B0N367
B	10	SER	-	expression tag	UNP A0A5B0N367
B	11	SER	-	expression tag	UNP A0A5B0N367
B	12	GLY	-	expression tag	UNP A0A5B0N367
B	13	VAL	-	expression tag	UNP A0A5B0N367
B	14	ASP	-	expression tag	UNP A0A5B0N367
B	15	LEU	-	expression tag	UNP A0A5B0N367
B	16	GLY	-	expression tag	UNP A0A5B0N367
B	17	THR	-	expression tag	UNP A0A5B0N367
B	18	GLU	-	expression tag	UNP A0A5B0N367
B	19	ASN	-	expression tag	UNP A0A5B0N367
B	20	LEU	-	expression tag	UNP A0A5B0N367
B	21	TYR	-	expression tag	UNP A0A5B0N367
B	22	PHE	-	expression tag	UNP A0A5B0N367
B	23	GLN	-	expression tag	UNP A0A5B0N367
B	24	SER	-	expression tag	UNP A0A5B0N367
B	25	ASN	-	expression tag	UNP A0A5B0N367

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	26	Total O 26 26	0	0
2	B	31	Total O 31 31	0	0

- Molecule 1: AvrSr35





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.12Å 115.27Å 143.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.89 – 2.06 44.89 – 2.06	Depositor EDS
% Data completeness (in resolution range)	97.7 (44.89-2.06) 97.8 (44.89-2.06)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.07Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.257 , 0.287 0.257 , 0.287	Depositor DCC
R_{free} test set	2758 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6188	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% 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

5.1 Standard geometry

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	0.93	4/3088 (0.1%)	1.37	6/4137 (0.1%)
1	B	0.88	1/3146 (0.0%)	1.38	6/4216 (0.1%)
All	All	0.91	5/6234 (0.1%)	1.38	12/8353 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	463	VAL	C-N	-7.07	1.23	1.33
1	A	543	PRO	C-O	-6.71	1.15	1.24
1	A	142	SER	CA-CB	-5.45	1.45	1.53
1	A	542	ASP	C-O	-5.22	1.20	1.24
1	A	504	PRO	C-O	-5.21	1.17	1.23

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	ASP	CA-CB-CG	6.79	119.39	112.60
1	B	328	ASP	CA-CB-CG	6.24	118.84	112.60
1	A	379	ASP	CA-CB-CG	6.04	118.64	112.60
1	A	230	PRO	CA-C-N	5.60	127.78	120.28
1	A	230	PRO	C-N-CA	5.60	127.78	120.28
1	B	554	ASN	N-CA-C	5.38	117.22	111.36
1	B	455	ASN	CA-C-N	5.25	127.63	120.54
1	B	455	ASN	C-N-CA	5.25	127.63	120.54
1	A	370	ASN	CA-C-N	5.16	127.19	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	370	ASN	C-N-CA	5.16	127.19	120.28
1	B	423	LEU	CA-C-N	5.04	127.29	120.38
1	B	423	LEU	C-N-CA	5.04	127.29	120.38

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	146	ARG	Sidechain
1	A	186	ARG	Sidechain

5.2 Too-close contacts

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	3039	0	3036	28	0
1	B	3092	0	3091	25	0
2	A	26	0	0	0	0
2	B	31	0	0	0	0
All	All	6188	0	6127	53	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 (53) 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:B:145:ILE:CD1	1:B:517:SER:HB3	1.74	1.18
1:B:145:ILE:HD11	1:B:517:SER:CB	1.80	1.11
1:B:186:ARG:HE	1:B:268:GLN:HB3	1.44	0.81
1:A:193:LEU:HD21	1:A:262:ILE:HD13	1.70	0.71
1:B:240:VAL:O	1:B:244:VAL:HG23	1.91	0.71
1:B:145:ILE:HD11	1:B:517:SER:HB3	0.85	0.70
1:B:161:ILE:HD11	1:B:522:LEU:HD23	1.76	0.66
1:B:328:ASP:OD2	1:B:337:LYS:HE2	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:551:ILE:HD13	1:B:555:ILE:HD11	1.77	0.65
1:B:145:ILE:HD13	1:B:514:ASN:O	1.97	0.64
1:B:244:VAL:HG13	1:B:259:ASN:ND2	2.14	0.63
1:B:328:ASP:CG	1:B:337:LYS:HE2	2.25	0.61
1:A:551:ILE:O	1:A:555:ILE:HG12	2.01	0.60
1:B:379:ASP:HB3	1:B:382:LYS:HD2	1.85	0.58
1:B:337:LYS:NZ	1:B:340:ASN:HD22	2.02	0.58
1:B:145:ILE:CD1	1:B:517:SER:CB	2.59	0.56
1:A:386:LEU:HD23	1:A:406:LEU:HD21	1.87	0.56
1:A:193:LEU:HD21	1:A:262:ILE:CD1	2.35	0.55
1:B:337:LYS:O	1:B:337:LYS:HD3	2.07	0.54
1:A:513:GLU:H	1:A:513:GLU:CD	2.15	0.54
1:B:186:ARG:NE	1:B:268:GLN:HB3	2.21	0.54
1:A:241:LEU:HD13	1:A:293:MSE:SE	2.58	0.53
1:B:230:PRO:O	1:B:234:ILE:HG12	2.09	0.53
1:B:186:ARG:HD3	1:B:269:ILE:HD13	1.90	0.53
1:A:230:PRO:O	1:A:234:ILE:HG12	2.09	0.52
1:A:188:GLU:OE2	1:A:500:ILE:HD12	2.11	0.52
1:A:145:ILE:HD11	1:A:518:TYR:HB2	1.93	0.50
1:A:375:MSE:HB3	1:A:409:LYS:HD2	1.94	0.49
1:A:389:PHE:C	1:A:389:PHE:CD1	2.91	0.48
1:B:161:ILE:HD11	1:B:522:LEU:CD2	2.43	0.48
1:A:186:ARG:NE	1:A:268:GLN:HB3	2.31	0.46
1:A:229:SER:O	1:A:230:PRO:C	2.59	0.46
1:A:316:MSE:SE	1:A:474:GLY:HA2	2.65	0.46
1:A:148:TYR:CE1	1:A:511:GLU:HG3	2.51	0.46
1:B:375:MSE:HB3	1:B:409:LYS:HD3	1.99	0.45
1:A:389:PHE:CD1	1:A:389:PHE:O	2.70	0.45
1:A:244:VAL:HG11	1:A:263:GLN:HG3	2.00	0.44
1:B:244:VAL:HG13	1:B:259:ASN:HD21	1.81	0.43
1:A:391:LYS:HA	1:A:391:LYS:HD2	1.72	0.43
1:A:370:ASN:HB2	1:A:429:TYR:CD2	2.53	0.43
1:A:465:LEU:HD11	1:A:526:ALA:HA	2.00	0.42
1:B:484:VAL:O	1:B:505:ILE:HD13	2.19	0.42
1:A:324:THR:CG2	1:A:358:THR:HG22	2.49	0.42
1:A:187:GLN:HE22	1:A:225:ASN:HB3	1.85	0.42
1:A:219:LYS:HA	1:A:219:LYS:HD3	1.85	0.42
1:A:244:VAL:CG1	1:A:263:GLN:HG3	2.50	0.41
1:A:509:HIS:ND1	1:A:509:HIS:C	2.79	0.41
1:A:144:ASP:HB3	1:A:514:ASN:HD21	1.86	0.41
1:B:551:ILE:CD1	1:B:555:ILE:HD11	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:ILE:HG23	1:B:287:LEU:HG	2.02	0.41
1:A:145:ILE:HD13	1:A:514:ASN:O	2.21	0.40
1:A:301:LYS:HE2	1:A:358:THR:HG21	2.03	0.40
1:B:288:ILE:HD12	1:B:343:LEU:HG	2.04	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	357/575 (62%)	349 (98%)	8 (2%)	0	100	100
1	B	365/575 (64%)	360 (99%)	5 (1%)	0	100	100
All	All	722/1150 (63%)	709 (98%)	13 (2%)	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	346/520 (66%)	331 (96%)	15 (4%)	26	20
1	B	351/520 (68%)	336 (96%)	15 (4%)	26	20
All	All	697/1040 (67%)	667 (96%)	30 (4%)	26	20

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	183	LEU
1	A	226	THR
1	A	227	LYS
1	A	229	SER
1	A	278	GLN
1	A	297	LEU
1	A	344	LYS
1	A	391	LYS
1	A	407	LEU
1	A	452	LEU
1	A	505	ILE
1	A	509	HIS
1	A	513	GLU
1	A	540	CYS
1	A	550	ARG
1	B	143	LYS
1	B	145	ILE
1	B	146	ARG
1	B	154	PRO
1	B	222	GLU
1	B	256	SER
1	B	287	LEU
1	B	315	LYS
1	B	337	LYS
1	B	372	GLU
1	B	410	ILE
1	B	444	ILE
1	B	452	LEU
1	B	500	ILE
1	B	551	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	187	GLN
1	A	189	ASN
1	A	218	ASN
1	A	257	GLN
1	A	319	ASN
1	A	468	GLN
1	A	471	GLN

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Mol	Chain	Res	Type
1	A	514	ASN
1	B	182	GLN
1	B	187	GLN
1	B	189	ASN
1	B	281	GLN
1	B	340	ASN
1	B	370	ASN
1	B	421	ASN
1	B	477	HIS
1	B	514	ASN
1	B	527	HIS
1	B	538	GLN
1	B	549	ASN
1	B	554	ASN

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	362/575 (62%)	0.83	51 (14%) 6 6	7, 27, 53, 81	0
1	B	368/575 (64%)	0.96	71 (19%) 3 3	8, 28, 56, 90	0
All	All	730/1150 (63%)	0.90	122 (16%) 4 4	7, 27, 54, 90	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	244	VAL	6.8
1	B	392	SER	6.1
1	A	557	VAL	5.7
1	B	515	LEU	5.3
1	B	142	SER	5.0
1	A	164	SER	4.9
1	A	555	ILE	4.8
1	B	500	ILE	4.4
1	B	143	LYS	4.3
1	B	162	LEU	4.3
1	A	141	ASN	4.3
1	B	146	ARG	4.0
1	B	513	GLU	4.0
1	B	201	LEU	3.9
1	A	556	PRO	3.8
1	B	199	LEU	3.7
1	B	401	GLU	3.7
1	B	209	ASN	3.7
1	B	145	ILE	3.6
1	B	402	HIS	3.5
1	A	509	HIS	3.4
1	A	226	THR	3.4
1	B	555	ILE	3.4
1	A	506	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	144	ASP	3.3
1	A	225	ASN	3.3
1	B	554	ASN	3.2
1	B	516	VAL	3.2
1	B	150	ALA	3.2
1	B	448	PHE	3.1
1	B	183	LEU	3.1
1	B	372	GLU	3.1
1	B	198	ILE	3.1
1	B	512	LYS	3.1
1	B	514	ASN	3.1
1	A	244	VAL	3.1
1	A	389	PHE	3.0
1	A	209	ASN	2.9
1	A	540	CYS	2.9
1	B	228	ILE	2.9
1	A	162	LEU	2.9
1	A	183	LEU	2.9
1	B	452	LEU	2.9
1	B	477	HIS	2.9
1	B	226	THR	2.9
1	B	509	HIS	2.9
1	A	228	ILE	2.8
1	A	405	ASP	2.8
1	B	533	ASP	2.8
1	A	227	LYS	2.8
1	B	489	SER	2.8
1	B	507	TYR	2.8
1	B	511	GLU	2.7
1	A	145	ILE	2.7
1	A	231	GLU	2.7
1	A	161	ILE	2.7
1	A	500	ILE	2.7
1	A	521	PHE	2.6
1	A	229	SER	2.6
1	A	507	TYR	2.6
1	B	517	SER	2.6
1	B	501	PHE	2.6
1	B	243	LYS	2.6
1	A	277	ASN	2.6
1	B	194	LYS	2.5
1	A	230	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	504	PRO	2.5
1	B	453	LYS	2.5
1	A	490	THR	2.5
1	A	142	SER	2.5
1	A	534	ASN	2.5
1	B	210	TRP	2.5
1	A	372	GLU	2.4
1	B	221	ASP	2.4
1	B	148	TYR	2.4
1	B	510	GLY	2.4
1	B	519	VAL	2.4
1	B	520	ASP	2.4
1	A	446	SER	2.4
1	B	490	THR	2.4
1	B	184	LYS	2.4
1	A	143	LYS	2.4
1	A	505	ILE	2.3
1	B	151	SER	2.3
1	B	196	GLN	2.3
1	A	552	LYS	2.3
1	B	499	LYS	2.3
1	B	508	LYS	2.3
1	B	252	SER	2.3
1	B	527	HIS	2.3
1	A	452	LEU	2.3
1	B	149	LEU	2.3
1	B	227	LYS	2.3
1	A	438	GLU	2.3
1	A	371	ASN	2.3
1	A	551	ILE	2.2
1	B	531	LEU	2.2
1	A	182	GLN	2.2
1	A	184	LYS	2.2
1	B	160	THR	2.2
1	B	161	ILE	2.2
1	B	506	ASP	2.2
1	A	548	LEU	2.2
1	A	146	ARG	2.2
1	B	253	LYS	2.2
1	B	197	ILE	2.2
1	B	521	PHE	2.2
1	A	392	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	505	ILE	2.1
1	A	406	LEU	2.1
1	A	453	LYS	2.1
1	A	483	LYS	2.1
1	A	232	GLU	2.1
1	A	407	LEU	2.1
1	B	182	GLN	2.1
1	B	523	TYR	2.1
1	A	234	ILE	2.1
1	B	153	PHE	2.1
1	A	533	ASP	2.0
1	B	485	PRO	2.0
1	B	503	ILE	2.0
1	B	450	ASP	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.