



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:13 PM UTC

PDB ID : 2QKW / pdb_00002qkw
Title : Structural basis for activation of plant immunity by bacterial effector protein AvrPto
Authors : Xing, W.M.; Zou, Y.; Liu, Q.; Hao, Q.; Zhou, J.M.; Chai, J.J.
Deposited on : 2007-07-11
Resolution : 3.20 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

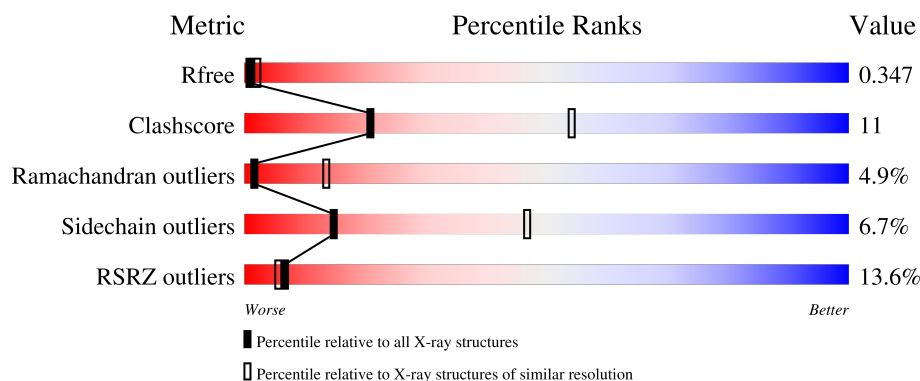
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	164	
2	B	321	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3135 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 Avirulence protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	101	Total	C	N	O	S	0	0	0
			798	481	152	158	7			

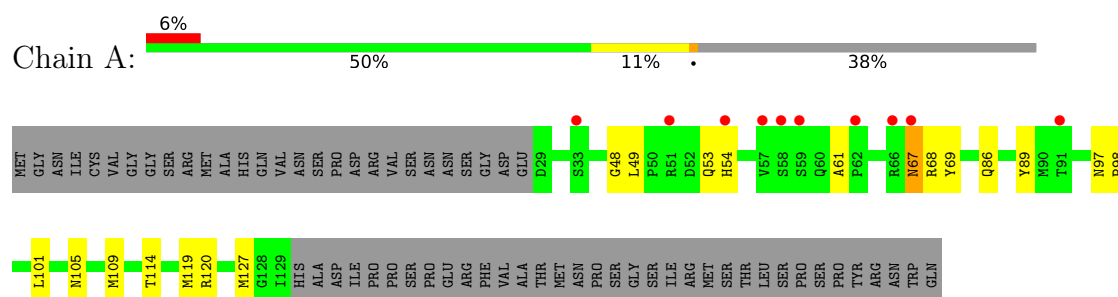
- Molecule 2 is a protein called Protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	292	Total	C	N	O	P	S	0	0
			2337	1481	402	441	2	11		

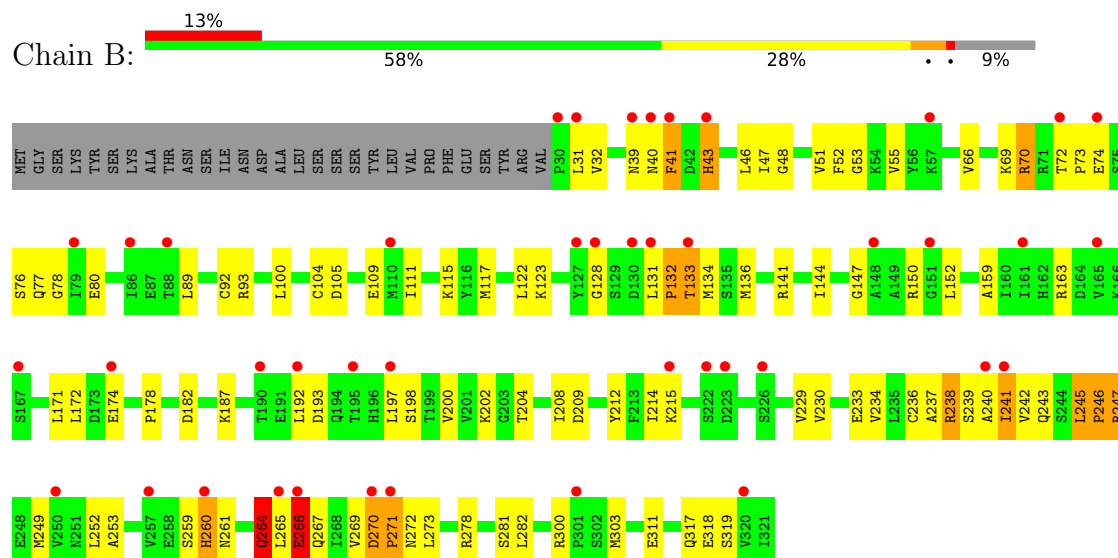
3 Residue-property plots [i](#)

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: Avirulence protein



• Molecule 2: Protein kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.47Å 94.59Å 98.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20 20.00 – 3.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (20.00-3.20) 96.6 (20.00-3.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.95Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.271 , 0.303 0.323 , 0.347	Depositor DCC
R_{free} test set	1009 reflections (6.76%)	wwPDB-VP
Wilson B-factor (Å ²)	86.6	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	3135	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, SEP

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	0.44	0/813	0.88	3/1099 (0.3%)
2	B	0.52	0/2361	0.92	6/3183 (0.2%)
All	All	0.50	0/3174	0.91	9/4282 (0.2%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	48	GLY	N-CA-C	7.44	120.51	112.33
2	B	318	GLU	N-CA-C	5.71	122.95	110.80
2	B	43	HIS	N-CA-C	5.65	118.37	109.96
1	A	61	ALA	CA-C-N	5.57	125.03	119.24
1	A	61	ALA	C-N-CA	5.57	125.03	119.24
2	B	78	GLY	N-CA-C	-5.47	107.88	114.66
2	B	319	SER	N-CA-C	5.30	118.33	110.48
1	A	67	ASN	N-CA-C	-5.28	106.79	113.18
2	B	266	GLU	N-CA-C	5.11	117.57	109.96

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	798	0	751	12	0
2	B	2337	0	2332	58	0
All	All	3135	0	3083	69	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 11.

All (69) 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:229:VAL:HG11	2:B:241:ILE:HD12	1.41	1.02
1:A:105:ASN:O	1:A:109:MET:HG2	1.81	0.80
2:B:229:VAL:CG1	2:B:241:ILE:HD12	2.13	0.79
2:B:260:HIS:HA	2:B:265:LEU:HA	1.67	0.77
2:B:229:VAL:HG22	2:B:253:ALA:HB2	1.76	0.68
2:B:241:ILE:HG12	2:B:242:VAL:N	2.11	0.66
1:A:53:GLN:HA	1:A:127:MET:HE1	1.78	0.65
2:B:53:GLY:HA2	2:B:73:PRO:HD2	1.78	0.65
2:B:229:VAL:HG11	2:B:241:ILE:CD1	2.22	0.64
1:A:86:GLN:HG3	1:A:105:ASN:ND2	2.14	0.61
2:B:159:ALA:HB2	2:B:192:LEU:HA	1.83	0.61
2:B:214:ILE:HG13	2:B:215:LYS:HG3	1.83	0.60
2:B:233:GLU:HG2	2:B:239:SER:HA	1.84	0.59
2:B:122:LEU:HD13	2:B:144:ILE:HG21	1.85	0.57
2:B:52:PHE:HE2	2:B:76:SER:HB2	1.68	0.57
2:B:278:ARG:HD2	2:B:317:GLN:HA	1.85	0.56
2:B:270:ASP:HB2	2:B:271:PRO:HD2	1.88	0.55
2:B:43:HIS:CE1	2:B:70:ARG:HH21	2.24	0.54
2:B:236:CYS:C	2:B:238:ARG:H	2.16	0.54
2:B:243:GLN:HG3	2:B:246:PRO:HD3	1.90	0.53
2:B:117:MET:HG3	2:B:171:LEU:HB3	1.92	0.52
2:B:259:SER:C	2:B:261:ASN:H	2.19	0.51
2:B:237:ALA:HB3	2:B:271:PRO:HG3	1.92	0.51
2:B:77:GLN:HE21	2:B:80:GLU:HB2	1.77	0.50
2:B:270:ASP:HB2	2:B:271:PRO:CD	2.42	0.50
2:B:187:LYS:HG2	2:B:197:LEU:HD11	1.94	0.49
2:B:197:LEU:HD23	2:B:197:LEU:H	1.77	0.49
1:A:49:LEU:HD21	1:A:54:HIS:HD2	1.78	0.49
2:B:237:ALA:CB	2:B:271:PRO:HG3	2.43	0.48
1:A:86:GLN:HA	1:A:98:PRO:HG3	1.97	0.47
2:B:209:ASP:CG	2:B:300:ARG:HH12	2.23	0.47
1:A:49:LEU:HA	1:A:120:ARG:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:163:ARG:NH2	2:B:202:LYS:HD2	2.29	0.47
2:B:237:ALA:C	2:B:239:SER:N	2.73	0.47
2:B:150:ARG:NH1	2:B:311:GLU:OE1	2.48	0.46
2:B:104:CYS:HB3	2:B:111:ILE:H	1.80	0.46
2:B:123:LYS:HG3	2:B:239:SER:OG	2.16	0.46
2:B:266:GLU:HB3	2:B:269:VAL:HG13	1.98	0.46
2:B:247:ARG:H	2:B:247:ARG:HD2	1.80	0.46
2:B:267:GLN:HG2	2:B:282:LEU:HD21	1.98	0.46
2:B:72:THR:N	2:B:73:PRO:CD	2.79	0.46
2:B:245:LEU:HB2	2:B:246:PRO:HD3	1.98	0.46
2:B:260:HIS:CE1	2:B:265:LEU:HG	2.51	0.46
2:B:200:VAL:O	2:B:212:TYR:OH	2.24	0.45
2:B:230:VAL:O	2:B:234:VAL:HG23	2.17	0.45
2:B:237:ALA:C	2:B:239:SER:H	2.24	0.45
2:B:259:SER:HB3	2:B:266:GLU:HB2	1.99	0.44
2:B:264:GLN:HB3	2:B:266:GLU:HG3	1.99	0.44
2:B:52:PHE:CE2	2:B:76:SER:HB2	2.49	0.44
2:B:89:LEU:HD23	2:B:100:LEU:HB2	1.99	0.44
2:B:136:MET:O	2:B:141:ARG:NH1	2.51	0.44
2:B:105:ASP:HA	2:B:109:GLU:O	2.18	0.44
2:B:147:GLY:HA3	2:B:178:PRO:HG2	2.00	0.43
2:B:41:PHE:CD1	2:B:41:PHE:C	2.96	0.43
2:B:236:CYS:HA	2:B:270:ASP:HA	2.00	0.42
2:B:238:ARG:C	2:B:240:ALA:H	2.26	0.42
1:A:89:TYR:CZ	1:A:97:ASN:HB2	2.55	0.42
2:B:247:ARG:C	2:B:249:MET:H	2.28	0.42
1:A:69:TYR:HB2	1:A:119:MET:HE2	2.01	0.42
2:B:41:PHE:C	2:B:41:PHE:HD1	2.28	0.42
2:B:55:VAL:HG22	2:B:69:LYS:HG3	2.02	0.42
1:A:67:ASN:C	1:A:69:TYR:N	2.79	0.41
2:B:132:PRO:HB2	2:B:133:THR:H	1.65	0.41
2:B:152:LEU:HB2	2:B:303:MET:HE2	2.03	0.41
2:B:241:ILE:HG23	2:B:242:VAL:H	1.85	0.41
1:A:97:ASN:O	2:B:204:THR:HA	2.21	0.41
1:A:97:ASN:HA	1:A:98:PRO:HD2	1.95	0.41
1:A:49:LEU:HD23	1:A:49:LEU:N	2.37	0.40
2:B:174:GLU:H	2:B:174:GLU:HG3	1.61	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	99/164 (60%)	91 (92%)	6 (6%)	2 (2%)	6	31
2	B	288/321 (90%)	241 (84%)	30 (10%)	17 (6%)	1	10
All	All	387/485 (80%)	332 (86%)	36 (9%)	19 (5%)	1	13

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	39	ASN
2	B	47	ILE
2	B	193	ASP
2	B	271	PRO
2	B	241	ILE
2	B	247	ARG
1	A	68	ARG
2	B	40	ASN
2	B	93	ARG
2	B	132	PRO
2	B	238	ARG
2	B	245	LEU
2	B	260	HIS
2	B	264	GLN
2	B	131	LEU
2	B	182	ASP
2	B	128	GLY
1	A	48	GLY
2	B	246	PRO

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	88/143 (62%)	86 (98%)	2 (2%)	44	70
2	B	255/282 (90%)	234 (92%)	21 (8%)	10	39
All	All	343/425 (81%)	320 (93%)	23 (7%)	15	47

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LEU
1	A	114	THR
2	B	31	LEU
2	B	32	VAL
2	B	41	PHE
2	B	46	LEU
2	B	51	VAL
2	B	66	VAL
2	B	70	ARG
2	B	74	GLU
2	B	92	CYS
2	B	115	LYS
2	B	133	THR
2	B	134	MET
2	B	172	LEU
2	B	208	ILE
2	B	252	LEU
2	B	264	GLN
2	B	266	GLU
2	B	270	ASP
2	B	272	ASN
2	B	273	LEU
2	B	281	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	54	HIS
1	A	67	ASN
1	A	86	GLN

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Mol	Chain	Res	Type
1	A	97	ASN
1	A	103	HIS
1	A	105	ASN
2	B	43	HIS
2	B	77	GLN
2	B	251	ASN
2	B	260	HIS
2	B	262	ASN
2	B	272	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	TPO	B	199	2	8,10,11	0.89	0	10,14,16	1.02	0
2	SEP	B	198	2	8,9,10	1.73	2 (25%)	7,12,14	1.19	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPO	B	199	2	-	2/9/11/13	-
2	SEP	B	198	2	-	5/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	198	SEP	P-O1P	3.68	1.61	1.50
2	B	198	SEP	P-O3P	2.02	1.62	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	198	SEP	OG-CB-CA	2.07	110.16	108.14

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	198	SEP	C-CA-CB-OG
2	B	198	SEP	CB-OG-P-O2P
2	B	198	SEP	CB-OG-P-O3P
2	B	199	TPO	N-CA-CB-OG1
2	B	199	TPO	CG2-CB-OG1-P
2	B	198	SEP	CB-OG-P-O1P
2	B	198	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

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	101/164 (61%)	1.02	10 (9%) 13 8	91, 97, 109, 110	0
2	B	290/321 (90%)	1.11	43 (14%) 5 4	81, 94, 110, 116	0
All	All	391/485 (80%)	1.09	53 (13%) 7 5	81, 95, 110, 116	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	62	PRO	4.3
1	A	59	SER	3.5
2	B	195	THR	3.4
2	B	127	TYR	3.4
2	B	72	THR	3.2
1	A	51	ARG	3.2
2	B	270	ASP	3.1
1	A	57	VAL	3.1
2	B	130	ASP	2.9
2	B	74	GLU	2.9
2	B	30	PRO	2.9
2	B	148	ALA	2.9
2	B	271	PRO	2.8
1	A	91	THR	2.8
2	B	197	LEU	2.7
2	B	88	THR	2.6
2	B	192	LEU	2.6
2	B	260	HIS	2.6
2	B	226	SER	2.6
1	A	58	SER	2.5
2	B	165	VAL	2.5
2	B	79	ILE	2.4
2	B	131	LEU	2.4
2	B	151	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	133	THR	2.4
2	B	167	SER	2.4
2	B	222	SER	2.3
2	B	223	ASP	2.3
2	B	57	LYS	2.3
2	B	301	PRO	2.3
2	B	128	GLY	2.3
2	B	190	THR	2.3
1	A	67	ASN	2.3
2	B	265	LEU	2.3
2	B	39	ASN	2.3
1	A	66	ARG	2.2
1	A	54	HIS	2.2
1	A	33	SER	2.2
2	B	31	LEU	2.2
2	B	40	ASN	2.2
2	B	174	GLU	2.2
2	B	240	ALA	2.2
2	B	250	VAL	2.1
2	B	241	ILE	2.1
2	B	266	GLU	2.1
2	B	110	MET	2.1
2	B	320	VAL	2.1
2	B	257	VAL	2.1
2	B	161	ILE	2.0
2	B	43	HIS	2.0
2	B	215	LYS	2.0
2	B	41	PHE	2.0
2	B	86	ILE	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SEP	B	198	10/11	0.62	0.21	101,101,106,106	0
2	TPO	B	199	11/12	0.92	0.09	99,100,105,105	0

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.