



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:53 PM UTC

PDB ID : 9KSG / pdb_00009ksg
Title : Crystal structure of RxLR145 effector
Authors : Zhang, X.G.
Deposited on : 2024-11-29
Resolution : 2.58 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

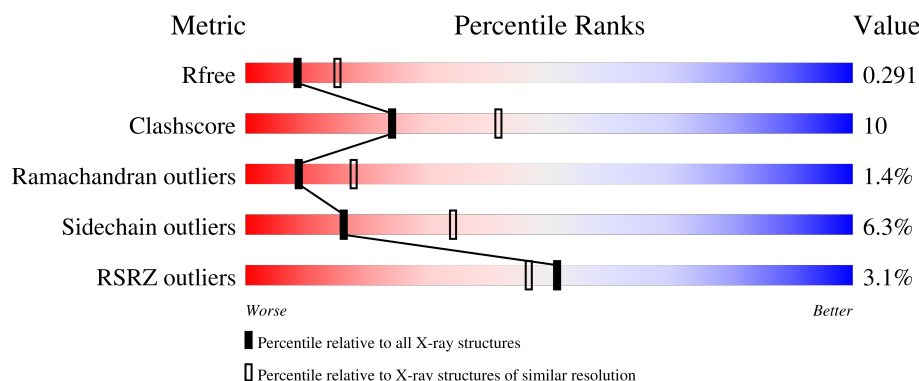
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	478	
1	B	478	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6631 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.

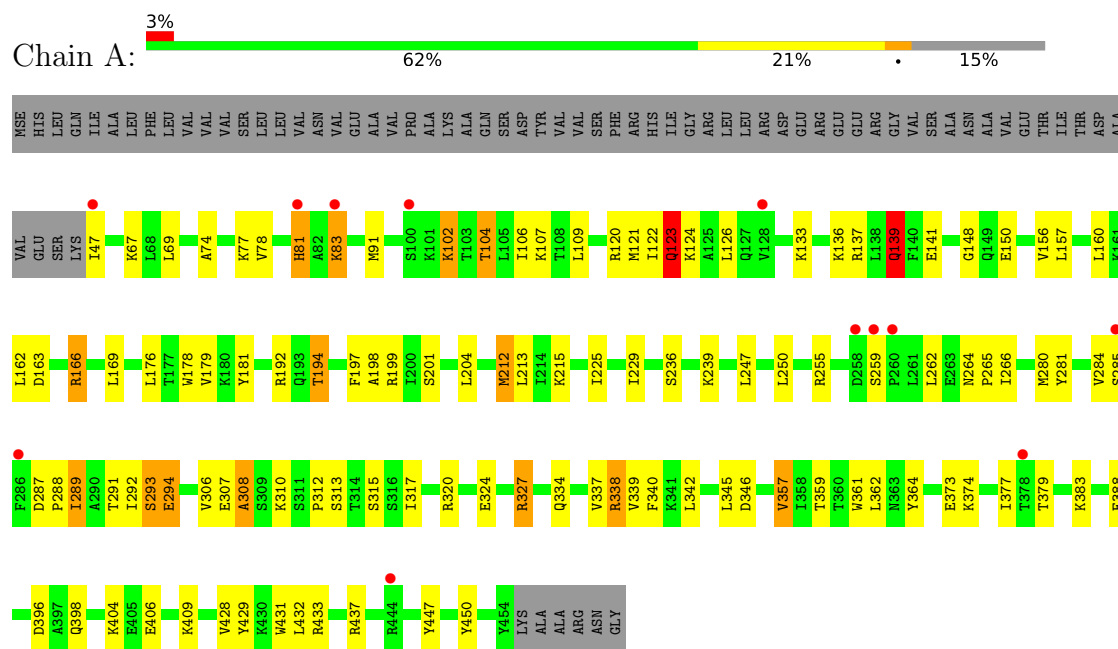
- Molecule 1 is a protein called RXLR effector Avh1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	Se	0	0	0
			3320	2131	563	619	7			
1	B	407	Total	C	N	O	Se	0	0	0
			3311	2126	561	617	7			

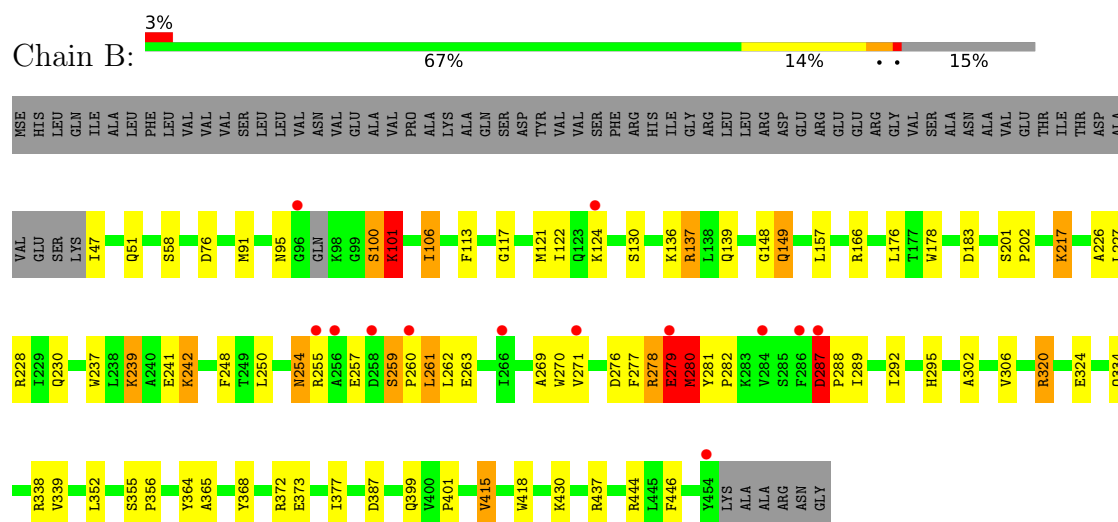
3 Residue-property plots

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: RXLR effector Avh1



• Molecule 1: RXLR effector Avh1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.03Å 89.59Å 147.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.15 – 2.58 43.15 – 2.58	Depositor EDS
% Data completeness (in resolution range)	98.7 (43.15-2.58) 98.3 (43.15-2.58)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.43 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.219 , 0.289 0.226 , 0.291	Depositor DCC
R_{free} test set	2000 reflections (6.55%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 25.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6631	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 67.21 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.3356e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.66	0/3384	0.97	5/4569 (0.1%)
1	B	0.69	0/3374	0.99	7/4554 (0.2%)
All	All	0.67	0/6758	0.98	12/9123 (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	B	0	4

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	GLN	CA-C-N	-11.76	107.27	123.03
1	B	149	GLN	C-N-CA	-11.76	107.27	123.03
1	A	78	VAL	N-CA-C	7.84	117.90	110.30
1	B	287	ASP	CA-C-N	-7.60	111.83	120.04
1	B	287	ASP	C-N-CA	-7.60	111.83	120.04
1	A	139	GLN	N-CA-C	-6.81	103.79	111.07
1	A	287	ASP	CA-C-N	5.82	125.29	119.24
1	A	287	ASP	C-N-CA	5.82	125.29	119.24
1	B	279	GLU	N-CA-C	5.63	122.80	110.80
1	A	123	GLN	CA-CB-CG	-5.53	103.05	114.10
1	B	280	MSE	N-CA-C	-5.10	99.94	110.80
1	B	100	SER	N-CA-C	5.03	120.80	114.31

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	259	SER	Peptide
1	B	278	ARG	Peptide
1	B	287	ASP	Peptide
1	B	95	ASN	Peptide

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	3320	0	3363	73	0
1	B	3311	0	3354	61	0
All	All	6631	0	6717	133	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 10.

All (133) 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:279:GLU:HG2	1:B:280:MSE:HB2	1.50	0.91
1:B:277:PHE:HA	1:B:279:GLU:OE2	1.74	0.87
1:A:320:ARG:NH1	1:A:324:GLU:OE2	2.13	0.82
1:B:279:GLU:CG	1:B:280:MSE:HB2	2.14	0.77
1:A:432:LEU:O	1:A:437:ARG:NH1	2.17	0.76
1:B:277:PHE:C	1:B:279:GLU:HB3	2.10	0.75
1:A:307:GLU:HA	1:A:310:LYS:NZ	2.03	0.74
1:A:194:THR:HG21	1:A:199:ARG:HH21	1.51	0.74
1:A:310:LYS:HZ3	1:A:310:LYS:H	1.36	0.74
1:A:362:LEU:HD13	1:A:406:GLU:HG2	1.70	0.73
1:A:122:ILE:HG21	1:A:139:GLN:HG3	1.71	0.72
1:A:123:GLN:OE1	1:A:176:LEU:HB2	1.90	0.71
1:B:100:SER:O	1:B:101:LYS:HB3	1.92	0.69
1:A:379:THR:O	1:A:383:LYS:HG2	1.93	0.68
1:A:307:GLU:HA	1:A:310:LYS:HZ1	1.57	0.68
1:B:260:PRO:HG2	1:B:263:GLU:HG3	1.76	0.67
1:B:279:GLU:HG2	1:B:280:MSE:CB	2.23	0.66
1:B:259:SER:HB2	1:B:261:LEU:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:LEU:HD13	1:A:178:TRP:CE2	2.32	0.64
1:B:279:GLU:HG2	1:B:280:MSE:N	2.11	0.64
1:A:281:TYR:O	1:A:284:VAL:HG22	1.97	0.64
1:A:396:ASP:OD1	1:A:433:ARG:NH2	2.25	0.64
1:A:109:LEU:HD13	1:A:121:MSE:HE1	1.78	0.64
1:B:260:PRO:O	1:B:262:LEU:N	2.27	0.63
1:B:277:PHE:HA	1:B:279:GLU:CD	2.23	0.62
1:B:368:TYR:OH	1:B:372:ARG:NH2	2.32	0.61
1:A:150:GLU:OE2	1:A:192:ARG:NH1	2.34	0.61
1:A:197:PHE:O	1:A:201:SER:HB2	1.99	0.61
1:A:289:ILE:HG12	1:A:324:GLU:HB3	1.84	0.59
1:A:289:ILE:O	1:A:293:SER:OG	2.18	0.59
1:B:287:ASP:CG	1:B:288:PRO:HD3	2.27	0.59
1:B:255:ARG:NH2	1:B:257:GLU:OE1	2.37	0.58
1:A:306:VAL:O	1:A:310:LYS:NZ	2.31	0.58
1:B:278:ARG:N	1:B:279:GLU:HB3	2.19	0.58
1:A:163:ASP:O	1:A:166:ARG:HB2	2.03	0.57
1:B:276:ASP:C	1:B:279:GLU:HB2	2.28	0.57
1:A:308:ALA:N	1:A:310:LYS:HZ1	2.02	0.57
1:A:69:LEU:HD22	1:A:83:LYS:CG	2.34	0.57
1:B:76:ASP:HB3	1:B:124:LYS:HZ2	1.69	0.57
1:A:122:ILE:CG2	1:A:139:GLN:HG3	2.35	0.56
1:A:262:LEU:HD13	1:A:317:ILE:HG23	1.87	0.56
1:A:339:VAL:HG21	1:A:364:TYR:CE2	2.41	0.56
1:B:279:GLU:OE1	1:B:281:TYR:N	2.39	0.56
1:B:279:GLU:CD	1:B:280:MSE:HB2	2.32	0.55
1:B:136:LYS:HZ2	1:B:137:ARG:HH12	1.56	0.54
1:B:437:ARG:O	1:B:444:ARG:NH1	2.41	0.54
1:A:379:THR:HG23	1:A:383:LYS:HE3	1.90	0.54
1:A:429:TYR:HB2	1:A:447:TYR:CE1	2.43	0.54
1:A:69:LEU:HD22	1:A:83:LYS:HG2	1.88	0.53
1:A:104:THR:HG21	1:A:106:ILE:HG22	1.89	0.53
1:A:104:THR:CG2	1:A:106:ILE:HG22	2.38	0.53
1:A:137:ARG:O	1:A:141:GLU:HG3	2.08	0.52
1:A:81:HIS:CE1	1:A:83:LYS:HB2	2.44	0.52
1:A:324:GLU:OE1	1:A:327:ARG:NH2	2.44	0.51
1:B:136:LYS:NZ	1:B:137:ARG:HH12	2.07	0.51
1:B:320:ARG:O	1:B:324:GLU:HG2	2.12	0.50
1:A:345:LEU:HD21	1:A:357:VAL:HG12	1.93	0.50
1:B:157:LEU:HD12	1:B:178:TRP:CZ2	2.47	0.50
1:A:213:LEU:HD11	1:A:229:ILE:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:GLU:HG2	1:B:255:ARG:NH1	2.27	0.49
1:A:398:GLN:OE1	1:A:437:ARG:NH2	2.46	0.49
1:B:279:GLU:CG	1:B:280:MSE:N	2.75	0.49
1:A:179:VAL:HG21	1:A:225:ILE:HD13	1.95	0.49
1:B:183:ASP:OD1	1:B:228:ARG:NH2	2.40	0.48
1:B:302:ALA:O	1:B:306:VAL:HG23	2.13	0.48
1:B:365:ALA:HB3	1:B:377:ILE:HD11	1.95	0.48
1:A:334:GLN:HE21	1:A:342:LEU:HD11	1.78	0.48
1:B:148:GLY:C	1:B:149:GLN:O	2.53	0.48
1:B:270:TRP:O	1:B:271:VAL:HB	2.13	0.48
1:B:117:GLY:O	1:B:121:MSE:HG3	2.14	0.48
1:B:288:PRO:O	1:B:292:ILE:HG12	2.14	0.48
1:B:415:VAL:HG13	1:B:446:PHE:CE2	2.48	0.48
1:A:307:GLU:CA	1:A:310:LYS:HZ1	2.26	0.47
1:A:361:TRP:CH2	1:A:377:ILE:HD12	2.49	0.47
1:B:254:ASN:HB3	1:B:295:HIS:CD2	2.49	0.47
1:B:248:PHE:CE2	1:B:295:HIS:HD2	2.33	0.47
1:B:387:ASP:OD2	1:B:418:TRP:NE1	2.44	0.47
1:A:377:ILE:HD13	1:A:377:ILE:HA	1.72	0.47
1:A:194:THR:HG22	1:A:198:ALA:HB3	1.97	0.47
1:B:122:ILE:HG21	1:B:139:GLN:HB2	1.97	0.47
1:B:415:VAL:HG13	1:B:446:PHE:CZ	2.50	0.47
1:A:156:VAL:HG21	1:A:181:TYR:CE2	2.49	0.47
1:B:399:GLN:O	1:B:401:PRO:HD3	2.15	0.46
1:B:106:ILE:HA	1:B:106:ILE:HD13	1.80	0.46
1:A:102:LYS:N	1:A:102:LYS:HD3	2.30	0.46
1:B:76:ASP:HA	1:B:124:LYS:NZ	2.31	0.46
1:A:266:ILE:HD13	1:A:266:ILE:HA	1.80	0.45
1:B:339:VAL:HG21	1:B:364:TYR:CE2	2.51	0.45
1:A:334:GLN:HA	1:A:338:ARG:NH1	2.32	0.45
1:B:280:MSE:C	1:B:282:PRO:HD3	2.42	0.45
1:A:162:LEU:HD22	1:A:169:LEU:HD12	1.99	0.45
1:B:289:ILE:HA	1:B:289:ILE:HD12	1.77	0.45
1:A:148:GLY:C	1:A:150:GLU:H	2.25	0.44
1:A:312:PRO:HA	1:A:315:SER:HB2	2.00	0.44
1:B:280:MSE:HE2	1:B:281:TYR:CZ	2.53	0.44
1:B:237:TRP:O	1:B:242:LYS:HB2	2.18	0.43
1:A:379:THR:O	1:A:383:LYS:HE2	2.18	0.43
1:A:428:VAL:HG21	1:A:450:TYR:CE2	2.53	0.43
1:A:69:LEU:HD22	1:A:83:LYS:HG3	1.99	0.43
1:A:194:THR:HG21	1:A:199:ARG:NH2	2.28	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:THR:HG22	1:A:106:ILE:N	2.33	0.43
1:A:308:ALA:H	1:A:310:LYS:NZ	2.16	0.43
1:A:334:GLN:NE2	1:A:338:ARG:HD2	2.33	0.43
1:B:122:ILE:HD13	1:B:139:GLN:HA	2.01	0.43
1:B:76:ASP:CB	1:B:124:LYS:HZ2	2.32	0.42
1:B:260:PRO:HG2	1:B:263:GLU:CG	2.48	0.42
1:A:337:VAL:O	1:A:340:PHE:HB3	2.19	0.42
1:A:264:ASN:HA	1:A:265:PRO:HD3	1.92	0.42
1:A:308:ALA:H	1:A:310:LYS:HZ1	1.65	0.42
1:B:121:MSE:HE3	1:B:121:MSE:HB3	1.92	0.42
1:B:239:LYS:C	1:B:241:GLU:H	2.27	0.42
1:A:288:PRO:O	1:A:292:ILE:HG13	2.20	0.42
1:A:123:GLN:HE21	1:A:123:GLN:HA	1.84	0.41
1:A:204:LEU:HD13	1:A:212:MSE:HE1	2.01	0.41
1:B:269:ALA:C	1:B:270:TRP:O	2.62	0.41
1:A:74:ALA:HB3	1:A:77:LYS:HD3	2.02	0.41
1:B:334:GLN:OE1	1:B:338:ARG:NH2	2.53	0.41
1:A:107:LYS:HE3	1:A:107:LYS:HB2	1.66	0.41
1:A:126:LEU:CD2	1:A:136:LYS:HD2	2.50	0.41
1:A:91:MSE:HE2	1:A:91:MSE:HB3	2.00	0.41
1:A:160:LEU:HD12	1:A:178:TRP:HB2	2.02	0.41
1:A:388:GLU:HG3	1:A:431:TRP:CD1	2.55	0.41
1:B:242:LYS:HE3	1:B:250:LEU:HD22	2.02	0.41
1:A:404:LYS:HB2	1:A:404:LYS:HE3	1.63	0.41
1:B:270:TRP:HE3	1:B:271:VAL:HG23	1.85	0.41
1:B:113:PHE:O	1:B:117:GLY:HA3	2.21	0.41
1:B:201:SER:N	1:B:202:PRO:HD2	2.36	0.41
1:B:217:LYS:HD2	1:B:227:LEU:CD2	2.51	0.41
1:A:247:LEU:HD12	1:A:250:LEU:HD23	2.03	0.40
1:A:291:THR:O	1:A:294:GLU:HG3	2.21	0.40
1:B:355:SER:HA	1:B:356:PRO:HD3	1.97	0.40
1:A:346:ASP:OD1	1:A:346:ASP:N	2.54	0.40
1:B:226:ALA:O	1:B:230:GLN:HB2	2.21	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	406/478 (85%)	391 (96%)	11 (3%)	4 (1%)	12	26
1	B	403/478 (84%)	374 (93%)	22 (6%)	7 (2%)	7	14
All	All	809/956 (85%)	765 (95%)	33 (4%)	11 (1%)	9	18

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	ARG
1	B	166	ARG
1	A	81	HIS
1	A	285	SER
1	A	308	ALA
1	B	320	ARG
1	B	242	LYS
1	B	261	LEU
1	B	101	LYS
1	B	279	GLU
1	B	280	MSE

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	359/409 (88%)	331 (92%)	28 (8%)	11	25
1	B	358/409 (88%)	341 (95%)	17 (5%)	23	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	717/818 (88%)	672 (94%)	45 (6%)	16	34

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	ILE
1	A	67	LYS
1	A	83	LYS
1	A	102	LYS
1	A	104	THR
1	A	120	ARG
1	A	123	GLN
1	A	124	LYS
1	A	133	LYS
1	A	139	GLN
1	A	194	THR
1	A	212	MSE
1	A	215	LYS
1	A	236	SER
1	A	239	LYS
1	A	255	ARG
1	A	259	SER
1	A	280	MSE
1	A	289	ILE
1	A	293	SER
1	A	294	GLU
1	A	313	SER
1	A	327	ARG
1	A	338	ARG
1	A	357	VAL
1	A	359	THR
1	A	374	LYS
1	A	409	LYS
1	B	47	ILE
1	B	51	GLN
1	B	58	SER
1	B	91	MSE
1	B	101	LYS
1	B	106	ILE
1	B	130	SER
1	B	137	ARG
1	B	176	LEU

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Mol	Chain	Res	Type
1	B	217	LYS
1	B	239	LYS
1	B	254	ASN
1	B	279	GLU
1	B	352	LEU
1	B	373	GLU
1	B	415	VAL
1	B	430	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	233	GLN
1	A	325	GLN
1	A	334	GLN
1	A	354	GLN
1	B	51	GLN
1	B	127	GLN
1	B	230	GLN
1	B	295	HIS
1	B	325	GLN

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	401/478 (83%)	0.29	12 (2%) 52 48	28, 44, 65, 82	0
1	B	400/478 (83%)	0.39	13 (3%) 49 44	27, 46, 69, 90	0
All	All	801/956 (83%)	0.34	25 (3%) 51 46	27, 45, 67, 90	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	279	GLU	4.6
1	B	258	ASP	4.4
1	A	260	PRO	3.9
1	B	96	GLY	3.8
1	A	47	ILE	3.8
1	B	260	PRO	3.4
1	B	287	ASP	3.4
1	A	286	PHE	3.3
1	A	83	LYS	3.2
1	A	259	SER	3.1
1	B	454	TYR	2.9
1	B	286	PHE	2.9
1	A	81	HIS	2.9
1	A	258	ASP	2.8
1	B	266	ILE	2.7
1	B	284	VAL	2.7
1	A	378	THR	2.7
1	A	285	SER	2.6
1	A	444	ARG	2.5
1	B	124	LYS	2.4
1	B	271	VAL	2.3
1	B	256	ALA	2.3
1	A	128	VAL	2.2
1	B	255	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	100	SER	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.