



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:04 AM UTC

PDB ID : 5MS2 / pdb\_00005ms2  
Title : Crystal structure of the Legionella pneumophila effector protein RavZ in complex with human LC3B  
Authors : Pantoom, S.; Vetter, I.R.; Wu, Y.W.  
Deposited on : 2016-12-30  
Resolution : 2.47 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](mailto: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>.

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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

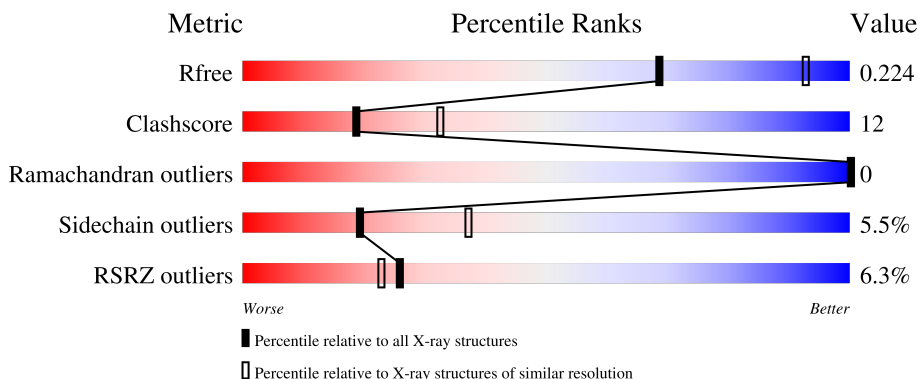
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.47 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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  $\geq 3$ , 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	433	
2	B	124	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4273 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 Legionella pneumophila effector protein RavZ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	405	3202	2029	518	645	10	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q5ZUV9
A	0	PRO	-	expression tag	UNP Q5ZUV9

- Molecule 2 is a protein called Microtubule-associated proteins 1A/1B light chain 3B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	115	960	614	168	175	3	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP Q9GZQ8
B	-3	HIS	-	expression tag	UNP Q9GZQ8
B	-2	MET	-	expression tag	UNP Q9GZQ8
B	-1	GLY	-	expression tag	UNP Q9GZQ8
B	0	CYS	-	expression tag	UNP Q9GZQ8

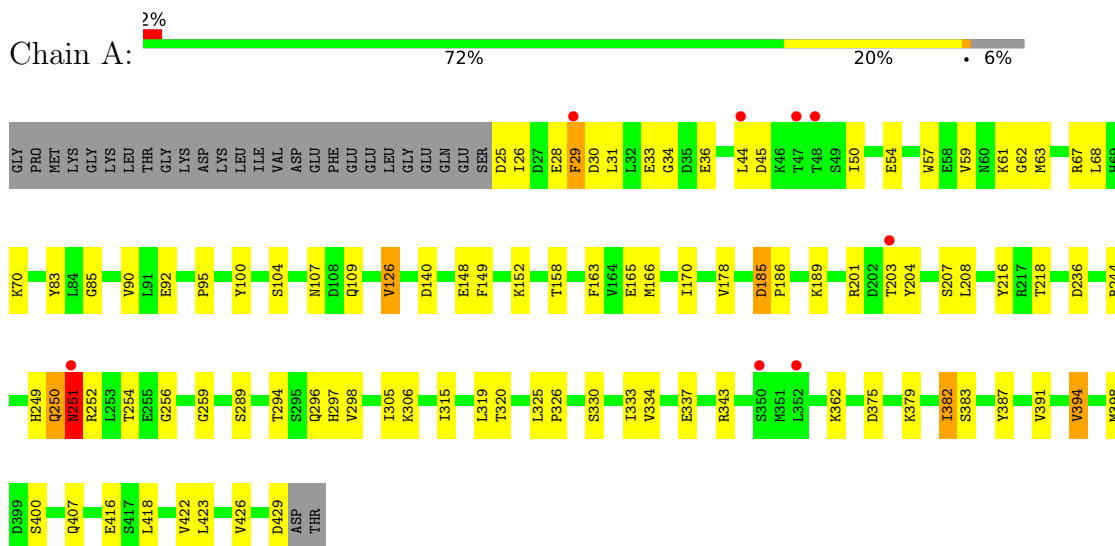
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total 106	O 106	0	0
3	B	5	Total 5	O 5	0	0

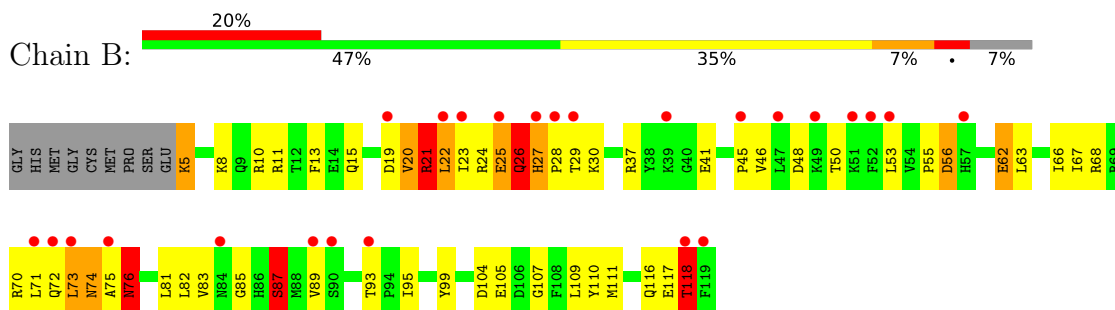
### 3 Residue-property plots [i](#)

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: Legionella pneumophila effector protein RavZ



- Molecule 2: Microtubule-associated proteins 1A/1B light chain 3B



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.55Å 69.55Å 90.17Å 90.00° 101.08° 90.00°	Depositor
Resolution (Å)	48.08 – 2.47 48.08 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.08-2.47) 99.9 (48.08-2.47)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.48Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.177 , 0.238 (Not available) , 0.224	Depositor DCC
$R_{free}$ test set	1131 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.3	Xtrriage
Anisotropy	0.585	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 61.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4273	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.63	1/3267 (0.0%)	1.05	14/4413 (0.3%)
2	B	0.56	0/978	1.22	14/1316 (1.1%)
All	All	0.61	1/4245 (0.0%)	1.09	28/5729 (0.5%)

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	1
2	B	0	4
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	29	PHE	CA-C	7.40	1.63	1.53

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	ASN	N-CA-C	-12.07	86.54	108.02
2	B	23	ILE	N-CA-C	-10.89	101.56	113.43
1	A	29	PHE	CA-C-O	9.14	136.11	120.85
1	A	30	ASP	N-CA-C	-8.46	102.51	112.92
1	A	251	ASN	CA-C-N	-8.15	112.24	122.84
1	A	251	ASN	C-N-CA	-8.15	112.24	122.84
1	A	249	HIS	CA-C-N	-7.69	111.76	123.14
1	A	249	HIS	C-N-CA	-7.69	111.76	123.14
2	B	74	ASN	N-CA-C	6.96	121.37	113.02
2	B	21	ARG	CA-C-N	-6.94	112.06	122.47
2	B	21	ARG	C-N-CA	-6.94	112.06	122.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	ASP	CA-C-N	6.92	126.53	119.19
1	A	185	ASP	C-N-CA	6.92	126.53	119.19
1	A	44	LEU	N-CA-C	6.75	118.63	111.28
2	B	118	THR	N-CA-C	6.69	118.94	110.24
2	B	87	SER	N-CA-C	6.50	117.05	107.88
2	B	25	GLU	N-CA-C	6.46	121.30	113.17
1	A	29	PHE	N-CA-C	6.26	121.02	107.49
2	B	27	HIS	CA-C-N	5.99	126.14	119.32
2	B	27	HIS	C-N-CA	5.99	126.14	119.32
1	A	400	SER	N-CA-C	5.96	116.83	108.00
2	B	89	VAL	N-CA-C	-5.75	107.13	112.83
1	A	400	SER	CB-CA-C	-5.74	108.31	116.34
2	B	26	GLN	N-CA-C	-5.69	106.11	113.16
1	A	203	THR	N-CA-C	-5.50	106.34	113.16
2	B	85	GLY	CA-C-N	5.38	131.00	122.94
2	B	85	GLY	C-N-CA	5.38	131.00	122.94
2	B	76	ASN	N-CA-CB	-5.18	102.82	110.49

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	250	GLN	Peptide
2	B	21	ARG	Peptide
2	B	22	LEU	Peptide
2	B	48	ASP	Peptide
2	B	73	LEU	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	3202	0	3173	56	1
2	B	960	0	979	45	0
3	A	106	0	0	0	0
3	B	5	0	0	3	0
All	All	4273	0	4152	99	1

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 12.

All (99) 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:24:ARG:NH1	2:B:25:GLU:OE1	1.98	0.97
2:B:82:LEU:HD12	2:B:87:SER:HB3	1.61	0.82
2:B:45:PRO:HG2	2:B:71:LEU:HD22	1.61	0.81
1:A:107:ASN:HB3	1:A:109:GLN:H	1.46	0.80
2:B:87:SER:OG	3:B:201:HOH:O	2.02	0.78
2:B:76:ASN:OD1	3:B:202:HOH:O	2.03	0.76
1:A:251:ASN:OD1	1:A:289:SER:OG	2.04	0.75
1:A:34:GLY:HA3	2:B:76:ASN:HD21	1.51	0.74
1:A:63:MET:HG3	1:A:259:GLY:HA3	1.71	0.72
2:B:70:ARG:O	2:B:72:GLN:NE2	2.23	0.71
2:B:13:PHE:HE2	2:B:105:GLU:HG3	1.58	0.69
2:B:26:GLN:N	2:B:26:GLN:OE1	2.28	0.67
2:B:10:ARG:HH22	2:B:50:THR:HG21	1.60	0.66
1:A:25:ASP:OD1	1:A:26:ILE:N	2.27	0.66
2:B:37:ARG:NH2	2:B:41:GLU:O	2.29	0.66
1:A:34:GLY:HA3	2:B:76:ASN:ND2	2.09	0.66
2:B:24:ARG:HH11	2:B:25:GLU:CD	2.05	0.64
2:B:68:ARG:NH1	2:B:75:ALA:HA	2.14	0.63
2:B:37:ARG:HD3	2:B:46:VAL:HG22	1.81	0.61
2:B:22:LEU:HD11	2:B:25:GLU:H	1.68	0.59
2:B:11:ARG:HD3	2:B:15:GLN:HB3	1.84	0.59
1:A:90:VAL:HG11	1:A:320:THR:O	2.04	0.57
2:B:25:GLU:HA	2:B:28:PRO:HA	1.85	0.57
1:A:109:GLN:NE2	1:A:158:THR:OG1	2.38	0.57
1:A:83:TYR:CZ	1:A:85:GLY:HA3	2.39	0.57
1:A:204:TYR:CD2	1:A:218:THR:HG21	2.40	0.57
2:B:22:LEU:CD1	2:B:25:GLU:H	2.19	0.55
1:A:294[A]:THR:HB	1:A:297:HIS:ND1	2.22	0.55
2:B:83:VAL:HG22	2:B:111:MET:HG2	1.89	0.54
1:A:387:TYR:CZ	1:A:423:LEU:HD13	2.43	0.54
1:A:29:PHE:CD1	1:A:31:LEU:HB2	2.43	0.54
2:B:73:LEU:HD23	2:B:74:ASN:H	1.72	0.54
1:A:294[A]:THR:HG22	1:A:296:GLN:H	1.72	0.54
1:A:423:LEU:O	1:A:426:VAL:HG12	2.07	0.53
1:A:163:PHE:CE1	1:A:178:VAL:HG13	2.43	0.53
2:B:67:ILE:HD12	2:B:81:LEU:HD11	1.89	0.53
2:B:8:LYS:NZ	2:B:104:ASP:OD2	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:VAL:HG11	1:A:208:LEU:HD13	1.91	0.52
1:A:201:ARG:HG2	1:A:252:ARG:HG3	1.92	0.52
1:A:33:GLU:HB2	3:B:202:HOH:O	2.10	0.51
1:A:28:GLU:HG2	1:A:29:PHE:H	1.74	0.51
1:A:294[B]:THR:HG22	1:A:297:HIS:ND1	2.26	0.51
2:B:116:GLN:HG2	2:B:118:THR:H	1.77	0.50
2:B:22:LEU:HG	2:B:26:GLN:OE1	2.12	0.50
2:B:66:ILE:O	2:B:70:ARG:HG3	2.12	0.50
2:B:30:LYS:HE3	2:B:55:PRO:HG3	1.94	0.50
2:B:20:VAL:HG11	2:B:107:GLY:HA3	1.94	0.50
1:A:294[B]:THR:HG23	1:A:296:GLN:H	1.78	0.49
2:B:117:GLU:O	2:B:117:GLU:HG2	2.13	0.49
1:A:201:ARG:NH1	1:A:254:THR:HG22	2.28	0.49
2:B:30:LYS:HB3	2:B:53:LEU:HG	1.95	0.49
2:B:11:ARG:NH1	2:B:19:ASP:OD1	2.46	0.49
1:A:343:ARG:HH12	1:A:362:LYS:HD2	1.78	0.48
2:B:10:ARG:NH2	2:B:50:THR:HG21	2.28	0.48
1:A:62:GLY:HA2	1:A:256:GLY:HA2	1.96	0.48
2:B:25:GLU:HA	2:B:28:PRO:CA	2.44	0.48
2:B:99:TYR:HD1	2:B:109:LEU:HB2	1.78	0.48
1:A:294[B]:THR:HG22	1:A:297:HIS:H	1.78	0.47
1:A:201:ARG:CG	1:A:252:ARG:HG3	2.42	0.47
1:A:333:ILE:O	1:A:337:GLU:HG3	2.14	0.47
2:B:11:ARG:HH11	2:B:15:GLN:HB3	1.79	0.47
1:A:57:TRP:CH2	1:A:59:VAL:HA	2.50	0.47
1:A:152:LYS:HB2	1:A:152:LYS:HE2	1.69	0.47
1:A:294[B]:THR:HG23	1:A:296:GLN:N	2.30	0.47
2:B:27:HIS:HB3	2:B:30:LYS:HB2	1.98	0.46
1:A:387:TYR:O	1:A:391:VAL:HG23	2.16	0.45
2:B:22:LEU:HD12	2:B:22:LEU:HA	1.72	0.45
1:A:375:ASP:OD1	1:A:379:LYS:NZ	2.44	0.45
1:A:59:VAL:HG21	1:A:298:VAL:HG13	1.98	0.45
1:A:189:LYS:HD3	1:A:236:ASP:HB3	1.99	0.45
1:A:63:MET:HE1	1:A:68:LEU:N	2.33	0.44
1:A:250:GLN:C	1:A:251:ASN:HD22	2.25	0.44
2:B:21:ARG:HG3	2:B:24:ARG:HH21	1.82	0.44
2:B:56:ASP:N	2:B:56:ASP:OD1	2.50	0.43
2:B:63:LEU:HD22	2:B:95:ILE:HD13	2.00	0.43
1:A:67:ARG:HB3	1:A:305:ILE:HD12	2.00	0.43
1:A:70:LYS:HA	1:A:315:ILE:HD11	1.99	0.43
1:A:29:PHE:CE1	1:A:31:LEU:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:ARG:O	2:B:24:ARG:NH2	2.52	0.43
1:A:189:LYS:NZ	1:A:236:ASP:OD2	2.49	0.43
1:A:325:LEU:HA	1:A:326:PRO:HD2	1.88	0.43
1:A:394:VAL:O	1:A:398:MET:HG2	2.19	0.43
1:A:54:GLU:O	1:A:306:LYS:HA	2.19	0.43
1:A:104:SER:CB	1:A:107:ASN:HB2	2.49	0.42
1:A:330:SER:O	1:A:334:VAL:HG23	2.18	0.42
1:A:185:ASP:HA	1:A:186:PRO:HD3	1.77	0.42
2:B:5:LYS:HE2	2:B:5:LYS:HB2	1.86	0.42
2:B:74:ASN:O	2:B:75:ALA:HB3	2.20	0.42
2:B:8:LYS:HE3	2:B:110:TYR:CZ	2.55	0.41
1:A:163:PHE:CZ	1:A:178:VAL:HG13	2.54	0.41
1:A:165:GLU:OE1	1:A:244:ARG:NH2	2.52	0.41
1:A:398:MET:HE1	1:A:407:GLN:HG3	2.02	0.41
1:A:100:TYR:CD2	1:A:319:LEU:HD12	2.55	0.41
1:A:126:VAL:HG13	1:A:216:TYR:CE1	2.55	0.41
1:A:382:ILE:HA	1:A:382:ILE:HD13	1.78	0.41
1:A:394:VAL:HG22	1:A:418:LEU:HD12	2.02	0.41
2:B:62:GLU:O	2:B:66:ILE:HG13	2.21	0.41
1:A:45:ASP:OD1	1:A:45:ASP:N	2.43	0.40
1:A:95:PRO:HB2	1:A:149:PHE:HE2	1.86	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:ASP:OD2	1:A:207:SER:OG[2_455]	2.03	0.17

## 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	277/433 (64%)	272 (98%)	5 (2%)	0	100	100
2	B	113/124 (91%)	107 (95%)	6 (5%)	0	100	100
All	All	390/557 (70%)	379 (97%)	11 (3%)	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	366/388 (94%)	350 (96%)	16 (4%)	25	47
2	B	109/116 (94%)	99 (91%)	10 (9%)	8	17
All	All	475/504 (94%)	449 (94%)	26 (6%)	19	37

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	GLU
1	A	50	ILE
1	A	61	LYS
1	A	92	GLU
1	A	126	VAL
1	A	140	ASP
1	A	148	GLU
1	A	166	MET
1	A	170	ILE
1	A	251	ASN
1	A	382	ILE
1	A	383	SER
1	A	394	VAL
1	A	416	GLU
1	A	422	VAL
1	A	429	ASP
2	B	5	LYS
2	B	20	VAL

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Mol	Chain	Res	Type
2	B	26	GLN
2	B	29	THR
2	B	56	ASP
2	B	62	GLU
2	B	76	ASN
2	B	87	SER
2	B	93	THR
2	B	118	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	226	GLN
1	A	257	ASN
1	A	353	ASN
2	B	43	GLN
2	B	76	ASN
2	B	77	GLN
2	B	86	HIS

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	405/433 (93%)	-0.27	8 (1%) 65 62	16, 33, 74, 122	2 (0%)
2	B	115/124 (92%)	1.12	25 (21%) 2 2	46, 89, 134, 147	0
All	All	520/557 (93%)	0.04	33 (6%) 26 23	16, 40, 106, 147	2 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	44	LEU	4.8
2	B	23	ILE	4.2
2	B	119	PHE	4.0
1	A	47	THR	3.9
1	A	29	PHE	3.8
2	B	73	LEU	3.6
2	B	89	VAL	3.4
2	B	93	THR	2.9
2	B	47	LEU	2.8
2	B	29	THR	2.7
1	A	352	LEU	2.7
1	A	350	SER	2.6
1	A	48	THR	2.6
1	A	203	THR	2.6
2	B	75	ALA	2.5
2	B	72	GLN	2.5
2	B	118	THR	2.4
1	A	251	ASN	2.4
2	B	28	PRO	2.3
2	B	53	LEU	2.3
2	B	51	LYS	2.3
2	B	19	ASP	2.3
2	B	25	GLU	2.3
2	B	27	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	71	LEU	2.3
2	B	57	HIS	2.2
2	B	45	PRO	2.2
2	B	22	LEU	2.2
2	B	90	SER	2.2
2	B	52	PHE	2.1
2	B	49	LYS	2.1
2	B	84	ASN	2.1
2	B	39	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.