



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:56 AM UTC

PDB ID : 5Y24 / pdb_00005y24
Title : Crystal structure of AimR from Bacillus phage SPbeta in complex with its signalling peptide
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Deposited on : 2017-07-24
Resolution : 1.92 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

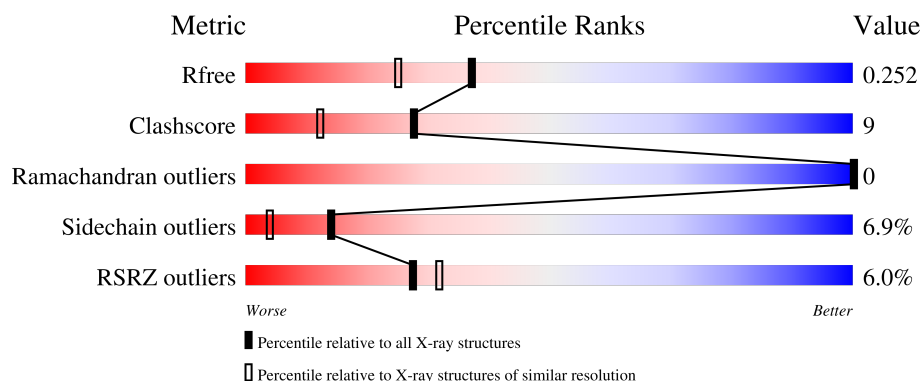
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.92 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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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	396	4% 71% 15% • 12%
1	B	396	6% 72% 14% • 12%
2	C	6	50% 50%
2	D	6	67% 33%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BR	A	402	-	-	X	-
3	BR	A	403	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6322 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 AimR transcriptional regulator.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	348	Total	C	N	O	S	Se	0	0	0
			2871	1835	476	542	6	12			
1	B	350	Total	C	N	O	S	Se	0	0	0
			2868	1832	478	540	6	12			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	387	LEU	-	expression tag	UNP O64094
A	388	GLU	-	expression tag	UNP O64094
A	389	HIS	-	expression tag	UNP O64094
A	390	HIS	-	expression tag	UNP O64094
A	391	HIS	-	expression tag	UNP O64094
A	392	HIS	-	expression tag	UNP O64094
A	393	HIS	-	expression tag	UNP O64094
A	394	HIS	-	expression tag	UNP O64094
A	395	HIS	-	expression tag	UNP O64094
A	396	HIS	-	expression tag	UNP O64094
B	387	LEU	-	expression tag	UNP O64094
B	388	GLU	-	expression tag	UNP O64094
B	389	HIS	-	expression tag	UNP O64094
B	390	HIS	-	expression tag	UNP O64094
B	391	HIS	-	expression tag	UNP O64094
B	392	HIS	-	expression tag	UNP O64094
B	393	HIS	-	expression tag	UNP O64094
B	394	HIS	-	expression tag	UNP O64094
B	395	HIS	-	expression tag	UNP O64094
B	396	HIS	-	expression tag	UNP O64094

- Molecule 2 is a protein called GLY-MET-PRO-ARG-GLY-ALA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	S	0	0	0
			40	23	9	7	1			
2	D	6	Total	C	N	O	S	0	0	0
			40	23	9	7	1			

- Molecule 3 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Br	0	0
			3	3		
3	B	2	Total	Br	0	0
			2	2		

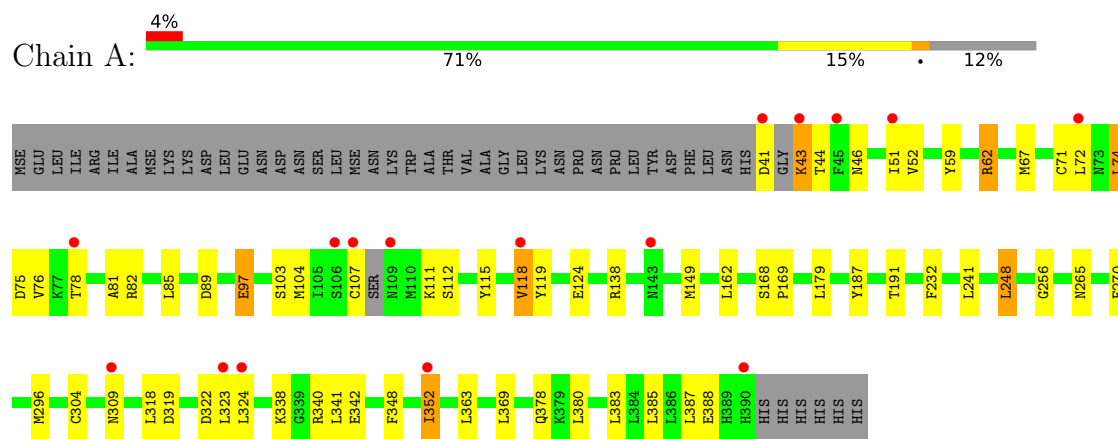
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	270	Total	O	0	0
			270	270		
4	C	5	Total	O	0	0
			5	5		
4	B	221	Total	O	0	0
			221	221		
4	D	2	Total	O	0	0
			2	2		

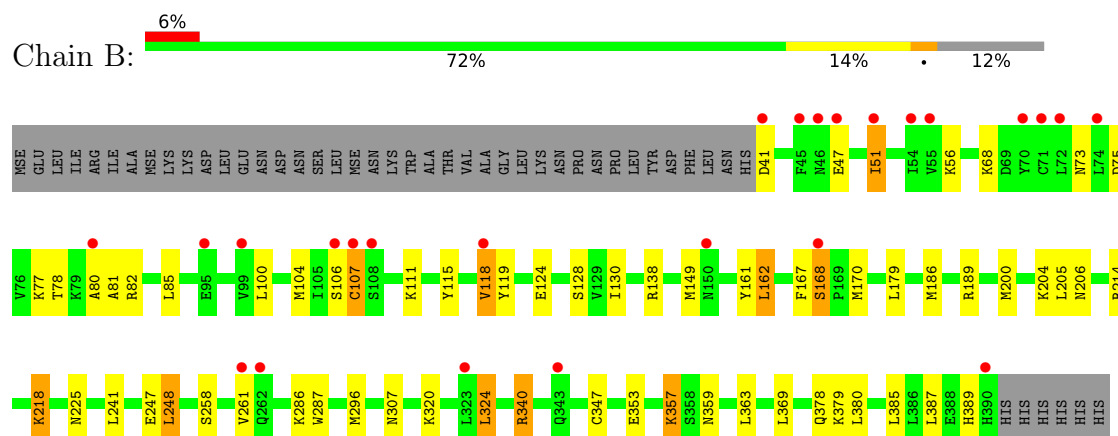
3 Residue-property plots

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: AimR transcriptional regulator



• Molecule 1: AimR transcriptional regulator



• Molecule 2: GLY-MET-PRO-ARG-GLY-ALA



• Molecule 2: GLY-MET-PRO-ARG-GLY-ALA



C1	M2	P3	R4	G5	A6
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4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	33.55Å 119.61Å 214.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.20 – 1.92 39.20 – 1.92	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.20-1.92) 99.8 (39.20-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.67 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.216 , 0.249 0.220 , 0.252	Depositor DCC
R_{free} test set	3298 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	30.1	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6322	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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: BR

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	0.52	0/2908	0.62	0/3888
1	B	0.40	1/2906 (0.0%)	0.51	0/3888
2	C	0.40	0/40	0.63	0/50
2	D	0.47	0/40	0.53	0/50
All	All	0.46	1/5894 (0.0%)	0.57	0/7876

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	379	LYS	C-O	-5.47	1.17	1.24

There are no bond angle outliers.

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	2871	0	2854	53	0
1	B	2868	0	2853	48	0
2	C	40	0	42	3	0
2	D	40	0	42	3	0
3	A	3	0	0	7	0
3	B	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	270	0	0	11	1
4	B	221	0	0	6	1
4	C	5	0	0	1	0
4	D	2	0	0	0	0
All	All	6322	0	5791	105	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 9.

All (105) 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:A:304:CYS:SG	3:A:401:BR:BR	2.41	1.34
3:A:402:BR:BR	4:A:658:HOH:O	2.06	1.28
1:A:107:CYS:SG	3:A:403:BR:BR	2.48	1.27
3:B:402:BR:BR	4:B:625:HOH:O	2.01	1.26
3:A:402:BR:BR	4:A:690:HOH:O	2.07	1.24
1:A:82:ARG:HG2	1:A:104:MSE:HE1	1.31	1.11
3:A:403:BR:BR	4:A:745:HOH:O	2.25	1.10
1:B:115:TYR:HA	1:B:149:MSE:HE2	1.44	1.00
1:B:167:PHE:HA	1:B:170:MSE:HE3	1.42	1.00
1:A:76:VAL:HG11	1:A:103:SER:OG	1.66	0.94
1:A:82:ARG:HG2	1:A:104:MSE:CE	1.98	0.94
1:A:115:TYR:HA	1:A:149:MSE:HE2	1.58	0.83
1:A:78:THR:HG23	1:A:81:ALA:H	1.51	0.76
1:A:43:LYS:HG3	1:A:44:THR:N	2.00	0.75
1:A:319:ASP:O	4:A:501:HOH:O	2.04	0.73
1:B:41:ASP:N	4:B:502:HOH:O	2.22	0.73
1:A:104:MSE:HE2	1:A:112:SER:HA	1.73	0.71
1:B:124:GLU:OE1	1:B:138:ARG:NH2	2.22	0.71
1:A:107:CYS:CB	3:A:403:BR:BR	2.95	0.70
1:B:186:MSE:HE1	1:B:189:ARG:HH21	1.57	0.69
1:A:43:LYS:O	4:A:502:HOH:O	2.10	0.68
1:A:124:GLU:OE1	1:A:138:ARG:NH2	2.28	0.66
1:B:100:LEU:HB3	1:B:104:MSE:HE3	1.78	0.65
1:B:167:PHE:HD1	1:B:170:MSE:CE	2.12	0.62
1:A:41:ASP:N	4:A:508:HOH:O	2.33	0.61
1:A:52:VAL:HA	1:A:67:MSE:CE	2.32	0.60
1:A:104:MSE:HE2	1:A:112:SER:CA	2.31	0.60
1:A:118:VAL:HG13	1:A:149:MSE:HE3	1.82	0.60
1:B:111:LYS:NZ	4:B:508:HOH:O	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:PHE:HD1	1:B:170:MSE:HE1	1.69	0.57
1:A:71:CYS:HA	1:A:74:LEU:HD22	1.87	0.56
1:B:118:VAL:HG22	1:B:149:MSE:HE3	1.86	0.56
1:B:162:LEU:HA	1:B:170:MSE:HE1	1.87	0.56
1:A:75:ASP:O	1:A:78:THR:HG22	2.06	0.55
1:A:82:ARG:CG	1:A:104:MSE:CE	2.81	0.55
1:B:161:TYR:CB	1:B:170:MSE:HE2	2.36	0.55
1:A:348:PHE:O	1:A:352:ILE:HG23	2.06	0.54
1:B:100:LEU:O	1:B:104:MSE:HG3	2.07	0.54
1:A:115:TYR:CA	1:A:149:MSE:HE2	2.35	0.54
1:B:118:VAL:HG13	1:B:149:MSE:HE3	1.90	0.54
1:A:322:ASP:HB2	4:A:501:HOH:O	2.06	0.54
1:B:320:LYS:NZ	4:B:509:HOH:O	2.40	0.54
1:A:118:VAL:HG22	1:A:149:MSE:HE3	1.91	0.52
1:B:347:CYS:SG	4:B:625:HOH:O	2.56	0.52
1:A:323:LEU:HG	4:A:501:HOH:O	2.08	0.52
1:A:104:MSE:HE2	1:A:112:SER:CB	2.40	0.52
1:B:206:ASN:OD1	2:D:4:ARG:NH1	2.42	0.52
1:B:296:MSE:HE1	2:D:3:PRO:HA	1.91	0.51
1:B:119:TYR:CD1	1:B:149:MSE:HE1	2.45	0.51
1:B:118:VAL:HG22	1:B:149:MSE:CE	2.41	0.51
1:B:241:LEU:HD13	1:B:248:LEU:HB3	1.91	0.51
1:B:307:ASN:OD1	1:B:340:ARG:NH2	2.34	0.50
1:B:161:TYR:C	1:B:170:MSE:HE2	2.36	0.50
1:A:118:VAL:CG1	1:A:149:MSE:HE3	2.41	0.50
1:B:115:TYR:CA	1:B:149:MSE:HE2	2.28	0.49
1:B:78:THR:HG23	1:B:81:ALA:H	1.78	0.49
1:B:200:MSE:HE1	1:B:204:LYS:HE2	1.94	0.49
1:A:296:MSE:HE1	2:C:3:PRO:HA	1.95	0.49
1:B:56:LYS:HE2	1:B:225:ASN:O	2.12	0.49
1:B:168:SER:HA	1:B:359:ASN:HD22	1.78	0.49
1:A:107:CYS:HB2	3:A:403:BR:BR	2.68	0.48
1:B:161:TYR:HB3	1:B:170:MSE:HE2	1.95	0.48
1:B:214:ARG:O	1:B:218:LYS:HG2	2.14	0.48
1:A:59:TYR:HB3	1:A:62:ARG:HG3	1.96	0.48
1:A:104:MSE:HG2	1:A:112:SER:HB3	1.96	0.48
1:A:322:ASP:OD2	4:A:503:HOH:O	2.20	0.47
1:A:318:LEU:HD12	1:A:341:LEU:HD22	1.97	0.47
1:B:286:LYS:HE3	1:B:287:TRP:CZ2	2.50	0.47
1:B:385:LEU:HD23	1:B:385:LEU:HA	1.63	0.46
1:B:82:ARG:HB3	1:B:115:TYR:CE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:VAL:CG2	1:A:149:MSE:HE3	2.47	0.45
1:A:119:TYR:CD1	1:A:149:MSE:HE1	2.52	0.45
1:B:118:VAL:CG2	1:B:149:MSE:HE3	2.47	0.45
1:B:167:PHE:HD1	1:B:170:MSE:HE3	1.81	0.44
1:A:385:LEU:HD23	1:A:385:LEU:HA	1.83	0.44
1:A:256:GLY:HA3	1:A:270:PHE:CZ	2.53	0.44
1:A:342:GLU:OE1	4:A:504:HOH:O	2.21	0.44
1:B:78:THR:HG23	1:B:80:ALA:N	2.33	0.43
1:A:104:MSE:HE2	1:A:112:SER:HB3	1.99	0.43
1:B:186:MSE:HE1	1:B:189:ARG:NH2	2.29	0.43
1:A:322:ASP:OD1	1:A:338:LYS:HE3	2.18	0.43
1:A:89:ASP:HA	1:A:97:GLU:OE2	2.18	0.43
1:B:258:SER:O	1:B:261:VAL:HG23	2.19	0.43
1:B:167:PHE:CD1	1:B:170:MSE:HE1	2.50	0.43
1:A:383:LEU:HD13	1:B:353:GLU:HB2	2.00	0.42
1:B:75:ASP:O	1:B:78:THR:HG22	2.18	0.42
1:A:118:VAL:HG22	1:A:149:MSE:CE	2.50	0.42
1:A:187:TYR:O	1:A:191:THR:HG23	2.19	0.42
4:B:551:HOH:O	2:D:4:ARG:HD3	2.19	0.42
2:C:4:ARG:NH2	4:C:101:HOH:O	2.53	0.42
1:B:51:ILE:H	1:B:51:ILE:HG13	1.50	0.42
1:A:168:SER:OG	1:A:169:PRO:HD3	2.20	0.42
1:A:76:VAL:HG11	1:A:103:SER:HG	1.79	0.42
1:B:118:VAL:CG1	1:B:149:MSE:HE3	2.49	0.42
1:A:265:ASN:HB3	4:A:540:HOH:O	2.20	0.41
1:A:232:PHE:CE1	2:C:5:GLY:HA3	2.55	0.41
1:A:52:VAL:HG22	1:A:67:MSE:HE3	2.03	0.41
1:B:77:LYS:NZ	1:B:107:CYS:HB2	2.36	0.41
1:B:130:ILE:HG21	1:B:138:ARG:HH21	1.85	0.41
1:B:357:LYS:HG3	1:B:389:HIS:CE1	2.56	0.41
1:A:104:MSE:CE	1:A:112:SER:HB3	2.50	0.41
1:A:115:TYR:HA	1:A:149:MSE:CE	2.40	0.40
1:A:241:LEU:HD13	1:A:248:LEU:HB3	2.01	0.40
1:A:387:LEU:HB3	1:B:387:LEU:HB3	2.03	0.40
1:B:320:LYS:O	1:B:324:LEU:HD13	2.21	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)
4:A:671:HOH:O	4:B:691:HOH:O[3_147]	2.11	0.09

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	343/396 (87%)	338 (98%)	5 (2%)	0	100	100
1	B	348/396 (88%)	342 (98%)	6 (2%)	0	100	100
2	C	4/6 (67%)	4 (100%)	0	0	100	100
2	D	4/6 (67%)	4 (100%)	0	0	100	100
All	All	699/804 (87%)	688 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	324/355 (91%)	302 (93%)	22 (7%)	14	4
1	B	322/355 (91%)	299 (93%)	23 (7%)	13	4
2	C	3/3 (100%)	3 (100%)	0	100	100
2	D	3/3 (100%)	3 (100%)	0	100	100
All	All	652/716 (91%)	607 (93%)	45 (7%)	14	4

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

Mol	Chain	Res	Type
1	A	43	LYS
1	A	46	ASN

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Mol	Chain	Res	Type
1	A	51	ILE
1	A	62	ARG
1	A	72	LEU
1	A	74	LEU
1	A	85	LEU
1	A	97	GLU
1	A	111	LYS
1	A	118	VAL
1	A	162	LEU
1	A	179	LEU
1	A	248	LEU
1	A	309	ASN
1	A	324	LEU
1	A	340	ARG
1	A	352	ILE
1	A	363	LEU
1	A	369	LEU
1	A	378	GLN
1	A	380	LEU
1	A	388	GLU
1	B	47	GLU
1	B	51	ILE
1	B	68	LYS
1	B	73	ASN
1	B	85	LEU
1	B	106	SER
1	B	107	CYS
1	B	118	VAL
1	B	128	SER
1	B	162	LEU
1	B	168	SER
1	B	179	LEU
1	B	205	LEU
1	B	218	LYS
1	B	247	GLU
1	B	248	LEU
1	B	324	LEU
1	B	340	ARG
1	B	357	LYS
1	B	363	LEU
1	B	369	LEU
1	B	378	GLN

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Mol	Chain	Res	Type
1	B	380	LEU

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	160	HIS
1	A	265	ASN
1	A	271	GLN
1	A	372	GLN
1	A	378	GLN
1	B	252	ASN
1	B	278	ASN
1	B	359	ASN
1	B	389	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	336/396 (84%)	0.40	16 (4%) 35 40	18, 35, 57, 84	0
1	B	338/396 (85%)	0.59	25 (7%) 20 24	22, 38, 65, 95	0
2	C	6/6 (100%)	0.04	0 100 100	23, 24, 28, 30	0
2	D	6/6 (100%)	0.13	0 100 100	24, 26, 35, 35	0
All	All	686/804 (85%)	0.49	41 (5%) 27 32	18, 36, 60, 95	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	99	VAL	5.2
1	B	323	LEU	4.8
1	B	74	LEU	4.1
1	B	107	CYS	4.1
1	B	55	VAL	3.8
1	B	51	ILE	3.7
1	B	261	VAL	3.5
1	A	107	CYS	3.4
1	A	323	LEU	3.3
1	A	390	HIS	3.3
1	B	54	ILE	3.2
1	B	390	HIS	2.8
1	A	51	ILE	2.7
1	A	45	PHE	2.7
1	B	41	ASP	2.6
1	B	70	TYR	2.6
1	B	106	SER	2.6
1	A	143	ASN	2.6
1	B	72	LEU	2.5
1	A	78	THR	2.4
1	B	95	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	343	GLN	2.4
1	B	150	ASN	2.4
1	A	43	LYS	2.4
1	B	80	ALA	2.4
1	B	45	PHE	2.3
1	A	118	VAL	2.3
1	B	46	ASN	2.3
1	A	352	ILE	2.2
1	B	108	SER	2.2
1	A	72	LEU	2.2
1	A	324	LEU	2.2
1	B	168	SER	2.2
1	A	41	ASP	2.1
1	A	109	ASN	2.1
1	A	309	ASN	2.1
1	B	262	GLN	2.1
1	A	106	SER	2.0
1	B	71	CYS	2.0
1	B	47	GLU	2.0
1	B	118	VAL	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](#)

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
3	BR	A	401	1/1	0.96	0.27	41,41,41,41	1
3	BR	B	401	1/1	0.96	0.18	49,49,49,49	0
3	BR	B	402	1/1	0.96	0.23	39,39,39,39	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	BR	A	402	1/1	0.97	0.22	38,38,38,38	1
3	BR	A	403	1/1	0.97	0.17	56,56,56,56	1

6.5 Other polymers [i](#)

There are no such residues in this entry.