WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Dec 2, 2023 – 11:29 pm GMT

PDB ID	:	2V8Z
Title	:	Crystal Structure of YagE, a prophage protein belonging to the dihydrodipicolinic acid synthase family from E. coli K12
Authors	:	Manicka, S.; Peleg, Y.; Unger, T.; Albeck, S.; Dym, O.; Greenblatt, H.M.; Bourenkov, G.; Lamzin, V.; Krishnaswamy, S.; Sussman, J.L.
Deposited on	:	2007-08-16
Resolution	:	2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

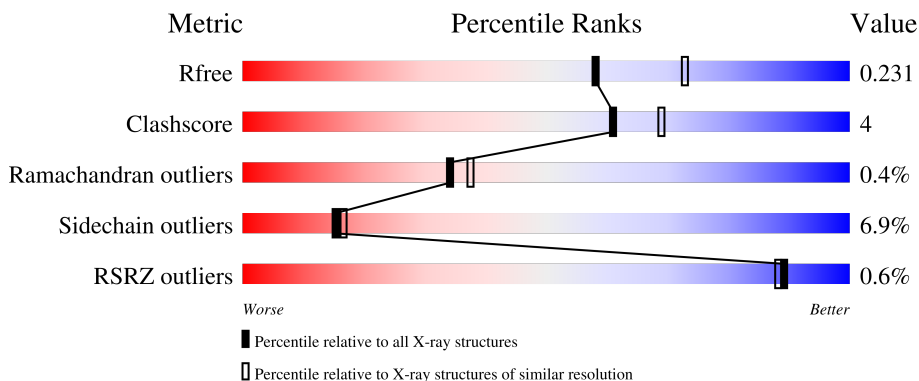|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.20 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	Percentile Ranks	Value
Rfree		0.231
Clashscore		4
Ramachandran outliers		0.4%
Sidechain outliers		6.9%
RSRZ outliers		0.6%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	343	74% 10% · · 13%
1	B	343	77% 8% · 13%
1	C	343	72% 11% · · 13%
1	D	343	73% 12% · 13%

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 9478 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 YAGE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2250	1443	381	420	6			
1	B	298	Total	C	N	O	S	0	0	0
			2257	1446	385	420	6			
1	C	298	Total	C	N	O	S	0	0	0
			2252	1444	383	419	6			
1	D	298	Total	C	N	O	S	0	0	0
			2255	1445	385	419	6			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	expression tag	UNP P75682
A	-16	GLY	-	expression tag	UNP P75682
A	-15	SER	-	expression tag	UNP P75682
A	-14	SER	-	expression tag	UNP P75682
A	-13	HIS	-	expression tag	UNP P75682
A	-12	HIS	-	expression tag	UNP P75682
A	-11	HIS	-	expression tag	UNP P75682
A	-10	HIS	-	expression tag	UNP P75682
A	-9	HIS	-	expression tag	UNP P75682
A	-8	HIS	-	expression tag	UNP P75682
A	-7	SER	-	expression tag	UNP P75682
A	-6	ALA	-	expression tag	UNP P75682
A	-5	GLY	-	expression tag	UNP P75682
A	-4	GLU	-	expression tag	UNP P75682
A	-3	ASN	-	expression tag	UNP P75682
A	-2	LEU	-	expression tag	UNP P75682
A	-1	TYR	-	expression tag	UNP P75682
A	0	PHE	-	expression tag	UNP P75682
A	1	GLN	-	expression tag	UNP P75682
A	2	GLY	-	expression tag	UNP P75682
A	310	CYS	-	expression tag	UNP P75682

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Chain	Residue	Modelled	Actual	Comment	Reference
A	311	GLY	-	expression tag	UNP P75682
A	312	ARG	-	expression tag	UNP P75682
A	313	THR	-	expression tag	UNP P75682
A	314	ARG	-	expression tag	UNP P75682
A	315	ALA	-	expression tag	UNP P75682
A	316	PRO	-	expression tag	UNP P75682
A	317	PRO	-	expression tag	UNP P75682
A	318	PRO	-	expression tag	UNP P75682
A	319	PRO	-	expression tag	UNP P75682
A	320	PRO	-	expression tag	UNP P75682
A	321	LEU	-	expression tag	UNP P75682
A	322	ARG	-	expression tag	UNP P75682
A	323	SER	-	expression tag	UNP P75682
A	324	GLY	-	expression tag	UNP P75682
A	325	CYS	-	expression tag	UNP P75682
B	-17	MET	-	expression tag	UNP P75682
B	-16	GLY	-	expression tag	UNP P75682
B	-15	SER	-	expression tag	UNP P75682
B	-14	SER	-	expression tag	UNP P75682
B	-13	HIS	-	expression tag	UNP P75682
B	-12	HIS	-	expression tag	UNP P75682
B	-11	HIS	-	expression tag	UNP P75682
B	-10	HIS	-	expression tag	UNP P75682
B	-9	HIS	-	expression tag	UNP P75682
B	-8	HIS	-	expression tag	UNP P75682
B	-7	SER	-	expression tag	UNP P75682
B	-6	ALA	-	expression tag	UNP P75682
B	-5	GLY	-	expression tag	UNP P75682
B	-4	GLU	-	expression tag	UNP P75682
B	-3	ASN	-	expression tag	UNP P75682
B	-2	LEU	-	expression tag	UNP P75682
B	-1	TYR	-	expression tag	UNP P75682
B	0	PHE	-	expression tag	UNP P75682
B	1	GLN	-	expression tag	UNP P75682
B	2	GLY	-	expression tag	UNP P75682
B	310	CYS	-	expression tag	UNP P75682
B	311	GLY	-	expression tag	UNP P75682
B	312	ARG	-	expression tag	UNP P75682
B	313	THR	-	expression tag	UNP P75682
B	314	ARG	-	expression tag	UNP P75682
B	315	ALA	-	expression tag	UNP P75682
B	316	PRO	-	expression tag	UNP P75682

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Chain	Residue	Modelled	Actual	Comment	Reference
B	317	PRO	-	expression tag	UNP P75682
B	318	PRO	-	expression tag	UNP P75682
B	319	PRO	-	expression tag	UNP P75682
B	320	PRO	-	expression tag	UNP P75682
B	321	LEU	-	expression tag	UNP P75682
B	322	ARG	-	expression tag	UNP P75682
B	323	SER	-	expression tag	UNP P75682
B	324	GLY	-	expression tag	UNP P75682
B	325	CYS	-	expression tag	UNP P75682
C	-17	MET	-	expression tag	UNP P75682
C	-16	GLY	-	expression tag	UNP P75682
C	-15	SER	-	expression tag	UNP P75682
C	-14	SER	-	expression tag	UNP P75682
C	-13	HIS	-	expression tag	UNP P75682
C	-12	HIS	-	expression tag	UNP P75682
C	-11	HIS	-	expression tag	UNP P75682
C	-10	HIS	-	expression tag	UNP P75682
C	-9	HIS	-	expression tag	UNP P75682
C	-8	HIS	-	expression tag	UNP P75682
C	-7	SER	-	expression tag	UNP P75682
C	-6	ALA	-	expression tag	UNP P75682
C	-5	GLY	-	expression tag	UNP P75682
C	-4	GLU	-	expression tag	UNP P75682
C	-3	ASN	-	expression tag	UNP P75682
C	-2	LEU	-	expression tag	UNP P75682
C	-1	TYR	-	expression tag	UNP P75682
C	0	PHE	-	expression tag	UNP P75682
C	1	GLN	-	expression tag	UNP P75682
C	2	GLY	-	expression tag	UNP P75682
C	310	CYS	-	expression tag	UNP P75682
C	311	GLY	-	expression tag	UNP P75682
C	312	ARG	-	expression tag	UNP P75682
C	313	THR	-	expression tag	UNP P75682
C	314	ARG	-	expression tag	UNP P75682
C	315	ALA	-	expression tag	UNP P75682
C	316	PRO	-	expression tag	UNP P75682
C	317	PRO	-	expression tag	UNP P75682
C	318	PRO	-	expression tag	UNP P75682
C	319	PRO	-	expression tag	UNP P75682
C	320	PRO	-	expression tag	UNP P75682
C	321	LEU	-	expression tag	UNP P75682
C	322	ARG	-	expression tag	UNP P75682

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Chain	Residue	Modelled	Actual	Comment	Reference
C	323	SER	-	expression tag	UNP P75682
C	324	GLY	-	expression tag	UNP P75682
C	325	CYS	-	expression tag	UNP P75682
D	-17	MET	-	expression tag	UNP P75682
D	-16	GLY	-	expression tag	UNP P75682
D	-15	SER	-	expression tag	UNP P75682
D	-14	SER	-	expression tag	UNP P75682
D	-13	HIS	-	expression tag	UNP P75682
D	-12	HIS	-	expression tag	UNP P75682
D	-11	HIS	-	expression tag	UNP P75682
D	-10	HIS	-	expression tag	UNP P75682
D	-9	HIS	-	expression tag	UNP P75682
D	-8	HIS	-	expression tag	UNP P75682
D	-7	SER	-	expression tag	UNP P75682
D	-6	ALA	-	expression tag	UNP P75682
D	-5	GLY	-	expression tag	UNP P75682
D	-4	GLU	-	expression tag	UNP P75682
D	-3	ASN	-	expression tag	UNP P75682
D	-2	LEU	-	expression tag	UNP P75682
D	-1	TYR	-	expression tag	UNP P75682
D	0	PHE	-	expression tag	UNP P75682
D	1	GLN	-	expression tag	UNP P75682
D	2	GLY	-	expression tag	UNP P75682
D	310	CYS	-	expression tag	UNP P75682
D	311	GLY	-	expression tag	UNP P75682
D	312	ARG	-	expression tag	UNP P75682
D	313	THR	-	expression tag	UNP P75682
D	314	ARG	-	expression tag	UNP P75682
D	315	ALA	-	expression tag	UNP P75682
D	316	PRO	-	expression tag	UNP P75682
D	317	PRO	-	expression tag	UNP P75682
D	318	PRO	-	expression tag	UNP P75682
D	319	PRO	-	expression tag	UNP P75682
D	320	PRO	-	expression tag	UNP P75682
D	321	LEU	-	expression tag	UNP P75682
D	322	ARG	-	expression tag	UNP P75682
D	323	SER	-	expression tag	UNP P75682
D	324	GLY	-	expression tag	UNP P75682
D	325	CYS	-	expression tag	UNP P75682

- Molecule 2 is water.

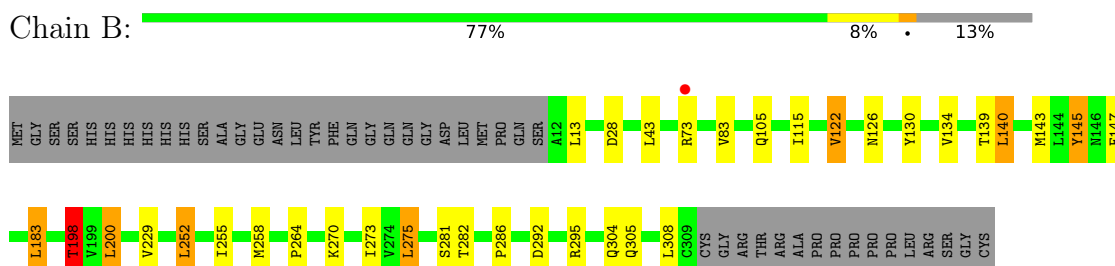| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	104	Total 104	O 104	0	0
2	B	144	Total 144	O 144	0	0
2	C	119	Total 119	O 119	0	0
2	D	97	Total 97	O 97	0	0

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.
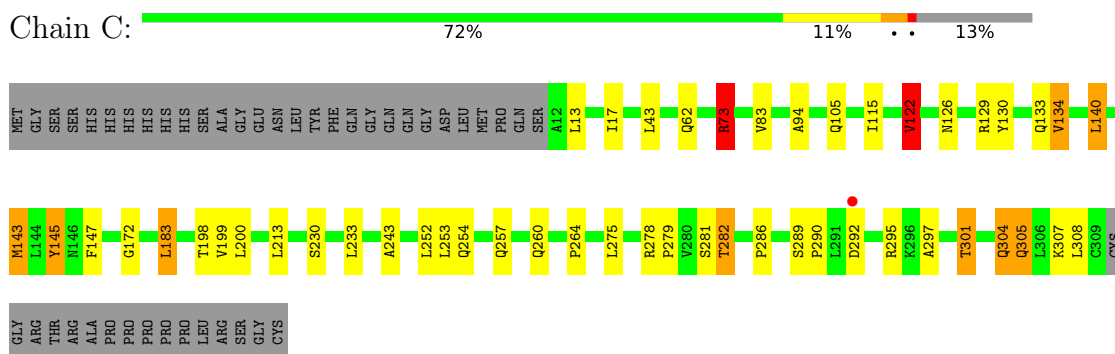
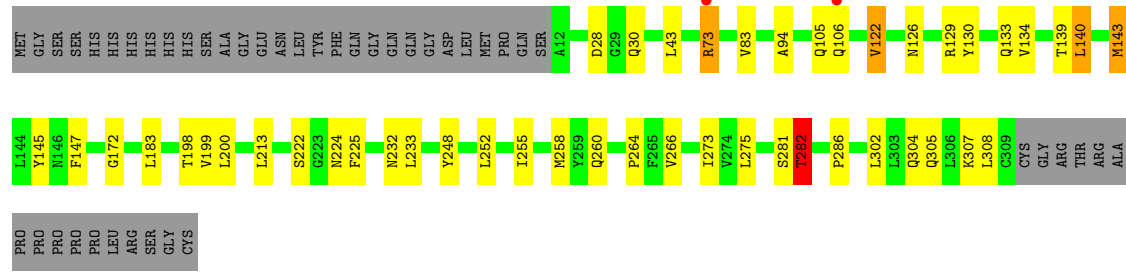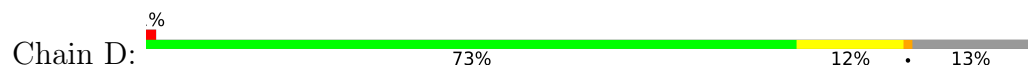• Molecule 1: YAGE

Chain A:

• Molecule 1: YAGE

Chain B:

• Molecule 1: YAGE

Chain C:

• Molecule 1: YAGE

Chain D:

73%   12%   ·   13%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER ALA GLY GLU ASN LEU TYR PHE GLN GLY GLN GLN GLY ASP LEU MET PRO GLN SER A12 D28 G29 Q30 L43 R73 V83 A94 Q105 Q106 V122 N126 R129 Y130 Q133 V134 T139 L140 M143

L144 Y145 N146 F147 G172 L183 T198 V199 L200 L213 S222 G223 N224 F225 N232 L233 Y248 L252 I255 M258 Y259 Q260 P264 F265 V266 I273 V274 L275 S281 I282 P286 L302 L303 Q304 Q305 L306 K307 L308 C309 CYS GLY ARG THR ARG ALA

PRO PRO PRO PRO LEU ARG SER GLY CYS

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	141.69Å 156.49Å 55.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.92 – 2.20 19.92 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.92-2.20) 99.8 (19.92-2.20)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.28 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , 0.232 0.190 , 0.231	Depositor DCC
R_{free} test set	3252 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	18.0	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 25.8	EDS
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9478	wwPDB-VP
Average B, all atoms (Å^2)	5.0	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 37.83 % 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 4.0417e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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	0.76	3/2298 (0.1%)	0.85	8/3133 (0.3%)
1	B	0.81	2/2305 (0.1%)	0.92	11/3141 (0.4%)
1	C	0.74	2/2300 (0.1%)	0.86	7/3135 (0.2%)
1	D	0.74	3/2303 (0.1%)	0.92	6/3139 (0.2%)
All	All	0.76	10/9206 (0.1%)	0.89	32/12548 (0.3%)

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
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	73	ARG	CZ-NH2	7.80	1.43	1.33
1	A	83	VAL	CB-CG1	-7.08	1.38	1.52
1	D	83	VAL	CB-CG2	-6.74	1.38	1.52
1	B	198	THR	CB-CG2	-6.61	1.30	1.52
1	A	83	VAL	CB-CG2	-6.48	1.39	1.52

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	73	ARG	NE-CZ-NH2	-21.42	109.59	120.30
1	B	73	ARG	NE-CZ-NH2	-15.16	112.72	120.30
1	B	73	ARG	NE-CZ-NH1	11.83	126.22	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	282	THR	N-CA-C	8.74	134.61	111.00
1	D	282	THR	N-CA-C	8.50	133.94	111.00

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	281	SER	Peptide
1	A	304	GLN	Peptide
1	B	281	SER	Peptide
1	B	304	GLN	Peptide
1	C	281	SER	Peptide

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	2250	0	2268	26	0
1	B	2257	0	2281	15	0
1	C	2252	0	2274	29	0
1	D	2255	0	2279	24	0
2	A	104	0	0	5	0
2	B	144	0	0	0	0
2	C	119	0	0	3	0
2	D	97	0	0	6	0
All	All	9478	0	9102	81	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.

The worst 5 of 81 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:105:GLN:HE22	1:B:139:THR:H	1.04	0.99
1:C:122:VAL:HG22	1:D:264:PRO:HD3	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:106:GLN:HG3	2:D:2031:HOH:O	1.75	0.84
1:A:122:VAL:HG22	1:B:264:PRO:HD3	1.61	0.83
1:A:188:HIS:CD2	2:A:2069:HOH:O	2.34	0.80

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	296/343 (86%)	289 (98%)	5 (2%)	2 (1%)	22	22
1	B	296/343 (86%)	292 (99%)	4 (1%)	0	100	100
1	C	296/343 (86%)	288 (97%)	6 (2%)	2 (1%)	22	22
1	D	296/343 (86%)	291 (98%)	4 (1%)	1 (0%)	41	46
All	All	1184/1372 (86%)	1160 (98%)	19 (2%)	5 (0%)	34	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	THR
1	A	305	GLN
1	C	282	THR
1	C	305	GLN
1	D	282	THR

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	240/280 (86%)	220 (92%)	20 (8%)	11	11
1	B	241/280 (86%)	229 (95%)	12 (5%)	24	30
1	C	240/280 (86%)	223 (93%)	17 (7%)	14	16
1	D	241/280 (86%)	224 (93%)	17 (7%)	14	16
All	All	962/1120 (86%)	896 (93%)	66 (7%)	15	16

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	183	LEU
1	D	200	LEU
1	D	308	LEU
1	B	145	TYR
1	B	143	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	62	GLN
1	C	260	GLN
1	B	105	GLN
1	C	257	GLN
1	B	102	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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(Å²)	Q<0.9
1	A	298/343 (86%)	-0.28	3 (1%)	82	81	2, 4, 11, 14	0
1	B	298/343 (86%)	-0.56	1 (0%)	94	93	2, 4, 11, 14	0
1	C	298/343 (86%)	-0.41	1 (0%)	94	93	2, 5, 11, 16	0
1	D	298/343 (86%)	-0.26	2 (0%)	87	86	2, 5, 12, 16	0
All	All	1192/1372 (86%)	-0.38	7 (0%)	89	88	2, 4, 11, 16	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	106	GLN	3.4
1	A	73	ARG	3.1
1	A	28	ASP	3.1
1	D	73	ARG	2.4
1	C	292	ASP	2.3

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 monosaccharides 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.