



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:33 AM UTC

PDB ID : 5NV5 / pdb_00005nv5
Title : Enterococcus faecalis FIC protein
Authors : Veyron, S.; Cherfils, J.
Deposited on : 2017-05-03
Resolution : 2.40 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
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

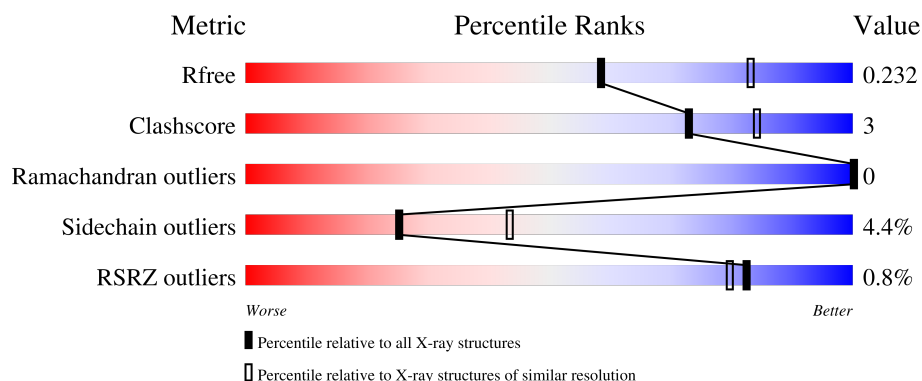
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	207	86% 10% .
1	B	207	% 83% 11% ..
1	C	207	87% 8% ..
1	D	207	% 81% 13% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7315 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 Fic family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	200	Total	C	N	O	S	0	0	0
			1666	1065	281	314	6			
1	B	198	Total	C	N	O	S	0	0	0
			1650	1054	279	312	5			
1	C	201	Total	C	N	O	S	0	0	0
			1676	1071	284	315	6			
1	D	198	Total	C	N	O	S	0	0	0
			1650	1054	279	312	5			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP U6S0Y1
A	2	HIS	-	expression tag	UNP U6S0Y1
A	3	HIS	-	expression tag	UNP U6S0Y1
A	4	HIS	-	expression tag	UNP U6S0Y1
A	5	HIS	-	expression tag	UNP U6S0Y1
A	6	HIS	-	expression tag	UNP U6S0Y1
A	7	HIS	-	expression tag	UNP U6S0Y1
A	32	ASN	LYS	conflict	UNP U6S0Y1
A	35	ARG	GLN	conflict	UNP U6S0Y1
A	45	ILE	VAL	conflict	UNP U6S0Y1
A	47	VAL	ILE	conflict	UNP U6S0Y1
A	142	ARG	GLN	conflict	UNP U6S0Y1
A	150	ASN	ASP	conflict	UNP U6S0Y1
A	205	ASP	GLU	conflict	UNP U6S0Y1
A	206	GLU	ASP	conflict	UNP U6S0Y1
B	1	MET	-	initiating methionine	UNP U6S0Y1
B	2	HIS	-	expression tag	UNP U6S0Y1
B	3	HIS	-	expression tag	UNP U6S0Y1
B	4	HIS	-	expression tag	UNP U6S0Y1
B	5	HIS	-	expression tag	UNP U6S0Y1
B	6	HIS	-	expression tag	UNP U6S0Y1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	7	HIS	-	expression tag	UNP U6S0Y1
B	32	ASN	LYS	conflict	UNP U6S0Y1
B	35	ARG	GLN	conflict	UNP U6S0Y1
B	45	ILE	VAL	conflict	UNP U6S0Y1
B	47	VAL	ILE	conflict	UNP U6S0Y1
B	142	ARG	GLN	conflict	UNP U6S0Y1
B	150	ASN	ASP	conflict	UNP U6S0Y1
B	205	ASP	GLU	conflict	UNP U6S0Y1
B	206	GLU	ASP	conflict	UNP U6S0Y1
C	1	MET	-	initiating methionine	UNP U6S0Y1
C	2	HIS	-	expression tag	UNP U6S0Y1
C	3	HIS	-	expression tag	UNP U6S0Y1
C	4	HIS	-	expression tag	UNP U6S0Y1
C	5	HIS	-	expression tag	UNP U6S0Y1
C	6	HIS	-	expression tag	UNP U6S0Y1
C	7	HIS	-	expression tag	UNP U6S0Y1
C	32	ASN	LYS	conflict	UNP U6S0Y1
C	35	ARG	GLN	conflict	UNP U6S0Y1
C	45	ILE	VAL	conflict	UNP U6S0Y1
C	47	VAL	ILE	conflict	UNP U6S0Y1
C	142	ARG	GLN	conflict	UNP U6S0Y1
C	150	ASN	ASP	conflict	UNP U6S0Y1
C	205	ASP	GLU	conflict	UNP U6S0Y1
C	206	GLU	ASP	conflict	UNP U6S0Y1
D	1	MET	-	initiating methionine	UNP U6S0Y1
D	2	HIS	-	expression tag	UNP U6S0Y1
D	3	HIS	-	expression tag	UNP U6S0Y1
D	4	HIS	-	expression tag	UNP U6S0Y1
D	5	HIS	-	expression tag	UNP U6S0Y1
D	6	HIS	-	expression tag	UNP U6S0Y1
D	7	HIS	-	expression tag	UNP U6S0Y1
D	32	ASN	LYS	conflict	UNP U6S0Y1
D	35	ARG	GLN	conflict	UNP U6S0Y1
D	45	ILE	VAL	conflict	UNP U6S0Y1
D	47	VAL	ILE	conflict	UNP U6S0Y1
D	142	ARG	GLN	conflict	UNP U6S0Y1
D	150	ASN	ASP	conflict	UNP U6S0Y1
D	205	ASP	GLU	conflict	UNP U6S0Y1
D	206	GLU	ASP	conflict	UNP U6S0Y1

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	200	Total 200	O 200	0	0
2	B	148	Total 148	O 148	0	0
2	C	194	Total 194	O 194	0	0
2	D	131	Total 131	O 131	0	0

- Molecule 1: Fic family protein



- | | |
|------|------|
| E206 | L207 |
| MET | HIS |
| | HIS |
| | HIS |
| | HIS |
| | HIS |
| | HIS |
| | MET |
| | LEU |
| | E10 |
| | N11 |
| | K12 |
| | I16 |
| | L21 |
| | N22 |
| | R23 |
| | I46 |
| | Y55 |
| | N58 |
| | E62 |
| | D83 |
| | I64 |
| | Y65 |
| | E66 |
| | F67 |
| | V71 |
| | Q74 |
| | V86 |
| | M87 |
| | H118 |
| | I130 |
| | K137 |
| | D145 |
| | P162 |
| | Y170 |
| | D178 |
| | K179 |
| | I180 |
| | T200 |
| | E201 |
| | Y202 |
| | D205 |

- | |
|------|
| MET |
| H1S |
| H1S |
| H1S |
| H1S |
| H1S |
| H7 |
| R35 |
| L36 |
| Y37 |
| N58 |
| E62 |
| D83 |
| I64 |
| N90 |
| V96 |
| E90 |
| L93 |
| M114 |
| H118 |
| V143 |
| D165 |
| L166 |
| N174 |
| I180 |
| R183 |
| E184 |
| I185 |
| D205 |
| E206 |
| I207 |

- | | |
|------|------|
| D205 | MET |
| E206 | HIS |
| L207 | HIS |
| | HIS |
| | HIS |
| | HIS |
| | HIS |
| | HIS |
| | MET |
| | LEU |
| | E10 |
| | N11 |
| | K12 |
| | L13 |
| | G14 |
| | I15 |
| | E20 |
| | L21 |
| | N22 |
| | E25 |
| | V28 |
| | K34 |
| | R35 |
| | L36 |
| | I42 |
| | I45 |
| | I64 |
| | Y65 |
| | R72 |
| | N75 |
| | I76 |
| | V86 |
| | M87 |
| | L93 |
| | M114 |
| | A117 |
| | H118 |
| | P119 |
| | E122 |
| | I130 |
| | K169 |
| | R183 |
| | V204 |

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	121.54Å 131.00Å 136.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.33 – 2.40 47.33 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.33-2.40) 99.8 (47.33-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.10.2, PHENIX	Depositor
R, R_{free}	0.164 , 0.226 0.173 , 0.232	Depositor DCC
R_{free} test set	2116 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtriage
Anisotropy	0.643	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7315	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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

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	0.89	0/1696	1.39	6/2282 (0.3%)
1	B	0.87	0/1680	1.41	11/2261 (0.5%)
1	C	0.91	1/1707 (0.1%)	1.35	4/2297 (0.2%)
1	D	0.90	1/1680 (0.1%)	1.40	8/2261 (0.4%)
All	All	0.89	2/6763 (0.0%)	1.39	29/9101 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	114	MET	SD-CE	-10.41	1.53	1.79
1	D	114	MET	SD-CE	-9.43	1.55	1.79

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	64	ILE	N-CA-C	6.85	117.70	111.81
1	B	130	ILE	CA-C-N	6.81	129.29	120.44
1	B	130	ILE	C-N-CA	6.81	129.29	120.44
1	A	62	GLU	N-CA-C	6.43	119.10	111.71
1	A	53	LEU	CA-C-N	6.22	128.61	120.28
1	A	53	LEU	C-N-CA	6.22	128.61	120.28
1	D	22	ASN	CA-C-N	5.73	127.89	120.44
1	D	22	ASN	C-N-CA	5.73	127.89	120.44
1	B	178	ASP	CA-CB-CG	5.72	118.32	112.60
1	C	80	ASN	CA-CB-CG	5.72	118.32	112.60
1	A	165	ASP	CA-CB-CG	5.67	118.27	112.60
1	C	90	GLU	CB-CG-CD	5.56	122.06	112.60
1	B	86	VAL	CA-C-N	5.54	127.70	120.28
1	B	86	VAL	C-N-CA	5.54	127.70	120.28
1	D	169	LYS	CA-C-N	5.51	127.61	120.44
1	D	169	LYS	C-N-CA	5.51	127.61	120.44
1	B	45	ILE	CA-C-N	5.51	128.93	121.05
1	B	45	ILE	C-N-CA	5.51	128.93	121.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	ASN	CA-C-N	5.34	127.38	120.44
1	A	22	ASN	C-N-CA	5.34	127.38	120.44
1	C	165	ASP	CA-CB-CG	5.30	117.90	112.60
1	D	130	ILE	CA-C-N	5.29	127.37	120.28
1	D	130	ILE	C-N-CA	5.29	127.37	120.28
1	B	145	ASP	N-CA-C	-5.15	98.93	107.99
1	D	65	TYR	CA-C-N	5.13	127.16	120.28
1	D	65	TYR	C-N-CA	5.13	127.16	120.28
1	B	67	PHE	CA-CB-CG	5.04	118.84	113.80
1	B	23	ARG	CA-C-N	5.00	126.86	120.56
1	B	23	ARG	C-N-CA	5.00	126.86	120.56

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	1666	0	1662	8	0
1	B	1650	0	1642	8	0
1	C	1676	0	1669	9	0
1	D	1650	0	1642	20	0
2	A	200	0	0	1	0
2	B	148	0	0	0	0
2	C	194	0	0	2	0
2	D	131	0	0	0	0
All	All	7315	0	6615	43	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 3.

All (43) 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:D:13:LEU:HD23	1:D:15:ILE:HD11	1.44	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:11:ASN:HD22	1:D:15:ILE:H	1.33	0.76
1:D:10:GLU:O	1:D:10:GLU:HG3	1.88	0.74
1:A:82:ARG:HD2	1:B:162:PRO:O	1.91	0.68
1:D:28:VAL:CG1	1:D:64:ILE:HD11	2.26	0.66
1:B:58:ASN:O	1:B:62:GLU:HB2	1.97	0.65
1:D:25:GLU:HA	1:D:64:ILE:HD13	1.78	0.64
1:D:13:LEU:HD23	1:D:15:ILE:CD1	2.25	0.64
1:D:72:ARG:HH21	1:D:75:ASN:HA	1.62	0.63
1:B:45:ILE:HG21	1:B:55:TYR:CD1	2.35	0.62
1:D:28:VAL:HG13	1:D:64:ILE:HD11	1.81	0.61
1:A:36:LEU:HD11	1:A:45:ILE:HD11	1.82	0.60
1:C:37:TYR:CE2	1:C:183:ARG:HG3	2.37	0.59
1:D:204:VAL:HA	1:D:207:LEU:HD12	1.85	0.58
1:B:23:ARG:HD3	1:B:202:TYR:OH	2.05	0.57
1:A:58:ASN:O	1:A:62:GLU:HB3	2.08	0.54
1:D:36:LEU:HD11	1:D:45:ILE:HD11	1.90	0.53
1:D:11:ASN:ND2	1:D:15:ILE:HB	2.25	0.52
1:A:72:ARG:HD2	1:A:76:ILE:HG12	1.93	0.51
1:D:93:LEU:CD2	1:D:114:MET:HE1	2.41	0.51
1:D:114:MET:HE3	1:D:117:ALA:HB3	1.92	0.50
1:C:93:LEU:CD2	1:C:114:MET:HE1	2.43	0.49
1:B:11:ASN:HD21	1:B:21:LEU:HD21	1.78	0.48
1:D:72:ARG:HG2	1:D:119:PRO:O	2.13	0.47
1:D:93:LEU:HD21	1:D:114:MET:HE1	1.96	0.47
1:C:174:ASN:HB3	2:C:457:HOH:O	2.15	0.46
1:C:93:LEU:HD21	1:C:114:MET:HE1	1.99	0.45
1:D:25:GLU:HA	1:D:64:ILE:CD1	2.46	0.45
1:C:114:MET:HA	1:C:114:MET:HE3	1.99	0.45
1:D:11:ASN:ND2	1:D:15:ILE:H	2.10	0.45
1:D:34:LYS:HE3	1:D:183:ARG:HH22	1.82	0.45
1:A:75:ASN:OD1	1:A:85:PRO:HA	2.18	0.44
1:B:170:TYR:CD1	1:C:166:LEU:HD21	2.52	0.43
1:C:58:ASN:O	1:C:62:GLU:HB3	2.18	0.43
1:D:36:LEU:HG	1:D:42:ILE:HB	2.00	0.43
1:D:76:ILE:HD12	1:D:118:HIS:HB3	2.01	0.42
1:C:143:VAL:HG13	1:C:180:ILE:HG22	2.03	0.41
1:A:58:ASN:HA	1:A:68:ALA:HB1	2.01	0.41
1:A:90:GLU:HG2	2:A:302:HOH:O	2.19	0.41
1:C:205:ASP:HB2	2:C:312:HOH:O	2.21	0.41
1:A:9:LEU:HD23	1:A:9:LEU:HA	1.90	0.40
1:B:137:LYS:HG3	1:B:180:ILE:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:LYS:HB2	1:B:64:ILE:O	2.21	0.40

There are no symmetry-related clashes.

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	198/207 (96%)	195 (98%)	3 (2%)	0	100	100
1	B	196/207 (95%)	189 (96%)	7 (4%)	0	100	100
1	C	199/207 (96%)	197 (99%)	2 (1%)	0	100	100
1	D	196/207 (95%)	190 (97%)	6 (3%)	0	100	100
All	All	789/828 (95%)	771 (98%)	18 (2%)	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	181/188 (96%)	175 (97%)	6 (3%)	33	55
1	B	179/188 (95%)	169 (94%)	10 (6%)	19	33
1	C	182/188 (97%)	174 (96%)	8 (4%)	25	43
1	D	179/188 (95%)	171 (96%)	8 (4%)	24	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	721/752 (96%)	689 (96%)	32 (4%)	25	43

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	ILE
1	A	86	VAL
1	A	118	HIS
1	A	121	ARG
1	A	179	LYS
1	A	205	ASP
1	B	12	LYS
1	B	21	LEU
1	B	45	ILE
1	B	66	GLU
1	B	71	VAL
1	B	74	GLN
1	B	87	MET
1	B	118	HIS
1	B	200	THR
1	B	205	ASP
1	C	7	HIS
1	C	35	ARG
1	C	86	VAL
1	C	90	GLU
1	C	118	HIS
1	C	166	LEU
1	C	185	ILE
1	C	205	ASP
1	D	10	GLU
1	D	13	LEU
1	D	20	GLU
1	D	86	VAL
1	D	87	MET
1	D	118	HIS
1	D	122	GLU
1	D	205	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	18	GLN
1	A	22	ASN
1	A	58	ASN
1	A	74	GLN
1	A	203	ASN
1	B	11	ASN
1	B	17	ASN
1	B	18	GLN
1	B	22	ASN
1	B	203	ASN
1	C	7	HIS
1	C	203	ASN
1	D	11	ASN
1	D	22	ASN
1	D	58	ASN
1	D	74	GLN
1	D	203	ASN

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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	200/207 (96%)	-0.58	1 (0%) 87 85	27, 43, 64, 89	0
1	B	198/207 (95%)	-0.35	2 (1%) 79 76	33, 49, 86, 106	0
1	C	201/207 (97%)	-0.56	1 (0%) 87 85	27, 43, 66, 82	0
1	D	198/207 (95%)	-0.29	2 (1%) 79 76	33, 52, 91, 110	0
All	All	797/828 (96%)	-0.45	6 (0%) 82 80	27, 46, 79, 110	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	11	ASN	3.7
1	A	9	LEU	3.3
1	D	10	GLU	3.0
1	B	16	ILE	2.7
1	B	10	GLU	2.2
1	C	7	HIS	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.