



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2016 – 11:22 AM EDT

PDB ID : 5DCQ  
Title : Crystal structure of bacterial adhesin, FNE from Streptococcus equi spp. equi.  
Authors : Tiouajni, M.; Graille, M.; van Tilbeurgh, H.  
Deposited on : 2015-08-24  
Resolution : 1.83 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027790  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027790

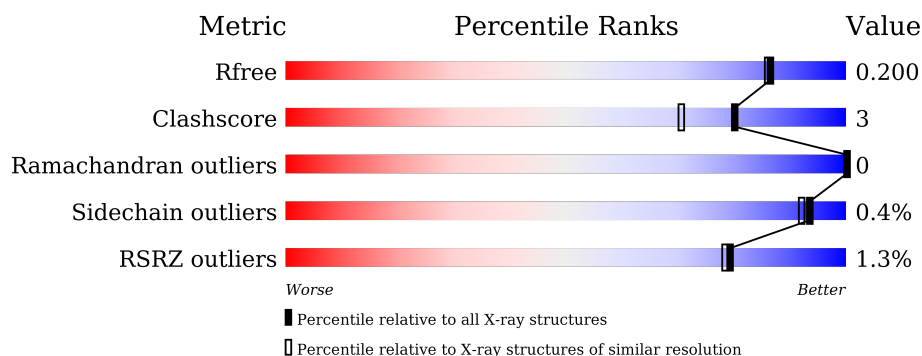
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.83 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))
$R_{free}$	91344	2634 (1.86-1.82)
Clashscore	102246	2862 (1.86-1.82)
Ramachandran outliers	100387	2831 (1.86-1.82)
Sidechain outliers	100360	2832 (1.86-1.82)
RSRZ outliers	91569	2639 (1.86-1.82)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	170	<div> <div>89%</div> <div>8%</div> </div>
1	B	170	<div> <div>83%</div> <div>8%</div> <div>9%</div> </div>
1	C	170	<div> <div>87%</div> <div>6%</div> <div>6%</div> </div>
2	D	271	<div> <div>70%</div> <div>27%</div> </div>
2	E	271	<div> <div>69%</div> <div>5%</div> <div>26%</div> </div>
2	F	271	<div> <div>66%</div> <div>8%</div> <div>27%</div> </div>

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	FMT	B	201	-	-	-	X
3	FMT	E	302	-	-	-	X
3	FMT	F	301	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9718 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 artificial repeat proteins (alphaREP3).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	3	0
			1227	766	218	240	3			
1	B	155	Total	C	N	O	S	0	1	0
			1192	742	212	235	3			
1	C	159	Total	C	N	O	S	0	1	0
			1235	769	223	240	3			

- Molecule 2 is a protein called Fibronectin-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	199	Total	C	N	O	S	0	0	0
			1635	1053	259	320	3			
2	E	200	Total	C	N	O	S	0	0	0
			1644	1059	261	321	3			
2	F	199	Total	C	N	O	S	0	2	0
			1647	1059	261	324	3			

There are 21 discrepancies between the modelled and reference sequences:

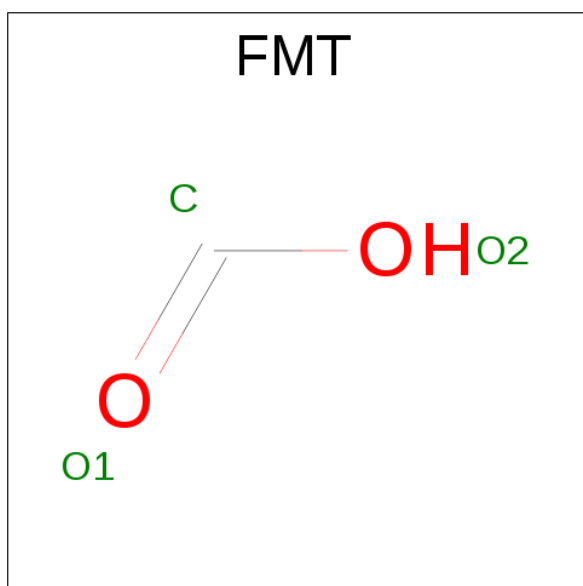
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	ALA	-	expression tag	UNP Q93ED6
D	266	HIS	-	expression tag	UNP Q93ED6
D	267	HIS	-	expression tag	UNP Q93ED6
D	268	HIS	-	expression tag	UNP Q93ED6
D	269	HIS	-	expression tag	UNP Q93ED6
D	270	HIS	-	expression tag	UNP Q93ED6
D	271	HIS	-	expression tag	UNP Q93ED6
E	1	ALA	-	expression tag	UNP Q93ED6
E	266	HIS	-	expression tag	UNP Q93ED6
E	267	HIS	-	expression tag	UNP Q93ED6
E	268	HIS	-	expression tag	UNP Q93ED6
E	269	HIS	-	expression tag	UNP Q93ED6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	270	HIS	-	expression tag	UNP Q93ED6
E	271	HIS	-	expression tag	UNP Q93ED6
F	1	ALA	-	expression tag	UNP Q93ED6
F	266	HIS	-	expression tag	UNP Q93ED6
F	267	HIS	-	expression tag	UNP Q93ED6
F	268	HIS	-	expression tag	UNP Q93ED6
F	269	HIS	-	expression tag	UNP Q93ED6
F	270	HIS	-	expression tag	UNP Q93ED6
F	271	HIS	-	expression tag	UNP Q93ED6

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 3 1 2	0	0
3	B	1	Total C O 3 1 2	0	0
3	C	1	Total C O 3 1 2	0	0
3	C	1	Total C O 3 1 2	0	0
3	C	1	Total C O 3 1 2	0	0
3	C	1	Total C O 3 1 2	0	0
3	D	1	Total C O 3 1 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	O	0	0
			3	1	2		
3	E	1	Total	C	O	0	0
			3	1	2		
3	E	1	Total	C	O	0	0
			3	1	2		
3	F	1	Total	C	O	0	0
			3	1	2		
3	F	1	Total	C	O	0	0
			3	1	2		


- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	156	Total	O	0	0
			156	156		
4	B	164	Total	O	0	0
			164	164		
4	C	161	Total	O	0	0
			161	161		
4	D	185	Total	O	0	0
			185	185		
4	E	198	Total	O	0	0
			198	198		
4	F	238	Total	O	0	0
			238	238		

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


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: artificial repeat proteins (alphaREP3)

Chain A: 




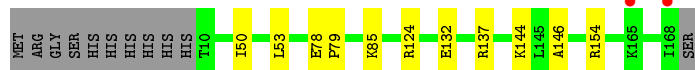
- Molecule 1: artificial repeat proteins (alphaREP3)

Chain B: 



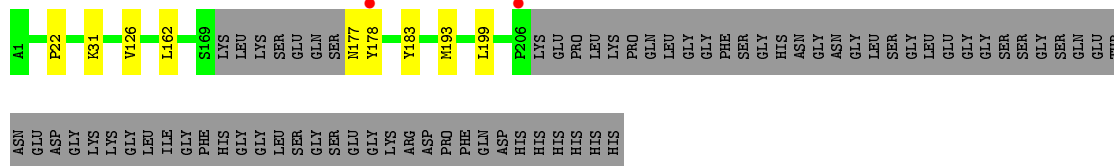
- Molecule 1: artificial repeat proteins (alphaREP3)

Chain C: 



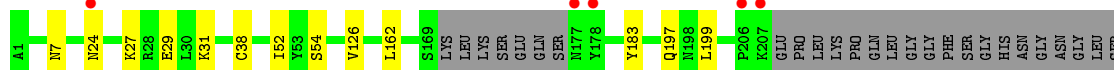
- Molecule 2: Fibronectin-binding protein

Chain D: 



- Molecule 2: Fibronectin-binding protein

Chain E: 



GLY	LEU	GLU	GLY	GLY	SER	SER	GLY	SER	GLN	GLU	THR	ASN	GLU	ASP	GLY	LYS	GLY	LEU	ILE	GLY	PHE	HIS	GLY	GLY	LEU	SER	GLY	SER	SER	GLU	GLY	LYS	ARG	ASP	PRO	PHE	GLN	ASP	HIS	HIS	HIS	HIS	HIS	HIS
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● Molecule 2: Fibronectin-binding protein



A1	M7	R11	C38	Q48	S54	Y75	I78	K87	K157	F161	K165	D168	S169	LYS	LEU	LEU	LYS	SER	GLU	GLN	SER	N177	Y178	Y183	H190	K194	Q197	M198	L199	P206	LYS	GLU	PRO	LEU	LYS	PRO	GLN	LEU	GLY	PHE	SER	GLY
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HIS	ASN	GLY	ASN	LEU	SER	GLY	LEU	GLU	GLY	GLY	SER	THR	ASN	GLU	ASP	GLY	LYS	LYS	GLY	LEU	ILE	GLY	PHE	HIS	GLY	GLY	LEU	SER	GLY	SER	GLU	GLY	LYS	ARG	ASP	PRO	PHE	GLN	ASP	HIS	HIS	HIS	HIS	HIS
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.69Å 113.69Å 152.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.83 45.20 – 1.83	Depositor EDS
% Data completeness (in resolution range)	97.8 (50.00-1.83) 97.8 (45.20-1.83)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.167 , 0.203 0.163 , 0.200	Depositor DCC
$R_{free}$ test set	4733 reflections (5.18%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.8	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.045 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9718	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.50% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMT

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	0.36	0/1240	0.47	0/1667
1	B	0.36	0/1204	0.47	0/1621
1	C	0.33	0/1247	0.44	0/1677
2	D	0.32	0/1681	0.47	0/2279
2	E	0.35	0/1690	0.50	0/2290
2	F	0.34	0/1693	0.48	0/2295
All	All	0.34	0/8755	0.47	0/11829

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	1227	0	1256	5	0
1	B	1192	0	1218	13	0
1	C	1235	0	1271	9	0
2	D	1635	0	1556	6	0
2	E	1644	0	1569	8	0
2	F	1647	0	1564	17	0
3	A	3	0	1	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	1	0	0
3	C	12	0	4	0	0
3	D	3	0	1	0	0
3	E	9	0	3	1	0
3	F	6	0	2	1	0
4	A	156	0	0	4	3
4	B	164	0	0	7	0
4	C	161	0	0	6	1
4	D	185	0	0	2	1
4	E	198	0	0	5	0
4	F	238	0	0	11	1
All	All	9718	0	8446	58	3

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 (58) 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:F:169:SER:OG	4:F:401:HOH:O	1.88	0.91
1:B:118:GLU:OE2	4:B:301:HOH:O	1.92	0.86
2:E:54:SER:O	4:E:401:HOH:O	1.93	0.86
2:E:31:LYS:NZ	4:E:402:HOH:O	2.19	0.74
1:C:146:ALA:O	1:C:154:ARG:NH1	2.22	0.73
1:A:109:GLU:OE1	4:A:301:HOH:O	2.11	0.68
2:E:31:LYS:HD2	4:E:562:HOH:O	1.93	0.68
2:F:168:ASP:OD2	4:F:403:HOH:O	2.11	0.68
1:C:132:GLU:OE1	4:C:301:HOH:O	2.12	0.67
1:C:85:LYS:NZ	4:C:303:HOH:O	2.22	0.67
2:F:54:SER:O	4:F:404:HOH:O	2.13	0.67
1:B:25:ASP:OD2	4:B:303:HOH:O	2.12	0.66
2:F:7:ASN:ND2	4:F:410:HOH:O	2.32	0.63
1:B:43:GLU:CD	1:B:43:GLU:H	2.04	0.61
1:A:109:GLU:OE2	4:A:302:HOH:O	2.15	0.60
1:B:139:ARG:NH2	4:B:311:HOH:O	2.34	0.60
1:B:116:LYS:NZ	4:B:304:HOH:O	2.15	0.59
1:C:78:GLU:OE1	4:C:302:HOH:O	2.17	0.57
1:B:97:LYS:NZ	4:B:305:HOH:O	2.15	0.56
2:F:177:ASN:OD1	2:F:178:TYR:N	2.38	0.56
1:B:47:GLU:OE2	2:F:194:LYS:NZ	2.39	0.54
2:F:48:GLN:OE1	4:F:405:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:ARG:HB3	1:B:152:PHE:CE2	2.43	0.53
1:A:51:LYS:HG2	4:A:352:HOH:O	2.09	0.52
3:E:301:FMT:O1	4:E:403:HOH:O	2.19	0.52
2:F:1:ALA:N	4:F:402:HOH:O	2.06	0.52
1:C:144:LYS:HE2	4:C:445:HOH:O	2.10	0.52
2:F:161:PHE:CE1	2:F:165:LYS:HE2	2.44	0.51
2:F:183:TYR:HB2	2:F:199:LEU:HB2	1.95	0.49
2:E:38:CYS:SG	2:E:197:GLN:HG2	2.54	0.47
2:F:87:LYS:NZ	4:F:409:HOH:O	2.31	0.47
2:D:183:TYR:HB2	2:D:199:LEU:HB2	1.96	0.46
1:B:14[A]:LYS:HB3	1:B:14[A]:LYS:HE3	1.59	0.46
2:F:157:LYS:HG3	4:F:448:HOH:O	2.17	0.45
1:C:137:ARG:NH2	4:C:320:HOH:O	2.50	0.44
1:B:139:ARG:NH1	4:B:302:HOH:O	2.11	0.44
1:C:124[B]:ARG:NH2	4:C:319:HOH:O	2.49	0.43
2:F:11:ARG:HE	2:F:11:ARG:HB3	1.62	0.43
2:D:193:MET:HG3	4:D:481:HOH:O	2.18	0.43
1:A:47:GLU:HG3	4:A:453:HOH:O	2.18	0.43
2:F:38:CYS:SG	2:F:197:GLN:OE1	2.77	0.43
2:D:177:ASN:HB2	2:D:178:TYR:H	1.66	0.43
2:F:190:HIS:CE1	4:F:504:HOH:O	2.73	0.42
1:B:154:ARG:NH2	4:B:315:HOH:O	2.40	0.42
3:F:301:FMT:O1	4:F:406:HOH:O	2.21	0.42
1:B:50:ILE:O	1:B:53:LEU:HB2	2.20	0.41
1:C:78:GLU:HB3	1:C:79:PRO:HD3	2.02	0.41
2:E:7:ASN:ND2	4:E:416:HOH:O	2.52	0.41
2:F:177:ASN:ND2	4:F:423:HOH:O	2.54	0.41
2:E:183:TYR:HB2	2:E:199:LEU:HB2	2.02	0.41
2:D:126:VAL:HG12	2:D:162:LEU:HD12	2.01	0.41
2:E:126:VAL:HG12	2:E:162:LEU:HD12	2.02	0.41
2:E:27:LYS:HB2	2:E:29:GLU:HG3	2.02	0.41
1:A:154:ARG:HH11	1:B:12:PRO:HB3	1.85	0.41
2:D:22:PRO:HD2	4:D:468:HOH:O	2.21	0.41
2:F:75:TYR:H	2:F:78:ILE:HG22	1.86	0.41
2:D:31:LYS:HB2	2:D:31:LYS:HE2	1.69	0.40
1:C:50:ILE:O	1:C:53:LEU:HB2	2.22	0.40

All (3) 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:425:HOH:O	4:D:571:HOH:O[5_554]	1.95	0.25
4:A:430:HOH:O	4:C:318:HOH:O[4_664]	2.10	0.10
4:A:318:HOH:O	4:F:504:HOH:O[4_664]	2.16	0.04

## 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	158/170 (93%)	157 (99%)	1 (1%)	0	100	100
1	B	154/170 (91%)	154 (100%)	0	0	100	100
1	C	159/170 (94%)	159 (100%)	0	0	100	100
2	D	195/271 (72%)	193 (99%)	2 (1%)	0	100	100
2	E	196/271 (72%)	193 (98%)	3 (2%)	0	100	100
2	F	197/271 (73%)	193 (98%)	4 (2%)	0	100	100
All	All	1059/1323 (80%)	1049 (99%)	10 (1%)	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	125/134 (93%)	121 (97%)	4 (3%)	46	26
1	B	121/134 (90%)	121 (100%)	0	100	100
1	C	126/134 (94%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	180/236 (76%)	180 (100%)	0	100	100
2	E	181/236 (77%)	179 (99%)	2 (1%)	80	72
2	F	182/236 (77%)	182 (100%)	0	100	100
All	All	915/1110 (82%)	909 (99%)	6 (1%)	93	84

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54[A]	LYS
1	A	54[B]	LYS
1	A	113[A]	LYS
1	A	113[B]	LYS
2	E	24	ASN
2	E	52	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	FMT	A	201	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	B	201	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	C	201	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	C	202	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	C	203	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	C	204	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	D	301	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	E	301	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	E	302	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	E	303	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	F	301	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	F	302	-	0,2,2	0.00	-	0,1,1	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FMT	A	201	-	-	0/0/0/0	0/0/0/0
3	FMT	B	201	-	-	0/0/0/0	0/0/0/0
3	FMT	C	201	-	-	0/0/0/0	0/0/0/0
3	FMT	C	202	-	-	0/0/0/0	0/0/0/0
3	FMT	C	203	-	-	0/0/0/0	0/0/0/0
3	FMT	C	204	-	-	0/0/0/0	0/0/0/0
3	FMT	D	301	-	-	0/0/0/0	0/0/0/0
3	FMT	E	301	-	-	0/0/0/0	0/0/0/0
3	FMT	E	302	-	-	0/0/0/0	0/0/0/0
3	FMT	E	303	-	-	0/0/0/0	0/0/0/0
3	FMT	F	301	-	-	0/0/0/0	0/0/0/0
3	FMT	F	302	-	-	0/0/0/0	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	301	FMT	1	0
3	F	301	FMT	1	0

## 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	157/170 (92%)	-0.54	0 100 100	14, 23, 47, 67	0
1	B	155/170 (91%)	-0.45	2 (1%) 79 78	14, 25, 51, 71	0
1	C	159/170 (93%)	-0.46	2 (1%) 79 78	14, 25, 51, 66	0
2	D	199/271 (73%)	-0.43	2 (1%) 84 83	17, 30, 52, 73	0
2	E	200/271 (73%)	-0.49	5 (2%) 61 57	13, 26, 52, 68	0
2	F	199/271 (73%)	-0.55	3 (1%) 76 74	13, 24, 44, 63	0
All	All	1069/1323 (80%)	-0.49	14 (1%) 79 78	13, 26, 50, 73	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	178	TYR	4.3
1	C	165	LYS	4.0
2	F	178	TYR	3.9
1	B	162	GLU	3.5
1	C	168	ILE	2.8
2	E	206	PRO	2.6
2	E	177	ASN	2.6
2	E	178	TYR	2.5
2	F	177	ASN	2.5
2	F	206	PRO	2.4
2	E	24	ASN	2.3
2	D	206	PRO	2.2
2	E	207	LYS	2.1
1	B	163	THR	2.0

### 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 [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	FMT	E	302	3/3	0.78	0.18	8.75	62,62,64,66	0
3	FMT	B	201	3/3	0.81	0.21	6.89	53,53,62,67	0
3	FMT	F	301	3/3	0.84	0.21	2.79	53,53,59,60	0
3	FMT	E	301	3/3	0.94	0.10	1.11	27,27,40,47	0
3	FMT	C	202	3/3	0.82	0.11	-0.12	51,51,56,58	0
3	FMT	C	201	3/3	0.97	0.05	-1.33	28,28,41,42	0
3	FMT	D	301	3/3	0.85	0.14	-	71,71,73,73	0
3	FMT	A	201	3/3	0.92	0.17	-	51,51,52,56	0
3	FMT	F	302	3/3	0.83	0.14	-	61,61,63,64	0
3	FMT	E	303	3/3	0.96	0.06	-	44,44,48,50	0
3	FMT	C	203	3/3	0.88	0.13	-	30,30,44,44	0
3	FMT	C	204	3/3	0.63	0.24	-	54,54,58,59	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.