



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:06 AM UTC

PDB ID : 7B8S / pdb_00007b8s
Title : Fusidic acid bound structure of bacterial efflux pump.
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Deposited on : 2020-12-13
Resolution : 2.30 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

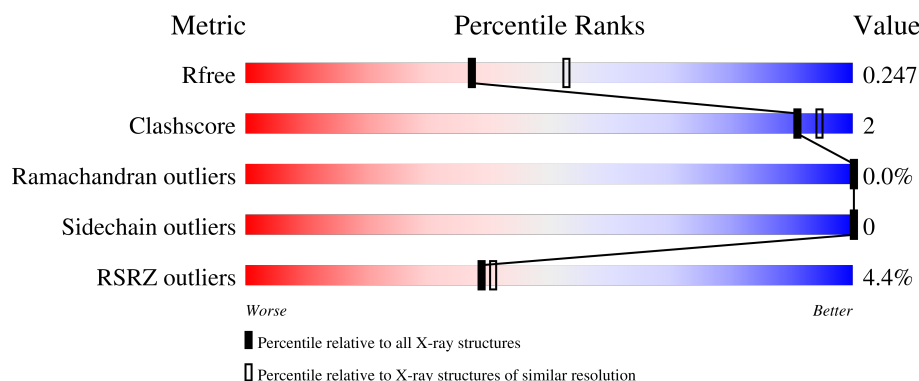
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	613	5% 91% 5%
1	B	613	2% 90% 6%
1	C	613	6% 92% 5%
2	D	169	2% 89% 7%
2	E	169	3% 87% 5% 8%

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Mol	Chain	Length	Quality of chain
2	F	169	6% 84% 8% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17656 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 Multidrug efflux pump subunit AcrB, Multidrug efflux pump subunit AcrB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	587	Total	C	N	O	S	0	0	0
			4465	2805	755	883	22			
1	B	576	Total	C	N	O	S	0	0	0
			4390	2756	744	868	22			
1	C	589	Total	C	N	O	S	0	0	0
			4487	2817	761	887	22			

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	38	SER	-	expression tag	UNP P31224
A	552	GLY	-	linker	UNP P31224
A	553	GLY	-	linker	UNP P31224
A	554	SER	-	linker	UNP P31224
A	555	GLY	-	linker	UNP P31224
A	556	GLY	-	linker	UNP P31224
A	557	SER	-	linker	UNP P31224
A	558	GLY	-	linker	UNP P31224
A	559	GLY	-	linker	UNP P31224
A	560	SER	-	linker	UNP P31224
A	870	SER	-	expression tag	UNP P31224
A	871	ALA	-	expression tag	UNP P31224
A	872	LEU	-	expression tag	UNP P31224
B	38	SER	-	expression tag	UNP P31224
B	552	GLY	-	linker	UNP P31224
B	553	GLY	-	linker	UNP P31224
B	554	SER	-	linker	UNP P31224
B	555	GLY	-	linker	UNP P31224
B	556	GLY	-	linker	UNP P31224
B	557	SER	-	linker	UNP P31224
B	558	GLY	-	linker	UNP P31224
B	559	GLY	-	linker	UNP P31224

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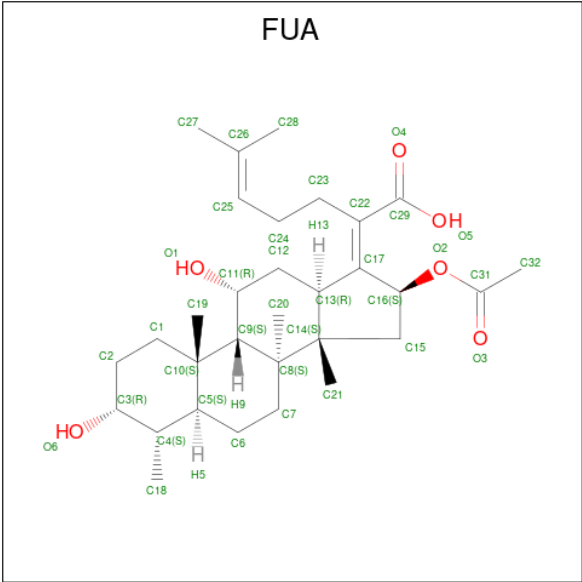
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Chain	Residue	Modelled	Actual	Comment	Reference
B	560	SER	-	linker	UNP P31224
B	870	SER	-	expression tag	UNP P31224
B	871	ALA	-	expression tag	UNP P31224
B	872	LEU	-	expression tag	UNP P31224
C	38	SER	-	expression tag	UNP P31224
C	552	GLY	-	linker	UNP P31224
C	553	GLY	-	linker	UNP P31224
C	554	SER	-	linker	UNP P31224
C	555	GLY	-	linker	UNP P31224
C	556	GLY	-	linker	UNP P31224
C	557	SER	-	linker	UNP P31224
C	558	GLY	-	linker	UNP P31224
C	559	GLY	-	linker	UNP P31224
C	560	SER	-	linker	UNP P31224
C	870	SER	-	expression tag	UNP P31224
C	871	ALA	-	expression tag	UNP P31224
C	872	LEU	-	expression tag	UNP P31224

- Molecule 2 is a protein called DARPin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	157	Total	C	N	O	S	0	0	0
			1197	754	213	229	1			
2	E	155	Total	C	N	O	S	0	0	0
			1173	739	205	228	1			
2	F	155	Total	C	N	O	S	0	0	0
			1173	739	205	228	1			

- Molecule 3 is FUSIDIC ACID (CCD ID: FUA) (formula: C₃₁H₄₈O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	C O	0	0
			37	31 6		

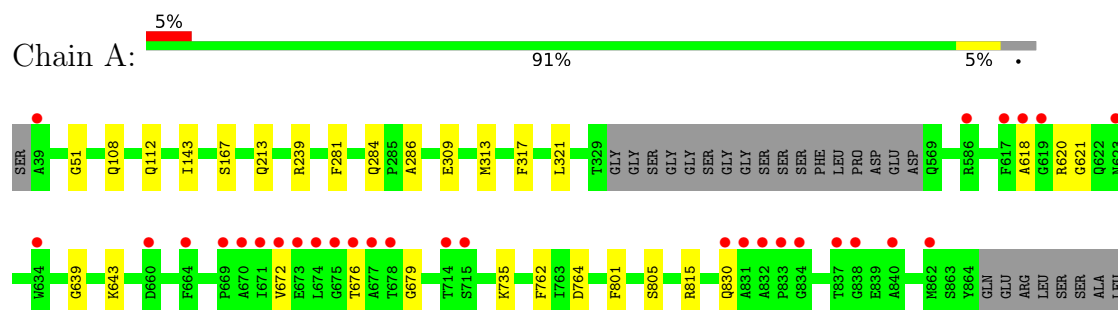
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	201	Total	O	0	0
			201	201		
4	B	246	Total	O	0	0
			246	246		
4	C	215	Total	O	0	0
			215	215		
4	D	22	Total	O	0	0
			22	22		
4	E	34	Total	O	0	0
			34	34		
4	F	16	Total	O	0	0
			16	16		

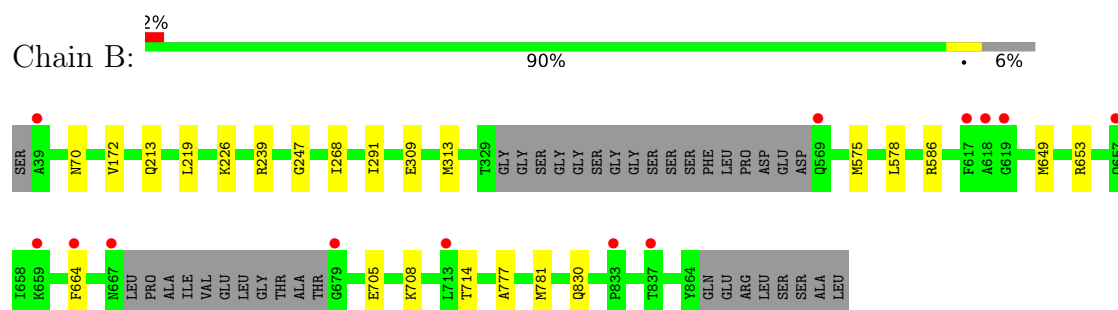
3 Residue-property plots [i](#)

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.

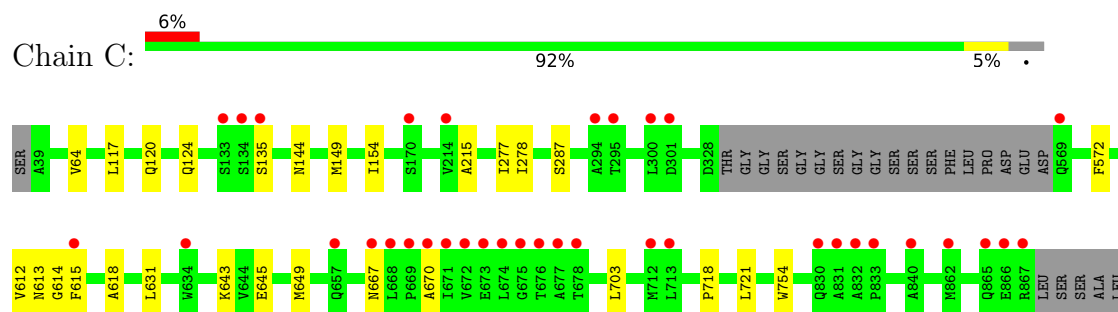
- Molecule 1: Multidrug efflux pump subunit AcrB, Multidrug efflux pump subunit AcrB



- Molecule 1: Multidrug efflux pump subunit AcrB, Multidrug efflux pump subunit AcrB

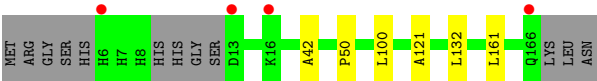


- Molecule 1: Multidrug efflux pump subunit AcrB, Multidrug efflux pump subunit AcrB

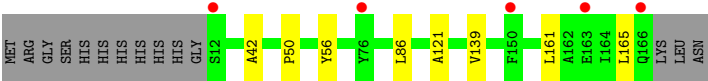
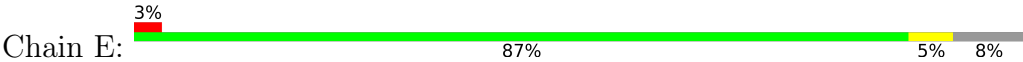


- Molecule 2: DARPin

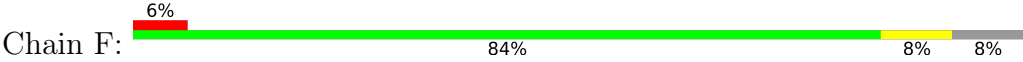




● Molecule 2: DARPin



● Molecule 2: DARPin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.71Å 145.24Å 175.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.83 – 2.30 49.83 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.83-2.30) 99.6 (49.83-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.201 , 0.247 0.203 , 0.247	Depositor DCC
R_{free} test set	6126 reflections (3.71%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.333	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 27.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17656	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 2.78% 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: FUA

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	0.10	0/4542	0.28	0/6158
1	B	0.11	0/4465	0.28	0/6049
1	C	0.10	0/4564	0.29	0/6186
2	D	0.08	0/1218	0.24	0/1655
2	E	0.09	0/1192	0.25	0/1621
2	F	0.09	0/1192	0.23	0/1621
All	All	0.10	0/17173	0.27	0/23290

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 [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	4465	0	4408	16	0
1	B	4390	0	4325	13	0
1	C	4487	0	4428	15	0
2	D	1197	0	1171	3	0
2	E	1173	0	1156	5	0
2	F	1173	0	1156	7	0
3	C	37	0	47	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	201	0	0	0	0
4	B	246	0	0	0	0
4	C	215	0	0	0	0
4	D	22	0	0	0	0
4	E	34	0	0	0	0
4	F	16	0	0	0	0
All	All	17656	0	16691	58	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 2.

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)
1:C:144:ASN:ND2	1:C:149:MET:SD	2.73	0.61
1:A:317:PHE:CD2	1:A:321:LEU:HD23	2.41	0.56
2:F:27:ASP:OD2	2:F:61:GLU:HG3	2.06	0.56
1:C:618:ALA:HB1	1:C:721:LEU:HD21	1.88	0.53
1:B:247:GLY:HA2	1:B:268:ILE:HD13	1.91	0.53
1:A:618:ALA:HB1	1:A:815:ARG:HH12	1.75	0.52
2:D:100:LEU:HD11	2:D:132:LEU:HD23	1.90	0.52
1:A:309:GLU:HG3	1:A:313:MET:HE3	1.91	0.51
1:A:801:PHE:O	1:A:805:SER:OG	2.26	0.51
2:E:121:ALA:HB1	2:E:161:LEU:HD21	1.93	0.50
2:F:67:LEU:HD11	2:F:99:LEU:HD23	1.92	0.50
2:D:42:ALA:O	2:D:50:PRO:HD3	2.13	0.49
2:D:121:ALA:HB1	2:D:161:LEU:HD21	1.94	0.49
1:A:281:PHE:O	1:A:284:GLN:HG2	2.13	0.48
1:B:578:LEU:CD2	1:B:586:ARG:HG2	2.43	0.48
1:C:612:VAL:HG11	1:C:615:PHE:CE2	2.49	0.48
1:B:219:LEU:HD23	1:C:754:TRP:CZ3	2.49	0.48
1:B:714:THR:HG23	1:B:830:GLN:HG3	1.95	0.48
1:B:649:MET:O	1:B:653:ARG:HG3	2.13	0.47
1:C:64:VAL:HG11	1:C:117:LEU:HB3	1.97	0.46
2:F:41:ASN:HD21	2:F:72:ASP:HB2	1.80	0.46
1:C:278:ILE:HB	1:C:613:ASN:HB3	1.97	0.46
2:F:121:ALA:HB1	2:F:161:LEU:HD21	1.97	0.46
3:C:901:FUA:H212	3:C:901:FUA:H72	1.82	0.45
2:E:139:VAL:HG23	2:E:165:LEU:CD2	2.47	0.45
1:C:645:GLU:HG3	1:C:649:MET:HE2	1.99	0.45
1:A:108:GLN:O	1:A:112:GLN:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:GLU:HG3	1:B:313:MET:HE3	1.99	0.44
1:C:703:LEU:HD11	1:C:718:PRO:HG3	2.00	0.44
1:B:213:GLN:OE1	1:B:239:ARG:HG2	2.18	0.44
1:A:620:ARG:HG2	1:A:621:GLY:N	2.33	0.43
1:A:672:VAL:O	1:A:676:THR:HG23	2.18	0.43
1:A:735:LYS:HD2	1:A:735:LYS:HA	1.89	0.43
1:B:172:VAL:HG13	1:B:291:ILE:HG23	2.00	0.43
1:B:705:GLU:OE1	1:B:708:LYS:HD2	2.18	0.42
1:C:667:ASN:HD21	1:C:670:ALA:HB2	1.84	0.42
1:C:572:PHE:HE2	1:C:631:LEU:HD21	1.83	0.42
2:E:42:ALA:O	2:E:50:PRO:HD3	2.20	0.42
1:A:639:GLY:O	1:A:643:LYS:NZ	2.47	0.42
1:A:143:ILE:HG22	1:A:286:ALA:HB2	2.02	0.42
1:C:277:ILE:HD13	1:C:614:GLY:HA3	2.00	0.42
1:A:167:SER:HB3	1:B:70:ASN:HB3	2.02	0.41
1:A:213:GLN:OE1	1:A:239:ARG:HG2	2.20	0.41
1:A:679:GLY:HA2	1:A:830:GLN:HA	2.02	0.41
1:A:762:PHE:CZ	1:A:764:ASP:HB2	2.55	0.41
1:B:575:MET:HE3	1:B:664:PHE:CD2	2.55	0.41
2:F:16:LYS:HE3	2:F:20:GLU:OE1	2.21	0.41
1:C:154:ILE:HG22	1:C:287:SER:HB3	2.03	0.41
2:F:44:ASP:OD2	2:F:48:TRP:HB2	2.19	0.41
1:C:120:GLN:HG3	1:C:124:GLN:OE1	2.21	0.41
3:C:901:FUA:H12	3:C:901:FUA:O1	2.21	0.41
1:C:643:LYS:HA	1:C:643:LYS:HD3	1.90	0.40
1:B:226:LYS:HE3	1:B:226:LYS:HB2	1.83	0.40
1:B:777:ALA:O	1:B:781:MET:HG2	2.21	0.40
2:E:139:VAL:HG23	2:E:165:LEU:HD23	2.02	0.40
1:A:51:GLY:C	1:C:215:ALA:HB1	2.46	0.40
2:E:56:TYR:HB2	2:E:86:LEU:HD13	2.03	0.40
2:F:68:LYS:HB2	2:F:68:LYS:HE3	1.88	0.40

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	583/613 (95%)	568 (97%)	15 (3%)	0	100	100
1	B	570/613 (93%)	555 (97%)	15 (3%)	0	100	100
1	C	585/613 (95%)	565 (97%)	19 (3%)	1 (0%)	43	55
2	D	153/169 (90%)	149 (97%)	4 (3%)	0	100	100
2	E	153/169 (90%)	149 (97%)	4 (3%)	0	100	100
2	F	153/169 (90%)	150 (98%)	3 (2%)	0	100	100
All	All	2197/2346 (94%)	2136 (97%)	60 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	135	SER

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	476/495 (96%)	476 (100%)	0	100	100
1	B	468/495 (94%)	468 (100%)	0	100	100
1	C	478/495 (97%)	478 (100%)	0	100	100
2	D	122/132 (92%)	122 (100%)	0	100	100
2	E	120/132 (91%)	120 (100%)	0	100	100
2	F	120/132 (91%)	120 (100%)	0	100	100
All	All	1784/1881 (95%)	1784 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	A	194	ASN
1	A	830	GLN
1	B	58	GLN
1	B	70	ASN
1	B	176	GLN
1	B	237	GLN
1	B	697	GLN
1	C	81	ASN
1	C	89	GLN
1	C	120	GLN
1	C	605	ASN
1	C	642	ASN
1	C	747	ASN
2	D	122	ASN
2	E	92	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 ⓘ

1 ligand is 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	FUA	C	901	-	39,40,40	1.62	2 (5%)	50,64,64	1.06	3 (6%)

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	FUA	C	901	-	-	7/16/92/92	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	901	FUA	C29-C22	-9.49	1.34	1.47
3	C	901	FUA	O5-C29	-2.49	1.23	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	901	FUA	O2-C16-C17	2.22	114.81	108.30
3	C	901	FUA	C7-C6-C5	-2.04	109.67	113.14
3	C	901	FUA	C1-C10-C9	2.02	113.69	109.16

There are no chirality outliers.

All (7) torsion outliers are listed below:

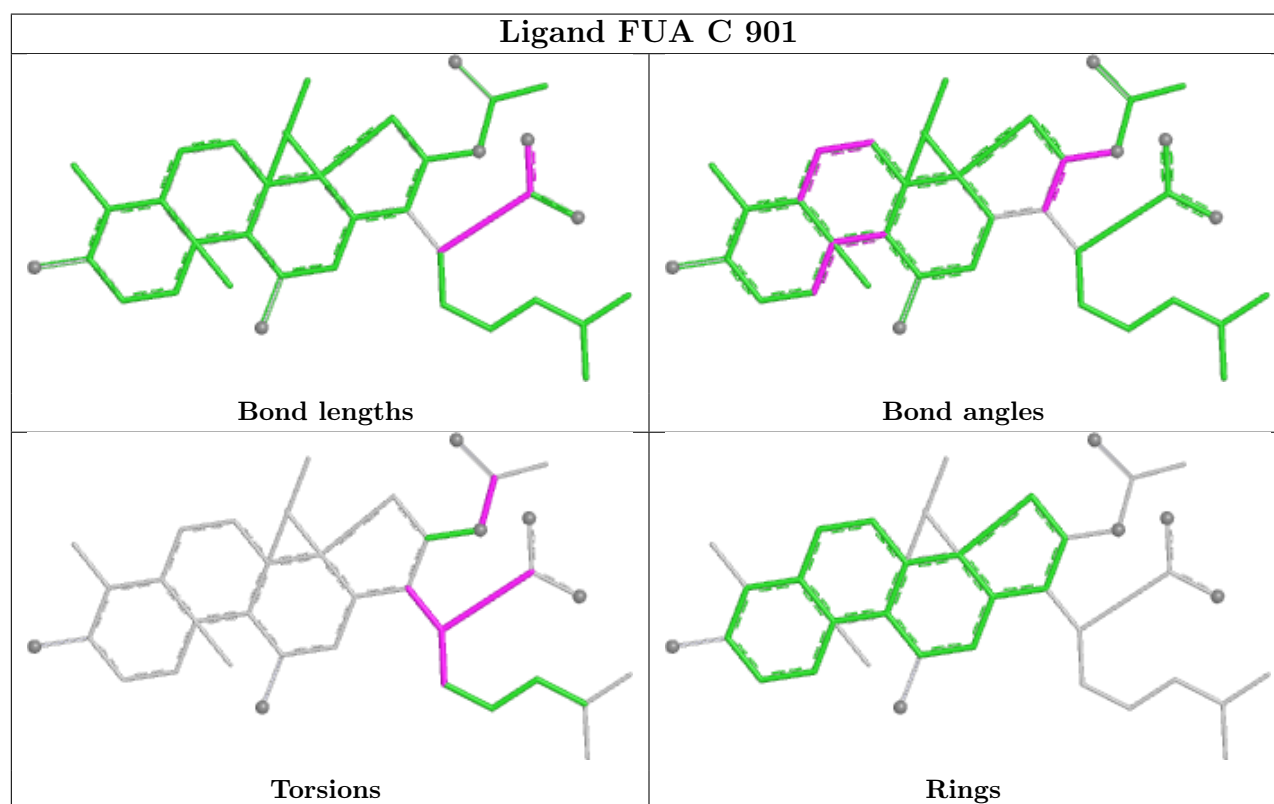
Mol	Chain	Res	Type	Atoms
3	C	901	FUA	C13-C17-C22-C29
3	C	901	FUA	C23-C22-C29-O4
3	C	901	FUA	C23-C22-C29-O5
3	C	901	FUA	C32-C31-O2-C16
3	C	901	FUA	O3-C31-O2-C16
3	C	901	FUA	C29-C22-C23-C24
3	C	901	FUA	C17-C22-C23-C24

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	901	FUA	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	587/613 (95%)	0.13	30 (5%) 33 35	21, 34, 67, 88	0
1	B	576/613 (93%)	0.01	13 (2%) 61 63	19, 32, 59, 78	0
1	C	589/613 (96%)	0.14	36 (6%) 27 29	18, 34, 63, 93	0
2	D	157/169 (92%)	0.58	4 (2%) 58 60	31, 47, 65, 79	0
2	E	155/169 (91%)	0.32	5 (3%) 50 52	26, 42, 62, 74	0
2	F	155/169 (91%)	0.92	10 (6%) 25 27	35, 51, 72, 89	0
All	All	2219/2346 (94%)	0.20	98 (4%) 39 41	18, 36, 65, 93	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	674	LEU	6.1
1	A	672	VAL	5.5
1	C	674	LEU	5.5
1	A	671	ILE	5.2
1	B	617	PHE	5.1
1	C	676	THR	5.1
1	C	672	VAL	4.9
1	C	634	TRP	4.8
1	A	634	TRP	4.7
1	A	670	ALA	4.2
1	C	668	LEU	4.1
1	C	677	ALA	4.0
2	E	12	SER	3.7
1	C	678	THR	3.6
1	A	39	ALA	3.5
1	C	865	GLN	3.5
1	A	834	GLY	3.5
1	A	664	PHE	3.5
1	B	618	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
2	F	12	SER	3.4
1	C	133	SER	3.3
2	F	14	LEU	3.3
1	C	569	GLN	3.3
1	C	673	GLU	3.1
2	F	166	GLN	3.1
1	A	660	ASP	3.0
1	A	623	ASN	3.0
2	F	76	TYR	2.9
1	A	676	THR	2.9
1	A	618	ALA	2.9
1	C	615	PHE	2.9
1	C	657	GLN	2.9
1	C	832	ALA	2.9
1	A	675	GLY	2.8
1	C	867	ARG	2.8
1	A	837	THR	2.8
1	C	671	ILE	2.8
1	C	134	SER	2.8
2	F	164	ILE	2.8
1	C	170	SER	2.8
1	A	831	ALA	2.8
1	C	866	GLU	2.7
2	E	76	TYR	2.7
1	A	830	GLN	2.7
2	D	166	GLN	2.7
1	A	838	GLY	2.7
1	C	300	LEU	2.7
1	B	664	PHE	2.6
2	D	13	ASP	2.6
1	A	714	THR	2.6
1	C	833	PRO	2.6
1	C	831	ALA	2.6
1	B	667	ASN	2.6
1	B	657	GLN	2.5
2	F	165	LEU	2.5
1	A	840	ALA	2.5
1	B	837	THR	2.5
1	A	617	PHE	2.5
2	D	6	HIS	2.5
1	C	669	PRO	2.5
2	F	91	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	862	MET	2.4
1	A	715	SER	2.4
1	B	659	LYS	2.4
1	C	862	MET	2.4
1	C	214	VAL	2.4
2	E	166	GLN	2.4
1	B	619	GLY	2.3
1	C	294	ALA	2.3
1	C	295	THR	2.3
1	C	667	ASN	2.3
1	B	39	ALA	2.3
1	C	830	GLN	2.3
1	A	669	PRO	2.2
1	C	675	GLY	2.2
2	F	15	GLY	2.2
1	A	678	THR	2.2
2	F	44	ASP	2.2
1	C	840	ALA	2.2
1	C	712	MET	2.2
1	B	679	GLY	2.2
1	A	833	PRO	2.2
1	C	713	LEU	2.1
2	E	163	GLU	2.1
1	A	677	ALA	2.1
1	B	569	GLN	2.1
2	F	150	PHE	2.1
1	A	619	GLY	2.1
1	A	586	ARG	2.1
1	C	135	SER	2.1
1	C	670	ALA	2.1
2	E	150	PHE	2.1
1	A	673	GLU	2.0
1	A	832	ALA	2.0
1	B	713	LEU	2.0
1	C	301	ASP	2.0
1	B	833	PRO	2.0
2	D	16	LYS	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](#)

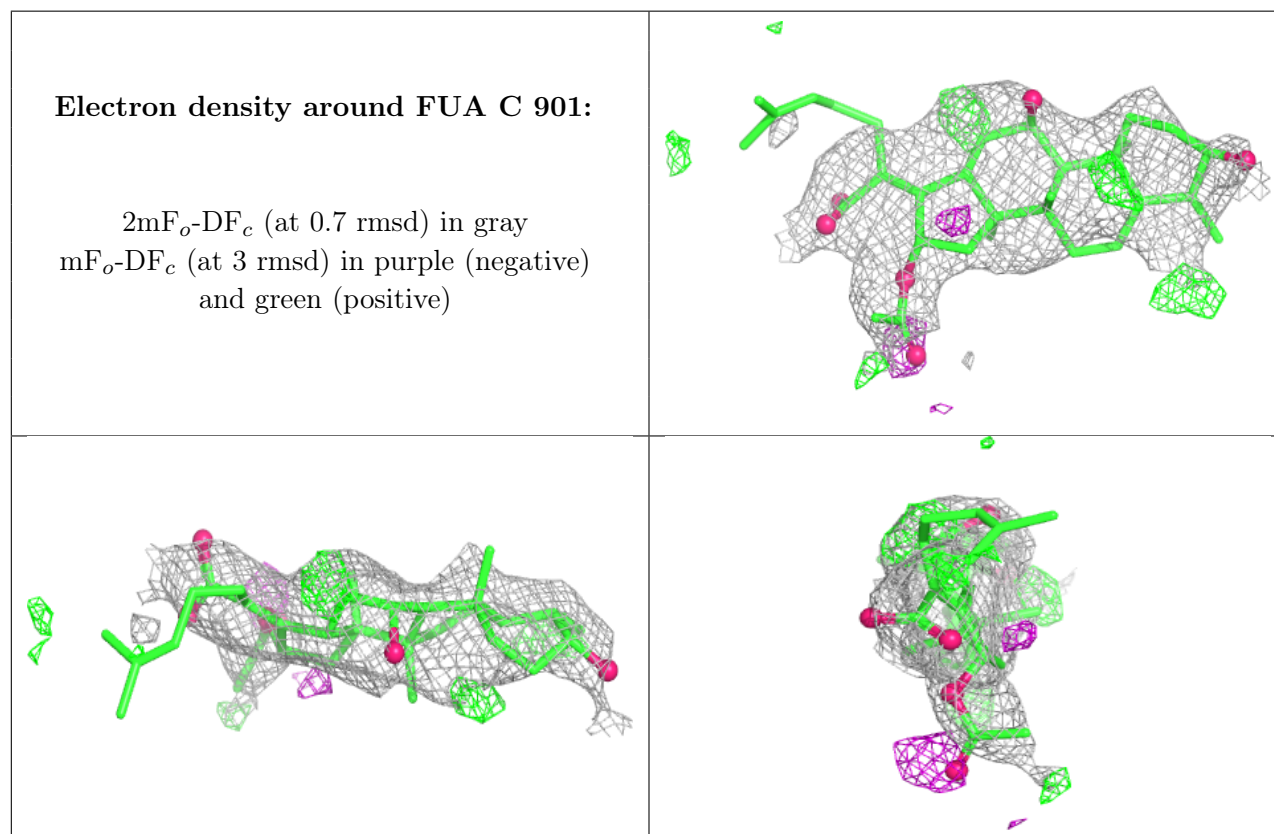
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
3	FUA	C	901	37/37	0.66	0.23	66,77,82,84	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.