



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:04 PM GMT

PDB ID : 3SOT  
Title : Crystal structure of a Multidomain protein including DUF1735 (BA-COVA\_03322) from Bacteroides ovatus at 2.80 Å resolution  
Authors : Joint Center for Structural Genomics (JCSG)  
Deposited on : 2011-06-30  
Resolution : 2.80 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

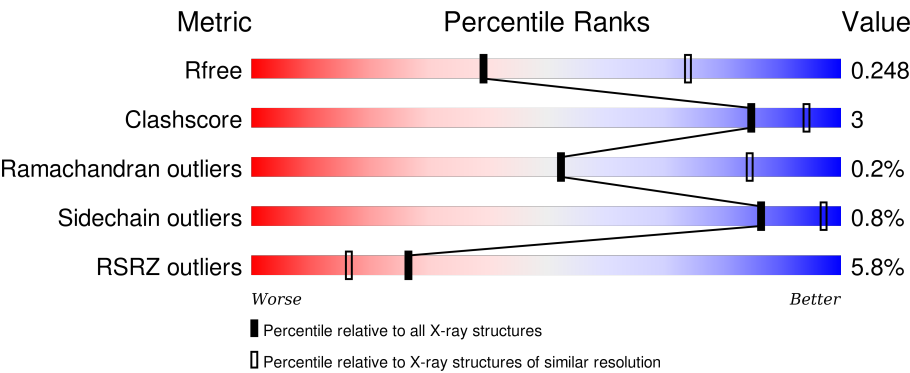
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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 <sub>free</sub>	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 >=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 <=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	319	<div><div>6%</div><div>88%5%7%</div></div>
1	B	319	<div><div>3%</div><div>85%7%9%</div></div>
1	C	319	<div><div>3%</div><div>83%8%8%</div></div>
1	D	319	<div><div>5%</div><div>86%7%7%</div></div>
1	E	319	<div><div>10%</div><div>83%9%7%</div></div>

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Mol	Chain	Length	Quality of chain
1	F	319	

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
2	EDO	A	340	-	-	-	X
2	EDO	B	341	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13888 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 Multidomain protein including DUF1735.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	Se	0	2	0
			2388	1521	380	475	1	11			
1	B	291	Total	C	N	O	S	Se	0	1	0
			2329	1483	372	462	1	11			
1	C	293	Total	C	N	O	S	Se	0	1	0
			2324	1483	371	458	1	11			
1	D	298	Total	C	N	O	S	Se	0	1	0
			2374	1513	377	472	1	11			
1	E	296	Total	C	N	O	S	Se	0	1	0
			2313	1477	368	456	1	11			
1	F	255	Total	C	N	O	Se		0	2	0
			2007	1274	323	399	11				

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	leader sequence	UNP A7LZP6
B	0	GLY	-	leader sequence	UNP A7LZP6
C	0	GLY	-	leader sequence	UNP A7LZP6
D	0	GLY	-	leader sequence	UNP A7LZP6
E	0	GLY	-	leader sequence	UNP A7LZP6
F	0	GLY	-	leader sequence	UNP A7LZP6

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		

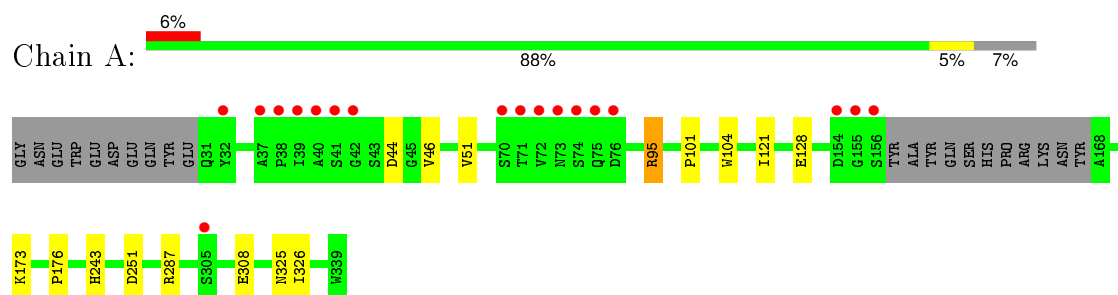
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total	O	0	0
			38	38		
3	B	38	Total	O	0	0
			38	38		
3	C	36	Total	O	0	0
			36	36		
3	D	16	Total	O	0	0
			16	16		
3	E	8	Total	O	0	0
			8	8		
3	F	1	Total	O	0	0
			1	1		

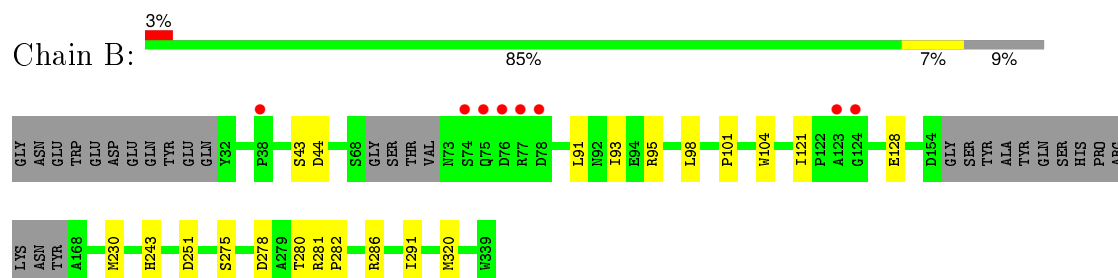
### 3 Residue-property plots [i](#)

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.

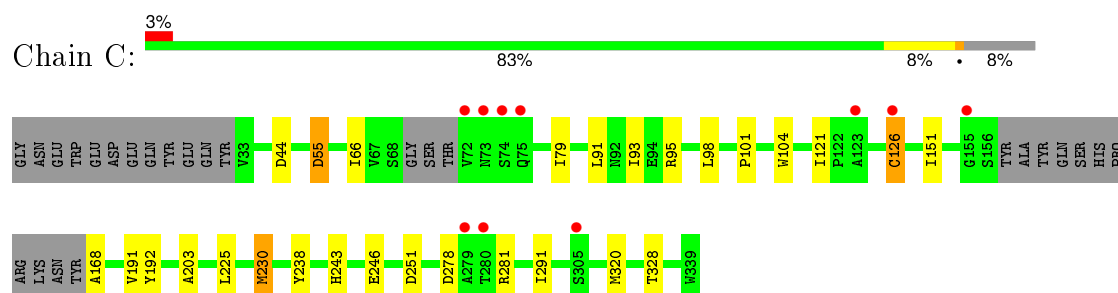
- Molecule 1: Multidomain protein including DUF1735



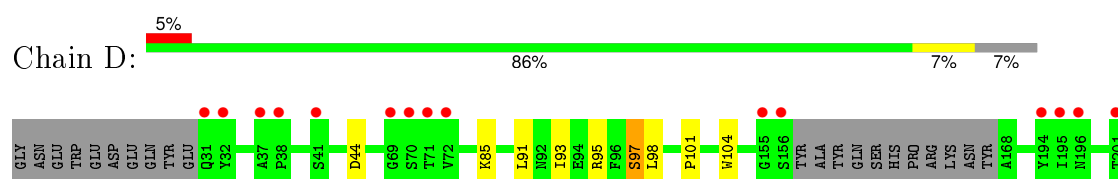
- Molecule 1: Multidomain protein including DUF1735

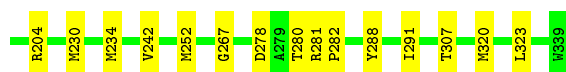


- Molecule 1: Multidomain protein including DUF1735

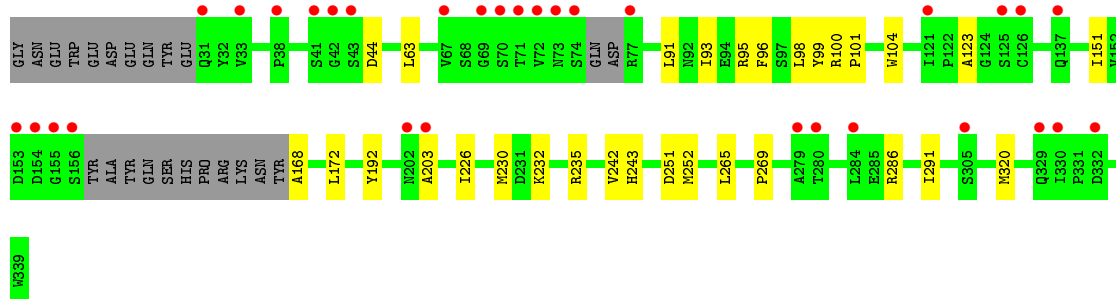
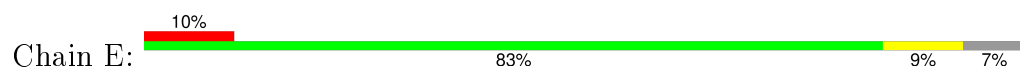


- Molecule 1: Multidomain protein including DUF1735

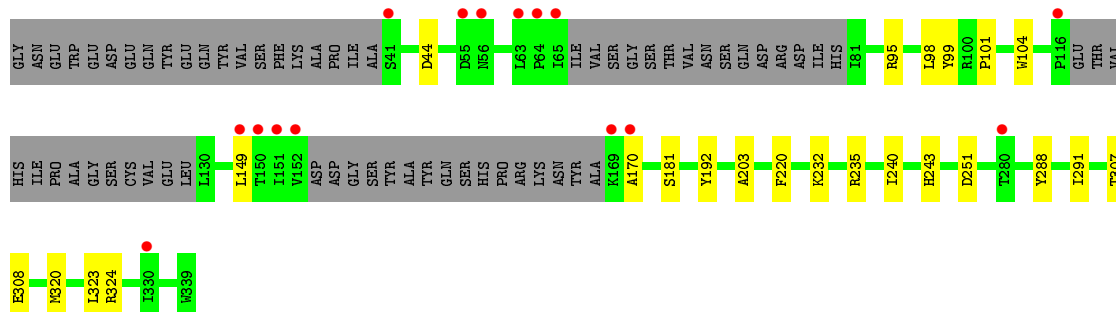




- Molecule 1: Multidomain protein including DUF1735



- Molecule 1: Multidomain protein including DUF1735



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.47Å 123.34Å 189.52Å 90.00° 99.28° 90.00°	Depositor
Resolution (Å)	29.97 – 2.80 29.97 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.97-2.80) 98.7 (29.97-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.16	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.95 (at 2.80Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, $R_{free}$	0.203 , 0.229 0.223 , 0.248	Depositor DCC
$R_{free}$ test set	2460 reflections (4.93%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.4	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 48.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	3 of 49927 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	13888	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	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 20.71 % 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 8.2011e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: EDO

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	0.51	0/2434	0.69	0/3287
1	B	0.51	1/2371 (0.0%)	0.70	0/3202
1	C	0.54	1/2366 (0.0%)	0.72	0/3196
1	D	0.49	0/2418	0.70	0/3267
1	E	0.49	0/2354	0.69	0/3183
1	F	0.48	0/2046	0.71	0/2761
All	All	0.51	2/13989 (0.0%)	0.70	0/18896

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	230	MSE	SE-CE	-6.80	1.55	1.95
1	B	230	MSE	SE-CE	-5.49	1.63	1.95

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	2388	0	2272	9	0
1	B	2329	0	2212	11	0
1	C	2324	0	2196	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2374	0	2262	15	0
1	E	2313	0	2168	19	0
1	F	2007	0	1824	13	0
2	A	4	0	6	0	0
2	B	4	0	6	0	0
2	C	8	0	12	0	0
3	A	38	0	0	0	0
3	B	38	0	0	1	0
3	C	36	0	0	2	0
3	D	16	0	0	2	0
3	E	8	0	0	0	0
3	F	1	0	0	0	0
All	All	13888	0	12958	77	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 (77) 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:E:226:ILE:HG23	1:E:230:MSE:HE2	1.64	0.79
1:D:44:ASP:HB2	1:D:91:LEU:HD11	1.73	0.71
1:E:230:MSE:HE3	1:E:235:ARG:HA	1.72	0.71
1:A:287:ARG:HH11	1:A:326:ILE:HG13	1.69	0.58
1:D:101:PRO:HA	1:D:104:TRP:CD1	2.41	0.56
1:D:204:ARG:HA	3:D:444:HOH:O	2.07	0.54
1:C:328:THR:HA	3:C:469:HOH:O	2.08	0.54
1:E:93:ILE:HD12	1:E:98:LEU:HG	1.91	0.53
1:D:230:MSE:HE3	1:D:234[B]:MSE:HB3	1.89	0.53
1:D:267:GLY:HA3	3:D:445:HOH:O	2.09	0.53
1:D:93:ILE:HD12	1:D:98:LEU:HG	1.90	0.53
1:E:230:MSE:HG3	1:E:235:ARG:HB3	1.90	0.52
1:B:291:ILE:HD11	1:B:320:MSE:HE3	1.91	0.52
1:B:93:ILE:HD12	1:B:98:LEU:HG	1.91	0.52
1:D:291:ILE:HD11	1:D:320:MSE:HE3	1.91	0.51
1:F:291:ILE:HD11	1:F:320:MSE:HE3	1.91	0.51
1:E:242:VAL:HG22	1:E:252:MSE:HG2	1.93	0.50
1:C:291:ILE:HD11	1:C:320:MSE:HE3	1.94	0.49
1:D:242:VAL:HG22	1:D:252:MSE:HG2	1.94	0.49
1:F:149:LEU:HB2	1:F:170:ALA:HB3	1.95	0.48
1:D:278:ASP:HB3	1:D:281:ARG:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:278:ASP:HB3	1:C:281:ARG:O	2.12	0.48
1:E:291:ILE:HD11	1:E:320:MSE:HE3	1.96	0.48
1:D:230:MSE:CE	1:D:234[B]:MSE:HB3	2.43	0.48
1:B:43:SER:HB3	3:B:347:HOH:O	2.13	0.47
1:C:230:MSE:HE1	1:C:238:TYR:CE2	2.49	0.47
1:C:55:ASP:HA	3:C:412:HOH:O	2.14	0.47
1:E:95:ARG:HD2	1:F:99:TYR:HB3	1.97	0.47
1:B:98:LEU:H	1:B:98:LEU:HD12	1.80	0.47
1:C:44:ASP:HB2	1:C:91:LEU:HD11	1.97	0.47
1:B:44:ASP:HB2	1:B:91:LEU:HD11	1.96	0.47
1:C:79:ILE:HD12	1:C:121:ILE:HD12	1.97	0.46
1:B:278:ASP:HB3	1:B:281:ARG:O	2.15	0.46
1:A:308:GLU:CD	1:B:286:ARG:HH12	2.20	0.46
1:E:44:ASP:HB2	1:E:91:LEU:HD11	1.98	0.46
1:D:98:LEU:HD12	1:D:98:LEU:H	1.80	0.45
1:F:98:LEU:HD12	1:F:98:LEU:H	1.80	0.45
1:D:93:ILE:O	1:D:97:SER:HA	2.17	0.45
1:C:151:ILE:HD12	1:C:168:ALA:HB3	1.99	0.45
1:A:287:ARG:NH1	1:A:326:ILE:HG13	2.31	0.45
1:C:93:ILE:HD12	1:C:98:LEU:HG	1.99	0.45
1:E:286:ARG:HH12	1:F:308:GLU:CD	2.21	0.44
1:F:44:ASP:HB3	1:F:95:ARG:HH11	1.82	0.44
1:F:288:TYR:CE1	1:F:323:LEU:HD13	2.52	0.44
1:C:98:LEU:HD12	1:C:98:LEU:H	1.82	0.44
1:B:121:ILE:HG12	1:B:128:GLU:HB2	1.98	0.44
1:F:243:HIS:HB3	1:F:251:ASP:HB2	2.00	0.43
1:E:63:LEU:HD22	1:E:172:LEU:HD11	2.01	0.43
1:B:101:PRO:HA	1:B:104:TRP:CD1	2.53	0.43
1:A:46:VAL:HG13	1:A:173:LYS:HB2	2.00	0.43
1:C:243:HIS:HB3	1:C:251:ASP:HB2	2.00	0.43
1:F:181:SER:O	1:F:324:ARG:NH2	2.52	0.43
1:A:101:PRO:HA	1:A:104:TRP:CD1	2.54	0.43
1:A:121:ILE:HG12	1:A:128:GLU:HB2	2.01	0.42
1:E:232:LYS:HA	1:E:235:ARG:HG2	2.01	0.42
1:F:101:PRO:HA	1:F:104:TRP:CD1	2.54	0.42
1:E:243:HIS:HB3	1:E:251:ASP:HB2	2.02	0.42
1:E:101:PRO:HA	1:E:104:TRP:CD1	2.55	0.42
1:A:243:HIS:HB3	1:A:251:ASP:HB2	2.00	0.42
1:E:98:LEU:HD12	1:E:98:LEU:H	1.85	0.42
1:E:96:PHE:HA	1:E:100:ARG:HH21	1.83	0.42
1:F:232:LYS:HA	1:F:235:ARG:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:192:TYR:CE1	1:F:203:ALA:HB2	2.55	0.42
1:B:280:THR:O	1:B:282:PRO:HD3	2.20	0.42
1:A:51:VAL:O	1:A:176:PRO:HA	2.20	0.41
1:D:95:ARG:HD2	1:E:99:TYR:HB3	2.03	0.41
1:C:191:VAL:HG21	1:C:225:LEU:HG	2.02	0.41
1:D:280:THR:O	1:D:282:PRO:HD3	2.21	0.41
1:E:192:TYR:CE1	1:E:203:ALA:HB2	2.54	0.41
1:C:192:TYR:CE1	1:C:203:ALA:HB2	2.56	0.41
1:E:265:LEU:HD11	1:E:269:PRO:HG3	2.03	0.40
1:E:151:ILE:HD12	1:E:168:ALA:HB3	2.04	0.40
1:D:288:TYR:CE2	1:D:323:LEU:HD13	2.56	0.40
1:B:243:HIS:HB3	1:B:251:ASP:HB2	2.03	0.40
1:F:220:PHE:HA	1:F:240:ILE:O	2.22	0.40
1:C:101:PRO:HA	1:C:104:TRP:CD1	2.57	0.40
1:A:44:ASP:HB3	1:A:95:ARG:CD	2.51	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	296/319 (93%)	288 (97%)	8 (3%)	0	100	100
1	B	286/319 (90%)	277 (97%)	9 (3%)	0	100	100
1	C	288/319 (90%)	274 (95%)	13 (4%)	1 (0%)	46	79
1	D	295/319 (92%)	286 (97%)	8 (3%)	1 (0%)	46	79
1	E	291/319 (91%)	279 (96%)	11 (4%)	1 (0%)	46	79
1	F	249/319 (78%)	241 (97%)	8 (3%)	0	100	100
All	All	1705/1914 (89%)	1645 (96%)	57 (3%)	3 (0%)	52	84

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	123	ALA
1	D	97	SER
1	C	126	CYS

### 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	259/280 (92%)	257 (99%)	2 (1%)	86	97
1	B	253/280 (90%)	251 (99%)	2 (1%)	86	97
1	C	248/280 (89%)	243 (98%)	5 (2%)	63	90
1	D	259/280 (92%)	257 (99%)	2 (1%)	86	97
1	E	243/280 (87%)	243 (100%)	0	100	100
1	F	205/280 (73%)	204 (100%)	1 (0%)	92	98
All	All	1467/1680 (87%)	1455 (99%)	12 (1%)	86	97

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	ARG
1	A	325	ASN
1	B	95	ARG
1	B	275	SER
1	C	55	ASP
1	C	66	ILE
1	C	95	ARG
1	C	126	CYS
1	C	246	GLU
1	D	85	LYS
1	D	307	THR
1	F	307	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	202	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

4 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	$\# Z  > 2$
2	EDO	A	340	-	3,3,3	0.53	0	2,2,2	0.23	0
2	EDO	B	341	-	3,3,3	0.55	0	2,2,2	0.19	0
2	EDO	C	342	-	3,3,3	0.58	0	2,2,2	0.15	0
2	EDO	C	343	-	3,3,3	0.51	0	2,2,2	0.48	0

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
2	EDO	A	340	-	-	0/1/1/1	0/0/0/0
2	EDO	B	341	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	C	342	-	-	0/1/1/1	0/0/0/0
2	EDO	C	343	-	-	0/1/1/1	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.

No monomer is involved in short contacts.

## 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, 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	288/319 (90%)	-0.17	18 (6%) 23 14	9, 33, 94, 116	0
1	B	281/319 (88%)	-0.26	8 (2%) 56 44	8, 27, 67, 98	0
1	C	283/319 (88%)	-0.12	10 (3%) 48 35	10, 32, 73, 131	0
1	D	288/319 (90%)	0.11	15 (5%) 31 20	14, 47, 93, 112	0
1	E	286/319 (89%)	0.36	31 (10%) 8 3	25, 53, 89, 122	0
1	F	245/319 (76%)	0.23	15 (6%) 25 15	29, 56, 95, 118	0
All	All	1671/1914 (87%)	0.02	97 (5%) 26 16	8, 41, 90, 131	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	69	GLY	6.8
1	F	152	VAL	6.4
1	D	32	TYR	6.3
1	A	38	PRO	6.0
1	E	74	SER	5.7
1	F	116	PRO	5.6
1	E	329	GLN	5.2
1	A	41	SER	4.9
1	E	155	GLY	4.9
1	C	155	GLY	4.7
1	E	280	THR	4.5
1	E	71	THR	4.5
1	E	156	SER	4.4
1	E	125	SER	4.2
1	D	194	TYR	4.1
1	C	74	SER	4.1
1	E	43	SER	4.1
1	A	39	ILE	4.0
1	A	32	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	72	VAL	4.0
1	A	70	SER	3.8
1	F	151	ILE	3.7
1	B	123	ALA	3.6
1	A	37	ALA	3.6
1	F	150	THR	3.6
1	D	71	THR	3.5
1	B	76	ASP	3.5
1	E	73	ASN	3.4
1	B	38	PRO	3.4
1	F	149	LEU	3.4
1	D	38	PRO	3.4
1	D	41	SER	3.4
1	F	41	SER	3.3
1	C	279	ALA	3.2
1	D	155	GLY	3.2
1	F	169	LYS	3.2
1	A	74	SER	3.2
1	C	126	CYS	3.2
1	D	195	ILE	3.1
1	A	71	THR	3.1
1	E	330	ILE	3.1
1	B	77	ARG	3.1
1	D	156	SER	3.1
1	C	280	THR	3.0
1	B	124	GLY	3.0
1	E	284	LEU	3.0
1	E	41	SER	3.0
1	F	56	ASN	2.9
1	A	156	SER	2.9
1	E	33	VAL	2.9
1	B	78	ASP	2.8
1	E	279	ALA	2.8
1	D	72	VAL	2.8
1	D	70	SER	2.8
1	E	42	GLY	2.8
1	E	72	VAL	2.8
1	C	73	ASN	2.7
1	E	154	ASP	2.7
1	A	42	GLY	2.7
1	A	154	ASP	2.7
1	A	75	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	40	ALA	2.7
1	F	64	PRO	2.6
1	E	31	GLN	2.6
1	F	55	ASP	2.6
1	E	70	SER	2.5
1	E	305	SER	2.5
1	A	73	ASN	2.5
1	B	75	GLN	2.4
1	C	75	GLN	2.4
1	F	280	THR	2.4
1	E	332	ASP	2.4
1	C	305	SER	2.4
1	D	196	ASN	2.4
1	E	153	ASP	2.4
1	E	126	CYS	2.4
1	B	74	SER	2.4
1	A	72	VAL	2.4
1	E	203	ALA	2.3
1	A	76	ASP	2.3
1	E	202	ASN	2.3
1	D	201	THR	2.3
1	E	67	VAL	2.3
1	E	38	PRO	2.2
1	F	170	ALA	2.2
1	A	155	GLY	2.2
1	D	31	GLN	2.1
1	D	37	ALA	2.1
1	A	305	SER	2.1
1	C	123	ALA	2.1
1	E	137	GLN	2.1
1	E	77	ARG	2.1
1	E	69	GLY	2.1
1	E	121	ILE	2.1
1	F	65	ILE	2.0
1	F	330	ILE	2.0
1	F	63	LEU	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( $\text{\AA}^2$ )	Q<0.9
2	EDO	A	340	4/4	0.92	0.24	4.90	45,46,47,50	0
2	EDO	B	341	4/4	0.95	0.19	2.38	34,35,37,37	0
2	EDO	C	342	4/4	0.88	0.16	-	41,43,44,45	0
2	EDO	C	343	4/4	0.92	0.22	-	47,47,49,55	0

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

There are no such residues in this entry.