



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 9, 2025 – 12:07 PM EST

PDB ID : 8W3E  
Title : Crystal structure of prefusion-stabilized RSV F protein UFCR1  
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Deposited on : 2024-02-22  
Resolution : 2.26 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

<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>.

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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 : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.21  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.004 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

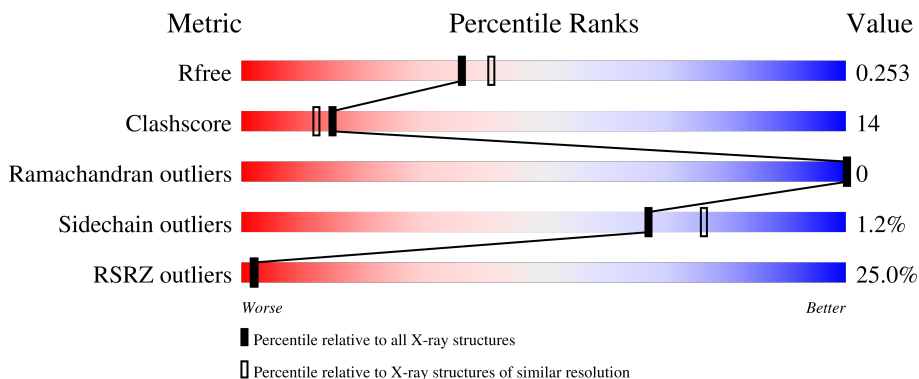
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.26 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))
$R_{free}$	164625	1763 (2.26-2.26)
Clashscore	180529	1919 (2.26-2.26)
Ramachandran outliers	177936	1884 (2.26-2.26)
Sidechain outliers	177891	1885 (2.26-2.26)
RSRZ outliers	164620	1763 (2.26-2.26)

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  $\geq 3$ , 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	F	507	

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	PEG	F	601	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3594 atoms, of which 16 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 Prefusion-stabilized RSV F protein UFCR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	F	444	3432	2159	570	680	23	0	1	0

- Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	F	1	17	4	10	3	0	0

- Molecule 3 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
			Total	C	H	O		
3	F	1	10	2	6	2	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	F	1	14	8	1	5	0	0

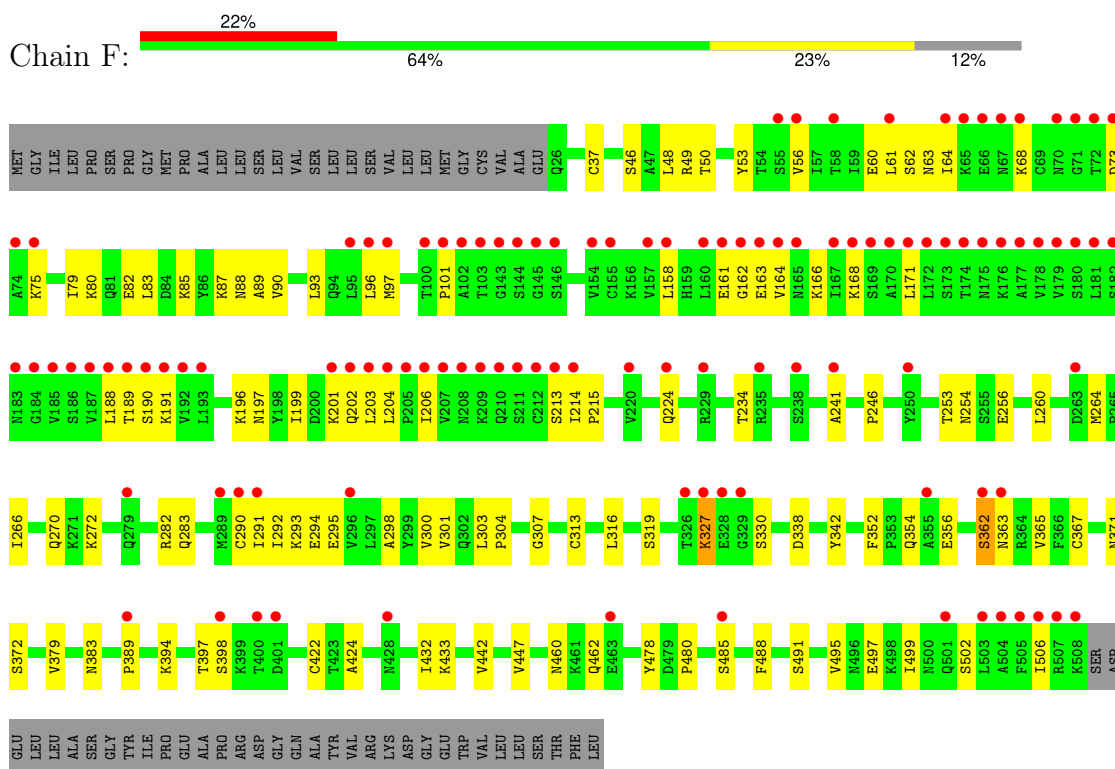
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	121	Total 121	O 121	0	0

### 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: Prefusion-stabilized RSV F protein UFCR1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	170.03Å 170.03Å 170.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.25 – 2.26 36.25 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.9 (36.25-2.26) 99.9 (36.25-2.26)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 2.27Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.227 , 0.253 0.226 , 0.253	Depositor DCC
$R_{free}$ test set	1962 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.4	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 36.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3594	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, PEG, 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	F	0.53	0/3485	0.85	0/4726

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	F	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	422	CYS	Mainchain

### 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	F	3432	0	3470	93	0
2	F	7	10	10	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	4	6	6	0	0
4	F	14	0	13	2	0
5	F	121	0	0	2	0
All	All	3578	16	3499	94	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 14.

All (94) 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:F:101:PRO:HG2	1:F:241:ALA:HB1	1.38	1.04
1:F:253:THR:HG23	1:F:256:GLU:OE1	1.65	0.94
1:F:93:LEU:CD1	1:F:234:THR:HG23	2.08	0.84
1:F:90:VAL:HG13	1:F:292:ILE:HD11	1.65	0.78
1:F:362:SER:OG	1:F:363:ASN:N	2.16	0.76
1:F:89:ALA:O	1:F:93:LEU:HD13	1.86	0.75
1:F:93:LEU:HD12	1:F:234:THR:HG23	1.67	0.74
2:F:601:PEG:H11	5:F:772:HOH:O	1.91	0.69
1:F:96:LEU:HD12	1:F:96:LEU:O	1.93	0.69
1:F:62:SER:OG	1:F:64:ILE:HG23	1.93	0.68
1:F:162:GLY:O	1:F:166:LYS:HG2	1.94	0.68
1:F:202:GLN:OE1	1:F:202:GLN:N	2.29	0.66
1:F:75:LYS:HD2	1:F:215:PRO:O	1.98	0.64
1:F:97:MET:SD	1:F:291:ILE:HG13	2.38	0.63
1:F:502:SER:O	1:F:506:ILE:HG13	1.98	0.62
1:F:197:ASN:HD21	1:F:201:LYS:HD2	1.64	0.61
1:F:73:ASP:OD2	1:F:214:ILE:HD12	2.00	0.61
1:F:61:LEU:O	1:F:196:LYS:HB2	2.00	0.61
1:F:290:CYS:SG	1:F:300:VAL:HG23	2.41	0.60
1:F:338:ASP:HB2	2:F:601:PEG:H12	1.83	0.60
1:F:56:VAL:HB	1:F:189:THR:HG22	1.84	0.59
1:F:83:LEU:O	1:F:87:LYS:HG3	2.03	0.59
1:F:478:TYR:O	1:F:480:PRO:HD3	2.03	0.58
1:F:206:ILE:HD13	1:F:213:SER:OG	2.03	0.58
1:F:63:ASN:HB2	1:F:295:GLU:HG2	1.86	0.57
1:F:37:CYS:SG	1:F:319:SER:HB3	2.45	0.57
1:F:260:LEU:O	1:F:264:MET:HG3	2.04	0.57
1:F:290:CYS:HB2	1:F:298:ALA:O	2.06	0.55
1:F:46:SER:HB3	1:F:313:CYS:SG	2.47	0.55
1:F:442:VAL:HG21	1:F:447:VAL:HG21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:171:LEU:HD13	1:F:191:LYS:HB2	1.88	0.55
1:F:188:LEU:HD23	1:F:260:LEU:CD1	2.38	0.54
1:F:197:ASN:ND2	1:F:201:LYS:HD2	2.22	0.54
1:F:163:GLU:HA	1:F:166:LYS:HG2	1.89	0.54
1:F:93:LEU:CD1	1:F:234:THR:CG2	2.84	0.54
1:F:53:TYR:HB3	1:F:264:MET:HE3	1.91	0.53
1:F:161:GLU:HG3	1:F:161:GLU:O	2.08	0.53
1:F:301:VAL:HG12	1:F:303:LEU:CD2	2.39	0.53
1:F:164:VAL:HG21	1:F:293:LYS:HE3	1.91	0.53
1:F:254:ASN:ND2	1:F:282:ARG:HH21	2.07	0.53
1:F:342:TYR:OH	2:F:601:PEG:H22	2.08	0.52
1:F:352:PHE:CE2	1:F:372:SER:HB3	2.44	0.52
1:F:293:LYS:HG2	1:F:294:GLU:HG3	1.92	0.51
1:F:398:SER:HA	1:F:485:SER:O	2.10	0.51
1:F:93:LEU:HD11	1:F:234:THR:OG1	2.10	0.51
1:F:432:ILE:HD11	1:F:447:VAL:HG22	1.92	0.51
1:F:93:LEU:HD11	1:F:234:THR:HG23	1.93	0.50
1:F:85:LYS:HA	1:F:88[B]:ASN:ND2	2.26	0.50
1:F:292:ILE:O	1:F:292:ILE:HG23	2.12	0.49
1:F:188:LEU:HD23	1:F:260:LEU:HD12	1.95	0.48
1:F:88[B]:ASN:OD1	1:F:89:ALA:N	2.46	0.48
1:F:90:VAL:HG13	1:F:292:ILE:CD1	2.40	0.48
1:F:48:LEU:HD22	1:F:367:CYS:HB2	1.95	0.48
1:F:164:VAL:O	1:F:168:LYS:HB2	2.14	0.48
1:F:327:LYS:NZ	1:F:330:SER:HB3	2.29	0.48
1:F:64:ILE:HG22	1:F:204:LEU:HD21	1.96	0.47
1:F:254:ASN:HD22	1:F:282:ARG:HH21	1.63	0.47
1:F:49:ARG:HG3	1:F:304:PRO:CB	2.45	0.47
1:F:301:VAL:HG12	1:F:303:LEU:HD23	1.96	0.46
1:F:497:GLU:HB2	4:F:603:NAG:H81	1.97	0.46
1:F:49:ARG:HG3	1:F:304:PRO:HB2	1.98	0.46
1:F:60:GLU:HG3	1:F:191:LYS:CE	2.45	0.46
1:F:389:PRO:HA	5:F:785:HOH:O	2.16	0.46
1:F:442:VAL:CG2	1:F:447:VAL:HG21	2.45	0.46
1:F:64:ILE:CD1	1:F:87:LYS:HE2	2.46	0.45
1:F:316:LEU:HD22	2:F:601:PEG:H41	1.98	0.44
1:F:379:VAL:HG22	2:F:601:PEG:H32	2.00	0.43
1:F:327:LYS:CE	1:F:330:SER:HB3	2.48	0.43
1:F:354:GLN:HE22	1:F:371:ASN:HB3	1.83	0.43
1:F:365:VAL:HG12	1:F:367:CYS:SG	2.58	0.43
1:F:495:VAL:O	1:F:499:ILE:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:163:GLU:HA	1:F:166:LYS:CG	2.48	0.43
1:F:203:LEU:O	1:F:206:ILE:HB	2.19	0.43
1:F:199:ILE:HG12	1:F:203:LEU:HD12	2.01	0.43
1:F:394:LYS:HA	1:F:491:SER:HA	2.01	0.42
1:F:316:LEU:HD22	2:F:601:PEG:C4	2.49	0.42
1:F:201:LYS:CB	1:F:202:GLN:OE1	2.68	0.42
1:F:201:LYS:HB2	1:F:202:GLN:OE1	2.20	0.42
1:F:497:GLU:HB2	4:F:603:NAG:C8	2.50	0.42
1:F:82:GLU:OE1	1:F:224:GLN:HG2	2.19	0.42
1:F:50:THR:OG1	1:F:307:GLY:HA3	2.20	0.42
1:F:53:TYR:CB	1:F:264:MET:CE	2.98	0.41
1:F:158:LEU:HD23	1:F:158:LEU:HA	1.61	0.41
1:F:60:GLU:HG3	1:F:191:LYS:HE2	2.02	0.41
1:F:53:TYR:HB3	1:F:264:MET:CE	2.50	0.41
1:F:266:ILE:HD12	1:F:270:GLN:HG2	2.03	0.41
1:F:383:ASN:HD21	2:F:601:PEG:C4	2.34	0.41
1:F:460:ASN:OD1	1:F:462:GLN:HB2	2.20	0.41
1:F:68:LYS:HA	1:F:80:LYS:HZ3	1.86	0.40
1:F:79:ILE:HD13	1:F:79:ILE:HA	1.92	0.40
1:F:356:GLU:H	1:F:356:GLU:CD	2.25	0.40
1:F:424:ALA:HB3	1:F:433:LYS:HB3	2.04	0.40
1:F:246:PRO:HB3	1:F:283:GLN:HA	2.03	0.40
1:F:397:THR:O	1:F:398:SER:HB3	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	F	443/507 (87%)	422 (95%)	21 (5%)	0	<a href="#">100</a> <a href="#">100</a>

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	F	406/457 (89%)	401 (99%)	5 (1%)	67 76

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	190	SER
1	F	272	LYS
1	F	327	LYS
1	F	362	SER
1	F	488	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	197	ASN
1	F	224	GLN
1	F	254	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

3 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	EDO	F	602	-	3,3,3	0.53	0	2,2,2	0.15	0
4	NAG	F	603	1	14,14,15	0.58	0	17,19,21	0.55	0
2	PEG	F	601	-	6,6,6	0.77	0	5,5,5	0.74	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	F	602	-	-	0/1/1/1	-
4	NAG	F	603	1	-	0/6/23/26	0/1/1/1
2	PEG	F	601	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	601	PEG	O1-C1-C2-O2
2	F	601	PEG	O2-C3-C4-O4
2	F	601	PEG	C4-C3-O2-C2

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	603	NAG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	601	PEG	7	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	F	444/507 (87%)	1.21	111 (25%) <b>2</b>   <b>2</b>	30, 56, 104, 138	1 (0%)

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	101	PRO	8.0
1	F	505	PHE	7.9
1	F	103	THR	6.9
1	F	102	ALA	6.6
1	F	167	ILE	6.5
1	F	160	LEU	6.2
1	F	144	SER	5.9
1	F	185	VAL	5.4
1	F	100	THR	5.4
1	F	506	ILE	5.3
1	F	174	THR	5.2
1	F	178	VAL	5.2
1	F	504	ALA	5.2
1	F	143	GLY	5.1
1	F	172	LEU	5.0
1	F	212	CYS	5.0
1	F	186	SER	4.9
1	F	211	SER	4.9
1	F	213	SER	4.8
1	F	181	LEU	4.8
1	F	328	GLU	4.7
1	F	208	ASN	4.7
1	F	508	LYS	4.5
1	F	400	THR	4.5
1	F	74	ALA	4.4
1	F	209	LYS	4.4
1	F	187	VAL	4.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	F	206	ILE	4.3
1	F	171	LEU	4.3
1	F	67	ASN	4.3
1	F	327	LYS	4.3
1	F	210	GLN	4.2
1	F	188	LEU	4.2
1	F	184	GLY	4.1
1	F	189	THR	4.0
1	F	68	LYS	4.0
1	F	179	VAL	3.9
1	F	73	ASP	3.9
1	F	65	LYS	3.9
1	F	205	PRO	3.8
1	F	175	ASN	3.8
1	F	180	SER	3.8
1	F	291	ILE	3.7
1	F	326	THR	3.7
1	F	507	ARG	3.6
1	F	145	GLY	3.6
1	F	398	SER	3.6
1	F	163	GLU	3.5
1	F	72	THR	3.5
1	F	155	CYS	3.5
1	F	164	VAL	3.4
1	F	214	ILE	3.4
1	F	182	SER	3.3
1	F	173	SER	3.3
1	F	168	LYS	3.3
1	F	329	GLY	3.2
1	F	95	LEU	3.2
1	F	158	LEU	3.2
1	F	503	LEU	3.2
1	F	170	ALA	3.1
1	F	177	ALA	3.1
1	F	64	ILE	3.1
1	F	290	CYS	3.1
1	F	207	VAL	3.1
1	F	401	ASP	3.0
1	F	202	GLN	3.0
1	F	204	LEU	3.0
1	F	161	GLU	2.9
1	F	71	GLY	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	F	55	SER	2.9
1	F	279	GLN	2.9
1	F	96	LEU	2.8
1	F	146	SER	2.8
1	F	176	LYS	2.7
1	F	362	SER	2.7
1	F	56	VAL	2.7
1	F	428	ASN	2.7
1	F	389	PRO	2.6
1	F	241	ALA	2.5
1	F	201	LYS	2.5
1	F	190	SER	2.5
1	F	485	SER	2.5
1	F	192	VAL	2.5
1	F	289	MET	2.4
1	F	157	VAL	2.4
1	F	238	SER	2.4
1	F	263	ASP	2.4
1	F	250	TYR	2.4
1	F	501	GLN	2.4
1	F	355	ALA	2.4
1	F	66	GLU	2.3
1	F	224	GLN	2.3
1	F	58	THR	2.3
1	F	97	MET	2.3
1	F	463	GLU	2.3
1	F	70	ASN	2.3
1	F	363	ASN	2.3
1	F	75	LYS	2.2
1	F	154	VAL	2.2
1	F	203	LEU	2.2
1	F	169	SER	2.1
1	F	165	ASN	2.1
1	F	183	ASN	2.1
1	F	191	LYS	2.1
1	F	296	VAL	2.1
1	F	162	GLY	2.1
1	F	193	LEU	2.1
1	F	229	ARG	2.0
1	F	235	ARG	2.0
1	F	220	VAL	2.0
1	F	61	LEU	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 monosaccharides 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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAG	F	603	14/15	0.49	0.23	77,96,105,105	0
2	PEG	F	601	7/7	0.83	0.32	30,45,62,62	0
3	EDO	F	602	4/4	0.96	0.17	36,44,53,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.