



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6QFK
Title : EngBF DARPin Fusion 4b G10
Authors : Ernst, P.; Pluckthun, A.; Mittl, P.R.E.
Deposited on : 2019-01-10
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

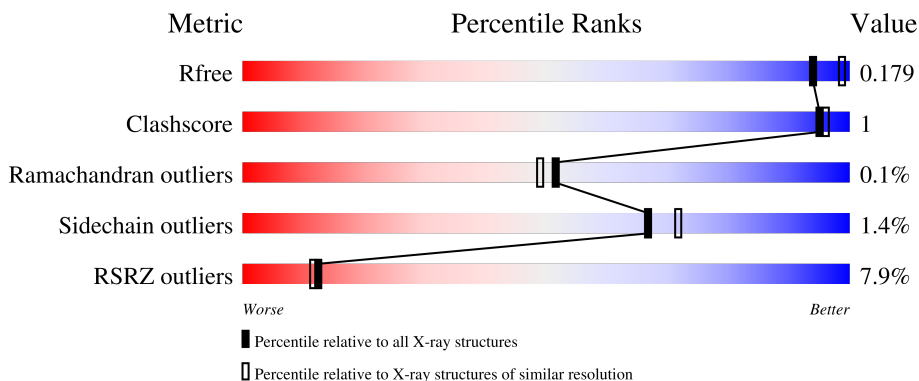
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

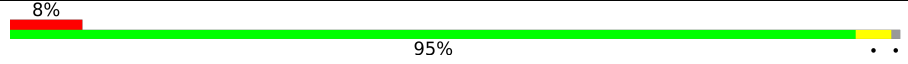
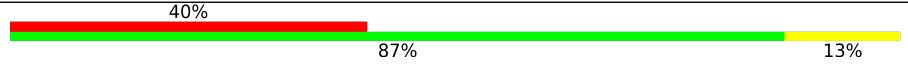
The reported resolution of this entry is 2.00 Å.

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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	1357	
2	B	15	

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
5	EDO	A	1709	-	-	-	X
6	MES	A	1711	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12243 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 PEGA domain-containing protein,PEGA domain-containing protein,EngBF DARPin fusion G10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1347	10412	6480	1781	2121	30	0	10	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	334	GLY	-	expression tag	UNP A0A414FD23
A	335	PRO	-	expression tag	UNP A0A414FD23
A	336	LEU	-	expression tag	UNP A0A414FD23
A	337	GLY	-	expression tag	UNP A0A414FD23
A	338	SER	-	expression tag	UNP A0A414FD23
A	339	MET	-	expression tag	UNP A0A414FD23
A	342	CYS	SER	conflict	UNP A0A414FD23
A	1309	ARG	GLN	conflict	UNP A0A414FD23

- Molecule 2 is a protein called V3-IF.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	15	113	75	20	18	0	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
3	A	4	4	4	0	0

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



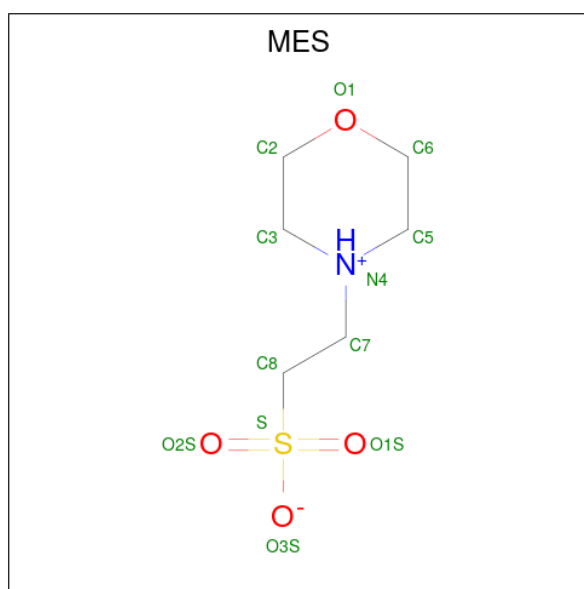
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

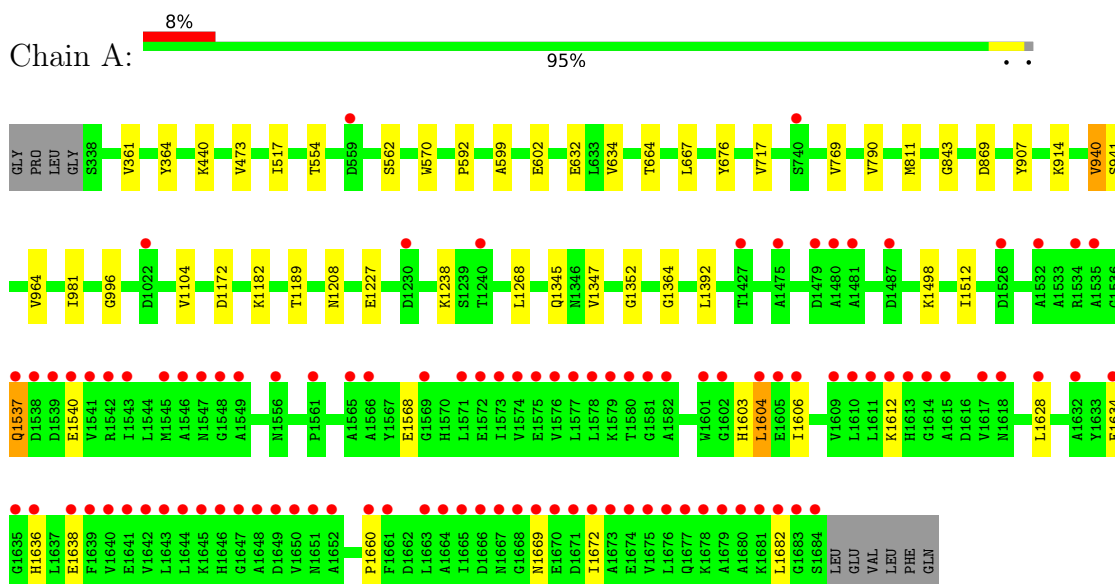
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1637	Total 1637	O 1637	0	0
7	B	1	Total 1	O 1	0	0

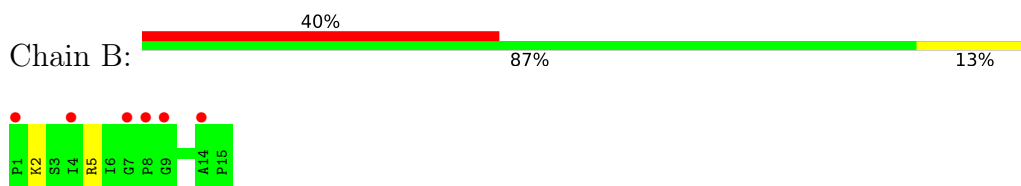
3 Residue-property plots

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: PEGA domain-containing protein, PEGA domain-containing protein, EngBF DARPin fusion G10



- Molecule 2: V3-IF



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	192.89Å 192.89Å 122.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.25 – 2.00 49.50 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.25-2.00) 100.0 (49.50-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.00Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.154 , 0.176 0.158 , 0.179	Depositor DCC
R_{free} test set	8747 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.1	Xtrriage
Anisotropy	0.118	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12243	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, MPD, MN, MES, DPR

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	0.52	0/10612	0.67	0/14393
2	B	0.42	0/109	0.68	0/145
All	All	0.51	0/10721	0.67	0/14538

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	10412	0	9955	25	0
2	B	113	0	116	0	0
3	A	4	0	0	0	0
4	A	8	0	14	0	0
5	A	44	0	66	1	0
6	A	24	0	26	0	0
7	A	1637	0	0	2	0
7	B	1	0	0	0	0
All	All	12243	0	10177	25	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 1.

The worst 5 of 25 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:A:964[B]:VAL:HG12	1:A:981:ILE:HG12	1.77	0.65
1:A:570:TRP:CD2	1:A:592:PRO:HB3	2.38	0.59
1:A:1604:LEU:HD11	1:A:1638:GLU:HG3	1.85	0.58
1:A:940:VAL:HG21	7:A:2110:HOH:O	2.08	0.53
1:A:1364:GLY:HA2	1:A:1392:LEU:HD13	1.93	0.51

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	1355/1357 (100%)	1304 (96%)	49 (4%)	2 (0%)	51	49
2	B	13/15 (87%)	12 (92%)	1 (8%)	0	100	100
All	All	1368/1372 (100%)	1316 (96%)	50 (4%)	2 (0%)	51	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	790	VAL
1	A	843	GLY

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	1108/1106 (100%)	1094 (99%)	14 (1%)	69	74
2	B	10/10 (100%)	8 (80%)	2 (20%)	1	0
All	All	1118/1116 (100%)	1102 (99%)	16 (1%)	67	72

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	2	LYS
1	A	1682	LEU
1	A	1568	GLU
1	A	1636	HIS
1	A	1537	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1646	HIS
1	A	1547	ASN
1	A	1280	GLN
1	A	1277	ASN
1	A	1443	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](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 4 are monoatomic - leaving 14 for Mogul analysis.

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
4	MPD	A	1705	-	7,7,7	0.64	0	9,10,10	0.35	0
5	EDO	A	1717	-	3,3,3	0.65	0	2,2,2	0.17	0
5	EDO	A	1710	-	3,3,3	0.58	0	2,2,2	0.24	0
5	EDO	A	1709	-	3,3,3	0.61	0	2,2,2	0.24	0
5	EDO	A	1706	-	3,3,3	0.77	0	2,2,2	0.11	0
5	EDO	A	1713	-	3,3,3	0.59	0	2,2,2	0.32	0
5	EDO	A	1716	-	3,3,3	0.50	0	2,2,2	0.42	0
5	EDO	A	1707	-	3,3,3	0.61	0	2,2,2	0.12	0
5	EDO	A	1715	-	3,3,3	0.54	0	2,2,2	0.29	0
6	MES	A	1708	-	12,12,12	0.78	0	14,16,16	0.43	0
5	EDO	A	1712	-	3,3,3	0.55	0	2,2,2	0.32	0
5	EDO	A	1718	-	3,3,3	0.60	0	2,2,2	0.22	0
5	EDO	A	1714	-	3,3,3	0.61	0	2,2,2	0.30	0
6	MES	A	1711	-	12,12,12	0.77	0	14,16,16	0.44	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
4	MPD	A	1705	-	-	2/5/5/5	-
5	EDO	A	1717	-	-	0/1/1/1	-
5	EDO	A	1710	-	-	0/1/1/1	-
5	EDO	A	1709	-	-	0/1/1/1	-
5	EDO	A	1706	-	-	1/1/1/1	-
5	EDO	A	1713	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	1716	-	-	0/1/1/1	-
5	EDO	A	1707	-	-	0/1/1/1	-
5	EDO	A	1715	-	-	0/1/1/1	-
6	MES	A	1708	-	-	0/6/14/14	0/1/1/1
5	EDO	A	1712	-	-	0/1/1/1	-
5	EDO	A	1718	-	-	0/1/1/1	-
5	EDO	A	1714	-	-	0/1/1/1	-
6	MES	A	1711	-	-	1/6/14/14	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1706	EDO	O1-C1-C2-O2
4	A	1705	MPD	C1-C2-C3-C4
4	A	1705	MPD	O2-C2-C3-C4
6	A	1711	MES	N4-C7-C8-S

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1707	EDO	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 [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	1347/1357 (99%)	-0.00	102 (7%) 13 13	25, 37, 90, 178	0
2	B	14/15 (93%)	2.21	6 (42%) 0 0	74, 82, 110, 120	0
All	All	1361/1372 (99%)	0.02	108 (7%) 12 11	25, 38, 92, 178	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1684	SER	9.8
1	A	1668	GLY	9.3
1	A	1682	LEU	8.9
1	A	1683	GLY	7.1
2	B	1	PRO	7.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
2	DPR	B	15	7/8	0.65	0.29	99,101,107,107	0

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, 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(Å ²)	Q<0.9
6	MES	A	1711	12/12	0.61	0.41	144,145,148,149	0
4	MPD	A	1705	8/8	0.74	0.26	101,104,105,105	0
5	EDO	A	1709	4/4	0.75	0.48	76,78,79,79	0
5	EDO	A	1710	4/4	0.76	0.18	81,82,82,82	0
5	EDO	A	1718	4/4	0.79	0.27	85,86,87,88	0
5	EDO	A	1717	4/4	0.79	0.30	79,80,80,80	0
5	EDO	A	1706	4/4	0.80	0.23	55,61,63,65	0
5	EDO	A	1713	4/4	0.81	0.13	88,88,88,88	0
5	EDO	A	1707	4/4	0.81	0.26	81,81,82,83	0
5	EDO	A	1714	4/4	0.84	0.17	76,78,80,80	0
5	EDO	A	1716	4/4	0.87	0.22	87,88,89,90	0
5	EDO	A	1712	4/4	0.88	0.21	79,80,80,81	0
5	EDO	A	1715	4/4	0.90	0.21	65,66,68,69	0
6	MES	A	1708	12/12	0.97	0.14	40,59,74,74	0
3	MN	A	1704	1/1	0.99	0.03	43,43,43,43	0
3	MN	A	1701	1/1	1.00	0.03	39,39,39,39	0
3	MN	A	1702	1/1	1.00	0.05	42,42,42,42	0
3	MN	A	1703	1/1	1.00	0.04	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.