wwPDB X-ray Structure Validation Summary Report (i)

Oct 17, 2022 – 10:14 pm BST

PDB ID	:	7ZRA
Title	:	Crystal structure of E.coli LexA in complex with nanobody NbSOS1(Nb14497)
Authors	:	Maso, L.; Vascon, F.; Chinellato, M.; Pardon, E.; Steyaert, J.; Angelini, A.; Tondi, D.; Cendron, L.
Deposited on	:	2022-05-04
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

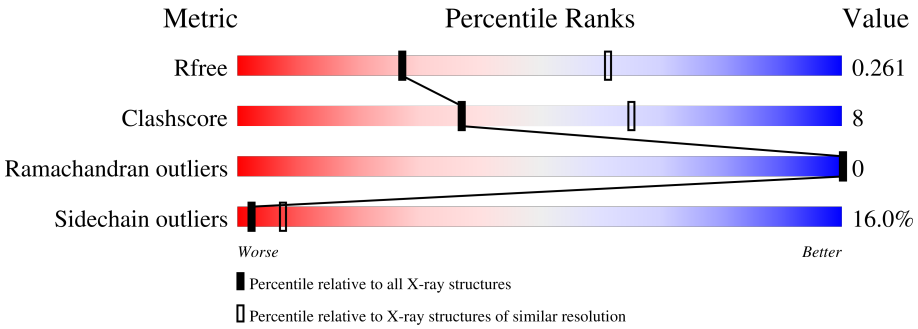
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (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 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	202	47% 16% · 36%
1	B	202	47% 15% · 37%
1	C	202	45% 16% · 36%
1	D	202	46% 17% 36%
2	E	132	64% 23% · 9%
2	F	132	67% 20% 5% 8%
2	G	132	70% 20% · 7%

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Mol	Chain	Length	Quality of chain
2	H	132	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7783 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.

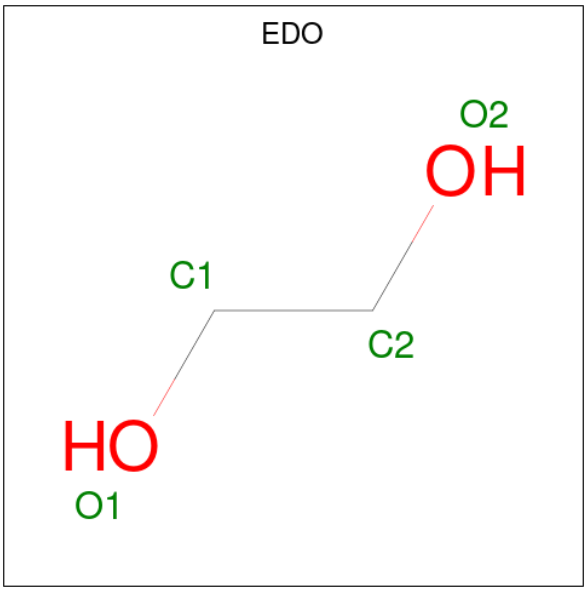
- Molecule 1 is a protein called LexA repressor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			1001	633	178	187	3			
1	C	129	Total	C	N	O	S	0	0	0
			1001	633	178	187	3			
1	B	128	Total	C	N	O	S	0	0	0
			992	628	177	184	3			
1	D	129	Total	C	N	O	S	0	1	0
			1017	645	180	189	3			

- Molecule 2 is a protein called Nanobody NbSOS1 (Nb14497).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	120	Total	C	N	O	S	0	0	0
			925	576	165	180	4			
2	G	123	Total	C	N	O	S	0	0	0
			947	588	170	185	4			
2	F	121	Total	C	N	O	S	0	0	0
			931	579	166	182	4			
2	H	122	Total	C	N	O	S	0	0	0
			937	582	167	184	4			

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 4 is water.

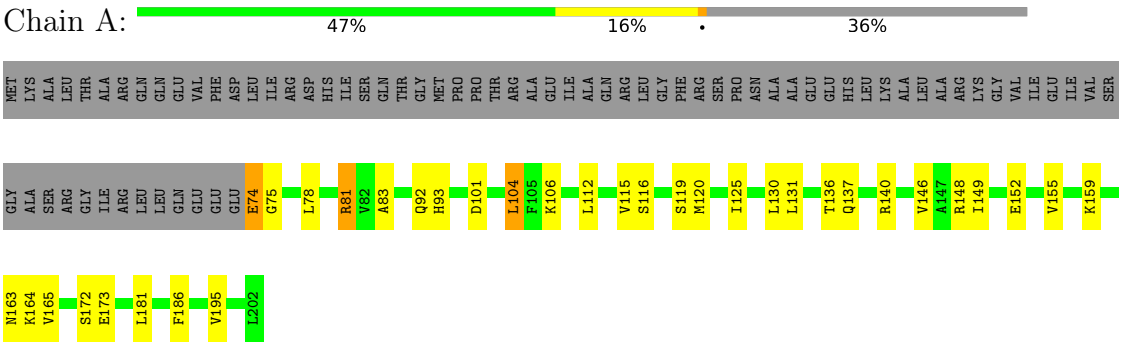
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total O 4 4	0	0
4	C	4	Total O 4 4	0	0
4	E	2	Total O 2 2	0	0
4	G	1	Total O 1 1	0	0
4	B	1	Total O 1 1	0	0
4	D	4	Total O 4 4	0	0
4	F	3	Total O 3 3	0	0
4	H	1	Total O 1 1	0	0

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. 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. 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.

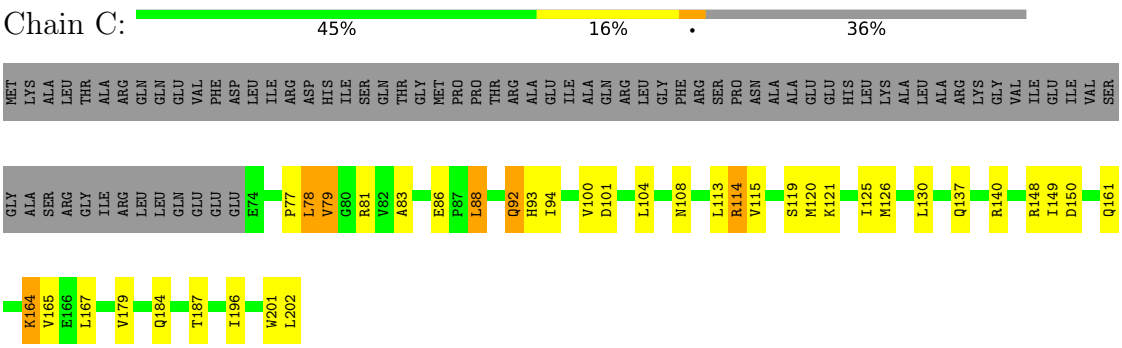
• Molecule 1: LexA repressor

Chain A:



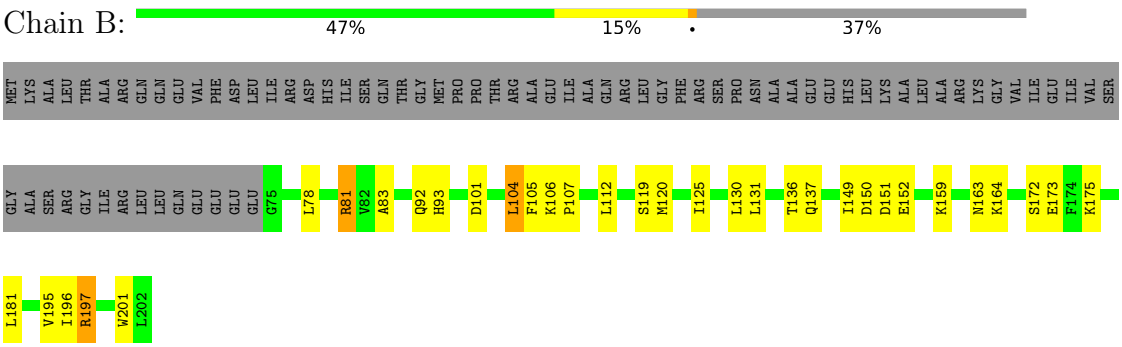
• Molecule 1: LexA repressor

Chain C:



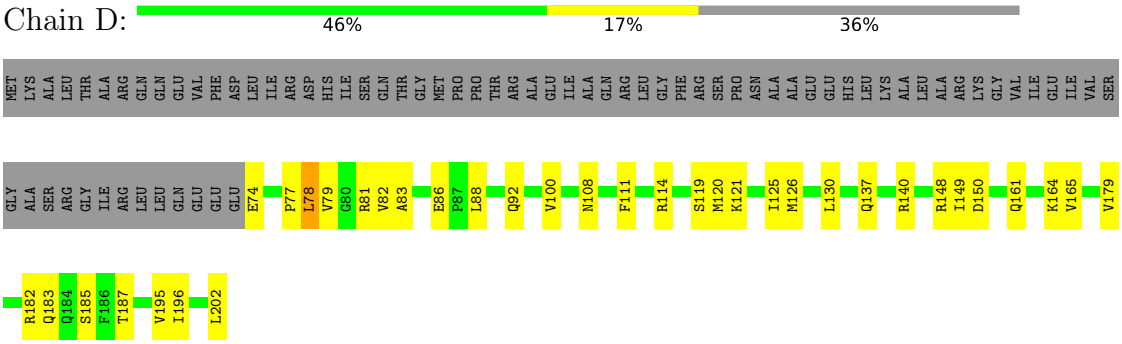
• Molecule 1: LexA repressor

Chain B:



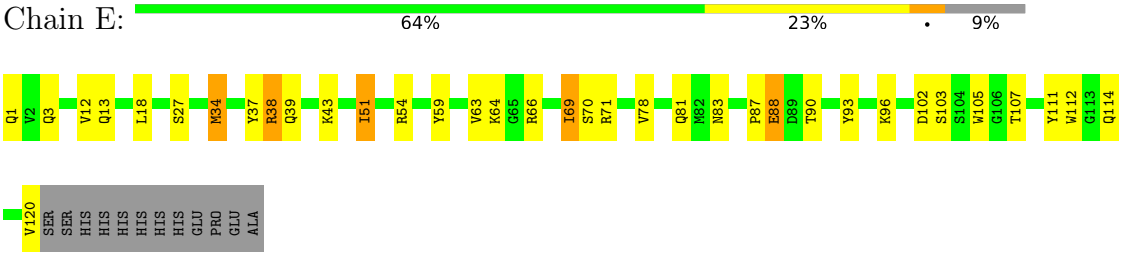
• Molecule 1: LexA repressor

Chain D:



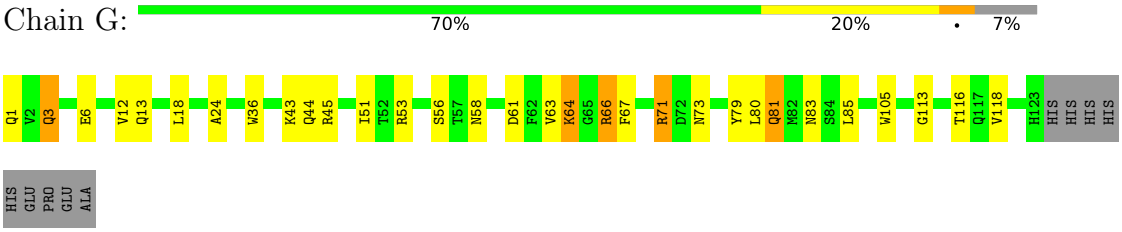
• Molecule 2: Nanobody NbSOS1 (Nb14497)

Chain E:



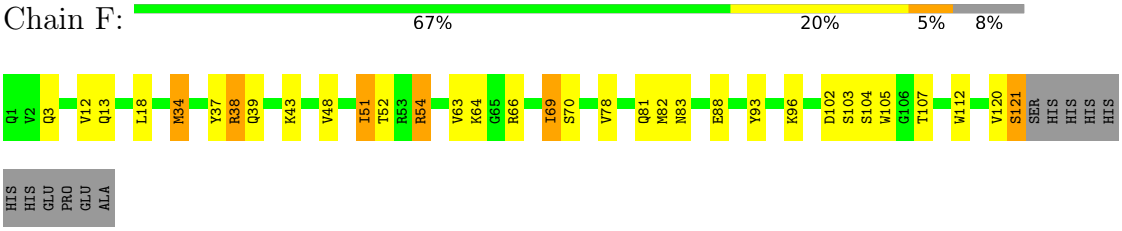
• Molecule 2: Nanobody NbSOS1 (Nb14497)

Chain G:



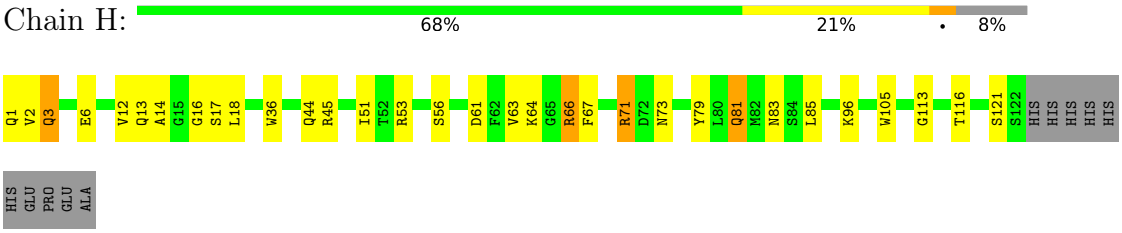
• Molecule 2: Nanobody NbSOS1 (Nb14497)

Chain F:



• Molecule 2: Nanobody NbSOS1 (Nb14497)

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	59.92Å 110.75Å 231.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.97 – 2.80 47.97 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.97-2.80) 99.2 (47.97-2.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.27 (at 2.81Å)	Xtriage
Refinement program	PHENIX 5.8.0267	Depositor
R, R_{free}	0.223 , 0.259 0.225 , 0.261	Depositor DCC
R_{free} test set	1819 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å^2)	100.7	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7783	wwPDB-VP
Average B, all atoms (Å^2)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.38	0/1016	0.67	0/1373
1	B	0.42	0/1007	0.73	0/1361
1	C	0.42	0/1016	0.68	0/1373
1	D	0.44	0/1030	0.78	0/1389
2	E	0.37	0/943	0.67	0/1275
2	F	0.43	0/949	0.75	0/1283
2	G	0.40	0/966	0.67	0/1306
2	H	0.41	0/955	0.68	0/1291
All	All	0.41	0/7882	0.71	0/10651

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	1001	0	1024	17	0
1	B	992	0	1018	19	0
1	C	1001	0	1024	19	0
1	D	1017	0	1046	16	0
2	E	925	0	896	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	931	0	901	16	0
2	G	947	0	913	13	0
2	H	937	0	906	13	0
3	A	4	0	6	1	0
3	C	8	0	12	0	0
4	A	4	0	0	0	0
4	B	1	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	0	0
4	E	2	0	0	0	0
4	F	3	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
All	All	7783	0	7746	121	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 8.

The worst 5 of 121 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:54:ARG:HH21	2:F:54:ARG:HG3	1.41	0.84
1:D:202[C]:LEU:HD22	2:H:96:LYS:HD3	1.67	0.77
2:F:54:ARG:HH21	2:F:54:ARG:CG	2.00	0.73
1:B:92:GLN:HB2	2:F:64:LYS:HB3	1.69	0.72
2:E:34:MET:HB3	2:E:78:VAL:HG21	1.73	0.71

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	127/202 (63%)	119 (94%)	8 (6%)	0	100	100
1	B	126/202 (62%)	120 (95%)	6 (5%)	0	100	100
1	C	127/202 (63%)	119 (94%)	8 (6%)	0	100	100
1	D	127/202 (63%)	121 (95%)	6 (5%)	0	100	100
2	E	118/132 (89%)	115 (98%)	3 (2%)	0	100	100
2	F	119/132 (90%)	115 (97%)	4 (3%)	0	100	100
2	G	121/132 (92%)	115 (95%)	6 (5%)	0	100	100
2	H	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
All	All	985/1336 (74%)	937 (95%)	48 (5%)	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	110/169 (65%)	95 (86%)	15 (14%)	3	11
1	B	109/169 (64%)	95 (87%)	14 (13%)	4	13
1	C	110/169 (65%)	94 (86%)	16 (14%)	3	9
1	D	112/169 (66%)	95 (85%)	17 (15%)	3	8
2	E	96/107 (90%)	78 (81%)	18 (19%)	1	5
2	F	97/107 (91%)	78 (80%)	19 (20%)	1	4
2	G	99/107 (92%)	83 (84%)	16 (16%)	2	7
2	H	98/107 (92%)	80 (82%)	18 (18%)	1	5
All	All	831/1104 (75%)	698 (84%)	133 (16%)	2	7

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	1	GLN
2	H	18	LEU

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Mol	Chain	Res	Type
2	H	85	LEU
2	E	114	GLN
2	E	107	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	1	GLN
2	H	73	ASN
2	H	58	ASN
2	G	58	ASN
2	F	32	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

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	A	301	-	3,3,3	0.42	0	2,2,2	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	EDO	C	302	-	3,3,3	0.09	0	2,2,2	0.11	0
3	EDO	C	301	-	3,3,3	0.08	0	2,2,2	0.20	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
3	EDO	A	301	-	-	1/1/1/1	-
3	EDO	C	302	-	-	1/1/1/1	-
3	EDO	C	301	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	EDO	O1-C1-C2-O2
3	C	302	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.