



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 12:43 PM UTC

PDB ID : 7ZAU / pdb_00007zau
Title : Fascin-1 in complex with Nb 3E11
Authors : Burgess, S.G.; Bayliss, R.
Deposited on : 2022-03-22
Resolution : 2.20 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

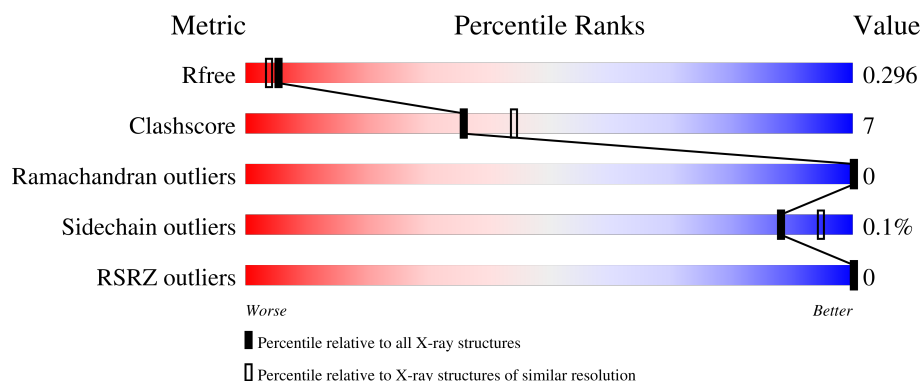
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	498	 84% 13% .
1	C	498	 78% 18% .
1	E	498	 79% 17% .
1	G	498	 83% 13% .
2	B	132	 80% 16% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	132	 83% 11% 6%
2	F	132	 78% 16% 6%
2	H	132	 78% 17% 5%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 19344 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 Fascin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	483	Total	C	N	O	S	0	1	0
			3697	2312	651	720	14			
1	C	480	Total	C	N	O	S	0	1	0
			3594	2248	627	705	14			
1	E	481	Total	C	N	O	S	0	0	0
			3624	2264	632	714	14			
1	G	480	Total	C	N	O	S	0	0	0
			3598	2252	626	706	14			

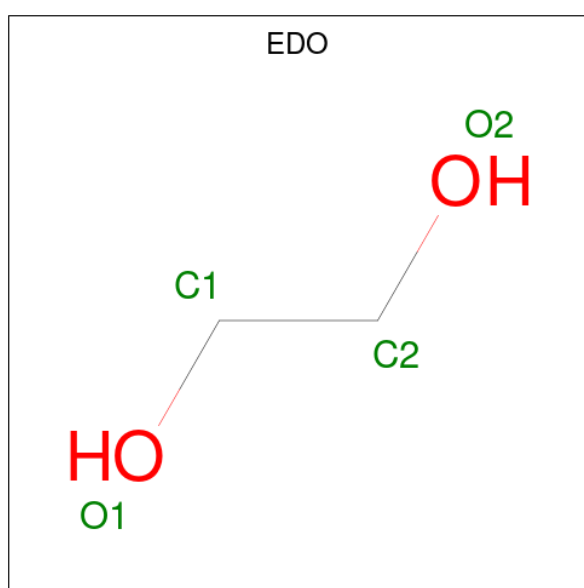
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q16658
A	-3	GLY	-	expression tag	UNP Q16658
A	-2	SER	-	expression tag	UNP Q16658
A	-1	GLU	-	expression tag	UNP Q16658
A	0	PHE	-	expression tag	UNP Q16658
C	-4	GLY	-	expression tag	UNP Q16658
C	-3	GLY	-	expression tag	UNP Q16658
C	-2	SER	-	expression tag	UNP Q16658
C	-1	GLU	-	expression tag	UNP Q16658
C	0	PHE	-	expression tag	UNP Q16658
E	-4	GLY	-	expression tag	UNP Q16658
E	-3	GLY	-	expression tag	UNP Q16658
E	-2	SER	-	expression tag	UNP Q16658
E	-1	GLU	-	expression tag	UNP Q16658
E	0	PHE	-	expression tag	UNP Q16658
G	-4	GLY	-	expression tag	UNP Q16658
G	-3	GLY	-	expression tag	UNP Q16658
G	-2	SER	-	expression tag	UNP Q16658
G	-1	GLU	-	expression tag	UNP Q16658
G	0	PHE	-	expression tag	UNP Q16658

- Molecule 2 is a protein called Nanobody 3E11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	126	Total	C	N	O	S	0	0	0
			960	608	164	183	5			
2	D	124	Total	C	N	O	S	0	0	0
			943	598	159	181	5			
2	F	124	Total	C	N	O	S	0	0	0
			931	591	156	179	5			
2	H	125	Total	C	N	O	S	0	0	0
			954	606	161	182	5			

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



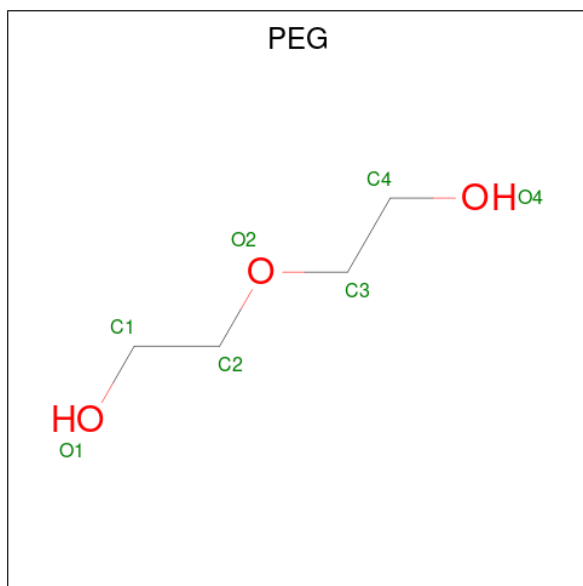
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		

Continued on next page...

Continued from previous page...

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			7	4	3		
4	E	1	Total	C	O	0	0
			7	4	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			7	4	3		
4	E	1	Total	C	O	0	0
			7	4	3		
4	G	1	Total	C	O	0	0
			7	4	3		

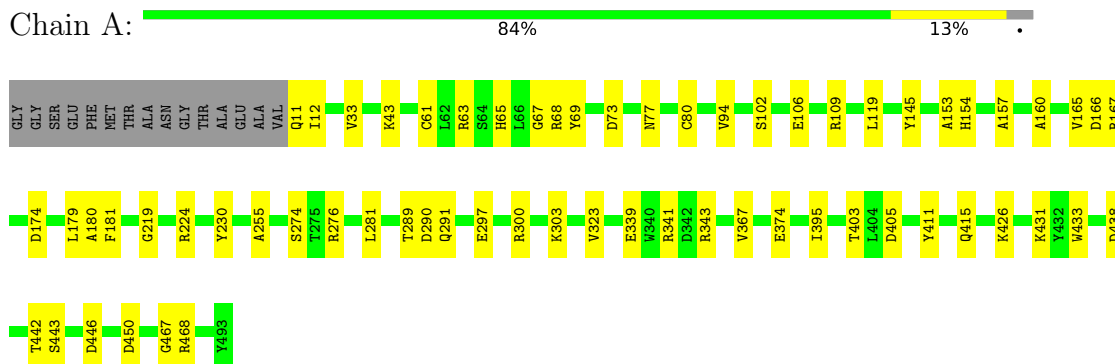
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	192	Total	O	0	0
			192	192		
5	B	85	Total	O	0	0
			85	85		
5	C	152	Total	O	0	0
			152	152		
5	D	44	Total	O	0	0
			44	44		
5	E	185	Total	O	0	0
			185	185		
5	F	57	Total	O	0	0
			57	57		
5	G	177	Total	O	0	0
			177	177		
5	H	52	Total	O	0	0
			52	52		

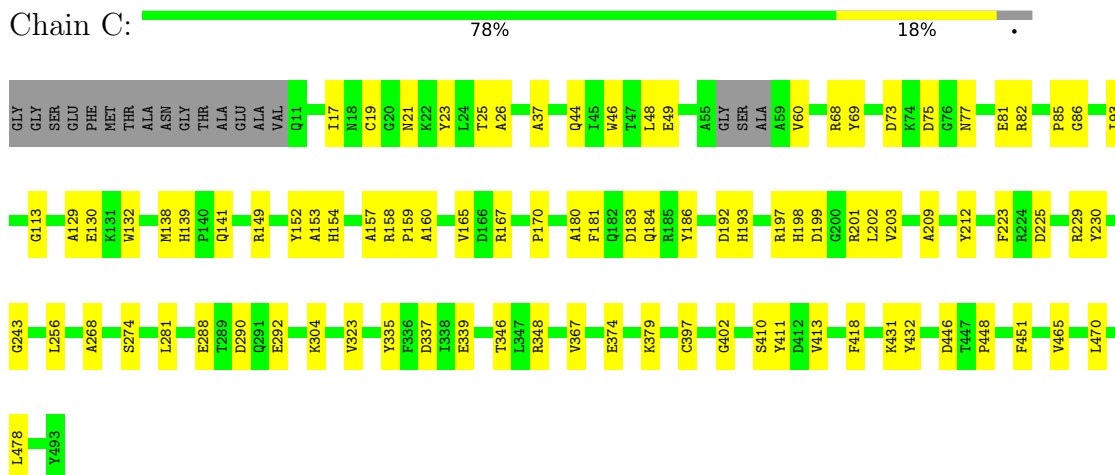
3 Residue-property plots [i](#)

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.

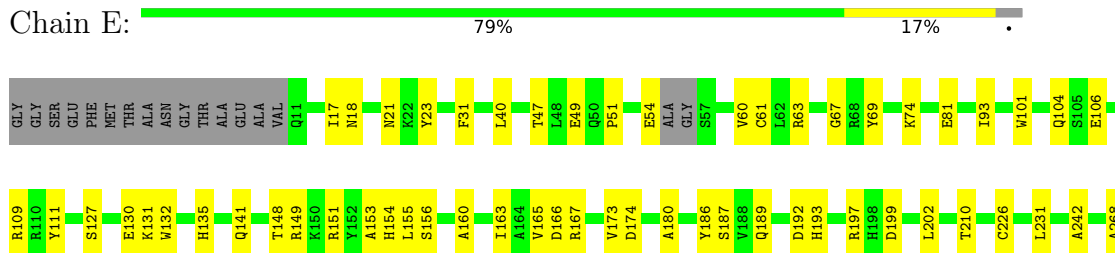
- Molecule 1: Fascin



- Molecule 1: Fascin



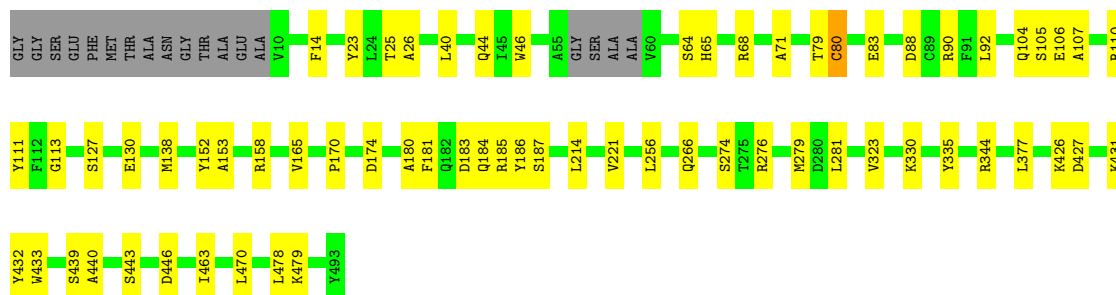
- Molecule 1: Fascin





• Molecule 1: Fascin

Chain G: 83% 13% .



• Molecule 2: Nanobody 3E11

Chain B: 80% 16% 5%



• Molecule 2: Nanobody 3E11

Chain D: 83% 11% 6%



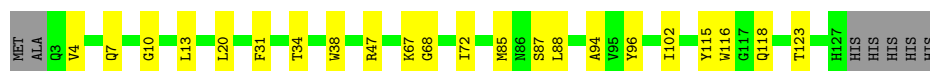
• Molecule 2: Nanobody 3E11

Chain F: 78% 16% 6%



• Molecule 2: Nanobody 3E11

Chain H: 78% 17% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.91Å 210.32Å 105.47Å 90.00° 91.26° 90.00°	Depositor
Resolution (Å)	59.44 – 2.20 59.44 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.5 (59.44-2.20) 91.1 (59.44-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.19_4085	Depositor
R, R_{free}	0.247 , 0.290 0.252 , 0.296	Depositor DCC
R_{free} test set	7940 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.562	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.247 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19344	wwPDB-VP
Average B, all atoms (Å ²)	60.0	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 39.37 % 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 3.2074e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: EDO, PEG

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	0.18	0/3777	0.41	1/5122 (0.0%)
1	C	0.19	0/3672	0.42	0/4994
1	E	0.18	0/3702	0.41	1/5031 (0.0%)
1	G	0.18	0/3675	0.42	0/4998
2	B	0.21	0/982	0.42	0/1331
2	D	0.13	0/965	0.39	0/1310
2	F	0.13	0/953	0.37	0/1295
2	H	0.25	0/976	0.43	0/1323
All	All	0.18	0/18702	0.41	2/25404 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	438	ASP	N-CA-C	-6.87	105.23	112.93
1	E	74	LYS	N-CA-C	-5.26	105.02	111.75

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	3697	0	3478	41	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3594	0	3282	61	0
1	E	3624	0	3344	54	0
1	G	3598	0	3305	49	0
2	B	960	0	909	12	0
2	D	943	0	883	9	0
2	F	931	0	866	17	0
2	H	954	0	909	15	0
3	A	20	0	30	3	0
3	B	4	0	6	1	0
3	C	8	0	12	1	0
3	E	20	0	30	5	0
3	G	8	0	12	1	0
3	H	4	0	6	2	0
4	C	7	0	10	1	0
4	E	21	0	30	0	0
4	G	7	0	10	1	0
5	A	192	0	0	3	0
5	B	85	0	0	1	0
5	C	152	0	0	3	0
5	D	44	0	0	0	0
5	E	185	0	0	5	0
5	F	57	0	0	5	0
5	G	177	0	0	0	0
5	H	52	0	0	0	0
All	All	19344	0	17122	258	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 7.

The worst 5 of 258 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)
3:E:506:EDO:H21	5:E:697:HOH:O	1.48	1.13
1:C:68:ARG:HD2	1:C:81:GLU:HA	1.50	0.92
2:F:47:ARG:CD	5:F:247:HOH:O	2.22	0.87
1:E:187:SER:HA	5:E:604:HOH:O	1.74	0.86
1:G:71:ALA:HB3	1:G:79:THR:OG1	1.80	0.81

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	482/498 (97%)	457 (95%)	25 (5%)	0	100	100
1	C	477/498 (96%)	434 (91%)	43 (9%)	0	100	100
1	E	477/498 (96%)	447 (94%)	30 (6%)	0	100	100
1	G	476/498 (96%)	440 (92%)	36 (8%)	0	100	100
2	B	124/132 (94%)	120 (97%)	4 (3%)	0	100	100
2	D	122/132 (92%)	119 (98%)	3 (2%)	0	100	100
2	F	122/132 (92%)	118 (97%)	4 (3%)	0	100	100
2	H	123/132 (93%)	121 (98%)	2 (2%)	0	100	100
All	All	2403/2520 (95%)	2256 (94%)	147 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	376/407 (92%)	376 (100%)	0	100	100
1	C	351/407 (86%)	351 (100%)	0	100	100
1	E	362/407 (89%)	362 (100%)	0	100	100
1	G	355/407 (87%)	353 (99%)	2 (1%)	78	89
2	B	97/108 (90%)	97 (100%)	0	100	100
2	D	95/108 (88%)	95 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	93/108 (86%)	93 (100%)	0	100	100
2	H	98/108 (91%)	98 (100%)	0	100	100
All	All	1827/2060 (89%)	1825 (100%)	2 (0%)	88	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	80	CYS
1	G	83	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	193	HIS
1	E	474	HIS
2	H	118	GLN
1	G	143	ASN
1	C	143	ASN

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 ⓘ

21 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	$\# Z > 2$
4	PEG	E	503	-	6,6,6	0.17	0	5,5,5	0.21	0
4	PEG	C	503	-	6,6,6	0.12	0	5,5,5	0.11	0
4	PEG	G	503	-	6,6,6	0.12	0	5,5,5	0.13	0
3	EDO	E	508	-	3,3,3	0.42	0	2,2,2	0.43	0
3	EDO	A	501	-	3,3,3	0.43	0	2,2,2	0.39	0
3	EDO	A	505	-	3,3,3	0.41	0	2,2,2	0.46	0
3	EDO	A	502	-	3,3,3	0.42	0	2,2,2	0.31	0
3	EDO	A	503	-	3,3,3	0.39	0	2,2,2	0.52	0
3	EDO	G	502	-	3,3,3	0.44	0	2,2,2	0.31	0
3	EDO	E	507	-	3,3,3	0.44	0	2,2,2	0.37	0
3	EDO	G	501	-	3,3,3	0.42	0	2,2,2	0.35	0
3	EDO	E	505	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	A	504	-	3,3,3	0.44	0	2,2,2	0.39	0
3	EDO	B	201	-	3,3,3	0.42	0	2,2,2	0.40	0
3	EDO	E	504	-	3,3,3	0.44	0	2,2,2	0.26	0
3	EDO	E	506	-	3,3,3	0.41	0	2,2,2	0.35	0
4	PEG	E	501	-	6,6,6	0.12	0	5,5,5	0.08	0
4	PEG	E	502	-	6,6,6	0.11	0	5,5,5	0.10	0
3	EDO	H	201	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	C	502	-	3,3,3	0.42	0	2,2,2	0.36	0
3	EDO	C	501	-	3,3,3	0.44	0	2,2,2	0.27	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	PEG	E	503	-	-	1/4/4/4	-
4	PEG	C	503	-	-	1/4/4/4	-
4	PEG	G	503	-	-	1/4/4/4	-
3	EDO	E	508	-	-	1/1/1/1	-
3	EDO	A	501	-	-	0/1/1/1	-
3	EDO	A	505	-	-	0/1/1/1	-
3	EDO	A	502	-	-	1/1/1/1	-
3	EDO	A	503	-	-	0/1/1/1	-
3	EDO	G	502	-	-	0/1/1/1	-
3	EDO	E	507	-	-	0/1/1/1	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	G	501	-	-	0/1/1/1	-
3	EDO	E	505	-	-	0/1/1/1	-
3	EDO	A	504	-	-	0/1/1/1	-
3	EDO	B	201	-	-	1/1/1/1	-
3	EDO	E	504	-	-	0/1/1/1	-
3	EDO	E	506	-	-	1/1/1/1	-
4	PEG	E	501	-	-	0/4/4/4	-
4	PEG	E	502	-	-	0/4/4/4	-
3	EDO	H	201	-	-	0/1/1/1	-
3	EDO	C	502	-	-	1/1/1/1	-
3	EDO	C	501	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	201	EDO	O1-C1-C2-O2
3	E	506	EDO	O1-C1-C2-O2
4	C	503	PEG	C4-C3-O2-C2
4	G	503	PEG	C4-C3-O2-C2
3	E	508	EDO	O1-C1-C2-O2

There are no ring outliers.

11 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	503	PEG	1	0
4	G	503	PEG	1	0
3	A	502	EDO	2	0
3	A	503	EDO	1	0
3	G	501	EDO	1	0
3	E	505	EDO	1	0
3	B	201	EDO	1	0
3	E	504	EDO	1	0
3	E	506	EDO	3	0
3	H	201	EDO	2	0
3	C	501	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	483/498 (96%)	-1.00	0 100 100	35, 56, 79, 94	1 (0%)
1	C	480/498 (96%)	-0.78	0 100 100	24, 63, 98, 111	1 (0%)
1	E	481/498 (96%)	-0.91	0 100 100	34, 59, 86, 102	0
1	G	480/498 (96%)	-0.83	0 100 100	38, 60, 95, 110	0
2	B	126/132 (95%)	-0.94	0 100 100	38, 52, 72, 80	0
2	D	124/132 (93%)	-0.70	0 100 100	44, 65, 81, 91	0
2	F	124/132 (93%)	-0.89	0 100 100	40, 58, 78, 90	0
2	H	125/132 (94%)	-1.02	0 100 100	38, 53, 68, 88	0
All	All	2423/2520 (96%)	-0.88	0 100 100	24, 59, 91, 111	2 (0%)

There are no RSRZ outliers to report.

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 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	EDO	E	504	4/4	0.96	0.06	75,80,80,82	0
3	EDO	E	508	4/4	0.96	0.08	60,60,63,64	0
3	EDO	G	501	4/4	0.96	0.09	60,63,68,68	0
4	PEG	E	501	7/7	0.96	0.05	85,91,93,95	0
4	PEG	E	503	7/7	0.96	0.10	52,59,69,70	0
3	EDO	A	501	4/4	0.97	0.05	66,70,71,73	0
3	EDO	A	502	4/4	0.97	0.08	47,56,58,67	0
3	EDO	A	504	4/4	0.97	0.08	62,66,68,71	0
3	EDO	H	201	4/4	0.97	0.08	49,52,53,57	0
4	PEG	C	503	7/7	0.97	0.09	58,61,63,72	0
3	EDO	C	501	4/4	0.97	0.07	53,56,56,64	0
4	PEG	E	502	7/7	0.97	0.06	53,65,70,71	0
3	EDO	C	502	4/4	0.97	0.08	61,68,76,77	0
4	PEG	G	503	7/7	0.97	0.08	49,59,62,69	0
3	EDO	B	201	4/4	0.98	0.12	46,47,52,56	0
3	EDO	E	505	4/4	0.98	0.05	46,47,47,54	0
3	EDO	E	507	4/4	0.98	0.07	42,49,53,56	0
3	EDO	A	503	4/4	0.98	0.06	50,53,56,59	0
3	EDO	A	505	4/4	0.98	0.07	64,66,69,73	0
3	EDO	G	502	4/4	0.98	0.06	57,57,59,61	0
3	EDO	E	506	4/4	0.99	0.06	51,52,56,61	0

6.5 Other polymers

There are no such residues in this entry.