



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:49 AM UTC

PDB ID : 3V5V / pdb_00003v5v
Title : UNLIGANDED E.CLOACAE C115D MURA
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Deposited on : 2011-12-16
Resolution : 2.70 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

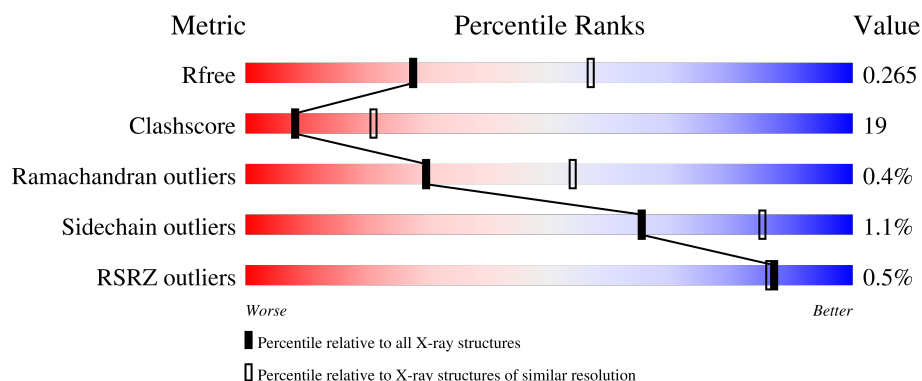
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	419	63% 35% .
1	B	419	66% 32% .
1	C	419	% 68% 30% .
1	D	419	% 65% 31% .

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	A	501	-	-	X	-
2	PEG	C	501	-	-	X	-
3	EDO	A	509	-	-	X	-
3	EDO	B	507	-	-	X	-
3	EDO	B	508	-	-	X	-
3	EDO	D	507	-	-	X	-
4	ACT	C	510	-	-	X	-
5	PGE	B	501	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13230 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 UDP-N-acetylglucosamine 1-carboxyvinyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	0	0
			3144	1977	554	600	13			
1	B	419	Total	C	N	O	S	0	0	0
			3144	1977	554	600	13			
1	C	419	Total	C	N	O	S	0	0	0
			3144	1977	554	600	13			
1	D	419	Total	C	N	O	S	0	0	0
			3144	1977	554	600	13			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	IAS	ASN	SEE REMARK 999	UNP P33038
A	115	ASP	CYS	engineered mutation	UNP P33038
B	67	IAS	ASN	SEE REMARK 999	UNP P33038
B	115	ASP	CYS	engineered mutation	UNP P33038
C	67	IAS	ASN	SEE REMARK 999	UNP P33038
C	115	ASP	CYS	engineered mutation	UNP P33038
D	67	IAS	ASN	SEE REMARK 999	UNP P33038
D	115	ASP	CYS	engineered mutation	UNP P33038

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			7	4	3		
2	A	1	Total	C	O	0	0
			7	4	3		
2	C	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



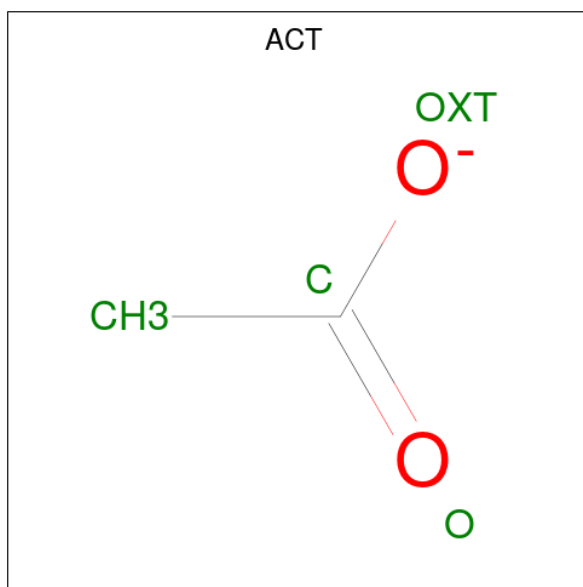
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0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

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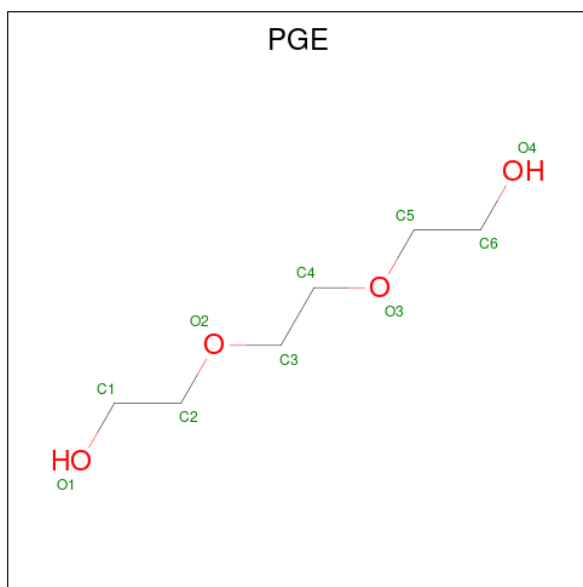
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0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

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 5 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		

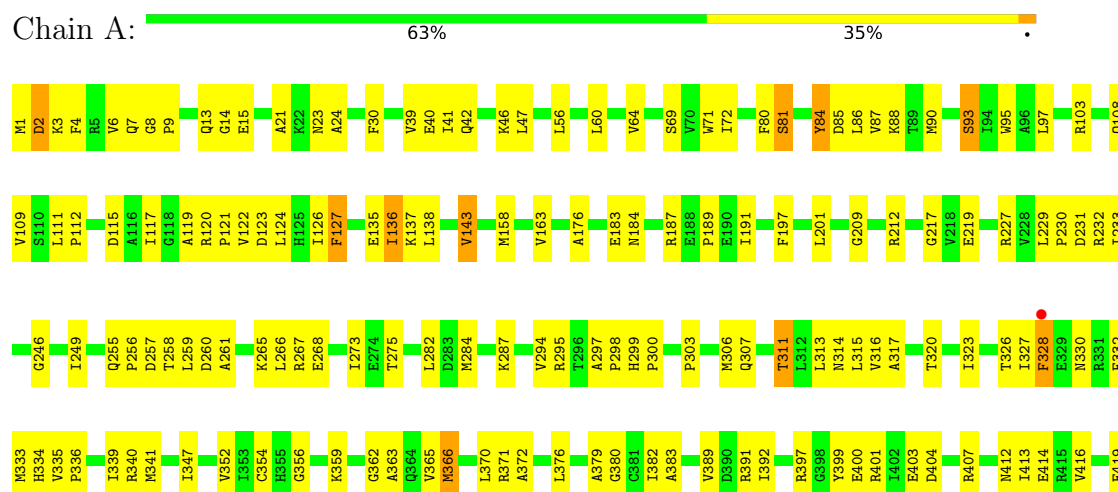
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	122	Total	O	0	0
			122	122		
6	B	131	Total	O	0	0
			131	131		
6	C	111	Total	O	0	0
			111	111		
6	D	112	Total	O	0	0
			112	112		

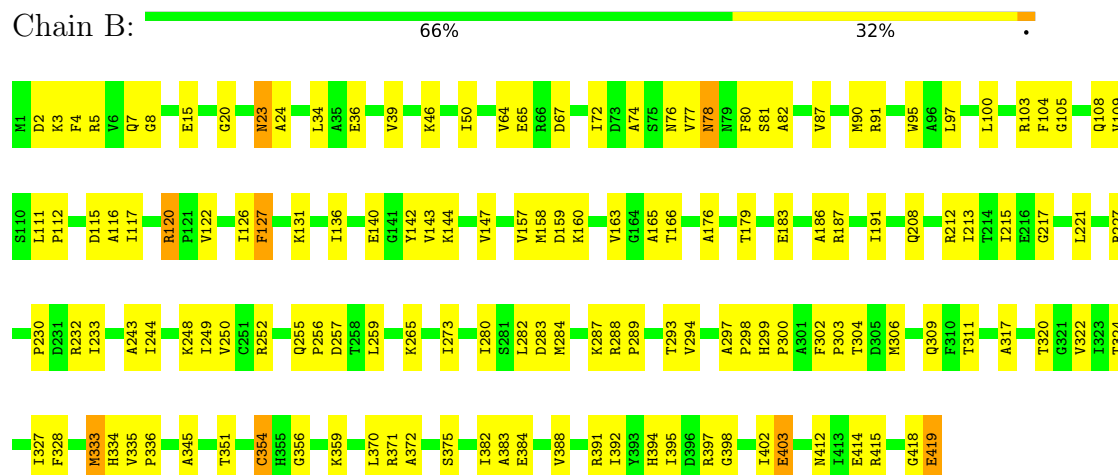
3 Residue-property plots

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: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

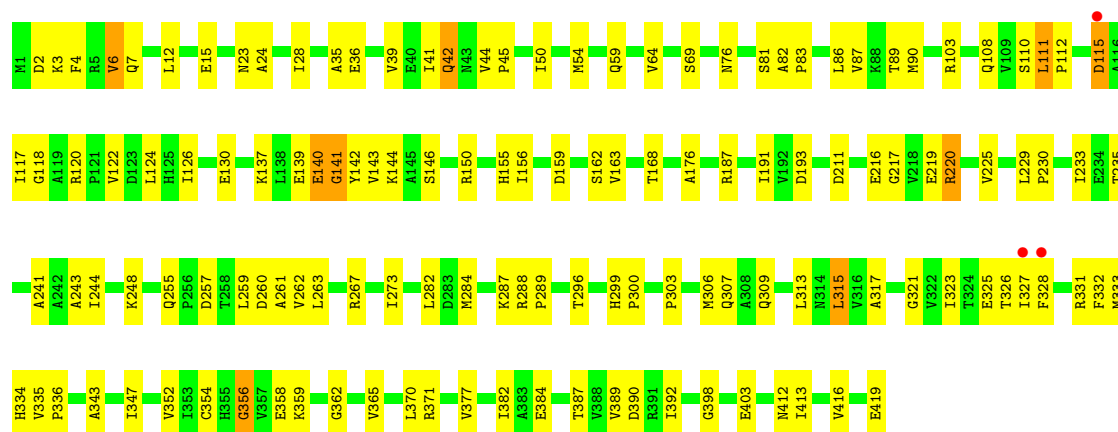


- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase

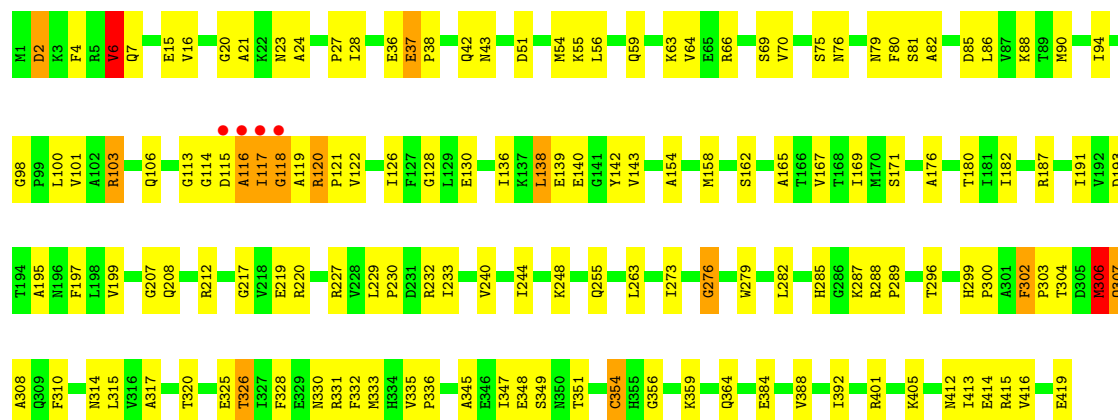


- Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase





● Molecule 1: UDP-N-acetylglucosamine 1-carboxyvinyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.14Å 101.69Å 213.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.70 19.89 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.89-2.70) 99.2 (19.89-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 2.71Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.191 , 0.264 0.191 , 0.265	Depositor DCC
R_{free} test set	1223 reflections (2.50%)	wwPDB-VP
Wilson B-factor (Å ²)	23.8	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13230	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: IAS, EDO, ACT, PGE, 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	0.55	0/3180	1.26	24/4308 (0.6%)
1	B	0.56	1/3180 (0.0%)	1.28	30/4308 (0.7%)
1	C	0.56	0/3180	1.32	39/4308 (0.9%)
1	D	0.64	3/3180 (0.1%)	1.29	26/4308 (0.6%)
All	All	0.58	4/12720 (0.0%)	1.29	119/17232 (0.7%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	307	GLN	C-O	-6.84	1.15	1.24
1	D	306	MET	C-O	-6.55	1.14	1.23
1	D	306	MET	SD-CE	-6.25	1.64	1.79
1	B	333	MET	SD-CE	5.02	1.92	1.79

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	118	GLY	N-CA-C	-10.61	97.11	112.81
1	C	307	GLN	N-CA-C	8.51	120.17	111.07
1	D	23	ASN	N-CA-C	8.11	122.27	112.38
1	C	76	ASN	N-CA-C	8.01	124.15	111.81
1	D	328	PHE	N-CA-C	7.77	121.45	110.50

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	3144	0	3215	148	0
1	B	3144	0	3215	131	0
1	C	3144	0	3215	129	0
1	D	3144	0	3215	118	0
2	A	14	0	19	12	0
2	C	7	0	10	14	0
2	D	7	0	9	0	0
3	A	32	0	48	9	0
3	B	28	0	42	15	0
3	C	32	0	48	5	0
3	D	40	0	60	15	0
4	A	4	0	3	0	0
4	C	4	0	3	4	0
5	B	10	0	14	10	0
6	A	122	0	0	5	0
6	B	131	0	0	4	0
6	C	111	0	0	4	0
6	D	112	0	0	1	0
All	All	13230	0	13116	503	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 19.

The worst 5 of 503 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:C:327:ILE:HG22	1:C:328:PHE:CD1	1.65	1.30
1:C:193:ASP:HB2	1:C:229:LEU:HD23	1.24	1.16
1:B:163:VAL:HG11	5:B:501:PGE:H62	1.10	1.10
1:A:230:PRO:HB2	3:A:509:EDO:H11	1.37	1.06
1:B:230:PRO:HB2	3:B:508:EDO:H12	1.39	1.01

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	415/419 (99%)	383 (92%)	30 (7%)	2 (0%)	24	48
1	B	415/419 (99%)	400 (96%)	14 (3%)	1 (0%)	43	68
1	C	415/419 (99%)	392 (94%)	22 (5%)	1 (0%)	43	68
1	D	415/419 (99%)	391 (94%)	22 (5%)	2 (0%)	24	48
All	All	1660/1676 (99%)	1566 (94%)	88 (5%)	6 (0%)	30	54

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	115	ASP
1	C	333	MET
1	D	120	ARG
1	A	2	ASP
1	A	115	ASP

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	329/329 (100%)	328 (100%)	1 (0%)	86	94
1	B	329/329 (100%)	325 (99%)	4 (1%)	63	84
1	C	329/329 (100%)	328 (100%)	1 (0%)	86	94
1	D	329/329 (100%)	321 (98%)	8 (2%)	43	72
All	All	1316/1316 (100%)	1302 (99%)	14 (1%)	65	85

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	63	LYS
1	D	117	ILE
1	D	351	THR
1	D	326	THR
1	D	348	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	79	ASN
1	C	307	GLN
1	D	412	ASN
1	C	344	HIS
1	B	344	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	IAS	D	67	1	6,7,8	0.93	0	3,8,10	0.95	0
1	IAS	C	67	1	6,7,8	1.03	0	3,8,10	1.01	0
1	IAS	A	67	1	6,7,8	1.03	0	3,8,10	0.94	0
1	IAS	B	67	1	6,7,8	0.99	0	3,8,10	0.98	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
1	IAS	D	67	1	-	0/7/7/8	-
1	IAS	C	67	1	-	0/7/7/8	-
1	IAS	A	67	1	-	0/7/7/8	-
1	IAS	B	67	1	-	0/7/7/8	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	67	IAS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

40 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	ACT	C	510	-	3,3,3	1.06	0	3,3,3	0.82	0
3	EDO	C	508	-	3,3,3	0.55	0	2,2,2	0.31	0
3	EDO	C	505	-	3,3,3	0.46	0	2,2,2	0.37	0
3	EDO	D	502	-	3,3,3	0.49	0	2,2,2	0.40	0
3	EDO	C	509	-	3,3,3	0.49	0	2,2,2	0.32	0
3	EDO	C	507	-	3,3,3	0.48	0	2,2,2	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PGE	B	501	-	9,9,9	0.45	0	8,8,8	0.29	0
2	PEG	A	502	-	6,6,6	1.58	1 (16%)	5,5,5	0.22	0
3	EDO	B	503	-	3,3,3	0.50	0	2,2,2	0.31	0
3	EDO	D	508	-	3,3,3	0.50	0	2,2,2	0.28	0
3	EDO	B	504	-	3,3,3	0.47	0	2,2,2	0.30	0
3	EDO	C	502	-	3,3,3	0.35	0	2,2,2	0.43	0
3	EDO	A	505	-	3,3,3	0.27	0	2,2,2	0.36	0
3	EDO	B	506	-	3,3,3	0.59	0	2,2,2	0.30	0
3	EDO	D	504	-	3,3,3	0.64	0	2,2,2	0.19	0
3	EDO	A	504	-	3,3,3	0.50	0	2,2,2	0.35	0
3	EDO	D	511	-	3,3,3	0.50	0	2,2,2	0.26	0
3	EDO	A	507	-	3,3,3	0.45	0	2,2,2	0.35	0
3	EDO	C	503	-	3,3,3	0.50	0	2,2,2	0.31	0
3	EDO	A	506	-	3,3,3	0.31	0	2,2,2	0.31	0
2	PEG	C	501	-	6,6,6	0.36	0	5,5,5	0.85	0
3	EDO	D	509	-	3,3,3	0.46	0	2,2,2	0.24	0
3	EDO	C	506	-	3,3,3	0.28	0	2,2,2	0.29	0
3	EDO	B	507	-	3,3,3	0.46	0	2,2,2	0.29	0
3	EDO	A	503	-	3,3,3	0.46	0	2,2,2	0.37	0
3	EDO	C	504	-	3,3,3	0.47	0	2,2,2	0.34	0
3	EDO	D	510	-	3,3,3	0.55	0	2,2,2	0.32	0
3	EDO	D	507	-	3,3,3	0.49	0	2,2,2	0.35	0
3	EDO	B	505	-	3,3,3	0.47	0	2,2,2	0.32	0
3	EDO	B	508	-	3,3,3	0.48	0	2,2,2	0.30	0
2	PEG	D	501	-	6,6,6	1.61	1 (16%)	5,5,5	0.21	0
2	PEG	A	501	-	6,6,6	0.29	0	5,5,5	1.34	1 (20%)
3	EDO	A	510	-	3,3,3	0.62	0	2,2,2	0.24	0
3	EDO	D	503	-	3,3,3	0.47	0	2,2,2	0.34	0
3	EDO	D	506	-	3,3,3	0.46	0	2,2,2	0.33	0
3	EDO	A	509	-	3,3,3	0.45	0	2,2,2	0.31	0
3	EDO	B	502	-	3,3,3	0.51	0	2,2,2	0.33	0
4	ACT	A	511	-	3,3,3	0.82	0	3,3,3	0.74	0
3	EDO	D	505	-	3,3,3	0.48	0	2,2,2	0.35	0
3	EDO	A	508	-	3,3,3	0.49	0	2,2,2	0.33	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	C	508	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	505	-	-	1/1/1/1	-
3	EDO	D	502	-	-	1/1/1/1	-
3	EDO	C	509	-	-	1/1/1/1	-
3	EDO	C	507	-	-	0/1/1/1	-
5	PGE	B	501	-	-	6/7/7/7	-
2	PEG	A	502	-	-	3/4/4/4	-
3	EDO	B	503	-	-	1/1/1/1	-
3	EDO	D	508	-	-	1/1/1/1	-
3	EDO	B	504	-	-	1/1/1/1	-
3	EDO	C	502	-	-	1/1/1/1	-
3	EDO	A	505	-	-	1/1/1/1	-
3	EDO	B	506	-	-	1/1/1/1	-
3	EDO	D	504	-	-	1/1/1/1	-
3	EDO	A	504	-	-	1/1/1/1	-
3	EDO	D	511	-	-	1/1/1/1	-
3	EDO	A	507	-	-	1/1/1/1	-
3	EDO	C	503	-	-	0/1/1/1	-
3	EDO	A	506	-	-	1/1/1/1	-
2	PEG	C	501	-	-	3/4/4/4	-
3	EDO	D	509	-	-	1/1/1/1	-
3	EDO	C	506	-	-	1/1/1/1	-
3	EDO	B	507	-	-	0/1/1/1	-
3	EDO	A	503	-	-	1/1/1/1	-
3	EDO	C	504	-	-	1/1/1/1	-
3	EDO	D	510	-	-	1/1/1/1	-
3	EDO	D	507	-	-	1/1/1/1	-
3	EDO	B	505	-	-	1/1/1/1	-
3	EDO	B	508	-	-	1/1/1/1	-
2	PEG	D	501	-	-	2/4/4/4	-
2	PEG	A	501	-	-	2/4/4/4	-
3	EDO	A	510	-	-	1/1/1/1	-
3	EDO	D	503	-	-	1/1/1/1	-
3	EDO	D	506	-	-	1/1/1/1	-
3	EDO	A	509	-	-	1/1/1/1	-
3	EDO	B	502	-	-	1/1/1/1	-
3	EDO	D	505	-	-	0/1/1/1	-
3	EDO	A	508	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	PEG	O1-C1	-3.68	1.23	1.42
2	A	502	PEG	O1-C1	-3.53	1.24	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	PEG	C3-O2-C2	2.31	123.36	113.26

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	PGE	C4-C3-O2-C2
5	B	501	PGE	O1-C1-C2-O2
2	A	501	PEG	O2-C3-C4-O4
2	A	502	PEG	O2-C3-C4-O4
2	D	501	PEG	O1-C1-C2-O2

There are no ring outliers.

23 monomers are involved in 84 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	510	ACT	4	0
3	D	502	EDO	1	0
3	C	507	EDO	1	0
5	B	501	PGE	10	0
3	B	503	EDO	2	0
3	D	508	EDO	3	0
3	C	502	EDO	2	0
3	D	504	EDO	1	0
3	D	511	EDO	1	0
3	A	507	EDO	2	0
3	C	503	EDO	1	0
2	C	501	PEG	14	0
3	D	509	EDO	1	0
3	C	506	EDO	1	0
3	B	507	EDO	9	0
3	A	503	EDO	2	0
3	D	507	EDO	4	0
3	B	508	EDO	4	0
2	A	501	PEG	12	0
3	A	510	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	503	EDO	2	0
3	A	509	EDO	4	0
3	D	505	EDO	2	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	418/419 (99%)	-0.43	1 (0%) 91 90	6, 21, 44, 80	0
1	B	418/419 (99%)	-0.56	0 100 100	6, 19, 38, 65	0
1	C	418/419 (99%)	-0.45	3 (0%) 84 83	6, 21, 49, 70	0
1	D	418/419 (99%)	-0.48	4 (0%) 79 78	5, 21, 42, 82	0
All	All	1672/1676 (99%)	-0.48	8 (0%) 87 86	5, 20, 43, 82	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	116	ALA	5.1
1	C	115	ASP	4.0
1	C	327	ILE	3.1
1	D	117	ILE	2.7
1	C	328	PHE	2.7

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
1	IAS	B	67	8/9	0.89	0.09	34,34,35,36	0
1	IAS	D	67	8/9	0.91	0.08	24,26,27,27	0
1	IAS	C	67	8/9	0.93	0.07	22,24,25,25	0
1	IAS	A	67	8/9	0.95	0.07	16,17,18,18	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
4	ACT	A	511	4/4	0.68	0.20	71,71,71,72	0
5	PGE	B	501	10/10	0.72	0.20	37,45,47,48	0
3	EDO	A	505	4/4	0.73	0.19	42,45,46,47	0
3	EDO	C	502	4/4	0.75	0.19	42,45,47,48	0
3	EDO	D	509	4/4	0.75	0.16	57,58,58,59	0
3	EDO	B	503	4/4	0.77	0.14	43,43,43,43	0
3	EDO	D	504	4/4	0.79	0.16	31,32,34,34	0
3	EDO	A	504	4/4	0.79	0.18	47,48,48,49	0
3	EDO	B	502	4/4	0.80	0.13	42,43,43,43	0
3	EDO	B	507	4/4	0.81	0.19	32,36,36,37	0
3	EDO	A	508	4/4	0.82	0.22	46,46,47,48	0
2	PEG	A	502	7/7	0.82	0.20	49,53,54,55	0
2	PEG	D	501	7/7	0.82	0.17	57,59,60,60	0
2	PEG	A	501	7/7	0.83	0.21	43,47,48,48	0
3	EDO	C	506	4/4	0.84	0.11	38,41,41,43	0
3	EDO	A	510	4/4	0.85	0.14	35,36,36,37	0
3	EDO	C	505	4/4	0.87	0.11	40,41,41,41	0
2	PEG	C	501	7/7	0.88	0.21	71,75,76,76	0
4	ACT	C	510	4/4	0.88	0.13	40,41,42,43	0
3	EDO	B	506	4/4	0.88	0.11	30,31,31,34	0
3	EDO	C	508	4/4	0.89	0.13	33,36,36,36	0
3	EDO	D	503	4/4	0.89	0.11	46,48,49,49	0
3	EDO	A	506	4/4	0.89	0.15	57,58,58,59	0
3	EDO	D	508	4/4	0.89	0.17	50,50,51,51	0
3	EDO	C	509	4/4	0.90	0.11	35,37,37,38	0
3	EDO	D	502	4/4	0.90	0.11	40,41,42,44	0
3	EDO	D	510	4/4	0.90	0.11	39,40,41,42	0
3	EDO	D	507	4/4	0.91	0.15	43,44,44,44	0
3	EDO	A	509	4/4	0.92	0.20	51,52,53,53	0
3	EDO	D	505	4/4	0.92	0.14	35,36,37,38	0
3	EDO	C	503	4/4	0.92	0.11	46,46,47,48	0
3	EDO	D	506	4/4	0.93	0.15	33,35,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	D	511	4/4	0.93	0.20	47,47,48,49	0
3	EDO	A	503	4/4	0.93	0.12	37,37,37,37	0
3	EDO	C	504	4/4	0.93	0.10	34,34,35,35	0
3	EDO	C	507	4/4	0.93	0.10	34,36,37,37	0
3	EDO	B	505	4/4	0.94	0.09	41,41,41,41	0
3	EDO	B	504	4/4	0.96	0.08	25,26,27,27	0
3	EDO	A	507	4/4	0.96	0.08	25,28,28,30	0
3	EDO	B	508	4/4	0.96	0.17	32,34,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.