



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:58 AM UTC

PDB ID : 6EB3 / pdb_00006eb3
Title : Structural and enzymatic characterization of an esterase from a metagenomic library
Authors : Guzzo, C.R.; Carvalho, C.F.; Teixeira, R.D.; Farah, C.S.
Deposited on : 2018-08-03
Resolution : 2.35 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

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

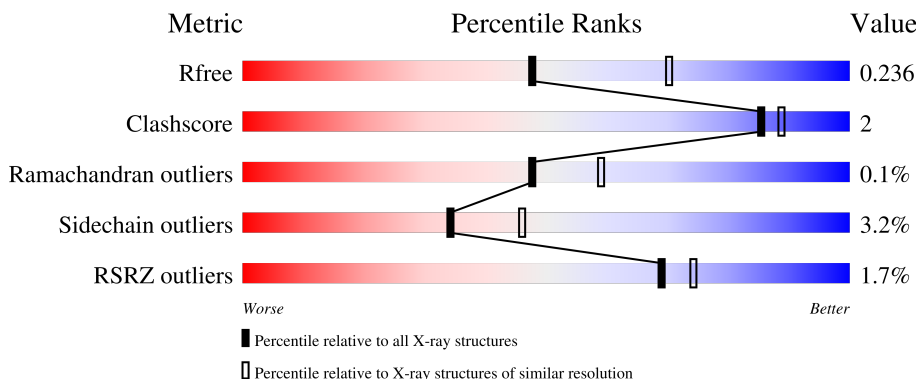
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	268	3% 88% 9% ..
1	B	268	2% 94% 5%
1	C	268	% 92% 6% .
1	D	268	94% 5% .

2 Entry composition [i](#)

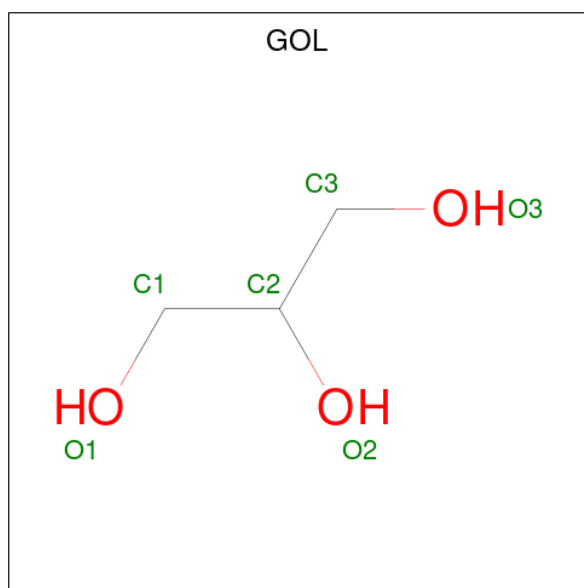
There are 9 unique types of molecules in this entry. The entry contains 8791 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Est1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	4	0
			2060	1326	353	371	10			
1	B	268	Total	C	N	O	S	0	6	0
			2112	1359	365	378	10			
1	C	262	Total	C	N	O	S	0	3	0
			2046	1317	351	368	10			
1	D	268	Total	C	N	O	S	0	3	0
			2082	1339	356	376	11			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



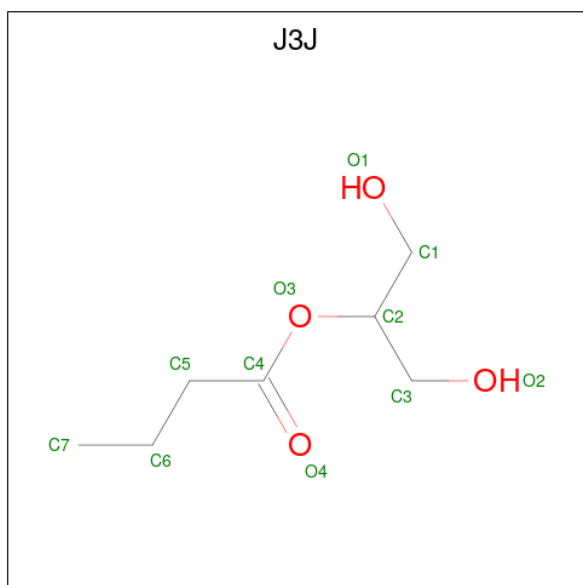
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is 1,3-dihydroxypropan-2-yl butanoate (CCD ID: J3J) (formula: $C_7H_{14}O_4$).



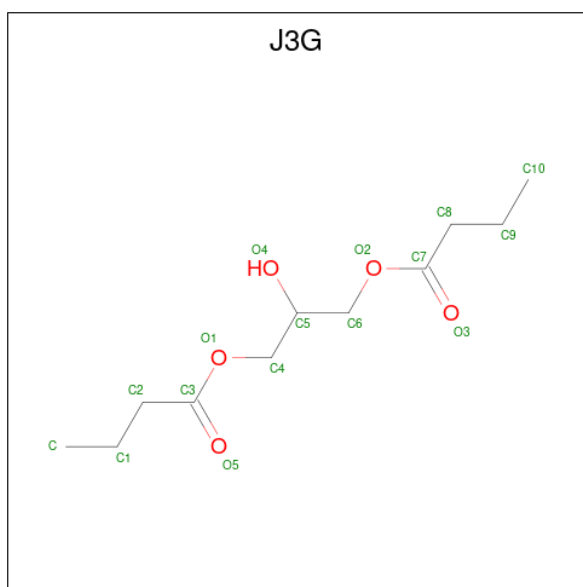
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	7	4		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 5 is 2-hydroxypropane-1,3-diyl dibutanoate (CCD ID: J3G) (formula: $C_{11}H_{20}O_5$).



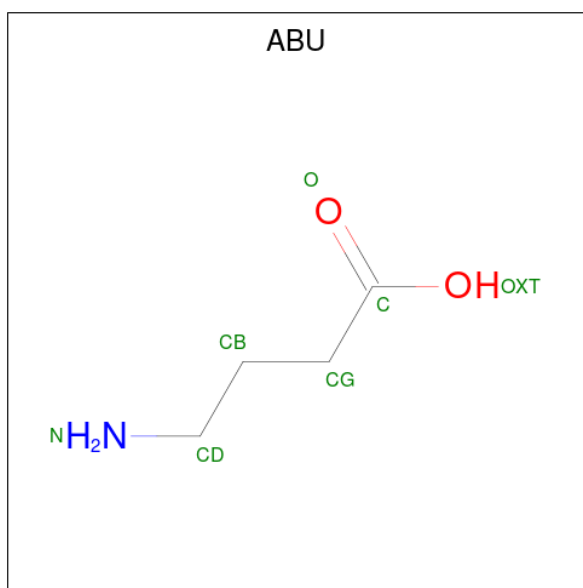
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			16	11	5		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

- Molecule 7 is GAMMA-AMINO-BUTANOIC ACID (CCD ID: ABU) (formula: $C_4H_9NO_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	4	2		
7	D	1	Total	C	O	0	0
			6	4	2		

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	D	1	Total	O	S	0	0
			5	4	1		
8	D	1	Total	O	S	0	0
			5	4	1		

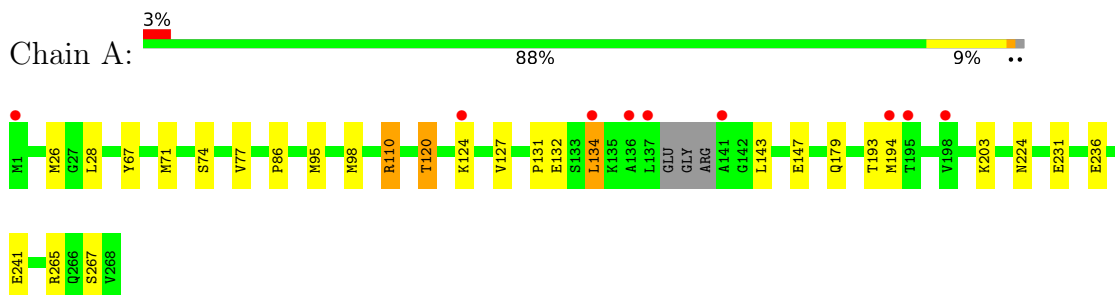
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	72	Total	O	0	0
			72	72		
9	B	87	Total	O	0	0
			87	87		
9	C	111	Total	O	0	0
			111	111		
9	D	121	Total	O	0	0
			121	121		

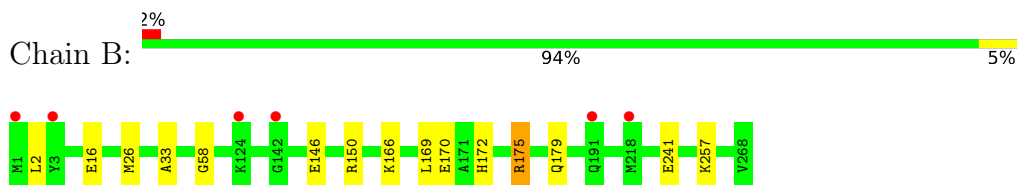
3 Residue-property plots [i](#)

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.

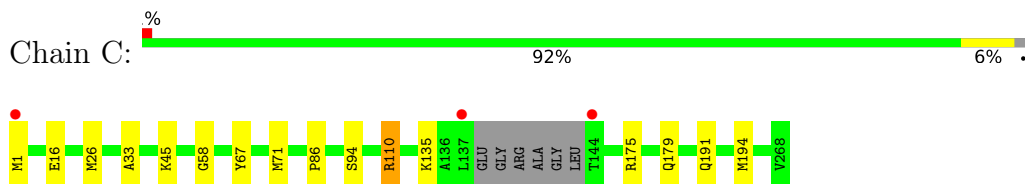
- Molecule 1: Est1



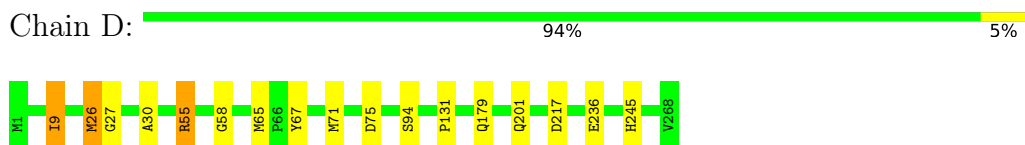
- Molecule 1: Est1



- Molecule 1: Est1



- Molecule 1: Est1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.65Å 105.95Å 145.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.87 – 2.35 19.87 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.87-2.35) 98.9 (19.87-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.35Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.193 , 0.233 0.196 , 0.236	Depositor DCC
R_{free} test set	2268 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.6	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	0.95	EDS
Total number of atoms	8791	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% 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: GOL, J3J, ABU, EDO, SO4, J3G, PO4

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	0.79	0/2117	0.97	6/2875 (0.2%)
1	B	0.75	1/2175 (0.0%)	0.89	1/2952 (0.0%)
1	C	0.76	0/2100	0.88	0/2850
1	D	0.78	0/2140	0.90	2/2903 (0.1%)
All	All	0.77	1/8532 (0.0%)	0.91	9/11580 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2	LEU	N-CA	5.33	1.52	1.46

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	127	VAL	CA-C-N	-9.75	110.03	120.66
1	A	127	VAL	C-N-CA	-9.75	110.03	120.66
1	B	241	GLU	N-CA-C	5.75	117.22	111.07
1	A	131	PRO	CA-C-N	5.51	127.98	120.54
1	A	131	PRO	C-N-CA	5.51	127.98	120.54
1	D	9	ILE	N-CA-CB	-5.33	102.08	111.93
1	A	132	GLU	CB-CA-C	-5.25	102.41	110.81
1	D	55	ARG	NE-CZ-NH2	-5.25	114.48	119.20
1	A	241	GLU	N-CA-C	5.24	116.80	111.14

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	2060	0	2086	13	0
1	B	2112	0	2145	4	0
1	C	2046	0	2078	9	0
1	D	2082	0	2117	13	0
2	A	18	0	24	2	0
2	D	6	0	8	0	0
3	A	11	0	0	0	0
4	B	4	0	6	0	0
4	C	8	0	12	0	0
5	B	16	0	0	0	0
6	B	5	0	0	0	0
7	C	6	0	0	0	0
7	D	6	0	0	0	0
8	C	10	0	0	0	0
8	D	10	0	0	0	0
9	A	72	0	0	0	0
9	B	87	0	0	0	0
9	C	111	0	0	1	0
9	D	121	0	0	0	0
All	All	8791	0	8476	37	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 2.

All (37) 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:D:55:ARG:HD3	1:D:71[A]:MET:HE3	1.68	0.74
1:D:26:MET:HE3	1:D:27:GLY:H	1.60	0.66
1:D:26:MET:HE2	1:D:30:ALA:CB	2.29	0.63
1:A:95:MET:HG3	1:A:98:MET:CE	2.32	0.60
1:B:33:ALA:O	1:B:175[A]:ARG:NH2	2.38	0.57
1:A:120:THR:HG23	1:A:224:ASN:CG	2.32	0.55
1:D:55:ARG:HD2	1:D:75:ASP:OD2	2.08	0.54
1:A:95:MET:HA	1:A:98:MET:HE2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:SER:HA	1:A:77[B]:VAL:HG22	1.92	0.52
1:D:55:ARG:CD	1:D:75:ASP:OD2	2.61	0.49
1:C:191:GLN:HA	1:C:191:GLN:OE1	2.12	0.48
1:A:28:LEU:HB2	2:A:301:GOL:H31	1.94	0.48
1:A:95:MET:HG3	1:A:98:MET:HE2	1.95	0.47
1:C:194:MET:CE	1:D:236:GLU:HG2	2.45	0.47
1:A:143:LEU:HB3	1:A:147:GLU:HG3	1.96	0.47
1:D:26:MET:HE3	1:D:27:GLY:N	2.27	0.46
1:A:236:GLU:OE2	1:A:265:ARG:NH2	2.39	0.46
1:B:150:ARG:NH1	1:B:170:GLU:OE2	2.50	0.45
1:C:45:LYS:NZ	9:C:404:HOH:O	2.48	0.45
1:D:58:GLY:HA2	1:D:179:GLN:HB3	1.99	0.45
1:C:194:MET:HE3	1:D:236:GLU:HG2	1.99	0.44
1:C:58:GLY:HA2	1:C:179:GLN:HB3	2.00	0.44
1:C:86:PRO:O	1:C:110[A]:ARG:NH1	2.50	0.44
1:D:217:ASP:OD2	1:D:245:HIS:HD2	2.00	0.44
1:D:65:MET:HE2	1:D:71[B]:MET:HE1	2.00	0.44
1:A:86:PRO:O	1:A:110[A]:ARG:NH1	2.51	0.43
1:B:58:GLY:HA2	1:B:179:GLN:HB3	2.00	0.43
1:A:67:TYR:CG	1:A:71:MET:HE1	2.54	0.43
1:A:98:MET:HE1	1:A:193:THR:HG22	2.00	0.42
1:C:1[B]:MET:HE3	1:C:1[B]:MET:HB2	1.82	0.42
1:A:28:LEU:HB2	2:A:301:GOL:C3	2.50	0.42
1:C:67:TYR:CG	1:C:71:MET:HE1	2.55	0.42
1:D:67:TYR:CG	1:D:71[A]:MET:HE1	2.55	0.41
1:B:172:HIS:O	1:B:175[A]:ARG:HG2	2.22	0.40
1:A:110[A]:ARG:HA	1:A:110[A]:ARG:HD2	1.96	0.40
1:C:33:ALA:O	1:C:175:ARG:HD2	2.22	0.40
1:D:26:MET:HE2	1:D:30:ALA:HB3	2.01	0.40

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	264/268 (98%)	258 (98%)	5 (2%)	1 (0%)	30	34
1	B	271/268 (101%)	266 (98%)	5 (2%)	0	100	100
1	C	260/268 (97%)	254 (98%)	6 (2%)	0	100	100
1	D	268/268 (100%)	264 (98%)	4 (2%)	0	100	100
All	All	1063/1072 (99%)	1042 (98%)	20 (2%)	1 (0%)	48	59

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	LEU

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	215/215 (100%)	204 (95%)	11 (5%)	21	26
1	B	221/215 (103%)	213 (96%)	8 (4%)	31	41
1	C	215/215 (100%)	209 (97%)	6 (3%)	38	51
1	D	218/215 (101%)	213 (98%)	5 (2%)	44	58
All	All	869/860 (101%)	839 (96%)	30 (4%)	34	42

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	MET
1	A	110[A]	ARG
1	A	110[B]	ARG
1	A	120	THR
1	A	124	LYS
1	A	134	LEU
1	A	179	GLN
1	A	194	MET
1	A	203	LYS
1	A	231	GLU

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Mol	Chain	Res	Type
1	A	267	SER
1	B	16	GLU
1	B	26	MET
1	B	146	GLU
1	B	166	LYS
1	B	169	LEU
1	B	175[A]	ARG
1	B	175[B]	ARG
1	B	257	LYS
1	C	16	GLU
1	C	26	MET
1	C	94	SER
1	C	110[A]	ARG
1	C	110[B]	ARG
1	C	135	LYS
1	D	9	ILE
1	D	26	MET
1	D	94	SER
1	D	131	PRO
1	D	201	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	B	54	ASN
1	B	106	HIS
1	C	18	GLN
1	C	54	ASN
1	D	54	ASN
1	D	109	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

16 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	$\# Z > 2$
2	GOL	A	303	-	5,5,5	0.35	0	5,5,5	0.11	0
8	SO4	C	303	-	4,4,4	0.45	0	6,6,6	0.13	0
3	J3J	A	304	-	10,10,10	1.63	1 (10%)	11,11,11	1.77	3 (27%)
4	EDO	B	301	-	3,3,3	0.51	0	2,2,2	0.17	0
8	SO4	D	303	-	4,4,4	0.46	0	6,6,6	0.15	0
5	J3G	B	302	-	15,15,15	1.56	2 (13%)	17,17,17	1.39	5 (29%)
2	GOL	A	301	-	5,5,5	0.29	0	5,5,5	0.61	0
8	SO4	D	302	-	4,4,4	0.46	0	6,6,6	0.15	0
6	PO4	B	303	-	4,4,4	0.80	0	6,6,6	0.69	0
7	ABU	D	301	-	5,5,6	1.02	0	5,5,6	1.17	0
2	GOL	A	302	-	5,5,5	0.45	0	5,5,5	0.63	0
2	GOL	D	304	-	5,5,5	0.41	0	5,5,5	0.19	0
4	EDO	C	304	-	3,3,3	0.47	0	2,2,2	0.32	0
8	SO4	C	302	-	4,4,4	0.47	0	6,6,6	0.19	0
7	ABU	C	301	-	5,5,6	0.95	0	5,5,6	1.11	0
4	EDO	C	305	-	3,3,3	0.44	0	2,2,2	0.35	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
2	GOL	A	303	-	-	2/4/4/4	-
3	J3J	A	304	-	-	2/11/11/11	-
4	EDO	B	301	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	J3G	B	302	-	-	6/16/16/16	-
2	GOL	A	301	-	-	0/4/4/4	-
7	ABU	D	301	-	-	0/3/3/4	-
2	GOL	A	302	-	-	2/4/4/4	-
2	GOL	D	304	-	-	2/4/4/4	-
4	EDO	C	304	-	-	1/1/1/1	-
7	ABU	C	301	-	-	1/3/3/4	-
4	EDO	C	305	-	-	1/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	304	J3J	O3-C4	4.72	1.47	1.34
5	B	302	J3G	O1-C3	4.39	1.46	1.33
5	B	302	J3G	O2-C7	3.76	1.44	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	304	J3J	O3-C4-C5	4.58	121.39	111.48
5	B	302	J3G	O1-C3-C2	2.83	120.45	111.83
5	B	302	J3G	O1-C3-O5	-2.33	117.79	123.63
5	B	302	J3G	O2-C7-C8	2.31	118.89	111.83
3	A	304	J3J	C3-C2-C1	-2.26	108.87	112.79
5	B	302	J3G	O2-C7-O3	-2.22	118.08	123.63
5	B	302	J3G	O1-C4-C5	2.13	115.87	105.85
3	A	304	J3J	O3-C4-O4	-2.01	119.00	123.70

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	302	GOL	C1-C2-C3-O3
2	A	303	GOL	C1-C2-C3-O3
3	A	304	J3J	O4-C4-O3-C2
3	A	304	J3J	C5-C4-O3-C2
5	B	302	J3G	O1-C4-C5-C6
5	B	302	J3G	O1-C4-C5-O4
2	D	304	GOL	O1-C1-C2-C3
2	A	302	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
2	A	303	GOL	O2-C2-C3-O3
5	B	302	J3G	C-C1-C2-C3
4	C	305	EDO	O1-C1-C2-O2
2	D	304	GOL	O1-C1-C2-O2
5	B	302	J3G	C7-C8-C9-C10
5	B	302	J3G	C2-C3-O1-C4
5	B	302	J3G	O5-C3-O1-C4
4	C	304	EDO	O1-C1-C2-O2
7	C	301	ABU	OXT-C-CG-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	GOL	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

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, 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	265/268 (98%)	0.22	9 (3%)	48	55	23, 48, 84, 98	4 (1%)
1	B	268/268 (100%)	0.03	6 (2%)	62	67	19, 41, 75, 90	6 (2%)
1	C	262/268 (97%)	-0.20	3 (1%)	78	82	21, 37, 64, 88	4 (1%)
1	D	268/268 (100%)	-0.20	0	100	100	18, 35, 58, 69	3 (1%)
All	All	1063/1072 (99%)	-0.04	18 (1%)	69	74	18, 40, 71, 98	17 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1[A]	MET	5.1
1	B	1[A]	MET	4.2
1	B	142	GLY	3.3
1	A	137	LEU	3.2
1	A	136	ALA	3.1
1	A	141	ALA	3.0
1	C	144	THR	2.9
1	A	124	LYS	2.7
1	A	1[A]	MET	2.7
1	A	195	THR	2.6
1	A	198	VAL	2.4
1	C	137	LEU	2.3
1	A	134	LEU	2.3
1	B	3[A]	TYR	2.3
1	A	194	MET	2.2
1	B	218	MET	2.0
1	B	124	LYS	2.0
1	B	191[A]	GLN	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 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
7	ABU	D	301	6/7	0.57	0.21	47,51,53,53	0
4	EDO	C	304	4/4	0.61	0.22	71,73,75,75	0
3	J3J	A	304	11/11	0.62	0.17	59,64,75,77	0
7	ABU	C	301	6/7	0.63	0.18	53,55,57,58	0
2	GOL	A	302	6/6	0.67	0.16	67,69,70,71	0
5	J3G	B	302	16/16	0.67	0.17	57,64,72,72	0
8	SO4	C	302	5/5	0.68	0.17	91,98,101,102	0
6	PO4	B	303	5/5	0.72	0.20	99,101,104,107	0
8	SO4	D	302	5/5	0.73	0.14	97,98,99,105	0
8	SO4	D	303	5/5	0.75	0.10	107,109,113,115	0
4	EDO	C	305	4/4	0.76	0.17	74,74,76,78	0
4	EDO	B	301	4/4	0.78	0.16	64,64,65,65	0
2	GOL	A	301	6/6	0.79	0.18	49,55,57,63	0
2	GOL	D	304	6/6	0.80	0.14	84,86,87,88	0
8	SO4	C	303	5/5	0.87	0.17	97,98,102,104	0
2	GOL	A	303	6/6	0.89	0.10	70,76,78,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.