



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:05 PM UTC

PDB ID : 6E8E / pdb_00006e8e
Title : Crystal structure of the Escherichia coli sliding clamp-MutL complex.
Authors : Guarne, A.; Almawi, A.W.
Deposited on : 2018-07-28
Resolution : 2.25 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

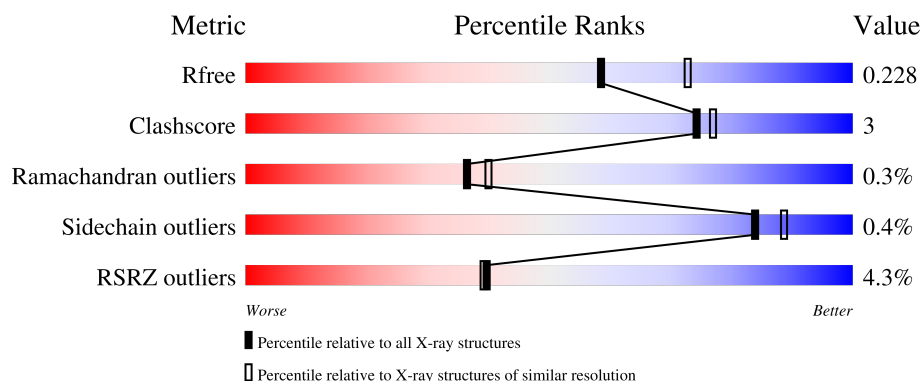
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

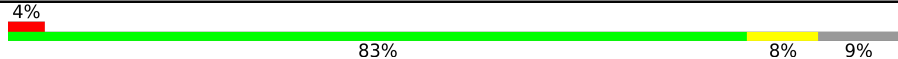
The reported resolution of this entry is 2.25 Å.

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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	517	
2	B	517	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7191 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 Beta sliding clamp,DNA mismatch repair protein MutL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	468	3522	2236	606	658	22	0	0	0

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0A988
A	2	GLY	-	expression tag	UNP P0A988
A	3	SER	-	expression tag	UNP P0A988
A	4	SER	-	expression tag	UNP P0A988
A	5	HIS	-	expression tag	UNP P0A988
A	6	HIS	-	expression tag	UNP P0A988
A	7	HIS	-	expression tag	UNP P0A988
A	8	HIS	-	expression tag	UNP P0A988
A	9	HIS	-	expression tag	UNP P0A988
A	10	HIS	-	expression tag	UNP P0A988
A	11	GLY	-	expression tag	UNP P0A988
A	12	SER	-	expression tag	UNP P0A988
A	13	GLY	-	expression tag	UNP P0A988
A	14	GLY	-	expression tag	UNP P0A988
A	15	GLY	-	expression tag	UNP P0A988
A	16	ASN	-	expression tag	UNP P0A988
A	17	ASN	-	expression tag	UNP P0A988
A	18	ASN	-	expression tag	UNP P0A988
A	19	ASN	-	expression tag	UNP P0A988
A	20	ASN	-	expression tag	UNP P0A988
A	21	ASN	-	expression tag	UNP P0A988
A	22	ASN	-	expression tag	UNP P0A988
A	23	ASN	-	expression tag	UNP P0A988
A	24	ASN	-	expression tag	UNP P0A988
A	25	ASN	-	expression tag	UNP P0A988
A	26	LEU	-	expression tag	UNP P0A988
A	27	GLY	-	expression tag	UNP P0A988

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Chain	Residue	Modelled	Actual	Comment	Reference
A	28	ILE	-	expression tag	UNP P0A988
A	29	GLU	-	expression tag	UNP P0A988
A	30	GLU	-	expression tag	UNP P0A988
A	31	ASN	-	expression tag	UNP P0A988
A	32	LEU	-	expression tag	UNP P0A988
A	33	TYR	-	expression tag	UNP P0A988
A	34	PHE	-	expression tag	UNP P0A988
A	35	GLN	-	expression tag	UNP P0A988
A	36	SER	-	expression tag	UNP P0A988
A	37	HIS	-	expression tag	UNP P0A988
A	38	MET	-	expression tag	UNP P0A988
A	405	VAL	-	linker	UNP P0A988
A	406	ASP	-	linker	UNP P0A988
A	407	SER	-	linker	UNP P0A988
A	408	GLY	-	linker	UNP P0A988
A	409	ALA	-	linker	UNP P0A988
A	410	SER	-	linker	UNP P0A988
A	411	GLY	-	linker	UNP P0A988
A	412	GLY	-	linker	UNP P0A988
A	413	SER	-	linker	UNP P0A988

- Molecule 2 is a protein called Beta sliding clamp,DNA mismatch repair protein MutL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	455	Total	C	N	O	S	0	0	0
			3417	2170	584	641	22			

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P0A988
B	2	GLY	-	expression tag	UNP P0A988
B	3	SER	-	expression tag	UNP P0A988
B	4	SER	-	expression tag	UNP P0A988
B	5	HIS	-	expression tag	UNP P0A988
B	6	HIS	-	expression tag	UNP P0A988
B	7	HIS	-	expression tag	UNP P0A988
B	8	HIS	-	expression tag	UNP P0A988
B	9	HIS	-	expression tag	UNP P0A988
B	10	HIS	-	expression tag	UNP P0A988
B	11	GLY	-	expression tag	UNP P0A988
B	12	SER	-	expression tag	UNP P0A988

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Chain	Residue	Modelled	Actual	Comment	Reference
B	13	GLY	-	expression tag	UNP P0A988
B	14	GLY	-	expression tag	UNP P0A988
B	15	GLY	-	expression tag	UNP P0A988
B	16	ASN	-	expression tag	UNP P0A988
B	17	ASN	-	expression tag	UNP P0A988
B	18	ASN	-	expression tag	UNP P0A988
B	19	ASN	-	expression tag	UNP P0A988
B	20	ASN	-	expression tag	UNP P0A988
B	21	ASN	-	expression tag	UNP P0A988
B	22	ASN	-	expression tag	UNP P0A988
B	23	ASN	-	expression tag	UNP P0A988
B	24	ASN	-	expression tag	UNP P0A988
B	25	ASN	-	expression tag	UNP P0A988
B	26	LEU	-	expression tag	UNP P0A988
B	27	GLY	-	expression tag	UNP P0A988
B	28	ILE	-	expression tag	UNP P0A988
B	29	GLU	-	expression tag	UNP P0A988
B	30	GLU	-	expression tag	UNP P0A988
B	31	ASN	-	expression tag	UNP P0A988
B	32	LEU	-	expression tag	UNP P0A988
B	33	TYR	-	expression tag	UNP P0A988
B	34	PHE	-	expression tag	UNP P0A988
B	35	GLN	-	expression tag	UNP P0A988
B	36	SER	-	expression tag	UNP P0A988
B	37	HIS	-	expression tag	UNP P0A988
B	38	MET	-	expression tag	UNP P0A988
B	405	VAL	-	linker	UNP P0A988
B	406	ASP	-	linker	UNP P0A988
B	407	SER	-	linker	UNP P0A988
B	408	GLY	-	linker	UNP P0A988
B	409	ALA	-	linker	UNP P0A988
B	410	SER	-	linker	UNP P0A988
B	411	GLY	-	linker	UNP P0A988
B	412	GLY	-	linker	UNP P0A988
B	413	SER	-	linker	UNP P0A988

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

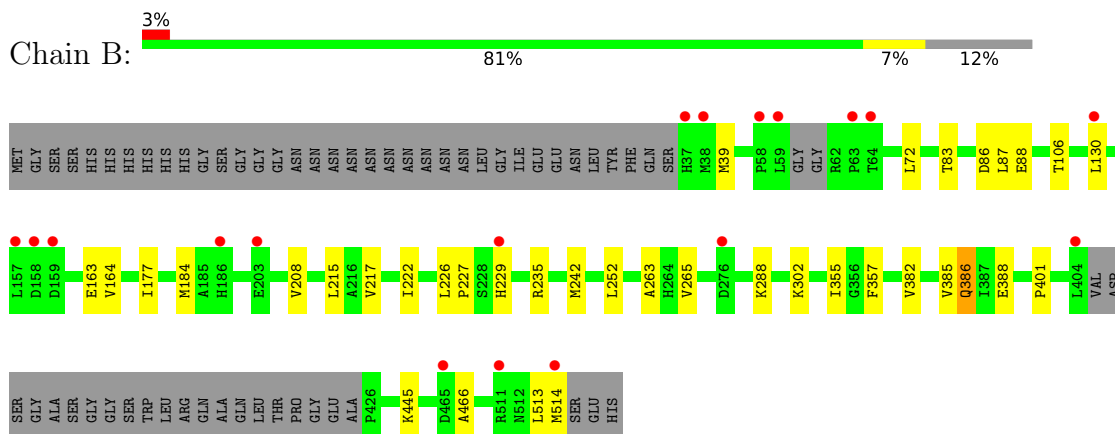


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	90	Total	O	0	0
			90	90		
5	B	101	Total	O	0	0
			101	101		

- Molecule 1: Beta sliding clamp, DNA mismatch repair protein MutL



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.39Å 103.21Å 141.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.83 – 2.25 46.83 – 2.25	Depositor EDS
% Data completeness (in resolution range)	96.6 (46.83-2.25) 96.6 (46.83-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.07Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.190 , 0.225 0.207 , 0.228	Depositor DCC
R_{free} test set	2000 reflections (2.97%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.0	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	7191	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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, CSO, SO4

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	1/3575 (0.0%)	0.75	5/4854 (0.1%)
2	B	0.46	2/3475 (0.1%)	0.76	2/4721 (0.0%)
All	All	0.50	3/7050 (0.0%)	0.75	7/9575 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	213	HIS	CA-C	5.48	1.59	1.52
2	B	215	LEU	CA-C	5.40	1.58	1.52
2	B	386	GLN	C-O	-5.31	1.17	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	88	GLU	N-CA-C	-10.01	101.57	113.88
1	A	88	GLU	N-CA-C	-8.34	103.62	113.88
1	A	62	ARG	C-N-CD	-7.18	95.57	125.00
1	A	466	ALA	N-CA-C	5.62	120.59	111.37
1	A	250	ASN	CA-C-N	-5.41	115.16	120.52
1	A	250	ASN	C-N-CA	-5.41	115.16	120.52
2	B	288	LYS	N-CA-C	-5.20	99.72	110.80

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	3522	0	3478	22	0
2	B	3417	0	3363	21	0
3	A	24	0	32	0	0
3	B	12	0	16	0	0
4	A	15	0	0	0	0
4	B	10	0	0	0	0
5	A	90	0	0	0	0
5	B	101	0	0	0	0
All	All	7191	0	6889	43	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 3.

All (43) 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:B:222:ILE:HD11	2:B:226:LEU:HD11	1.44	0.99
1:A:164:VAL:HG22	1:A:227:PRO:HG2	1.55	0.88
1:A:222:ILE:HD11	1:A:226:LEU:HD11	1.63	0.80
2:B:106:THR:HB	2:B:130:LEU:HD21	1.73	0.68
1:A:262:ARG:HD3	1:A:264:HIS:NE2	2.11	0.66
2:B:164:VAL:HG22	2:B:227:PRO:HG2	1.80	0.62
2:B:445:LYS:HE3	2:B:466:ALA:O	2.03	0.58
1:A:262:ARG:HD3	1:A:264:HIS:CE1	2.39	0.58
2:B:513:LEU:O	2:B:514:MET:HG2	2.06	0.56
2:B:184:MET:HE1	2:B:235:ARG:HA	1.88	0.56
2:B:208:VAL:HG22	2:B:217:VAL:HG23	1.88	0.54
2:B:163:GLU:OE1	2:B:229:HIS:HE1	1.92	0.53
1:A:252:LEU:HD11	1:A:263:ALA:HB1	1.91	0.52
2:B:355:ILE:HD11	2:B:401:PRO:HB3	1.91	0.52
1:A:184:MET:HE3	1:A:196:MET:HB2	1.91	0.52
2:B:39:MET:HE2	2:B:130:LEU:HD11	1.94	0.50
1:A:177:ILE:HD11	1:A:241:LEU:HD23	1.94	0.50
2:B:513:LEU:O	2:B:514:MET:CG	2.61	0.48
1:A:262:ARG:HH11	1:A:264:HIS:CE1	2.32	0.47
1:A:262:ARG:HH11	1:A:264:HIS:HE1	1.63	0.47
1:A:252:LEU:HD13	1:A:265:VAL:CG2	2.45	0.47
1:A:465:ASP:OD1	1:A:465:ASP:C	2.58	0.47
2:B:39:MET:HE2	2:B:130:LEU:CD1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:VAL:HA	1:A:431:PRO:HG3	1.99	0.45
2:B:513:LEU:O	2:B:514:MET:SD	2.75	0.44
1:A:319:VAL:HG12	1:A:332:ALA:HB2	2.00	0.44
1:A:355:ILE:HD11	1:A:401:PRO:HB3	1.99	0.43
2:B:252:LEU:HD13	2:B:265:VAL:HG23	1.99	0.43
2:B:513:LEU:C	2:B:514:MET:HG2	2.43	0.43
1:A:85:THR:HG21	1:A:155:PRO:HG2	2.00	0.43
2:B:386:GLN:NE2	2:B:388:GLU:OE2	2.52	0.42
1:A:252:LEU:HD13	1:A:265:VAL:HG23	2.01	0.42
2:B:357:PHE:CZ	2:B:385:VAL:HG21	2.54	0.42
1:A:175:ARG:HG2	1:A:220:MET:HE2	2.02	0.42
1:A:482:ASN:O	1:A:486:LEU:HG	2.20	0.42
2:B:252:LEU:HD11	2:B:263:ALA:HB1	2.00	0.42
2:B:72:LEU:HB3	2:B:83:THR:HB	2.01	0.41
1:A:108:VAL:HG11	1:A:135:MET:SD	2.60	0.41
1:A:215:LEU:C	1:A:215:LEU:HD23	2.46	0.41
2:B:86:ASP:O	2:B:87:LEU:HB2	2.21	0.41
1:A:106:THR:HG21	1:A:130:LEU:HD21	2.03	0.41
1:A:43:VAL:HG21	1:A:48:LEU:HD13	2.03	0.40
2:B:177:ILE:HG21	2:B:242:MET:HG2	2.02	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	461/517 (89%)	451 (98%)	8 (2%)	2 (0%)	30	31
2	B	449/517 (87%)	439 (98%)	9 (2%)	1 (0%)	43	50
All	All	910/1034 (88%)	890 (98%)	17 (2%)	3 (0%)	36	40

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	382	VAL
1	A	382	VAL
1	A	63	PRO

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	365/436 (84%)	363 (100%)	2 (0%)	81	87
2	B	355/437 (81%)	354 (100%)	1 (0%)	86	90
All	All	720/873 (82%)	717 (100%)	3 (0%)	84	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	214	ARG
1	A	294	LEU
2	B	302	LYS

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	186	HIS
2	B	54	GLN
2	B	229	HIS
2	B	255	GLN
2	B	373	ASN
2	B	468	HIS
2	B	484	GLN

5.3.3 RNA ⓘ

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.

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	CSO	A	428	1	3,6,7	0.79	0	1,6,8	0.16	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	CSO	A	428	1	-	0/1/5/7	-

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 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	GOL	A	603	-	5,5,5	0.41	0	5,5,5	0.40	0
4	SO4	A	607	-	4,4,4	0.36	0	6,6,6	0.13	0
4	SO4	A	605	-	4,4,4	0.23	0	6,6,6	0.10	0
4	SO4	A	606	-	4,4,4	0.23	0	6,6,6	0.15	0
4	SO4	B	603	-	4,4,4	0.23	0	6,6,6	0.06	0
3	GOL	A	604	-	5,5,5	0.37	0	5,5,5	0.24	0
3	GOL	A	602	-	5,5,5	0.34	0	5,5,5	0.68	0
3	GOL	B	602	-	5,5,5	0.38	0	5,5,5	0.33	0
3	GOL	A	601	-	5,5,5	0.36	0	5,5,5	0.39	0
3	GOL	B	601	-	5,5,5	0.37	0	5,5,5	0.21	0
4	SO4	B	604	-	4,4,4	0.24	0	6,6,6	0.11	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	GOL	A	603	-	-	4/4/4/4	-
3	GOL	A	604	-	-	0/4/4/4	-
3	GOL	A	602	-	-	0/4/4/4	-
3	GOL	B	602	-	-	0/4/4/4	-
3	GOL	A	601	-	-	0/4/4/4	-
3	GOL	B	601	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	603	GOL	C1-C2-C3-O3
3	B	601	GOL	O1-C1-C2-C3
3	A	603	GOL	O1-C1-C2-C3
3	A	603	GOL	O2-C2-C3-O3
3	B	601	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	A	603	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	467/517 (90%)	0.37	22 (4%)	36 35	31, 47, 73, 91	0
2	B	455/517 (88%)	0.37	18 (3%)	42 42	33, 48, 69, 104	0
All	All	922/1034 (89%)	0.37	40 (4%)	40 39	31, 47, 71, 104	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	514	MET	4.3
2	B	404	LEU	4.2
1	A	64	THR	4.0
2	B	63	PRO	3.9
1	A	63	PRO	3.8
1	A	158	ASP	3.7
2	B	64	THR	3.7
1	A	291	ASP	3.5
2	B	158	ASP	3.4
1	A	34	PHE	3.3
1	A	241	LEU	3.2
1	A	27	GLY	3.0
1	A	426	PRO	3.0
1	A	466	ALA	3.0
1	A	32	LEU	2.9
2	B	37	HIS	2.9
2	B	130	LEU	2.8
2	B	157	LEU	2.8
2	B	203	GLU	2.8
1	A	28	ILE	2.8
1	A	514	MET	2.7
2	B	186	HIS	2.7
2	B	58	PRO	2.7
1	A	264	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	382	VAL	2.7
1	A	506	ALA	2.5
1	A	59	LEU	2.5
2	B	465	ASP	2.5
1	A	61	GLY	2.5
2	B	59	LEU	2.4
2	B	159	ASP	2.3
2	B	229	HIS	2.3
2	B	276	ASP	2.2
2	B	38	MET	2.2
1	A	65	LEU	2.1
1	A	404	LEU	2.1
2	B	511	ARG	2.1
1	A	157	LEU	2.1
1	A	62	ARG	2.1
1	A	33	TYR	2.0

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
1	CSO	A	428	7/8	0.90	0.11	51,52,64,68	0

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(Å ²)	Q<0.9
4	SO4	B	604	5/5	0.54	0.14	89,95,102,123	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	601	6/6	0.76	0.18	54,61,63,72	0
3	GOL	A	602	6/6	0.76	0.21	52,64,74,83	0
4	SO4	A	607	5/5	0.78	0.10	72,73,79,103	0
3	GOL	A	603	6/6	0.79	0.18	48,63,64,67	0
3	GOL	A	601	6/6	0.87	0.14	53,57,65,70	0
3	GOL	B	602	6/6	0.93	0.11	40,45,49,49	0
3	GOL	A	604	6/6	0.95	0.09	44,48,48,53	0
4	SO4	A	605	5/5	0.95	0.10	57,58,66,69	0
4	SO4	B	603	5/5	0.96	0.10	52,53,55,56	0
4	SO4	A	606	5/5	0.97	0.07	53,53,54,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.