



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 10:27 am BST

PDB ID : 4M0V
Title : Crystal structure of E.coli SbcD with Mn²⁺
Authors : Liu, S.; Tian, L.F.; Yan, X.X.; Liang, D.C.
Deposited on : 2013-08-02
Resolution : 1.83 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

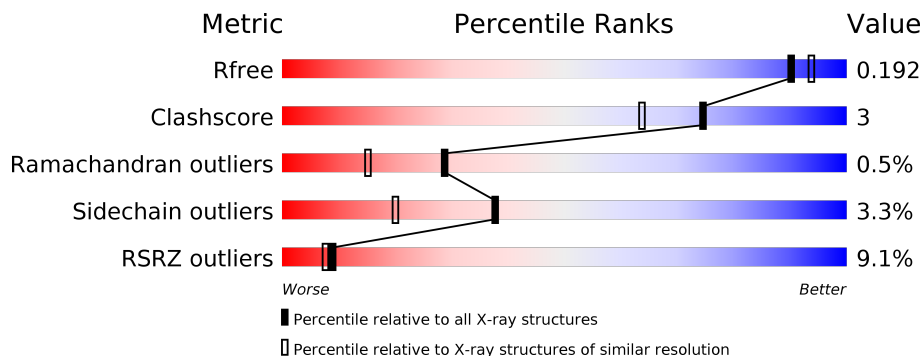
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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 on 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	354	10% (Poor fit) 82% (0 outliers) 10% (1 outlier) 6% (2 outliers)
1	B	354	7% (Poor fit) 92% (0 outliers) 5% (1 outlier) 6% (2 outliers)
1	C	354	7% (Poor fit) 86% (0 outliers) 9% (1 outlier) 8% (2 outliers)
1	D	354	10% (Poor fit) 89% (0 outliers) 8% (1 outlier) 3% (2 outliers)

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MN	C	403	-	-	-	X

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 11308 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 Exonuclease subunit SbcD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	332	Total	C	N	O	S	0	5	0
			2509	1593	439	468	9			
1	B	342	Total	C	N	O	S	0	5	0
			2600	1648	455	488	9			
1	C	345	Total	C	N	O	S	0	9	0
			2680	1709	466	494	11			
1	D	345	Total	C	N	O	S	0	7	0
			2651	1689	465	486	11			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP E8Y9D8
A	-12	SER	-	EXPRESSION TAG	UNP E8Y9D8
A	-11	HIS	-	EXPRESSION TAG	UNP E8Y9D8
A	-10	HIS	-	EXPRESSION TAG	UNP E8Y9D8
A	-9	HIS	-	EXPRESSION TAG	UNP E8Y9D8
A	-8	HIS	-	EXPRESSION TAG	UNP E8Y9D8
A	-7	HIS	-	EXPRESSION TAG	UNP E8Y9D8
A	-6	HIS	-	EXPRESSION TAG	UNP E8Y9D8
A	-5	SER	-	EXPRESSION TAG	UNP E8Y9D8
A	-4	MET	-	EXPRESSION TAG	UNP E8Y9D8
A	-3	ASP	-	EXPRESSION TAG	UNP E8Y9D8
A	-2	ILE	-	EXPRESSION TAG	UNP E8Y9D8
A	-1	GLU	-	EXPRESSION TAG	UNP E8Y9D8
A	0	PHE	-	EXPRESSION TAG	UNP E8Y9D8
B	-13	MET	-	EXPRESSION TAG	UNP E8Y9D8
B	-12	SER	-	EXPRESSION TAG	UNP E8Y9D8
B	-11	HIS	-	EXPRESSION TAG	UNP E8Y9D8
B	-10	HIS	-	EXPRESSION TAG	UNP E8Y9D8
B	-9	HIS	-	EXPRESSION TAG	UNP E8Y9D8
B	-8	HIS	-	EXPRESSION TAG	UNP E8Y9D8
B	-7	HIS	-	EXPRESSION TAG	UNP E8Y9D8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	EXPRESSION TAG	UNP E8Y9D8
B	-5	SER	-	EXPRESSION TAG	UNP E8Y9D8
B	-4	MET	-	EXPRESSION TAG	UNP E8Y9D8
B	-3	ASP	-	EXPRESSION TAG	UNP E8Y9D8
B	-2	ILE	-	EXPRESSION TAG	UNP E8Y9D8
B	-1	GLU	-	EXPRESSION TAG	UNP E8Y9D8
B	0	PHE	-	EXPRESSION TAG	UNP E8Y9D8
C	-13	MET	-	EXPRESSION TAG	UNP E8Y9D8
C	-12	SER	-	EXPRESSION TAG	UNP E8Y9D8
C	-11	HIS	-	EXPRESSION TAG	UNP E8Y9D8
C	-10	HIS	-	EXPRESSION TAG	UNP E8Y9D8
C	-9	HIS	-	EXPRESSION TAG	UNP E8Y9D8
C	-8	HIS	-	EXPRESSION TAG	UNP E8Y9D8
C	-7	HIS	-	EXPRESSION TAG	UNP E8Y9D8
C	-6	HIS	-	EXPRESSION TAG	UNP E8Y9D8
C	-5	SER	-	EXPRESSION TAG	UNP E8Y9D8
C	-4	MET	-	EXPRESSION TAG	UNP E8Y9D8
C	-3	ASP	-	EXPRESSION TAG	UNP E8Y9D8
C	-2	ILE	-	EXPRESSION TAG	UNP E8Y9D8
C	-1	GLU	-	EXPRESSION TAG	UNP E8Y9D8
C	0	PHE	-	EXPRESSION TAG	UNP E8Y9D8
D	-13	MET	-	EXPRESSION TAG	UNP E8Y9D8
D	-12	SER	-	EXPRESSION TAG	UNP E8Y9D8
D	-11	HIS	-	EXPRESSION TAG	UNP E8Y9D8
D	-10	HIS	-	EXPRESSION TAG	UNP E8Y9D8
D	-9	HIS	-	EXPRESSION TAG	UNP E8Y9D8
D	-8	HIS	-	EXPRESSION TAG	UNP E8Y9D8
D	-7	HIS	-	EXPRESSION TAG	UNP E8Y9D8
D	-6	HIS	-	EXPRESSION TAG	UNP E8Y9D8
D	-5	SER	-	EXPRESSION TAG	UNP E8Y9D8
D	-4	MET	-	EXPRESSION TAG	UNP E8Y9D8
D	-3	ASP	-	EXPRESSION TAG	UNP E8Y9D8
D	-2	ILE	-	EXPRESSION TAG	UNP E8Y9D8
D	-1	GLU	-	EXPRESSION TAG	UNP E8Y9D8
D	0	PHE	-	EXPRESSION TAG	UNP E8Y9D8

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Mn 2 2	0	0
3	A	2	Total Mn 2 2	0	0
3	D	2	Total Mn 2 2	0	0
3	C	2	Total Mn 2 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	164	Total O 164 164	0	0

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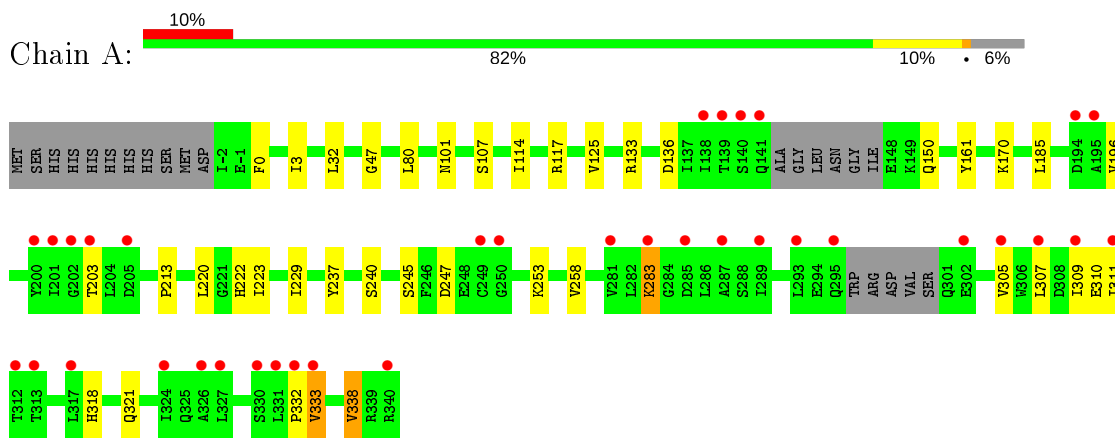
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	194	Total 194	O 194	0	0
4	C	236	Total 236	O 236	0	0
4	D	242	Total 242	O 242	0	0

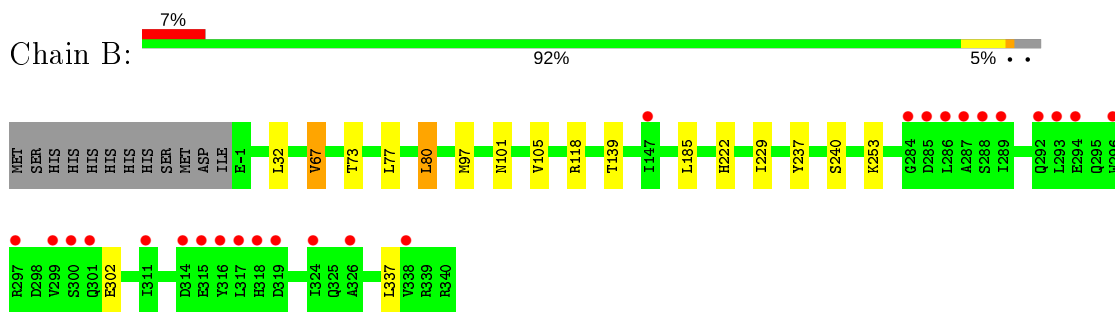
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

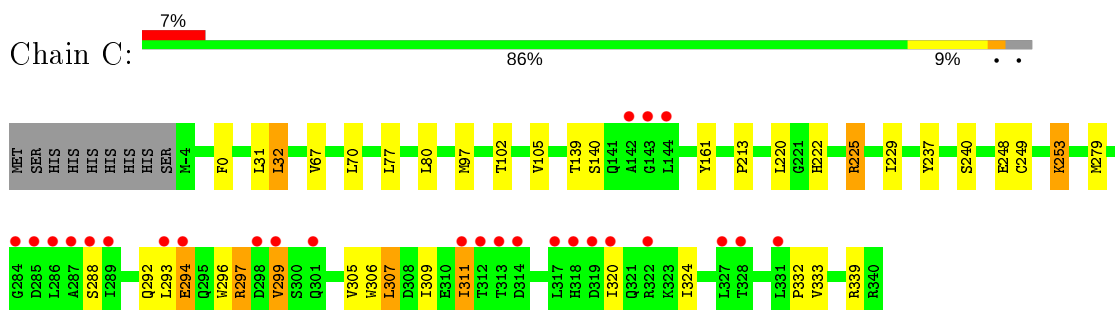
- Molecule 1: Exonuclease subunit SbcD



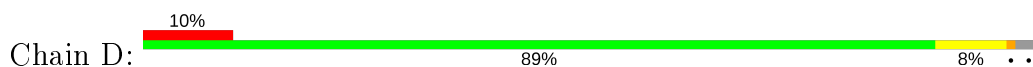
- Molecule 1: Exonuclease subunit SbcD

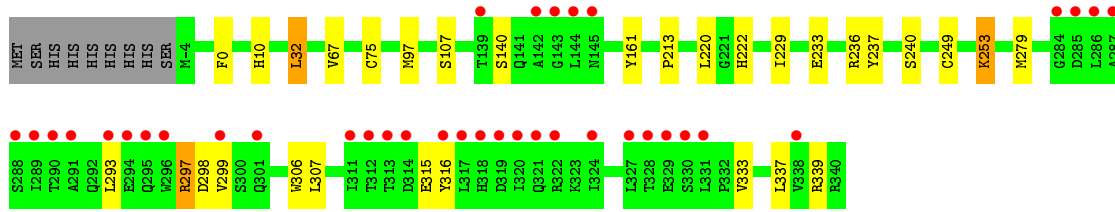


- Molecule 1: Exonuclease subunit SbcD



- Molecule 1: Exonuclease subunit SbcD





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	62.16Å 69.23Å 95.19Å 72.24° 84.00° 83.48°	Depositor
Resolution (Å)	19.97 – 1.83 46.93 – 1.83	Depositor EDS
% Data completeness (in resolution range)	97.7 (19.97-1.83) 97.7 (46.93-1.83)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.13 (at 1.83Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.162 , 0.199 0.155 , 0.192	Depositor DCC
R_{free} test set	6330 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtrriage
Anisotropy	0.458	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11308	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.79% 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: GOL, MN

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	0.37	0/2567	0.55	0/3512
1	B	0.35	0/2662	0.56	1/3646 (0.0%)
1	C	0.40	0/2742	0.59	0/3750
1	D	0.40	0/2714	0.59	0/3713
All	All	0.38	0/10685	0.57	1/14621 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	80	LEU	CA-CB-CG	5.15	127.15	115.30

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	2509	0	2359	21	0
1	B	2600	0	2461	7	0
1	C	2680	0	2595	22	0
1	D	2651	0	2555	16	0
2	A	6	0	8	0	0
2	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	6	0	8	0	0
2	D	6	0	8	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	164	0	0	0	0
4	B	194	0	0	0	0
4	C	236	0	0	1	0
4	D	242	0	0	1	0
All	All	11308	0	10002	66	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 (66) 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:A:332:PRO:O	1:A:333:VAL:HG13	1.55	1.06
1:A:332:PRO:O	1:A:333:VAL:CG1	2.30	0.79
1:C:311:ILE:HD11	1:C:324:ILE:HD11	1.67	0.77
1:A:133[A]:ARG:NH1	1:A:136:ASP:OD2	2.26	0.68
1:D:279[A]:MET:HG2	1:D:306:TRP:HB2	1.78	0.65
1:C:249:CYS:SG	4:C:707:HOH:O	2.55	0.65
1:D:10:HIS:NE2	4:D:742:HOH:O	2.29	0.65
1:C:220:LEU:HD12	1:C:229[A]:ILE:HD13	1.83	0.61
1:D:249:CYS:HB3	1:D:279[B]:MET:HE2	1.83	0.59
1:C:67:VAL:HG11	1:C:97:MET:SD	2.42	0.59
1:C:294:GLU:OE1	1:C:297:ARG:NH2	2.34	0.58
1:C:279[B]:MET:HG2	1:C:306:TRP:HB2	1.86	0.58
1:D:307:LEU:HD23	1:D:333:VAL:HB	1.85	0.58
1:C:299:VAL:HA	1:C:332:PRO:HG3	1.85	0.58
1:D:315:GLU:O	1:D:316:TYR:CB	2.51	0.58
1:A:220:LEU:HD12	1:A:229:ILE:HD13	1.85	0.58
1:D:67:VAL:HG11	1:D:97:MET:SD	2.44	0.58
1:A:283:LYS:HA	1:A:310:GLU:O	2.04	0.58
1:B:67:VAL:HG11	1:B:97:MET:SD	2.45	0.57
1:A:332:PRO:C	1:A:333:VAL:HG13	2.26	0.54
1:D:220:LEU:HD12	1:D:229:ILE:HD13	1.90	0.53
1:C:229[B]:ILE:HD11	1:C:237:TYR:CD2	2.44	0.53
1:A:150:GLN:HA	1:A:203:THR:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:67:VAL:HG21	1:B:97:MET:SD	2.51	0.51
1:D:337:LEU:HD21	1:D:339:ARG:HD3	1.93	0.51
1:A:161:TYR:HB3	1:A:213:PRO:HD3	1.92	0.50
1:B:80:LEU:HD13	1:B:105:VAL:HB	1.94	0.50
1:A:245:SER:OG	1:A:247:ASP:OD1	2.26	0.50
1:B:67:VAL:HG23	1:B:77:LEU:HD23	1.96	0.48
1:A:196:VAL:HG11	1:A:223:ILE:HD13	1.96	0.48
1:C:161:TYR:HB3	1:C:213:PRO:HD3	1.96	0.47
1:A:309:ILE:HB	1:A:338:VAL:HG12	1.96	0.47
1:B:73:THR:O	1:B:118:ARG:NH1	2.47	0.47
1:C:220:LEU:HD12	1:C:229[A]:ILE:CD1	2.46	0.46
1:A:240:SER:O	1:A:253[A]:LYS:HD3	2.16	0.46
1:A:170:LYS:HE3	1:A:170:LYS:HB2	1.69	0.46
1:C:139:THR:HA	1:C:140:SER:HA	1.65	0.46
1:C:240:SER:O	1:C:253[B]:LYS:HD3	2.16	0.46
1:A:3:ILE:HG13	1:A:258:VAL:HB	1.99	0.45
1:C:296:TRP:NE1	1:C:305:VAL:HG21	2.32	0.45
1:C:307:LEU:HD22	1:C:333:VAL:HB	1.99	0.45
1:D:229:ILE:HD11	1:D:237:TYR:CD2	2.52	0.45
1:C:32:LEU:HA	1:C:32:LEU:HD12	1.82	0.45
1:C:70:LEU:CD2	1:C:77:LEU:HB2	2.47	0.45
1:D:233:GLU:O	1:D:236:ARG:HD3	2.17	0.44
1:A:318:HIS:O	1:A:321:GLN:HB2	2.18	0.44
1:D:161:TYR:HB3	1:D:213:PRO:HD3	2.00	0.43
1:D:240:SER:O	1:D:253[B]:LYS:HD3	2.18	0.43
1:D:67:VAL:HG21	1:D:97:MET:SD	2.58	0.43
1:D:297:ARG:O	1:D:298:ASP:CB	2.67	0.43
1:B:229[B]:ILE:HD11	1:B:237:TYR:CD2	2.53	0.43
1:A:0:PHE:O	1:A:117:ARG:NH1	2.51	0.42
1:A:47:GLY:HA2	1:A:80:LEU:O	2.18	0.42
1:A:114:ILE:HD13	1:A:125:VAL:HG22	2.01	0.42
1:C:253[A]:LYS:HE3	1:C:253[A]:LYS:HA	2.01	0.42
1:A:229:ILE:HD11	1:A:237:TYR:CD2	2.54	0.42
1:C:309[B]:ILE:HG22	1:C:311:ILE:HG12	2.01	0.42
1:A:305:VAL:CG1	1:A:333:VAL:HG11	2.50	0.42
1:C:225:ARG:NH1	1:C:248:GLU:OE1	2.53	0.41
1:C:97:MET:HB3	1:C:102:THR:HB	2.02	0.41
1:A:305:VAL:HG22	1:A:307:LEU:HD22	2.02	0.41
1:C:80:LEU:HD13	1:C:105:VAL:HB	2.03	0.41
1:B:240:SER:O	1:B:253[A]:LYS:HD3	2.20	0.41
1:C:288:SER:O	1:C:292:GLN:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:32:LEU:HD12	1:D:32:LEU:HA	1.88	0.40
1:D:339:ARG:HB2	1:D:339:ARG:HE	1.63	0.40

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	331/354 (94%)	317 (96%)	11 (3%)	3 (1%)	17	6
1	B	345/354 (98%)	334 (97%)	10 (3%)	1 (0%)	41	27
1	C	352/354 (99%)	340 (97%)	10 (3%)	2 (1%)	25	12
1	D	350/354 (99%)	337 (96%)	12 (3%)	1 (0%)	41	27
All	All	1378/1416 (97%)	1328 (96%)	43 (3%)	7 (0%)	29	15

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	311	ILE
1	C	222	HIS
1	D	222	HIS
1	A	222	HIS
1	B	222	HIS
1	C	299	VAL
1	A	333	VAL

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	251/303 (83%)	245 (98%)	6 (2%)	49	32
1	B	265/303 (88%)	258 (97%)	7 (3%)	46	29
1	C	278/303 (92%)	264 (95%)	14 (5%)	24	8
1	D	273/303 (90%)	262 (96%)	11 (4%)	31	14
All	All	1067/1212 (88%)	1029 (96%)	38 (4%)	38	17

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	LEU
1	A	101	ASN
1	A	107	SER
1	A	185	LEU
1	A	283	LYS
1	A	338	VAL
1	B	32	LEU
1	B	67	VAL
1	B	101	ASN
1	B	139	THR
1	B	185	LEU
1	B	302	GLU
1	B	337	LEU
1	C	0	PHE
1	C	31[A]	LEU
1	C	31[B]	LEU
1	C	32	LEU
1	C	225	ARG
1	C	253[A]	LYS
1	C	253[B]	LYS
1	C	293	LEU
1	C	294	GLU
1	C	297	ARG
1	C	307	LEU
1	C	311	ILE
1	C	320	ILE
1	C	339	ARG
1	D	0	PHE
1	D	32	LEU
1	D	75[A]	CYS

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Mol	Chain	Res	Type
1	D	75[B]	CYS
1	D	107	SER
1	D	140	SER
1	D	253[A]	LYS
1	D	253[B]	LYS
1	D	293	LEU
1	D	297	ARG
1	D	299	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	C	401	-	5,5,5	0.35	0	5,5,5	0.31	0
2	GOL	B	401	-	5,5,5	0.52	0	5,5,5	1.09	0
2	GOL	D	401	-	5,5,5	0.57	0	5,5,5	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	401	-	5,5,5	0.35	0	5,5,5	0.28	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	C	401	-	-	0/4/4/4	-
2	GOL	B	401	-	-	2/4/4/4	-
2	GOL	D	401	-	-	2/4/4/4	-
2	GOL	A	401	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	GOL	C1-C2-C3-O3
2	B	401	GOL	O2-C2-C3-O3
2	D	401	GOL	O1-C1-C2-C3
2	D	401	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	332/354 (93%)	0.19	36 (10%) 5 4	15, 33, 74, 89	89 (26%)
1	B	342/354 (96%)	0.00	25 (7%) 15 13	15, 30, 66, 78	79 (23%)
1	C	345/354 (97%)	0.15	26 (7%) 14 13	12, 25, 60, 70	34 (9%)
1	D	345/354 (97%)	0.14	37 (10%) 6 4	10, 25, 71, 89	28 (8%)
All	All	1364/1416 (96%)	0.12	124 (9%) 9 8	10, 28, 69, 89	230 (16%)

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	331	LEU	10.2
1	B	316	TYR	10.0
1	B	317	LEU	9.4
1	A	313	THR	7.2
1	C	143	GLY	7.2
1	D	311	ILE	7.1
1	D	299	VAL	6.6
1	C	142	ALA	6.3
1	D	317	LEU	6.0
1	D	312	THR	5.9
1	A	140	SER	5.6
1	A	332	PRO	5.5
1	A	312	THR	5.5
1	A	295	GLN	5.5
1	C	144	LEU	5.4
1	B	289	ILE	5.1
1	D	316	TYR	4.9
1	A	139	THR	4.8
1	D	287	ALA	4.7
1	D	289	ILE	4.4
1	B	314	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	319	ASP	4.3
1	D	320	ILE	4.2
1	A	309	ILE	4.0
1	A	333	VAL	4.0
1	D	286	LEU	3.9
1	A	202	GLY	3.9
1	C	287	ALA	3.8
1	C	322	ARG	3.8
1	A	311	ILE	3.8
1	B	300	SER	3.7
1	C	320	ILE	3.7
1	D	294	GLU	3.7
1	C	284	GLY	3.7
1	D	318	HIS	3.7
1	B	318	HIS	3.6
1	A	287	ALA	3.5
1	D	284	GLY	3.5
1	A	330	SER	3.4
1	A	141	GLN	3.4
1	B	301	GLN	3.3
1	A	293	LEU	3.3
1	A	302	GLU	3.3
1	C	286	LEU	3.3
1	C	298	ASP	3.2
1	D	285	ASP	3.2
1	D	143	GLY	3.2
1	A	201	ILE	3.2
1	D	321	GLN	3.2
1	A	283	LYS	3.1
1	D	328	THR	3.1
1	A	327	LEU	3.1
1	D	322	ARG	3.0
1	D	293	LEU	3.0
1	D	291	ALA	3.0
1	D	144	LEU	3.0
1	D	338	VAL	2.9
1	C	328	THR	2.9
1	D	288	SER	2.9
1	D	295	GLN	2.9
1	D	301	GLN	2.9
1	C	314	ASP	2.9
1	B	311	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	299	VAL	2.9
1	A	324	ILE	2.8
1	D	290	THR	2.8
1	B	285	ASP	2.8
1	B	299	VAL	2.8
1	C	312	THR	2.8
1	A	317	LEU	2.8
1	A	281	VAL	2.8
1	D	331	LEU	2.7
1	D	324	ILE	2.7
1	C	285	ASP	2.7
1	A	326	ALA	2.7
1	A	203	THR	2.7
1	C	288	SER	2.7
1	D	330	SER	2.6
1	B	324	ILE	2.6
1	B	294	GLU	2.6
1	D	319	ASP	2.6
1	B	338	VAL	2.6
1	C	293	LEU	2.5
1	D	327	LEU	2.5
1	B	288	SER	2.5
1	C	313	THR	2.5
1	A	307	LEU	2.5
1	C	289	ILE	2.5
1	B	326	ALA	2.5
1	A	200	TYR	2.5
1	D	313	THR	2.5
1	C	294	GLU	2.5
1	B	315	GLU	2.4
1	C	311	ILE	2.4
1	B	284	GLY	2.4
1	C	331	LEU	2.4
1	A	305	VAL	2.4
1	D	142	ALA	2.4
1	A	340	ARG	2.3
1	B	286	LEU	2.3
1	A	285	ASP	2.3
1	C	318	HIS	2.3
1	B	147	ILE	2.3
1	A	289	ILE	2.2
1	D	314	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	301	GLN	2.2
1	B	287	ALA	2.2
1	C	319	ASP	2.2
1	D	296	TRP	2.2
1	A	194	ASP	2.2
1	A	195	ALA	2.2
1	D	329	GLU	2.2
1	B	293	LEU	2.1
1	A	250	GLY	2.1
1	A	205	ASP	2.1
1	A	138	ILE	2.1
1	C	327	LEU	2.1
1	A	249	CYS	2.1
1	D	145	ASN	2.1
1	B	297	ARG	2.1
1	B	296	TRP	2.1
1	D	139	THR	2.0
1	B	292	GLN	2.0
1	C	317	LEU	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 carbohydrates 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
3	MN	D	403	1/1	0.26	0.32	19,19,19,19	1
3	MN	C	403	1/1	0.32	0.46	23,23,23,23	1
3	MN	B	403	1/1	0.74	0.25	82,82,82,82	1
3	MN	A	402	1/1	0.78	0.14	63,63,63,63	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MN	B	402	1/1	0.88	0.18	67,67,67,67	1
2	GOL	D	401	6/6	0.88	0.16	30,31,32,33	0
2	GOL	B	401	6/6	0.90	0.17	24,27,29,31	0
3	MN	A	403	1/1	0.93	0.20	67,67,67,67	1
3	MN	C	402	1/1	0.93	0.30	69,69,69,69	1
2	GOL	A	401	6/6	0.94	0.17	23,28,29,32	0
2	GOL	C	401	6/6	0.95	0.15	28,29,31,33	0
3	MN	D	402	1/1	0.98	0.32	57,57,57,57	1

6.5 Other polymers [i](#)

There are no such residues in this entry.