



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:15 PM UTC

PDB ID : 5NAF / pdb_00005naf
Title : Co-crystal structure of an MeCP2 peptide with TBLR1 WD40 domain
Authors : Kruusvee, V.; Cook, A.G.
Deposited on : 2017-02-27
Resolution : 2.49 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

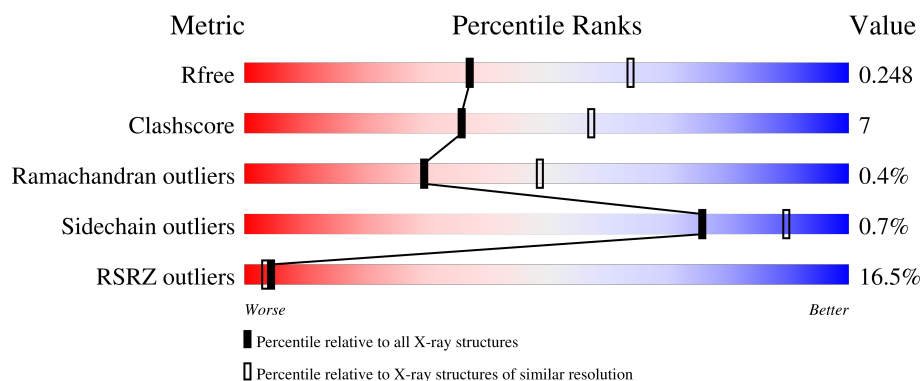
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	402	2% 74% 13% 12%
1	B	402	% 73% 13% 13%
1	C	402	22% 73% 11% 16%
1	D	402	31% 73% 9% 18%
2	E	25	12% 28% 16% 56%

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Mol	Chain	Length	Quality of chain
2	F	25	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10400 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 F-box-like/WD repeat-containing protein TBL1XR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	0	0
			2654	1669	457	513	15			
1	B	348	Total	C	N	O	S	0	0	0
			2616	1651	452	498	15			
1	C	339	Total	C	N	O	S	0	0	0
			2235	1395	399	430	11			
1	D	331	Total	C	N	O	S	0	0	0
			2114	1309	384	410	11			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	113	MET	-	initiating methionine	UNP Q8BHJ5
A	114	GLY	-	expression tag	UNP Q8BHJ5
A	115	SER	-	expression tag	UNP Q8BHJ5
A	116	SER	-	expression tag	UNP Q8BHJ5
A	117	HIS	-	expression tag	UNP Q8BHJ5
A	118	HIS	-	expression tag	UNP Q8BHJ5
A	119	HIS	-	expression tag	UNP Q8BHJ5
A	120	HIS	-	expression tag	UNP Q8BHJ5
A	121	HIS	-	expression tag	UNP Q8BHJ5
A	122	HIS	-	expression tag	UNP Q8BHJ5
A	123	SER	-	expression tag	UNP Q8BHJ5
A	124	SER	-	expression tag	UNP Q8BHJ5
A	125	GLY	-	expression tag	UNP Q8BHJ5
A	126	LEU	-	expression tag	UNP Q8BHJ5
A	127	GLU	-	expression tag	UNP Q8BHJ5
A	128	VAL	-	expression tag	UNP Q8BHJ5
A	129	LEU	-	expression tag	UNP Q8BHJ5
A	130	PHE	-	expression tag	UNP Q8BHJ5
A	131	GLN	-	expression tag	UNP Q8BHJ5
A	132	GLY	-	expression tag	UNP Q8BHJ5
A	133	PRO	-	expression tag	UNP Q8BHJ5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	113	MET	-	initiating methionine	UNP Q8BHIJ5
B	114	GLY	-	expression tag	UNP Q8BHIJ5
B	115	SER	-	expression tag	UNP Q8BHIJ5
B	116	SER	-	expression tag	UNP Q8BHIJ5
B	117	HIS	-	expression tag	UNP Q8BHIJ5
B	118	HIS	-	expression tag	UNP Q8BHIJ5
B	119	HIS	-	expression tag	UNP Q8BHIJ5
B	120	HIS	-	expression tag	UNP Q8BHIJ5
B	121	HIS	-	expression tag	UNP Q8BHIJ5
B	122	HIS	-	expression tag	UNP Q8BHIJ5
B	123	SER	-	expression tag	UNP Q8BHIJ5
B	124	SER	-	expression tag	UNP Q8BHIJ5
B	125	GLY	-	expression tag	UNP Q8BHIJ5
B	126	LEU	-	expression tag	UNP Q8BHIJ5
B	127	GLU	-	expression tag	UNP Q8BHIJ5
B	128	VAL	-	expression tag	UNP Q8BHIJ5
B	129	LEU	-	expression tag	UNP Q8BHIJ5
B	130	PHE	-	expression tag	UNP Q8BHIJ5
B	131	GLN	-	expression tag	UNP Q8BHIJ5
B	132	GLY	-	expression tag	UNP Q8BHIJ5
B	133	PRO	-	expression tag	UNP Q8BHIJ5
C	113	MET	-	initiating methionine	UNP Q8BHIJ5
C	114	GLY	-	expression tag	UNP Q8BHIJ5
C	115	SER	-	expression tag	UNP Q8BHIJ5
C	116	SER	-	expression tag	UNP Q8BHIJ5
C	117	HIS	-	expression tag	UNP Q8BHIJ5
C	118	HIS	-	expression tag	UNP Q8BHIJ5
C	119	HIS	-	expression tag	UNP Q8BHIJ5
C	120	HIS	-	expression tag	UNP Q8BHIJ5
C	121	HIS	-	expression tag	UNP Q8BHIJ5
C	122	HIS	-	expression tag	UNP Q8BHIJ5
C	123	SER	-	expression tag	UNP Q8BHIJ5
C	124	SER	-	expression tag	UNP Q8BHIJ5
C	125	GLY	-	expression tag	UNP Q8BHIJ5
C	126	LEU	-	expression tag	UNP Q8BHIJ5
C	127	GLU	-	expression tag	UNP Q8BHIJ5
C	128	VAL	-	expression tag	UNP Q8BHIJ5
C	129	LEU	-	expression tag	UNP Q8BHIJ5
C	130	PHE	-	expression tag	UNP Q8BHIJ5
C	131	GLN	-	expression tag	UNP Q8BHIJ5
C	132	GLY	-	expression tag	UNP Q8BHIJ5
C	133	PRO	-	expression tag	UNP Q8BHIJ5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	113	MET	-	initiating methionine	UNP Q8BHJ5
D	114	GLY	-	expression tag	UNP Q8BHJ5
D	115	SER	-	expression tag	UNP Q8BHJ5
D	116	SER	-	expression tag	UNP Q8BHJ5
D	117	HIS	-	expression tag	UNP Q8BHJ5
D	118	HIS	-	expression tag	UNP Q8BHJ5
D	119	HIS	-	expression tag	UNP Q8BHJ5
D	120	HIS	-	expression tag	UNP Q8BHJ5
D	121	HIS	-	expression tag	UNP Q8BHJ5
D	122	HIS	-	expression tag	UNP Q8BHJ5
D	123	SER	-	expression tag	UNP Q8BHJ5
D	124	SER	-	expression tag	UNP Q8BHJ5
D	125	GLY	-	expression tag	UNP Q8BHJ5
D	126	LEU	-	expression tag	UNP Q8BHJ5
D	127	GLU	-	expression tag	UNP Q8BHJ5
D	128	VAL	-	expression tag	UNP Q8BHJ5
D	129	LEU	-	expression tag	UNP Q8BHJ5
D	130	PHE	-	expression tag	UNP Q8BHJ5
D	131	GLN	-	expression tag	UNP Q8BHJ5
D	132	GLY	-	expression tag	UNP Q8BHJ5
D	133	PRO	-	expression tag	UNP Q8BHJ5

- Molecule 2 is a protein called Methyl-CpG-binding protein 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	11	Total	C	N	O	0	0	0
			81	52	18	11			
2	F	10	Total	C	N	O	0	0	0
			72	47	14	11			

- 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	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		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

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

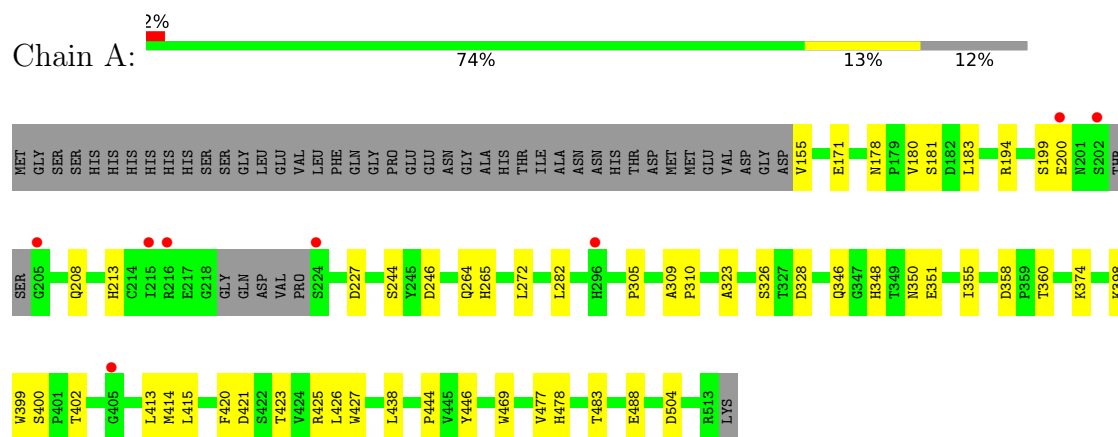
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	202	Total	O	0	0
			202	202		
4	B	187	Total	O	0	0
			187	187		
4	C	74	Total	O	0	0
			74	74		
4	D	40	Total	O	0	0
			40	40		
4	E	5	Total	O	0	0
			5	5		
4	F	6	Total	O	0	0
			6	6		

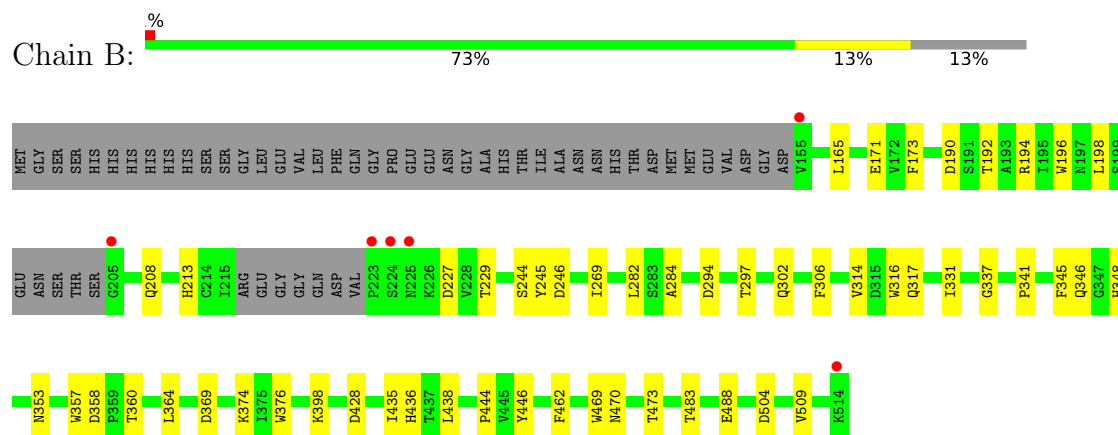
3 Residue-property plots

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.

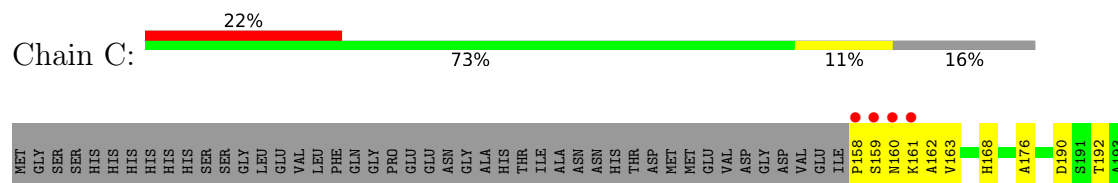
- Molecule 1: F-box-like/WD repeat-containing protein TBL1XR1

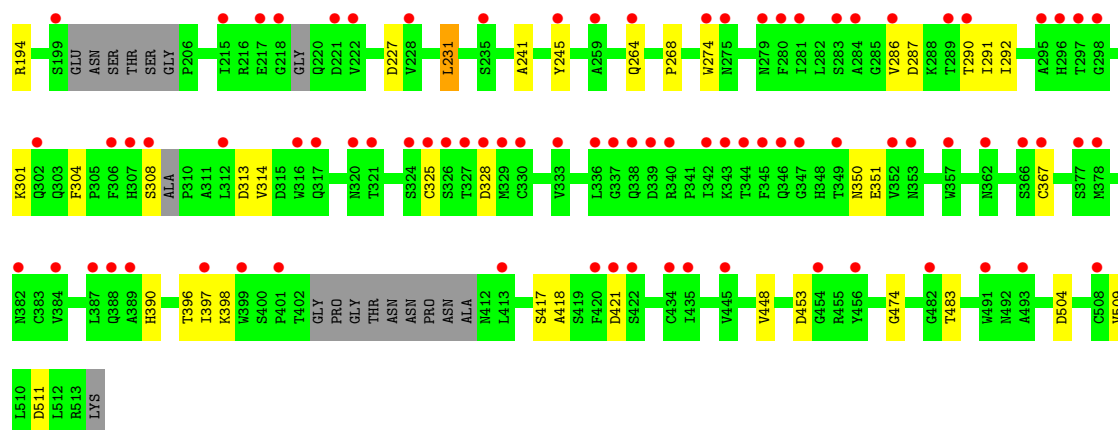


- Molecule 1: F-box-like/WD repeat-containing protein TBL1XR1

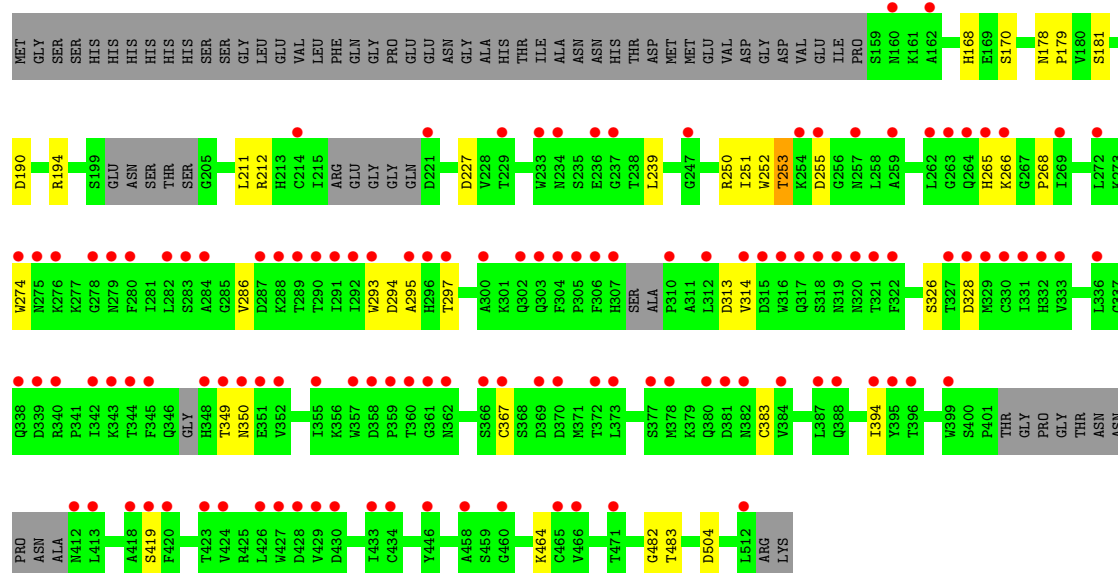
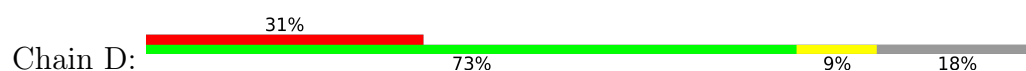


- Molecule 1: F-box-like/WD repeat-containing protein TBL1XR1

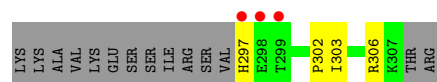
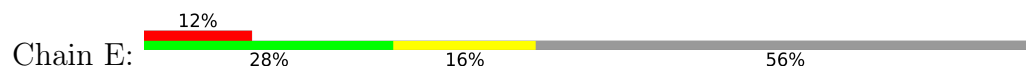




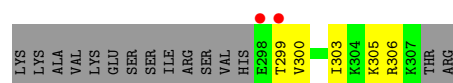
• Molecule 1: F-box-like/WD repeat-containing protein TBL1XR1



• Molecule 2: Methyl-CpG-binding protein 2



• Molecule 2: Methyl-CpG-binding protein 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.63Å 58.64Å 155.10Å 97.63° 91.17° 90.24°	Depositor
Resolution (Å)	49.64 – 2.49 49.64 – 2.49	Depositor EDS
% Data completeness (in resolution range)	97.5 (49.64-2.49) 97.6 (49.64-2.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.48Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.203 , 0.248 0.204 , 0.248	Depositor DCC
R_{free} test set	2513 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 77.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.033 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10400	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.55% 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

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	0.17	0/2720	0.40	0/3710
1	B	0.18	0/2682	0.40	0/3658
1	C	0.20	0/2286	0.44	1/3138 (0.0%)
1	D	0.23	0/2157	0.43	0/2966
2	E	0.22	0/82	0.41	0/109
2	F	0.20	0/72	0.57	0/95
All	All	0.19	0/9999	0.42	1/13676 (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	C	231	LEU	CB-CG-CD2	-6.24	91.97	110.70

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	2654	0	2472	37	0
1	B	2616	0	2456	34	1
1	C	2235	0	1708	33	0
1	D	2114	0	1569	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	81	0	77	3	0
2	F	72	0	80	4	0
3	A	42	0	56	0	1
3	B	30	0	40	0	0
3	C	6	0	8	0	0
3	D	36	0	47	0	0
4	A	202	0	0	5	1
4	B	187	0	0	3	1
4	C	74	0	0	6	0
4	D	40	0	0	3	0
4	E	5	0	0	1	0
4	F	6	0	0	0	0
All	All	10400	0	8513	134	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 134 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:265:HIS:HE2	1:D:293:TRP:HZ2	1.11	0.92
1:A:194:ARG:HH11	1:A:208:GLN:NE2	1.68	0.91
1:B:302:GLN:HE22	1:B:337:GLY:H	1.23	0.87
1:A:194:ARG:HH11	1:A:208:GLN:HE21	1.18	0.84
1:D:483:THR:OG1	1:D:504:ASP:OD2	1.95	0.83

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:346:GLN:NE2	3:A:605:GOL:O3[1_565]	2.16	0.04
4:A:844:HOH:O	4:B:859:HOH:O[1_545]	2.19	0.01

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	346/402 (86%)	329 (95%)	15 (4%)	2 (1%)	21	38
1	B	342/402 (85%)	328 (96%)	13 (4%)	1 (0%)	36	55
1	C	329/402 (82%)	312 (95%)	16 (5%)	1 (0%)	36	55
1	D	319/402 (79%)	304 (95%)	14 (4%)	1 (0%)	36	55
2	E	9/25 (36%)	9 (100%)	0	0	100	100
2	F	8/25 (32%)	8 (100%)	0	0	100	100
All	All	1353/1658 (82%)	1290 (95%)	58 (4%)	5 (0%)	30	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	266	LYS
1	C	264	GLN
1	A	199	SER
1	A	200	GLU
1	B	213	HIS

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	276/338 (82%)	275 (100%)	1 (0%)	84	93
1	B	273/338 (81%)	272 (100%)	1 (0%)	84	93
1	C	159/338 (47%)	158 (99%)	1 (1%)	78	91
1	D	141/338 (42%)	139 (99%)	2 (1%)	59	81
2	E	6/24 (25%)	6 (100%)	0	100	100
2	F	7/24 (29%)	6 (86%)	1 (14%)	3	6
All	All	862/1400 (62%)	856 (99%)	6 (1%)	76	89

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	253	THR
1	D	367	CYS
2	F	299	THR
1	B	171	GLU
1	A	171	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	385	HIS
1	B	412	ASN
1	D	213	HIS
1	C	385	HIS
1	D	160	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

19 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	C	601	-	5,5,5	0.37	0	5,5,5	0.29	0
3	GOL	D	601	-	5,5,5	0.38	0	5,5,5	0.31	0
3	GOL	A	602	-	5,5,5	0.38	0	5,5,5	0.33	0
3	GOL	A	604	-	5,5,5	0.38	0	5,5,5	0.39	0
3	GOL	A	603	-	5,5,5	0.37	0	5,5,5	0.30	0
3	GOL	B	605	-	5,5,5	0.37	0	5,5,5	0.28	0
3	GOL	A	607	-	5,5,5	0.37	0	5,5,5	0.23	0
3	GOL	D	605	-	5,5,5	0.38	0	5,5,5	0.29	0
3	GOL	D	603	-	5,5,5	0.38	0	5,5,5	0.33	0
3	GOL	D	604	-	5,5,5	0.38	0	5,5,5	0.33	0
3	GOL	A	601	-	5,5,5	0.35	0	5,5,5	0.29	0
3	GOL	B	601	-	5,5,5	0.38	0	5,5,5	0.31	0
3	GOL	A	605	-	5,5,5	0.36	0	5,5,5	0.42	0
3	GOL	A	606	-	5,5,5	0.38	0	5,5,5	0.19	0
3	GOL	D	606	-	5,5,5	0.79	0	5,5,5	0.65	0
3	GOL	B	603	-	5,5,5	0.37	0	5,5,5	0.34	0
3	GOL	D	602	-	5,5,5	0.38	0	5,5,5	0.31	0
3	GOL	B	604	-	5,5,5	0.41	0	5,5,5	0.26	0
3	GOL	B	602	-	5,5,5	0.38	0	5,5,5	0.23	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	C	601	-	-	2/4/4/4	-
3	GOL	D	601	-	-	2/4/4/4	-
3	GOL	A	602	-	-	2/4/4/4	-
3	GOL	A	604	-	-	3/4/4/4	-
3	GOL	A	603	-	-	2/4/4/4	-
3	GOL	B	605	-	-	4/4/4/4	-
3	GOL	A	607	-	-	2/4/4/4	-
3	GOL	D	605	-	-	2/4/4/4	-
3	GOL	D	603	-	-	2/4/4/4	-
3	GOL	D	604	-	-	2/4/4/4	-
3	GOL	A	601	-	-	1/4/4/4	-
3	GOL	B	601	-	-	2/4/4/4	-
3	GOL	A	605	-	-	0/4/4/4	-
3	GOL	A	606	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	D	606	-	-	0/4/4/4	-
3	GOL	B	603	-	-	2/4/4/4	-
3	GOL	D	602	-	-	2/4/4/4	-
3	GOL	B	604	-	-	2/4/4/4	-
3	GOL	B	602	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	GOL	O1-C1-C2-C3
3	A	603	GOL	O1-C1-C2-C3
3	A	604	GOL	O1-C1-C2-C3
3	A	607	GOL	O1-C1-C2-C3
3	B	603	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	605	GOL	0	1

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	352/402 (87%)	0.05	8 (2%) 61 57	17, 28, 50, 127	0
1	B	348/402 (86%)	0.13	6 (1%) 69 65	18, 29, 48, 97	0
1	C	339/402 (84%)	1.42	87 (25%) 1 1	29, 70, 109, 135	0
1	D	331/402 (82%)	1.74	124 (37%) 1 1	32, 75, 125, 155	0
2	E	11/25 (44%)	0.94	3 (27%) 1 1	30, 35, 86, 89	0
2	F	10/25 (40%)	0.95	2 (20%) 3 2	28, 40, 61, 77	0
All	All	1391/1658 (83%)	0.82	230 (16%) 4 3	17, 44, 109, 155	0

The worst 5 of 230 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	308	SER	5.7
1	D	349	THR	5.3
1	B	223	PRO	4.9
1	D	289	THR	4.8
1	C	280	PHE	4.7

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(Å ²)	Q<0.9
3	GOL	D	604	6/6	0.47	0.18	68,71,75,78	0
3	GOL	D	606	6/6	0.56	0.18	67,70,71,74	0
3	GOL	C	601	6/6	0.67	0.15	63,66,67,67	0
3	GOL	D	601	6/6	0.70	0.16	68,74,76,77	0
3	GOL	B	603	6/6	0.72	0.26	61,70,75,75	0
3	GOL	A	606	6/6	0.75	0.17	62,67,69,72	0
3	GOL	D	602	6/6	0.75	0.16	52,53,54,55	0
3	GOL	D	605	6/6	0.77	0.14	68,71,73,73	0
3	GOL	B	605	6/6	0.78	0.15	47,50,54,57	0
3	GOL	B	602	6/6	0.78	0.17	45,49,52,53	0
3	GOL	D	603	6/6	0.78	0.13	58,61,64,65	0
3	GOL	A	601	6/6	0.79	0.20	64,68,69,69	0
3	GOL	B	604	6/6	0.82	0.21	40,57,61,62	0
3	GOL	A	604	6/6	0.82	0.19	39,45,46,47	0
3	GOL	B	601	6/6	0.82	0.13	60,61,62,64	0
3	GOL	A	605	6/6	0.83	0.17	59,60,62,63	0
3	GOL	A	603	6/6	0.84	0.21	57,60,63,67	0
3	GOL	A	602	6/6	0.84	0.15	63,65,66,66	0
3	GOL	A	607	6/6	0.91	0.11	53,56,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.