



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 27, 2021 – 12:12 PM JST

PDB ID : 7DBN
Title : HIV-1 reverse transcriptase mutant Q151M/Y115F/F116Y/M184V/F160M:
DNA:dCTP ternary complex
Authors : Yasutake, Y.; Hattori, S.I.; Tamura, N.; Maeda, K.
Deposited on : 2020-10-21
Resolution : 2.67 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:

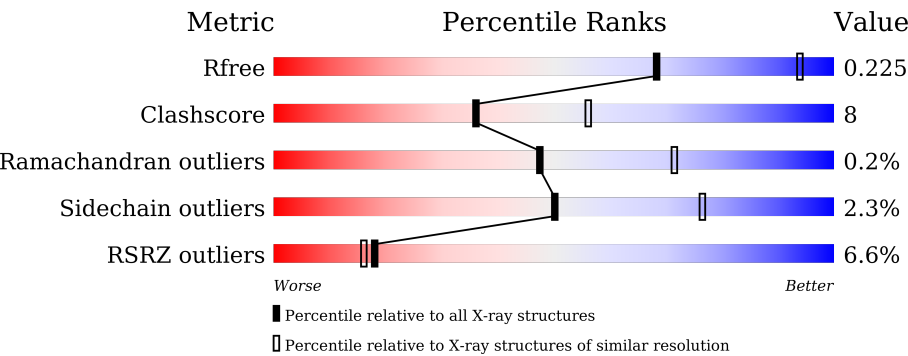
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.22
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.22

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 2.67 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	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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	557	<div><div>6%</div><div><div></div><div>80%</div><div>18%</div><div>..</div></div></div>
1	C	557	<div><div>8%</div><div><div></div><div>83%</div><div>16%</div><div>.</div></div></div>
2	B	444	<div><div>9%</div><div><div></div><div>71%</div><div>18%</div><div>.</div><div>9%</div></div></div>
2	D	444	<div><div>3%</div><div><div></div><div>80%</div><div>12%</div><div>9%</div></div></div>
3	E	38	<div><div></div><div><div></div><div>68%</div><div>18%</div><div>5%</div><div>8%</div></div></div>
3	F	38	<div><div></div><div><div></div><div>76%</div><div>18%</div><div>5%</div></div></div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	A	602	-	-	X	-
6	MG	A	603	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 17447 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 HIV-1 reverse transcriptase p66 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	0	0	0
			4494	2907	750	829	8			
1	C	553	Total	C	N	O	S	0	0	0
			4494	2907	750	829	8			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP D3XFN5
A	0	VAL	-	expression tag	UNP D3XFN5
A	115	PHE	TYR	engineered mutation	UNP D3XFN5
A	116	TYR	PHE	engineered mutation	UNP D3XFN5
A	151	MET	GLN	engineered mutation	UNP D3XFN5
A	160	MET	PHE	engineered mutation	UNP D3XFN5
A	162	SER	CYS	engineered mutation	UNP D3XFN5
A	184	VAL	MET	engineered mutation	UNP D3XFN5
A	280	SER	CYS	engineered mutation	UNP D3XFN5
C	-1	MET	-	expression tag	UNP D3XFN5
C	0	VAL	-	expression tag	UNP D3XFN5
C	115	PHE	TYR	engineered mutation	UNP D3XFN5
C	116	TYR	PHE	engineered mutation	UNP D3XFN5
C	151	MET	GLN	engineered mutation	UNP D3XFN5
C	160	MET	PHE	engineered mutation	UNP D3XFN5
C	162	SER	CYS	engineered mutation	UNP D3XFN5
C	184	VAL	MET	engineered mutation	UNP D3XFN5
C	280	SER	CYS	engineered mutation	UNP D3XFN5

- Molecule 2 is a protein called HIV-1 RT p51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	406	Total	C	N	O	S	0	0	0
			3347	2178	557	606	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	406	Total	C	N	O	S	0	0	0
			3347	2178	557	606	6			

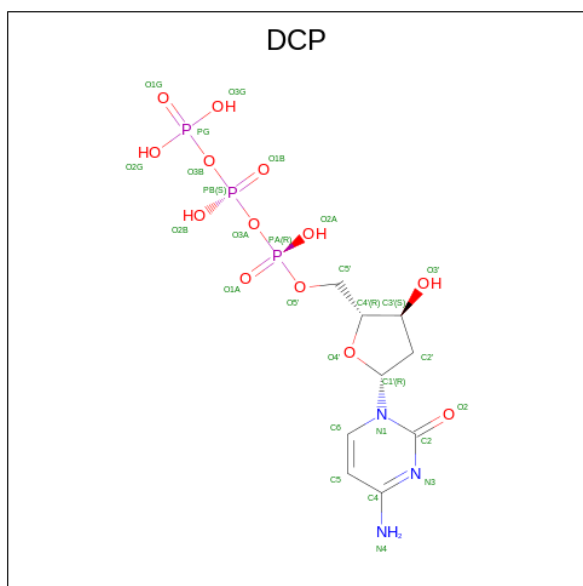
There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	expression tag	UNP P12497
B	-14	ALA	-	expression tag	UNP P12497
B	-13	HIS	-	expression tag	UNP P12497
B	-12	HIS	-	expression tag	UNP P12497
B	-11	HIS	-	expression tag	UNP P12497
B	-10	HIS	-	expression tag	UNP P12497
B	-9	HIS	-	expression tag	UNP P12497
B	-8	HIS	-	expression tag	UNP P12497
B	-7	ALA	-	expression tag	UNP P12497
B	-6	LEU	-	expression tag	UNP P12497
B	-5	GLU	-	expression tag	UNP P12497
B	-4	VAL	-	expression tag	UNP P12497
B	-3	LEU	-	expression tag	UNP P12497
B	-2	PHE	-	expression tag	UNP P12497
B	-1	GLN	-	expression tag	UNP P12497
B	0	GLY	-	expression tag	UNP P12497
B	162	SER	CYS	engineered mutation	UNP P12497
B	280	SER	CYS	engineered mutation	UNP P12497
D	-15	MET	-	expression tag	UNP P12497
D	-14	ALA	-	expression tag	UNP P12497
D	-13	HIS	-	expression tag	UNP P12497
D	-12	HIS	-	expression tag	UNP P12497
D	-11	HIS	-	expression tag	UNP P12497
D	-10	HIS	-	expression tag	UNP P12497
D	-9	HIS	-	expression tag	UNP P12497
D	-8	HIS	-	expression tag	UNP P12497
D	-7	ALA	-	expression tag	UNP P12497
D	-6	LEU	-	expression tag	UNP P12497
D	-5	GLU	-	expression tag	UNP P12497
D	-4	VAL	-	expression tag	UNP P12497
D	-3	LEU	-	expression tag	UNP P12497
D	-2	PHE	-	expression tag	UNP P12497
D	-1	GLN	-	expression tag	UNP P12497
D	0	GLY	-	expression tag	UNP P12497
D	162	SER	CYS	engineered mutation	UNP P12497
D	280	SER	CYS	engineered mutation	UNP P12497

- Molecule 3 is a DNA chain called DNA/RNA (38-MER).

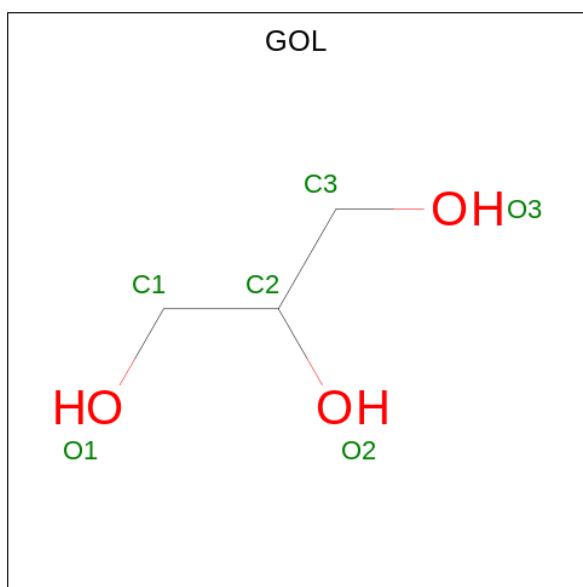
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	35	Total	C	N	O	P	0	0	0
			721	340	130	216	35			
3	F	38	Total	C	N	O	P	0	0	0
			780	370	142	231	37			

- Molecule 4 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: $C_9H_{16}N_3O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
4	C	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		
6	C	1	Total	Mg	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	56	Total	O	0	0
			56	56		
7	B	28	Total	O	0	0
			28	28		
7	E	21	Total	O	0	0
			21	21		

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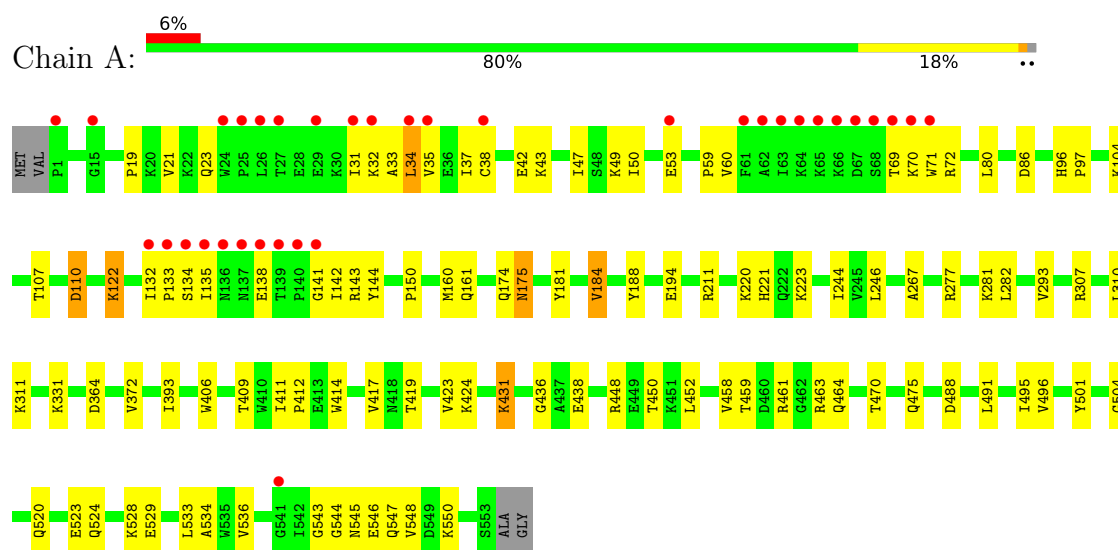
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	38	Total 38	O 38	0	0
7	D	25	Total 25	O 25	0	0
7	F	14	Total 14	O 14	0	0

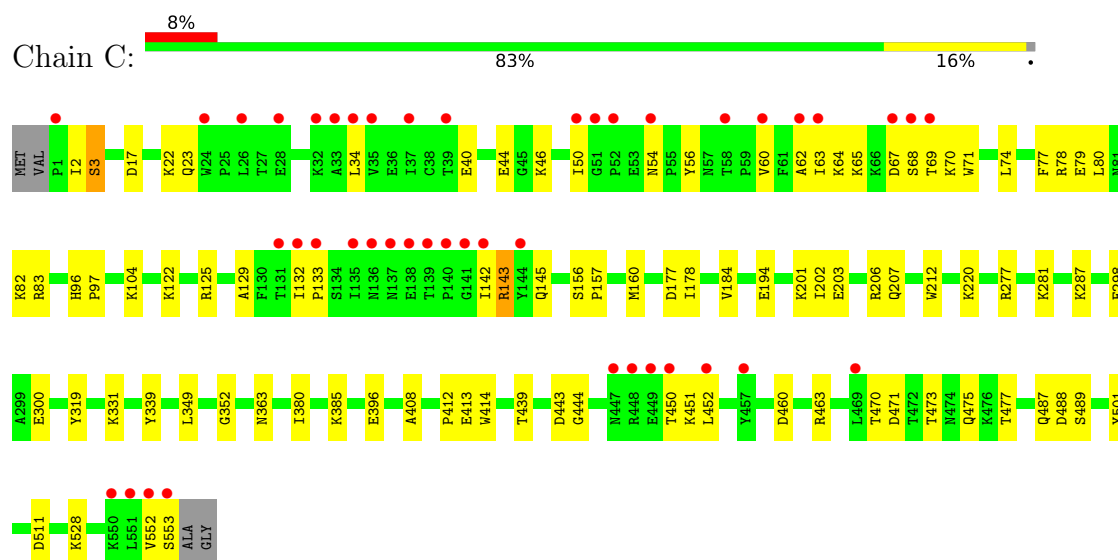
3 Residue-property plots [i](#)

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: HIV-1 reverse transcriptase p66 subunit

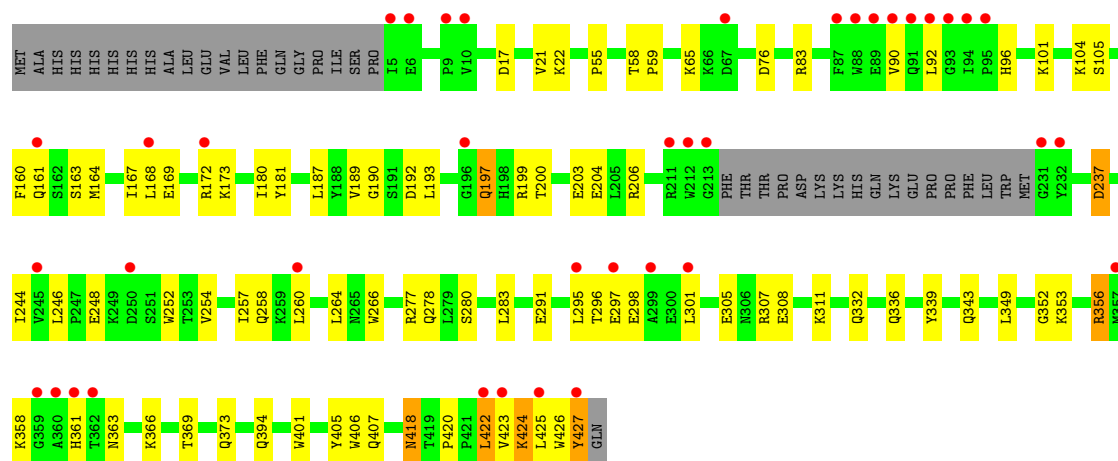


- Molecule 1: HIV-1 reverse transcriptase p66 subunit

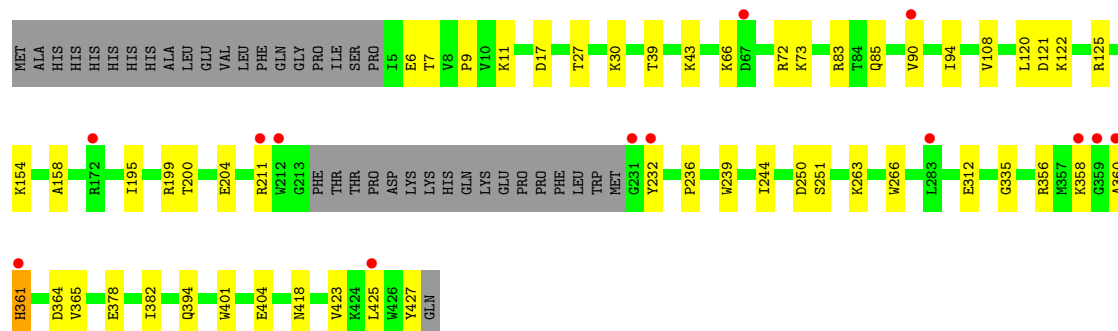
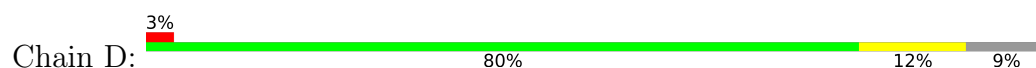


- Molecule 2: HIV-1 RT p51 subunit





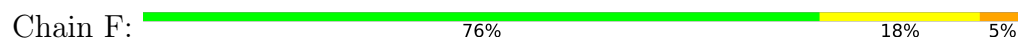
• Molecule 2: HIV-1 RT p51 subunit



• Molecule 3: DNA/RNA (38-MER)



• Molecule 3: DNA/RNA (38-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	285.68Å 285.68Å 96.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.90 – 2.67 48.90 – 2.67	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.90-2.67) 100.0 (48.90-2.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.69Å)	Xtriage
Refinement program	PHENIX (1.14_3260)	Depositor
R, R_{free}	0.177 , 0.225 0.176 , 0.225	Depositor DCC
R_{free} test set	4205 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	59.5	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17447	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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: MG, GOL, OMC, DCP

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	0.43	2/4611 (0.0%)	0.58	3/6262 (0.0%)
1	C	0.38	0/4611	0.53	0/6262
2	B	0.39	0/3441	0.54	0/4673
2	D	0.37	0/3441	0.53	0/4673
3	E	0.74	0/760	1.00	1/1172 (0.1%)
3	F	0.65	0/827	0.96	2/1276 (0.2%)
All	All	0.43	2/17691 (0.0%)	0.60	6/24318 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	175	ASN	C-N	8.32	1.50	1.34
1	A	53	GLU	CG-CD	-7.20	1.41	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	GLU	OE1-CD-OE2	10.24	135.59	123.30
1	A	34	LEU	CA-CB-CG	6.77	130.88	115.30
3	F	31	DG	O4'-C4'-C3'	-6.32	101.97	104.50
3	E	31	DG	O4'-C4'-C3'	-6.14	102.04	104.50
3	F	28	DG	O4'-C4'-C3'	-5.28	102.39	104.50
1	A	175	ASN	C-N-CD	-5.11	109.37	120.60

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	4494	0	4553	96	0
1	C	4494	0	4553	64	0
2	B	3347	0	3379	74	0
2	D	3347	0	3379	42	0
3	E	721	0	397	5	0
3	F	780	0	432	4	0
4	A	28	0	12	1	0
4	C	28	0	12	2	0
5	A	6	0	8	4	0
5	B	6	0	8	0	0
5	C	6	0	8	1	0
5	D	6	0	8	0	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	A	56	0	0	5	0
7	B	28	0	0	1	0
7	C	38	0	0	1	0
7	D	25	0	0	0	0
7	E	21	0	0	0	0
7	F	14	0	0	0	0
All	All	17447	0	16749	273	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 8.

All (273) 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:D:266:TRP:CE3	2:D:425:LEU:HD21	1.74	1.21
1:A:450:THR:CG2	1:A:452:LEU:HD12	2.03	0.89
2:D:266:TRP:CE3	2:D:425:LEU:CD2	2.58	0.85
2:D:266:TRP:CZ3	2:D:425:LEU:HD21	2.16	0.80
2:B:168:LEU:HD12	2:B:172:ARG:HH21	1.46	0.78
2:B:248:GLU:HB2	2:B:307:ARG:HH22	1.48	0.78
1:A:450:THR:HG21	1:A:452:LEU:HD12	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:THR:HG22	1:A:461:ARG:H	1.51	0.76
1:A:23:GLN:OE1	1:A:60:VAL:HG12	1.88	0.74
1:A:452:LEU:CD2	1:A:470:THR:HG22	2.17	0.73
1:A:31:ILE:HA	1:A:34:LEU:HD12	1.69	0.73
1:C:451:LYS:HB3	1:C:471:ASP:HA	1.69	0.73
3:F:3:DC:H2'	3:F:4:OMC:C6	2.23	0.73
2:B:296:THR:HG22	2:B:298:GLU:H	1.54	0.73
1:A:452:LEU:HD21	1:A:470:THR:HG22	1.71	0.72
2:B:424:LYS:HG3	2:B:427:TYR:HB2	1.72	0.72
2:B:92:LEU:O	2:B:161:GLN:NE2	2.23	0.72
1:C:34:LEU:HB3	1:C:132:ILE:HD13	1.71	0.72
1:C:50:ILE:HD12	1:C:54:ASN:ND2	2.05	0.71
1:A:458:VAL:HG12	1:A:464:GLN:HG2	1.71	0.71
2:B:163:SER:O	2:B:167:ILE:HG13	1.92	0.69
1:C:450:THR:HG23	1:C:452:LEU:H	1.58	0.69
5:C:602:GOL:H11	2:D:394:GLN:HB2	1.74	0.69
1:C:470:THR:O	1:C:471:ASP:OD1	2.09	0.69
1:A:122:LYS:CD	7:A:717:HOH:O	2.40	0.68
1:A:23:GLN:OE1	1:A:59:PRO:HA	1.94	0.68
2:B:424:LYS:HE2	2:B:424:LYS:HA	1.76	0.68
1:A:135:ILE:HG22	1:A:135:ILE:O	1.93	0.67
1:A:31:ILE:O	1:A:34:LEU:HB2	1.96	0.66
1:A:436:GLY:O	1:A:461:ARG:NH2	2.28	0.65
2:B:58:THR:HG23	2:B:76:ASP:O	1.97	0.65
1:C:50:ILE:HD12	1:C:54:ASN:HD22	1.60	0.65
1:A:221:HIS:NE2	1:A:223:LYS:HE2	2.11	0.65
2:D:66:LYS:HD3	2:D:66:LYS:H	1.62	0.65
1:A:459:THR:HG22	1:A:461:ARG:N	2.11	0.65
1:A:122:LYS:HD2	7:A:717:HOH:O	1.96	0.65
2:B:356:ARG:C	2:B:356:ARG:HD2	2.17	0.65
1:A:143:ARG:HH11	1:A:143:ARG:HG2	1.61	0.64
1:A:23:GLN:NE2	1:A:60:VAL:H	1.96	0.64
2:B:332:GLN:OE1	2:B:424:LYS:HD2	1.98	0.63
1:C:2:ILE:HD11	1:C:46:LYS:HD3	1.80	0.63
2:D:195:ILE:HG13	2:D:199:ARG:HE	1.62	0.63
1:A:331:LYS:NZ	1:A:364:ASP:OD2	2.31	0.63
1:A:34:LEU:HA	1:A:37:ILE:HD12	1.80	0.63
2:B:193:LEU:HD13	2:B:197:GLN:HE22	1.64	0.63
1:A:546:GLU:HG3	1:A:550:LYS:HE3	1.80	0.63
2:B:308:GLU:HA	2:B:311:LYS:HB2	1.80	0.62
2:B:104:LYS:HB3	2:B:192:ASP:HA	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:3:DC:H2'	3:E:4:OMC:C6	2.35	0.61
2:B:424:LYS:HA	2:B:424:LYS:CE	2.30	0.61
2:B:180:ILE:HG12	2:B:189:VAL:HG13	1.82	0.61
1:C:34:LEU:HD21	1:C:62:ALA:HB2	1.80	0.61
2:B:296:THR:HG22	2:B:298:GLU:N	2.15	0.61
1:A:543:GLY:HA3	2:B:283:LEU:O	2.02	0.60
1:C:287:LYS:NZ	7:C:701:HOH:O	2.33	0.60
1:A:220:LYS:NZ	4:A:601:DCP:O1G	2.32	0.59
2:D:90:VAL:HG21	2:D:158:ALA:HA	1.83	0.59
2:D:39:THR:O	2:D:43:LYS:HG2	2.03	0.59
1:A:536:VAL:HG23	1:A:545:ASN:HD22	1.66	0.59
1:C:54:ASN:HD21	1:C:129:ALA:HB2	1.67	0.59
1:C:203:GLU:O	1:C:207:GLN:HG2	2.03	0.57
1:A:450:THR:HG22	1:A:452:LEU:HD12	1.82	0.57
1:C:412:PRO:O	1:C:414:TRP:HD1	1.88	0.57
2:B:248:GLU:HB2	2:B:307:ARG:NH2	2.17	0.56
1:C:489:SER:OG	1:C:528:LYS:NZ	2.21	0.56
2:B:356:ARG:HD2	2:B:356:ARG:O	2.05	0.56
2:B:308:GLU:HG2	2:B:311:LYS:HD2	1.88	0.56
1:C:3:SER:HB2	1:C:212:TRP:O	2.05	0.56
1:A:122:LYS:HD3	7:A:717:HOH:O	2.03	0.56
3:F:1:DC:H2'	3:F:2:OMC:C6	2.41	0.55
1:A:31:ILE:HD13	1:A:133:PRO:O	2.07	0.55
1:C:34:LEU:HB3	1:C:132:ILE:CD1	2.37	0.55
1:A:406:TRP:CZ2	2:B:420:PRO:HG3	2.42	0.55
1:A:32:LYS:HA	1:A:35:VAL:HB	1.89	0.55
2:B:90:VAL:HG12	2:B:90:VAL:O	2.07	0.55
2:B:168:LEU:HD12	2:B:172:ARG:NH2	2.21	0.55
1:C:50:ILE:CD1	1:C:54:ASN:ND2	2.69	0.55
1:C:50:ILE:CD1	1:C:54:ASN:HD22	2.21	0.54
1:A:520:GLN:O	1:A:524:GLN:HG3	2.06	0.54
2:D:90:VAL:HA	2:D:94:ILE:HD12	1.90	0.54
2:D:9:PRO:HA	2:D:121:ASP:OD2	2.08	0.54
2:D:244:ILE:HG12	2:D:425:LEU:CD1	2.38	0.54
1:A:372:VAL:HG11	1:A:411:ILE:HG23	1.90	0.54
1:A:23:GLN:HE22	1:A:60:VAL:H	1.54	0.54
2:B:277:ARG:HG3	2:B:278:GLN:HG3	1.90	0.53
1:A:122:LYS:HD3	1:A:122:LYS:H	1.74	0.53
1:A:21:VAL:CG2	1:A:59:PRO:HD3	2.39	0.53
1:A:23:GLN:CD	1:A:60:VAL:H	2.12	0.53
2:B:356:ARG:HD3	2:B:358:LYS:CG	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:378:GLU:O	2:D:382:ILE:HG13	2.09	0.53
2:D:108:VAL:HG21	2:D:232:TYR:CE1	2.44	0.52
1:C:40:GLU:OE1	1:C:44:GLU:HG3	2.09	0.52
1:C:177:ASP:OD1	1:C:177:ASP:N	2.41	0.52
1:A:459:THR:CG2	1:A:461:ARG:H	2.22	0.52
2:B:169:GLU:O	2:B:173:LYS:HB2	2.09	0.52
1:C:487:GLN:HG3	1:C:488:ASP:OD1	2.10	0.52
1:A:49:LYS:HG2	1:A:144:TYR:CE2	2.46	0.51
1:C:64:LYS:NZ	1:C:70:LYS:O	2.43	0.51
2:B:254:VAL:HG13	2:B:283:LEU:HD22	1.93	0.51
1:A:409:THR:CB	5:A:602:GOL:H2	2.41	0.51
1:A:409:THR:HB	5:A:602:GOL:H2	1.92	0.51
1:A:448:ARG:NH2	3:E:18:DT:C4	2.79	0.51
1:A:504:GLY:HA2	2:B:420:PRO:HG2	1.92	0.51
2:B:356:ARG:HD3	2:B:358:LYS:HG2	1.92	0.51
1:C:17:ASP:OD1	1:C:56:TYR:OH	2.28	0.51
1:A:104:LYS:NZ	1:A:194:GLU:OE2	2.42	0.51
2:B:252:TRP:CD1	2:B:295:LEU:HD21	2.46	0.51
2:B:96:HIS:HA	2:B:181:TYR:CE1	2.46	0.51
1:C:132:ILE:O	1:C:142:ILE:HG22	2.11	0.51
2:D:263:LYS:HG3	2:D:425:LEU:HB2	1.93	0.51
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.93	0.51
2:D:425:LEU:C	2:D:425:LEU:HD12	2.30	0.51
1:C:77:PHE:CD1	1:C:80:LEU:HD23	2.46	0.50
1:A:134:SER:HB2	1:A:141:GLY:HA2	1.93	0.50
1:A:406:TRP:HE1	2:B:418:ASN:ND2	2.09	0.50
1:A:452:LEU:HD23	1:A:470:THR:HA	1.94	0.50
1:C:396:GLU:CD	1:C:396:GLU:H	2.15	0.50
1:C:23:GLN:HE22	1:C:60:VAL:H	1.60	0.49
1:C:501:TYR:OH	3:F:21:DA:OP1	2.26	0.49
2:D:30:LYS:NZ	2:D:404:GLU:OE1	2.44	0.49
1:A:438:GLU:OE2	1:A:459:THR:HG21	2.12	0.49
3:E:1:DC:H2'	3:E:2:OMC:C6	2.47	0.49
1:C:50:ILE:CG1	1:C:143:ARG:HB3	2.42	0.49
2:B:422:LEU:HD23	2:B:422:LEU:H	1.78	0.49
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.93	0.49
1:C:463:ARG:NH2	1:C:488:ASP:O	2.45	0.49
1:C:473:THR:O	1:C:477:THR:HG23	2.12	0.49
1:A:417:VAL:HG22	1:A:419:THR:HG23	1.95	0.49
2:B:203:GLU:OE2	2:B:206:ARG:NH2	2.46	0.48
5:A:602:GOL:H31	2:B:394:GLN:CG	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:58:THR:CG2	2:B:76:ASP:O	2.61	0.48
2:B:200:THR:O	2:B:204:GLU:HG3	2.13	0.48
2:D:263:LYS:HE2	2:D:425:LEU:O	2.14	0.48
1:A:495:ILE:HB	1:A:533:LEU:CD1	2.44	0.48
2:B:356:ARG:HH11	2:B:361:HIS:HB2	1.79	0.48
1:C:339:TYR:CZ	1:C:352:GLY:HA3	2.49	0.47
1:C:178:ILE:HD11	1:C:201:LYS:HG3	1.95	0.47
1:A:70:LYS:HG3	1:A:71:TRP:N	2.30	0.47
1:A:504:GLY:CA	2:B:420:PRO:HG2	2.45	0.47
2:B:101:LYS:HG2	7:B:622:HOH:O	2.14	0.47
1:A:463:ARG:NH2	1:A:488:ASP:O	2.47	0.47
1:A:33:ALA:O	1:A:37:ILE:HG13	2.15	0.47
1:A:143:ARG:HG2	1:A:143:ARG:NH1	2.30	0.47
1:A:38:CYS:HB3	1:A:47:ILE:HD11	1.97	0.47
1:A:107:THR:OG1	1:A:223:LYS:NZ	2.47	0.47
1:C:220:LYS:NZ	4:C:601:DCP:O2G	2.36	0.47
1:C:78:ARG:O	1:C:82:LYS:HG2	2.15	0.46
1:A:406:TRP:HE1	2:B:418:ASN:HD21	1.63	0.46
1:C:104:LYS:NZ	1:C:194:GLU:OE1	2.45	0.46
1:A:495:ILE:HB	1:A:533:LEU:HD13	1.98	0.46
1:C:444:GLY:HA2	1:C:552:VAL:HG11	1.97	0.46
1:A:491:LEU:HB3	1:A:529:GLU:HB2	1.98	0.46
1:C:22:LYS:HD3	1:C:22:LYS:HA	1.62	0.46
2:D:66:LYS:HZ2	2:D:232:TYR:HD2	1.62	0.46
1:C:380:ILE:HD12	2:D:27:THR:HG22	1.97	0.46
1:A:23:GLN:OE1	1:A:60:VAL:N	2.49	0.46
1:C:298:GLU:OE2	1:C:298:GLU:N	2.35	0.46
1:A:438:GLU:HG3	1:A:461:ARG:HG3	1.97	0.45
1:A:86:ASP:O	2:B:55:PRO:HB3	2.17	0.45
3:E:23:DC:H2"	3:E:24:DG:C8	2.51	0.45
2:D:356:ARG:CD	2:D:361:HIS:HB2	2.46	0.45
1:C:50:ILE:HG21	1:C:145:GLN:HB3	1.98	0.45
2:B:65:LYS:HA	2:B:407:GLN:OE1	2.16	0.45
2:B:343:GLN:HG3	2:B:349:LEU:HD11	1.99	0.45
1:A:32:LYS:HE2	1:A:32:LYS:HB3	1.72	0.45
2:B:237:ASP:N	2:B:237:ASP:OD2	2.49	0.45
1:C:63:ILE:HG12	1:C:74:LEU:HD12	1.98	0.45
2:D:423:VAL:HG12	2:D:423:VAL:O	2.17	0.45
1:C:17:ASP:OD2	1:C:56:TYR:OH	2.31	0.45
1:C:96:HIS:CG	1:C:97:PRO:HD2	2.51	0.45
2:D:356:ARG:NE	2:D:361:HIS:HB2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:ARG:HD2	7:A:735:HOH:O	2.17	0.45
1:C:23:GLN:NE2	1:C:60:VAL:H	2.15	0.45
2:D:122:LYS:HD3	2:D:125:ARG:NH2	2.32	0.45
1:A:132:ILE:HB	1:A:142:ILE:CG2	2.46	0.45
1:A:161:GLN:HE21	1:A:184:VAL:HG22	1.82	0.45
2:B:160:PHE:O	2:B:160:PHE:CD2	2.70	0.45
2:B:199:ARG:O	2:B:203:GLU:HG2	2.17	0.45
1:C:202:ILE:O	1:C:206:ARG:HG3	2.17	0.45
1:A:244:ILE:HD13	1:A:267:ALA:HB2	1.99	0.45
1:A:282:LEU:HB3	1:A:293:VAL:HG11	1.98	0.45
2:B:164:MET:CE	2:B:187:LEU:HD11	2.47	0.45
1:A:42:GLU:OE2	1:A:49:LYS:HG3	2.17	0.44
1:A:43:LYS:HD2	1:A:43:LYS:HA	1.66	0.44
1:A:70:LYS:HG3	1:A:71:TRP:H	1.81	0.44
1:A:533:LEU:HD12	1:A:533:LEU:HA	1.82	0.44
2:B:168:LEU:CD1	2:B:172:ARG:HH21	2.24	0.44
1:A:496:VAL:HG22	1:A:534:ALA:HB3	1.98	0.44
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.53	0.44
1:C:451:LYS:N	1:C:451:LYS:HD3	2.32	0.44
2:B:90:VAL:HG12	2:B:92:LEU:HG	1.99	0.44
2:D:6:GLU:HG2	2:D:7:THR:N	2.32	0.44
1:A:520:GLN:O	1:A:523:GLU:HG2	2.18	0.44
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.53	0.44
1:A:110:ASP:HB2	1:A:220:LYS:HB3	2.00	0.44
2:B:193:LEU:HD13	2:B:197:GLN:NE2	2.31	0.44
2:B:258:GLN:HG3	2:B:283:LEU:HD13	1.99	0.44
2:D:365:VAL:HG11	2:D:401:TRP:HB2	2.00	0.44
1:A:524:GLN:O	1:A:528:LYS:HG2	2.17	0.43
1:A:50:ILE:HG13	1:A:143:ARG:HB3	1.99	0.43
1:C:65:LYS:HE3	1:C:71:TRP:O	2.17	0.43
1:A:544:GLY:O	1:A:548:VAL:HG12	2.18	0.43
1:A:181:TYR:HB2	1:A:188:TYR:HB3	2.00	0.43
1:C:203:GLU:OE1	1:C:206:ARG:NH1	2.51	0.43
1:A:409:THR:OG1	5:A:602:GOL:H2	2.18	0.43
2:D:358:LYS:HG2	2:D:360:ALA:H	1.84	0.43
1:A:393:ILE:O	1:A:414:TRP:CZ3	2.72	0.43
1:C:122:LYS:HG2	1:C:125:ARG:NH1	2.34	0.43
1:C:408:ALA:HB1	2:D:364:ASP:HB3	2.01	0.43
2:B:266:TRP:NE1	2:B:425:LEU:HD22	2.34	0.42
2:B:423:VAL:CG2	2:B:425:LEU:HB2	2.49	0.42
2:B:425:LEU:HD23	2:B:426:TRP:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:236:PRO:HA	2:D:239:TRP:CD2	2.54	0.42
1:A:69:THR:O	1:A:69:THR:OG1	2.35	0.42
1:C:69:THR:HB	1:C:70:LYS:HG2	2.01	0.42
2:D:17:ASP:O	2:D:83:ARG:HD3	2.19	0.42
7:A:701:HOH:O	1:C:331:LYS:HE2	2.18	0.42
2:B:426:TRP:O	2:B:427:TYR:HD1	2.01	0.42
4:C:601:DCP:O5'	4:C:601:DCP:H6	2.18	0.42
2:D:108:VAL:HG21	2:D:232:TYR:CZ	2.55	0.42
2:B:373:GLN:HG3	2:B:406:TRP:CZ3	2.55	0.42
2:D:6:GLU:HG2	2:D:7:THR:H	1.85	0.42
1:C:201:LYS:HA	1:C:201:LYS:HD3	1.79	0.42
1:A:23:GLN:HA	1:A:59:PRO:HB3	2.00	0.42
1:C:64:LYS:HE3	1:C:64:LYS:HB3	1.40	0.42
1:C:470:THR:C	1:C:471:ASP:OD1	2.57	0.42
1:A:431:LYS:HB2	1:A:431:LYS:HE2	1.76	0.42
1:A:393:ILE:HG23	1:A:414:TRP:CH2	2.55	0.42
1:A:536:VAL:CG2	1:A:545:ASN:HD22	2.33	0.42
2:B:336:GLN:OE1	2:B:353:LYS:HE2	2.19	0.42
2:D:66:LYS:H	2:D:66:LYS:CD	2.28	0.42
1:A:246:LEU:HD11	1:A:310:LEU:HD12	2.01	0.42
1:C:319:TYR:HA	1:C:349:LEU:HD21	2.02	0.42
1:C:439:THR:N	1:C:460:ASP:OD2	2.40	0.41
1:A:307:ARG:O	1:A:311:LYS:HG3	2.19	0.41
2:D:72:ARG:HD3	2:D:73:LYS:O	2.21	0.41
2:D:211:ARG:O	2:D:211:ARG:HG3	2.20	0.41
2:B:105:SER:O	2:B:190:GLY:HA2	2.20	0.41
2:B:244:ILE:HD13	2:B:425:LEU:HD11	2.01	0.41
1:A:184:VAL:HG21	3:E:33:DG:H1'	2.03	0.41
2:B:297:GLU:H	2:B:297:GLU:HG3	1.67	0.41
2:B:308:GLU:CA	2:B:311:LYS:HB2	2.50	0.41
2:B:356:ARG:HD3	2:B:358:LYS:HG3	2.02	0.41
1:C:17:ASP:CG	1:C:56:TYR:OH	2.59	0.41
1:C:79:GLU:HG3	1:C:83:ARG:HE	1.85	0.41
1:C:443:ASP:OD2	1:C:444:GLY:N	2.53	0.41
2:D:335:GLY:HA3	2:D:356:ARG:HG2	2.02	0.41
2:B:254:VAL:HG23	2:B:291:GLU:O	2.20	0.41
2:D:312:GLU:H	2:D:312:GLU:HG3	1.68	0.41
1:A:19:PRO:HG3	1:A:80:LEU:HB2	2.03	0.41
1:A:132:ILE:HB	1:A:142:ILE:HG22	2.02	0.41
2:B:104:LYS:CB	2:B:192:ASP:HA	2.49	0.41
1:C:67:ASP:O	1:C:68:SER:OG	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:475:GLN:HB3	1:C:501:TYR:CE2	2.56	0.41
2:B:363:ASN:HB3	2:B:366:LYS:HB3	2.02	0.41
2:D:11:LYS:O	2:D:85:GLN:HG2	2.21	0.41
2:D:195:ILE:HD12	2:D:195:ILE:HA	1.88	0.41
3:F:10:DC:H2"	3:F:11:DG:C8	2.56	0.41
1:A:31:ILE:O	1:A:35:VAL:HG23	2.21	0.40
2:B:21:VAL:HB	2:B:59:PRO:HD3	2.03	0.40
1:A:135:ILE:HG22	1:A:138:GLU:HB3	2.03	0.40
2:D:11:LYS:HB2	2:D:11:LYS:HE3	1.86	0.40
2:D:122:LYS:HD3	2:D:125:ARG:CZ	2.50	0.40
2:B:90:VAL:O	2:B:90:VAL:CG1	2.69	0.40
2:B:257:ILE:HG22	2:B:283:LEU:HD11	2.03	0.40
1:C:156:SER:HB2	1:C:157:PRO:HD3	2.03	0.40
1:C:363:ASN:HA	1:C:511:ASP:OD1	2.20	0.40
2:D:120:LEU:HD23	2:D:125:ARG:HG2	2.04	0.40
1:A:412:PRO:HG3	2:B:401:TRP:CH2	2.56	0.40
2:B:339:TYR:CZ	2:B:352:GLY:HA3	2.56	0.40
2:D:200:THR:O	2:D:204:GLU:HG3	2.21	0.40
2:B:17:ASP:O	2:B:83:ARG:NH1	2.52	0.40
2:B:369:THR:HG21	2:B:405:TYR:HB2	2.03	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	551/557 (99%)	535 (97%)	15 (3%)	1 (0%)	47	71
1	C	551/557 (99%)	528 (96%)	21 (4%)	2 (0%)	34	58
2	B	402/444 (90%)	390 (97%)	12 (3%)	0	100	100
2	D	402/444 (90%)	389 (97%)	13 (3%)	0	100	100
All	All	1906/2002 (95%)	1842 (97%)	61 (3%)	3 (0%)	47	71

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	VAL
1	C	184	VAL
1	C	133	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	492/494 (100%)	479 (97%)	13 (3%)	46	73
1	C	492/494 (100%)	483 (98%)	9 (2%)	59	81
2	B	365/400 (91%)	353 (97%)	12 (3%)	38	64
2	D	365/400 (91%)	359 (98%)	6 (2%)	62	83
All	All	1714/1788 (96%)	1674 (98%)	40 (2%)	50	76

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	ARG
1	A	110	ASP
1	A	122	LYS
1	A	150	PRO
1	A	160	MET
1	A	174	GLN
1	A	175	ASN
1	A	211	ARG
1	A	277	ARG
1	A	281	LYS
1	A	424	LYS
1	A	431	LYS
1	A	547	GLN
2	B	22	LYS
2	B	197	GLN
2	B	237	ASP
2	B	260	LEU

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Mol	Chain	Res	Type
2	B	280	SER
2	B	301	LEU
2	B	305	GLU
2	B	356	ARG
2	B	418	ASN
2	B	422	LEU
2	B	424	LYS
2	B	427	TYR
1	C	3	SER
1	C	143	ARG
1	C	160	MET
1	C	277	ARG
1	C	281	LYS
1	C	300	GLU
1	C	385	LYS
1	C	413	GLU
1	C	553	SER
2	D	154	LYS
2	D	250	ASP
2	D	251	SER
2	D	361	HIS
2	D	418	ASN
2	D	427	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	428	GLN
1	A	464	GLN
1	A	483	HIS
1	A	509	GLN
1	A	545	ASN
2	B	161	GLN
2	B	174	GLN
2	B	182	GLN
2	B	197	GLN
2	B	235	HIS
2	B	269	GLN
2	B	278	GLN
2	B	334	GLN
2	B	418	ASN
1	C	54	ASN

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Mol	Chain	Res	Type
1	C	221	HIS
1	C	278	GLN
1	C	334	GLN
1	C	373	GLN
1	C	487	GLN
1	C	520	GLN
2	D	137	ASN
2	D	182	GLN
2	D	255	ASN
2	D	418	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	OMC	E	2	3	15,22,23	3.71	6 (40%)	17,31,34	1.06	1 (5%)
3	OMC	F	2	3	15,22,23	3.79	6 (40%)	17,31,34	1.27	1 (5%)
3	OMC	F	4	3	15,22,23	3.72	6 (40%)	17,31,34	1.31	2 (11%)
3	OMC	E	4	3	15,22,23	3.60	6 (40%)	17,31,34	1.45	2 (11%)

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	OMC	E	2	3	-	0/7/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OMC	F	2	3	-	0/7/27/28	0/2/2/2
3	OMC	F	4	3	-	0/7/27/28	0/2/2/2
3	OMC	E	4	3	-	0/7/27/28	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	2	OMC	C6-N1	9.07	1.47	1.35
3	E	2	OMC	C6-N1	9.07	1.47	1.35
3	F	4	OMC	C6-N1	9.01	1.47	1.35
3	E	4	OMC	C6-N1	8.30	1.46	1.35
3	F	4	OMC	C4-N3	6.88	1.46	1.35
3	F	2	OMC	C4-N3	6.86	1.46	1.35
3	E	2	OMC	C4-N3	6.70	1.46	1.35
3	E	4	OMC	C4-N3	6.60	1.46	1.35
3	E	4	OMC	C2-N3	5.52	1.49	1.38
3	F	2	OMC	C6-C5	5.40	1.50	1.38
3	F	4	OMC	C2-N3	5.26	1.48	1.38
3	F	2	OMC	C2-N3	5.19	1.48	1.38
3	E	4	OMC	C6-C5	5.03	1.49	1.38
3	E	2	OMC	C6-C5	5.01	1.49	1.38
3	F	4	OMC	C6-C5	5.00	1.49	1.38
3	E	2	OMC	C2-N3	4.67	1.47	1.38
3	E	2	OMC	C4-N4	4.28	1.47	1.35
3	F	2	OMC	C4-N4	4.23	1.47	1.35
3	E	4	OMC	C4-N4	4.17	1.47	1.35
3	F	4	OMC	C4-N4	4.05	1.47	1.35
3	E	2	OMC	C5-C4	3.40	1.49	1.41
3	F	2	OMC	C5-C4	3.30	1.49	1.41
3	F	4	OMC	C5-C4	2.85	1.48	1.41
3	E	4	OMC	C5-C4	2.67	1.47	1.41

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	4	OMC	C2-N3-C4	4.26	120.66	116.34
3	F	2	OMC	C2-N3-C4	4.14	120.53	116.34
3	F	4	OMC	C2-N3-C4	3.80	120.20	116.34
3	E	2	OMC	C2-N3-C4	3.32	119.71	116.34
3	E	4	OMC	N4-C4-N3	3.05	121.31	116.49
3	F	4	OMC	N4-C4-N3	2.68	120.73	116.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	2	OMC	1	0
3	F	2	OMC	1	0
3	F	4	OMC	1	0
3	E	4	OMC	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	$\# Z > 2$
4	DCP	C	601	6	23,29,29	3.83	12 (52%)	30,45,45	1.27	3 (10%)
5	GOL	D	501	-	5,5,5	0.72	0	5,5,5	1.12	0
5	GOL	B	501	-	5,5,5	1.07	0	5,5,5	0.90	0
5	GOL	C	602	-	5,5,5	0.08	0	5,5,5	0.32	0
5	GOL	A	602	-	5,5,5	0.99	0	5,5,5	1.03	0
4	DCP	A	601	6	23,29,29	3.94	12 (52%)	30,45,45	1.31	4 (13%)

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
4	DCP	C	601	6	-	4/19/34/34	0/2/2/2
5	GOL	D	501	-	-	0/4/4/4	-
5	GOL	B	501	-	-	2/4/4/4	-
5	GOL	C	602	-	-	2/4/4/4	-
5	GOL	A	602	-	-	2/4/4/4	-
4	DCP	A	601	6	-	5/19/34/34	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	DCP	C6-N1	8.41	1.46	1.35
4	C	601	DCP	C6-N1	8.14	1.45	1.35
4	A	601	DCP	O4'-C4'	7.73	1.62	1.45
4	C	601	DCP	O4'-C4'	7.54	1.61	1.45
4	A	601	DCP	C2-N3	6.26	1.50	1.38
4	A	601	DCP	C4-N3	6.25	1.45	1.35
4	A	601	DCP	C3'-C4'	-6.23	1.35	1.53
4	C	601	DCP	C3'-C4'	-6.06	1.36	1.53
4	C	601	DCP	C4-N3	6.02	1.45	1.35
4	C	601	DCP	C2-N3	5.85	1.49	1.38
4	A	601	DCP	C6-C5	5.66	1.50	1.38
4	C	601	DCP	C6-C5	5.60	1.50	1.38
4	C	601	DCP	O4'-C1'	-5.11	1.30	1.42
4	A	601	DCP	O4'-C1'	-5.10	1.30	1.42
4	A	601	DCP	C4-N4	4.26	1.47	1.35
4	C	601	DCP	C4-N4	4.22	1.47	1.35
4	A	601	DCP	C5-C4	3.04	1.48	1.41
4	C	601	DCP	C5-C4	2.79	1.47	1.41
4	A	601	DCP	PA-O5'	2.72	1.70	1.59
4	A	601	DCP	O3'-C3'	2.65	1.49	1.43
4	C	601	DCP	O3'-C3'	2.59	1.48	1.43
4	C	601	DCP	PA-O5'	2.58	1.69	1.59
4	C	601	DCP	C2'-C1'	2.38	1.59	1.52
4	A	601	DCP	C2'-C1'	2.30	1.58	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	601	DCP	C2-N3-C4	4.68	121.08	116.34
4	A	601	DCP	C2-N3-C4	4.23	120.63	116.34
4	A	601	DCP	C2'-C1'-N1	-2.73	107.98	114.27
4	A	601	DCP	PB-O3B-PG	-2.71	123.52	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	601	DCP	PB-O3B-PG	-2.34	124.80	132.83
4	C	601	DCP	N4-C4-N3	2.06	119.75	116.49
4	A	601	DCP	N4-C4-N3	2.00	119.66	116.49

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	601	DCP	C5'-O5'-PA-O2A
4	A	601	DCP	PB-O3B-PG-O2G
4	C	601	DCP	PB-O3A-PA-O5'
4	C	601	DCP	PB-O3B-PG-O2G
5	B	501	GOL	O2-C2-C3-O3
5	A	602	GOL	O1-C1-C2-C3
5	B	501	GOL	C1-C2-C3-O3
5	C	602	GOL	O1-C1-C2-C3
5	A	602	GOL	O1-C1-C2-O2
5	C	602	GOL	O1-C1-C2-O2
4	A	601	DCP	PB-O3A-PA-O5'
4	A	601	DCP	C5'-O5'-PA-O3A
4	A	601	DCP	C5'-O5'-PA-O1A
4	C	601	DCP	PA-O3A-PB-O2B
4	C	601	DCP	PB-O3B-PG-O1G

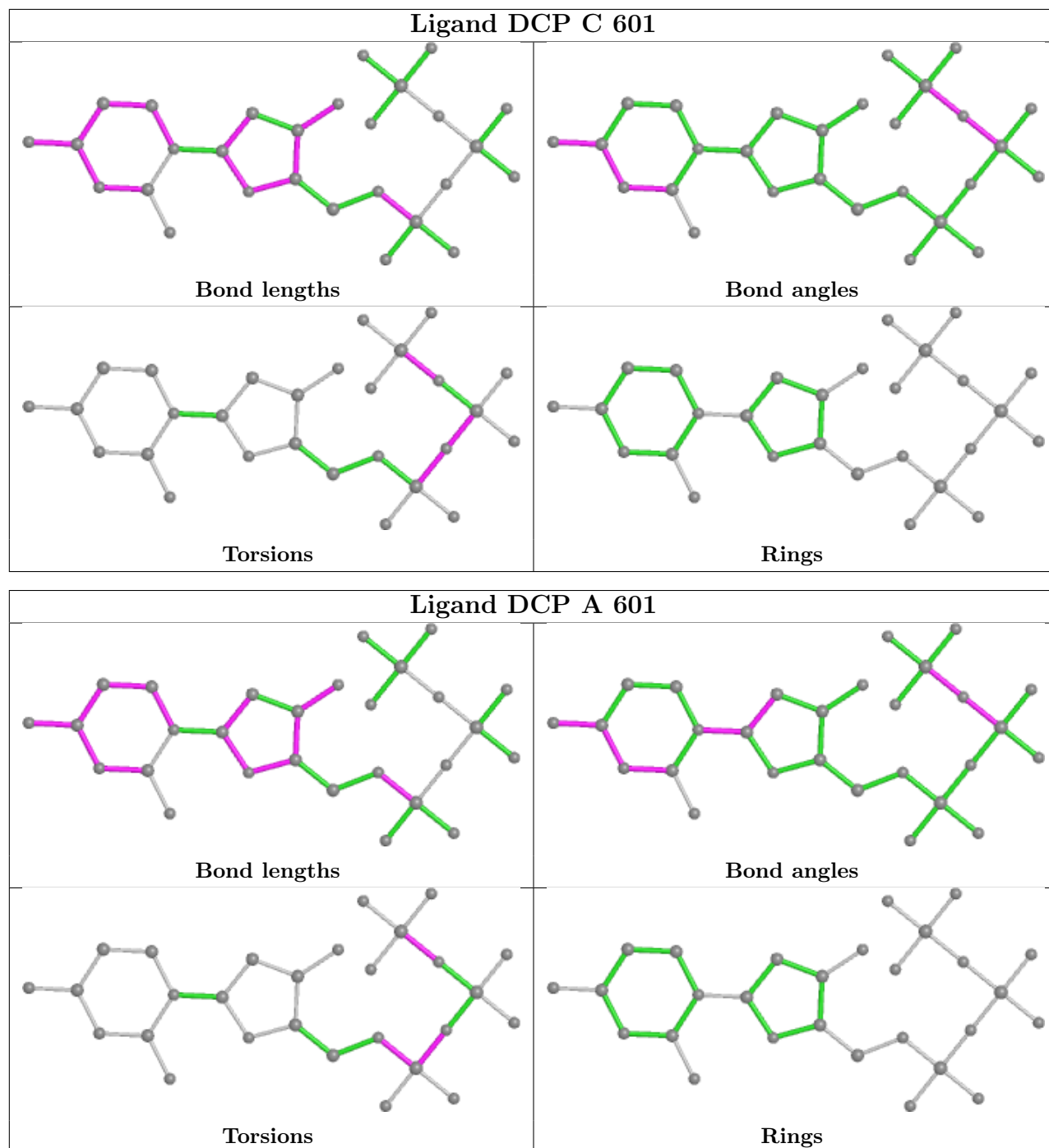
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	601	DCP	2	0
5	C	602	GOL	1	0
5	A	602	GOL	4	0
4	A	601	DCP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	553/557 (99%)	0.25	35 (6%)	20	18	35, 65, 120, 201	0
1	C	553/557 (99%)	0.31	44 (7%)	12	10	35, 69, 124, 215	0
2	B	406/444 (91%)	0.52	39 (9%)	8	6	38, 78, 151, 204	0
2	D	406/444 (91%)	0.10	13 (3%)	47	47	35, 63, 110, 176	0
3	E	33/38 (86%)	-0.22	0	100	100	41, 62, 92, 140	0
3	F	36/38 (94%)	-0.12	0	100	100	45, 73, 135, 166	0
All	All	1987/2078 (95%)	0.28	131 (6%)	18	16	35, 68, 129, 215	0

All (131) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	SER	14.1
2	D	231	GLY	9.7
1	A	69	THR	9.5
1	A	137	ASN	8.9
2	B	93	GLY	8.8
1	C	136	ASN	7.9
2	B	360	ALA	7.1
1	A	140	PRO	6.9
2	B	361	HIS	6.9
1	C	135	ILE	6.8
2	B	94	ILE	6.7
2	B	88	TRP	6.6
2	B	301	LEU	6.5
1	A	27	THR	6.2
1	A	138	GLU	6.2
1	C	140	PRO	6.1
2	B	92	LEU	5.9
1	C	132	ILE	5.8
2	D	360	ALA	5.6

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Mol	Chain	Res	Type	RSRZ
2	B	91	GLN	5.6
2	B	359	GLY	5.5
1	C	142	ILE	5.5
2	D	232	TYR	5.4
1	C	137	ASN	5.3
2	B	89	GLU	5.2
1	A	34	LEU	5.2
2	B	90	VAL	5.0
2	B	231	GLY	5.0
1	A	29	GLU	4.9
1	A	141	GLY	4.7
2	D	359	GLY	4.7
1	A	63	ILE	4.6
2	B	212	TRP	4.5
2	B	357	MET	4.5
2	D	67	ASP	4.4
1	A	65	LYS	4.4
1	A	139	THR	4.4
1	A	25	PRO	4.4
1	A	24	TRP	4.3
1	C	133	PRO	4.3
1	A	133	PRO	4.3
1	A	61	PHE	4.2
1	A	32	LYS	4.2
2	B	213	GLY	4.1
1	A	135	ILE	4.1
1	A	26	LEU	4.0
1	A	136	ASN	3.9
1	A	66	LYS	3.8
1	C	26	LEU	3.8
1	C	33	ALA	3.7
2	B	245	VAL	3.7
2	D	425	LEU	3.7
1	C	58	THR	3.7
1	C	34	LEU	3.7
2	B	362	THR	3.7
1	C	50	ILE	3.7
1	C	553	SER	3.6
2	B	297	GLU	3.6
2	D	283	LEU	3.6
1	A	132	ILE	3.5
1	C	551	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	70	LYS	3.5
2	B	168	LEU	3.5
2	B	295	LEU	3.4
1	A	71	TRP	3.4
2	B	95	PRO	3.4
1	C	67	ASP	3.4
2	D	212	TRP	3.3
1	A	35	VAL	3.3
2	B	5	ILE	3.3
1	C	452	LEU	3.3
1	C	68	SER	3.3
1	C	35	VAL	3.3
1	C	141	GLY	3.2
1	A	53	GLU	3.2
1	A	67	ASP	3.2
1	C	552	VAL	3.2
1	C	24	TRP	3.1
1	C	1	PRO	3.1
1	C	144	TYR	3.1
1	C	39	THR	3.1
2	D	361	HIS	3.0
2	B	422	LEU	3.0
1	A	64	LYS	3.0
2	B	260	LEU	3.0
1	C	28	GLU	2.9
1	A	1	PRO	2.9
1	C	139	THR	2.8
1	C	131	THR	2.8
2	B	67	ASP	2.8
1	C	550	LYS	2.7
2	D	358	LYS	2.7
1	C	69	THR	2.7
1	C	52	PRO	2.6
1	C	449	GLU	2.6
2	B	6	GLU	2.6
1	A	62	ALA	2.6
2	B	10	VAL	2.5
2	B	87	PHE	2.5
1	C	448	ARG	2.5
1	C	62	ALA	2.4
1	C	37	ILE	2.4
2	B	423	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	211	ARG	2.4
2	B	250	ASP	2.4
1	A	134	SER	2.4
2	B	196	GLY	2.4
1	C	32	LYS	2.4
1	C	138	GLU	2.4
1	A	15	GLY	2.4
1	C	51	GLY	2.4
2	B	427	TYR	2.4
1	A	31	ILE	2.3
2	B	161	GLN	2.3
1	C	54	ASN	2.3
1	C	457	TYR	2.3
2	B	425	LEU	2.2
2	B	232	TYR	2.2
1	A	38	CYS	2.2
2	D	211	ARG	2.2
2	B	172	ARG	2.1
1	C	447	ASN	2.1
1	C	63	ILE	2.1
1	A	541	GLY	2.1
1	C	469	LEU	2.1
2	D	172	ARG	2.1
2	B	9	PRO	2.1
2	B	299	ALA	2.1
1	C	450	THR	2.1
1	C	60	VAL	2.0
2	D	90	VAL	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
3	OMC	E	2	21/22	0.98	0.21	41,49,59,60	0
3	OMC	F	2	21/22	0.98	0.18	53,58,62,69	0
3	OMC	F	4	21/22	0.98	0.19	40,45,50,52	0
3	OMC	E	4	21/22	0.99	0.19	31,44,48,50	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

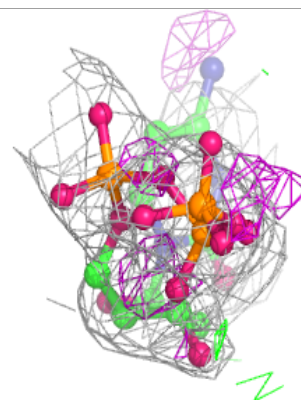
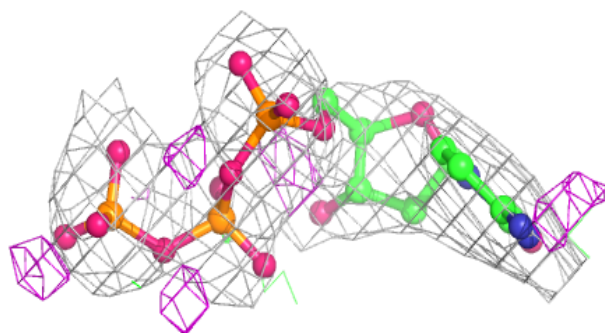
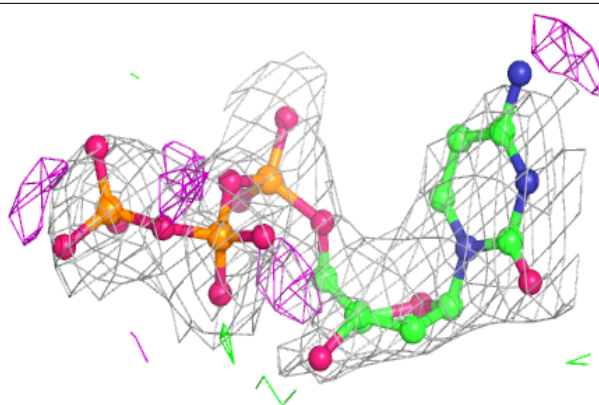
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	MG	C	603	1/1	0.52	0.33	144,144,144,144	1
6	MG	A	603	1/1	0.76	0.46	42,42,42,42	1
5	GOL	A	602	6/6	0.83	0.27	68,76,80,83	0
4	DCP	A	601	28/28	0.89	0.23	74,96,151,154	0
5	GOL	C	602	6/6	0.93	0.21	64,67,69,70	0
4	DCP	C	601	28/28	0.94	0.17	64,91,126,135	0
5	GOL	D	501	6/6	0.95	0.23	48,58,59,63	0
5	GOL	B	501	6/6	0.96	0.23	41,56,64,70	0

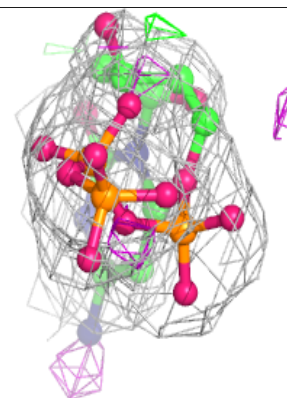
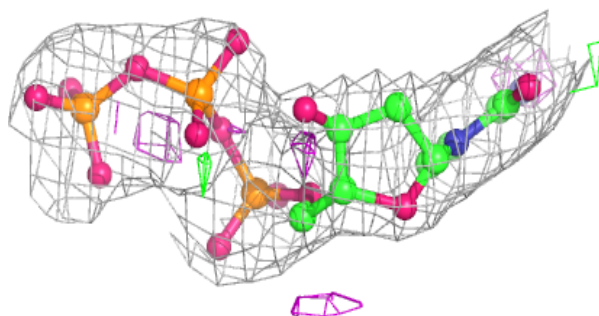
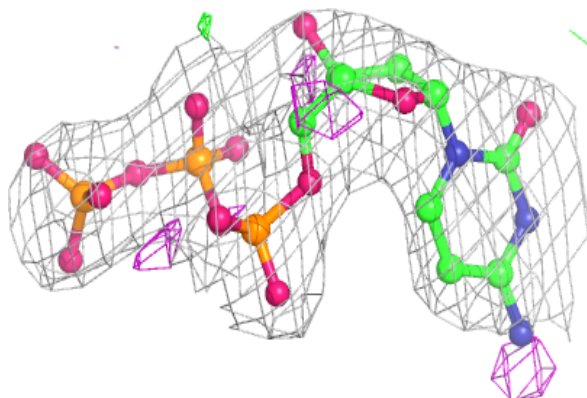
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around DCP A 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around DCP C 601:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.