



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:09 am GMT

PDB ID : 3GQC
Title : Structure of human Rev1-DNA-dNTP ternary complex
Authors : Swan, M.K.; Aggarwal, A.K.
Deposited on : 2009-03-24
Resolution : 2.50 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

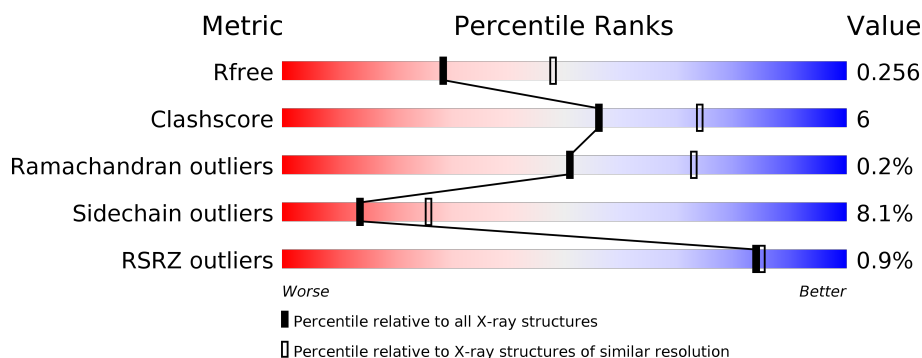
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	504	<div> <div></div> <div>72% 13% 14%</div> </div>
1	B	504	<div> <div></div> <div>73% 13% 13%</div> </div>
1	C	504	<div> <div></div> <div>70% 12% 16%</div> </div>
1	D	504	<div> <div></div> <div>74% 10% 14%</div> </div>
2	E	12	<div> <div></div> <div>50% 42% 8%</div> </div>
2	G	12	<div> <div></div> <div>67% 25% 8%</div> </div>

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Mol	Chain	Length	Quality of chain
2	I	12	
2	K	12	
3	F	16	
3	H	16	
3	J	16	
3	L	16	

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	MG	D	210	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15522 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 DNA repair protein REV1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	435	Total	C	N	O	S	0	0	0
			3318	2085	591	615	27			
1	B	440	Total	C	N	O	S	0	0	0
			3312	2078	594	614	26			
1	C	423	Total	C	N	O	S	0	0	0
			3189	2003	566	594	26			
1	D	433	Total	C	N	O	S	0	0	0
			3206	2016	573	591	26			

- Molecule 2 is a DNA chain called 5'-D(*AP*TP*CP*CP*TP*CP*CP*CP*CP*TP*AP*(D OC))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	12	Total	C	N	O	P	0	0	0
			231	113	37	70	11			
2	G	12	Total	C	N	O	P	0	0	0
			231	113	37	70	11			
2	I	12	Total	C	N	O	P	0	0	0
			231	113	37	70	11			
2	K	12	Total	C	N	O	P	0	0	0
			231	113	37	70	11			

- Molecule 3 is a DNA chain called 5'-D(*TP*AP*AP*GP*GP*TP*AP*GP*GP*GP*GP*A P*GP*GP*AP*T)-3'.

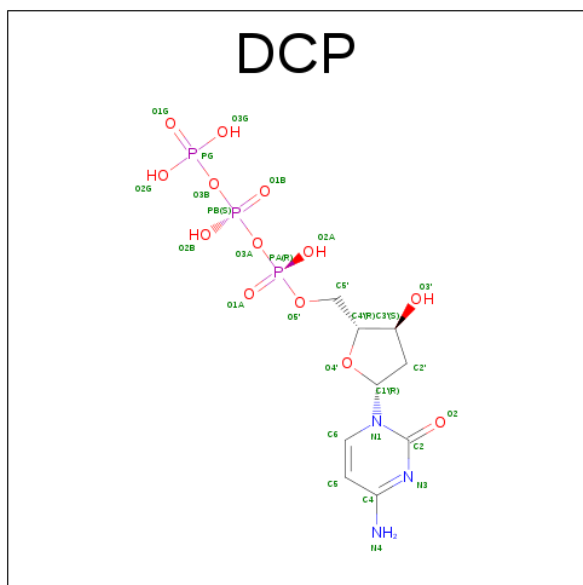
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	16	Total	C	N	O	P	0	0	0
			338	160	71	92	15			
3	H	16	Total	C	N	O	P	0	0	0
			338	160	71	92	15			
3	J	16	Total	C	N	O	P	0	0	0
			338	160	71	92	15			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	16	Total	C	N	O	P	0	0	0
			338	160	71	92	15			

- Molecule 4 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: $C_9H_{16}N_3O_{13}P_3$).



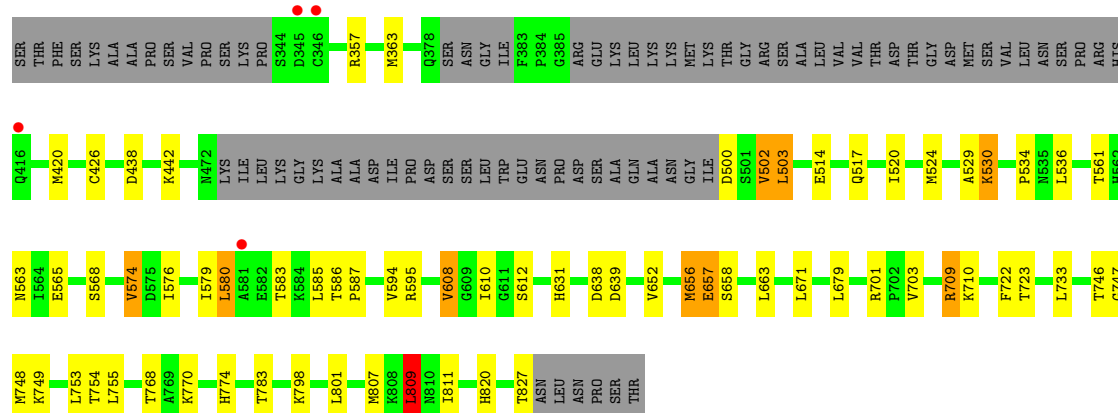
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
4	B	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
4	C	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
4	D	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

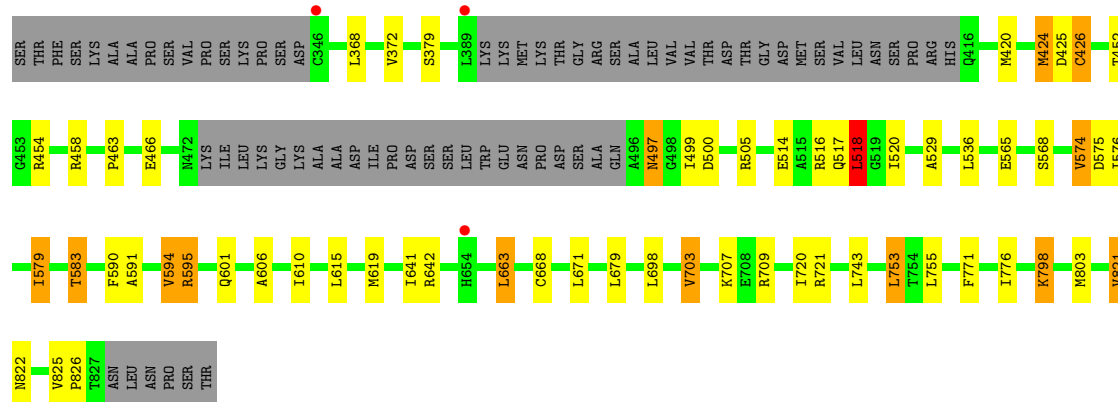
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Mg	0	0
			2	2		
5	A	4	Total	Mg	0	0
			4	4		
5	D	4	Total	Mg	0	0
			4	4		
5	C	3	Total	Mg	0	0
			3	3		

- Molecule 6 is water.

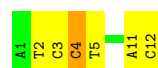
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	38	Total O 38 38	0	0
6	B	15	Total O 15 15	0	0
6	C	17	Total O 17 17	0	0
6	D	10	Total O 10 10	0	0
6	E	2	Total O 2 2	0	0
6	F	1	Total O 1 1	0	0
6	G	1	Total O 1 1	0	0
6	H	5	Total O 5 5	0	0
6	I	1	Total O 1 1	0	0
6	J	3	Total O 3 3	0	0
6	K	1	Total O 1 1	0	0
6	L	2	Total O 2 2	0	0



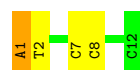
- Molecule 1: DNA repair protein REV1



- Molecule 2: 5'-D(*AP*TP*CP*CP*TP*CP*CP*CP*CP*TP*AP*(DOC))-3'



- Molecule 2: 5'-D(*AP*TP*CP*CP*TP*CP*CP*CP*CP*TP*AP*(DOC))-3'



- Molecule 2: 5'-D(*AP*TP*CP*CP*TP*CP*CP*CP*CP*TP*AP*(DOC))-3'



- Molecule 2: 5'-D(*AP*TP*CP*CP*TP*CP*CP*CP*CP*TP*AP*(DOC))-3'

Chain K:  58% 42%



- Molecule 3: 5'-D(*TP*AP*AP*GP*GP*TP*AP*GP*GP*GP*GP*AP*GP*GP*AP*T)-3',

Chain F:  63% 38%



- Molecule 3: 5'-D(*TP*AP*AP*GP*GP*TP*AP*GP*GP*GP*GP*AP*GP*GP*AP*T)-3',

Chain H:  63% 38%



- Molecule 3: 5'-D(*TP*AP*AP*GP*GP*TP*AP*GP*GP*GP*GP*AP*GP*GP*AP*T)-3',

Chain J:  25% 63% 13%



- Molecule 3: 5'-D(*TP*AP*AP*GP*GP*TP*AP*GP*GP*GP*GP*AP*GP*GP*AP*T)-3',

Chain L:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.44Å 172.78Å 129.19Å 90.00° 90.65° 90.00°	Depositor
Resolution (Å)	43.07 – 2.50 43.06 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.4 (43.07-2.50) 94.4 (43.06-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.214 , 0.267 0.205 , 0.256	Depositor DCC
R_{free} test set	8037 reflections (11.09%)	DCC
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.428	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.109 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15522	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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: DOC, MG, 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	0.50	0/3377	0.61	0/4562
1	B	0.47	0/3372	0.60	0/4565
1	C	0.50	0/3245	0.62	1/4387 (0.0%)
1	D	0.45	0/3263	0.58	1/4421 (0.0%)
2	E	0.89	0/236	1.55	1/360 (0.3%)
2	G	1.12	1/236 (0.4%)	1.51	2/360 (0.6%)
2	I	0.93	0/236	1.42	2/360 (0.6%)
2	K	0.86	1/236 (0.4%)	1.46	1/360 (0.3%)
3	F	1.02	0/382	1.67	7/591 (1.2%)
3	H	0.94	0/382	1.51	5/591 (0.8%)
3	J	2.35	9/382 (2.4%)	2.23	17/591 (2.9%)
3	L	0.82	0/382	1.52	6/591 (1.0%)
All	All	0.67	11/15729 (0.1%)	0.88	43/21739 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	J	0	1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	16	DT	C5-C7	23.85	1.64	1.50
3	J	16	DT	N1-C6	20.49	1.52	1.38
3	J	15	DA	C2-N3	13.44	1.45	1.33
3	J	16	DT	N3-C4	13.14	1.49	1.38
3	J	15	DA	N9-C4	10.75	1.44	1.37
2	G	1	DA	O5'-C5'	10.24	1.67	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	16	DT	C4-C5	9.03	1.53	1.45
3	J	15	DA	N7-C5	8.66	1.44	1.39
3	J	15	DA	C5-C6	7.22	1.47	1.41
2	K	1	DA	O5'-C5'	6.09	1.57	1.42
3	J	15	DA	C6-N6	5.37	1.38	1.33

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	16	DT	C4-C5-C7	21.41	131.84	119.00
3	J	16	DT	C6-C5-C7	-16.16	113.20	122.90
3	J	13	DG	O4'-C1'-N9	13.70	117.59	108.00
3	J	5	DG	O4'-C1'-N9	-12.72	99.09	108.00
3	L	5	DG	O4'-C1'-N9	-10.47	100.67	108.00
3	F	4	DG	O4'-C4'-C3'	-9.42	100.35	106.00
3	J	15	DA	C5-C6-N1	8.68	122.04	117.70
3	J	15	DA	C6-N1-C2	-8.05	113.77	118.60
3	L	10	DG	O4'-C1'-N9	7.93	113.55	108.00
3	F	13	DG	O4'-C1'-N9	7.36	113.15	108.00
3	J	16	DT	C4-C5-C6	-7.35	113.59	118.00
3	J	4	DG	O4'-C4'-C3'	-7.28	101.59	104.50
3	J	12	DA	P-O3'-C3'	7.13	128.25	119.70
3	J	15	DA	N1-C6-N6	-6.82	114.51	118.60
3	F	2	DA	O4'-C1'-N9	-6.75	103.27	108.00
3	H	10	DG	O4'-C1'-N9	6.70	112.69	108.00
3	J	16	DT	N3-C4-C5	6.53	119.12	115.20
3	J	10	DG	O4'-C1'-N9	6.50	112.55	108.00
3	J	16	DT	C5-C4-O4	-6.21	120.56	124.90
1	D	518	LEU	CA-CB-CG	6.18	129.51	115.30
3	J	16	DT	N3-C2-O2	-6.14	118.61	122.30
3	L	6	DT	O4'-C1'-C2'	-6.09	101.03	105.90
3	F	2	DA	O4'-C4'-C3'	-6.09	102.06	104.50
3	F	8	DG	O4'-C1'-N9	6.08	112.26	108.00
2	I	10	DT	C6-C5-C7	-5.91	119.35	122.90
2	E	4	DC	O4'-C1'-N1	5.84	112.09	108.00
3	L	8	DG	O4'-C1'-N9	5.78	112.05	108.00
3	J	13	DG	C1'-O4'-C4'	-5.75	104.35	110.10
3	L	4	DG	O4'-C4'-C3'	-5.74	102.20	104.50
2	G	7	DC	O4'-C1'-N1	5.71	112.00	108.00
3	F	13	DG	P-O3'-C3'	5.60	126.42	119.70
2	K	5	DT	C4-C5-C7	5.46	122.28	119.00
2	G	8	DC	O4'-C1'-N1	5.43	111.80	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	8	DG	P-O3'-C3'	5.29	126.05	119.70
3	F	10	DG	P-O3'-C3'	5.23	125.97	119.70
3	H	15	DA	P-O3'-C3'	5.18	125.91	119.70
3	J	13	DG	C3'-C2'-C1'	-5.16	96.31	102.50
2	I	2	DT	O4'-C1'-N1	5.13	111.59	108.00
3	H	5	DG	O4'-C1'-N9	-5.12	104.41	108.00
3	J	13	DG	P-O3'-C3'	5.09	125.80	119.70
3	L	6	DT	C5-C4-O4	-5.05	121.37	124.90
3	H	6	DT	C5-C4-O4	-5.03	121.38	124.90
1	C	809	LEU	CA-CB-CG	5.01	126.82	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	J	16	DT	Sidechain

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	3318	0	3257	45	0
1	B	3312	0	3202	36	0
1	C	3189	0	3106	38	0
1	D	3206	0	3092	36	0
2	E	231	0	137	4	0
2	G	231	0	137	6	0
2	I	231	0	137	2	0
2	K	231	0	137	2	0
3	F	338	0	181	1	0
3	H	338	0	181	1	0
3	J	338	0	181	5	0
3	L	338	0	181	2	0
4	A	28	0	12	1	0
4	B	28	0	12	0	0
4	C	28	0	12	0	0
4	D	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	4	0	0	0	0
5	B	2	0	0	0	0
5	C	3	0	0	0	0
5	D	4	0	0	0	0
6	A	38	0	0	4	0
6	B	15	0	0	1	0
6	C	17	0	0	1	0
6	D	10	0	0	0	0
6	E	2	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	5	0	0	0	0
6	I	1	0	0	0	0
6	J	3	0	0	0	0
6	K	1	0	0	0	0
6	L	2	0	0	0	0
All	All	15522	0	13977	169	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 6.

All (169) 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:G:1:DA:O5'	2:G:1:DA:C5'	1.67	1.42
1:D:424:MET:HE2	1:D:606:ALA:HB2	1.42	1.02
1:B:722:PHE:HD1	1:B:814:MET:HE3	1.32	0.94
1:C:709:ARG:HD3	1:C:746:THR:HG21	1.58	0.85
1:D:424:MET:CE	1:D:606:ALA:HB2	2.08	0.83
1:B:709:ARG:NH2	3:H:7:DA:OP1	2.14	0.81
1:D:565:GLU:HB2	1:D:703:VAL:HG23	1.65	0.78
1:D:424:MET:HE2	1:D:606:ALA:CB	2.15	0.76
2:E:4:DC:H2''	2:E:5:DT:O5'	1.86	0.75
1:A:782:ARG:C	1:A:803:MET:HE1	2.07	0.75
1:C:500:ASP:HA	1:C:503:LEU:HD22	1.72	0.71
1:B:424:MET:HE1	1:B:553:LEU:HD13	1.71	0.71
1:B:722:PHE:HD1	1:B:814:MET:CE	2.04	0.71
1:C:524:MET:HE3	1:C:529:ALA:HB2	1.74	0.70
1:C:520:ILE:HG23	1:C:524:MET:HE2	1.76	0.68
1:A:799:ALA:O	1:A:803:MET:HG3	1.93	0.68
1:A:754:THR:HG23	1:A:820:HIS:HB2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:507:GLU:OE2	1:B:523:GLY:HA2	1.95	0.65
1:A:376:GLN:NE2	1:A:705:THR:HB	2.11	0.65
1:D:591:ALA:HB2	1:D:610:ILE:HD11	1.78	0.65
1:D:458:ARG:NH1	1:D:771:PHE:HD1	1.95	0.65
1:D:595:ARG:HG2	1:D:595:ARG:HH11	1.62	0.64
1:D:497:ASN:HA	1:D:500:ASP:HB2	1.80	0.64
1:A:524:MET:CE	1:A:529:ALA:HA	2.28	0.64
1:D:452:THR:HG22	1:D:454:ARG:H	1.62	0.63
1:C:583:THR:CB	1:C:585:LEU:H	2.12	0.62
1:B:722:PHE:CD1	1:B:814:MET:HE3	2.24	0.62
1:D:575:ASP:HB2	1:D:703:VAL:HG11	1.81	0.62
1:C:652:VAL:HG22	1:C:656:MET:CE	2.31	0.61
1:A:524:MET:HE3	1:A:529:ALA:HA	1.83	0.60
1:A:524:MET:HE1	1:A:532:LEU:HD12	1.83	0.60
1:B:451:GLY:O	1:B:530:LYS:HE2	2.02	0.60
1:B:668:CYS:O	1:B:672:GLN:HG3	2.01	0.59
1:C:709:ARG:NH2	3:J:7:DA:OP1	2.34	0.59
1:D:615:LEU:O	1:D:619:MET:HG3	2.02	0.58
6:A:14:HOH:O	1:C:768:THR:HG23	2.04	0.58
1:B:497:ASN:C	1:B:497:ASN:HD22	2.08	0.57
1:A:516:ARG:C	1:A:518:LEU:H	2.07	0.57
1:D:743:LEU:HD21	1:D:821:VAL:HG21	1.87	0.56
1:A:656:MET:SD	1:A:683:PHE:CE1	2.99	0.56
1:C:652:VAL:HG22	1:C:656:MET:HE2	1.88	0.56
1:C:420:MET:HE3	1:C:576:ILE:HD13	1.88	0.56
1:A:565:GLU:HB2	1:A:703:VAL:HG13	1.87	0.56
1:D:368:LEU:O	1:D:372:VAL:HG23	2.05	0.56
1:B:424:MET:HE3	1:B:553:LEU:HD22	1.88	0.55
1:C:768:THR:HG22	1:C:770:LYS:O	2.06	0.55
1:D:709:ARG:NH1	3:L:7:DA:OP1	2.39	0.55
1:A:420:MET:HE2	1:A:610:ILE:HD11	1.88	0.55
2:G:1:DA:HO5'	2:G:1:DA:C5'	2.11	0.55
1:B:425:ASP:O	1:B:426:CYS:C	2.45	0.54
1:C:420:MET:HE2	1:C:610:ILE:HD11	1.88	0.54
2:E:2:DT:H2''	2:E:3:DC:OP2	2.08	0.53
1:B:444:VAL:HG12	1:B:537:GLN:HB2	1.91	0.53
1:A:646:VAL:HG21	1:A:660:LEU:HD13	1.89	0.53
1:B:424:MET:HE1	1:B:553:LEU:CD1	2.39	0.53
1:C:595:ARG:HD3	1:C:608:VAL:HG13	1.91	0.53
1:A:599:LYS:NZ	1:A:605:ALA:HB2	2.24	0.53
1:A:709:ARG:HD3	1:A:746:THR:HG21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:709:ARG:NH2	3:F:7:DA:OP1	2.43	0.52
1:C:709:ARG:CD	1:C:746:THR:HG21	2.34	0.52
1:B:458:ARG:NH1	1:B:771:PHE:HD1	2.09	0.51
1:A:619:MET:HE1	1:A:641:ILE:CD1	2.41	0.51
1:A:784:VAL:N	1:A:803:MET:HE3	2.25	0.51
1:A:768:THR:HG22	6:A:42:HOH:O	2.10	0.51
1:D:420:MET:HE3	1:D:576:ILE:HD13	1.93	0.51
1:C:574:VAL:HG22	1:C:576:ILE:HG23	1.91	0.51
2:K:7:DC:H2'	2:K:8:DC:C6	2.46	0.51
1:B:646:VAL:HG11	1:B:660:LEU:HD13	1.93	0.50
1:B:740:GLN:HG3	1:B:791:ASP:O	2.10	0.50
2:G:1:DA:C4'	2:G:1:DA:O5'	2.53	0.50
1:A:357:ARG:HG2	1:A:358:LEU:N	2.27	0.50
1:C:574:VAL:HG22	1:C:576:ILE:CG2	2.42	0.50
1:B:420:MET:HE3	1:B:576:ILE:HD13	1.94	0.50
1:D:568:SER:HB2	2:K:12:DOC:H4'	1.94	0.50
2:E:11:DA:H2''	2:E:12:DOC:H5''	1.94	0.50
1:A:526:PHE:CE2	1:A:536:LEU:HD13	2.46	0.50
1:C:524:MET:CE	1:C:529:ALA:HB2	2.42	0.50
1:C:565:GLU:HB2	1:C:703:VAL:HG13	1.93	0.49
1:B:722:PHE:CD1	1:B:814:MET:CE	2.90	0.49
3:L:14:DG:H2'	3:L:15:DA:C8	2.47	0.49
1:A:783:THR:C	1:A:803:MET:HE3	2.33	0.48
1:B:704:ARG:HH21	1:B:706:GLU:H	1.60	0.48
1:C:722:PHE:HB2	1:C:811:ILE:HG22	1.94	0.48
1:A:619:MET:HE3	1:A:641:ILE:HD12	1.94	0.48
1:C:652:VAL:HG13	1:C:656:MET:HB3	1.94	0.48
1:C:514:GLU:CD	1:C:514:GLU:H	2.15	0.48
1:D:425:ASP:O	1:D:426:CYS:C	2.50	0.48
1:C:502:VAL:HG13	1:C:502:VAL:O	2.13	0.48
1:A:565:GLU:HG3	1:A:704:ARG:O	2.14	0.47
1:C:580:LEU:HD21	1:C:587:PRO:HG3	1.96	0.47
1:A:500:ASP:HA	1:A:503:LEU:HD22	1.96	0.47
1:B:549:VAL:HG13	1:B:602:THR:HB	1.96	0.47
1:A:619:MET:CE	1:A:641:ILE:CD1	2.92	0.47
1:A:420:MET:HG3	1:A:608:VAL:HG13	1.96	0.47
1:A:420:MET:HB2	1:A:610:ILE:HD13	1.96	0.47
1:C:709:ARG:HA	3:J:8:DG:OP1	2.15	0.47
1:B:420:MET:HE1	1:B:590:PHE:CD2	2.50	0.47
1:D:641:ILE:O	1:D:668:CYS:HB2	2.15	0.47
1:B:754:THR:HB	1:B:820:HIS:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:807:MET:HB3	1:C:809:LEU:HD13	1.97	0.47
1:D:575:ASP:HB2	1:D:703:VAL:CG1	2.44	0.47
2:I:10:DT:H2''	2:I:11:DA:C8	2.50	0.47
1:A:526:PHE:HE2	1:A:536:LEU:HD13	1.80	0.46
1:A:509:ALA:O	4:A:101:DCP:H2'1	2.15	0.46
1:B:431:VAL:O	1:B:434:ARG:HB2	2.15	0.46
1:B:386:ARG:HD3	1:B:560:TYR:O	2.16	0.46
1:D:426:CYS:HA	4:D:101:DCP:PB	2.56	0.46
1:B:351:ASN:HB3	6:B:78:HOH:O	2.16	0.46
1:A:568:SER:HB3	2:E:12:DOC:H4'	1.97	0.45
1:D:574:VAL:HG22	1:D:576:ILE:HG23	1.98	0.45
1:A:466:GLU:HA	1:A:776:ILE:HD11	1.98	0.45
1:A:768:THR:CG2	6:A:42:HOH:O	2.63	0.45
3:J:6:DT:H2''	3:J:7:DA:C8	2.52	0.45
1:B:591:ALA:HB1	1:B:608:VAL:HG21	1.98	0.45
1:D:520:ILE:HD12	1:D:529:ALA:HB1	1.99	0.45
1:A:376:GLN:HE21	1:A:705:THR:HB	1.81	0.45
1:A:385:GLY:O	1:A:389:LEU:HG	2.16	0.45
1:A:615:LEU:O	1:A:619:MET:HG3	2.17	0.45
1:D:514:GLU:H	1:D:514:GLU:CD	2.18	0.45
1:C:798:LYS:HA	1:C:798:LYS:HD2	1.80	0.44
1:D:516:ARG:C	1:D:518:LEU:H	2.21	0.44
1:D:753:LEU:O	1:D:803:MET:HE3	2.16	0.44
2:G:1:DA:H2''	2:G:2:DT:H5''	2.00	0.44
1:A:713:SER:HA	1:A:739:ILE:HD11	1.99	0.44
1:B:587:PRO:HB3	1:B:610:ILE:HG21	2.00	0.44
1:A:782:ARG:O	1:A:803:MET:HE1	2.16	0.44
1:D:590:PHE:O	1:D:594:VAL:HG12	2.17	0.44
1:D:825:VAL:HA	1:D:826:PRO:HD2	1.73	0.44
1:C:754:THR:HB	1:C:820:HIS:HB2	2.00	0.44
1:B:520:ILE:HD11	1:B:533:CYS:HB3	1.99	0.44
1:C:701:ARG:NH2	6:C:48:HOH:O	2.50	0.43
1:A:704:ARG:HA	1:A:704:ARG:HD2	1.83	0.43
1:C:520:ILE:HA	1:C:524:MET:HE2	2.00	0.43
1:C:568:SER:HB3	2:I:12:DOC:H4'	1.99	0.43
1:D:595:ARG:CG	1:D:595:ARG:HH11	2.31	0.43
1:B:601:GLN:HA	1:B:601:GLN:OE1	2.19	0.43
1:C:657:GLU:HG3	1:C:658:SER:N	2.33	0.43
2:G:1:DA:H2''	2:G:2:DT:C5'	2.48	0.43
6:A:15:HOH:O	1:B:454:ARG:HD3	2.18	0.42
1:C:747:GLY:O	1:C:748:MET:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:774:HIS:CD2	3:J:4:DG:C8	3.07	0.42
1:A:728:ALA:O	1:A:732:LEU:HG	2.19	0.42
1:B:420:MET:HE1	1:B:590:PHE:HD2	1.84	0.42
1:B:517:GLN:HE21	1:B:517:GLN:HB3	1.61	0.42
1:D:466:GLU:HA	1:D:776:ILE:HD11	2.02	0.42
3:J:2:DA:H2'	3:J:3:DA:C8	2.55	0.42
1:D:463:PRO:HB3	1:D:505:ARG:NH2	2.35	0.42
2:G:1:DA:C2	2:G:2:DT:C2	3.07	0.42
1:C:530:LYS:HE3	1:C:534:PRO:O	2.20	0.42
1:D:663:LEU:HA	1:D:663:LEU:HD12	1.89	0.42
1:A:422:VAL:O	1:A:571:GLU:HA	2.20	0.42
1:D:574:VAL:HG22	1:D:576:ILE:CG2	2.50	0.42
1:B:796:ILE:O	1:B:800:MET:HG2	2.20	0.41
1:A:638:ASP:O	1:A:642:ARG:HG3	2.19	0.41
1:A:528:HIS:O	1:A:531:GLN:HB2	2.20	0.41
1:D:579:ILE:O	1:D:583:THR:OG1	2.31	0.41
1:A:524:MET:HE3	1:A:529:ALA:CA	2.49	0.41
1:B:610:ILE:HB	1:B:631:HIS:HA	2.02	0.41
1:D:424:MET:CE	1:D:606:ALA:CB	2.88	0.41
1:C:749:LYS:HG3	1:C:827:THR:HG22	2.01	0.41
1:A:425:ASP:O	1:A:426:CYS:C	2.58	0.41
1:B:514:GLU:CD	1:B:514:GLU:H	2.24	0.41
1:D:720:ILE:O	1:D:721:ARG:HD3	2.20	0.41
1:B:675:THR:HG22	1:B:677:ALA:N	2.36	0.41
1:C:514:GLU:O	1:C:517:GLN:HB2	2.21	0.41
1:C:561:THR:HB	1:C:579:ILE:HD11	2.03	0.40
1:A:622:ARG:HE	1:A:622:ARG:HB2	1.73	0.40
1:D:798:LYS:HE3	1:D:798:LYS:HA	2.03	0.40
1:C:807:MET:HB3	1:C:809:LEU:CD1	2.52	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	427/504 (85%)	415 (97%)	12 (3%)	0	100	100
1	B	434/504 (86%)	423 (98%)	9 (2%)	2 (0%)	32	53
1	C	415/504 (82%)	400 (96%)	14 (3%)	1 (0%)	51	73
1	D	427/504 (85%)	418 (98%)	8 (2%)	1 (0%)	51	73
All	All	1703/2016 (84%)	1656 (97%)	43 (2%)	4 (0%)	51	73

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	426	CYS
1	D	426	CYS
1	C	426	CYS
1	B	471	GLN

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	348/429 (81%)	326 (94%)	22 (6%)	21	38
1	B	339/429 (79%)	309 (91%)	30 (9%)	12	22
1	C	331/429 (77%)	299 (90%)	32 (10%)	9	18
1	D	323/429 (75%)	298 (92%)	25 (8%)	15	28
All	All	1341/1716 (78%)	1232 (92%)	109 (8%)	14	26

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	375	LEU
1	A	417	SER
1	A	438	ASP
1	A	473	LYS
1	A	503	LEU
1	A	535	ASN
1	A	536	LEU

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Mol	Chain	Res	Type
1	A	578	GLU
1	A	600	ASP
1	A	601	GLN
1	A	622	ARG
1	A	647	THR
1	A	658	SER
1	A	663	LEU
1	A	671	LEU
1	A	674	MET
1	A	704	ARG
1	A	709	ARG
1	A	735	LEU
1	A	739	ILE
1	A	754	THR
1	A	755	LEU
1	B	366	CYS
1	B	386	ARG
1	B	434	ARG
1	B	497	ASN
1	B	517	GLN
1	B	530	LYS
1	B	536	LEU
1	B	548	GLU
1	B	573	LEU
1	B	579	ILE
1	B	580	LEU
1	B	600	ASP
1	B	608	VAL
1	B	612	SER
1	B	631	HIS
1	B	646	VAL
1	B	657	GLU
1	B	662	SER
1	B	679	LEU
1	B	703	VAL
1	B	704	ARG
1	B	723	THR
1	B	726	LYS
1	B	732	LEU
1	B	733	LEU
1	B	753	LEU
1	B	755	LEU

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Mol	Chain	Res	Type
1	B	756	LYS
1	B	780	ILE
1	B	827	THR
1	C	357	ARG
1	C	363	MET
1	C	438	ASP
1	C	442	LYS
1	C	502	VAL
1	C	503	LEU
1	C	530	LYS
1	C	536	LEU
1	C	563	ASN
1	C	574	VAL
1	C	580	LEU
1	C	586	THR
1	C	594	VAL
1	C	608	VAL
1	C	612	SER
1	C	631	HIS
1	C	638	ASP
1	C	639	ASP
1	C	656	MET
1	C	657	GLU
1	C	663	LEU
1	C	671	LEU
1	C	679	LEU
1	C	709	ARG
1	C	710	LYS
1	C	723	THR
1	C	733	LEU
1	C	753	LEU
1	C	755	LEU
1	C	783	THR
1	C	801	LEU
1	C	809	LEU
1	D	379	SER
1	D	424	MET
1	D	497	ASN
1	D	499	ILE
1	D	517	GLN
1	D	518	LEU
1	D	536	LEU

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Mol	Chain	Res	Type
1	D	574	VAL
1	D	579	ILE
1	D	583	THR
1	D	594	VAL
1	D	595	ARG
1	D	601	GLN
1	D	642	ARG
1	D	663	LEU
1	D	671	LEU
1	D	679	LEU
1	D	698	LEU
1	D	703	VAL
1	D	707	LYS
1	D	753	LEU
1	D	755	LEU
1	D	798	LYS
1	D	821	VAL
1	D	822	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	435	ASN
1	A	535	ASN
1	A	631	HIS
1	B	497	ASN
1	B	672	GLN
1	C	563	ASN
1	C	648	ASN
1	D	517	GLN
1	D	551	GLN

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$
2	DOC	E	12	3,2	13,19,20	0.69	0	12,26,29	0.99	0
2	DOC	G	12	3,2	13,19,20	0.74	0	12,26,29	1.09	1 (8%)
2	DOC	I	12	3,2	13,19,20	0.79	0	12,26,29	0.95	0
2	DOC	K	12	3,2	13,19,20	0.75	0	12,26,29	1.09	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	DOC	E	12	3,2	-	0/3/18/19	0/2/2/2
2	DOC	G	12	3,2	-	0/3/18/19	0/2/2/2
2	DOC	I	12	3,2	-	0/3/18/19	0/2/2/2
2	DOC	K	12	3,2	-	0/3/18/19	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	12	DOC	C2'-C3'-C4'	2.04	106.52	102.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	12	DOC	2	0
2	I	12	DOC	1	0
2	K	12	DOC	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 13 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$
4	DCP	A	101	5	23,29,29	1.23	1 (4%)	25,45,45	1.08	1 (4%)
4	DCP	B	101	5	23,29,29	1.30	1 (4%)	25,45,45	1.29	2 (8%)
4	DCP	C	101	5	23,29,29	1.28	1 (4%)	25,45,45	1.22	2 (8%)
4	DCP	D	101	5	23,29,29	1.27	1 (4%)	25,45,45	1.28	2 (8%)

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	A	101	5	-	0/18/34/34	0/2/2/2
4	DCP	B	101	5	-	0/18/34/34	0/2/2/2
4	DCP	C	101	5	-	0/18/34/34	0/2/2/2
4	DCP	D	101	5	-	0/18/34/34	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	101	DCP	C6-N1	4.97	1.42	1.35
4	D	101	DCP	C6-N1	5.23	1.42	1.35
4	C	101	DCP	C6-N1	5.45	1.43	1.35
4	B	101	DCP	C6-N1	5.50	1.43	1.35

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	101	DCP	C6-N1-C2	-3.71	115.26	121.28
4	B	101	DCP	C6-N1-C2	-3.66	115.35	121.28
4	D	101	DCP	C6-N1-C2	-3.52	115.57	121.28
4	A	101	DCP	C6-N1-C2	-3.20	116.09	121.28
4	B	101	DCP	N4-C4-N3	2.15	120.27	116.64
4	C	101	DCP	N4-C4-N3	2.19	120.32	116.64
4	D	101	DCP	N4-C4-N3	2.47	120.80	116.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	101	DCP	1	0
4	D	101	DCP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	435/504 (86%)	0.22	5 (1%) 80 81	24, 41, 58, 76	0
1	B	440/504 (87%)	0.19	4 (0%) 84 85	27, 41, 54, 78	0
1	C	423/504 (83%)	-0.04	4 (0%) 84 85	26, 41, 58, 70	0
1	D	433/504 (85%)	0.21	3 (0%) 87 88	30, 42, 56, 69	0
2	E	11/12 (91%)	-0.36	0 100 100	24, 37, 42, 45	0
2	G	11/12 (91%)	-0.21	0 100 100	32, 42, 47, 48	0
2	I	11/12 (91%)	-0.22	0 100 100	26, 32, 38, 38	0
2	K	11/12 (91%)	-0.29	0 100 100	35, 39, 46, 49	0
3	F	16/16 (100%)	-0.08	0 100 100	39, 50, 57, 59	0
3	H	16/16 (100%)	-0.18	0 100 100	33, 43, 52, 55	0
3	J	16/16 (100%)	-0.19	0 100 100	14, 27, 35, 38	0
3	L	16/16 (100%)	-0.37	0 100 100	37, 44, 51, 52	0
All	All	1839/2128 (86%)	0.12	16 (0%) 84 85	14, 41, 57, 78	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	471	GLN	5.0
1	C	346	CYS	3.9
1	D	346	CYS	3.7
1	A	499	ILE	3.6
1	C	581	ALA	3.3
1	B	346	CYS	2.9
1	C	345	ASP	2.9
1	A	389	LEU	2.8
1	A	470	TYR	2.7
1	A	477	GLY	2.6
1	B	641	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	389	LEU	2.3
1	A	500	ASP	2.1
1	C	416	GLN	2.1
1	D	654	HIS	2.1
1	B	379	SER	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	DOC	G	12	18/19	0.87	0.20	-	41,44,51,51	0
2	DOC	I	12	18/19	0.93	0.15	-	30,32,44,45	0
2	DOC	K	12	18/19	0.86	0.18	-	42,44,47,48	0
2	DOC	E	12	18/19	0.91	0.15	-	29,31,40,40	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	MG	D	210	1/1	0.99	0.24	3.36	30,30,30,30	0
5	MG	B	212	1/1	0.88	0.20	1.58	54,54,54,54	0
5	MG	A	209	1/1	0.93	0.18	1.52	40,40,40,40	0
5	MG	C	213	1/1	0.65	0.13	-1.05	44,44,44,44	0
5	MG	D	207	1/1	0.93	0.12	-1.26	41,41,41,41	0
4	DCP	B	101	28/28	0.96	0.13	-1.29	32,40,52,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	DCP	C	101	28/28	0.98	0.10	-1.38	24,29,35,36	0
5	MG	D	214	1/1	0.72	0.13	-1.83	50,50,50,50	0
4	DCP	D	101	28/28	0.97	0.10	-1.95	35,40,53,54	0
5	MG	A	211	1/1	0.84	0.10	-2.47	49,49,49,49	0
5	MG	B	203	1/1	0.96	0.08	-2.99	34,34,34,34	0
4	DCP	A	101	28/28	0.98	0.10	-3.06	21,25,33,35	0
5	MG	C	205	1/1	0.97	0.05	-4.90	25,25,25,25	0
5	MG	A	201	1/1	0.98	0.03	-5.90	20,20,20,20	0
5	MG	A	202	1/1	0.94	0.50	-	33,33,33,33	1
5	MG	C	206	1/1	0.96	0.38	-	33,33,33,33	1
5	MG	D	208	1/1	0.98	0.39	-	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.