



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:09 PM GMT

PDB ID : 4KOE
Title : Quinolone(Trovaflaxacin)-DNA cleavage complex of type IV topoisomerase from *S. pneumoniae*
Authors : Laponogov, I.; Pan, X.-S.; Veselkov, D.A.; Fisher, L.M.; Sanderson, M.R.
Deposited on : 2013-05-11
Resolution : 3.02 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

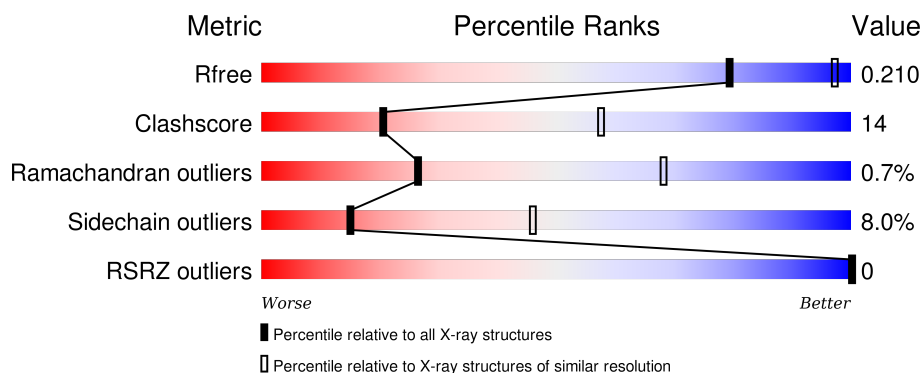
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 3.02 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.





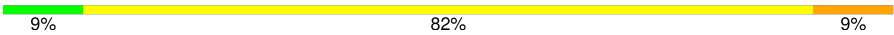
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1773 (3.04-3.00)
Clashscore	102246	2117 (3.04-3.00)
Ramachandran outliers	100387	2050 (3.04-3.00)
Sidechain outliers	100360	2053 (3.04-3.00)
RSRZ outliers	91569	1788 (3.04-3.00)

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	496	 74% 20% • •
1	B	496	 73% 21% • •
2	C	268	 62% 13% • 22%
2	D	268	 57% 18% • 23%
3	E	7	 14% 71% 14%

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Mol	Chain	Length	Quality of chain
4	F	11	 27% 55% 18%
5	G	7	 29% 71%
6	H	11	 9% 82% 9%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 11133 atoms, of which 28 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 topoisomerase 4 subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	0	0	0
			3737	2366	647	711	13			
1	B	482	Total	C	N	O	S	0	0	0
			3709	2354	637	705	13			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	257	THR	ILE	ENGINEERED MUTATION	UNP P72525
A	489	LEU	-	EXPRESSION TAG	UNP P72525
A	490	GLU	-	EXPRESSION TAG	UNP P72525
A	491	HIS	-	EXPRESSION TAG	UNP P72525
A	492	HIS	-	EXPRESSION TAG	UNP P72525
A	493	HIS	-	EXPRESSION TAG	UNP P72525
A	494	HIS	-	EXPRESSION TAG	UNP P72525
A	495	HIS	-	EXPRESSION TAG	UNP P72525
A	496	HIS	-	EXPRESSION TAG	UNP P72525
B	257	THR	ILE	ENGINEERED MUTATION	UNP P72525
B	489	LEU	-	EXPRESSION TAG	UNP P72525
B	490	GLU	-	EXPRESSION TAG	UNP P72525
B	491	HIS	-	EXPRESSION TAG	UNP P72525
B	492	HIS	-	EXPRESSION TAG	UNP P72525
B	493	HIS	-	EXPRESSION TAG	UNP P72525
B	494	HIS	-	EXPRESSION TAG	UNP P72525
B	495	HIS	-	EXPRESSION TAG	UNP P72525
B	496	HIS	-	EXPRESSION TAG	UNP P72525

- Molecule 2 is a protein called DNA topoisomerase 4 subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	208	Total	C	N	O	S	0	0	0
			1436	912	252	266	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	207	Total	C	N	O	S	0	0	0
			1427	906	249	266	6			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	380	MET	-	EXPRESSION TAG	UNP Q59961
C	381	GLY	-	EXPRESSION TAG	UNP Q59961
C	382	HIS	-	EXPRESSION TAG	UNP Q59961
C	383	HIS	-	EXPRESSION TAG	UNP Q59961
C	384	HIS	-	EXPRESSION TAG	UNP Q59961
C	385	HIS	-	EXPRESSION TAG	UNP Q59961
C	386	HIS	-	EXPRESSION TAG	UNP Q59961
C	387	HIS	-	EXPRESSION TAG	UNP Q59961
C	388	HIS	-	EXPRESSION TAG	UNP Q59961
C	389	HIS	-	EXPRESSION TAG	UNP Q59961
C	390	HIS	-	EXPRESSION TAG	UNP Q59961
C	391	HIS	-	EXPRESSION TAG	UNP Q59961
C	392	SER	-	EXPRESSION TAG	UNP Q59961
C	393	SER	-	EXPRESSION TAG	UNP Q59961
C	394	GLY	-	EXPRESSION TAG	UNP Q59961
C	395	HIS	-	EXPRESSION TAG	UNP Q59961
C	396	ILE	-	EXPRESSION TAG	UNP Q59961
C	397	ASP	-	EXPRESSION TAG	UNP Q59961
C	398	ASP	-	EXPRESSION TAG	UNP Q59961
C	399	ASP	-	EXPRESSION TAG	UNP Q59961
C	400	ASP	-	EXPRESSION TAG	UNP Q59961
C	401	LYS	-	EXPRESSION TAG	UNP Q59961
C	402	HIS	-	EXPRESSION TAG	UNP Q59961
C	403	MET	-	EXPRESSION TAG	UNP Q59961
C	460	ILE	VAL	ENGINEERED MUTATION	UNP Q59961
C	644	ALA	THR	ENGINEERED MUTATION	UNP Q59961
D	380	MET	-	EXPRESSION TAG	UNP Q59961
D	381	GLY	-	EXPRESSION TAG	UNP Q59961
D	382	HIS	-	EXPRESSION TAG	UNP Q59961
D	383	HIS	-	EXPRESSION TAG	UNP Q59961
D	384	HIS	-	EXPRESSION TAG	UNP Q59961
D	385	HIS	-	EXPRESSION TAG	UNP Q59961
D	386	HIS	-	EXPRESSION TAG	UNP Q59961
D	387	HIS	-	EXPRESSION TAG	UNP Q59961
D	388	HIS	-	EXPRESSION TAG	UNP Q59961
D	389	HIS	-	EXPRESSION TAG	UNP Q59961

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Chain	Residue	Modelled	Actual	Comment	Reference
D	390	HIS	-	EXPRESSION TAG	UNP Q59961
D	391	HIS	-	EXPRESSION TAG	UNP Q59961
D	392	SER	-	EXPRESSION TAG	UNP Q59961
D	393	SER	-	EXPRESSION TAG	UNP Q59961
D	394	GLY	-	EXPRESSION TAG	UNP Q59961
D	395	HIS	-	EXPRESSION TAG	UNP Q59961
D	396	ILE	-	EXPRESSION TAG	UNP Q59961
D	397	ASP	-	EXPRESSION TAG	UNP Q59961
D	398	ASP	-	EXPRESSION TAG	UNP Q59961
D	399	ASP	-	EXPRESSION TAG	UNP Q59961
D	400	ASP	-	EXPRESSION TAG	UNP Q59961
D	401	LYS	-	EXPRESSION TAG	UNP Q59961
D	402	HIS	-	EXPRESSION TAG	UNP Q59961
D	403	MET	-	EXPRESSION TAG	UNP Q59961
D	460	ILE	VAL	ENGINEERED MUTATION	UNP Q59961
D	644	ALA	THR	ENGINEERED MUTATION	UNP Q59961

- Molecule 3 is a DNA chain called E-site DNA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	P	0	0	0
			140	69	27	38	6			

- Molecule 4 is a DNA chain called E-site DNA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	11	Total	C	N	O	P	0	0	0
			225	108	39	67	11			

- Molecule 5 is a DNA chain called E-site DNA3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	7	Total	C	N	O	P	0	0	0
			139	68	25	40	6			

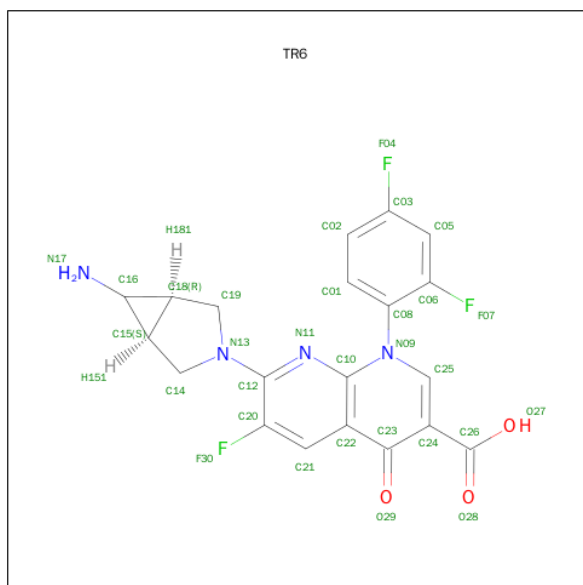
- Molecule 6 is a DNA chain called E-site DNA4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	11	Total	C	N	O	P	0	0	0
			226	107	43	65	11			

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	2	Total Mg 2 2	0	0
7	A	2	Total Mg 2 2	0	0
7	D	1	Total Mg 1 1	0	0
7	C	1	Total Mg 1 1	0	0

- Molecule 8 is TROVAFLOXACIN (three-letter code: TR6) (formula: $C_{20}H_{15}F_3N_4O_3$).

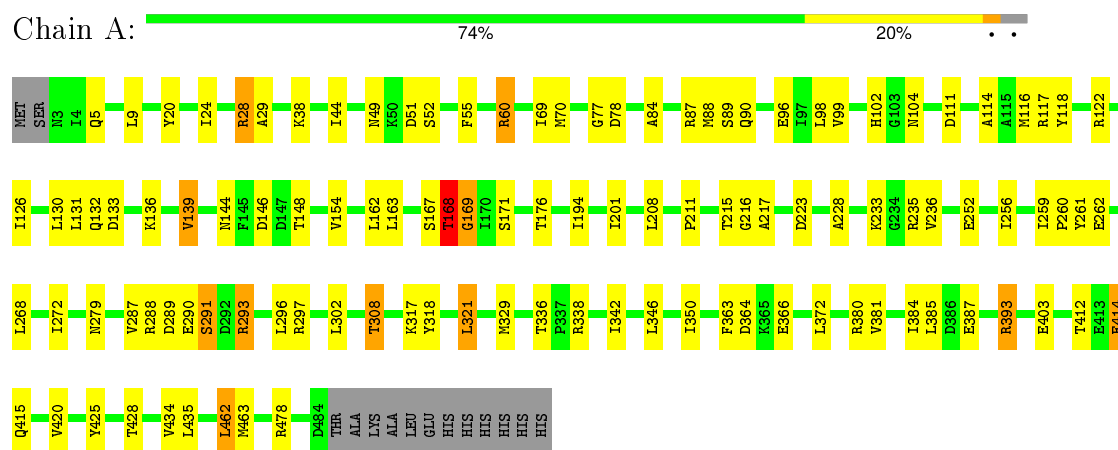


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	F	1	Total	C	F	H	N	O	0	0
			44	20	3	14	4	3		
8	H	1	Total	C	F	H	N	O	0	0
			44	20	3	14	4	3		

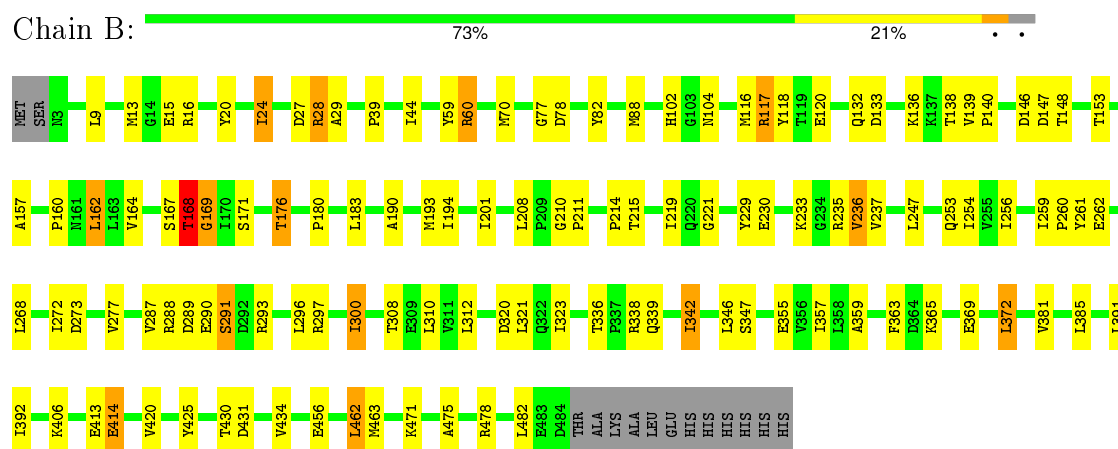
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

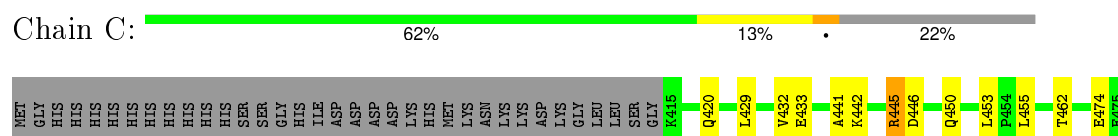
• Molecule 1: DNA topoisomerase 4 subunit A

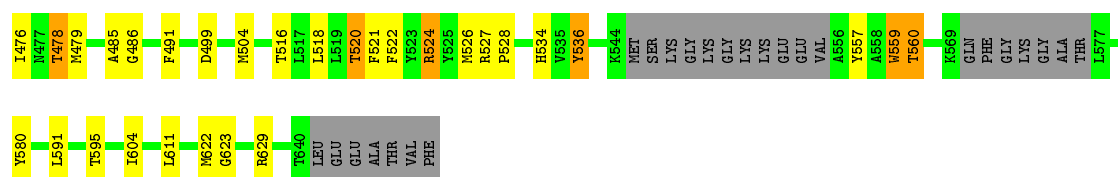


• Molecule 1: DNA topoisomerase 4 subunit A



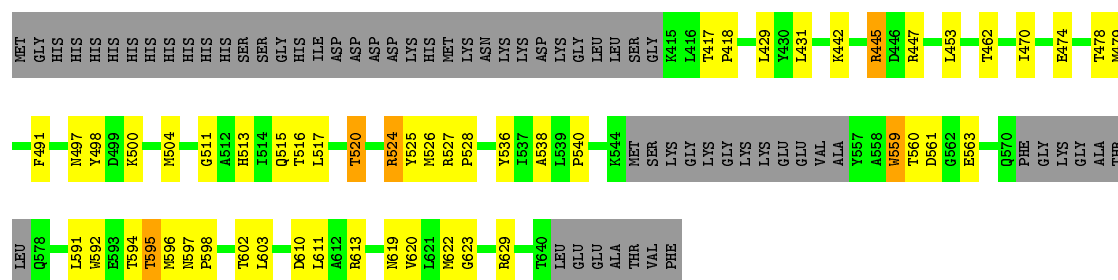
• Molecule 2: DNA topoisomerase 4 subunit B





• Molecule 2: DNA topoisomerase 4 subunit B

Chain D: 57% 18% 23%



• Molecule 3: E-site DNA1

Chain E: 14% 71% 14%



• Molecule 4: E-site DNA2

Chain F: 27% 55% 18%



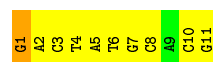
• Molecule 5: E-site DNA3

Chain G: 29% 71%



• Molecule 6: E-site DNA4

Chain H: 9% 82% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	158.04Å 158.04Å 210.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	62.42 – 3.02 62.42 – 3.02	Depositor EDS
% Data completeness (in resolution range)	99.9 (62.42-3.02) 100.0 (62.42-3.02)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.72 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.175 , 0.210 0.176 , 0.210	Depositor DCC
R_{free} test set	3025 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	69.4	Xtriage
Anisotropy	0.591	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 47.9	EDS
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 60127 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11133	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, TR6

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	0/3798	0.59	0/5144
1	B	0.44	0/3770	0.61	0/5112
2	C	0.34	0/1462	0.53	0/1999
2	D	0.32	0/1453	0.51	0/1986
3	E	0.69	0/157	1.47	3/241 (1.2%)
4	F	0.79	0/251	1.64	11/385 (2.9%)
5	G	0.81	0/155	1.51	2/238 (0.8%)
6	H	0.78	0/253	1.50	5/388 (1.3%)
All	All	0.44	0/11299	0.71	21/15493 (0.1%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	6	DT	O4'-C4'-C3'	-7.66	101.40	106.00
6	H	2	DA	O4'-C1'-N9	-6.70	103.31	108.00
4	F	1	DA	C1'-O4'-C4'	-6.46	103.64	110.10
6	H	1	DG	O4'-C1'-C2'	-6.38	100.79	105.90
3	E	15	DT	N3-C4-O4	6.23	123.64	119.90
4	F	6	DT	C4'-C3'-C2'	-6.05	97.65	103.10
4	F	6	DT	O4'-C1'-N1	6.01	112.21	108.00
6	H	1	DG	O5'-P-OP2	-6.01	100.29	105.70
4	F	3	DT	N3-C4-O4	6.00	123.50	119.90
4	F	1	DA	O4'-C1'-C2'	-5.93	101.16	105.90
4	F	10	DT	C1'-O4'-C4'	-5.92	104.18	110.10
3	E	11	DT	O4'-C1'-N1	-5.92	103.86	108.00
6	H	8	DC	O4'-C1'-N1	5.91	112.14	108.00
6	H	1	DG	P-O5'-C5'	-5.71	111.76	120.90
5	G	11	DT	N3-C4-O4	5.52	123.21	119.90
4	F	3	DT	O4'-C1'-N1	5.47	111.83	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	3	DT	C5-C4-O4	-5.40	121.12	124.90
5	G	15	DT	N3-C4-O4	5.28	123.07	119.90
3	E	10	DA	O4'-C1'-N9	5.12	111.58	108.00
4	F	6	DT	C1'-O4'-C4'	-5.11	104.99	110.10
4	F	7	DT	N3-C4-O4	5.05	122.93	119.90

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	3737	0	3650	104	0
1	B	3709	0	3617	96	0
2	C	1436	0	1222	40	0
2	D	1427	0	1208	41	0
3	E	140	0	78	7	0
4	F	225	0	126	15	0
5	G	139	0	78	6	0
6	H	226	0	124	21	0
7	A	2	0	0	0	0
7	B	2	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	F	30	14	14	1	0
8	H	30	14	14	1	0
All	All	11105	28	10131	305	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 14.

All (305) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:ARG:HB3	1:A:293:ARG:HH11	1.06	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:ARG:HG3	1:A:28:ARG:HH11	0.96	1.08
1:B:70:MET:HE1	1:B:78:ASP:HB3	1.32	1.08
1:A:146:ASP:HB3	1:A:148:THR:HG22	1.35	1.08
1:A:60:ARG:HB2	1:A:60:ARG:HH11	1.16	1.08
1:A:70:MET:HE1	1:A:78:ASP:HB3	1.36	1.05
1:B:146:ASP:HB3	1:B:148:THR:HG23	1.36	1.02
1:A:169:GLY:HA2	1:A:176:THR:HG22	1.43	1.00
1:B:28:ARG:HG3	1:B:28:ARG:HH11	1.22	0.99
4:F:3:DT:H4'	4:F:4:DC:OP1	1.62	0.98
1:B:291:SER:HB3	1:B:296:LEU:HA	1.44	0.96
2:C:524:ARG:HH11	2:C:524:ARG:HG3	1.27	0.96
1:A:293:ARG:CB	1:A:293:ARG:HH11	1.78	0.95
1:A:28:ARG:HG3	1:A:28:ARG:NH1	1.75	0.94
2:D:524:ARG:HH11	2:D:524:ARG:HB3	1.33	0.94
1:A:60:ARG:HH11	1:A:60:ARG:CB	1.79	0.93
1:A:393:ARG:HH11	1:A:393:ARG:HG2	1.31	0.92
2:D:431:LEU:HD13	2:D:479:MET:HE1	1.52	0.90
2:D:491:PHE:CE2	2:D:526:MET:HG2	2.08	0.88
2:C:524:ARG:HH11	2:C:524:ARG:CG	1.85	0.88
1:A:60:ARG:HB2	1:A:60:ARG:NH1	1.89	0.86
1:A:256:ILE:HD13	1:A:321:LEU:HD21	1.57	0.86
1:B:288:ARG:NH1	1:B:290:GLU:OE2	2.07	0.86
2:D:431:LEU:HD13	2:D:479:MET:CE	2.07	0.83
1:A:293:ARG:NH1	1:A:293:ARG:HB3	1.91	0.83
1:B:29:ALA:HB3	1:B:171:SER:HB3	1.58	0.83
1:A:211:PRO:O	1:A:478:ARG:NH2	2.13	0.80
3:E:9:DC:H2''	3:E:10:DA:H5''	1.66	0.78
3:E:9:DC:N4	4:F:11:DG:O6	2.13	0.78
1:A:118:TYR:HE2	4:F:1:DA:C5'	1.97	0.77
1:A:60:ARG:HH11	1:A:60:ARG:CG	1.98	0.76
1:B:146:ASP:HB3	1:B:148:THR:CG2	2.16	0.76
2:D:520:THR:HG21	2:D:622:MET:HG3	1.66	0.75
2:D:611:LEU:O	2:D:611:LEU:HD13	1.86	0.75
1:B:24:ILE:HG23	1:B:171:SER:HB2	1.67	0.75
1:A:70:MET:CE	1:A:78:ASP:HB3	2.14	0.74
1:B:167:SER:C	1:B:168:THR:HG22	2.06	0.74
2:C:524:ARG:NH1	2:C:524:ARG:HG3	2.01	0.74
1:A:144:ASN:HD21	1:A:148:THR:CG2	2.00	0.74
1:A:146:ASP:HB3	1:A:148:THR:CG2	2.16	0.74
2:D:474:GLU:O	2:D:478:THR:HG23	1.88	0.74
2:C:557:TYR:HE2	2:C:580:TYR:HH	1.34	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:3:DC:H4'	6:H:4:DT:OP1	1.87	0.73
1:A:393:ARG:HG2	1:A:393:ARG:NH1	2.02	0.72
2:C:474:GLU:O	2:C:478:THR:HG23	1.90	0.72
1:B:59:TYR:HB3	1:B:120:GLU:HB3	1.72	0.71
2:D:623:GLY:O	2:D:629:ARG:NH2	2.24	0.71
2:D:602:THR:O	2:D:603:LEU:HD23	1.91	0.71
1:A:118:TYR:HE2	4:F:1:DA:H5''	1.55	0.70
2:D:516:THR:O	2:D:520:THR:HG23	1.91	0.70
1:A:96:GLU:HG2	1:A:126:ILE:HD13	1.74	0.70
1:B:194:ILE:CD1	1:B:463:MET:HE2	2.21	0.69
1:A:235:ARG:NH2	4:F:11:DG:O3'	2.24	0.69
1:B:211:PRO:O	1:B:478:ARG:NH2	2.25	0.69
1:B:169:GLY:HA3	1:B:176:THR:HG22	1.75	0.69
1:B:169:GLY:CA	1:B:176:THR:HG22	2.23	0.68
1:A:169:GLY:HA2	1:A:176:THR:CG2	2.20	0.68
1:B:24:ILE:CG2	1:B:171:SER:HB2	2.24	0.68
5:G:9:DC:H42	6:H:11:DG:H1	1.41	0.68
1:A:412:THR:OG1	1:A:415:GLN:HG3	1.94	0.68
1:B:28:ARG:CG	1:B:28:ARG:HH11	2.01	0.67
1:A:169:GLY:CA	1:A:176:THR:HG22	2.22	0.67
6:H:10:DC:H2''	6:H:11:DG:C5'	2.24	0.67
1:A:350:ILE:HA	1:A:463:MET:HE3	1.77	0.67
1:B:9:LEU:HD23	1:B:9:LEU:C	2.15	0.67
6:H:10:DC:H2''	6:H:11:DG:H5''	1.77	0.67
2:D:524:ARG:HH11	2:D:524:ARG:CB	2.07	0.66
1:A:393:ARG:HH11	1:A:393:ARG:CG	2.06	0.66
1:B:24:ILE:HD11	1:B:28:ARG:NE	2.10	0.65
1:B:194:ILE:HD11	1:B:463:MET:CE	2.26	0.65
5:G:13:DC:H2''	5:G:14:DA:O5'	1.97	0.65
4:F:1:DA:H2''	4:F:2:DG:C8	2.32	0.64
1:B:261:TYR:CD2	1:B:262:GLU:HG3	2.32	0.64
1:B:9:LEU:HD23	1:B:9:LEU:O	1.97	0.63
1:B:132:GLN:O	1:B:133:ASP:HB2	1.98	0.63
1:A:144:ASN:HD21	1:A:148:THR:HG23	1.62	0.63
2:D:491:PHE:CD2	2:D:526:MET:HG2	2.33	0.63
1:B:193:MET:HE1	1:B:347:SER:HB3	1.79	0.63
1:A:20:TYR:O	1:A:24:ILE:HG12	1.99	0.62
2:C:486:GLY:O	2:C:491:PHE:HD2	1.83	0.62
1:B:194:ILE:HD11	1:B:463:MET:HE2	1.82	0.61
2:C:462:THR:HG21	2:C:521:PHE:HD2	1.65	0.61
1:A:117:ARG:HE	1:B:77:GLY:HA2	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:538:ALA:O	2:D:540:PRO:HD3	2.00	0.61
1:B:235:ARG:NH2	6:H:11:DG:O3'	2.32	0.60
1:B:24:ILE:HD11	1:B:28:ARG:HE	1.66	0.60
1:A:393:ARG:NH1	1:A:393:ARG:CG	2.63	0.60
2:D:500:LYS:HG2	2:D:536:TYR:CE2	2.37	0.60
1:A:118:TYR:CE2	4:F:1:DA:H5''	2.34	0.60
2:C:485:ALA:HB3	2:C:491:PHE:CE2	2.37	0.60
1:A:434:VAL:HG13	1:A:435:LEU:N	2.16	0.60
3:E:9:DC:C2'	3:E:10:DA:H5''	2.32	0.60
1:B:431:ASP:O	1:B:434:VAL:HG12	2.02	0.60
1:A:290:GLU:HB2	1:A:297:ARG:HG2	1.82	0.59
6:H:5:DA:H2''	6:H:6:DT:H5''	1.83	0.59
3:E:9:DC:N3	4:F:11:DG:N1	2.49	0.59
1:B:44:ILE:HD12	1:B:88:MET:HE2	1.83	0.59
2:C:527:ARG:N	2:C:528:PRO:HD2	2.18	0.59
2:D:611:LEU:C	2:D:611:LEU:HD13	2.23	0.59
3:E:13:DA:H2''	3:E:14:DA:O5'	2.03	0.59
2:C:516:THR:O	2:C:520:THR:HG22	2.04	0.58
1:A:235:ARG:HH12	4:F:11:DG:H4'	1.68	0.58
1:B:355:GLU:OE2	1:B:355:GLU:HA	2.04	0.58
1:B:82:TYR:CD1	1:B:116:MET:HB3	2.39	0.58
1:B:60:ARG:HB2	1:B:60:ARG:HH11	1.68	0.58
1:B:194:ILE:HD13	1:B:463:MET:HE2	1.86	0.58
2:C:623:GLY:O	2:C:629:ARG:NH2	2.33	0.58
2:D:559:TRP:N	2:D:559:TRP:HE3	2.02	0.57
1:B:70:MET:CE	1:B:78:ASP:HB3	2.20	0.57
1:B:168:THR:HA	1:B:176:THR:O	2.04	0.57
1:B:60:ARG:CB	1:B:60:ARG:HH11	2.17	0.57
2:D:513:HIS:O	2:D:516:THR:HB	2.04	0.57
2:C:433:GLU:HG2	2:C:433:GLU:O	2.03	0.57
1:A:216:GLY:O	1:A:217:ALA:HB3	2.04	0.56
2:C:524:ARG:CB	2:C:524:ARG:HH11	2.18	0.56
6:H:3:DC:H2'	6:H:4:DT:C6	2.39	0.56
2:D:527:ARG:N	2:D:528:PRO:HD2	2.21	0.56
2:C:499:ASP:O	2:C:534:HIS:ND1	2.38	0.56
1:B:146:ASP:O	1:B:147:ASP:HB2	2.04	0.56
2:C:559:TRP:CE3	2:C:559:TRP:N	2.74	0.56
1:A:169:GLY:HA3	1:A:176:THR:O	2.05	0.56
2:D:559:TRP:N	2:D:559:TRP:CE3	2.74	0.55
1:A:5:GLN:O	2:C:604:ILE:HA	2.06	0.55
1:B:259:ILE:HB	1:B:260:PRO:CD	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:GLU:HG2	1:A:126:ILE:CD1	2.36	0.55
1:A:261:TYR:CD2	1:A:262:GLU:HG3	2.40	0.55
1:A:118:TYR:CE2	4:F:1:DA:C5'	2.85	0.55
6:H:6:DT:H2''	6:H:7:DG:H5'	1.88	0.55
1:A:317:LYS:HE3	1:A:318:TYR:CE2	2.42	0.55
2:C:516:THR:O	2:C:520:THR:CG2	2.55	0.55
1:A:201:ILE:H	1:A:201:ILE:HD12	1.72	0.55
1:B:9:LEU:HD21	1:B:13:MET:HG3	1.88	0.55
1:B:193:MET:CE	1:B:347:SER:HB3	2.38	0.54
2:D:592:TRP:HA	2:D:596:MET:HB2	1.89	0.54
1:B:406:LYS:HE2	1:B:413:GLU:HA	1.90	0.54
1:A:29:ALA:O	1:A:38:LYS:HE2	2.08	0.54
1:B:9:LEU:CD2	1:B:9:LEU:C	2.76	0.54
2:C:611:LEU:HD13	2:C:611:LEU:O	2.08	0.53
1:B:118:TYR:HE2	6:H:1:DG:C5'	2.22	0.53
1:A:403:GLU:OE2	1:A:403:GLU:HA	2.09	0.53
6:H:11:DG:H8	6:H:11:DG:H3'	1.73	0.53
1:A:29:ALA:HB3	1:A:171:SER:HB3	1.90	0.53
2:D:594:THR:OG1	2:D:595:THR:HG22	2.09	0.53
1:A:414:GLU:CD	1:A:414:GLU:H	2.12	0.53
1:A:293:ARG:CG	1:A:293:ARG:HH11	2.21	0.53
1:A:252:GLU:OE1	1:A:308:THR:HG21	2.08	0.52
1:B:289:ASP:OD2	1:B:291:SER:OG	2.28	0.52
1:B:272:ILE:HG22	1:B:287:VAL:HG21	1.91	0.52
1:B:219:ILE:HB	1:B:482:LEU:HD23	1.90	0.52
1:B:29:ALA:CB	1:B:171:SER:HB3	2.35	0.52
1:A:87:ARG:HA	1:A:90:GLN:HG3	1.91	0.52
6:H:10:DC:H2''	6:H:11:DG:H5'	1.92	0.52
1:A:24:ILE:HG22	1:A:171:SER:HB2	1.92	0.51
2:D:610:ASP:OD1	2:D:613:ARG:HB2	2.11	0.51
1:A:136:LYS:HG2	1:A:363:PHE:CD2	2.46	0.51
2:C:520:THR:HG21	2:C:622:MET:HG3	1.91	0.51
1:A:28:ARG:CG	1:A:28:ARG:HH11	1.87	0.51
2:D:504:MET:HG3	2:D:538:ALA:HB3	1.93	0.51
2:C:432:VAL:HG22	2:C:504:MET:CE	2.41	0.51
1:A:288:ARG:NH1	1:A:290:GLU:OE2	2.44	0.51
1:B:233:LYS:HG3	1:B:339:GLN:OE1	2.10	0.51
1:A:293:ARG:NH1	1:A:293:ARG:CB	2.62	0.50
2:D:431:LEU:CD1	2:D:479:MET:HE1	2.35	0.50
5:G:13:DC:H42	6:H:7:DG:H1	1.57	0.50
2:C:476:ILE:HD12	2:C:521:PHE:CE2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:536:TYR:N	2:C:536:TYR:CD2	2.79	0.50
1:A:256:ILE:CD1	1:A:321:LEU:HD21	2.35	0.50
1:B:194:ILE:HD11	1:B:463:MET:HE1	1.92	0.50
1:A:169:GLY:CA	1:A:176:THR:CG2	2.87	0.50
1:B:167:SER:C	1:B:168:THR:CG2	2.77	0.49
1:B:28:ARG:CG	1:B:28:ARG:NH1	2.69	0.49
1:B:169:GLY:HA2	1:B:176:THR:HG22	1.90	0.49
6:H:11:DG:H3'	6:H:11:DG:C8	2.48	0.49
1:A:296:LEU:HD23	1:A:296:LEU:C	2.31	0.49
1:A:420:VAL:HG13	1:B:425:TYR:HB3	1.94	0.49
6:H:3:DC:H2'	6:H:4:DT:C5	2.48	0.49
1:B:256:ILE:HD13	1:B:321:LEU:HD21	1.95	0.49
2:C:559:TRP:O	2:C:560:THR:CB	2.60	0.49
1:A:60:ARG:NH1	1:A:60:ARG:CG	2.66	0.49
1:A:302:LEU:CD1	1:A:308:THR:HB	2.42	0.49
1:B:296:LEU:C	1:B:296:LEU:HD23	2.33	0.49
2:D:525:TYR:O	2:D:526:MET:HG3	2.13	0.49
8:F:101:TR6:C01	8:F:101:TR6:N11	2.73	0.48
1:A:259:ILE:HB	1:A:260:PRO:HD2	1.95	0.48
1:B:391:LEU:HD23	1:B:391:LEU:C	2.34	0.48
1:B:210:GLY:HA2	1:B:229:TYR:OH	2.13	0.48
1:A:51:ASP:O	1:A:52:SER:HB2	2.12	0.48
1:A:77:GLY:HA2	1:B:117:ARG:HE	1.79	0.48
2:D:560:THR:O	2:D:563:GLU:N	2.46	0.48
2:C:441:ALA:O	2:C:445:ARG:HB3	2.13	0.48
1:A:28:ARG:CG	1:A:28:ARG:NH1	2.56	0.48
2:C:559:TRP:HE3	2:C:559:TRP:N	2.12	0.48
1:B:162:LEU:HA	1:B:162:LEU:HD23	1.71	0.48
1:A:144:ASN:HD21	1:A:148:THR:HG22	1.78	0.48
1:B:342:ILE:HA	1:B:342:ILE:HD12	1.60	0.48
1:A:20:TYR:CE1	1:A:24:ILE:HD11	2.49	0.47
1:A:272:ILE:HG22	1:A:287:VAL:HG21	1.95	0.47
3:E:9:DC:C3'	3:E:10:DA:H5''	2.45	0.47
1:A:259:ILE:HB	1:A:260:PRO:CD	2.44	0.47
1:B:321:LEU:HA	1:B:321:LEU:HD23	1.75	0.47
2:C:479:MET:CE	2:C:522:PHE:HZ	2.28	0.47
1:A:55:PHE:HA	1:A:122:ARG:HD2	1.97	0.47
2:D:516:THR:HG22	2:D:517:LEU:N	2.29	0.47
2:C:486:GLY:O	2:C:491:PHE:CD2	2.67	0.47
1:A:136:LYS:HE2	1:A:364:ASP:OD1	2.15	0.47
6:H:11:DG:C3'	6:H:11:DG:C8	2.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:LYS:O	1:B:369:GLU:HG3	2.15	0.47
1:A:293:ARG:NH1	1:A:293:ARG:CG	2.79	0.46
1:B:190:ALA:O	1:B:194:ILE:HG13	2.14	0.46
1:A:434:VAL:CG1	1:A:435:LEU:N	2.78	0.46
2:C:446:ASP:O	2:C:450:GLN:HB2	2.16	0.46
1:A:228:ALA:HA	1:A:233:LYS:O	2.14	0.46
1:A:350:ILE:HG12	1:A:463:MET:CE	2.45	0.46
1:B:9:LEU:CD2	1:B:13:MET:HG3	2.46	0.46
1:A:425:TYR:HB3	1:B:420:VAL:HG13	1.98	0.46
1:B:167:SER:O	1:B:168:THR:HG22	2.15	0.46
1:B:236:VAL:HG13	1:B:237:VAL:N	2.30	0.46
2:C:455:LEU:CD1	2:C:518:LEU:HD11	2.46	0.46
1:A:49:ASN:HB2	1:A:131:LEU:HD13	1.98	0.46
1:B:28:ARG:NH1	1:B:28:ARG:HG3	2.03	0.45
2:C:516:THR:HG22	2:C:622:MET:CE	2.46	0.45
1:B:160:PRO:O	1:B:164:VAL:HG23	2.16	0.45
2:D:592:TRP:CE2	2:D:597:ASN:HB2	2.51	0.45
1:B:140:PRO:HG2	1:B:153:THR:OG1	2.16	0.45
1:A:384:ILE:HB	1:A:387:GLU:HG2	1.99	0.45
1:B:60:ARG:HB2	1:B:60:ARG:NH1	2.30	0.45
2:D:462:THR:HG22	2:D:470:ILE:HD13	1.99	0.45
1:B:169:GLY:HA3	1:B:176:THR:O	2.17	0.45
1:B:430:THR:O	1:B:430:THR:HG23	2.16	0.45
2:C:432:VAL:HG22	2:C:504:MET:HE3	1.98	0.45
2:D:597:ASN:HA	2:D:598:PRO:HD3	1.85	0.44
8:H:101:TR6:N11	8:H:101:TR6:C01	2.78	0.44
1:B:320:ASP:OD1	1:B:323:ILE:HG22	2.17	0.44
4:F:3:DT:H2'	4:F:4:DC:C5	2.53	0.44
1:B:414:GLU:H	1:B:414:GLU:CD	2.21	0.44
2:D:491:PHE:CD1	2:D:528:PRO:HG2	2.53	0.44
1:A:167:SER:C	1:A:168:THR:HG22	2.37	0.44
1:A:20:TYR:CZ	1:A:24:ILE:HG13	2.53	0.43
2:C:491:PHE:CE1	2:C:528:PRO:HG2	2.54	0.43
1:B:342:ILE:HG23	1:B:346:LEU:HD12	1.99	0.43
1:B:273:ASP:O	1:B:277:VAL:HG23	2.18	0.43
1:A:235:ARG:NH1	4:F:11:DG:H4'	2.33	0.43
6:H:6:DT:C2'	6:H:7:DG:H5'	2.47	0.43
2:D:511:GLY:O	2:D:515:GLN:HG3	2.18	0.43
2:D:594:THR:OG1	2:D:595:THR:CG2	2.66	0.43
4:F:1:DA:H2''	4:F:2:DG:N7	2.33	0.43
1:A:291:SER:O	2:D:447:ARG:NH1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:442:LYS:O	2:D:445:ARG:HD3	2.19	0.43
6:H:11:DG:C8	6:H:11:DG:H5'	2.53	0.43
1:A:428:THR:HG22	1:B:392:ILE:O	2.18	0.43
2:D:497:ASN:HB2	2:D:498:TYR:CE2	2.54	0.43
1:A:132:GLN:O	1:A:133:ASP:HB2	2.19	0.42
1:B:15:GLU:OE1	1:B:16:ARG:NH1	2.52	0.42
1:B:290:GLU:OE1	1:B:297:ARG:NH1	2.48	0.42
1:B:201:ILE:HD12	1:B:201:ILE:N	2.35	0.42
1:A:118:TYR:CE2	4:F:1:DA:OP2	2.67	0.42
1:A:139:VAL:HG22	1:A:154:VAL:HG13	2.02	0.42
1:A:28:ARG:CZ	3:E:14:DA:H4'	2.49	0.42
5:G:9:DC:N4	6:H:11:DG:H1	2.12	0.42
1:A:289:ASP:OD2	1:A:291:SER:OG	2.32	0.42
1:A:168:THR:HA	1:A:176:THR:O	2.18	0.42
2:C:476:ILE:HD12	2:C:521:PHE:CD2	2.54	0.42
1:A:89:SER:HA	1:A:99:VAL:O	2.20	0.42
1:A:44:ILE:HG12	1:A:69:ILE:HD13	2.02	0.42
1:A:393:ARG:HD2	1:A:393:ARG:HA	1.72	0.42
1:B:118:TYR:HE2	6:H:1:DG:H5''	1.83	0.42
2:D:619:ASN:O	2:D:620:VAL:C	2.57	0.42
1:B:24:ILE:HA	1:B:24:ILE:HD12	1.68	0.42
2:D:431:LEU:HD22	2:D:479:MET:HE2	2.02	0.42
2:C:526:MET:HE3	2:C:526:MET:HB3	1.82	0.42
1:B:247:LEU:HD11	1:B:253:GLN:HB2	2.02	0.42
2:C:524:ARG:NH1	2:C:524:ARG:CG	2.56	0.41
1:B:463:MET:HE2	1:B:463:MET:HB3	1.42	0.41
1:B:471:LYS:O	1:B:475:ALA:HB2	2.19	0.41
1:A:84:ALA:O	1:A:88:MET:HG3	2.20	0.41
1:A:118:TYR:HE2	4:F:1:DA:H5'	1.78	0.41
2:C:516:THR:CG2	2:C:622:MET:SD	3.09	0.41
1:A:291:SER:HB3	1:A:296:LEU:HA	2.03	0.41
1:A:104:ASN:HB3	1:A:114:ALA:HB2	2.02	0.41
2:D:417:THR:HA	2:D:418:PRO:HD3	1.90	0.41
1:B:357:ILE:HD12	1:B:463:MET:HG2	2.02	0.41
1:A:387:GLU:H	1:A:387:GLU:CD	2.24	0.41
1:A:346:LEU:HD23	1:A:346:LEU:HA	1.83	0.41
1:B:372:LEU:O	1:B:372:LEU:HD22	2.21	0.41
1:B:462:LEU:HD23	1:B:462:LEU:HA	1.87	0.41
1:A:98:LEU:HD22	1:A:130:LEU:HD12	2.03	0.41
1:A:194:ILE:HG12	1:A:463:MET:HE1	2.02	0.41
1:A:261:TYR:CE2	1:A:262:GLU:HG3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:479:MET:CE	2:C:522:PHE:CZ	3.04	0.41
1:B:312:LEU:HD12	1:B:312:LEU:HA	1.88	0.41
2:D:560:THR:O	2:D:561:ASP:C	2.59	0.40
2:C:442:LYS:O	2:C:445:ARG:HD3	2.22	0.40
1:B:20:TYR:O	1:B:24:ILE:HB	2.21	0.40
5:G:9:DC:N3	6:H:11:DG:N2	2.62	0.40
2:C:491:PHE:CD1	2:C:528:PRO:HG2	2.56	0.40
1:A:163:LEU:HA	1:A:163:LEU:HD23	1.89	0.40
1:A:462:LEU:HD23	1:A:462:LEU:HA	1.80	0.40
1:B:138:THR:HA	1:B:359:ALA:CB	2.52	0.40
5:G:13:DC:N4	6:H:7:DG:H1	2.18	0.40
2:C:491:PHE:CZ	2:C:526:MET:HE3	2.57	0.40
1:B:136:LYS:HG2	1:B:363:PHE:CD2	2.56	0.40
1:B:180:PRO:HG2	1:B:214:PRO:HD3	2.03	0.40
2:D:611:LEU:C	2:D:611:LEU:CD1	2.90	0.40
1:B:254:ILE:HB	1:B:300:ILE:HB	2.03	0.40
1:B:27:ASP:C	1:B:39:PRO:HG2	2.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	480/496 (97%)	457 (95%)	20 (4%)	3 (1%)	30	71
1	B	480/496 (97%)	449 (94%)	26 (5%)	5 (1%)	19	59
2	C	202/268 (75%)	195 (96%)	6 (3%)	1 (0%)	34	75
2	D	201/268 (75%)	184 (92%)	17 (8%)	0	100	100
All	All	1363/1528 (89%)	1285 (94%)	69 (5%)	9 (1%)	26	68

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	157	ALA
1	B	168	THR
1	A	168	THR
2	C	560	THR
1	A	329	MET
1	A	169	GLY
1	B	104	ASN
1	B	221	GLY
1	B	169	GLY

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	379/431 (88%)	349 (92%)	30 (8%)	15	47
1	B	375/431 (87%)	346 (92%)	29 (8%)	16	48
2	C	108/224 (48%)	97 (90%)	11 (10%)	9	32
2	D	107/224 (48%)	99 (92%)	8 (8%)	17	50
All	All	969/1310 (74%)	891 (92%)	78 (8%)	15	46

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	28	ARG
1	A	60	ARG
1	A	102	HIS
1	A	111	ASP
1	A	116	MET
1	A	139	VAL
1	A	162	LEU
1	A	168	THR
1	A	208	LEU
1	A	215	THR
1	A	223	ASP
1	A	236	VAL

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Mol	Chain	Res	Type
1	A	268	LEU
1	A	279	ASN
1	A	291	SER
1	A	293	ARG
1	A	308	THR
1	A	321	LEU
1	A	336	THR
1	A	338	ARG
1	A	342	ILE
1	A	366	GLU
1	A	372	LEU
1	A	380	ARG
1	A	381	VAL
1	A	385	LEU
1	A	393	ARG
1	A	414	GLU
1	A	462	LEU
1	B	24	ILE
1	B	28	ARG
1	B	60	ARG
1	B	102	HIS
1	B	117	ARG
1	B	139	VAL
1	B	162	LEU
1	B	168	THR
1	B	176	THR
1	B	183	LEU
1	B	208	LEU
1	B	215	THR
1	B	230	GLU
1	B	236	VAL
1	B	268	LEU
1	B	291	SER
1	B	293	ARG
1	B	300	ILE
1	B	308	THR
1	B	310	LEU
1	B	336	THR
1	B	338	ARG
1	B	342	ILE
1	B	372	LEU
1	B	381	VAL

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Mol	Chain	Res	Type
1	B	385	LEU
1	B	414	GLU
1	B	456	GLU
1	B	462	LEU
2	C	420	GLN
2	C	429	LEU
2	C	445	ARG
2	C	453	LEU
2	C	478	THR
2	C	520	THR
2	C	524	ARG
2	C	536	TYR
2	C	559	TRP
2	C	591	LEU
2	C	595	THR
2	D	429	LEU
2	D	445	ARG
2	D	453	LEU
2	D	520	THR
2	D	524	ARG
2	D	559	TRP
2	D	591	LEU
2	D	595	THR

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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
8	TR6	F	101	7	27,34,34	1.89	7 (25%)	29,53,53	2.43	12 (41%)
8	TR6	H	101	7	27,34,34	1.77	8 (29%)	29,53,53	2.30	9 (31%)

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
8	TR6	F	101	7	-	0/7/29/29	0/4/5/5
8	TR6	H	101	7	-	0/7/29/29	0/4/5/5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	F	101	TR6	C12-C20	-3.77	1.37	1.42
8	H	101	TR6	C12-C20	-3.62	1.37	1.42
8	F	101	TR6	C19-C18	-2.98	1.49	1.53
8	F	101	TR6	C14-C15	-2.63	1.49	1.53
8	H	101	TR6	F04-C03	-2.63	1.30	1.36
8	H	101	TR6	C19-C18	-2.47	1.49	1.53
8	F	101	TR6	F04-C03	-2.34	1.31	1.36
8	H	101	TR6	C14-C15	-2.16	1.50	1.53
8	H	101	TR6	C10-N09	-2.01	1.34	1.39
8	H	101	TR6	C12-N11	2.63	1.34	1.31
8	F	101	TR6	C12-N11	2.93	1.34	1.31
8	H	101	TR6	C12-N13	3.38	1.44	1.36
8	F	101	TR6	C12-N13	3.88	1.45	1.36
8	F	101	TR6	C21-C20	4.35	1.39	1.35
8	H	101	TR6	C21-C20	4.66	1.40	1.35

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	101	TR6	C14-N13-C12	-7.30	103.09	123.52
8	H	101	TR6	C14-N13-C12	-6.24	106.06	123.52
8	F	101	TR6	C20-C12-N13	-3.51	119.61	123.89
8	H	101	TR6	C02-C03-C05	-2.94	119.55	123.35
8	F	101	TR6	C02-C03-C05	-2.94	119.56	123.35
8	F	101	TR6	C22-C10-N11	-2.79	120.22	123.53
8	H	101	TR6	C24-C23-C22	-2.67	117.34	121.87
8	H	101	TR6	C20-C12-N13	-2.60	120.71	123.89
8	H	101	TR6	C22-C10-N11	-2.54	120.51	123.53
8	F	101	TR6	C24-C23-C22	-2.40	117.80	121.87
8	H	101	TR6	C21-C20-C12	-2.38	119.99	121.71
8	F	101	TR6	F30-C20-C12	-2.25	118.08	119.77
8	F	101	TR6	C21-C20-C12	-2.17	120.14	121.71
8	H	101	TR6	F30-C20-C12	-2.03	118.24	119.77
8	F	101	TR6	C12-N11-C10	2.10	122.29	118.68
8	F	101	TR6	C23-C22-C10	2.44	120.56	117.89
8	F	101	TR6	N11-C12-N13	2.61	120.99	116.81
8	F	101	TR6	C06-C05-C03	3.19	119.96	116.63
8	H	101	TR6	C06-C05-C03	3.47	120.25	116.63
8	F	101	TR6	C19-N13-C12	5.21	138.09	123.52
8	H	101	TR6	C19-N13-C12	5.74	139.59	123.52

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
8	F	101	TR6	1	0
8	H	101	TR6	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	482/496 (97%)	-0.61	0 100 100	42, 63, 104, 136	0
1	B	482/496 (97%)	-0.60	0 100 100	43, 60, 91, 127	0
2	C	208/268 (77%)	-0.55	0 100 100	68, 98, 145, 187	0
2	D	207/268 (77%)	-0.52	0 100 100	69, 104, 142, 164	0
3	E	7/7 (100%)	-0.27	0 100 100	62, 67, 103, 137	0
4	F	11/11 (100%)	-0.33	0 100 100	68, 89, 127, 132	0
5	G	7/7 (100%)	-0.23	0 100 100	59, 65, 100, 127	0
6	H	11/11 (100%)	-0.38	0 100 100	70, 80, 125, 125	0
All	All	1415/1564 (90%)	-0.58	0 100 100	42, 69, 127, 187	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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(\AA^2)	Q<0.9
8	TR6	F	101	30/30	0.95	0.23	0.97	66,83,105,120	0
8	TR6	H	101	30/30	0.95	0.22	0.16	61,77,92,110	0
7	MG	B	501	1/1	0.74	0.13	-1.98	90,90,90,90	0
7	MG	A	501	1/1	0.89	0.07	-3.12	81,81,81,81	0
7	MG	C	701	1/1	0.90	0.50	-	59,59,59,59	0
7	MG	B	502	1/1	0.95	0.55	-	73,73,73,73	0
7	MG	A	502	1/1	0.89	0.43	-	74,74,74,74	0
7	MG	D	701	1/1	0.85	0.41	-	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.