



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2018 – 10:57 PM EST

PDB ID : 5Y7G
Title : Crystal structure of nuclease
Authors : Cho, Y.; Jin, H.
Deposited on : 2017-08-17
Resolution : 3.40 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
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
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) : rb-20030736

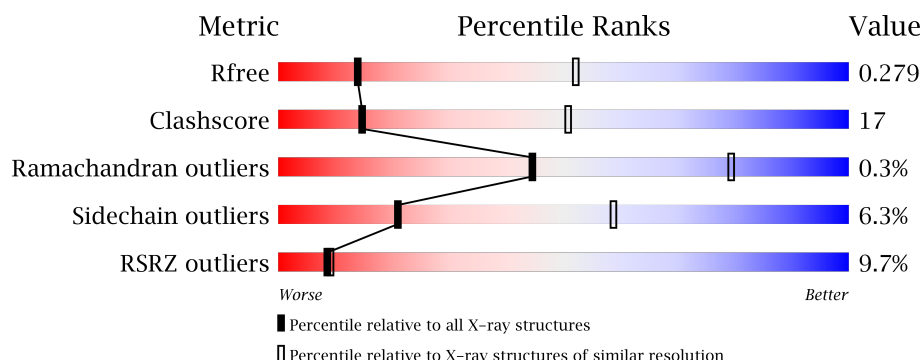
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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	1679 (3.50-3.30)
Clashscore	112137	1832 (3.50-3.30)
Ramachandran outliers	110173	1789 (3.50-3.30)
Sidechain outliers	110143	1789 (3.50-3.30)
RSRZ outliers	101464	1709 (3.50-3.30)

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	580	<div> <div>4%</div> <div>59%</div> <div>30%</div> <div>7%</div> </div>
1	B	580	<div> <div>7%</div> <div>60%</div> <div>31%</div> <div>6%</div> </div>
1	C	580	<div> <div>16%</div> <div>61%</div> <div>30%</div> <div>7%</div> </div>
2	D	10	<div> <div>20%</div> <div>50%</div> <div>30%</div> </div>
2	F	10	<div> <div>40%</div> <div>50%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
2	H	10	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>30%10%90%</div>
3	E	24	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>4%25%50%25%</div>
3	G	24	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>13%38%54%8%</div>
3	I	24	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>4%29%71%</div>
4	J	14	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>36%29%43%29%</div>
4	L	14	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>21%14%71%14%</div>
4	N	14	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> <div>7%7%86%7%</div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16164 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 Fanconi-associated nuclease 1 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	542	Total	C	N	O	S	0	0	0
			4406	2816	799	771	20			
1	B	543	Total	C	N	O	S	0	0	0
			4424	2827	800	777	20			
1	C	540	Total	C	N	O	S	0	0	0
			4401	2813	794	774	20			

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP Q9I2N0
A	-19	GLY	-	expression tag	UNP Q9I2N0
A	-18	SER	-	expression tag	UNP Q9I2N0
A	-17	SER	-	expression tag	UNP Q9I2N0
A	-16	HIS	-	expression tag	UNP Q9I2N0
A	-15	HIS	-	expression tag	UNP Q9I2N0
A	-14	HIS	-	expression tag	UNP Q9I2N0
A	-13	HIS	-	expression tag	UNP Q9I2N0
A	-12	HIS	-	expression tag	UNP Q9I2N0
A	-11	HIS	-	expression tag	UNP Q9I2N0
A	-10	SER	-	expression tag	UNP Q9I2N0
A	-9	SER	-	expression tag	UNP Q9I2N0
A	-8	GLY	-	expression tag	UNP Q9I2N0
A	-7	LEU	-	expression tag	UNP Q9I2N0
A	-6	VAL	-	expression tag	UNP Q9I2N0
A	-5	PRO	-	expression tag	UNP Q9I2N0
A	-4	ARG	-	expression tag	UNP Q9I2N0
A	-3	GLY	-	expression tag	UNP Q9I2N0
A	-2	SER	-	expression tag	UNP Q9I2N0
A	-1	HIS	-	expression tag	UNP Q9I2N0
A	0	MET	-	expression tag	UNP Q9I2N0
B	-20	MET	-	expression tag	UNP Q9I2N0
B	-19	GLY	-	expression tag	UNP Q9I2N0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	SER	-	expression tag	UNP Q9I2N0
B	-17	SER	-	expression tag	UNP Q9I2N0
B	-16	HIS	-	expression tag	UNP Q9I2N0
B	-15	HIS	-	expression tag	UNP Q9I2N0
B	-14	HIS	-	expression tag	UNP Q9I2N0
B	-13	HIS	-	expression tag	UNP Q9I2N0
B	-12	HIS	-	expression tag	UNP Q9I2N0
B	-11	HIS	-	expression tag	UNP Q9I2N0
B	-10	SER	-	expression tag	UNP Q9I2N0
B	-9	SER	-	expression tag	UNP Q9I2N0
B	-8	GLY	-	expression tag	UNP Q9I2N0
B	-7	LEU	-	expression tag	UNP Q9I2N0
B	-6	VAL	-	expression tag	UNP Q9I2N0
B	-5	PRO	-	expression tag	UNP Q9I2N0
B	-4	ARG	-	expression tag	UNP Q9I2N0
B	-3	GLY	-	expression tag	UNP Q9I2N0
B	-2	SER	-	expression tag	UNP Q9I2N0
B	-1	HIS	-	expression tag	UNP Q9I2N0
B	0	MET	-	expression tag	UNP Q9I2N0
C	-20	MET	-	expression tag	UNP Q9I2N0
C	-19	GLY	-	expression tag	UNP Q9I2N0
C	-18	SER	-	expression tag	UNP Q9I2N0
C	-17	SER	-	expression tag	UNP Q9I2N0
C	-16	HIS	-	expression tag	UNP Q9I2N0
C	-15	HIS	-	expression tag	UNP Q9I2N0
C	-14	HIS	-	expression tag	UNP Q9I2N0
C	-13	HIS	-	expression tag	UNP Q9I2N0
C	-12	HIS	-	expression tag	UNP Q9I2N0
C	-11	HIS	-	expression tag	UNP Q9I2N0
C	-10	SER	-	expression tag	UNP Q9I2N0
C	-9	SER	-	expression tag	UNP Q9I2N0
C	-8	GLY	-	expression tag	UNP Q9I2N0
C	-7	LEU	-	expression tag	UNP Q9I2N0
C	-6	VAL	-	expression tag	UNP Q9I2N0
C	-5	PRO	-	expression tag	UNP Q9I2N0
C	-4	ARG	-	expression tag	UNP Q9I2N0
C	-3	GLY	-	expression tag	UNP Q9I2N0
C	-2	SER	-	expression tag	UNP Q9I2N0
C	-1	HIS	-	expression tag	UNP Q9I2N0
C	0	MET	-	expression tag	UNP Q9I2N0

- Molecule 2 is a DNA chain called DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			
2	F	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			
2	H	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	24	Total	C	N	O	P	0	0	0
			488	234	84	146	24			
3	G	24	Total	C	N	O	P	0	0	0
			487	233	84	146	24			
3	I	24	Total	C	N	O	P	0	0	0
			488	234	84	146	24			

- Molecule 4 is a DNA chain called DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	14	Total	C	N	O	P	0	0	0
			284	136	53	81	14			
4	L	14	Total	C	N	O	P	0	0	0
			284	136	53	81	14			
4	N	13	Total	C	N	O	P	0	0	0
			264	126	51	74	13			

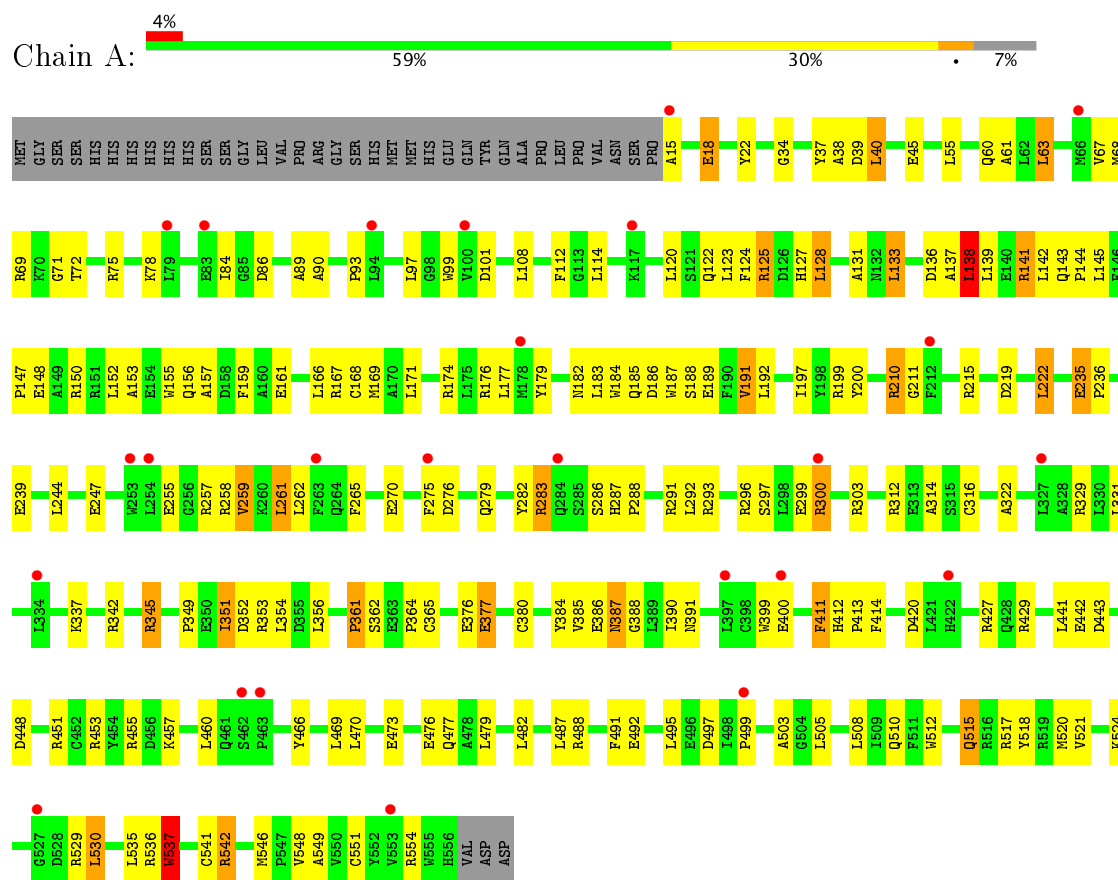
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ca	0	0
			2	2		
5	A	2	Total	Ca	0	0
			2	2		
5	C	1	Total	Ca	0	0
			1	1		

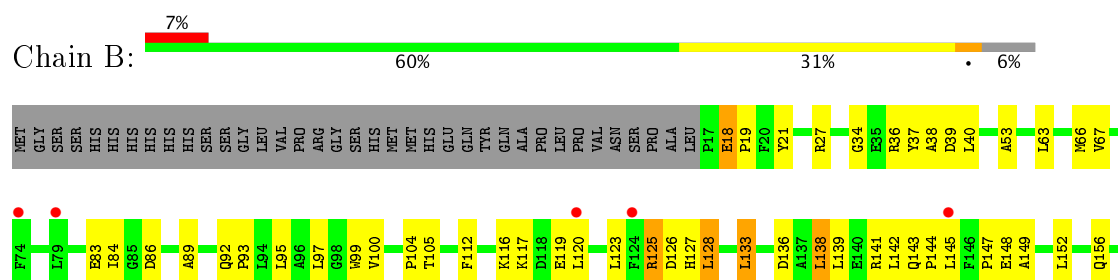
3 Residue-property plots [i](#)

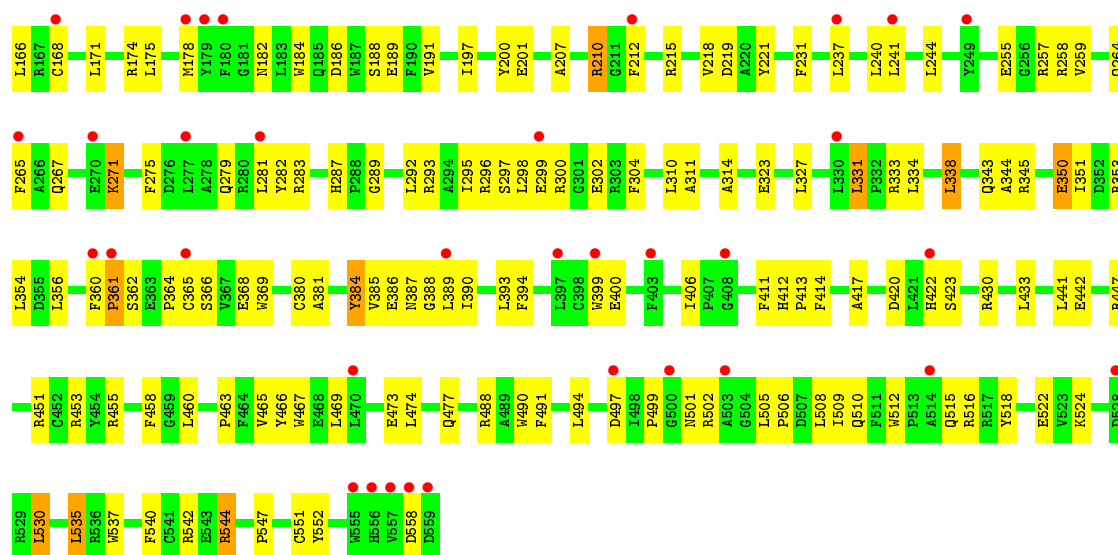
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Fanconi-associated nuclease 1 homolog

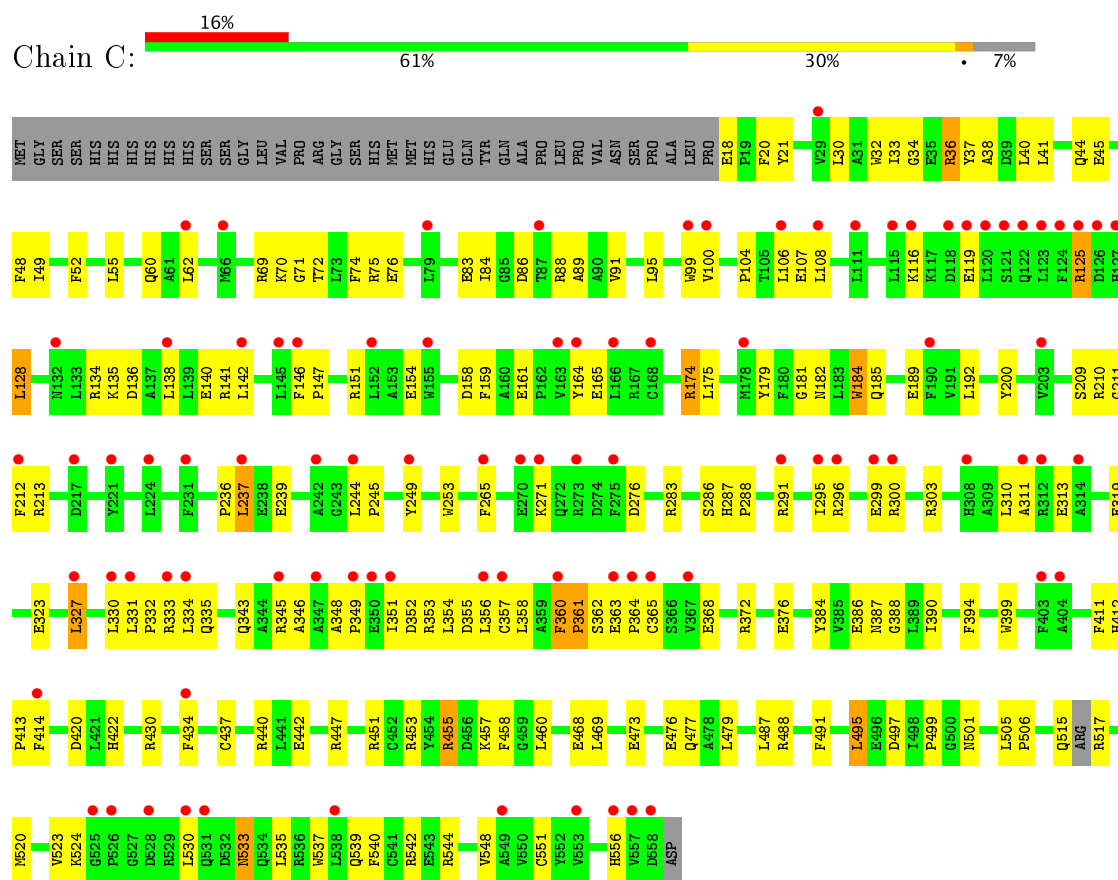


• Molecule 1: Fanconi-associated nuclease 1 homolog

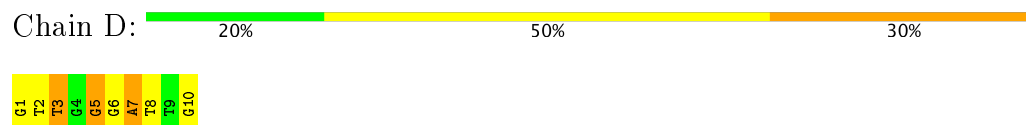




• Molecule 1: Fanconi-associated nuclease 1 homolog

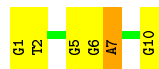


• Molecule 2: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')



- Molecule 2: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')

Chain F: 



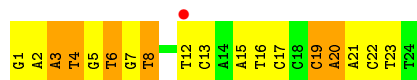
- Molecule 2: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')

Chain H: 



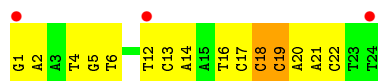
- Molecule 3: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*T
P*CP*CP*CP*AP*AP*CP*TP*T)-3')

Chain E: 



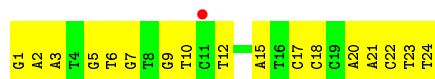
- Molecule 3: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*T
P*CP*CP*CP*AP*AP*CP*TP*T)-3')

Chain G: 



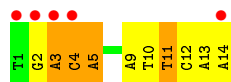
- Molecule 3: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*T
P*CP*CP*CP*AP*AP*CP*TP*T)-3')

Chain I: 

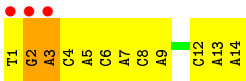


- Molecule 4: DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3')

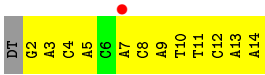
Chain J: 



- Molecule 4: DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3')



● Molecule 4: DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	140.29Å 143.26Å 172.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.58 – 3.40 46.03 – 3.17	Depositor EDS
% Data completeness (in resolution range)	95.6 (33.58-3.40) 94.4 (46.03-3.17)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.10.1-2155_1069: ???)	Depositor
R, R_{free}	0.221 , 0.280 0.218 , 0.279	Depositor DCC
R_{free} test set	2367 reflections (5.11%)	DCC
Wilson B-factor (Å ²)	105.5	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 64.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.004 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	16164	wwPDB-VP
Average B, all atoms (Å ²)	163.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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: CA

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	0.62	1/4522 (0.0%)	0.87	7/6125 (0.1%)
1	B	0.55	1/4541 (0.0%)	0.79	4/6150 (0.1%)
1	C	0.47	0/4516	0.72	1/6115 (0.0%)
2	D	1.26	2/236 (0.8%)	1.25	2/364 (0.5%)
2	F	1.09	1/236 (0.4%)	1.10	0/364
2	H	0.76	0/236	1.11	0/364
3	E	1.43	6/545 (1.1%)	1.18	5/838 (0.6%)
3	G	1.17	3/544 (0.6%)	1.15	1/836 (0.1%)
3	I	1.00	0/545	1.12	0/838
4	J	1.42	3/318 (0.9%)	1.17	2/487 (0.4%)
4	L	1.08	1/318 (0.3%)	1.05	1/487 (0.2%)
4	N	0.82	0/296	0.94	0/453
All	All	0.71	18/16853 (0.1%)	0.88	23/23421 (0.1%)

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
1	A	0	2
1	B	0	1
All	All	0	3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	12	DT	C1'-N1	8.56	1.60	1.49
3	E	4	DT	C3'-O3'	-8.22	1.33	1.44
2	F	7	DA	C3'-O3'	-7.67	1.33	1.44
2	D	7	DA	C3'-O3'	-7.26	1.34	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	4	DC	C3'-O3'	-6.70	1.35	1.44
1	B	490	TRP	CB-CG	-6.52	1.38	1.50
4	J	5	DA	C3'-O3'	-6.19	1.35	1.44
1	A	537	TRP	CB-CG	-6.09	1.39	1.50
3	E	19	DC	C3'-O3'	-5.76	1.36	1.44
2	D	5	DG	C3'-O3'	-5.67	1.36	1.44
3	E	20	DA	C3'-O3'	-5.59	1.36	1.44
3	E	3	DA	C3'-O3'	-5.58	1.36	1.44
4	J	11	DT	C3'-O3'	-5.46	1.36	1.44
3	G	19	DC	C3'-O3'	-5.39	1.36	1.44
3	E	1	DG	N9-C4	-5.38	1.33	1.38
3	E	6	DT	N1-C2	-5.16	1.33	1.38
3	G	18	DC	C3'-O3'	-5.10	1.37	1.44
4	L	3	DA	N9-C4	5.05	1.40	1.37

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	7	DA	O5'-P-OP2	-8.03	98.47	105.70
4	J	3	DA	O5'-P-OP2	-7.43	99.01	105.70
1	A	377	GLU	C-N-CD	-7.32	104.49	120.60
4	L	2	DG	O4'-C4'-C3'	-6.84	101.76	104.50
3	E	4	DT	O4'-C4'-C3'	-6.81	101.78	104.50
3	G	12	DT	O4'-C1'-N1	6.62	112.63	108.00
1	A	537	TRP	CA-CB-CG	-6.52	101.31	113.70
1	A	261	LEU	CA-CB-CG	-6.38	100.64	115.30
3	E	4	DT	O4'-C1'-N1	5.88	112.12	108.00
3	E	4	DT	C1'-O4'-C4'	-5.85	104.25	110.10
1	C	237	LEU	CA-CB-CG	5.66	128.32	115.30
1	A	377	GLU	C-N-CA	5.65	145.72	122.00
1	A	470	LEU	CA-CB-CG	5.57	128.10	115.30
3	E	8	DT	N3-C4-O4	5.54	123.22	119.90
1	A	138	LEU	CB-CG-CD1	-5.51	101.63	111.00
1	A	530	LEU	CB-CG-CD2	-5.37	101.87	111.00
1	B	128	LEU	CA-CB-CG	-5.33	103.04	115.30
1	B	535	LEU	CB-CG-CD1	-5.25	102.08	111.00
1	B	441	LEU	CB-CG-CD2	-5.21	102.14	111.00
2	D	3	DT	N3-C4-O4	5.19	123.01	119.90
4	J	11	DT	N3-C4-O4	5.16	123.00	119.90
1	B	338	LEU	CA-CB-CG	5.08	127.00	115.30
3	E	8	DT	C5-C4-O4	-5.04	121.38	124.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	361	PRO	Peptide
1	A	71	GLY	Peptide
1	B	361	PRO	Peptide

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	4406	0	4306	149	1
1	B	4424	0	4317	139	0
1	C	4401	0	4293	129	1
2	D	211	0	115	16	0
2	F	211	0	115	5	0
2	H	211	0	115	14	0
3	E	488	0	273	16	0
3	G	487	0	270	15	0
3	I	488	0	273	20	0
4	J	284	0	158	11	0
4	L	284	0	158	16	0
4	N	264	0	146	11	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	1	0	0	0	0
All	All	16164	0	14539	524	1

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 17.

All (524) 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:342:ARG:NH1	4:J:14:DA:OP1	1.91	1.03
1:B:387:ASN:HB3	1:B:505:LEU:HB2	1.48	0.96
3:E:21:DA:H2"	3:E:22:DC:H5"	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:21:DA:H2''	3:G:22:DC:H5''	1.49	0.94
4:N:9:DA:H2''	4:N:10:DT:H5''	1.50	0.93
1:C:276:ASP:OD2	1:C:303:ARG:NH1	2.04	0.91
1:C:21:TYR:OH	2:H:10:DG:OP2	1.94	0.85
1:C:390:ILE:HD13	1:C:505:LEU:HD13	1.56	0.85
1:A:45:GLU:HG2	1:A:171:LEU:HD11	1.61	0.82
2:D:6:DG:H2'	2:D:7:DA:C8	2.15	0.81
2:D:7:DA:H2''	2:D:8:DT:H5'	1.62	0.80
2:D:1:DG:H2''	2:D:2:DT:H5''	1.62	0.79
1:B:333:ARG:NH2	3:G:4:DT:O3'	2.15	0.79
1:A:279:GLN:HE21	1:A:283:ARG:HH21	1.32	0.78
1:A:189:GLU:OE2	1:A:200:TYR:OH	2.02	0.78
1:B:174:ARG:NH2	1:B:219:ASP:OD2	2.15	0.78
1:C:345:ARG:NH1	3:I:3:DA:OP1	2.17	0.78
4:N:12:DC:H2'	4:N:13:DA:C8	2.21	0.76
1:A:361:PRO:HB2	1:A:362:SER:HA	1.69	0.74
4:J:2:DG:H2''	4:J:3:DA:C8	2.23	0.73
1:C:36:ARG:HH11	1:C:36:ARG:HB3	1.53	0.73
1:A:69:ARG:HH22	1:A:78:LYS:HB3	1.53	0.73
1:C:332:PRO:HG3	1:C:343:GLN:HB2	1.69	0.73
1:B:37:TYR:HD2	1:B:40:LEU:HD12	1.54	0.73
1:A:15:ALA:N	2:D:10:DG:O3'	2.22	0.72
1:C:271:LYS:NZ	3:I:7:DG:OP2	2.22	0.72
2:H:1:DG:N2	3:I:23:DT:O2	2.22	0.72
2:D:5:DG:H2''	2:D:6:DG:H8	1.54	0.72
1:B:447:ARG:HB3	1:B:451:ARG:HH21	1.54	0.71
1:A:270:GLU:OE2	1:A:293:ARG:NH2	2.21	0.71
1:A:15:ALA:N	2:D:10:DG:HO3'	1.89	0.71
1:A:312:ARG:HD2	1:A:331:LEU:HD11	1.73	0.70
1:C:299:GLU:HG3	1:C:334:LEU:HD21	1.74	0.69
1:B:21:TYR:OH	2:F:10:DG:OP2	2.09	0.69
1:C:40:LEU:HD21	1:C:213:ARG:O	1.92	0.69
1:C:533:ASN:HD22	1:C:533:ASN:H	1.41	0.68
1:C:75:ARG:NH2	1:C:161:GLU:OE1	2.26	0.68
1:A:112:PHE:HA	1:A:120:LEU:HD11	1.74	0.68
1:C:69:ARG:NE	1:C:71:GLY:H	1.92	0.68
1:B:413:PRO:HG2	1:B:414:PHE:CE2	2.29	0.67
1:B:189:GLU:OE2	1:B:200:TYR:OH	2.11	0.67
3:E:12:DT:OP1	3:E:12:DT:H4'	1.94	0.67
3:E:22:DC:H2''	3:E:23:DT:H5''	1.77	0.67
1:A:413:PRO:HG2	1:A:414:PHE:CE2	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:331:LEU:HD13	1:C:343:GLN:HE22	1.59	0.66
1:C:387:ASN:HB3	1:C:505:LEU:HB2	1.78	0.66
2:H:3:DT:H2''	2:H:4:DG:H5''	1.78	0.66
1:B:241:LEU:HD11	1:B:281:LEU:HD11	1.76	0.66
3:E:4:DT:H2'	3:E:5:DG:C8	2.31	0.66
1:C:37:TYR:CZ	1:C:210:ARG:HB2	2.30	0.66
1:B:275:PHE:CE2	1:B:300:ARG:HB3	2.30	0.66
1:B:112:PHE:HA	1:B:120:LEU:HD11	1.77	0.65
3:E:15:DA:H1'	3:E:16:DT:H5'	1.78	0.65
1:C:345:ARG:HG2	1:C:346:ALA:H	1.61	0.65
1:C:184:TRP:CD1	1:C:185:GLN:HG3	2.31	0.65
2:H:4:DG:H2''	2:H:5:DG:C8	2.33	0.65
1:B:497:ASP:O	1:B:501:ASN:HB2	1.97	0.64
1:B:123:LEU:HD13	1:B:156:GLN:HB3	1.78	0.64
1:B:380:CYS:SG	1:B:512:TRP:NE1	2.70	0.64
4:L:13:DA:H2''	4:L:14:DA:H8	1.63	0.63
4:L:13:DA:H2''	4:L:14:DA:C8	2.32	0.63
2:D:2:DT:H2''	2:D:3:DT:H5''	1.80	0.63
1:B:530:LEU:HD12	1:B:530:LEU:H	1.64	0.63
1:C:37:TYR:OH	1:C:211:GLY:N	2.25	0.63
3:G:5:DG:H2''	3:G:6:DT:H5''	1.80	0.63
1:B:27:ARG:HH12	1:B:53:ALA:HA	1.65	0.62
1:C:286:SER:HA	1:C:291:ARG:HH12	1.65	0.62
4:J:3:DA:H1'	4:J:4:DC:H5''	1.81	0.62
2:D:5:DG:H2''	2:D:6:DG:C8	2.33	0.62
1:A:400:GLU:HB2	1:A:453:ARG:HH21	1.64	0.62
1:C:356:LEU:HD13	1:C:358:LEU:HD21	1.81	0.62
1:A:386:GLU:C	1:A:388:GLY:H	2.03	0.62
3:I:9:DG:H2''	3:I:10:DT:H5''	1.81	0.62
1:B:138:LEU:O	1:B:142:LEU:HB2	2.00	0.61
1:C:48:PHE:HB3	1:C:52:PHE:CZ	2.35	0.61
1:A:497:ASP:OD2	1:A:499:PRO:HD2	2.00	0.61
3:G:17:DC:H2'	3:G:18:DC:C6	2.34	0.61
1:A:412:HIS:HB2	1:A:413:PRO:HD2	1.83	0.60
1:B:353:ARG:HG2	1:B:552:TYR:HE2	1.65	0.60
3:I:5:DG:H2''	3:I:6:DT:H5'	1.84	0.60
1:B:364:PRO:HA	1:B:365:CYS:HB3	1.83	0.60
1:A:364:PRO:HA	1:A:365:CYS:HB3	1.84	0.60
1:A:442:GLU:HG2	1:A:488:ARG:HH22	1.66	0.60
2:H:6:DG:H2''	2:H:7:DA:C8	2.37	0.60
1:A:128:LEU:HA	1:A:141:ARG:NH2	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:442:GLU:OE2	1:C:488:ARG:NE	2.35	0.59
1:A:136:ASP:OD1	1:A:136:ASP:N	2.35	0.59
1:C:331:LEU:HD13	1:C:343:GLN:NE2	2.17	0.59
3:G:1:DG:H5'	3:G:2:DA:H8	1.68	0.59
4:L:1:DT:H1'	4:L:2:DG:N7	2.17	0.59
1:B:473:GLU:O	1:B:477:GLN:HG3	2.03	0.58
1:C:323:GLU:O	1:C:327:LEU:HB2	2.04	0.58
4:L:5:DA:H2''	4:L:6:DC:H5''	1.84	0.58
1:C:457:LYS:HD2	1:C:460:LEU:HD12	1.86	0.58
1:A:128:LEU:HD11	1:A:138:LEU:HD11	1.86	0.58
4:N:7:DA:H2''	4:N:8:DC:H5'	1.86	0.58
1:B:201:GLU:HB2	1:B:460:LEU:HD13	1.84	0.58
1:C:287:HIS:CG	1:C:288:PRO:HD2	2.39	0.58
1:A:385:VAL:HA	1:A:469:LEU:HD21	1.84	0.58
1:A:45:GLU:OE1	1:A:215:ARG:NH1	2.35	0.58
1:C:372:ARG:NH1	1:C:376:GLU:OE1	2.36	0.58
1:B:422:HIS:ND1	1:B:499:PRO:HG3	2.18	0.57
1:B:104:PRO:HD2	1:B:152:LEU:HD23	1.86	0.57
3:E:13:DC:H5'	3:E:13:DC:C6	2.39	0.57
1:C:55:LEU:HD11	1:C:99:TRP:HZ3	1.68	0.57
1:B:412:HIS:HB2	1:B:413:PRO:HD2	1.87	0.57
3:I:12:DT:H6	3:I:12:DT:H5''	1.69	0.57
4:N:10:DT:H2''	4:N:11:DT:H5''	1.87	0.57
1:C:361:PRO:O	1:C:362:SER:HB2	2.04	0.57
1:C:33:ILE:HG21	1:C:175:LEU:HD22	1.87	0.57
1:A:156:GLN:CD	1:A:159:PHE:HB2	2.25	0.56
1:A:293:ARG:O	1:A:297:SER:HB2	2.05	0.56
1:A:55:LEU:HB2	1:A:60:GLN:HG3	1.87	0.56
1:C:108:LEU:HD21	1:C:142:LEU:HB3	1.87	0.56
1:A:127:HIS:O	1:A:128:LEU:HD13	2.05	0.56
1:A:322:ALA:HB2	1:A:536:ARG:CZ	2.36	0.56
2:H:8:DT:H1'	2:H:9:DT:H5'	1.87	0.56
1:B:178:MET:HE3	1:B:218:VAL:HG11	1.87	0.56
3:I:1:DG:H2'	3:I:2:DA:C8	2.41	0.56
1:A:40:LEU:HD21	1:A:215:ARG:HA	1.87	0.56
1:B:37:TYR:CD2	1:B:40:LEU:HD12	2.36	0.56
2:F:1:DG:H1'	2:F:2:DT:H5'	1.88	0.56
3:G:1:DG:H5'	3:G:2:DA:C8	2.40	0.56
1:A:86:ASP:HB3	1:A:89:ALA:HB3	1.87	0.56
1:C:244:LEU:HD11	1:C:265:PHE:HE2	1.71	0.56
2:H:5:DG:H2''	2:H:6:DG:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:GLN:HG3	1:A:159:PHE:HB2	1.88	0.55
1:A:541:CYS:HB3	1:A:546:MET:HB2	1.88	0.55
1:A:128:LEU:CD1	1:A:138:LEU:HD11	2.36	0.55
1:A:329:ARG:HG2	1:A:345:ARG:HH22	1.72	0.55
1:A:349:PRO:HB2	1:A:542:ARG:HD2	1.89	0.55
1:C:520:MET:HB2	1:C:548:VAL:HG12	1.88	0.55
1:A:524:LYS:HE3	1:A:530:LEU:HA	1.89	0.55
1:C:108:LEU:HD22	1:C:146:PHE:HB2	1.89	0.55
1:B:381:ALA:O	1:B:510:GLN:HA	2.06	0.55
1:C:412:HIS:HB2	1:C:413:PRO:HD2	1.88	0.55
1:A:39:ASP:OD2	1:A:210:ARG:NH2	2.39	0.55
1:B:63:LEU:O	1:B:67:VAL:HG23	2.07	0.55
4:L:2:DG:H2''	4:L:3:DA:C8	2.42	0.55
1:B:210:ARG:HD2	1:B:212:PHE:O	2.07	0.55
1:C:44:GLN:O	1:C:48:PHE:HD2	1.90	0.55
1:A:210:ARG:HA	1:A:411:PHE:HB3	1.88	0.55
1:C:34:GLY:O	1:C:38:ALA:HB2	2.06	0.55
1:B:95:LEU:HD23	1:B:100:VAL:O	2.07	0.55
1:C:422:HIS:ND1	1:C:499:PRO:HG3	2.22	0.55
1:A:128:LEU:HG	1:A:138:LEU:HD11	1.89	0.54
1:C:104:PRO:HG2	1:C:106:LEU:HD11	1.89	0.54
1:B:171:LEU:O	1:B:175:LEU:HG	2.08	0.54
1:A:316:CYS:SG	1:B:338:LEU:HA	2.47	0.54
2:D:7:DA:C2'	2:D:8:DT:H5'	2.34	0.54
3:I:17:DC:H2'	3:I:18:DC:C6	2.42	0.54
1:A:138:LEU:HD12	1:A:142:LEU:HD12	1.88	0.54
1:C:116:LYS:HB2	1:C:119:GLU:HG3	1.90	0.54
1:B:255:GLU:OE2	1:B:258:ARG:NH2	2.40	0.54
1:C:36:ARG:NH2	1:C:209:SER:O	2.33	0.54
1:A:299:GLU:OE2	1:A:337:LYS:NZ	2.41	0.54
3:G:17:DC:H2'	3:G:18:DC:C5	2.43	0.54
4:J:12:DC:H2'	4:J:13:DA:C5	2.42	0.54
2:D:2:DT:H2'	2:D:3:DT:H71	1.88	0.54
1:C:368:GLU:HG3	1:C:523:VAL:HB	1.88	0.54
1:A:184:TRP:CE3	1:A:185:GLN:HG2	2.42	0.53
1:B:125:ARG:HG2	1:B:126:ASP:N	2.23	0.53
1:B:302:GLU:HA	1:B:304:PHE:CE2	2.43	0.53
1:C:45:GLU:OE2	1:C:174:ARG:NH1	2.41	0.53
1:B:354:LEU:O	1:B:551:CYS:HA	2.09	0.53
1:A:387:ASN:O	1:A:391:ASN:HB2	2.08	0.53
1:C:134:ARG:HG2	3:I:21:DA:H5'	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:VAL:HG11	1:C:164:TYR:CZ	2.43	0.53
1:A:179:TYR:HH	1:A:414:PHE:HE2	1.56	0.53
1:B:27:ARG:HH22	1:B:53:ALA:HB2	1.73	0.53
1:C:151:ARG:N	1:C:154:GLU:HB2	2.23	0.53
1:C:20:PHE:CZ	1:C:83:GLU:HB3	2.43	0.53
1:C:136:ASP:O	1:C:140:GLU:HB2	2.08	0.53
1:A:377:GLU:H	1:A:380:CYS:HB3	1.74	0.53
1:C:437:CYS:O	1:C:440:ARG:HG3	2.08	0.53
3:G:13:DC:H2''	3:G:14:DA:C8	2.44	0.53
1:C:49:ILE:HA	1:C:52:PHE:CD2	2.44	0.52
1:B:116:LYS:HB2	1:B:119:GLU:HG3	1.91	0.52
1:B:127:HIS:C	1:B:128:LEU:HG	2.30	0.52
1:A:122:GLN:O	1:A:125:ARG:HD2	2.09	0.52
1:B:186:ASP:HB3	1:B:188:SER:H	1.74	0.52
1:B:366:SER:HB2	1:B:369:TRP:HD1	1.74	0.52
1:C:182:ASN:HB3	1:C:184:TRP:CD1	2.44	0.52
3:I:2:DA:H2''	3:I:3:DA:C8	2.44	0.52
4:L:12:DC:H2''	4:L:13:DA:C8	2.44	0.52
1:C:36:ARG:HB3	1:C:36:ARG:NH1	2.21	0.52
1:B:289:GLY:O	1:B:293:ARG:HG2	2.09	0.52
4:J:2:DG:H2''	4:J:3:DA:H8	1.72	0.52
1:B:293:ARG:O	1:B:297:SER:HB2	2.09	0.52
1:B:314:ALA:HB1	1:B:327:LEU:HD11	1.92	0.52
1:C:363:GLU:HB3	1:C:364:PRO:HD2	1.92	0.52
1:A:127:HIS:CD2	1:A:145:LEU:HD23	2.45	0.52
1:A:270:GLU:CD	1:A:293:ARG:HH21	2.11	0.51
1:A:291:ARG:HD3	1:A:314:ALA:HB2	1.92	0.51
1:B:350:GLU:HG3	1:B:351:ILE:N	2.25	0.51
1:C:533:ASN:N	1:C:533:ASN:HD22	2.08	0.51
1:A:152:LEU:HD21	1:A:159:PHE:CE2	2.45	0.51
3:E:5:DG:H2'	3:E:6:DT:H71	1.92	0.51
1:A:386:GLU:C	1:A:388:GLY:N	2.64	0.51
3:G:1:DG:H2'	3:G:1:DG:N3	2.26	0.51
3:I:23:DT:H2''	3:I:24:DT:H5''	1.93	0.51
1:A:376:GLU:HG3	1:A:380:CYS:O	2.10	0.51
1:B:136:ASP:OD1	1:B:136:ASP:N	2.44	0.51
1:C:360:PHE:HD2	1:C:556:HIS:O	1.94	0.51
1:A:390:ILE:HD13	1:A:505:LEU:HD23	1.93	0.51
1:A:503:ALA:HB1	4:J:5:DA:OP1	2.10	0.51
4:L:2:DG:H5''	4:L:2:DG:H8	1.75	0.51
1:A:275:PHE:CE2	1:A:300:ARG:HB3	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:236:PRO:HG2	1:C:239:GLU:HG3	1.93	0.51
1:C:37:TYR:CE2	1:C:210:ARG:HD2	2.45	0.51
1:C:135:LYS:HB2	3:I:21:DA:OP2	2.11	0.51
1:C:291:ARG:HD3	1:C:319:GLU:OE2	2.11	0.51
1:C:335:GLN:OE1	1:C:343:GLN:HG3	2.10	0.51
1:A:122:GLN:O	1:A:125:ARG:HB3	2.11	0.50
1:A:255:GLU:O	1:A:259:VAL:HB	2.11	0.50
1:B:400:GLU:OE1	1:B:453:ARG:NH2	2.44	0.50
1:A:530:LEU:HB3	1:A:535:LEU:HD13	1.92	0.50
1:B:237:LEU:HD23	1:B:240:LEU:HD12	1.94	0.50
1:B:530:LEU:HB2	1:B:535:LEU:HD13	1.93	0.50
1:C:33:ILE:HD13	1:C:175:LEU:HD22	1.92	0.50
1:A:236:PRO:HG2	1:A:239:GLU:HG3	1.92	0.50
1:B:353:ARG:HG2	1:B:552:TYR:CE2	2.46	0.50
2:H:4:DG:H2''	2:H:5:DG:H8	1.76	0.50
1:B:442:GLU:OE2	1:B:488:ARG:NH2	2.45	0.50
1:C:390:ILE:N	1:C:390:ILE:HD12	2.27	0.50
2:F:5:DG:H2''	2:F:6:DG:C8	2.47	0.50
4:J:12:DC:H2'	4:J:13:DA:C8	2.46	0.50
1:A:473:GLU:O	1:A:477:GLN:HG3	2.11	0.50
1:B:361:PRO:HB2	1:B:362:SER:HA	1.93	0.50
1:B:417:ALA:HB2	1:B:463:PRO:HD3	1.93	0.50
1:A:123:LEU:CD2	1:A:156:GLN:HB3	2.42	0.50
1:A:211:GLY:HA2	1:A:411:PHE:CE2	2.47	0.50
1:B:128:LEU:CD1	1:B:141:ARG:HG2	2.42	0.50
1:B:302:GLU:HA	1:B:304:PHE:CZ	2.47	0.50
1:C:390:ILE:H	1:C:390:ILE:HD12	1.77	0.50
1:C:451:ARG:O	1:C:455:ARG:HD2	2.12	0.50
1:C:52:PHE:HD1	1:C:99:TRP:CH2	2.30	0.50
2:D:6:DG:H2''	2:D:7:DA:O5'	2.12	0.49
2:H:8:DT:H4'	2:H:9:DT:OP1	2.11	0.49
1:B:34:GLY:O	1:B:38:ALA:HB2	2.12	0.49
1:B:333:ARG:HG3	1:B:334:LEU:N	2.27	0.49
1:C:72:THR:O	1:C:165:GLU:HA	2.12	0.49
3:I:5:DG:C2'	3:I:6:DT:H5'	2.41	0.49
1:B:133:LEU:CD1	1:B:138:LEU:HD13	2.41	0.49
1:B:360:PHE:CD2	1:B:361:PRO:HD2	2.48	0.49
1:C:107:GLU:HG2	1:C:108:LEU:N	2.28	0.49
1:C:134:ARG:O	1:C:138:LEU:HG	2.11	0.49
1:C:41:LEU:HA	1:C:45:GLU:OE1	2.12	0.49
1:C:353:ARG:NH1	1:C:355:ASP:OD2	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:GLU:O	1:C:49:ILE:HG13	2.12	0.49
1:B:385:VAL:HA	1:B:469:LEU:HD21	1.95	0.49
2:H:1:DG:N2	3:I:23:DT:C2	2.80	0.49
1:B:390:ILE:HD12	1:B:390:ILE:H	1.77	0.48
1:B:506:PRO:HA	1:B:522:GLU:OE1	2.13	0.48
3:E:6:DT:H2''	3:E:7:DG:H8	1.78	0.48
1:B:36:ARG:HH22	1:B:207:ALA:HA	1.78	0.48
2:D:1:DG:C8	2:D:2:DT:H72	2.48	0.48
1:A:387:ASN:HA	1:A:505:LEU:HD22	1.94	0.48
1:A:399:TRP:NE1	1:A:457:LYS:HE3	2.28	0.48
1:A:512:TRP:HE3	1:A:517:ARG:HB3	1.78	0.48
1:C:364:PRO:HA	1:C:365:CYS:HB3	1.95	0.48
1:A:108:LEU:HG	1:A:139:LEU:HD11	1.95	0.48
2:D:1:DG:C2'	2:D:2:DT:H5''	2.39	0.48
4:L:8:DC:H2''	4:L:9:DA:H8	1.79	0.48
1:B:128:LEU:HD13	1:B:141:ARG:HB3	1.95	0.48
1:B:333:ARG:HG3	1:B:334:LEU:H	1.79	0.48
1:C:434:PHE:CZ	1:C:495:LEU:HD11	2.48	0.48
1:C:91:VAL:HG11	1:C:164:TYR:OH	2.14	0.48
1:A:131:ALA:O	1:A:133:LEU:HD23	2.13	0.48
1:A:186:ASP:HB3	1:A:188:SER:H	1.79	0.48
1:A:293:ARG:NH1	1:A:296:ARG:HG2	2.29	0.48
1:B:18:GLU:HG3	1:B:18:GLU:H	1.41	0.48
2:H:5:DG:H2''	2:H:6:DG:C8	2.48	0.48
1:C:244:LEU:HD11	1:C:265:PHE:CE2	2.49	0.48
2:H:6:DG:H2''	2:H:7:DA:H8	1.79	0.48
1:B:279:GLN:HG3	1:B:298:LEU:HG	1.96	0.47
1:B:299:GLU:HG3	1:B:334:LEU:HD21	1.95	0.47
1:B:399:TRP:HZ3	1:B:465:VAL:HG21	1.79	0.47
1:C:107:GLU:HG2	1:C:108:LEU:H	1.77	0.47
1:C:413:PRO:HG2	1:C:414:PHE:CE2	2.49	0.47
1:A:156:GLN:CG	1:A:159:PHE:HB2	2.43	0.47
3:G:18:DC:H2''	3:G:19:DC:C5'	2.45	0.47
1:B:264:GLN:O	1:B:267:GLN:HB2	2.14	0.47
1:A:127:HIS:C	1:A:128:LEU:HD13	2.34	0.47
1:A:128:LEU:HD22	1:A:128:LEU:N	2.30	0.47
1:A:133:LEU:HD12	1:A:137:ALA:CB	2.44	0.47
1:C:399:TRP:HE1	1:C:457:LYS:HE3	1.79	0.47
3:E:5:DG:H2''	3:E:6:DT:H6	1.78	0.47
2:H:4:DG:H4'	2:H:4:DG:OP1	2.14	0.47
1:A:150:ARG:HD2	1:A:155:TRP:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:386:GLU:C	1:C:388:GLY:H	2.18	0.47
3:E:6:DT:H2''	3:E:7:DG:C8	2.49	0.47
1:A:147:PRO:HD2	1:A:148:GLU:OE1	2.14	0.47
1:A:261:LEU:HD12	1:A:261:LEU:HA	1.61	0.47
3:E:21:DA:C2'	3:E:22:DC:H5''	2.32	0.47
3:E:3:DA:H2''	3:E:4:DT:H6	1.80	0.47
3:G:4:DT:H2''	3:G:5:DG:O5'	2.15	0.47
1:A:153:ALA:O	1:A:157:ALA:HA	2.15	0.47
1:A:247:GLU:N	1:A:247:GLU:OE1	2.47	0.47
4:L:2:DG:H5''	4:L:2:DG:C8	2.50	0.47
4:N:4:DC:H2''	4:N:5:DA:C8	2.50	0.47
1:A:123:LEU:HD12	1:A:124:PHE:CE1	2.50	0.47
1:B:145:LEU:O	1:B:147:PRO:HD3	2.15	0.47
1:B:182:ASN:HB2	1:B:184:TRP:CD1	2.50	0.47
1:B:360:PHE:CG	1:B:361:PRO:HD2	2.50	0.47
4:L:1:DT:H1'	4:L:2:DG:C8	2.49	0.47
1:B:147:PRO:HD2	1:B:148:GLU:OE1	2.15	0.47
1:B:386:GLU:C	1:B:388:GLY:H	2.17	0.47
1:B:389:LEU:HD22	1:B:474:LEU:HD11	1.97	0.47
1:B:368:GLU:HB2	1:B:384:TYR:HE2	1.80	0.46
1:B:385:VAL:HG21	1:B:389:LEU:CB	2.46	0.46
1:C:420:ASP:OD2	1:C:430:ARG:NH1	2.47	0.46
1:A:143:GLN:N	1:A:144:PRO:HD2	2.30	0.46
1:A:385:VAL:HG12	1:A:469:LEU:CD2	2.45	0.46
1:B:143:GLN:N	1:B:144:PRO:HD2	2.30	0.46
1:B:117:LYS:N	3:G:20:DA:OP1	2.48	0.46
4:J:11:DT:H2''	4:J:12:DC:H5''	1.98	0.46
4:J:9:DA:H1'	4:J:10:DT:H5'	1.97	0.46
1:A:138:LEU:O	1:A:142:LEU:N	2.44	0.46
1:A:520:MET:HB2	1:A:548:VAL:HG12	1.97	0.46
1:A:97:LEU:HD13	1:A:99:TRP:CZ3	2.51	0.46
1:B:112:PHE:CG	1:B:139:LEU:HD13	2.50	0.46
1:C:32:TRP:CE2	1:C:36:ARG:HG3	2.51	0.46
4:N:11:DT:H2''	4:N:12:DC:O4'	2.14	0.46
1:B:420:ASP:O	1:B:423:SER:HB2	2.15	0.46
1:A:128:LEU:HD13	1:A:128:LEU:N	2.29	0.46
1:A:128:LEU:CG	1:A:138:LEU:HD11	2.44	0.46
1:A:90:ALA:O	1:A:93:PRO:HD2	2.16	0.46
1:A:451:ARG:O	1:A:455:ARG:HG2	2.16	0.46
1:B:469:LEU:HD12	1:B:469:LEU:HA	1.60	0.46
1:C:295:ILE:CG2	1:C:330:LEU:HD13	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:18:DC:H2''	3:G:19:DC:H5'	1.98	0.46
4:L:5:DA:C4	4:L:6:DC:C5	3.04	0.46
1:A:287:HIS:CG	1:A:288:PRO:HD2	2.51	0.46
1:C:55:LEU:HD11	1:C:99:TRP:CZ3	2.49	0.46
1:A:166:LEU:HG	1:A:169:MET:HG2	1.97	0.46
1:A:171:LEU:HD12	1:A:171:LEU:HA	1.66	0.46
3:E:2:DA:H8	3:E:2:DA:OP2	1.99	0.46
4:N:2:DG:H3'	4:N:3:DA:H8	1.81	0.46
1:A:191:VAL:HG21	2:D:10:DG:C8	2.51	0.46
1:C:330:LEU:HD23	1:C:333:ARG:NH2	2.31	0.45
1:C:388:GLY:HA3	1:C:469:LEU:CD2	2.46	0.45
1:A:156:GLN:NE2	1:A:159:PHE:HB2	2.31	0.45
1:A:262:LEU:HA	1:A:262:LEU:HD23	1.69	0.45
1:A:282:TYR:CZ	1:A:293:ARG:HB3	2.51	0.45
1:B:394:PHE:HB2	1:B:491:PHE:CE1	2.51	0.45
3:I:20:DA:H2''	3:I:21:DA:H8	1.81	0.45
4:L:7:DA:H2''	4:L:8:DC:H6	1.80	0.45
1:C:345:ARG:HG2	1:C:346:ALA:N	2.28	0.45
1:B:241:LEU:CD1	1:B:281:LEU:HD11	2.43	0.45
1:B:295:ILE:HG12	1:B:310:LEU:HB3	1.99	0.45
1:B:386:GLU:HA	1:B:506:PRO:O	2.17	0.45
1:B:66:MET:CE	1:B:166:LEU:HB2	2.46	0.45
1:A:152:LEU:HD21	1:A:159:PHE:CD2	2.52	0.45
1:C:33:ILE:HD11	1:C:179:TYR:HB2	1.99	0.45
4:L:5:DA:H2''	4:L:6:DC:H6	1.82	0.45
1:C:473:GLU:O	1:C:477:GLN:HG3	2.16	0.45
1:A:179:TYR:OH	1:A:414:PHE:HE2	2.00	0.45
1:C:245:PRO:HG3	1:C:249:TYR:CZ	2.52	0.45
1:A:479:LEU:HA	1:A:479:LEU:HD23	1.59	0.45
1:A:22:TYR:OH	1:A:61:ALA:HB1	2.17	0.45
1:C:286:SER:HA	1:C:291:ARG:NH1	2.30	0.45
3:E:16:DT:H2''	3:E:17:DC:H5''	1.99	0.45
1:A:63:LEU:O	1:A:67:VAL:HG23	2.17	0.44
1:C:501:ASN:HB3	1:C:537:TRP:CZ3	2.52	0.44
1:C:76:GLU:HG3	1:C:164:TYR:HE2	1.81	0.44
3:I:20:DA:H2''	3:I:21:DA:C8	2.53	0.44
1:A:384:TYR:HA	1:A:508:LEU:HD23	2.00	0.44
1:C:296:ARG:HE	1:C:300:ARG:HD2	1.82	0.44
1:C:479:LEU:HD23	1:C:479:LEU:HA	1.87	0.44
1:A:322:ALA:HB2	1:A:536:ARG:NH2	2.32	0.44
1:C:88:ARG:O	1:C:91:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:LEU:HA	1:A:244:LEU:HD23	1.71	0.44
1:A:75:ARG:HD2	1:A:114:LEU:O	2.16	0.44
1:C:351:ILE:O	1:C:351:ILE:HG13	2.17	0.44
1:C:399:TRP:NE1	1:C:457:LYS:HE3	2.33	0.44
1:C:86:ASP:HB3	1:C:89:ALA:HB3	2.00	0.44
1:B:182:ASN:OD1	1:B:184:TRP:CD1	2.70	0.44
1:B:518:TYR:CE2	1:B:547:PRO:HG2	2.53	0.44
1:B:40:LEU:HD22	1:B:215:ARG:N	2.32	0.44
1:A:97:LEU:HD13	1:A:99:TRP:CE3	2.53	0.44
1:C:125:ARG:HA	1:C:128:LEU:HD13	1.98	0.44
1:A:521:VAL:HA	1:A:549:ALA:O	2.18	0.44
4:N:9:DA:C2'	4:N:10:DT:H5''	2.36	0.44
4:N:13:DA:H2''	4:N:14:DA:O5'	2.17	0.44
1:B:40:LEU:O	1:B:215:ARG:NH2	2.43	0.44
1:B:406:ILE:HG13	1:B:430:ARG:CZ	2.48	0.44
1:A:184:TRP:CD2	1:A:185:GLN:HG2	2.53	0.43
1:C:497:ASP:OD1	1:C:499:PRO:HD2	2.18	0.43
1:A:259:VAL:HG21	1:A:286:SER:OG	2.18	0.43
1:B:530:LEU:HD22	1:B:535:LEU:HD11	2.00	0.43
1:C:352:ASP:OD2	1:C:542:ARG:NH1	2.52	0.43
1:B:524:LYS:HE3	1:B:530:LEU:HA	2.01	0.43
4:J:13:DA:H2''	4:J:14:DA:OP2	2.18	0.43
1:A:150:ARG:HD2	1:A:155:TRP:CE2	2.53	0.43
1:B:458:PHE:HA	1:B:467:TRP:CH2	2.53	0.43
1:B:505:LEU:HA	1:B:506:PRO:HD3	1.82	0.43
4:L:7:DA:H2''	4:L:8:DC:C6	2.53	0.43
4:N:7:DA:C2'	4:N:8:DC:H5'	2.47	0.43
1:A:37:TYR:CE2	1:A:210:ARG:HD3	2.53	0.43
2:F:6:DG:H2''	2:F:7:DA:C8	2.53	0.43
1:A:482:LEU:HA	1:A:482:LEU:HD23	1.75	0.43
1:B:384:TYR:HA	1:B:508:LEU:HD23	1.99	0.43
1:C:95:LEU:HA	1:C:100:VAL:O	2.18	0.43
1:C:487:LEU:HD23	1:C:487:LEU:HA	1.79	0.43
3:E:19:DC:H2''	3:E:20:DA:C8	2.54	0.43
1:A:138:LEU:HD13	1:A:138:LEU:HA	1.54	0.43
1:B:361:PRO:HB2	1:B:362:SER:CA	2.48	0.43
1:C:310:LEU:HA	1:C:310:LEU:HD12	1.71	0.43
1:C:62:LEU:HD13	1:C:84:ILE:HD12	2.01	0.43
1:A:176:ARG:NH2	1:A:183:LEU:HD22	2.34	0.43
1:A:192:LEU:HD12	1:A:197:ILE:HB	2.00	0.43
1:A:388:GLY:HA2	1:A:466:TYR:CD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:LEU:HD23	1:A:356:LEU:HA	1.88	0.42
1:A:420:ASP:HB2	1:A:429:ARG:HH12	1.84	0.42
1:A:427:ARG:HG3	1:A:495:LEU:HD13	2.01	0.42
1:B:221:TYR:OH	1:B:257:ARG:NH2	2.52	0.42
1:A:292:LEU:HD12	1:A:292:LEU:HA	1.55	0.42
1:A:331:LEU:HA	1:A:331:LEU:HD23	1.90	0.42
1:B:535:LEU:HA	1:B:535:LEU:HD12	1.73	0.42
1:C:348:ALA:HB3	1:C:351:ILE:CG2	2.48	0.42
1:C:354:LEU:HD23	1:C:551:CYS:HB2	2.01	0.42
1:A:529:ARG:HD3	1:A:529:ARG:HA	1.72	0.42
1:B:314:ALA:CB	1:B:327:LEU:HD11	2.48	0.42
1:C:542:ARG:HD2	1:C:542:ARG:HA	1.61	0.42
1:A:177:LEU:HD23	1:A:222:LEU:HD22	2.02	0.42
1:B:293:ARG:HD2	1:B:293:ARG:HA	1.79	0.42
1:C:30:LEU:HA	1:C:30:LEU:HD23	1.80	0.42
1:A:329:ARG:HG2	1:A:345:ARG:NH2	2.33	0.42
1:A:386:GLU:O	1:A:388:GLY:N	2.53	0.42
1:A:413:PRO:HG2	1:A:414:PHE:CD2	2.54	0.42
1:A:515:GLN:H	1:A:515:GLN:HG2	1.76	0.42
3:G:16:DT:H2"	3:G:17:DC:C6	2.54	0.42
1:A:182:ASN:HB3	1:A:184:TRP:CD1	2.54	0.42
1:A:276:ASP:OD1	1:A:303:ARG:NH1	2.49	0.42
1:A:505:LEU:HD11	1:A:537:TRP:CE2	2.55	0.42
1:B:197:ILE:HD13	1:B:197:ILE:HA	1.81	0.42
1:B:300:ARG:HD2	3:G:6:DT:OP1	2.19	0.42
1:C:95:LEU:HD12	1:C:100:VAL:O	2.20	0.42
1:C:394:PHE:HB2	1:C:491:PHE:CD1	2.55	0.42
1:C:540:PHE:CE1	1:C:544:ARG:CZ	3.03	0.42
2:D:5:DG:C2'	2:D:6:DG:C8	3.02	0.42
1:A:123:LEU:HD21	1:A:156:GLN:HB3	2.01	0.42
1:B:279:GLN:HE21	1:B:283:ARG:HH11	1.66	0.42
1:B:390:ILE:HD12	1:B:390:ILE:N	2.34	0.42
1:B:466:TYR:CD1	1:B:466:TYR:N	2.88	0.42
1:B:92:GLN:HB2	1:B:93:PRO:HD3	2.01	0.42
1:A:34:GLY:O	1:A:38:ALA:HB2	2.19	0.42
1:B:145:LEU:C	1:B:147:PRO:HD3	2.40	0.42
1:C:181:GLY:HA2	1:C:212:PHE:HE2	1.84	0.42
1:C:40:LEU:HA	1:C:40:LEU:HD23	1.77	0.42
1:C:69:ARG:HG2	1:C:74:PHE:HE2	1.83	0.42
1:B:387:ASN:CB	1:B:505:LEU:HB2	2.33	0.42
1:B:97:LEU:HD22	1:B:99:TRP:CZ2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:ILE:O	1:A:352:ASP:HB2	2.20	0.42
1:A:487:LEU:HD22	1:A:491:PHE:CZ	2.54	0.42
1:A:354:LEU:O	1:A:551:CYS:HA	2.20	0.42
1:B:393:LEU:HD23	1:B:393:LEU:HA	1.90	0.42
1:B:244:LEU:HD23	1:B:244:LEU:HA	1.72	0.41
1:B:386:GLU:C	1:B:388:GLY:N	2.73	0.41
1:B:259:VAL:HG12	1:B:287:HIS:HB2	2.02	0.41
1:C:158:ASP:O	1:C:159:PHE:HB2	2.20	0.41
1:A:192:LEU:HA	1:A:192:LEU:HD13	1.86	0.41
1:B:390:ILE:HD13	1:B:505:LEU:HD13	2.02	0.41
1:C:349:PRO:HG2	1:C:539:GLN:HG3	2.01	0.41
1:C:530:LEU:HB3	1:C:535:LEU:HD13	2.01	0.41
3:I:23:DT:H2''	3:I:24:DT:C6	2.55	0.41
1:A:138:LEU:O	1:A:142:LEU:HB2	2.20	0.41
1:A:174:ARG:NH2	1:A:219:ASP:OD2	2.39	0.41
1:A:510:GLN:O	1:A:518:TYR:HA	2.20	0.41
1:B:36:ARG:NH2	1:B:207:ALA:HA	2.36	0.41
1:B:296:ARG:NH2	1:B:300:ARG:HG3	2.35	0.41
1:B:385:VAL:CG2	1:B:389:LEU:H	2.34	0.41
1:C:515:GLN:O	1:C:517:ARG:HA	2.19	0.41
1:A:385:VAL:HG12	1:A:469:LEU:HD21	2.01	0.41
1:A:427:ARG:CG	1:A:495:LEU:HD13	2.50	0.41
1:B:105:THR:HG22	1:B:149:ALA:HB1	2.01	0.41
1:C:524:LYS:HA	1:C:524:LYS:HD3	1.88	0.41
3:I:21:DA:H2'	3:I:22:DC:O4'	2.21	0.41
1:A:167:ARG:HH21	1:A:167:ARG:HG2	1.84	0.41
1:B:494:LEU:HD11	1:B:502:ARG:HA	2.02	0.41
1:C:390:ILE:HD11	1:C:520:MET:CE	2.51	0.41
1:A:222:LEU:HA	1:A:222:LEU:HD12	1.88	0.41
1:B:39:ASP:N	1:B:39:ASP:OD1	2.53	0.41
1:B:86:ASP:HB3	1:B:89:ALA:HB3	2.03	0.41
1:A:159:PHE:CZ	1:A:161:GLU:HB3	2.56	0.41
1:A:199:ARG:HE	1:A:460:LEU:HD11	1.86	0.41
1:A:261:LEU:HD21	1:A:265:PHE:CZ	2.55	0.41
1:C:505:LEU:HA	1:C:506:PRO:HD3	1.92	0.41
1:B:282:TYR:CZ	1:B:293:ARG:HB3	2.56	0.41
1:B:311:ALA:HB1	1:B:331:LEU:HD13	2.02	0.41
1:B:406:ILE:HG12	1:B:406:ILE:H	1.58	0.41
1:C:311:ALA:HB1	1:C:327:LEU:HD11	2.03	0.41
1:C:354:LEU:O	1:C:551:CYS:HA	2.21	0.41
3:E:7:DG:C8	3:E:8:DT:H72	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:PHE:CG	1:A:139:LEU:HD13	2.56	0.41
1:B:231:PHE:HB2	1:B:265:PHE:CE1	2.55	0.41
4:L:3:DA:H1'	4:L:4:DC:H5'	2.03	0.41
4:L:8:DC:H2''	4:L:9:DA:C8	2.56	0.41
1:B:171:LEU:HA	1:B:171:LEU:HD23	1.83	0.40
1:B:389:LEU:HD23	1:B:509:ILE:CD1	2.52	0.40
1:C:505:LEU:HD23	1:C:505:LEU:HA	1.75	0.40
3:I:15:DA:H2'	3:I:15:DA:OP2	2.21	0.40
4:N:8:DC:H6	4:N:8:DC:H2'	1.70	0.40
1:A:68:MET:HG2	1:A:187:TRP:HD1	1.86	0.40
1:B:40:LEU:HD22	1:B:215:ARG:HB2	2.03	0.40
1:B:430:ARG:O	1:B:433:LEU:N	2.55	0.40
2:H:8:DT:H2''	2:H:9:DT:H71	2.03	0.40
1:B:271:LYS:HE3	1:B:271:LYS:HB3	1.77	0.40
1:B:292:LEU:HD13	1:B:323:GLU:HG3	2.04	0.40
1:B:83:GLU:HG2	1:B:84:ILE:HG13	2.04	0.40
1:C:189:GLU:OE1	1:C:200:TYR:OH	2.35	0.40
1:C:192:LEU:HA	1:C:192:LEU:HD23	1.87	0.40
4:J:12:DC:H2'	4:J:13:DA:N7	2.36	0.40
1:C:348:ALA:HB3	1:C:351:ILE:HG22	2.03	0.40
2:D:1:DG:H2''	2:D:2:DT:C5'	2.43	0.40
3:I:21:DA:H2''	3:I:22:DC:H5'	2.04	0.40
1:A:189:GLU:HG2	1:A:414:PHE:HB3	2.02	0.40
1:B:351:ILE:HG13	1:B:353:ARG:HE	1.86	0.40
1:B:356:LEU:HA	1:B:356:LEU:HD23	1.91	0.40
1:B:386:GLU:O	1:B:388:GLY:N	2.54	0.40
1:B:540:PHE:CE1	1:B:544:ARG:CZ	3.05	0.40
1:C:49:ILE:HA	1:C:52:PHE:CE2	2.57	0.40
2:F:5:DG:H2''	2:F:6:DG:H8	1.85	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:GLU:O	1:C:447:ARG:NH2[3_545]	2.18	0.02

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	540/580 (93%)	520 (96%)	18 (3%)	2 (0%)	38	75
1	B	541/580 (93%)	523 (97%)	16 (3%)	2 (0%)	38	75
1	C	536/580 (92%)	511 (95%)	24 (4%)	1 (0%)	51	84
All	All	1617/1740 (93%)	1554 (96%)	58 (4%)	5 (0%)	44	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	361	PRO
1	A	18	GLU
1	B	344	ALA
1	B	19	PRO
1	A	235	GLU

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	441/478 (92%)	406 (92%)	35 (8%)	14	48
1	B	444/478 (93%)	422 (95%)	22 (5%)	28	65
1	C	442/478 (92%)	416 (94%)	26 (6%)	23	60
All	All	1327/1434 (92%)	1244 (94%)	83 (6%)	21	59

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLU
1	A	40	LEU
1	A	63	LEU
1	A	72	THR
1	A	84	ILE
1	A	101	ASP
1	A	125	ARG
1	A	128	LEU
1	A	133	LEU
1	A	138	LEU
1	A	141	ARG
1	A	168	CYS
1	A	191	VAL
1	A	210	ARG
1	A	222	LEU
1	A	235	GLU
1	A	257	ARG
1	A	258	ARG
1	A	259	VAL
1	A	283	ARG
1	A	300	ARG
1	A	345	ARG
1	A	351	ILE
1	A	353	ARG
1	A	387	ASN
1	A	411	PHE
1	A	441	LEU
1	A	443	ASP
1	A	448	ASP
1	A	476	GLU
1	A	492	GLU
1	A	515	GLN
1	A	537	TRP
1	A	542	ARG
1	A	554	ARG
1	B	18	GLU
1	B	125	ARG
1	B	133	LEU
1	B	138	LEU
1	B	168	CYS
1	B	191	VAL
1	B	210	ARG
1	B	271	LYS

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Mol	Chain	Res	Type
1	B	331	LEU
1	B	343	GLN
1	B	345	ARG
1	B	350	GLU
1	B	384	TYR
1	B	411	PHE
1	B	455	ARG
1	B	515	GLN
1	B	516	ARG
1	B	530	LEU
1	B	537	TRP
1	B	542	ARG
1	B	544	ARG
1	B	558	ASP
1	C	18	GLU
1	C	36	ARG
1	C	60	GLN
1	C	70	LYS
1	C	125	ARG
1	C	128	LEU
1	C	141	ARG
1	C	147	PRO
1	C	174	ARG
1	C	184	TRP
1	C	237	LEU
1	C	253	TRP
1	C	283	ARG
1	C	313	GLU
1	C	327	LEU
1	C	357	CYS
1	C	360	PHE
1	C	384	TYR
1	C	411	PHE
1	C	453	ARG
1	C	455	ARG
1	C	458	PHE
1	C	468	GLU
1	C	476	GLU
1	C	495	LEU
1	C	533	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	ASN
1	A	279	GLN
1	C	343	GLN
1	C	531	GLN
1	C	533	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	542/580 (93%)	0.43	25 (4%) 33 30	80, 130, 180, 258	0
1	B	543/580 (93%)	0.48	39 (7%) 16 17	105, 148, 200, 248	0
1	C	540/580 (93%)	0.83	91 (16%) 2 2	119, 185, 246, 291	0
2	D	10/10 (100%)	0.07	0 100 100	135, 155, 227, 236	0
2	F	10/10 (100%)	-0.21	0 100 100	141, 160, 230, 255	0
2	H	10/10 (100%)	0.74	3 (30%) 1 1	190, 195, 246, 261	0
3	E	24/24 (100%)	-0.09	1 (4%) 37 34	126, 159, 201, 221	0
3	G	24/24 (100%)	0.39	3 (12%) 4 5	154, 196, 248, 275	0
3	I	24/24 (100%)	0.12	1 (4%) 37 34	185, 205, 249, 272	0
4	J	14/14 (100%)	0.99	5 (35%) 0 0	120, 155, 194, 200	0
4	L	14/14 (100%)	0.87	3 (21%) 1 1	188, 211, 230, 240	0
4	N	13/14 (92%)	1.03	1 (7%) 14 14	174, 206, 249, 263	0
All	All	1768/1884 (93%)	0.56	172 (9%) 8 9	80, 155, 230, 291	0

All (172) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	365	CYS	9.9
1	C	558	ASP	8.2
1	C	125	ARG	7.7
1	B	559	ASP	7.4
1	C	142	LEU	6.1
1	C	124	PHE	5.9
1	C	525	GLY	5.6
1	B	277	LEU	5.3
1	C	330	LEU	5.3
1	B	249	TYR	5.3
1	C	557	VAL	5.2

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Mol	Chain	Res	Type	RSRZ
1	C	111	LEU	5.0
1	C	163	VAL	5.0
1	C	132	ASN	4.9
1	C	120	LEU	4.8
1	B	555	TRP	4.7
1	B	237	LEU	4.6
1	C	364	PRO	4.4
1	B	557	VAL	4.3
1	C	308	HIS	4.2
1	C	270	GLU	4.2
1	C	164	TYR	4.2
1	C	331	LEU	4.1
1	C	115	LEU	4.0
1	C	296	ARG	4.0
1	C	300	ARG	4.0
1	C	556	HIS	4.0
1	B	556	HIS	3.9
1	C	367	VAL	3.9
1	C	549	ALA	3.9
1	C	311	ALA	3.9
1	C	249	TYR	3.9
1	C	123	LEU	3.8
1	C	434	PHE	3.8
1	B	365	CYS	3.8
1	C	62	LEU	3.7
1	B	179	TYR	3.7
1	B	124	PHE	3.6
1	C	414	PHE	3.6
1	A	15	ALA	3.6
1	C	100	VAL	3.5
1	C	334	LEU	3.5
1	C	127	HIS	3.5
1	C	273	ARG	3.5
1	C	146	PHE	3.5
1	C	295	ILE	3.4
1	C	116	LYS	3.4
1	C	327	LEU	3.4
4	J	4	DC	3.4
1	C	291	ARG	3.4
1	A	275	PHE	3.3
1	C	530	LEU	3.3
1	C	237	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	29	VAL	3.2
1	C	349	PRO	3.1
1	C	360	PHE	3.1
1	C	212	PHE	3.1
1	B	397	LEU	3.1
1	C	106	LEU	3.1
1	A	499	PRO	3.0
4	L	1	DT	3.0
1	C	121	SER	3.0
1	C	79	LEU	3.0
1	C	108	LEU	3.0
1	B	299	GLU	3.0
1	A	100	VAL	3.0
1	C	312	ARG	2.9
1	C	404	ALA	2.9
1	B	470	LEU	2.9
1	C	553	VAL	2.9
1	C	351	ILE	2.9
1	B	422	HIS	2.9
1	C	363	GLU	2.9
4	J	14	DA	2.9
1	C	122	GLN	2.9
1	C	231	PHE	2.9
1	C	314	ALA	2.8
1	C	178	MET	2.8
3	I	11	DC	2.8
1	C	357	CYS	2.8
2	H	1	DG	2.8
1	B	408	GLY	2.8
4	J	2	DG	2.7
1	B	265	PHE	2.7
1	B	500	GLY	2.7
4	J	3	DA	2.7
1	C	299	GLU	2.7
3	G	24	DT	2.7
1	A	117	LYS	2.7
1	B	178	MET	2.7
1	C	350	GLU	2.6
1	A	300	ARG	2.6
1	A	422	HIS	2.6
1	C	203	VAL	2.6
2	H	4	DG	2.6

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Mol	Chain	Res	Type	RSRZ
3	G	1	DG	2.6
1	C	526	PRO	2.6
1	A	178	MET	2.6
1	B	558	ASP	2.6
2	H	3	DT	2.6
3	G	12	DT	2.6
1	C	138	LEU	2.6
1	A	66	MET	2.6
1	C	275	PHE	2.5
1	A	253	TRP	2.5
1	B	180	PHE	2.5
1	C	244	LEU	2.5
4	L	2	DG	2.5
1	B	79	LEU	2.5
1	A	79	LEU	2.4
1	C	356	LEU	2.4
1	A	397	LEU	2.4
1	B	497	ASP	2.4
1	C	66	MET	2.4
1	A	83	GLU	2.4
1	B	145	LEU	2.4
1	B	399	TRP	2.4
1	A	527	GLY	2.4
4	J	1	DT	2.4
1	C	145	LEU	2.4
1	B	360	PHE	2.4
1	C	221	TYR	2.4
3	E	12	DT	2.4
1	B	212	PHE	2.4
1	C	217	ASP	2.4
1	C	166	LEU	2.4
1	C	118	ASP	2.3
1	B	361	PRO	2.3
1	C	87	THR	2.3
1	B	503	ALA	2.3
4	L	3	DA	2.3
1	B	403	PHE	2.3
4	N	7	DA	2.3
1	C	528	ASP	2.3
1	C	224	LEU	2.3
1	A	400	GLU	2.3
1	A	327	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	120	LEU	2.3
1	B	168	CYS	2.3
1	C	126	ASP	2.3
1	B	270	GLU	2.2
1	A	263	PHE	2.2
1	A	254	LEU	2.2
1	B	74	PHE	2.2
1	C	155	TRP	2.2
1	A	463	PRO	2.2
1	A	94	LEU	2.2
1	C	403	PHE	2.2
1	A	284	GLN	2.2
1	C	265	PHE	2.2
1	B	389	LEU	2.1
1	A	462	SER	2.1
1	B	281	LEU	2.1
1	C	152	LEU	2.1
1	C	99	TRP	2.1
1	A	212	PHE	2.1
1	A	553	VAL	2.1
1	C	242	ALA	2.1
1	C	347	ALA	2.1
1	B	241	LEU	2.1
1	C	538	LEU	2.1
1	B	528	ASP	2.1
1	C	190	PHE	2.0
1	C	345	ARG	2.0
1	C	119	GLU	2.0
1	B	514	ALA	2.0
1	C	271	LYS	2.0
1	C	168	CYS	2.0
1	C	531	GLN	2.0
1	A	334	LEU	2.0
1	B	330	LEU	2.0
1	C	333	ARG	2.0

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 [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	CA	A	601	1/1	0.98	0.28	-0.00	92,92,92,92	0
5	CA	B	601	1/1	0.99	0.23	-0.18	142,142,142,142	0
5	CA	C	601	1/1	0.94	0.21	-0.71	189,189,189,189	0
5	CA	B	602	1/1	0.94	0.18	-0.81	148,148,148,148	0
5	CA	A	602	1/1	0.96	0.25	-0.89	142,142,142,142	0

6.5 Other polymers [i](#)

There are no such residues in this entry.