



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 09:02 PM UTC

PDB ID : 1F66 / pdb_00001f66
Title : 2.6 Å CRYSTAL STRUCTURE OF A NUCLEOSOME CORE PARTICLE
CONTAINING THE VARIANT HISTONE H2A.Z
Authors : Suto, R.K.; Clarkson, M.J.; Tremethick, D.J.; Luger, K.
Deposited on : 2000-06-20
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

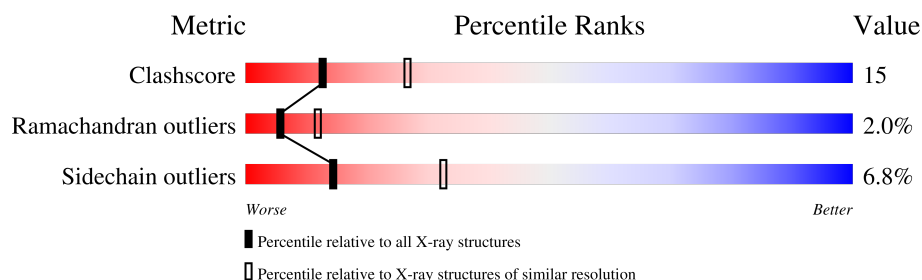
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	I	146	39% 58% .
1	J	146	47% 47% 5%
2	A	136	57% 12% . . 26%
2	E	136	59% 14% . . 24%
3	B	103	52% 24% . 22%
3	F	103	58% 17% 8% . 17%
4	C	128	55% 18% . . 20%
4	G	128	56% 19% 7% . 16%

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Mol	Chain	Length	Quality of chain
5	D	126	50%22%••25%
5	H	126	58%13%•25%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12397 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 DNA chain called PALINDROMIC 146 BASE PAIR DNA FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	I	146	Total	C	N	O	P	0	0	0
			2990	1430	541	874	145			
1	J	146	Total	C	N	O	P	0	0	0
			2990	1430	541	874	145			

- Molecule 2 is a protein called HISTONE H3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	100	Total	C	N	O	S	0	0	0
			826	521	160	142	3			
2	E	103	Total	C	N	O	S	0	0	0
			841	530	163	145	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	434	GLU	GLY	conflict	UNP Q7ZT64
A	517	VAL	ILE	conflict	UNP Q7ZT64
E	634	GLU	GLY	conflict	UNP Q7ZT64
E	717	VAL	ILE	conflict	UNP Q7ZT64

- Molecule 3 is a protein called HISTONE H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	80	Total	C	N	O	S	0	0	0
			638	401	125	111	1			
3	F	86	Total	C	N	O	S	0	0	0
			694	436	140	117	1			

- Molecule 4 is a protein called HISTONE H2A.Z.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	C	103	Total	C	N	O	0	0	0
			781	490	152	139			
4	G	107	Total	C	N	O	0	0	0
			807	506	158	143			

- Molecule 5 is a protein called HISTONE H2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			
5	H	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1229	THR	SER	conflict	UNP P02281
H	1429	THR	SER	conflict	UNP P02281

- Molecule 6 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	I	7	Total	Mn	0	0
			7	7		
6	J	5	Total	Mn	0	0
			5	5		
6	C	1	Total	Mn	0	0
			1	1		
6	E	1	Total	Mn	0	0
			1	1		
6	G	1	Total	Mn	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	I	62	Total	O	0	0
			62	62		
7	J	56	Total	O	0	0
			56	56		
7	A	27	Total	O	0	0
			27	27		

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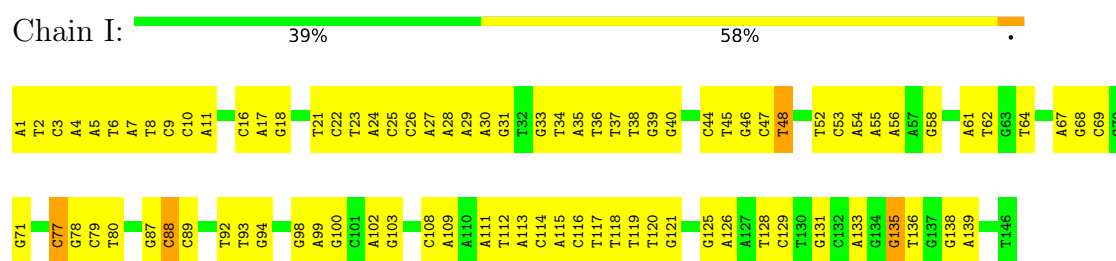
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	24	Total 24	O 24	0	0
7	C	31	Total 31	O 31	0	0
7	D	25	Total 25	O 25	0	0
7	E	43	Total 43	O 43	0	0
7	F	26	Total 26	O 26	0	0
7	G	16	Total 16	O 16	0	0
7	H	15	Total 15	O 15	0	0

3 Residue-property plots [i](#)

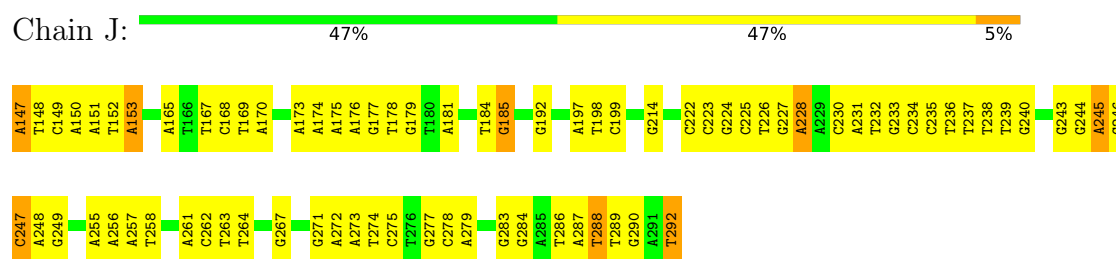
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

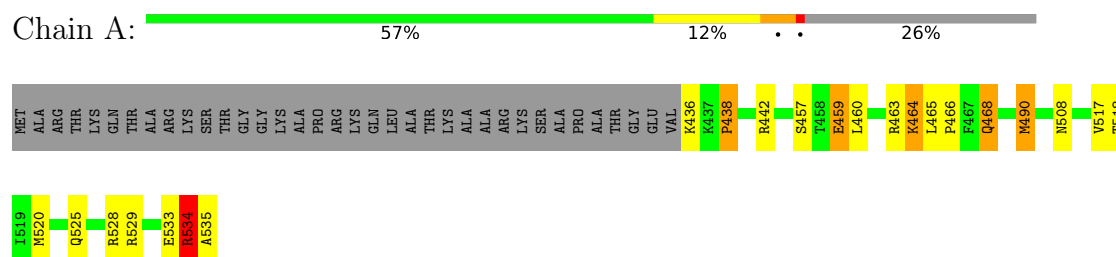
• Molecule 1: PALINDROMIC 146 BASE PAIR DNA FRAGMENT



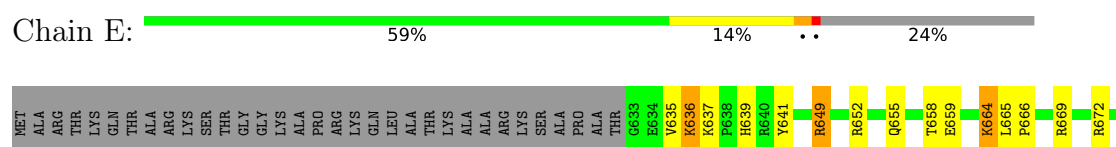
• Molecule 1: PALINDROMIC 146 BASE PAIR DNA FRAGMENT



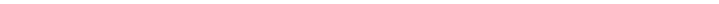
• Molecule 2: HISTONE H3

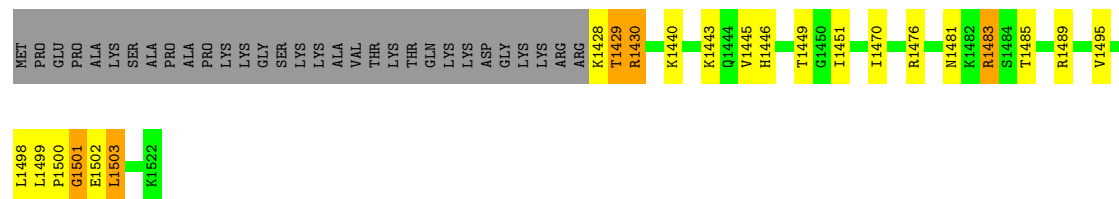


• Molecule 2: HISTONE H3



- Molecule 5: HISTONE H2B

Chain H:  58% 13% 0 25%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.66Å 183.21Å 109.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.60	Depositor
% Data completeness (in resolution range)	99.6 (25.00-2.60)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.193 , 0.249	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12397	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MN

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	I	0.40	0/3354	0.80	2/5175 (0.0%)
1	J	0.40	0/3354	0.84	1/5175 (0.0%)
2	A	1.02	2/838 (0.2%)	1.23	2/1122 (0.2%)
2	E	1.15	0/853	1.33	5/1142 (0.4%)
3	B	1.09	0/645	1.24	5/862 (0.6%)
3	F	1.25	4/702 (0.6%)	1.30	5/937 (0.5%)
4	C	1.11	2/792 (0.3%)	1.34	10/1068 (0.9%)
4	G	0.96	1/818 (0.1%)	1.24	10/1100 (0.9%)
5	D	1.07	2/756 (0.3%)	1.25	5/1015 (0.5%)
5	H	0.98	0/756	1.24	4/1015 (0.4%)
All	All	0.80	11/12868 (0.1%)	1.04	49/18611 (0.3%)

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	I	0	8
1	J	0	10
3	B	0	1
5	D	0	1
All	All	0	20

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	250	ILE	CA-CB	6.51	1.62	1.54
2	A	518	THR	CA-CB	6.37	1.62	1.53
4	G	1110	ILE	CA-C	5.71	1.58	1.53
4	C	857	ILE	CA-CB	5.69	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	913	ILE	CA-CB	-5.54	1.47	1.54
2	A	520	MET	SD-CE	5.50	1.93	1.79
3	F	297	LEU	C-O	-5.42	1.17	1.24
3	F	243	VAL	CA-CB	-5.33	1.47	1.54
5	D	1255	ALA	CA-CB	-5.18	1.45	1.53
3	F	231	LYS	CA-C	5.10	1.59	1.52
5	D	1238	VAL	CA-CB	5.04	1.60	1.54

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	464	LYS	N-CA-C	12.66	124.62	111.07
2	E	635	VAL	N-CA-C	-10.91	102.20	111.91
2	E	717	VAL	N-CA-C	-9.33	104.05	113.10
3	B	28	GLY	N-CA-C	-8.65	103.93	114.66
4	C	839	ARG	N-CA-C	-8.39	103.16	112.72
1	J	227	DG	C5'-C4'-C3'	-8.30	102.45	114.90
4	G	1118	ILE	N-CA-C	-7.22	100.27	109.58
2	E	664	LYS	N-CA-C	7.08	118.78	111.14
4	G	1039	ARG	N-CA-C	-6.79	102.25	111.55
5	D	1298	LEU	N-CA-C	6.78	120.77	112.23
3	B	46	ILE	N-CA-C	6.72	117.52	108.11
3	F	219	ARG	N-CA-C	6.66	124.99	110.80
4	C	827	PHE	CA-C-N	6.23	127.62	119.84
4	C	827	PHE	C-N-CA	6.23	127.62	119.84
3	B	44	LYS	N-CA-C	6.15	120.81	113.12
3	F	246	ILE	N-CA-C	6.14	116.72	107.75
4	G	1119	GLY	N-CA-C	6.11	127.66	113.18
4	C	842	SER	CB-CA-C	-6.04	109.01	117.23
4	C	883	PRO	N-CA-C	-6.04	105.14	113.53
5	D	1235	ALA	N-CA-C	5.95	118.53	111.33
4	C	879	LYS	N-CA-C	5.90	120.64	112.90
1	I	48	DT	C5'-C4'-C3'	-5.83	106.15	114.90
2	A	517	VAL	N-CA-C	-5.75	107.67	113.20
5	D	1315	VAL	N-CA-C	-5.74	105.52	110.74
4	G	1110	ILE	CA-C-N	-5.69	113.90	119.76
4	G	1110	ILE	C-N-CA	-5.69	113.90	119.76
5	H	1498	LEU	N-CA-C	5.67	120.33	112.90
3	B	29	ILE	N-CA-C	-5.64	98.52	107.15
3	F	229	ILE	N-CA-C	-5.63	98.39	106.55
2	E	655	GLN	CA-C-N	-5.62	113.27	122.54
2	E	655	GLN	C-N-CA	-5.62	113.27	122.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	849	THR	N-CA-C	5.55	120.05	113.16
4	C	884	ARG	CB-CG-CD	5.54	124.03	111.30
4	G	1027	PHE	CA-C-N	5.50	126.71	119.84
4	G	1027	PHE	C-N-CA	5.50	126.71	119.84
5	H	1429	THR	N-CA-C	5.48	118.27	110.10
4	C	832	ILE	N-CA-C	-5.48	105.18	110.72
3	F	251	TYR	N-CA-C	5.48	116.93	111.07
5	H	1430	ARG	N-CA-C	5.47	118.12	109.96
3	B	40	ARG	N-CA-C	-5.46	105.72	112.38
3	F	228	GLY	N-CA-C	-5.42	107.94	114.66
4	G	1040	THR	N-CA-C	5.40	118.39	109.85
4	C	895	GLU	N-CA-C	5.19	117.02	111.36
1	I	79	DC	C2'-C3'-O3'	-5.15	103.78	111.50
4	G	1069	ALA	N-CA-C	-5.15	105.75	111.36
5	D	1288	SER	N-CA-C	-5.14	106.27	112.54
5	H	1470	ILE	N-CA-C	5.11	115.34	110.53
4	G	1120	LYS	N-CA-C	-5.06	100.03	110.80
5	D	1268	GLU	N-CA-C	-5.03	105.69	111.07

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	98	TYR	Sidechain
5	D	1239	TYR	Sidechain
1	I	121	DG	Sidechain
1	I	131	DG	Sidechain
1	I	133	DA	Sidechain
1	I	135	DG	Sidechain
1	I	64	DT	Sidechain
1	I	67	DA	Sidechain
1	I	77	DC	Sidechain
1	I	88	DC	Sidechain
1	J	147	DA	Sidechain
1	J	153	DA	Sidechain
1	J	185	DG	Sidechain
1	J	214	DG	Sidechain
1	J	228	DA	Sidechain
1	J	238	DT	Sidechain
1	J	245	DA	Sidechain
1	J	247	DC	Sidechain
1	J	288	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	J	292	DT	Sidechain

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	I	2990	0	1651	84	0
1	J	2990	0	1651	96	0
2	A	826	0	871	24	0
2	E	841	0	884	27	0
3	B	638	0	676	17	0
3	F	694	0	742	19	0
4	C	781	0	824	42	0
4	G	807	0	856	39	0
5	D	745	0	773	30	0
5	H	745	0	773	22	0
6	C	1	0	0	0	0
6	E	1	0	0	0	0
6	G	1	0	0	0	0
6	I	7	0	0	0	0
6	J	5	0	0	0	0
7	A	27	0	0	0	0
7	B	24	0	0	2	0
7	C	31	0	0	0	0
7	D	25	0	0	2	0
7	E	43	0	0	1	0
7	F	26	0	0	1	0
7	G	16	0	0	1	0
7	H	15	0	0	2	0
7	I	62	0	0	5	0
7	J	56	0	0	3	0
All	All	12397	0	9701	329	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 15.

All (329) 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)
7:J:1048:HOH:O	4:G:1034:ARG:HD2	1.49	1.08
5:D:1243:LYS:HE2	5:D:1243:LYS:HA	1.40	1.03
2:A:464:LYS:HE2	2:A:490:MET:HE1	1.44	0.98
4:C:839:ARG:HH11	4:C:839:ARG:HB2	1.26	0.98
2:E:636:LYS:HG2	2:E:637:LYS:H	1.26	0.97
4:C:822:ARG:NH2	5:D:1322:LYS:HB2	1.80	0.95
4:G:1057:ILE:HD13	5:H:1495:VAL:HG21	1.51	0.91
3:B:84:MET:HE1	3:B:102:GLY:HA3	1.53	0.91
4:C:839:ARG:HB2	4:C:839:ARG:NH1	1.89	0.87
2:E:649:ARG:HG3	2:E:649:ARG:HH11	1.38	0.87
4:G:1053:TYR:HE1	4:G:1057:ILE:HD11	1.41	0.86
4:C:857:ILE:HD12	5:D:1307:ALA:HB1	1.58	0.85
5:H:1476:ARG:HD2	7:H:262:HOH:O	1.77	0.85
2:A:528:ARG:HH12	2:A:535:ALA:HB3	1.41	0.83
5:D:1254:LYS:HG2	7:D:7:HOH:O	1.77	0.83
4:G:1119:GLY:C	4:G:1121:LYS:H	1.84	0.81
1:J:287:DA:H2''	1:J:288:DT:H5'	1.63	0.81
2:E:636:LYS:HG2	2:E:637:LYS:N	1.91	0.81
1:J:257:DA:H2''	1:J:258:DT:H71	1.63	0.79
4:C:841:THR:HG23	4:C:841:THR:O	1.83	0.79
4:C:839:ARG:HH11	4:C:839:ARG:CB	1.95	0.79
3:B:95:ARG:HD3	7:B:123:HOH:O	1.81	0.78
2:A:464:LYS:CE	2:A:490:MET:HE1	2.13	0.78
1:J:197:DA:H2''	1:J:198:DT:H5'	1.66	0.78
4:G:1053:TYR:CE1	4:G:1057:ILE:HD11	2.18	0.78
3:B:84:MET:HE1	3:B:102:GLY:CA	2.13	0.77
4:C:840:THR:HG22	4:C:841:THR:N	1.99	0.77
5:H:1501:GLY:HA2	7:H:168:HOH:O	1.85	0.77
1:I:113:DA:H2''	1:I:114:DC:O5'	1.85	0.76
4:C:840:THR:HG22	4:C:841:THR:H	1.50	0.76
4:G:1019:ARG:HH22	4:G:1033:HIS:CD2	2.02	0.76
1:J:245:DA:H2''	1:J:246:DG:H5''	1.67	0.75
2:A:534:ARG:NE	2:A:534:ARG:HA	2.00	0.75
1:J:237:DT:H4'	2:A:463:ARG:CZ	2.18	0.74
3:F:297:LEU:O	3:F:302:GLY:HA2	1.86	0.73
1:I:125:DG:H1'	1:I:126:DA:H5'	1.70	0.73
1:J:234:DC:H4'	1:J:235:DC:OP1	1.86	0.73
4:G:1057:ILE:CD1	5:H:1495:VAL:HG21	2.18	0.73
1:I:61:DA:H2''	1:I:62:DT:H5'	1.70	0.73
1:J:149:DC:H2''	1:J:150:DA:O5'	1.89	0.72
1:J:248:DA:H2''	1:J:249:DG:C8	2.25	0.72
1:J:151:DA:H2''	1:J:152:DT:H5''	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:840:THR:CG2	4:C:841:THR:N	2.53	0.72
1:I:5:DA:H2''	1:I:6:DT:H5''	1.71	0.71
2:A:436:LYS:O	2:A:438:PRO:HD3	1.91	0.71
4:G:1057:ILE:HD13	5:H:1495:VAL:CG2	2.21	0.71
1:J:257:DA:C2'	1:J:258:DT:H71	2.20	0.71
1:I:27:DA:H2	1:J:267:DG:H22	1.40	0.70
1:J:246:DG:H2''	1:J:247:DC:C6	2.27	0.70
1:I:31:DG:H5''	4:C:818:SER:HA	1.74	0.69
4:C:857:ILE:HG13	5:D:1295:VAL:HG21	1.73	0.69
1:I:21:DT:H2''	1:I:22:DC:O5'	1.92	0.69
1:I:22:DC:H2'	1:I:23:DT:H71	1.75	0.69
4:C:828:PRO:HG3	5:D:1237:TYR:CE2	2.27	0.69
1:J:185:DG:H4'	4:G:1045:ARG:HD2	1.75	0.69
4:C:839:ARG:O	4:C:839:ARG:HG2	1.92	0.69
4:G:1120:LYS:O	4:G:1120:LYS:HD3	1.93	0.69
5:H:1481:ASN:O	5:H:1483:ARG:HG2	1.93	0.69
1:J:197:DA:C2'	1:J:198:DT:H5'	2.24	0.68
2:E:664:LYS:HD2	7:E:268:HOH:O	1.94	0.68
1:J:230:DC:H2''	1:J:231:DA:C8	2.29	0.67
1:J:287:DA:H2''	1:J:288:DT:C5'	2.25	0.67
3:F:287:VAL:HG11	3:F:302:GLY:H	1.59	0.67
4:C:834:ARG:HG2	4:C:834:ARG:HH11	1.59	0.66
4:C:840:THR:O	4:C:841:THR:HB	1.95	0.66
1:I:31:DG:H1	1:J:262:DC:H42	1.44	0.66
1:I:22:DC:N4	1:J:271:DG:H1	1.94	0.66
3:F:292:ARG:HB3	3:F:292:ARG:NH1	2.12	0.65
1:J:248:DA:H2''	1:J:249:DG:H8	1.59	0.65
2:E:649:ARG:HG3	2:E:649:ARG:NH1	2.07	0.65
1:I:22:DC:H42	1:J:271:DG:H1	1.44	0.65
4:G:1016:ALA:O	4:G:1017:VAL:HB	1.95	0.65
1:J:151:DA:H2''	1:J:152:DT:C5'	2.27	0.64
1:I:103:DG:H5''	5:D:1229:THR:CG2	2.28	0.64
1:J:292:DT:H5'	2:E:636:LYS:HZ1	1.63	0.64
4:C:828:PRO:HG3	5:D:1237:TYR:CZ	2.32	0.64
5:D:1243:LYS:HE2	5:D:1243:LYS:CA	2.22	0.64
1:I:27:DA:C3'	5:D:1228:LYS:HZ1	2.10	0.64
1:I:103:DG:H5''	5:D:1229:THR:HG23	1.78	0.63
1:J:151:DA:C2'	1:J:152:DT:H5''	2.28	0.63
1:I:1:DA:H2''	1:I:2:DT:OP2	1.99	0.63
1:J:239:DT:H2''	1:J:240:DG:C8	2.34	0.63
4:C:840:THR:HG23	4:C:844:GLY:HA3	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:249:DG:H5''	5:H:1428:LYS:HA	1.80	0.62
2:A:528:ARG:NH1	2:A:535:ALA:OXT	2.33	0.62
1:J:246:DG:H2''	1:J:247:DC:C5	2.34	0.62
4:G:1119:GLY:C	4:G:1121:LYS:N	2.57	0.62
4:C:841:THR:O	4:C:841:THR:CG2	2.47	0.61
1:J:197:DA:H1'	1:J:198:DT:H5'	1.82	0.61
3:F:229:ILE:HG13	3:F:258:LEU:HD23	1.82	0.61
1:I:44:DC:H1'	1:I:45:DT:H5'	1.81	0.61
1:J:292:DT:H5'	2:E:636:LYS:NZ	2.15	0.61
4:C:822:ARG:HH22	5:D:1322:LYS:HB2	1.65	0.60
1:J:165:DA:H4'	4:G:1080:ARG:NH2	2.16	0.60
5:D:1243:LYS:HA	5:D:1243:LYS:CE	2.25	0.60
1:I:27:DA:H2	1:J:267:DG:N2	2.00	0.59
3:F:287:VAL:CG1	3:F:302:GLY:H	2.15	0.59
5:D:1294:ALA:O	5:D:1298:LEU:HD12	2.02	0.59
1:I:71:DG:OP2	7:I:1045:HOH:O	2.17	0.59
1:I:24:DA:H1'	1:I:25:DC:H5'	1.83	0.59
1:J:184:DT:H2''	1:J:185:DG:N7	2.18	0.59
1:I:34:DT:H5''	7:I:1023:HOH:O	2.03	0.58
1:J:149:DC:H2'	1:J:150:DA:C8	2.39	0.58
1:J:235:DC:H2''	1:J:236:DT:OP2	2.03	0.58
2:E:636:LYS:CG	2:E:637:LYS:H	2.10	0.58
1:I:111:DA:H2''	1:I:112:DT:OP2	2.03	0.58
1:I:94:DG:H1	1:J:199:DC:H42	1.51	0.58
4:G:1082:THR:HB	4:G:1083:PRO:CD	2.34	0.58
1:J:286:DT:H2''	1:J:287:DA:O5'	2.04	0.57
1:I:61:DA:C2'	1:I:62:DT:H5'	2.34	0.57
1:J:277:DG:H3'	4:C:879:LYS:HD2	1.86	0.57
3:B:31:LYS:NZ	3:B:55:ARG:HH12	2.03	0.57
3:F:275:HIS:O	5:H:1489:ARG:NH2	2.35	0.57
1:J:175:DA:C2'	1:J:176:DA:C8	2.88	0.57
1:I:135:DG:H2''	1:I:136:DT:OP2	2.05	0.56
4:C:840:THR:O	4:C:841:THR:CB	2.53	0.56
1:I:17:DA:C2	1:I:18:DG:C2	2.93	0.56
1:I:111:DA:H4'	4:G:1045:ARG:HE	1.69	0.56
1:I:118:DT:H2''	1:I:119:DT:H72	1.88	0.56
1:J:177:DG:H5''	4:G:1018:SER:HA	1.88	0.56
1:I:100:DG:H5''	2:E:683:ARG:HD2	1.86	0.56
1:I:111:DA:H4'	4:G:1045:ARG:NE	2.21	0.55
1:J:165:DA:H4'	4:G:1080:ARG:CZ	2.37	0.55
4:C:842:SER:C	4:C:844:GLY:H	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:68:DG:OP1	2:A:442:ARG:HD3	2.06	0.55
4:C:884:ARG:O	4:C:884:ARG:HG3	2.01	0.55
1:I:4:DA:C2	1:J:290:DG:N2	2.75	0.55
1:I:55:DA:H2''	1:I:56:DA:C8	2.40	0.55
1:I:36:DT:H2''	1:I:37:DT:OP2	2.07	0.55
2:E:665:LEU:HB3	2:E:666:PRO:HD3	1.88	0.55
2:A:534:ARG:HA	2:A:534:ARG:HE	1.69	0.54
1:J:232:DT:H2''	1:J:233:DG:H8	1.72	0.54
1:J:228:DA:OP2	3:B:35:ARG:NH2	2.34	0.54
1:J:175:DA:H2''	1:J:176:DA:C8	2.43	0.54
4:C:834:ARG:HG2	4:C:834:ARG:NH1	2.23	0.54
1:I:22:DC:H2''	1:I:23:DT:O5'	2.08	0.54
3:F:287:VAL:HG11	3:F:302:GLY:N	2.22	0.53
1:J:147:DA:H2''	1:J:148:DT:C6	2.43	0.53
1:J:192:DG:H2'	7:J:1058:HOH:O	2.08	0.53
1:I:26:DC:C2	1:I:27:DA:C2	2.97	0.53
5:D:1276:ARG:HD2	7:D:34:HOH:O	2.07	0.53
3:B:52:GLU:OE2	3:B:55:ARG:NH1	2.41	0.53
3:B:76:ALA:O	3:B:77:LYS:HB2	2.09	0.53
1:I:118:DT:C2'	1:I:119:DT:H72	2.39	0.52
1:J:277:DG:OP2	4:C:879:LYS:NZ	2.42	0.52
4:C:837:LYS:O	4:C:840:THR:HB	2.09	0.52
1:I:2:DT:H2''	1:I:3:DC:O5'	2.09	0.52
1:I:36:DT:H1'	1:I:37:DT:H5'	1.90	0.52
1:I:58:DG:H8	7:I:1011:HOH:O	1.93	0.52
1:J:147:DA:H2''	1:J:148:DT:H6	1.74	0.52
4:G:1045:ARG:HG2	4:G:1045:ARG:HH11	1.75	0.52
1:J:169:DT:H72	1:J:170:DA:H62	1.74	0.52
1:J:199:DC:OP1	3:F:218:HIS:NE2	2.43	0.52
4:C:840:THR:HG22	4:G:1042:SER:HA	1.92	0.52
3:F:292:ARG:HB3	3:F:292:ARG:HH11	1.74	0.52
1:I:119:DT:H4'	1:I:120:DT:OP1	2.09	0.52
1:J:249:DG:OP1	5:H:1429:THR:HG22	2.10	0.52
2:A:465:LEU:N	2:A:466:PRO:CD	2.74	0.51
1:J:272:DA:H2''	1:J:273:DA:O5'	2.11	0.51
1:I:7:DA:C2	1:J:287:DA:C2	2.98	0.51
1:J:258:DT:OP1	4:C:837:LYS:NZ	2.44	0.51
4:G:1045:ARG:HD3	5:H:1485:THR:OG1	2.11	0.51
5:H:1445:VAL:HG12	5:H:1446:HIS:CD2	2.46	0.51
1:I:46:DG:H2''	1:I:47:DC:H6	1.76	0.51
1:I:54:DA:H61	1:J:239:DT:H3	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:30:THR:HB	3:B:32:PRO:HD2	1.93	0.51
1:J:234:DC:O2	1:J:235:DC:N3	2.44	0.50
4:C:841:THR:HA	4:G:1040:THR:O	2.11	0.50
1:I:38:DT:H2''	1:I:39:DG:N7	2.27	0.50
1:I:92:DT:C6	1:I:93:DT:H72	2.47	0.50
2:E:733:GLU:O	2:E:734:ARG:HB2	2.11	0.50
1:I:28:DA:H2''	1:I:29:DA:OP2	2.11	0.50
4:C:882:THR:HB	4:C:883:PRO:CD	2.41	0.50
3:B:30:THR:CB	3:B:32:PRO:HD2	2.42	0.50
2:E:719:ILE:HG13	3:F:250:ILE:HG13	1.93	0.50
1:I:8:DT:H2''	1:I:9:DC:C6	2.47	0.50
1:J:292:DT:C5'	2:E:636:LYS:NZ	2.75	0.50
1:J:225:DC:H2''	1:J:226:DT:H71	1.94	0.50
1:I:61:DA:OP1	3:B:23:ARG:NH2	2.40	0.49
1:I:30:DA:H2''	1:I:31:DG:OP2	2.12	0.49
1:J:178:DT:H2''	1:J:179:DG:H8	1.78	0.49
1:I:6:DT:H2''	1:I:7:DA:C8	2.47	0.49
1:J:271:DG:H8	7:J:1045:HOH:O	1.95	0.49
2:A:508:ASN:HD21	4:G:1117:LEU:HD11	1.78	0.49
2:E:734:ARG:O	2:E:735:ALA:HB2	2.13	0.49
1:I:27:DA:H4'	5:D:1228:LYS:NZ	2.28	0.48
2:A:468:GLN:HE21	2:A:468:GLN:HB2	1.47	0.48
4:G:1041:THR:O	4:G:1042:SER:C	2.54	0.48
4:G:1026:GLN:OE1	5:H:1440:LYS:HD3	2.13	0.48
1:J:197:DA:C1'	1:J:198:DT:H5'	2.44	0.48
1:J:234:DC:O2	1:J:235:DC:C2	2.66	0.48
1:J:178:DT:H2''	1:J:179:DG:C8	2.48	0.48
1:J:288:DT:H2''	1:J:289:DT:H5'	1.94	0.48
5:H:1443:LYS:NZ	5:H:1449:THR:O	2.44	0.48
1:I:118:DT:H2''	1:I:119:DT:C7	2.44	0.48
1:I:61:DA:H1'	1:I:62:DT:H5'	1.95	0.48
1:J:147:DA:C8	1:J:148:DT:H72	2.49	0.48
1:I:108:DC:H2''	1:I:109:DA:N7	2.29	0.47
1:I:47:DC:H2''	1:I:48:DT:H71	1.96	0.47
5:D:1243:LYS:CA	5:D:1243:LYS:CE	2.89	0.47
1:J:245:DA:C2'	1:J:246:DG:H5''	2.42	0.47
1:I:54:DA:H2''	1:I:55:DA:C8	2.50	0.47
2:A:528:ARG:NH1	2:A:535:ALA:HB3	2.18	0.47
3:F:259:LYS:HE3	3:F:263:GLU:OE2	2.15	0.47
1:I:47:DC:H2''	1:I:48:DT:C7	2.44	0.47
5:D:1251:ILE:HG21	5:D:1256:MET:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:88:DC:H2''	1:I:89:DC:C6	2.50	0.47
2:A:457:SER:HB2	2:A:459:GLU:OE2	2.15	0.47
5:D:1245:VAL:HG23	5:D:1246:HIS:CD2	2.49	0.46
1:I:46:DG:H2''	1:I:47:DC:C6	2.50	0.46
1:J:152:DT:H2''	1:J:153:DA:C8	2.50	0.46
2:A:533:GLU:O	2:A:534:ARG:O	2.33	0.46
2:E:733:GLU:O	2:E:734:ARG:HD3	2.15	0.46
3:F:219:ARG:HB2	3:F:220:LYS:H	1.26	0.46
4:G:1019:ARG:NH2	4:G:1033:HIS:CD2	2.79	0.46
4:G:1082:THR:HB	4:G:1083:PRO:HD2	1.96	0.46
1:J:261:DA:H2''	1:J:262:DC:H5'	1.98	0.46
1:I:40:DG:OP1	5:D:1285:THR:HB	2.15	0.46
5:D:1239:TYR:O	5:D:1243:LYS:HG2	2.16	0.46
2:E:734:ARG:HA	2:E:734:ARG:HD2	1.54	0.46
1:I:98:DG:H4'	1:I:99:DA:OP1	2.16	0.45
1:J:287:DA:C2'	1:J:288:DT:H5'	2.41	0.45
4:G:1045:ARG:HG2	4:G:1045:ARG:NH1	2.32	0.45
1:J:175:DA:H2''	1:J:176:DA:O5'	2.16	0.45
4:C:845:ARG:HD3	5:D:1285:THR:OG1	2.16	0.45
5:H:1489:ARG:HH11	5:H:1489:ARG:HG2	1.81	0.45
1:J:283:DG:H2''	1:J:284:DG:C8	2.52	0.45
4:G:1026:GLN:N	4:G:1059:GLU:OE1	2.47	0.45
5:H:1489:ARG:HG2	5:H:1489:ARG:NH1	2.32	0.45
1:J:283:DG:H2''	1:J:284:DG:OP2	2.16	0.44
4:C:817:VAL:HG13	4:C:821:GLN:HB3	1.99	0.44
5:D:1299:LEU:N	5:D:1299:LEU:HD23	2.31	0.44
1:I:10:DC:H1'	1:I:11:DA:C8	2.52	0.44
4:C:882:THR:HB	4:C:883:PRO:HD2	1.98	0.44
5:H:1451:ILE:HG23	5:H:1451:ILE:O	2.16	0.44
1:J:243:DG:H2''	1:J:244:DG:C8	2.52	0.44
4:G:1101:LYS:HA	4:G:1101:LYS:HD3	1.64	0.44
4:G:1114:HIS:HB3	7:G:142:HOH:O	2.17	0.44
1:I:102:DA:H2''	1:I:103:DG:OP2	2.16	0.44
1:I:113:DA:C2	1:J:181:DA:C2	3.05	0.44
3:B:89:ALA:O	3:B:93:GLN:HG3	2.16	0.44
1:I:31:DG:OP1	4:C:819:ARG:HG3	2.17	0.44
1:I:27:DA:C4'	5:D:1228:LYS:HZ1	2.31	0.44
1:I:87:DG:H4'	1:I:88:DC:OP1	2.18	0.44
1:J:147:DA:C2'	1:J:148:DT:C7	2.96	0.44
4:C:914:HIS:CE1	2:E:709:LEU:HD21	2.53	0.44
5:D:1277:LEU:HD12	5:D:1277:LEU:HA	1.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:679:LYS:HG3	3:F:274:GLU:OE2	2.18	0.44
2:A:528:ARG:HH12	2:A:535:ALA:CB	2.22	0.43
3:B:31:LYS:N	3:B:32:PRO:CD	2.81	0.43
1:J:277:DG:P	4:C:879:LYS:NZ	2.92	0.43
4:G:1067:GLU:HA	5:H:1446:HIS:HE2	1.82	0.43
1:I:80:DT:OP2	7:I:1054:HOH:O	2.21	0.43
1:J:249:DG:P	5:H:1429:THR:HG22	2.57	0.43
1:I:34:DT:H2''	1:I:35:DA:O5'	2.18	0.43
1:J:274:DT:H2''	1:J:275:DC:OP2	2.17	0.43
1:I:5:DA:C2'	1:I:6:DT:H5''	2.45	0.43
1:J:278:DC:H2''	1:J:279:DA:N7	2.34	0.43
1:I:52:DT:H2''	1:I:53:DC:C6	2.53	0.43
2:E:649:ARG:HH11	2:E:649:ARG:CG	2.16	0.43
3:F:289:ALA:O	3:F:293:GLN:HG3	2.17	0.43
1:I:125:DG:H1'	1:I:126:DA:C5'	2.46	0.43
7:I:1065:HOH:O	2:E:652:ARG:HD2	2.19	0.43
4:C:870:GLY:HA3	5:D:1246:HIS:CD2	2.54	0.43
2:E:672:ARG:HG2	2:E:672:ARG:HH11	1.83	0.43
2:A:529:ARG:CD	2:A:529:ARG:C	2.92	0.42
1:J:147:DA:H2'	1:J:148:DT:H72	2.01	0.42
2:A:529:ARG:C	2:A:529:ARG:HD3	2.44	0.42
2:A:525:GLN:O	2:A:534:ARG:NH2	2.53	0.42
3:F:218:HIS:C	3:F:219:ARG:HG2	2.43	0.42
1:J:247:DC:OP1	3:B:79:LYS:N	2.39	0.42
3:B:31:LYS:HZ3	3:B:55:ARG:HH12	1.67	0.42
4:C:884:ARG:HB2	2:E:658:THR:HG21	2.00	0.42
1:I:77:DC:H2''	1:I:78:DG:C8	2.55	0.42
1:I:116:DC:H2''	1:I:117:DT:OP2	2.19	0.42
2:A:460:LEU:HD12	2:A:464:LYS:HE2	2.02	0.42
2:A:534:ARG:O	2:A:535:ALA:HB2	2.20	0.42
1:I:114:DC:H2''	1:I:115:DA:C8	2.55	0.42
1:J:147:DA:H2'	1:J:148:DT:C7	2.50	0.42
4:C:891:ARG:HA	4:C:891:ARG:HD3	1.68	0.42
1:I:94:DG:H1	1:J:199:DC:N4	2.15	0.42
1:J:167:DT:H2''	1:J:168:DC:OP2	2.19	0.41
2:A:529:ARG:HD3	2:A:529:ARG:O	2.20	0.41
3:F:231:LYS:HB3	3:F:232:PRO:HD3	2.02	0.41
1:I:69:DC:H42	1:J:224:DG:H1	1.68	0.41
1:J:272:DA:H1'	1:J:273:DA:H5'	2.01	0.41
2:A:465:LEU:HB3	2:A:466:PRO:HD3	2.01	0.41
4:C:887:GLN:HG2	4:C:907:GLY:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:1053:TYR:CE1	4:G:1057:ILE:CD1	2.98	0.41
1:I:16:DC:O2	1:I:17:DA:C2	2.73	0.41
1:I:33:DG:C2	1:J:261:DA:C2	3.08	0.41
2:E:639:HIS:HE1	2:E:641:TYR:CE2	2.37	0.41
2:E:669:ARG:HD2	3:F:225:ASN:OD1	2.20	0.41
3:B:31:LYS:NZ	7:B:109:HOH:O	2.38	0.41
2:E:641:TYR:CE2	2:E:649:ARG:NH2	2.88	0.41
3:F:259:LYS:HE2	3:F:259:LYS:HB3	1.73	0.41
1:J:175:DA:H2'	1:J:176:DA:C8	2.56	0.41
1:J:255:DA:C6	1:J:256:DA:C6	3.09	0.41
2:E:734:ARG:O	2:E:735:ALA:CB	2.68	0.41
4:G:1095:GLU:HB3	5:H:1503:LEU:HD22	2.02	0.41
1:I:31:DG:H1	1:J:262:DC:N4	2.16	0.41
1:I:138:DG:H2''	1:I:139:DA:OP2	2.20	0.41
1:J:225:DC:H2''	1:J:226:DT:C7	2.50	0.41
3:B:24:ASP:OD1	3:B:25:ASN:N	2.54	0.41
4:C:857:ILE:HG13	5:D:1295:VAL:CG2	2.47	0.41
5:H:1443:LYS:HA	5:H:1443:LYS:HD3	1.66	0.41
1:I:128:DT:H2''	1:I:129:DC:OP2	2.21	0.41
4:G:1091:ARG:HD3	4:G:1091:ARG:HA	1.70	0.41
1:J:257:DA:C4	1:J:258:DT:C5	3.09	0.40
1:J:263:DT:H2''	1:J:264:DT:OP2	2.19	0.40
5:D:1299:LEU:HA	5:D:1300:PRO:HD3	1.89	0.40
4:G:1036:LEU:HD23	4:G:1036:LEU:HA	1.95	0.40
1:J:173:DA:H2''	1:J:174:DA:OP2	2.21	0.40
3:B:61:PHE:HE1	3:B:95:ARG:HD2	1.87	0.40
4:C:842:SER:C	4:C:844:GLY:N	2.79	0.40
3:F:302:GLY:N	7:F:305:HOH:O	2.54	0.40
1:I:10:DC:H2''	1:I:11:DA:H8	1.85	0.40
1:I:27:DA:C4'	5:D:1228:LYS:NZ	2.85	0.40
1:J:175:DA:H8	1:J:175:DA:C5'	2.33	0.40
4:G:1017:VAL:O	4:G:1018:SER:CB	2.69	0.40
4:G:1017:VAL:O	4:G:1021:GLN:HB3	2.21	0.40
1:J:151:DA:H1'	1:J:152:DT:H5''	2.03	0.40
2:A:457:SER:CB	2:A:459:GLU:OE2	2.69	0.40
5:D:1228:LYS:HG2	5:D:1229:THR:H	1.85	0.40
2:E:733:GLU:O	2:E:734:ARG:CB	2.69	0.40
5:H:1499:LEU:HA	5:H:1500:PRO:HD3	1.74	0.40
1:J:222:DC:H2''	1:J:223:DC:C5	2.56	0.40
4:G:1017:VAL:HG12	4:G:1018:SER:N	2.37	0.40
5:H:1430:ARG:HH11	5:H:1430:ARG:HG2	1.86	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	
2	A	98/136 (72%)	94 (96%)	2 (2%)	2 (2%)	6	12
2	E	101/136 (74%)	96 (95%)	3 (3%)	2 (2%)	6	12
3	B	78/103 (76%)	78 (100%)	0	0	100	100
3	F	84/103 (82%)	77 (92%)	4 (5%)	3 (4%)	2	4
4	C	101/128 (79%)	93 (92%)	5 (5%)	3 (3%)	3	6
4	G	105/128 (82%)	94 (90%)	8 (8%)	3 (3%)	3	6
5	D	93/126 (74%)	91 (98%)	1 (1%)	1 (1%)	11	25
5	H	93/126 (74%)	89 (96%)	3 (3%)	1 (1%)	11	25
All	All	753/986 (76%)	712 (95%)	26 (4%)	15 (2%)	6	12

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	534	ARG
4	C	841	THR
5	D	1301	GLY
2	E	636	LYS
4	G	1017	VAL
5	H	1501	GLY
4	C	843	HIS
4	C	840	THR
3	F	220	LYS
3	F	301	GLY
4	G	1042	SER
2	A	438	PRO
4	G	1018	SER
2	E	734	ARG

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Mol	Chain	Res	Type
3	F	219	ARG

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	
2	A	87/112 (78%)	83 (95%)	4 (5%)	24	49
2	E	88/112 (79%)	85 (97%)	3 (3%)	32	60
3	B	65/79 (82%)	62 (95%)	3 (5%)	24	49
3	F	71/79 (90%)	65 (92%)	6 (8%)	10	22
4	C	81/97 (84%)	74 (91%)	7 (9%)	10	22
4	G	83/97 (86%)	74 (89%)	9 (11%)	6	13
5	D	81/106 (76%)	73 (90%)	8 (10%)	7	16
5	H	81/106 (76%)	78 (96%)	3 (4%)	30	57
All	All	637/788 (81%)	594 (93%)	43 (7%)	14	32

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	459	GLU
2	A	468	GLN
2	A	490	MET
2	A	534	ARG
3	B	44	LYS
3	B	47	SER
3	B	92	ARG
4	C	832	ILE
4	C	839	ARG
4	C	840	THR
4	C	841	THR
4	C	878	VAL
4	C	884	ARG
4	C	904	ILE

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Mol	Chain	Res	Type
5	D	1232	GLU
5	D	1239	TYR
5	D	1268	GLU
5	D	1270	ILE
5	D	1282	LYS
5	D	1299	LEU
5	D	1309	SER
5	D	1313	LYS
2	E	649	ARG
2	E	659	GLU
2	E	734	ARG
3	F	219	ARG
3	F	224	ASP
3	F	247	SER
3	F	259	LYS
3	F	263	GLU
3	F	292	ARG
4	G	1018	SER
4	G	1019	ARG
4	G	1040	THR
4	G	1041	THR
4	G	1045	ARG
4	G	1067	GLU
4	G	1078	VAL
4	G	1084	ARG
4	G	1118	ILE
5	H	1483	ARG
5	H	1502	GLU
5	H	1503	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	485	GLN
2	A	508	ASN
3	B	25	ASN
3	B	75	HIS
4	C	914	HIS
5	D	1281	ASN
2	E	639	HIS
4	G	1021	GLN
4	G	1033	HIS

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Mol	Chain	Res	Type
4	G	1043	HIS
4	G	1114	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 15 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.