



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:30 AM GMT

PDB ID : 3AZL
Title : Crystal Structure of Human Nucleosome Core Particle Containing H4K77Q mutation
Authors : Iwasaki, W.; Tachiwana, H.; Kawaguchi, K.; Shibata, T.; Kagawa, W.; Kurumizaka, H.
Deposited on : 2011-05-25
Resolution : 2.70 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

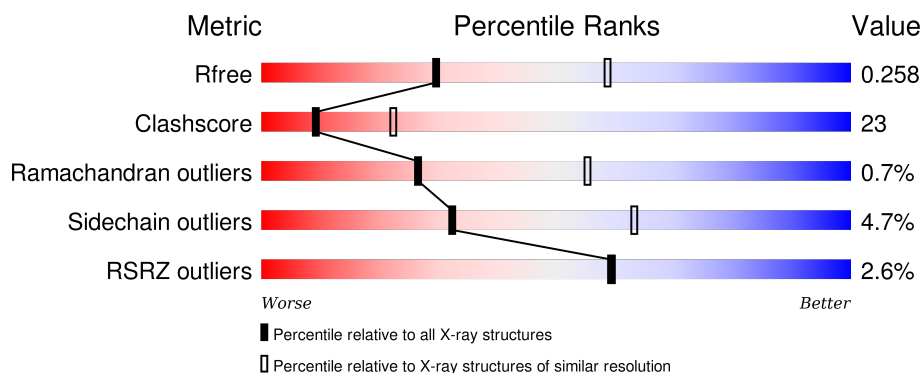
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	139	
1	E	139	
2	B	106	
2	F	106	
3	C	133	

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Mol	Chain	Length	Quality of chain
3	G	133	
4	D	129	
4	H	129	
5	I	146	
5	J	146	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	MN	E	1001	-	-	-	X
7	MN	I	1004	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12153 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 Histone H3.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	97	Total	C	N	O	S	0	0	0
			801	505	155	137	4			
1	E	99	Total	C	N	O	S	0	0	0
			816	514	158	140	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP P68431
A	-2	SER	-	EXPRESSION TAG	UNP P68431
A	-1	HIS	-	EXPRESSION TAG	UNP P68431
E	-3	GLY	-	EXPRESSION TAG	UNP P68431
E	-2	SER	-	EXPRESSION TAG	UNP P68431
E	-1	HIS	-	EXPRESSION TAG	UNP P68431

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	78	Total	C	N	O	S	0	0	0
			619	390	120	108	1			
2	F	86	Total	C	N	O	S	0	0	0
			694	435	140	118	1			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	EXPRESSION TAG	UNP P62805
B	-2	SER	-	EXPRESSION TAG	UNP P62805
B	-1	HIS	-	EXPRESSION TAG	UNP P62805
B	77	GLN	LYS	ENGINEERED MUTATION	UNP P62805
F	-3	GLY	-	EXPRESSION TAG	UNP P62805
F	-2	SER	-	EXPRESSION TAG	UNP P62805

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	HIS	-	EXPRESSION TAG	UNP P62805
F	77	GLN	LYS	ENGINEERED MUTATION	UNP P62805

- Molecule 3 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	108	Total	C	N	O	0	0	0
			835	526	165	144			
3	G	105	Total	C	N	O	0	0	0
			810	511	158	141			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	EXPRESSION TAG	UNP P04908
C	-2	SER	-	EXPRESSION TAG	UNP P04908
C	-1	HIS	-	EXPRESSION TAG	UNP P04908
G	-3	GLY	-	EXPRESSION TAG	UNP P04908
G	-2	SER	-	EXPRESSION TAG	UNP P04908
G	-1	HIS	-	EXPRESSION TAG	UNP P04908

- Molecule 4 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	94	Total	C	N	O	S	0	0	0
			736	462	134	138	2			
4	H	93	Total	C	N	O	S	0	0	0
			725	456	130	137	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	GLY	-	EXPRESSION TAG	UNP P06899
D	-2	SER	-	EXPRESSION TAG	UNP P06899
D	-1	HIS	-	EXPRESSION TAG	UNP P06899
H	-3	GLY	-	EXPRESSION TAG	UNP P06899
H	-2	SER	-	EXPRESSION TAG	UNP P06899
H	-1	HIS	-	EXPRESSION TAG	UNP P06899

- Molecule 5 is a DNA chain called 146-MER DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	145	Total	C	N	O	P	0	0	0
			2970	1421	538	867	144			
5	J	145	Total	C	N	O	P	0	0	0
			2969	1421	535	869	144			

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	1	Total	Cl	0	0
			1	1		
6	A	1	Total	Cl	0	0
			1	1		
6	C	1	Total	Cl	0	0
			1	1		
6	E	1	Total	Cl	0	0
			1	1		

- Molecule 7 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	J	4	Total	Mn	0	0
			4	4		
7	I	6	Total	Mn	0	0
			6	6		
7	E	1	Total	Mn	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	21	Total	O	0	0
			21	21		
8	B	15	Total	O	0	0
			15	15		
8	C	19	Total	O	0	0
			19	19		
8	D	10	Total	O	0	0
			10	10		
8	E	36	Total	O	0	0
			36	36		
8	F	23	Total	O	0	0
			23	23		

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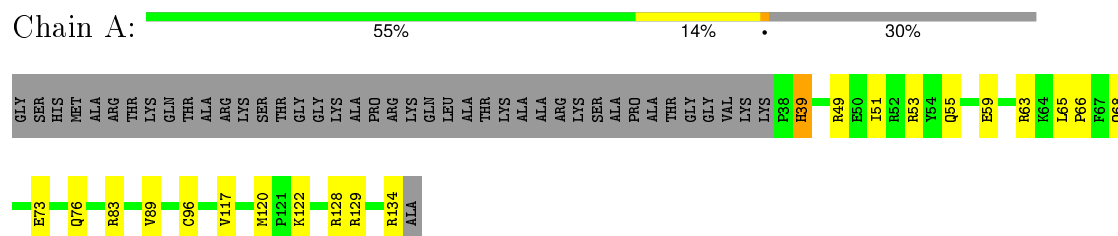
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	G	9	Total 9	O 9	0	0
8	H	9	Total 9	O 9	0	0
8	I	9	Total 9	O 9	0	0
8	J	12	Total 12	O 12	0	0

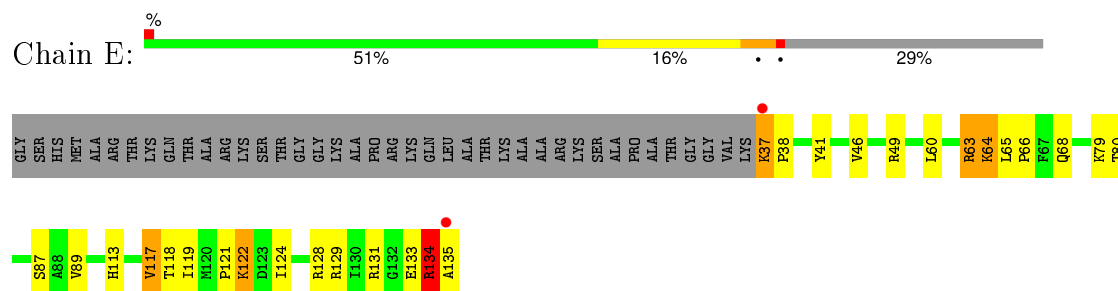
3 Residue-property plots [i](#)

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

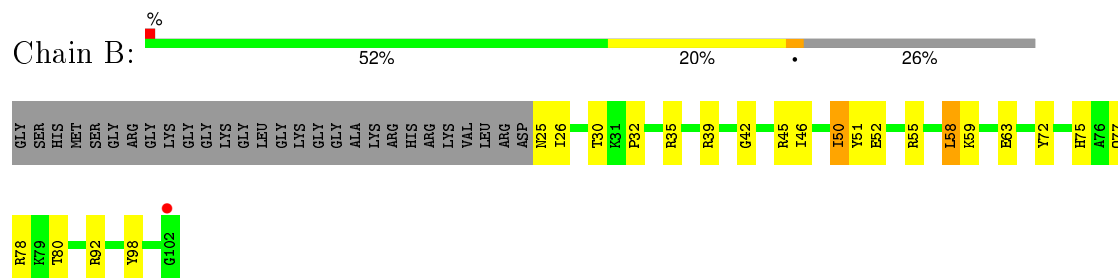
• Molecule 1: Histone H3.1



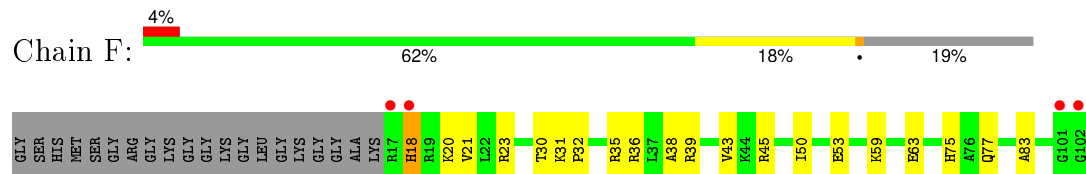
• Molecule 1: Histone H3.1



• Molecule 2: Histone H4



• Molecule 2: Histone H4



• Molecule 3: Histone H2A type 1-B/E

G131
C132
A133
G134
G135
T136
G137
G138
A139
T140
A141
T142
T143
G144
A145
DT

● Molecule 5: 146-MER DNA



DA
T148
C149
A150
A151
T152
A153
T154
C155
C158
G159
T160
G161
C162
A163
G164
A165
T166
T167
C168
T169
A170
C171
C172
A173
A174
A175
A176
G177
T178
G179
T180
A181
T182
T183
T184
G185
G186
A187
A188
A189
C190
T191
G192
C193
T194
C195
C196
A197
T198
C199
A200
A201
A202
G205
C206
A207

T210
T211
C212
G217
T220
T221
C222
A223
G224
C225
T226
G227
A228
A229
C230
A231
T232
G233
C234
C235
T236
T237
T238
T239
G240
A241
T242
G243
G244
A245
G246
C247
A248
G249
T250
T251
T252
C253
C254
A255
A256
A257
T258
A259
C260
A261
C262
T263
T264
T265
T266
G267
G268
T269
A270
G271
A272
A273

T274
C275
A279
G280
G281
T282
G283
G284
A285
T286
A287
T288
T289
T292

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.58Å 109.64Å 182.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.98 – 2.70 42.98 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (42.98-2.70) 99.8 (42.98-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.28 (at 2.69Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.208 , 0.259 0.208 , 0.258	Depositor DCC
R_{free} test set	2996 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	53.4	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 60.4	EDS
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 59257 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12153	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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: MN, CL

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	0.46	0/813	0.67	0/1090
1	E	0.55	0/828	0.72	0/1109
2	B	0.48	0/626	0.68	0/838
2	F	0.53	0/702	0.77	0/938
3	C	0.47	0/845	0.66	0/1139
3	G	0.41	0/820	0.62	0/1107
4	D	0.46	0/747	0.66	0/1004
4	H	0.46	0/736	0.62	0/990
5	I	0.42	0/3332	0.81	0/5141
5	J	0.41	0/3330	0.82	0/5138
All	All	0.45	0/12779	0.75	0/18494

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
2	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	51	TYR	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	A	801	0	839	26	0
1	E	816	0	856	36	0
2	B	619	0	654	28	0
2	F	694	0	737	24	0
3	C	835	0	897	39	0
3	G	810	0	866	26	0
4	D	736	0	758	32	0
4	H	725	0	745	25	0
5	I	2970	0	1640	163	0
5	J	2969	0	1641	159	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
6	E	1	0	0	1	0
6	G	1	0	0	1	0
7	E	1	0	0	0	0
7	I	6	0	0	0	0
7	J	4	0	0	0	0
8	A	21	0	0	4	0
8	B	15	0	0	1	0
8	C	19	0	0	1	0
8	D	10	0	0	1	0
8	E	36	0	0	1	0
8	F	23	0	0	3	0
8	G	9	0	0	3	0
8	H	9	0	0	1	0
8	I	9	0	0	1	0
8	J	12	0	0	5	0
All	All	12153	0	9633	494	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 23.

All (494) 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)
5:J:285:DA:H2''	5:J:286:DT:H5'	1.23	1.16
5:J:192:DG:H2''	5:J:193:DC:H5''	1.24	1.12
5:I:104:DT:H2''	5:I:105:DT:H5''	1.43	1.00
5:I:23:DT:H2''	5:I:24:DA:H5''	1.40	0.99
5:J:239:DT:H2''	5:J:240:DG:H5''	1.46	0.97
5:I:131:DG:H2''	5:I:132:DC:C5	2.00	0.96
5:J:192:DG:C2'	5:J:193:DC:H5''	1.98	0.94
5:J:149:DC:H2''	5:J:150:DA:H5'	1.49	0.94
5:I:51:DA:H2''	5:I:52:DT:H5'	1.48	0.93
5:I:52:DT:H2''	5:I:53:DC:H5''	1.50	0.91
5:I:55:DA:H2''	5:I:56:DA:H5''	1.53	0.90
5:I:42:DA:H2''	5:I:43:DA:H5'	1.55	0.87
5:I:93:DT:H2''	5:I:94:DG:H5'	1.57	0.87
5:J:281:DG:H2''	5:J:282:DT:H5'	1.55	0.87
5:I:55:DA:C2'	5:I:56:DA:H5''	2.05	0.87
5:I:142:DT:H2''	5:I:143:DT:H5'	1.54	0.86
5:J:266:DT:H2''	5:J:267:DG:N7	1.90	0.85
4:H:37:TYR:H	4:H:63:ASN:HD21	1.24	0.85
3:C:62:ILE:HD11	3:C:83:LEU:HD22	1.58	0.85
5:J:248:DA:H2''	5:J:249:DG:H5'	1.58	0.85
5:I:52:DT:C2'	5:I:53:DC:H5''	2.07	0.84
5:J:164:DG:H2''	5:J:165:DA:H5''	1.59	0.84
5:I:43:DA:H2''	5:I:44:DC:H5''	1.61	0.83
5:I:31:DG:H2''	5:I:32:DT:H5'	1.60	0.83
5:J:172:DC:H2''	5:J:173:DA:H5''	1.62	0.82
5:I:99:DA:H2''	5:I:100:DG:H5'	1.61	0.81
5:J:192:DG:H2''	5:J:193:DC:C5'	2.09	0.81
5:J:286:DT:C2'	5:J:287:DA:H5''	2.11	0.81
4:D:46:LYS:HA	4:D:46:LYS:HE2	1.63	0.80
5:I:36:DT:H1'	5:I:37:DT:H5'	1.64	0.80
1:E:63:ARG:NH1	1:E:63:ARG:H	1.79	0.79
5:I:50:DC:H2''	5:I:51:DA:H5''	1.62	0.79
5:I:55:DA:C3'	5:I:56:DA:H5''	2.13	0.79
5:J:150:DA:H2''	5:J:151:DA:OP2	1.82	0.79
5:J:181:DA:H1'	5:J:182:DT:H5''	1.65	0.79
5:J:189:DA:H2''	5:J:190:DC:O5'	1.81	0.79
3:G:102:ILE:HG23	4:H:61:ILE:HD13	1.65	0.78
3:C:84:GLN:HE22	3:C:88:ARG:HE	1.27	0.78
5:J:270:DA:H2''	5:J:271:DG:O5'	1.84	0.78
5:J:235:DC:H2''	5:J:236:DT:C7	2.13	0.78
5:I:23:DT:C2'	5:I:24:DA:H5''	2.14	0.78
4:H:88:THR:HG23	5:J:186:DG:OP1	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:17:ARG:HH12	3:G:31:HIS:HD2	1.31	0.78
5:J:266:DT:H2''	5:J:267:DG:C8	2.20	0.77
5:I:17:DA:H2''	5:I:18:DG:H5''	1.67	0.77
5:I:43:DA:C2'	5:I:44:DC:H5''	2.15	0.76
5:J:286:DT:H2''	5:J:287:DA:H5''	1.65	0.76
5:J:239:DT:C2'	5:J:240:DG:H5''	2.15	0.76
5:I:50:DC:H2''	5:I:51:DA:C5'	2.14	0.76
4:D:118:VAL:O	4:D:122:THR:HG23	1.86	0.75
5:I:104:DT:H2''	5:I:105:DT:C5'	2.15	0.75
5:I:104:DT:C2'	5:I:105:DT:H5''	2.17	0.74
1:E:133:GLU:O	1:E:134:ARG:HB2	1.87	0.74
5:J:286:DT:H1'	5:J:287:DA:H5''	1.68	0.74
5:I:115:DA:H2''	5:I:116:DC:H5''	1.70	0.74
5:J:241:DA:H1'	5:J:242:DT:H5'	1.69	0.74
5:J:262:DC:H4'	5:J:263:DT:OP1	1.87	0.73
3:G:42:ARG:HB2	4:H:88:THR:HB	1.69	0.73
5:I:8:DT:H2''	5:I:9:DC:OP2	1.89	0.73
5:J:182:DT:H2''	5:J:183:DT:H5'	1.70	0.73
1:E:63:ARG:HB2	1:E:63:ARG:HH11	1.54	0.73
2:B:59:LYS:O	2:B:63:GLU:HG3	1.88	0.72
5:J:285:DA:C2'	5:J:286:DT:H5'	2.12	0.72
5:I:16:DC:H2''	5:I:17:DA:OP2	1.89	0.72
5:J:244:DG:H1'	5:J:245:DA:H5'	1.70	0.72
5:J:284:DG:H2''	5:J:285:DA:H8	1.54	0.72
1:E:68:GLN:HG3	1:E:89:VAL:HG11	1.72	0.72
5:J:165:DA:H2''	5:J:166:DT:H5'	1.71	0.71
5:I:34:DT:H2''	5:I:35:DA:H8	1.54	0.71
5:I:35:DA:H2''	5:I:36:DT:OP2	1.90	0.70
1:E:37:LYS:N	1:E:38:PRO:HA	2.07	0.70
5:I:3:DC:H2''	5:I:4:DA:C8	2.26	0.70
3:G:31:HIS:CD2	3:G:48:PRO:HG2	2.27	0.70
5:J:211:DT:H2''	5:J:212:DC:H5'	1.74	0.70
5:J:182:DT:H1'	5:J:183:DT:H5''	1.73	0.69
5:J:284:DG:H2''	5:J:285:DA:C8	2.26	0.69
3:C:62:ILE:HD11	3:C:83:LEU:CD2	2.23	0.69
5:J:253:DC:H3'	8:J:2008:HOH:O	1.93	0.69
5:I:134:DG:H2''	5:I:135:DG:H5'	1.75	0.69
3:C:55:LEU:O	3:C:59:THR:HG23	1.93	0.68
5:J:271:DG:H2''	5:J:272:DA:H5'	1.76	0.68
1:A:120:MET:HA	2:B:50:ILE:HD11	1.76	0.68
2:F:59:LYS:O	2:F:63:GLU:HG3	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:79:LYS:HD3	1:E:80:THR:N	2.09	0.68
5:I:106:DT:H1'	5:I:107:DC:H5"	1.76	0.67
4:H:119:THR:HG22	4:H:120:LYS:N	2.08	0.67
5:I:50:DC:C2'	5:I:51:DA:H5"	2.24	0.67
1:A:63:ARG:HH12	2:B:30:THR:CG2	2.08	0.67
5:I:52:DT:H2"	5:I:53:DC:C5'	2.23	0.66
5:J:286:DT:C1'	5:J:287:DA:H5"	2.25	0.66
4:H:37:TYR:H	4:H:63:ASN:ND2	1.90	0.66
5:I:110:DA:H2"	5:I:111:DA:OP2	1.95	0.66
5:I:55:DA:H4'	5:I:55:DA:OP1	1.96	0.66
1:E:49:ARG:HG3	1:E:49:ARG:HH11	1.61	0.66
5:J:179:DG:H2"	5:J:180:DT:OP2	1.95	0.66
2:B:92:ARG:HB3	2:B:92:ARG:NH1	2.10	0.66
5:I:54:DA:H4'	5:I:54:DA:OP1	1.95	0.66
5:J:187:DA:H2"	5:J:188:DA:O5'	1.96	0.66
5:J:205:DG:H2"	5:J:206:DC:H5'	1.77	0.66
5:I:31:DG:H2"	5:I:32:DT:C5'	2.25	0.65
5:I:26:DC:H2"	5:I:27:DA:C8	2.30	0.65
1:A:120:MET:HA	2:B:50:ILE:CD1	2.26	0.65
5:I:26:DC:H2"	5:I:27:DA:C5	2.32	0.65
5:I:115:DA:C2'	5:I:116:DC:H5"	2.27	0.65
1:A:120:MET:CA	2:B:50:ILE:HD11	2.27	0.65
3:C:102:ILE:HG23	4:D:61:ILE:HD13	1.78	0.65
5:J:241:DA:H2"	5:J:242:DT:OP2	1.94	0.65
5:I:43:DA:H2"	5:I:44:DC:C5'	2.26	0.65
5:I:26:DC:H2"	5:I:27:DA:N7	2.11	0.65
5:J:161:DG:H2"	5:J:162:DC:OP2	1.95	0.65
5:I:10:DC:H2"	5:I:11:DA:C8	2.32	0.64
5:J:205:DG:H1'	5:J:206:DC:H5"	1.79	0.64
1:E:63:ARG:CB	1:E:63:ARG:HH11	2.11	0.64
5:J:250:DT:H2"	5:J:251:DT:OP2	1.97	0.63
3:G:76:THR:O	4:H:52:THR:HG23	1.98	0.63
4:D:88:THR:HG23	5:I:39:DG:OP1	1.98	0.63
3:G:17:ARG:HH12	3:G:31:HIS:CD2	2.14	0.63
5:J:153:DA:H1'	5:J:154:DT:H5"	1.79	0.63
2:B:92:ARG:HH21	4:D:101:LEU:HD12	1.64	0.63
3:G:110:ASN:HA	8:G:2006:HOH:O	1.98	0.63
3:C:30:VAL:HG13	4:D:70:PHE:HE1	1.64	0.63
2:F:31:LYS:HB3	2:F:32:PRO:HD3	1.81	0.62
5:J:233:DG:H2"	5:J:234:DC:OP2	1.96	0.62
1:E:121:PRO:HB3	2:F:53:GLU:HG3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:34:DT:H2"	5:I:35:DA:C8	2.35	0.62
5:J:249:DG:H1'	5:J:250:DT:H5"	1.82	0.62
5:J:167:DT:H1'	5:J:168:DC:H5"	1.81	0.62
1:E:41:TYR:OH	5:I:7:DA:H5'	2.00	0.62
5:I:118:DT:H2"	5:I:119:DT:OP2	1.99	0.61
5:I:108:DC:H2"	5:I:109:DA:C8	2.35	0.61
5:I:99:DA:C2'	5:I:100:DG:H5'	2.29	0.61
5:I:137:DG:H2"	5:I:138:DG:OP2	2.00	0.61
3:C:67:GLY:HA3	4:D:49:HIS:CD2	2.36	0.61
3:C:92:GLU:HG2	4:D:103:PRO:HG2	1.82	0.61
5:J:255:DA:H2"	5:J:256:DA:OP2	2.00	0.60
3:C:87:ILE:HD12	3:C:102:ILE:HD11	1.82	0.60
5:I:17:DA:C2'	5:I:18:DG:H5"	2.29	0.60
5:J:159:DC:H1'	5:J:160:DT:H5'	1.83	0.60
5:I:129:DC:H2"	5:I:130:DT:C7	2.31	0.60
5:J:235:DC:H2"	5:J:236:DT:H71	1.81	0.60
5:J:252:DT:H2"	5:J:253:DC:O5'	2.02	0.60
1:A:49:ARG:HD2	5:J:155:DC:OP1	2.02	0.60
5:J:259:DA:H2"	5:J:260:DC:H5'	1.84	0.60
4:H:88:THR:CG2	5:J:186:DG:OP1	2.49	0.60
5:I:113:DA:H1'	5:I:114:DC:H5"	1.83	0.60
5:I:23:DT:H2"	5:I:24:DA:C5'	2.25	0.59
5:I:93:DT:H2"	5:I:94:DG:C5'	2.30	0.59
3:C:51:LEU:HD13	4:D:73:ILE:HG21	1.84	0.59
4:D:122:THR:C	4:D:124:ALA:H	2.04	0.59
5:J:239:DT:H2"	5:J:240:DG:C5'	2.28	0.59
5:I:144:DG:H1'	5:I:145:DA:H5"	1.84	0.59
4:D:42:TYR:CE2	4:D:46:LYS:HD2	2.37	0.59
5:J:242:DT:H2"	5:J:243:DG:H5'	1.84	0.59
5:J:195:DC:H1'	5:J:196:DC:C5	2.37	0.59
5:I:139:DA:H2"	5:I:140:DT:H5'	1.84	0.59
3:C:101:THR:HG21	8:F:2011:HOH:O	2.03	0.59
3:C:50:TYR:OH	4:D:95:GLN:HG3	2.02	0.59
5:I:62:DT:H2"	5:I:63:DG:H5'	1.84	0.58
5:I:46:DG:H2"	5:I:47:DC:C6	2.37	0.58
5:I:22:DC:H1'	5:I:23:DT:H5"	1.85	0.58
2:F:35:ARG:HG2	2:F:35:ARG:HH11	1.68	0.58
5:J:246:DG:H1'	5:J:247:DC:H5'	1.86	0.58
5:J:261:DA:H2"	5:J:262:DC:OP2	2.04	0.58
2:B:46:ILE:O	5:J:227:DG:H3'	2.04	0.58
3:C:31:HIS:ND1	3:C:48:PRO:HG3	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:63:DG:H2"	5:I:64:DT:OP2	2.04	0.57
5:J:164:DG:C2'	5:J:165:DA:H5"	2.32	0.57
5:J:182:DT:H2"	5:J:183:DT:C5'	2.34	0.57
5:J:236:DT:H2"	5:J:237:DT:OP2	2.04	0.57
5:J:286:DT:H2"	5:J:287:DA:C5'	2.35	0.57
5:J:264:DT:H2"	5:J:265:DT:OP2	2.04	0.57
5:I:114:DC:H2"	5:I:115:DA:C8	2.40	0.57
5:I:9:DC:H1'	5:I:10:DC:H5"	1.87	0.57
1:A:63:ARG:HH12	2:B:30:THR:HG23	1.69	0.57
5:J:234:DC:H2"	5:J:235:DC:C5	2.41	0.56
4:H:111:VAL:O	4:H:115:THR:HG23	2.06	0.56
5:J:248:DA:H2"	5:J:249:DG:C5'	2.33	0.56
4:D:37:TYR:H	4:D:63:ASN:HD21	1.52	0.56
5:I:135:DG:H2"	5:I:136:DT:H5'	1.88	0.56
5:I:122:DG:H1'	5:I:123:DT:H5"	1.86	0.56
2:F:45:ARG:CZ	5:I:80:DT:H4'	2.35	0.56
5:J:243:DG:H2"	5:J:244:DG:OP2	2.05	0.56
4:D:80:LEU:HD21	4:D:96:THR:CG2	2.36	0.56
5:I:24:DA:H2"	5:I:25:DC:C6	2.41	0.56
3:C:35:ARG:HD3	8:J:2011:HOH:O	2.05	0.56
3:C:15:LYS:HB2	3:C:20:ARG:HH12	1.70	0.56
5:J:230:DC:H2"	5:J:231:DA:C8	2.41	0.56
1:A:65:LEU:HB3	1:A:66:PRO:HD3	1.87	0.55
5:I:142:DT:C2'	5:I:143:DT:H5'	2.33	0.55
5:I:129:DC:H2"	5:I:130:DT:H73	1.87	0.55
5:I:63:DG:H1'	5:I:64:DT:H5'	1.88	0.55
5:I:51:DA:C2'	5:I:52:DT:H5'	2.28	0.55
2:F:77:GLN:HG2	8:F:2022:HOH:O	2.06	0.55
5:I:77:DA:C2	5:J:217:DG:N2	2.75	0.55
1:E:60:LEU:HD12	1:E:64:LYS:HE3	1.88	0.55
1:A:39:HIS:ND1	1:A:39:HIS:C	2.60	0.55
5:I:43:DA:H1'	5:I:44:DC:H5"	1.88	0.55
5:J:241:DA:H1'	5:J:242:DT:C5'	2.36	0.55
1:A:96:CYS:SG	2:B:58:LEU:HD21	2.47	0.55
5:I:31:DG:H1'	5:I:32:DT:H5"	1.89	0.54
2:F:35:ARG:O	2:F:39:ARG:HG2	2.08	0.54
4:D:31:ARG:HG3	4:D:31:ARG:O	2.06	0.54
5:I:73:DA:H2"	5:I:74:DT:H5'	1.87	0.54
5:J:154:DT:H5'	5:J:154:DT:H6	1.72	0.54
5:I:92:DT:H1'	5:I:93:DT:H5"	1.89	0.54
2:B:32:PRO:HA	2:B:35:ARG:HG3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:51:ASP:HB3	8:H:209:HOH:O	2.06	0.54
4:D:88:THR:CG2	5:I:39:DG:OP1	2.55	0.54
5:J:201:DA:H2''	5:J:202:DA:OP2	2.08	0.54
5:J:229:DA:H2''	5:J:230:DC:H5'	1.89	0.54
3:G:73:ASN:HB2	8:G:2007:HOH:O	2.08	0.54
1:E:63:ARG:HH11	1:E:63:ARG:H	1.54	0.54
1:E:63:ARG:NH2	2:F:30:THR:H	2.06	0.54
5:I:58:DG:H2'	5:I:59:DG:C8	2.43	0.54
5:I:88:DC:H2''	5:I:89:DC:C6	2.42	0.54
5:I:96:DT:H2''	5:I:97:DG:OP2	2.09	0.54
4:D:79:ARG:HG2	4:D:83:TYR:CZ	2.42	0.54
3:G:92:GLU:HB3	4:H:106:LEU:HD22	1.90	0.53
5:I:37:DT:H2''	5:I:38:DT:OP2	2.07	0.53
5:I:49:DC:H2''	5:I:50:DC:OP2	2.07	0.53
5:J:181:DA:H1'	5:J:182:DT:C5'	2.35	0.53
1:A:49:ARG:HD2	5:J:155:DC:P	2.49	0.53
5:I:50:DC:H2''	5:I:51:DA:H5'	1.88	0.53
5:J:179:DG:H1'	5:J:180:DT:H5''	1.90	0.53
1:E:65:LEU:HB3	1:E:66:PRO:HD3	1.90	0.53
5:J:154:DT:H2''	5:J:155:DC:O5'	2.08	0.53
5:I:128:DT:H2''	5:I:129:DC:C6	2.44	0.53
1:A:51:ILE:HD12	2:B:42:GLY:HA2	1.91	0.53
1:E:122:LYS:HB3	6:E:1002:CL:CL	2.46	0.53
3:G:45:ALA:O	3:G:48:PRO:HD2	2.09	0.52
2:F:23:ARG:HD3	8:F:2020:HOH:O	2.09	0.52
5:I:138:DG:H2''	5:I:139:DA:OP2	2.08	0.52
5:I:63:DG:H1'	5:I:64:DT:C5'	2.39	0.52
3:C:87:ILE:HD12	3:C:102:ILE:CD1	2.40	0.52
5:J:259:DA:H2''	5:J:260:DC:C5'	2.39	0.52
5:J:177:DG:H1'	5:J:178:DT:H5''	1.90	0.52
5:J:182:DT:H6	5:J:182:DT:H5'	1.74	0.52
5:J:197:DA:H2''	5:J:198:DT:H5'	1.90	0.52
5:I:141:DA:H1'	5:I:142:DT:H5''	1.92	0.52
5:I:58:DG:C2'	5:I:59:DG:C8	2.93	0.52
5:J:183:DT:H2'	5:J:184:DT:H71	1.92	0.52
1:A:63:ARG:HH12	2:B:30:THR:HG21	1.75	0.52
1:E:129:ARG:HD3	1:E:135:ALA:HA	1.91	0.52
3:C:26:PRO:HD3	4:D:40:TYR:CD1	2.44	0.52
5:I:28:DA:H1'	5:I:29:DA:C8	2.45	0.51
3:G:81:ARG:HD3	3:G:81:ARG:O	2.10	0.51
3:C:42:ARG:NH1	5:I:38:DT:H4'	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:87:ILE:HD13	3:C:97:LEU:CD1	2.40	0.51
3:C:31:HIS:CD2	3:C:35:ARG:HH11	2.28	0.51
2:B:26:ILE:CG1	2:B:55:ARG:HB3	2.41	0.51
5:I:103:DG:H1'	5:I:104:DT:H5''	1.92	0.51
1:A:73:GLU:OE2	2:B:25:ASN:HB2	2.11	0.51
5:J:172:DC:C2'	5:J:173:DA:H5''	2.38	0.51
2:F:30:THR:OG1	2:F:32:PRO:HD2	2.10	0.51
1:A:63:ARG:HH21	5:J:237:DT:H5''	1.76	0.51
1:A:83:ARG:O	2:B:80:THR:HA	2.11	0.51
5:I:5:DA:H1'	5:I:6:DT:H5''	1.92	0.51
5:J:242:DT:H1'	5:J:243:DG:C5'	2.41	0.51
5:J:153:DA:H1'	5:J:154:DT:C5'	2.40	0.51
5:I:1:DA:H1'	5:I:2:DT:C6	2.46	0.51
1:E:63:ARG:NH2	2:F:30:THR:HG23	2.26	0.51
2:F:20:LYS:HG2	2:F:21:VAL:N	2.26	0.51
5:J:287:DA:H1'	5:J:288:DT:H5'	1.94	0.50
2:F:30:THR:CB	2:F:32:PRO:HD2	2.41	0.50
1:A:76:GLN:HA	1:A:76:GLN:NE2	2.26	0.50
5:J:279:DA:H1'	5:J:280:DG:H5'	1.93	0.50
4:H:80:LEU:HD11	4:H:96:THR:HG22	1.93	0.50
5:I:119:DT:H2''	5:I:120:DT:OP2	2.10	0.50
5:I:86:DT:H2''	5:I:87:DG:C8	2.47	0.50
5:J:241:DA:C1'	5:J:242:DT:H5'	2.40	0.50
5:J:245:DA:H2''	5:J:246:DG:OP2	2.12	0.50
5:J:170:DA:H1'	5:J:171:DC:H5''	1.92	0.50
4:D:33:ARG:HD2	5:J:269:DT:H4'	1.93	0.50
3:C:87:ILE:HD13	3:C:97:LEU:HD12	1.92	0.50
5:J:260:DC:H2''	5:J:261:DA:C8	2.47	0.50
5:J:179:DG:H1'	5:J:180:DT:C5'	2.42	0.50
5:I:73:DA:H1'	5:I:74:DT:H5''	1.93	0.50
4:D:84:ASN:O	4:D:86:ARG:HG3	2.12	0.50
5:J:266:DT:H2''	5:J:267:DG:C5	2.47	0.49
4:D:53:GLY:HA3	8:I:2007:HOH:O	2.12	0.49
5:I:43:DA:C1'	5:I:44:DC:H5''	2.41	0.49
4:H:119:THR:CG2	4:H:120:LYS:N	2.76	0.49
5:I:9:DC:H2''	5:I:10:DC:H5'	1.94	0.49
5:I:115:DA:H2''	5:I:116:DC:C5'	2.41	0.49
3:G:81:ARG:NH2	3:G:107:VAL:O	2.45	0.49
5:I:100:DG:H1'	5:I:101:DC:C6	2.48	0.49
5:I:48:DT:H1'	5:I:49:DC:C6	2.48	0.49
5:I:41:DA:H2''	5:I:42:DA:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:153:DA:H2''	5:J:154:DT:OP2	2.13	0.49
5:J:227:DG:H2''	5:J:228:DA:OP2	2.12	0.49
5:I:143:DT:H2''	5:I:144:DG:C8	2.48	0.49
2:B:92:ARG:HB3	2:B:92:ARG:CZ	2.42	0.49
5:I:29:DA:H2''	5:I:30:DA:H8	1.76	0.49
1:A:96:CYS:SG	2:B:58:LEU:CD2	3.01	0.49
5:J:190:DC:H5'	8:J:2012:HOH:O	2.12	0.49
3:C:26:PRO:HD3	4:D:40:TYR:CG	2.48	0.49
5:I:99:DA:H1'	5:I:100:DG:C5'	2.42	0.49
1:E:133:GLU:O	1:E:134:ARG:CB	2.55	0.48
1:E:37:LYS:N	1:E:38:PRO:CA	2.75	0.48
5:I:5:DA:C2'	5:I:6:DT:H5''	2.43	0.48
5:J:181:DA:H2''	5:J:182:DT:OP2	2.13	0.48
3:C:15:LYS:HB2	3:C:20:ARG:NH1	2.27	0.48
3:C:29:ARG:HD2	3:C:32:ARG:HH22	1.78	0.48
1:E:49:ARG:HG3	1:E:49:ARG:NH1	2.28	0.48
2:B:58:LEU:O	2:B:58:LEU:HD22	2.13	0.48
4:D:31:ARG:HH11	4:D:31:ARG:HG2	1.78	0.48
3:C:58:LEU:O	3:C:62:ILE:HG23	2.14	0.48
4:D:69:ILE:HG22	4:D:73:ILE:HD12	1.96	0.48
5:I:35:DA:H1'	5:I:36:DT:H5'	1.94	0.48
5:J:182:DT:H1'	5:J:183:DT:C5'	2.42	0.48
1:E:37:LYS:HB2	1:E:38:PRO:O	2.13	0.48
1:E:37:LYS:N	1:E:37:LYS:HD3	2.27	0.48
5:J:200:DA:H1'	5:J:201:DA:H5'	1.96	0.48
5:J:242:DT:H1'	5:J:243:DG:H5''	1.96	0.48
5:I:26:DC:H4'	5:I:26:DC:OP1	2.13	0.48
5:I:57:DA:H2''	5:I:58:DG:C8	2.49	0.47
1:A:68:GLN:HE21	1:A:89:VAL:HG21	1.79	0.47
5:I:5:DA:H2''	5:I:6:DT:C5'	2.45	0.47
5:I:52:DT:C1'	5:I:53:DC:H5''	2.44	0.47
3:C:62:ILE:HD12	3:C:62:ILE:O	2.14	0.47
3:G:79:ILE:HG12	3:G:82:HIS:CE1	2.49	0.47
5:J:226:DT:H2''	5:J:227:DG:C8	2.50	0.47
5:I:14:DT:H4'	5:I:15:DG:H5'	1.96	0.47
5:J:158:DC:H1'	5:J:159:DC:H5''	1.97	0.47
3:C:42:ARG:HB2	4:D:88:THR:HB	1.96	0.47
5:J:258:DT:H2''	5:J:259:DA:C8	2.50	0.47
1:E:49:ARG:HD3	5:I:8:DT:OP1	2.15	0.46
5:J:265:DT:H2''	5:J:266:DT:O5'	2.15	0.46
5:J:166:DT:H2'	5:J:167:DT:H71	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:27:DA:C6	5:I:28:DA:C6	3.03	0.46
3:G:24:GLN:HG3	4:H:47:GLN:OE1	2.15	0.46
5:J:220:DT:H1'	5:J:221:DT:H5''	1.96	0.46
5:I:115:DA:H1'	5:I:116:DC:H5''	1.97	0.46
5:J:281:DG:C2'	5:J:282:DT:H5'	2.37	0.46
3:C:115:LEU:CD2	1:E:117:VAL:HG22	2.45	0.46
5:I:133:DA:H1'	5:I:134:DG:H5''	1.98	0.46
5:I:90:DT:H2''	5:I:91:DT:H5'	1.98	0.46
3:G:92:GLU:OE1	4:H:105:GLU:HB2	2.14	0.46
1:A:53:ARG:HG2	8:A:2019:HOH:O	2.15	0.46
5:I:52:DT:H1'	5:I:53:DC:H5''	1.97	0.46
5:J:182:DT:C1'	5:J:183:DT:H5''	2.43	0.46
5:I:46:DG:H2''	5:I:47:DC:C5	2.50	0.46
2:F:45:ARG:NH2	5:I:80:DT:H4'	2.31	0.46
2:B:52:GLU:OE2	2:B:55:ARG:NH1	2.49	0.46
1:A:128:ARG:NH1	8:A:2021:HOH:O	2.50	0.46
5:J:280:DG:H1'	5:J:281:DG:H5''	1.99	0.45
5:J:281:DG:H2''	5:J:282:DT:C5'	2.38	0.45
1:A:51:ILE:O	1:A:55:GLN:HG3	2.16	0.45
5:I:101:DC:H2''	5:I:102:DA:O4'	2.16	0.45
4:D:122:THR:C	4:D:124:ALA:N	2.69	0.45
3:C:15:LYS:CB	3:C:20:ARG:NH1	2.79	0.45
1:E:46:VAL:HG21	5:I:82:DA:H3'	1.97	0.45
1:A:122:LYS:HG2	1:E:113:HIS:HE1	1.81	0.45
8:A:2020:HOH:O	3:G:111:ILE:HD12	2.16	0.45
5:I:40:DG:H2''	5:I:41:DA:H5'	1.97	0.45
5:J:176:DA:H2''	5:J:177:DG:OP2	2.17	0.45
5:I:20:DT:H2''	5:I:21:DT:OP2	2.16	0.45
4:D:31:ARG:CG	4:D:31:ARG:O	2.64	0.45
5:J:224:DG:C2'	5:J:225:DC:H5''	2.47	0.45
2:F:20:LYS:HG2	2:F:21:VAL:H	1.81	0.45
2:F:30:THR:HB	2:F:32:PRO:HD2	1.99	0.45
5:I:15:DG:H2''	5:I:16:DC:OP2	2.16	0.45
2:F:18:HIS:N	2:F:18:HIS:ND1	2.64	0.45
5:I:125:DG:H2''	5:I:126:DA:O5'	2.17	0.45
3:G:18:SER:O	3:G:22:GLY:N	2.50	0.45
3:G:44:GLY:HA3	6:G:1001:CL:CL	2.54	0.45
5:I:131:DG:H2''	5:I:132:DC:C4	2.48	0.44
5:I:116:DC:H2'	5:I:117:DT:H71	1.99	0.44
1:E:134:ARG:HE	1:E:134:ARG:HB3	1.47	0.44
5:J:210:DT:H2''	5:J:211:DT:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:123:DT:H6	5:I:123:DT:H2'	1.67	0.44
5:I:58:DG:H2''	5:I:59:DG:C8	2.52	0.44
3:G:79:ILE:HB	3:G:80:PRO:CD	2.47	0.44
5:I:8:DT:H1'	5:I:9:DC:H5'	1.99	0.44
5:J:271:DG:OP1	5:J:271:DG:H4'	2.18	0.44
5:J:221:DT:H1'	5:J:222:DC:H5'	2.00	0.44
3:G:85:LEU:O	3:G:89:ASN:HB2	2.18	0.44
5:I:6:DT:H2''	5:I:7:DA:C8	2.53	0.44
5:I:95:DA:H2''	5:I:96:DT:OP2	2.17	0.44
1:E:122:LYS:HE2	8:E:2030:HOH:O	2.17	0.44
8:B:2004:HOH:O	3:G:101:THR:HG21	2.17	0.44
5:J:282:DT:H2''	5:J:283:DG:C8	2.52	0.44
2:F:38:ALA:HB1	2:F:43:VAL:HB	2.00	0.44
5:J:235:DC:H2''	5:J:236:DT:C5	2.52	0.44
5:J:210:DT:H2'	5:J:211:DT:H71	1.99	0.44
5:I:106:DT:H2''	5:I:107:DC:H5'	2.00	0.44
5:J:225:DC:H2''	5:J:226:DT:C6	2.52	0.44
5:J:273:DA:H2''	5:J:274:DT:OP2	2.18	0.43
5:J:282:DT:H6	5:J:282:DT:H2'	1.70	0.43
3:C:84:GLN:HG3	3:C:105:GLY:HA3	2.00	0.43
5:J:263:DT:H1'	5:J:264:DT:H5'	1.99	0.43
1:A:76:GLN:HA	1:A:76:GLN:HE21	1.81	0.43
1:E:124:ILE:O	1:E:128:ARG:HG3	2.19	0.43
5:I:99:DA:H1'	5:I:100:DG:H5'	2.00	0.43
5:J:151:DA:H2''	5:J:152:DT:OP2	2.17	0.43
5:I:36:DT:C2'	5:I:37:DT:H71	2.47	0.43
5:I:54:DA:C4'	5:I:54:DA:OP1	2.64	0.43
3:G:73:ASN:O	3:G:74:LYS:HB2	2.18	0.43
5:I:136:DT:H2'	5:I:136:DT:H6	1.69	0.43
1:A:122:LYS:HG2	1:E:113:HIS:CE1	2.54	0.43
5:J:205:DG:H1'	5:J:206:DC:C5'	2.48	0.43
4:D:34:LYS:HG2	5:J:270:DA:OP1	2.18	0.43
2:F:21:VAL:HG12	2:F:23:ARG:HG3	2.01	0.43
1:A:117:VAL:HG12	1:A:117:VAL:O	2.19	0.43
1:E:87:SER:HB3	2:F:83:ALA:HB2	1.99	0.43
3:C:37:GLY:HA3	3:C:39:TYR:CE2	2.54	0.43
4:H:123:SER:O	4:H:124:ALA:C	2.57	0.43
5:I:5:DA:H2''	5:I:6:DT:H5''	1.99	0.43
5:J:224:DG:H2''	5:J:225:DC:H5''	2.01	0.43
1:E:119:ILE:HG13	2:F:50:ILE:HG13	2.01	0.43
5:J:287:DA:H2'	5:J:288:DT:H72	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:49:HIS:HB3	4:H:52:THR:OG1	2.19	0.43
2:B:35:ARG:O	2:B:39:ARG:HG2	2.19	0.43
5:J:197:DA:H1'	5:J:198:DT:C5'	2.49	0.43
5:J:188:DA:H2''	5:J:189:DA:O5'	2.19	0.42
5:I:111:DA:C8	5:I:112:DT:H72	2.54	0.42
2:B:78:ARG:CD	5:J:248:DA:H5'	2.49	0.42
5:I:47:DC:N4	5:J:245:DA:N6	2.67	0.42
3:C:84:GLN:HE22	3:C:88:ARG:NE	2.04	0.42
5:I:17:DA:H1'	5:I:18:DG:H5''	2.01	0.42
1:E:134:ARG:O	1:E:134:ARG:NE	2.52	0.42
1:E:118:THR:HA	2:F:45:ARG:HB3	2.01	0.42
5:J:165:DA:H2'	5:J:166:DT:H72	2.00	0.42
5:I:18:DG:H2''	5:I:19:DA:C8	2.54	0.42
4:H:102:LEU:HA	4:H:103:PRO:HD3	1.90	0.42
2:B:98:TYR:CD1	4:H:64:SER:HB3	2.53	0.42
4:D:80:LEU:HD21	4:D:96:THR:HG21	2.00	0.42
5:I:58:DG:H8	5:I:58:DG:H5''	1.83	0.42
5:I:102:DA:H2''	5:I:103:DG:C8	2.55	0.42
5:J:189:DA:C2'	5:J:190:DC:O5'	2.61	0.42
5:J:197:DA:H1'	5:J:198:DT:H5''	2.01	0.42
4:H:33:ARG:HH11	4:H:33:ARG:HB3	1.84	0.42
5:J:173:DA:H2''	5:J:174:DA:C8	2.55	0.42
4:D:42:TYR:O	4:D:46:LYS:HG2	2.20	0.42
2:F:36:ARG:O	2:F:39:ARG:HB2	2.20	0.42
3:C:38:ASN:HA	8:C:2013:HOH:O	2.20	0.42
5:I:91:DT:H1'	5:I:92:DT:H5'	2.02	0.42
5:J:249:DG:H2''	5:J:250:DT:H5'	2.02	0.42
5:I:34:DT:C2'	5:I:35:DA:C8	3.01	0.42
5:J:182:DT:C2'	5:J:183:DT:C5'	2.97	0.42
5:I:29:DA:H2''	5:I:30:DA:C8	2.54	0.42
3:G:81:ARG:HD3	3:G:81:ARG:C	2.40	0.42
5:J:274:DT:H2''	5:J:275:DC:OP2	2.20	0.42
5:J:288:DT:H1'	5:J:289:DT:H5'	2.00	0.41
3:G:17:ARG:HG2	4:H:121:TYR:HE1	1.85	0.41
3:C:35:ARG:CD	8:J:2011:HOH:O	2.65	0.41
4:H:46:LYS:HA	4:H:46:LYS:HD3	1.82	0.41
5:I:40:DG:H1'	5:I:41:DA:H5''	2.02	0.41
5:I:117:DT:H2''	5:I:118:DT:OP2	2.19	0.41
5:J:268:DG:H2''	5:J:269:DT:C6	2.56	0.41
4:D:86:ARG:NH1	8:D:210:HOH:O	2.50	0.41
5:I:7:DA:C2	5:J:287:DA:C2	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:166:DT:C2'	5:J:167:DT:H71	2.51	0.41
5:I:109:DA:H2''	5:I:110:DA:OP2	2.20	0.41
2:B:75:HIS:C	2:B:77:GLN:H	2.22	0.41
1:E:63:ARG:HE	5:J:207:DA:H5''	1.84	0.41
5:I:26:DC:C2'	5:I:27:DA:N7	2.81	0.41
2:B:58:LEU:C	2:B:58:LEU:HD22	2.40	0.41
2:F:75:HIS:HD2	4:H:96:THR:OG1	2.04	0.41
5:J:183:DT:H5'	5:J:183:DT:H6	1.86	0.41
3:G:44:GLY:O	3:G:48:PRO:HD3	2.21	0.41
3:C:31:HIS:CD2	3:C:35:ARG:NH1	2.89	0.41
3:C:13:LYS:HD3	3:C:15:LYS:NZ	2.36	0.41
3:C:81:ARG:NH2	3:C:107:VAL:O	2.39	0.41
5:J:210:DT:C2'	5:J:211:DT:H71	2.51	0.41
2:B:26:ILE:HG13	2:B:55:ARG:HD3	2.03	0.41
1:E:131:ARG:HD3	1:E:133:GLU:OE2	2.20	0.41
5:J:159:DC:H2''	5:J:160:DT:O5'	2.20	0.41
3:C:26:PRO:HB2	3:C:29:ARG:HB3	2.03	0.41
5:I:7:DA:H2''	5:I:8:DT:OP2	2.21	0.41
4:D:32:SER:HB2	5:I:103:DG:OP1	2.21	0.41
5:I:120:DT:H2''	5:I:121:DG:C8	2.56	0.41
4:H:87:SER:OG	5:J:185:DG:H3'	2.20	0.41
5:J:242:DT:H1'	5:J:243:DG:H5'	2.03	0.41
3:G:112:GLN:HG2	8:G:2002:HOH:O	2.21	0.41
5:J:184:DT:O3'	5:J:185:DG:C8	2.74	0.41
3:C:84:GLN:HE21	3:C:102:ILE:HD12	1.86	0.41
5:J:190:DC:C5'	8:J:2012:HOH:O	2.69	0.40
2:B:45:ARG:CZ	5:J:227:DG:H4'	2.50	0.40
1:A:134:ARG:HD2	8:A:2021:HOH:O	2.20	0.40
5:I:99:DA:H1'	5:I:100:DG:H5''	2.02	0.40
5:I:31:DG:C2'	5:I:32:DT:C5'	2.97	0.40
5:J:231:DA:H2''	5:J:232:DT:OP2	2.22	0.40
5:I:84:DC:H2''	5:I:85:DA:C8	2.56	0.40
4:H:37:TYR:N	4:H:63:ASN:HD21	2.03	0.40
5:I:113:DA:C2	5:J:181:DA:C2	3.10	0.40
5:J:195:DC:H1'	5:J:196:DC:C6	2.57	0.40
5:J:280:DG:H1'	5:J:281:DG:C5'	2.51	0.40
5:I:14:DT:H1'	5:I:15:DG:C5	2.57	0.40
5:I:59:DG:H2''	5:I:60:DC:OP2	2.20	0.40
2:B:72:TYR:OH	2:B:92:ARG:HD2	2.21	0.40
5:J:154:DT:C6	5:J:154:DT:H5'	2.54	0.40
5:J:225:DC:H2''	5:J:226:DT:C5	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:82:DA:C6	5:I:83:DA:C6	3.09	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	95/139 (68%)	93 (98%)	2 (2%)	0	100	100
1	E	97/139 (70%)	94 (97%)	2 (2%)	1 (1%)	19	45
2	B	76/106 (72%)	74 (97%)	2 (3%)	0	100	100
2	F	84/106 (79%)	82 (98%)	2 (2%)	0	100	100
3	C	106/133 (80%)	101 (95%)	5 (5%)	0	100	100
3	G	103/133 (77%)	97 (94%)	6 (6%)	0	100	100
4	D	92/129 (71%)	88 (96%)	2 (2%)	2 (2%)	8	22
4	H	91/129 (70%)	89 (98%)	0	2 (2%)	8	22
All	All	744/1014 (73%)	718 (96%)	21 (3%)	5 (1%)	26	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	134	ARG
4	D	32	SER
4	D	104	GLY
4	H	104	GLY
4	H	123	SER

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	85/113 (75%)	82 (96%)	3 (4%)	43	74
1	E	86/113 (76%)	80 (93%)	6 (7%)	19	42
2	B	63/81 (78%)	61 (97%)	2 (3%)	46	77
2	F	71/81 (88%)	70 (99%)	1 (1%)	74	92
3	C	85/102 (83%)	77 (91%)	8 (9%)	11	25
3	G	83/102 (81%)	79 (95%)	4 (5%)	31	62
4	D	80/107 (75%)	79 (99%)	1 (1%)	76	92
4	H	79/107 (74%)	74 (94%)	5 (6%)	22	48
All	All	632/806 (78%)	602 (95%)	30 (5%)	32	63

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	HIS
1	A	59	GLU
1	A	129	ARG
2	B	50	ILE
2	B	58	LEU
3	C	29	ARG
3	C	42	ARG
3	C	59	THR
3	C	62	ILE
3	C	71	ARG
3	C	81	ARG
3	C	99	ARG
3	C	101	THR
4	D	88	THR
1	E	37	LYS
1	E	63	ARG
1	E	64	LYS
1	E	117	VAL
1	E	122	LYS

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Mol	Chain	Res	Type
1	E	134	ARG
2	F	18	HIS
3	G	73	ASN
3	G	81	ARG
3	G	101	THR
3	G	118	LYS
4	H	36	SER
4	H	88	THR
4	H	106	LEU
4	H	109	HIS
4	H	119	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	76	GLN
1	A	108	ASN
2	B	64	ASN
2	B	75	HIS
3	C	24	GLN
3	C	84	GLN
4	D	63	ASN
1	E	68	GLN
1	E	76	GLN
2	F	75	HIS
3	G	31	HIS
3	G	73	ASN
4	H	63	ASN
4	H	95	GLN

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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 [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	97/139 (69%)	-0.04	0 100 100	32, 45, 73, 103	0
1	E	99/139 (71%)	0.05	2 (2%) 68 69	27, 38, 68, 106	0
2	B	78/106 (73%)	-0.04	1 (1%) 79 79	31, 44, 65, 89	0
2	F	86/106 (81%)	0.10	4 (4%) 35 34	24, 38, 65, 112	0
3	C	108/133 (81%)	0.08	4 (3%) 45 45	25, 43, 77, 137	0
3	G	105/133 (78%)	-0.07	2 (1%) 70 70	31, 48, 78, 99	0
4	D	94/129 (72%)	0.12	2 (2%) 67 68	29, 45, 76, 110	0
4	H	93/129 (72%)	0.04	0 100 100	31, 47, 85, 106	0
5	I	145/146 (99%)	0.29	7 (4%) 34 33	48, 98, 143, 163	0
5	J	145/146 (99%)	0.29	5 (3%) 49 49	51, 102, 149, 156	0
All	All	1050/1306 (80%)	0.10	27 (2%) 59 59	24, 50, 130, 163	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	11	ARG	9.1
2	F	102	GLY	7.3
3	C	12	ALA	6.9
1	E	37	LYS	4.6
3	C	13	LYS	4.3
5	I	55	DA	3.9
1	E	135	ALA	3.7
5	J	263	DT	2.8
5	J	162	DC	2.8
5	I	106	DT	2.8
5	I	56	DA	2.8
2	B	102	GLY	2.6
5	J	148	DT	2.6

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Mol	Chain	Res	Type	RSRZ
5	I	44	DC	2.5
3	G	14	ALA	2.5
3	G	118	LYS	2.5
2	F	18	HIS	2.5
5	I	42	DA	2.5
4	D	32	SER	2.5
3	C	118	LYS	2.4
2	F	17	ARG	2.3
4	D	124	ALA	2.3
5	I	33	DG	2.3
5	I	104	DT	2.2
5	J	262	DC	2.1
5	J	233	DG	2.1
2	F	101	GLY	2.0

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

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
7	MN	E	1001	1/1	0.99	0.26	4.42	39,39,39,39	0
7	MN	I	1004	1/1	0.88	0.20	2.58	96,96,96,96	0
6	CL	G	1001	1/1	0.96	0.19	1.06	54,54,54,54	0
6	CL	C	1001	1/1	0.97	0.10	-3.03	51,51,51,51	0
7	MN	I	1005	1/1	0.74	0.07	-	112,112,112,112	0
6	CL	A	1001	1/1	0.96	0.10	-	63,63,63,63	0
6	CL	E	1002	1/1	0.98	0.15	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	MN	I	1006	1/1	0.63	0.22	-	128,128,128,128	0
7	MN	J	1001	1/1	0.94	0.12	-	101,101,101,101	0
7	MN	I	1001	1/1	0.43	0.22	-	131,131,131,131	0
7	MN	I	1002	1/1	0.79	0.15	-	133,133,133,133	0
7	MN	J	1004	1/1	0.89	0.19	-	77,77,77,77	0
7	MN	J	1003	1/1	0.97	0.09	-	78,78,78,78	0
7	MN	I	1003	1/1	0.92	0.27	-	90,90,90,90	0
7	MN	J	1002	1/1	0.90	0.15	-	92,92,92,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.