Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 06:02 PM EDT

PDB ID	:	3X1T
Title	:	Crystal structure of nucleosome core particle consisting of mouse testis specific histone variants H2aa and H2ba
Authors	:	Sivaraman, P.; Kumarevel, T.S.
Deposited on	:	2014-11-27
Resolution	:	2.81 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 (i) 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 (1)) were used in the production of this report:

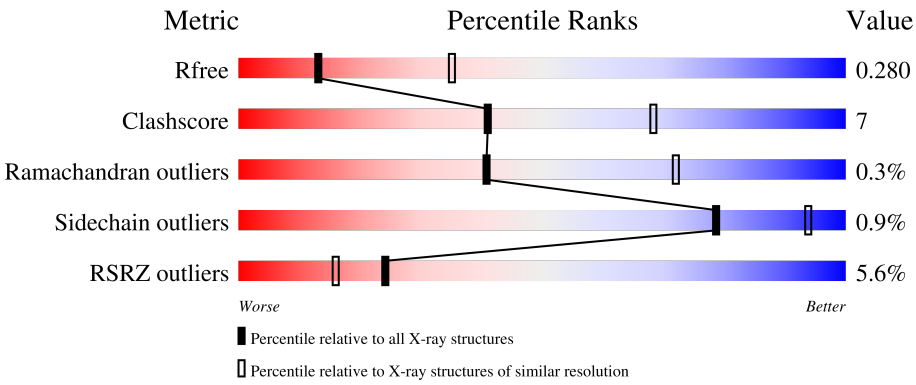
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.81 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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	I	146	18%, 47%, 53%
1	J	146	18%, 58%, 42%
2	A	135	%, 61%, 11%, 27%
2	E	135	%, 62%, 10%, 27%
3	B	102	73%, 7%, 21%

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Mol	Chain	Length	Quality of chain
3	F	102	% 80% 5% 15%
4	C	128	74% 8% 18%
4	G	128	% 73% 9% • 17%
5	D	126	66% 7% • 26%
5	H	126	64% 10% 26%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 12181 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 DNA (146-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	I	146	2990	1431	540	874	145	0	0	0
1	J	146	2990	1431	540	874	145	0	0	0

- Molecule 2 is a protein called Histone H3.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	98	807	508	156	139	4	0	0	0
2	E	98	807	508	156	139	4	0	0	0

- Molecule 3 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	B	81	646	407	126	112	1	0	0	0
3	F	87	703	442	142	118	1	0	0	0

- Molecule 4 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	C	105	809	509	159	141	0	0	0
4	G	106	818	515	161	142	0	0	0

- Molecule 5 is a protein called Histone H2B type 1-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	D	93	734	462	130	140	2	0	0	0
5	H	93	734	462	130	140	2	0	0	0

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
6	I	11	11	11	0	0
6	J	7	7	7	0	0
6	A	1	1	1	0	0
6	D	2	2	2	0	0
6	G	1	1	1	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
7	J	5	5	5	0	0
7	B	1	1	1	0	0
7	D	2	2	2	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	I	23	23	23	0	0
8	J	8	8	8	0	0
8	A	7	7	7	0	0
8	B	5	5	5	0	0
8	C	8	8	8	0	0

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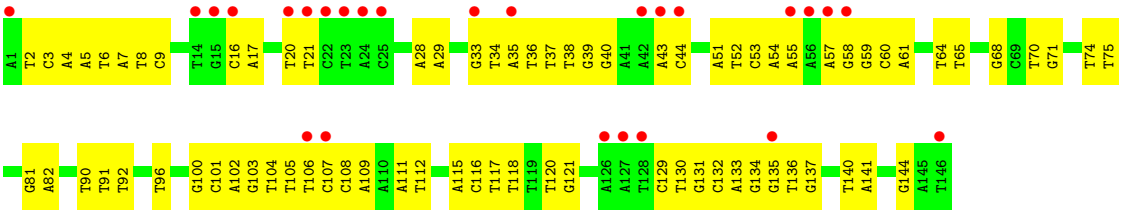
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	D	4	4	4	0	0
			Total	O		
8	E	19	19	19	0	0
			Total	O		
8	F	14	14	14	0	0
			Total	O		
8	G	19	19	19	0	0
			Total	O		
8	H	6	6	6	0	0

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

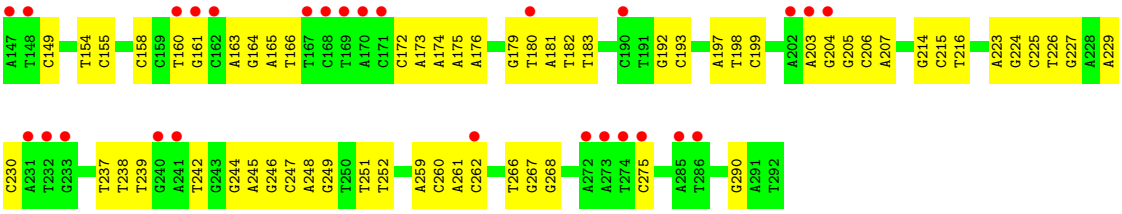
• Molecule 1: DNA (146-MER)

Chain I:



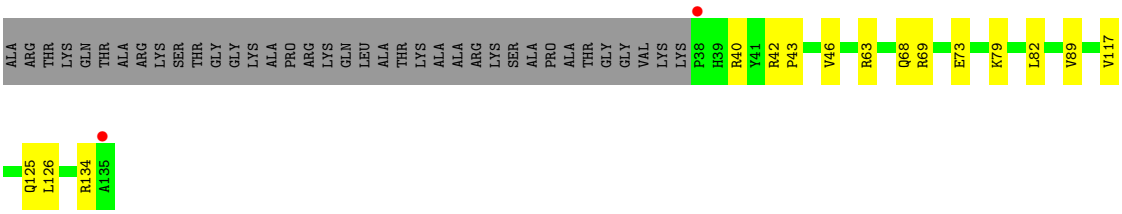
• Molecule 1: DNA (146-MER)

Chain J:



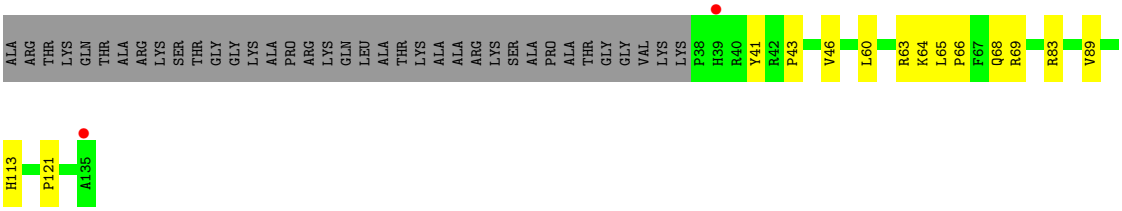
• Molecule 2: Histone H3.1

Chain A:



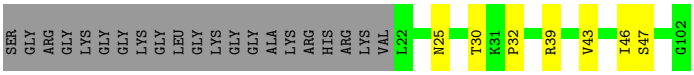
• Molecule 2: Histone H3.1

Chain E:



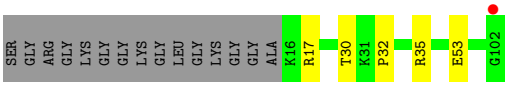
- Molecule 3: Histone H4

Chain B:



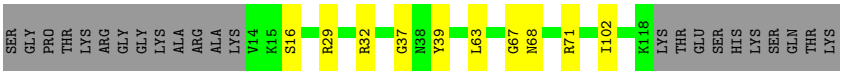
- Molecule 3: Histone H4

Chain F:



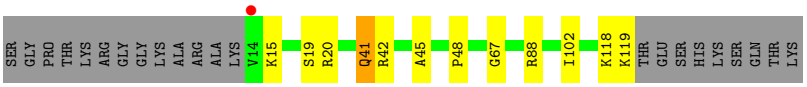
- Molecule 4: Histone H2A

Chain C:



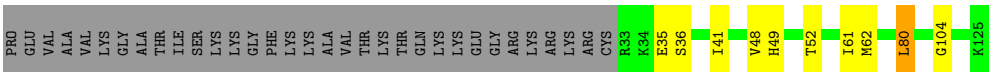
- Molecule 4: Histone H2A

Chain G:



- Molecule 5: Histone H2B type 1-A

Chain D:



- Molecule 5: Histone H2B type 1-A

Chain H:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	105.77Å 109.60Å 181.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.96 – 2.81 38.05 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.2 (34.96-2.81) 99.2 (38.05-2.81)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.43 (at 2.81Å)	Xtriage
Refinement program	REFMAC, PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.209 , 0.266 0.228 , 0.280	Depositor DCC
R_{free} test set	2629 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	55.7	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 51.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.029 for k,h,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	12181	wwPDB-VP
Average B, all atoms (Å^2)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	I	0.51	0/3354	0.91	0/5175
1	J	0.49	0/3354	0.91	0/5175
2	A	0.31	0/819	0.46	0/1097
2	E	0.32	0/819	0.45	0/1097
3	B	0.27	0/653	0.47	0/873
3	F	0.30	0/711	0.46	0/948
4	C	0.28	0/819	0.43	0/1107
4	G	0.29	0/828	0.45	0/1118
5	D	0.30	0/745	0.46	0/1000
5	H	0.32	0/745	0.50	0/1000
All	All	0.42	0/12847	0.75	0/18590

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	2990	0	1652	62	0
1	J	2990	0	1652	53	0
2	A	807	0	844	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	807	0	844	11	0
3	B	646	0	687	4	0
3	F	703	0	755	5	0
4	C	809	0	861	9	0
4	G	818	0	874	9	0
5	D	734	0	760	8	0
5	H	734	0	760	11	0
6	A	1	0	0	0	0
6	D	2	0	0	0	0
6	G	1	0	0	0	0
6	I	11	0	0	0	0
6	J	7	0	0	0	0
7	B	1	0	0	0	0
7	D	2	0	0	0	0
7	J	5	0	0	1	0
8	A	7	0	0	0	0
8	B	5	0	0	0	0
8	C	8	0	0	0	0
8	D	4	0	0	0	0
8	E	19	0	0	0	0
8	F	14	0	0	0	0
8	G	19	0	0	0	0
8	H	6	0	0	2	0
8	I	23	0	0	0	0
8	J	8	0	0	0	0
All	All	12181	0	9689	147	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 7.

All (147) 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:I:55:DA:H61	1:J:238:DT:H3	1.28	0.81
1:J:205:DG:H2"	1:J:206:DC:H5"	1.65	0.78
5:H:122:THR:O	5:H:125:LYS:NZ	2.16	0.78
1:I:115:DA:H2"	1:I:116:DC:H5"	1.68	0.75
1:J:259:DA:H2"	1:J:260:DC:H5"	1.70	0.72
4:G:67:GLY:HA3	5:H:49:HIS:CD2	2.25	0.71
2:E:121:PRO:HB3	3:F:53:GLU:HG3	1.73	0.71
1:J:164:DG:H2"	1:J:165:DA:H5"	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:5:DA:H2"	1:I:6:DT:H5"	1.74	0.69
4:C:68:ASN:OD1	4:C:71:ARG:NH2	2.25	0.69
1:I:129:DC:N3	1:J:163:DA:N6	2.42	0.66
1:I:2:DT:H2"	1:I:3:DC:H5"	1.79	0.65
1:J:181:DA:H2"	1:J:182:DT:H5"	1.80	0.64
2:A:73:GLU:OE1	3:B:25:ASN:ND2	2.26	0.63
2:A:125:GLN:HG2	2:A:134:ARG:HH12	1.64	0.62
1:I:106:DT:H2"	1:I:107:DC:H5"	1.81	0.62
4:G:118:LYS:HG3	4:G:119:LYS:HG3	1.80	0.62
1:J:261:DA:H2"	1:J:262:DC:H5"	1.80	0.62
4:C:102:ILE:HG23	5:D:61:ILE:HD13	1.83	0.61
1:J:268:DG:C8	1:J:268:DG:H5'	2.36	0.61
4:C:32:ARG:NH2	5:D:35:GLU:OE2	2.25	0.61
1:J:246:DG:H2"	1:J:247:DC:H5"	1.81	0.60
1:I:120:DT:H2"	1:I:121:DG:C8	2.36	0.60
4:G:41:GLN:HG2	4:G:42:ARG:HG3	1.84	0.60
1:J:206:DC:H2"	1:J:207:DA:C8	2.38	0.59
1:I:136:DT:H2'	1:I:137:DG:C8	2.37	0.59
1:I:64:DT:H1'	1:I:65:DT:H5'	1.85	0.59
1:I:130:DT:H2"	1:I:131:DG:H5"	1.86	0.58
1:J:154:DT:H2"	1:J:155:DC:H5"	1.84	0.58
4:G:41:GLN:OE1	5:H:87:SER:HB2	2.06	0.56
1:J:247:DC:H2"	1:J:248:DA:N7	2.21	0.56
5:H:125:LYS:N	5:H:125:LYS:HD3	2.21	0.55
1:J:251:DT:H2"	1:J:252:DT:H5'	1.88	0.55
1:J:179:DG:H2"	1:J:180:DT:H5"	1.89	0.55
1:J:182:DT:H2"	1:J:183:DT:H5"	1.89	0.54
1:J:199:DC:OP1	3:F:17:ARG:NH2	2.41	0.54
1:J:226:DT:H2"	1:J:227:DG:C8	2.43	0.53
1:I:108:DC:H2"	1:I:109:DA:N7	2.23	0.53
1:I:51:DA:H2"	1:I:52:DT:H5"	1.91	0.52
1:I:118:DT:H6	1:I:118:DT:H5'	1.75	0.52
1:J:247:DC:H2"	1:J:248:DA:C8	2.45	0.52
1:I:58:DG:H4'	1:I:58:DG:OP1	2.11	0.51
1:I:70:DT:H2"	1:I:71:DG:C8	2.45	0.51
1:I:20:DT:H1'	1:I:21:DT:H5"	1.92	0.51
1:I:90:DT:OP2	2:E:69:ARG:NH2	2.44	0.51
1:J:197:DA:H2"	1:J:198:DT:H5"	1.92	0.51
1:I:101:DC:H2"	1:I:102:DA:O4'	2.11	0.51
1:J:160:DT:H2"	1:J:161:DG:C8	2.46	0.51
1:J:174:DA:H2"	1:J:175:DA:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:82:DA:H3'	2:E:46:VAL:HG21	1.93	0.50
3:B:39:ARG:NH1	3:B:43:VAL:O	2.44	0.50
1:I:29:DA:OP1	4:C:32:ARG:NH1	2.44	0.50
1:I:43:DA:H2"	1:I:44:DC:H5"	1.93	0.50
2:E:68:GLN:HG3	2:E:89:VAL:HG11	1.93	0.50
1:I:57:DA:H2"	1:I:58:DG:O4'	2.12	0.50
2:E:60:LEU:HD12	2:E:64:LYS:HE2	1.93	0.50
1:I:102:DA:H2"	1:I:103:DG:C8	2.47	0.50
1:I:68:DG:OP1	2:A:42:ARG:NE	2.41	0.49
1:I:117:DT:H1'	1:I:118:DT:H5"	1.94	0.49
1:I:68:DG:H5'	2:A:43:PRO:HG2	1.94	0.49
1:I:6:DT:H2"	1:I:7:DA:C8	2.48	0.49
4:G:15:LYS:HE2	4:G:19:SER:HB3	1.95	0.49
5:H:49:HIS:HB3	8:H:203:HOH:O	2.11	0.49
4:C:67:GLY:HA3	5:D:49:HIS:CD2	2.48	0.48
1:I:129:DC:H6	1:I:129:DC:H5'	1.78	0.48
1:I:105:DT:H1'	1:I:106:DT:H5'	1.95	0.48
1:J:237:DT:P	2:A:69:ARG:HH22	2.36	0.48
4:C:37:GLY:HA3	4:C:39:TYR:CE2	2.48	0.48
1:I:131:DG:H2"	1:I:132:DC:C6	2.48	0.48
1:J:268:DG:N7	7:J:312:CL:CL	2.84	0.48
1:I:59:DG:H4'	2:A:63:ARG:NH2	2.28	0.48
1:I:100:DG:H5"	2:E:83:ARG:HD2	1.96	0.48
2:A:79:LYS:HB3	2:A:82:LEU:HD11	1.96	0.48
1:I:28:DA:H2"	1:I:29:DA:C8	2.49	0.47
1:I:40:DG:H5"	1:I:40:DG:H8	1.79	0.47
1:I:60:DC:H2"	1:I:61:DA:C8	2.49	0.47
1:J:215:DC:H5'	2:E:43:PRO:HG2	1.97	0.47
1:I:34:DT:H2"	1:I:35:DA:H8	1.80	0.47
1:I:74:DT:H1'	1:I:75:DT:H5'	1.96	0.47
1:I:58:DG:H2"	1:I:59:DG:C8	2.49	0.47
1:J:175:DA:H2"	1:J:176:DA:C8	2.50	0.47
1:I:38:DT:H2"	1:I:39:DG:C8	2.50	0.46
1:J:229:DA:H3'	2:A:46:VAL:HG21	1.97	0.46
1:I:52:DT:H1'	1:I:53:DC:H5'	1.97	0.46
4:C:29:ARG:NH1	5:D:36:SER:O	2.48	0.46
1:I:54:DA:H61	1:J:239:DT:H3	1.63	0.46
1:J:203:DA:H2"	1:J:204:DG:C8	2.52	0.45
1:J:266:DT:H2"	1:J:267:DG:C8	2.51	0.45
1:J:227:DG:H3'	3:B:46:ILE:O	2.16	0.45
4:G:102:ILE:HG23	5:H:61:ILE:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:41:ILE:HD13	5:D:62:MET:HB3	1.99	0.45
1:J:163:DA:H2"	1:J:164:DG:C8	2.51	0.45
1:J:237:DT:H4'	2:A:63:ARG:CZ	2.47	0.44
2:A:126:LEU:HD22	2:E:113:HIS:CG	2.52	0.44
5:D:80:LEU:HD12	5:D:80:LEU:HA	1.77	0.44
1:I:140:DT:H2"	1:I:141:DA:C8	2.52	0.44
1:J:173:DA:H2"	1:J:174:DA:C8	2.53	0.44
1:J:215:DC:H2"	1:J:216:DT:H71	1.99	0.44
1:J:248:DA:H2"	1:J:249:DG:C8	2.52	0.44
1:I:33:DG:N2	1:J:260:DC:O2	2.49	0.44
1:I:121:DG:H5"	5:H:40:TYR:OH	2.17	0.44
5:H:124:SER:C	5:H:125:LYS:HD3	2.38	0.44
4:G:45:ALA:O	4:G:48:PRO:HD2	2.18	0.44
1:I:16:DC:H2"	1:I:17:DA:C8	2.53	0.44
2:A:68:GLN:HG3	2:A:89:VAL:HG11	2.00	0.44
1:I:135:DG:H1	1:J:158:DC:H42	1.66	0.44
1:J:165:DA:H2"	1:J:166:DT:H5'	2.00	0.44
5:H:107:ALA:O	5:H:111:VAL:HG23	2.18	0.43
1:J:154:DT:C2'	1:J:155:DC:H5"	2.48	0.43
2:E:63:ARG:HD3	2:E:63:ARG:HA	1.69	0.43
1:I:4:DA:H2"	1:I:5:DA:C8	2.53	0.43
1:I:134:DG:H1'	1:I:135:DG:H5'	2.01	0.43
1:J:223:DA:H2"	1:J:224:DG:C8	2.54	0.43
1:J:214:DG:H2"	1:J:215:DC:C6	2.54	0.43
4:C:63:LEU:HD23	4:C:63:LEU:HA	1.90	0.43
1:I:92:DT:H6	1:I:92:DT:H2'	1.68	0.43
1:J:224:DG:H2"	1:J:225:DC:C5	2.54	0.43
5:D:48:VAL:O	5:D:49:HIS:ND1	2.47	0.43
1:I:108:DC:H2"	1:I:109:DA:C8	2.54	0.42
1:J:275:DC:H6	1:J:275:DC:H5'	1.84	0.42
1:J:290:DG:H5"	2:E:41:TYR:HA	2.02	0.42
1:I:132:DC:H2"	1:I:133:DA:C8	2.54	0.42
1:I:144:DG:H1	1:J:149:DC:H42	1.67	0.42
1:I:100:DG:N2	1:J:193:DC:O2	2.45	0.42
2:E:65:LEU:HB3	2:E:66:PRO:HD3	2.00	0.42
1:I:96:DT:H6	1:I:96:DT:H2'	1.73	0.42
1:J:192:DG:H1'	1:J:193:DC:H5"	2.01	0.42
1:I:104:DT:H2"	1:I:105:DT:H5"	2.01	0.42
1:J:230:DC:H5"	2:A:40:ARG:HG2	2.01	0.41
3:B:30:THR:HB	3:B:32:PRO:HD2	2.02	0.41
1:I:36:DT:H2"	1:I:37:DT:H5"	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:180:DT:H2"	1:J:181:DA:C8	2.56	0.41
1:J:244:DG:H2"	1:J:245:DA:C8	2.55	0.41
1:I:29:DA:OP2	4:C:32:ARG:HD3	2.21	0.41
1:I:81:DG:P	3:F:35:ARG:HH22	2.43	0.41
1:I:81:DG:OP2	3:F:35:ARG:NH2	2.46	0.41
1:J:242:DT:H6	1:J:242:DT:H2'	1.72	0.41
3:F:30:THR:HB	3:F:32:PRO:HD2	2.03	0.41
4:G:20:ARG:HB3	5:H:124:SER:OG	2.21	0.41
1:I:111:DA:H1'	1:I:112:DT:H5'	2.03	0.40
1:J:172:DC:H2"	1:J:173:DA:C8	2.56	0.40
5:H:79:ARG:NH1	8:H:204:HOH:O	2.40	0.40
1:I:91:DT:H2"	1:I:92:DT:H5'	2.03	0.40
1:I:8:DT:H1'	1:I:9:DC:H5"	2.03	0.40
5:D:49:HIS:HB3	5:D:52:THR:HB	2.04	0.40
4:G:88:ARG:HD3	4:G:88:ARG:HA	1.74	0.40
1:J:197:DA:C2'	1:J:198:DT:H5"	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	96/135 (71%)	96 (100%)	0	0	100	100
2	E	96/135 (71%)	95 (99%)	1 (1%)	0	100	100
3	B	79/102 (78%)	77 (98%)	2 (2%)	0	100	100
3	F	85/102 (83%)	82 (96%)	3 (4%)	0	100	100
4	C	103/128 (80%)	101 (98%)	2 (2%)	0	100	100
4	G	104/128 (81%)	101 (97%)	3 (3%)	0	100	100
5	D	91/126 (72%)	90 (99%)	0	1 (1%)	14	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	H	91/126 (72%)	90 (99%)	0	1 (1%)	14	41
All	All	745/982 (76%)	732 (98%)	11 (2%)	2 (0%)	41	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	D	104	GLY
5	H	104	GLY

5.3.2 Protein sidechains (i)

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	85/110 (77%)	84 (99%)	1 (1%)	71	92
2	E	85/110 (77%)	85 (100%)	0	100	100
3	B	66/78 (85%)	65 (98%)	1 (2%)	65	89
3	F	72/78 (92%)	72 (100%)	0	100	100
4	C	83/101 (82%)	82 (99%)	1 (1%)	71	92
4	G	84/101 (83%)	83 (99%)	1 (1%)	71	92
5	D	82/109 (75%)	81 (99%)	1 (1%)	71	92
5	H	82/109 (75%)	81 (99%)	1 (1%)	71	92
All	All	639/796 (80%)	633 (99%)	6 (1%)	78	94

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	117	VAL
3	B	47	SER
4	C	16	SER
5	D	80	LEU
4	G	41	GLN
5	H	48	VAL

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

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 30 ligands modelled in this entry, 30 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 (i)

6.1 Protein, DNA and RNA chains (i)

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	I	146/146 (100%)	1.11	26 (17%) 1 1	47, 102, 138, 156	0
1	J	146/146 (100%)	0.99	27 (18%) 1 1	53, 103, 139, 146	0
2	A	98/135 (72%)	0.17	2 (2%) 65 56	31, 46, 71, 108	0
2	E	98/135 (72%)	0.10	2 (2%) 65 56	24, 34, 60, 100	0
3	B	81/102 (79%)	0.08	0 100 100	33, 44, 63, 107	0
3	F	87/102 (85%)	0.11	1 (1%) 80 75	24, 35, 56, 96	0
4	C	105/128 (82%)	-0.07	0 100 100	22, 37, 58, 93	0
4	G	106/128 (82%)	-0.02	1 (0%) 84 80	32, 48, 72, 101	0
5	D	93/126 (73%)	0.07	0 100 100	27, 40, 62, 111	0
5	H	93/126 (73%)	0.05	0 100 100	31, 48, 73, 105	0
All	All	1053/1274 (82%)	0.34	59 (5%) 24 16	22, 47, 126, 156	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	146	DT	15.1
1	I	43	DA	6.7
1	J	148	DT	6.2
1	I	56	DA	6.1
2	E	135	ALA	5.9
1	J	162	DC	5.9
1	J	147	DA	5.1
1	I	57	DA	4.8
1	I	24	DA	4.6
1	I	58	DG	4.5
4	G	14	VAL	4.5
1	J	161	DG	4.4
1	I	106	DT	4.4

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Mol	Chain	Res	Type	RSRZ
1	J	169	DT	4.0
1	I	44	DC	4.0
1	I	55	DA	3.8
1	I	42	DA	3.8
1	J	273	DA	3.6
1	I	35	DA	3.6
1	I	23	DT	3.4
1	J	233	DG	3.4
1	I	22	DC	3.3
2	A	135	ALA	3.2
1	I	15	DG	3.2
1	I	21	DT	3.2
1	J	203	DA	3.1
1	I	128	DT	3.1
1	J	232	DT	3.1
1	J	231	DA	3.0
1	J	240	DG	3.0
1	J	204	DG	3.0
1	J	274	DT	3.0
3	F	102	GLY	3.0
1	J	241	DA	2.9
1	J	285	DA	2.9
1	I	14	DT	2.8
1	J	202	DA	2.8
1	J	170	DA	2.7
1	J	262	DC	2.7
1	I	135	DG	2.6
1	I	126	DA	2.6
1	J	180	DT	2.5
1	J	160	DT	2.5
1	J	167	DT	2.5
1	J	171	DC	2.5
1	J	168	DC	2.5
1	I	16	DC	2.4
1	I	107	DC	2.4
2	A	38	PRO	2.4
1	I	20	DT	2.4
1	I	33	DG	2.4
1	J	275	DC	2.3
1	J	286	DT	2.3
1	J	272	DA	2.3
1	J	190	DC	2.2

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Mol	Chain	Res	Type	RSRZ
1	I	1	DA	2.2
1	I	127	DA	2.2
1	I	25	DC	2.2
2	E	39	HIS	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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
6	MN	I	210	1/1	0.51	0.11	119,119,119,119	0
7	CL	J	309	1/1	0.53	0.17	90,90,90,90	0
6	MN	I	211	1/1	0.56	0.11	128,128,128,128	0
6	MN	I	201	1/1	0.57	0.21	119,119,119,119	0
6	MN	J	307	1/1	0.60	0.10	139,139,139,139	0
6	MN	J	301	1/1	0.66	0.12	130,130,130,130	0
7	CL	J	312	1/1	0.74	0.11	88,88,88,88	0
6	MN	A	201	1/1	0.76	0.16	111,111,111,111	0
6	MN	I	207	1/1	0.77	0.16	104,104,104,104	0
6	MN	I	204	1/1	0.82	0.11	99,99,99,99	0
7	CL	J	311	1/1	0.83	0.11	93,93,93,93	0
6	MN	I	209	1/1	0.86	0.22	117,117,117,117	0
6	MN	J	304	1/1	0.89	0.07	109,109,109,109	0
6	MN	I	205	1/1	0.90	0.09	91,91,91,91	0
6	MN	J	303	1/1	0.90	0.08	115,115,115,115	0
7	CL	J	310	1/1	0.90	0.12	95,95,95,95	0
6	MN	I	202	1/1	0.90	0.39	134,134,134,134	0
6	MN	I	208	1/1	0.90	0.09	114,114,114,114	0
6	MN	I	206	1/1	0.92	0.06	109,109,109,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	MN	J	306	1/1	0.92	0.10	80,80,80,80	0
6	MN	G	201	1/1	0.93	0.09	69,69,69,69	0
7	CL	J	308	1/1	0.94	0.18	88,88,88,88	0
7	CL	D	203	1/1	0.95	0.09	49,49,49,49	0
6	MN	J	302	1/1	0.97	0.08	109,109,109,109	0
6	MN	J	305	1/1	0.97	0.16	80,80,80,80	0
7	CL	B	201	1/1	0.97	0.19	69,69,69,69	0
6	MN	I	203	1/1	0.97	0.05	98,98,98,98	0
7	CL	D	204	1/1	0.98	0.21	77,77,77,77	0
6	MN	D	202	1/1	0.99	0.12	55,55,55,55	0
6	MN	D	201	1/1	0.99	0.16	46,46,46,46	0

6.5 Other polymers (i)

There are no such residues in this entry.