



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:32 AM UTC

PDB ID : 2CV5 / pdb\_00002cv5  
Title : Crystal structure of human nucleosome core particle  
Authors : Tsunaka, Y.; Kajimura, N.; Tate, S.; Morikawa, K.  
Deposited on : 2005-05-31  
Resolution : 2.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

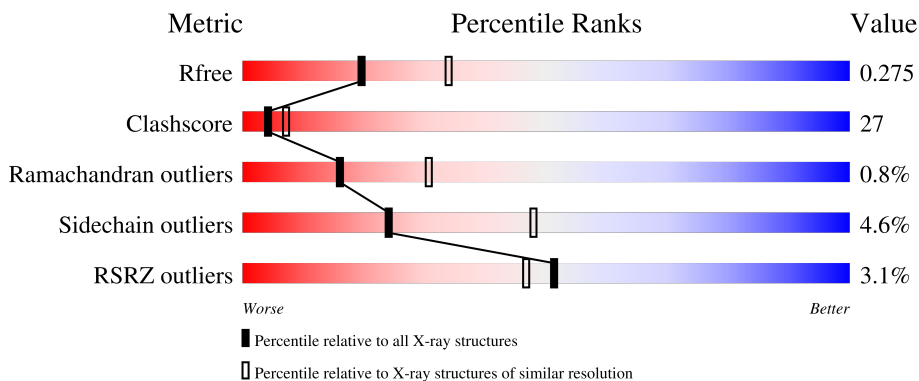
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	
1	J	146	
2	A	136	
2	E	136	
3	B	103	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
3	F	103	
4	C	130	
4	G	130	
5	D	126	
5	H	126	

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	CL	E	2003	-	-	X	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 12471 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	97	801	505	155	137	4	0	0	0
2	E	99	816	514	158	140	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	78	619	391	120	107	1	0	0	0
3	F	85	683	430	136	116	1	0	0	0

- Molecule 4 is a protein called Histone H2A.a.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	C	108	835	526	165	144	0	0	0
4	G	104	805	508	157	140	0	0	0

- Molecule 5 is a protein called Histone H2B K.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	96	Total	C	N	O	S	0	0	0
			754	473	138	141	2			
5	H	94	Total	C	N	O	S	0	0	0
			735	461	134	138	2			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	I	3	Total	Mn	0	0
			3	3		
6	J	5	Total	Mn	0	0
			5	5		
6	D	1	Total	Mn	0	0
			1	1		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	I	94	Total	O	0	0
			94	94		
8	J	79	Total	O	0	0
			79	79		
8	A	26	Total	O	0	0
			26	26		
8	B	23	Total	O	0	0
			23	23		
8	C	42	Total	O	0	0
			42	42		
8	D	21	Total	O	0	0
			21	21		

*Continued on next page...*

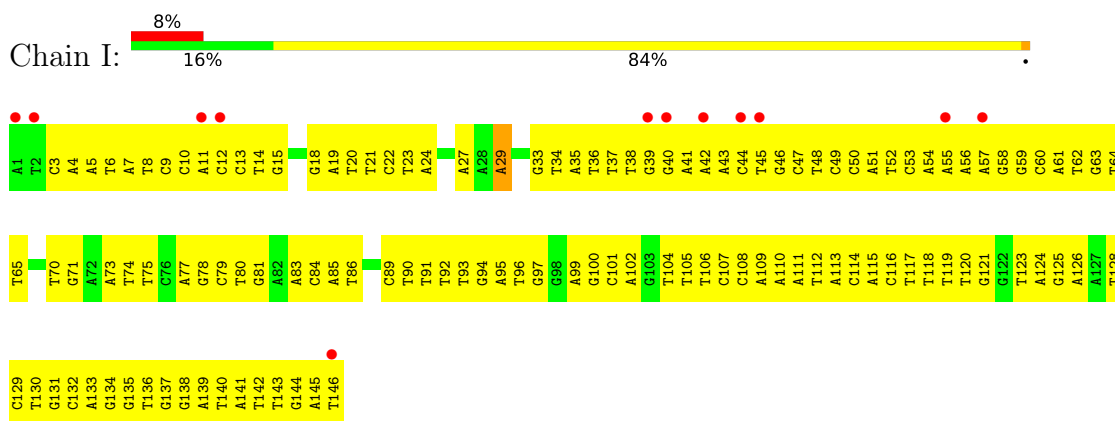
*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
8	E	52	Total 52	O 52	0	0
8	F	39	Total 39	O 39	0	0
8	G	38	Total 38	O 38	0	0
8	H	16	Total 16	O 16	0	0

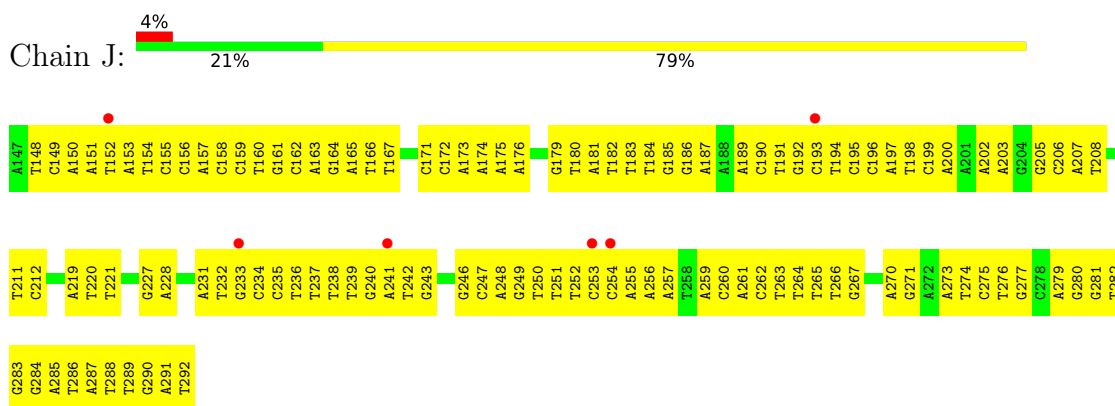
### 3 Residue-property plots

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.

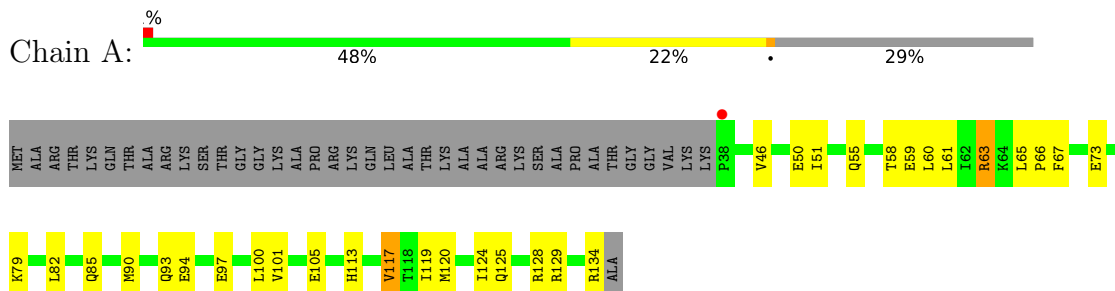
- Molecule 1: DNA (146-MER)



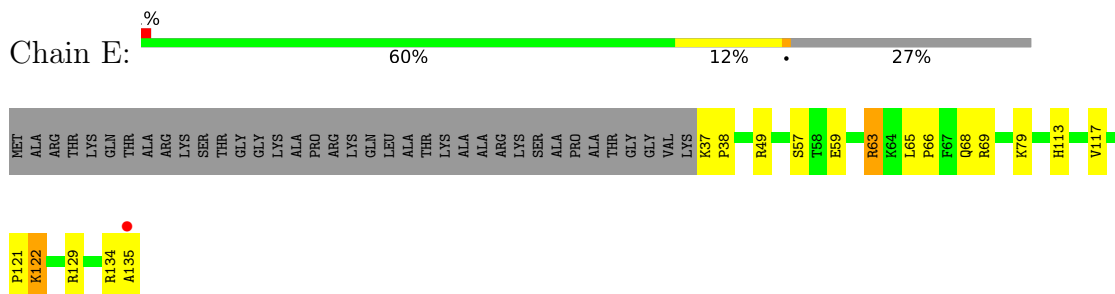
- Molecule 1: DNA (146-MER)



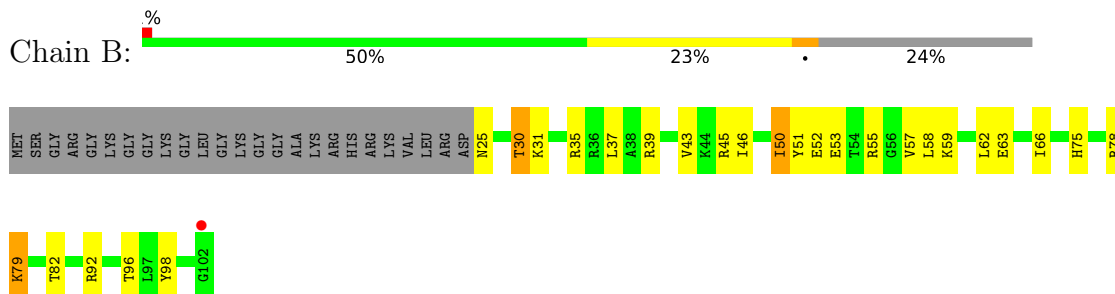
- Molecule 2: Histone H3.1



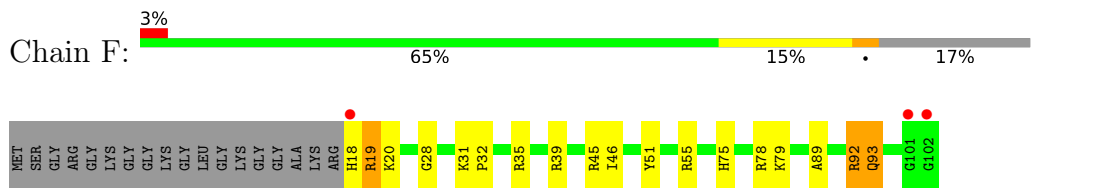
• Molecule 2: Histone H3.1



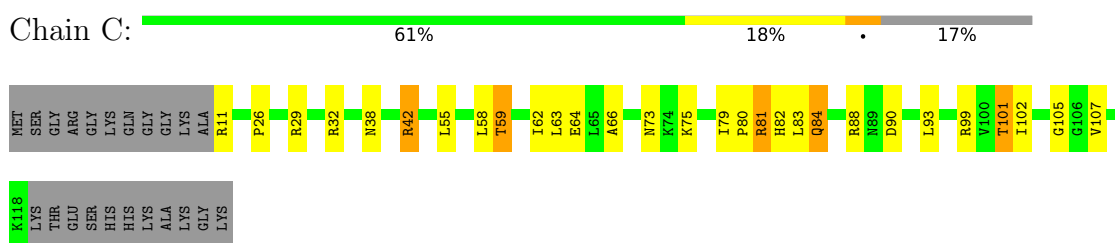
• Molecule 3: Histone H4



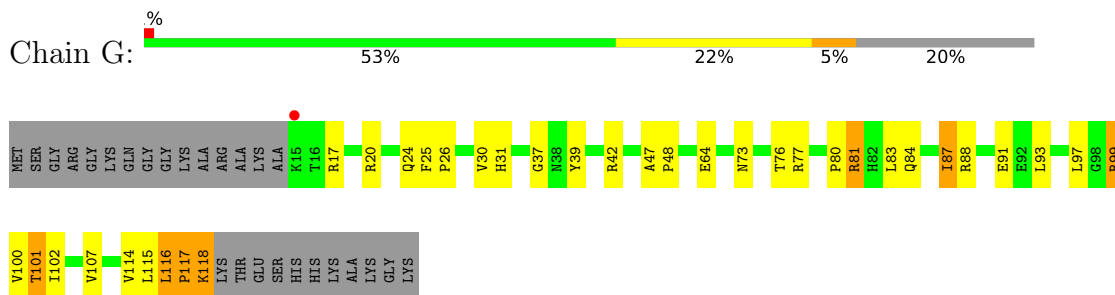
• Molecule 3: Histone H4



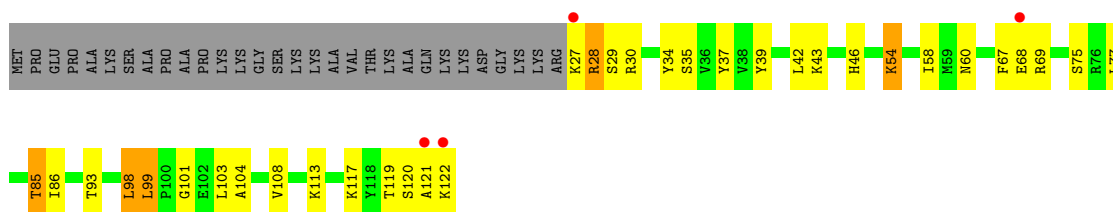
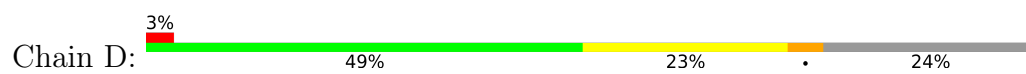
• Molecule 4: Histone H2A.a



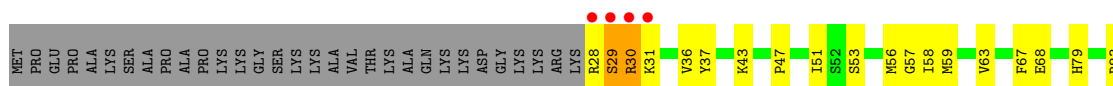
• Molecule 4: Histone H2A.a



• Molecule 5: Histone H2B K



- Molecule 5: Histone H2B K



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.56Å 108.37Å 169.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 50.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.0 (50.00-2.50) 96.0 (50.00-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.55 (at 2.51Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.224 , 0.277 0.222 , 0.275	Depositor DCC
$R_{free}$ test set	6241 reflections (10.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.8	Xtrriage
Anisotropy	0.549	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 46.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	12471	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.30	0/3354	0.76	1/5175 (0.0%)
1	J	0.30	0/3354	0.76	0/5175
2	A	0.47	0/813	0.89	1/1090 (0.1%)
2	E	0.55	0/828	0.86	1/1109 (0.1%)
3	B	0.49	0/626	0.99	4/837 (0.5%)
3	F	0.58	0/691	0.94	2/923 (0.2%)
4	C	0.51	0/845	0.91	1/1139 (0.1%)
4	G	0.48	0/815	0.99	8/1100 (0.7%)
5	D	0.51	0/765	0.94	2/1025 (0.2%)
5	H	0.51	0/746	0.87	1/1003 (0.1%)
All	All	0.42	0/12837	0.84	21/18576 (0.1%)

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	50	ILE	N-CA-C	7.15	117.91	110.62
4	G	24	GLN	N-CA-C	-6.89	104.87	113.55
4	G	87	ILE	N-CA-C	6.45	116.61	110.42
2	A	117	VAL	N-CA-C	-6.30	107.15	113.20
3	B	46	ILE	N-CA-C	6.29	117.18	108.12

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	2990	0	1652	218	0
1	J	2990	0	1652	180	0
2	A	801	0	839	42	0
2	E	816	0	856	27	0
3	B	619	0	659	37	0
3	F	683	0	729	22	0
4	C	835	0	897	30	0
4	G	805	0	861	38	0
5	D	754	0	782	41	0
5	H	735	0	756	41	0
6	D	1	0	0	0	0
6	I	3	0	0	0	0
6	J	5	0	0	0	0
7	A	1	0	0	0	0
7	C	1	0	0	0	0
7	E	1	0	0	2	0
7	G	1	0	0	0	0
8	A	26	0	0	4	0
8	B	23	0	0	2	0
8	C	42	0	0	3	0
8	D	21	0	0	3	0
8	E	52	0	0	4	0
8	F	39	0	0	1	0
8	G	38	0	0	2	0
8	H	16	0	0	3	0
8	I	94	0	0	2	0
8	J	79	0	0	0	0
All	All	12471	0	9683	594	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 27.

The worst 5 of 594 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:J:194:DT:H2''	1:J:195:DC:H5''	1.20	1.14
1:I:51:DA:H2''	1:I:52:DT:H5''	1.29	1.14
1:I:139:DA:H2''	1:I:140:DT:H5'	1.26	1.11
2:A:63:ARG:HH11	2:A:63:ARG:HB2	0.91	1.07

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:155:DC:H2''	1:J:156:DC:H5'	1.35	1.06

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	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
2	E	97/136 (71%)	95 (98%)	2 (2%)	0	100	100
3	B	76/103 (74%)	75 (99%)	1 (1%)	0	100	100
3	F	83/103 (81%)	80 (96%)	3 (4%)	0	100	100
4	C	106/130 (82%)	101 (95%)	5 (5%)	0	100	100
4	G	102/130 (78%)	98 (96%)	3 (3%)	1 (1%)	12	24
5	D	94/126 (75%)	89 (95%)	4 (4%)	1 (1%)	11	22
5	H	92/126 (73%)	88 (96%)	0	4 (4%)	2	2
All	All	745/990 (75%)	718 (96%)	21 (3%)	6 (1%)	16	31

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	H	120	SER
5	D	101	GLY
5	H	29	SER
5	H	30	ARG
5	H	101	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	85/111 (77%)	82 (96%)	3 (4%)	32	58
2	E	86/111 (78%)	82 (95%)	4 (5%)	23	47
3	B	63/79 (80%)	63 (100%)	0	100	100
3	F	70/79 (89%)	67 (96%)	3 (4%)	26	51
4	C	85/100 (85%)	80 (94%)	5 (6%)	18	37
4	G	83/100 (83%)	78 (94%)	5 (6%)	17	36
5	D	82/105 (78%)	76 (93%)	6 (7%)	13	27
5	H	80/105 (76%)	77 (96%)	3 (4%)	29	56
All	All	634/790 (80%)	605 (95%)	29 (5%)	24	48

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	63	ARG
5	H	102	GLU
2	E	122	LYS
4	G	101	THR
2	E	79	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
4	G	31	HIS
5	H	79	HIS
5	H	92	GLN
5	H	44	GLN
5	D	46	HIS

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	I	146/146 (100%)	0.68	12 (8%) 17 15	26, 56, 119, 132	0
1	J	146/146 (100%)	0.58	6 (4%) 41 37	27, 58, 112, 128	0
2	A	97/136 (71%)	-0.19	1 (1%) 79 76	15, 30, 52, 60	0
2	E	99/136 (72%)	-0.35	1 (1%) 79 76	9, 21, 42, 59	0
3	B	78/103 (75%)	-0.21	1 (1%) 75 71	16, 28, 40, 53	0
3	F	85/103 (82%)	-0.36	3 (3%) 47 42	9, 20, 37, 53	0
4	C	108/130 (83%)	-0.25	0 100 100	13, 27, 46, 73	0
4	G	104/130 (80%)	-0.19	1 (0%) 79 76	14, 26, 50, 65	0
5	D	96/126 (76%)	-0.12	4 (4%) 40 36	14, 25, 67, 86	0
5	H	94/126 (74%)	-0.14	4 (4%) 40 35	14, 27, 53, 95	0
All	All	1053/1282 (82%)	0.01	33 (3%) 51 47	9, 30, 84, 132	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	102	GLY	4.4
3	B	102	GLY	3.8
5	H	29	SER	3.6
5	D	122	LYS	3.3
2	E	135	ALA	3.2

### 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 oligosaccharides 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
6	MN	I	1007	1/1	0.94	0.13	72,72,72,72	0
6	MN	I	1005	1/1	0.95	0.13	60,60,60,60	0
6	MN	J	1006	1/1	0.95	0.17	69,69,69,69	0
6	MN	I	1004	1/1	0.96	0.07	57,57,57,57	0
7	CL	E	2003	1/1	0.96	0.08	42,42,42,42	0
6	MN	J	1009	1/1	0.97	0.09	50,50,50,50	0
7	CL	A	2004	1/1	0.97	0.06	44,44,44,44	0
6	MN	J	1001	1/1	0.97	0.07	49,49,49,49	0
6	MN	J	1003	1/1	0.98	0.07	57,57,57,57	0
7	CL	G	2002	1/1	0.98	0.03	31,31,31,31	0
7	CL	C	2001	1/1	0.99	0.06	34,34,34,34	0
6	MN	D	1008	1/1	0.99	0.03	28,28,28,28	0
6	MN	J	1002	1/1	0.99	0.05	48,48,48,48	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.