wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 07:29 AM GMT

PDB ID	:	3AYW
Title	:	Crystal Structure of Human Nucleosome Core Particle Containing H3K56Q mutation
Authors	:	Iwasaki, W.; Tachiwana, H.; Kawaguchi, K.; Shibata, T.; Kagawa, W.; Kurumizaka, H.
Deposited on	:	2011-05-19
Resolution	:	2.90 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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

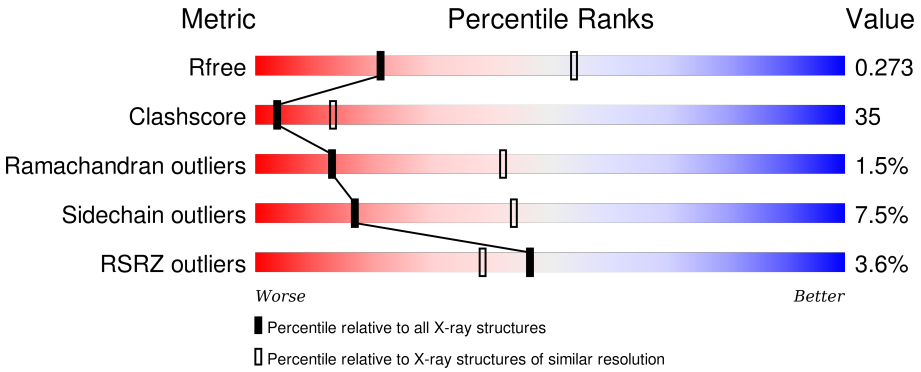
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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 <=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	% 33% 33% · 30%
1	E	139	45% 20% · 30%
2	B	106	39% 30% 5% 26%
2	F	106	50% 26% · 21%
3	C	133	% 38% 38% 5% 19%

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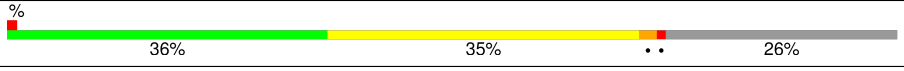
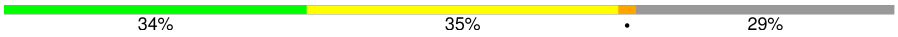
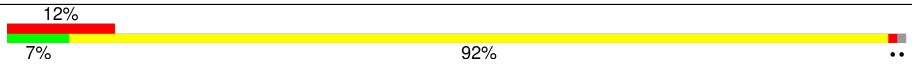
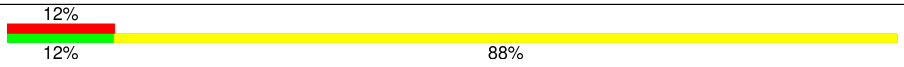
Mol	Chain	Length	Quality of chain
3	G	133	
4	D	129	
4	H	129	
5	I	146	
5	J	146	

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
6	CL	A	1001	-	-	X	-
7	MN	D	201	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11972 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	504	155	138	4			
1	E	97	Total	C	N	O	S	0	0	0
			799	504	153	138	4			

There are 8 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
A	56	GLN	LYS	ENGINEERED MUTATION	UNP P68431
E	-3	GLY	-	EXPRESSION TAG	UNP P68431
E	-2	SER	-	EXPRESSION TAG	UNP P68431
E	-1	HIS	-	EXPRESSION TAG	UNP P68431
E	56	GLN	LYS	ENGINEERED MUTATION	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	391	120	107	1			
2	F	84	Total	C	N	O	S	0	0	0
			673	424	133	115	1			

There are 6 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
F	-3	GLY	-	EXPRESSION TAG	UNP P62805

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	SER	-	EXPRESSION TAG	UNP P62805
F	-1	HIS	-	EXPRESSION TAG	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	103	Total	C	N	O	0	0	0
			796	502	155	139			

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	96	Total	C	N	O	S	0	0	0
			755	474	138	141	2			
4	H	92	Total	C	N	O	S	0	0	0
			719	453	129	135	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	146	Total	C	N	O	P	0	0	0
			2990	1431	540	874	145			

- 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	D	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).

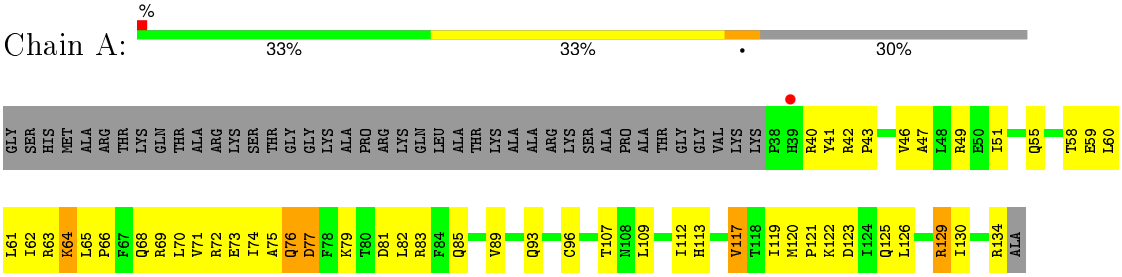
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	J	5	Total	Mn	0	0
			5	5		
7	I	5	Total	Mn	0	0
			5	5		
7	D	1	Total	Mn	0	0
			1	1		

3 Residue-property plots (i)

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

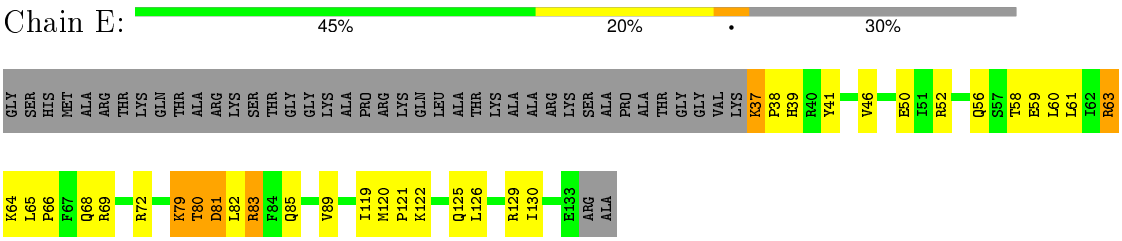
- Molecule 1: Histone H3.1

Chain A:



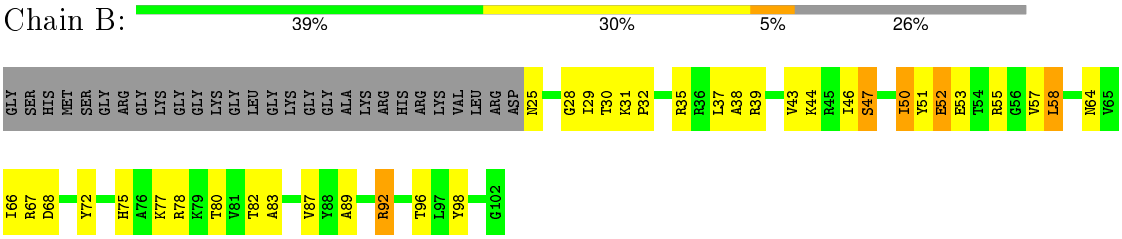
- Molecule 1: Histone H3.1

Chain E:



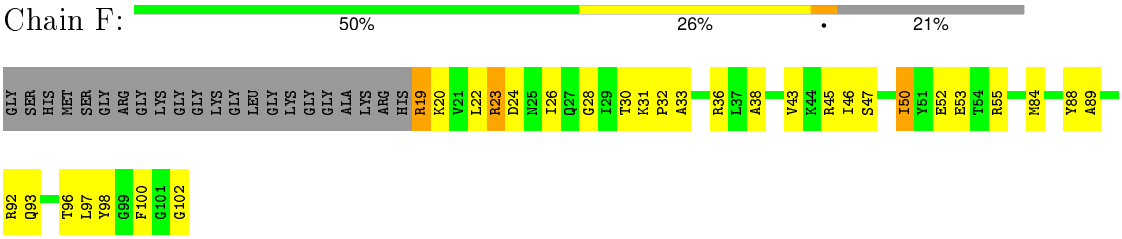
- Molecule 2: Histone H4

Chain B:



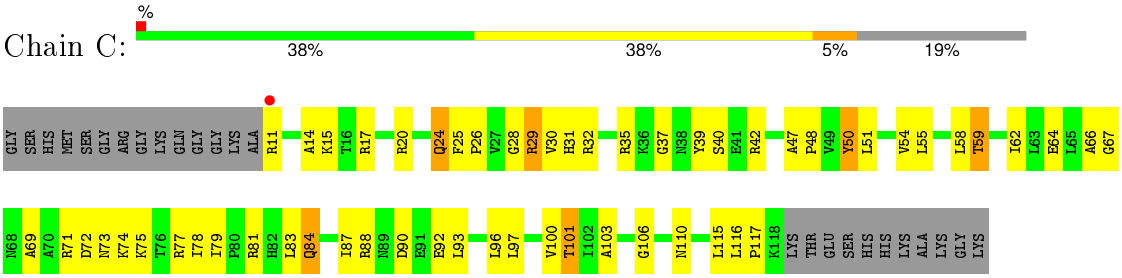
- Molecule 2: Histone H4

Chain F:



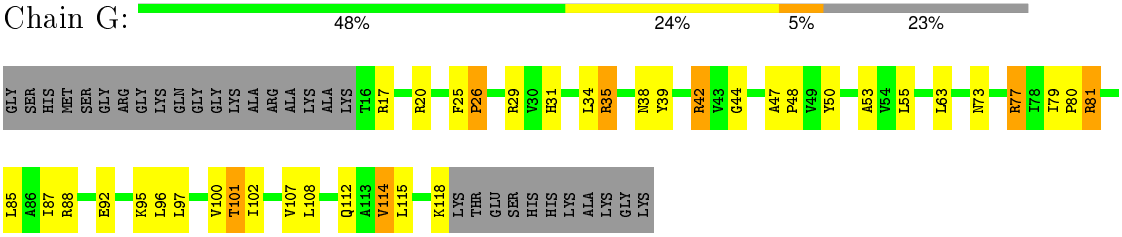
• Molecule 3: Histone H2A type 1-B/E

Chain C:



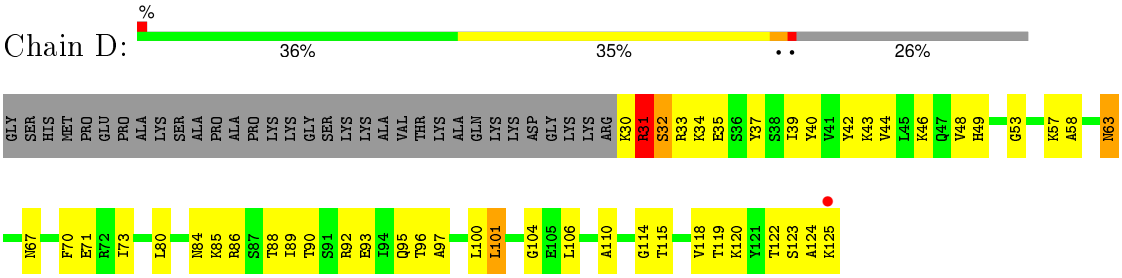
• Molecule 3: Histone H2A type 1-B/E

Chain G:



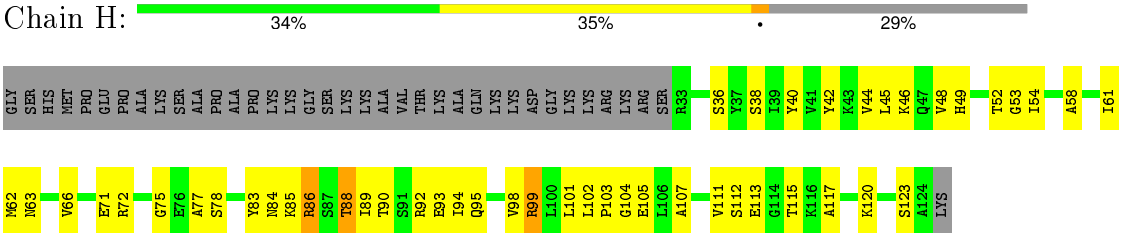
• Molecule 4: Histone H2B type 1-J

Chain D:



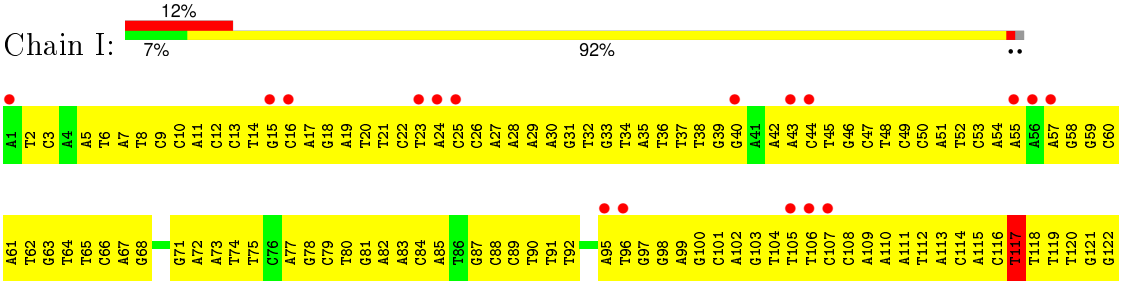
• Molecule 4: Histone H2B type 1-J

Chain H:



• Molecule 5: 146-MER DNA

Chain I:



- Molecule 5: 146-MER DNA

Chain J:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	105.95Å 109.48Å 181.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.99 – 2.90 38.99 – 2.90	Depositor EDS
% Data completeness (in resolution range)	86.1 (38.99-2.90) 86.1 (38.99-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 2.90Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.218 , 0.273 0.219 , 0.273	Depositor DCC
R_{free} test set	2057 reflections (5.02%)	DCC
Wilson B-factor (Å^2)	60.1	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 59.0	EDS
Estimated twinning fraction	0.054 for k,h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Outliers	0 of 40980 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	11972	wwPDB-VP
Average B, all atoms (Å^2)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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, 0.375 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	0.40	0/813	0.63	0/1091
1	E	0.44	0/811	0.65	0/1089
2	B	0.41	0/626	0.69	0/837
2	F	0.45	0/680	0.73	0/908
3	C	0.39	0/845	0.64	0/1139
3	G	0.38	0/806	0.62	0/1089
4	D	0.41	0/766	0.66	0/1026
4	H	0.39	0/730	0.62	0/982
5	I	0.39	0/3332	0.78	1/5141 (0.0%)
5	J	0.37	0/3354	0.79	0/5175
All	All	0.39	0/12763	0.73	1/18477 (0.0%)

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
5	I	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	I	117	DT	N1-C1'-C2'	5.08	122.25	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	I	117	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	A	801	0	834	72	0
1	E	799	0	833	46	0
2	B	619	0	659	44	0
2	F	673	0	722	40	0
3	C	835	0	897	81	0
3	G	796	0	848	57	0
4	D	755	0	784	70	0
4	H	719	0	740	55	0
5	I	2970	0	1640	237	0
5	J	2990	0	1652	215	0
6	A	1	0	0	2	0
6	D	1	0	0	0	0
6	E	1	0	0	1	0
6	G	1	0	0	1	0
7	D	1	0	0	0	0
7	I	5	0	0	0	0
7	J	5	0	0	0	0
All	All	11972	0	9609	761	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 35.

The worst 5 of 761 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:248:DA:H2"	5:J:249:DG:H5"	1.24	1.16
5:J:152:DT:H2"	5:J:153:DA:H5"	1.26	1.14
5:J:277:DG:H2"	5:J:278:DC:H5'	1.28	1.12
5:I:43:DA:H2"	5:I:44:DC:H5"	1.15	1.10
5:I:5:DA:H2"	5:I:6:DT:H5"	1.34	1.08

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%)	1 (1%)	1 (1%)	17 51
1	E	95/139 (68%)	89 (94%)	6 (6%)	0	100 100
2	B	76/106 (72%)	71 (93%)	5 (7%)	0	100 100
2	F	82/106 (77%)	79 (96%)	3 (4%)	0	100 100
3	C	106/133 (80%)	96 (91%)	8 (8%)	2 (2%)	10 35
3	G	101/133 (76%)	96 (95%)	2 (2%)	3 (3%)	5 22
4	D	94/129 (73%)	83 (88%)	8 (8%)	3 (3%)	5 20
4	H	90/129 (70%)	77 (86%)	11 (12%)	2 (2%)	8 31
All	All	739/1014 (73%)	684 (93%)	44 (6%)	11 (2%)	13 42

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	72	ASP
4	D	31	ARG
4	H	123	SER
4	D	104	GLY
3	G	38	ASN

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	
1	A	85/113 (75%)	79 (93%)	6 (7%)	18	47
1	E	85/113 (75%)	79 (93%)	6 (7%)	18	47
2	B	63/81 (78%)	58 (92%)	5 (8%)	15	41
2	F	69/81 (85%)	64 (93%)	5 (7%)	18	46
3	C	85/102 (83%)	77 (91%)	8 (9%)	11	32
3	G	82/102 (80%)	75 (92%)	7 (8%)	13	37
4	D	82/107 (77%)	77 (94%)	5 (6%)	23	56
4	H	78/107 (73%)	73 (94%)	5 (6%)	22	53
All	All	629/806 (78%)	582 (92%)	47 (8%)	17	44

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	63	ASN
1	E	79	LYS
4	H	86	ARG
4	D	101	LEU
1	E	80	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	49	HIS
4	D	63	ASN
3	G	73	ASN
3	C	84	GLN
3	G	38	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 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, 95^{th} 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%)	0.02	1 (1%) 84 82	31, 49, 71, 104	0
1	E	97/139 (69%)	-0.08	0 100 100	24, 42, 64, 95	0
2	B	78/106 (73%)	-0.06	0 100 100	30, 47, 67, 87	0
2	F	84/106 (79%)	-0.03	0 100 100	23, 40, 65, 83	0
3	C	108/133 (81%)	-0.12	1 (0%) 85 84	27, 45, 76, 123	0
3	G	103/133 (77%)	-0.16	0 100 100	33, 52, 74, 85	0
4	D	96/129 (74%)	-0.01	1 (1%) 84 82	32, 48, 92, 118	0
4	H	92/129 (71%)	-0.07	0 100 100	30, 52, 78, 99	0
5	I	145/146 (99%)	0.60	17 (11%) 6 4	48, 100, 152, 173	0
5	J	146/146 (100%)	0.63	18 (12%) 5 3	49, 103, 147, 185	0
All	All	1046/1306 (80%)	0.12	38 (3%) 46 38	23, 53, 134, 185	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	I	56	DA	7.2
5	J	147	DA	7.2
5	I	55	DA	6.0
4	D	125	LYS	6.0
5	I	106	DT	5.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	D	201	1/1	0.98	0.28	3.55	46,46,46,46	0
6	CL	D	202	1/1	0.91	0.15	-1.45	53,53,53,53	0
6	CL	G	1001	1/1	0.99	0.14	-1.69	44,44,44,44	0
7	MN	I	1001	1/1	0.68	0.14	-	121,121,121,121	0
7	MN	J	1001	1/1	0.80	0.14	-	119,119,119,119	0
7	MN	I	1005	1/1	0.86	0.07	-	95,95,95,95	0
7	MN	J	1004	1/1	0.97	0.13	-	65,65,65,65	0
7	MN	I	1002	1/1	0.84	0.09	-	126,126,126,126	0
6	CL	A	1001	1/1	0.95	0.07	-	69,69,69,69	0
7	MN	J	1002	1/1	0.96	0.10	-	101,101,101,101	0
7	MN	J	1003	1/1	0.90	0.14	-	103,103,103,103	0
7	MN	I	1003	1/1	0.94	0.17	-	86,86,86,86	0
7	MN	J	1005	1/1	0.97	0.04	-	108,108,108,108	0
7	MN	I	1004	1/1	0.97	0.07	-	102,102,102,102	0
6	CL	E	1001	1/1	0.99	0.08	-	53,53,53,53	0

6.5 Other polymers (i)

There are no such residues in this entry.