wwPDB X-ray Structure Validation Summary Report (i)

Oct 30, 2023 – 02:05 PM JST

PDB ID	:	5B40
Title	:	The nucleosome structure containing H2B-K120 and H4-K31 monoubiquitinations
Authors	:	Machida, S.; Sekine, S.; Nishiyama, Y.; Horikoshi, N.; Kurumizaka, H.
Deposited on	:	2016-03-22
Resolution	:	3.33 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
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:

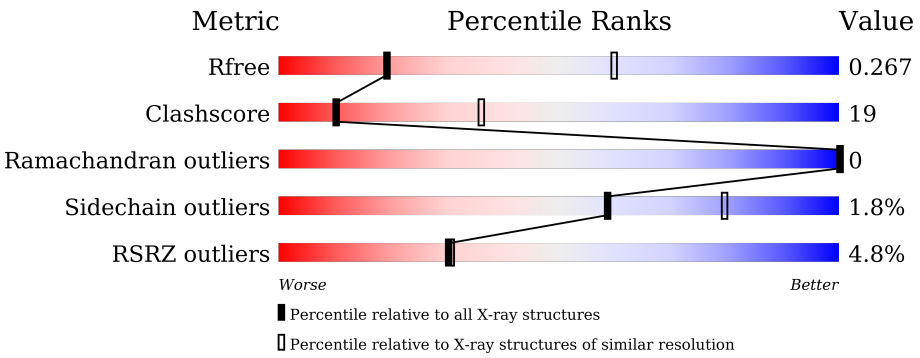
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.33 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	1060 (3.38-3.30)
Clashscore	141614	1111 (3.38-3.30)
Ramachandran outliers	138981	1090 (3.38-3.30)
Sidechain outliers	138945	1089 (3.38-3.30)
RSRZ outliers	127900	1028 (3.38-3.30)

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	A	139	6%, 40%, 26%, •, 32%
1	E	139	8%, 37%, 29%, •, 32%
2	B	106	6%, 46%, 27%, 26%
2	F	106	5%, 45%, 30%, 25%
3	C	133	2%, 55%, 23%, •, 22%
3	G	133	3%, 47%, 30%, •, 22%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	129	2% 49% 23% 28%
4	H	129	4% 49% 22% 29%
5	I	146	% 26% 69% 5%
5	J	146	% 29% 68%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 11817 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 H3.2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	94	772	488	147	135	2	0	0	0
1	E	95	778	491	148	137	2	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q71DI3
A	-2	SER	-	expression tag	UNP Q71DI3
A	-1	HIS	-	expression tag	UNP Q71DI3
A	110	ALA	CYS	engineered mutation	UNP Q71DI3
E	-3	GLY	-	expression tag	UNP Q71DI3
E	-2	SER	-	expression tag	UNP Q71DI3
E	-1	HIS	-	expression tag	UNP Q71DI3
E	110	ALA	CYS	engineered mutation	UNP Q71DI3

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	78	616	388	119	107	2	0	0	0
2	F	80	638	402	124	110	2	0	0	0

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	31	CYS	LYS	engineered mutation	UNP P62805

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	GLY	-	expression tag	UNP P62805
F	-2	SER	-	expression tag	UNP P62805
F	-1	HIS	-	expression tag	UNP P62805
F	31	CYS	LYS	engineered mutation	UNP P62805

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	104	801	505	156	140	0	0	0
3	G	104	805	508	157	140	0	0	0

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
			Total	C	N	O	S			
4	D	93	722	453	129	137	3	0	0	0
4	H	91	705	444	124	134	3	0	0	0

There are 8 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
D	120	CYS	LYS	engineered mutation	UNP P06899
H	-3	GLY	-	expression tag	UNP P06899
H	-2	SER	-	expression tag	UNP P06899
H	-1	HIS	-	expression tag	UNP P06899
H	120	CYS	LYS	engineered mutation	UNP P06899

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

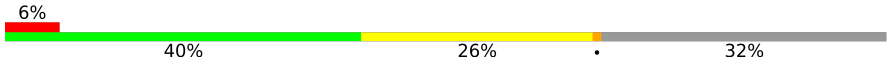
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	I	146	2990	1431	540	874	145	0	0	0
			Total	C	N	O	P			
5	J	146	2990	1431	540	874	145	0	0	0

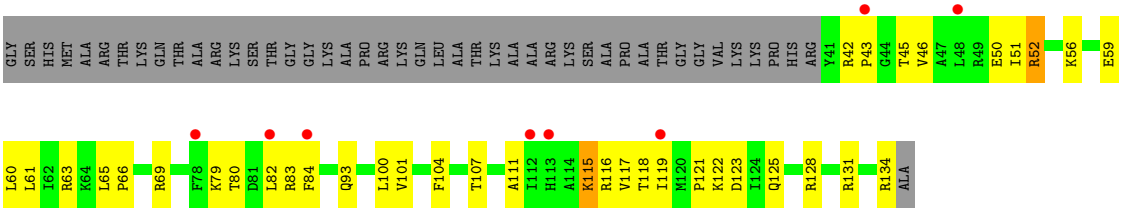
3 Residue-property plots (i)

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: Histone H3.2

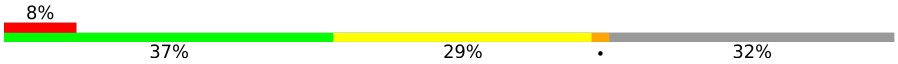
Chain A:

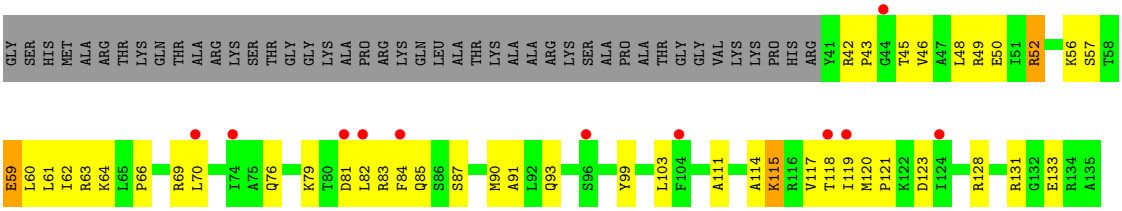




- Molecule 1: Histone H3.2

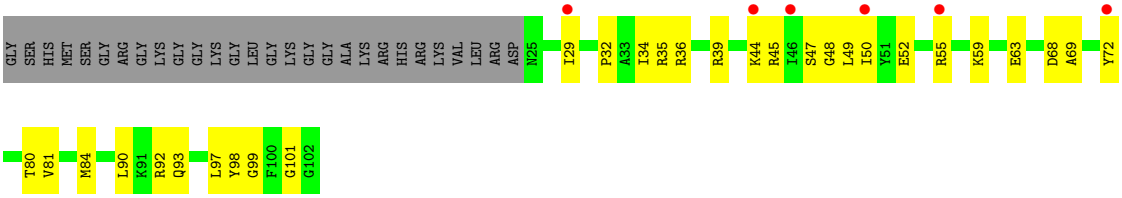
Chain E:





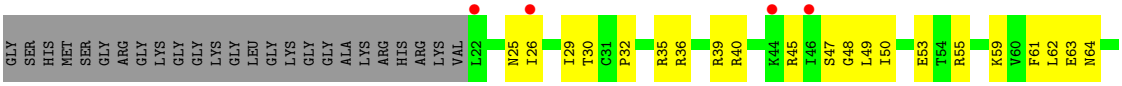
- Molecule 2: Histone H4

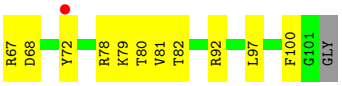
Chain B:



- Molecule 2: Histone H4

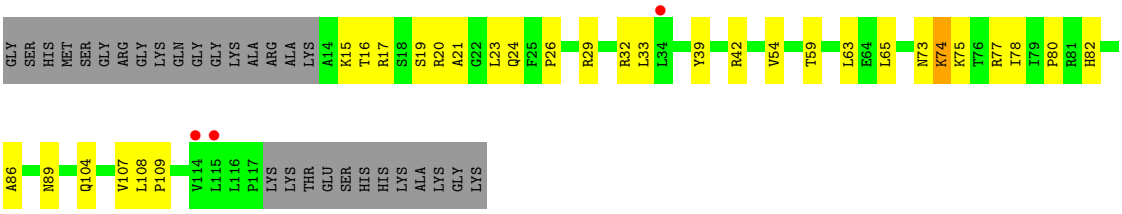
Chain F:





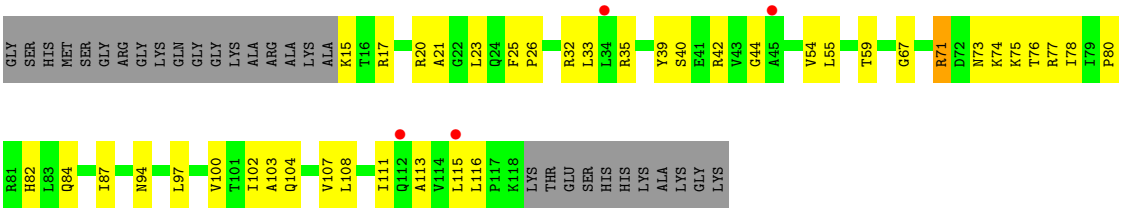
• Molecule 3: Histone H2A type 1-B/E

Chain C:



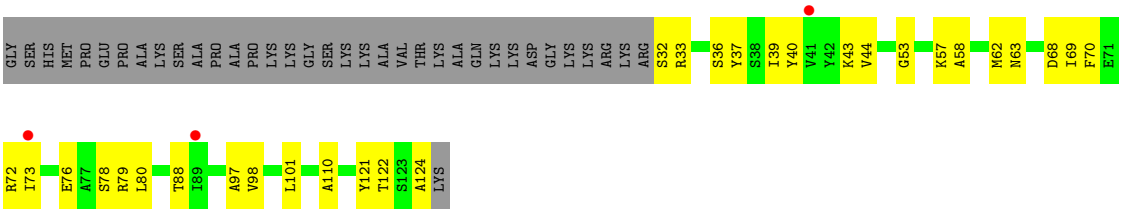
• Molecule 3: Histone H2A type 1-B/E

Chain G:



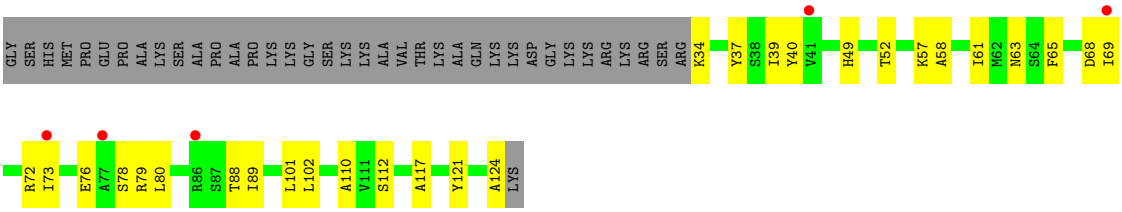
• Molecule 4: Histone H2B type 1-J

Chain D:



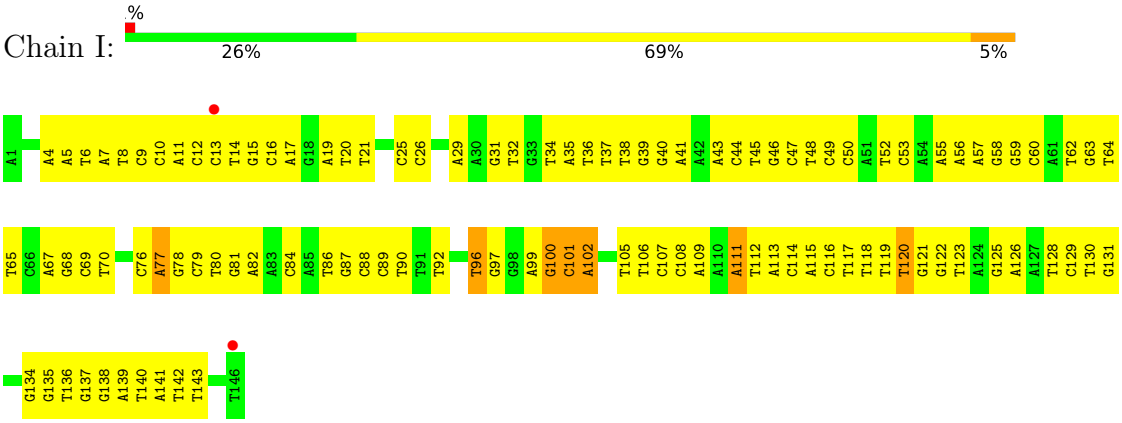
• Molecule 4: Histone H2B type 1-J

Chain H:



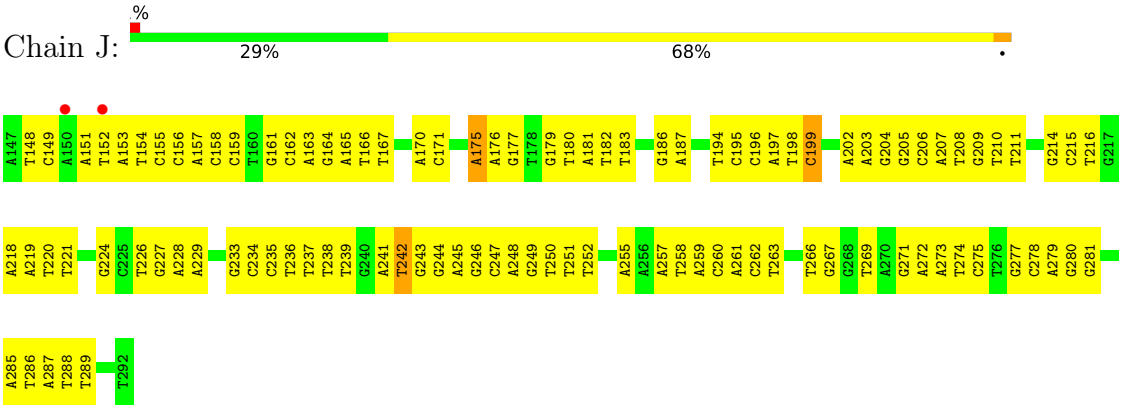
• Molecule 5: DNA (146-MER)

Chain I:



- Molecule 5: DNA (146-MER)

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	100.42Å 100.42Å 186.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.39 – 3.33 44.18 – 3.33	Depositor EDS
% Data completeness (in resolution range)	97.6 (39.39-3.33) 97.7 (44.18-3.33)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.79 (at 3.32Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.201 , 0.263 0.205 , 0.267	Depositor DCC
R_{free} test set	1997 reflections (6.66%)	wwPDB-VP
Wilson B-factor (Å^2)	101.4	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 74.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	0.068 for -h,-k,l 0.458 for h,-h-k,-l 0.068 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11817	wwPDB-VP
Average B, all atoms (Å^2)	122.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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)

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	0.66	0/782	0.85	0/1049
1	E	0.69	0/788	0.92	0/1056
2	B	0.72	0/623	0.93	0/834
2	F	0.71	0/645	0.89	1/865 (0.1%)
3	C	0.67	0/811	0.90	0/1096
3	G	0.67	0/815	1.00	1/1100 (0.1%)
4	D	0.70	0/733	0.81	0/987
4	H	0.67	0/716	0.86	1/965 (0.1%)
5	I	0.91	3/3354 (0.1%)	1.10	10/5175 (0.2%)
5	J	0.89	2/3354 (0.1%)	1.07	2/5175 (0.0%)
All	All	0.81	5/12621 (0.0%)	1.01	15/18302 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	175	DA	C3'-O3'	-6.71	1.35	1.44
5	I	81	DG	C3'-O3'	-6.45	1.35	1.44
5	J	224	DG	C3'-O3'	-6.12	1.35	1.44
5	I	77	DA	C3'-O3'	-6.04	1.36	1.44
5	I	49	DC	C1'-N1	5.26	1.56	1.49

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	I	120	DT	O4'-C1'-N1	6.84	112.79	108.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	J	199	DC	O4'-C1'-N1	5.82	112.08	108.00
3	G	108	LEU	CA-CB-CG	5.56	128.09	115.30
5	I	50	DC	O5'-P-OP1	-5.46	100.78	105.70
5	I	101	DC	P-O5'-C5'	-5.45	112.17	120.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	115	LYS	Peptide

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	A	772	0	811	39	0
1	E	778	0	816	53	0
2	B	616	0	651	27	0
2	F	638	0	676	35	0
3	C	801	0	853	37	0
3	G	805	0	861	45	0
4	D	722	0	737	34	0
4	H	705	0	719	32	0
5	I	2990	0	1652	108	0
5	J	2990	0	1652	107	0
All	All	11817	0	9428	397	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 19.

The worst 5 of 397 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:E:49:ARG:HD3	1:E:52:ARG:HE	1.14	1.07
5:J:182:DT:H2"	5:J:183:DT:H5"	1.52	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:62:ILE:HD13	2:F:29:ILE:HD12	1.54	0.89
3:G:104:GLN:HE21	4:H:57:LYS:HB3	1.36	0.89
3:G:15:LYS:O	3:G:20:ARG:NH2	2.08	0.87

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	92/139 (66%)	87 (95%)	5 (5%)	0	100	100
1	E	93/139 (67%)	86 (92%)	7 (8%)	0	100	100
2	B	76/106 (72%)	68 (90%)	8 (10%)	0	100	100
2	F	78/106 (74%)	72 (92%)	6 (8%)	0	100	100
3	C	102/133 (77%)	97 (95%)	5 (5%)	0	100	100
3	G	102/133 (77%)	98 (96%)	4 (4%)	0	100	100
4	D	91/129 (70%)	89 (98%)	2 (2%)	0	100	100
4	H	89/129 (69%)	89 (100%)	0	0	100	100
All	All	723/1014 (71%)	686 (95%)	37 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	81/112 (72%)	77 (95%)	4 (5%)	25	58
1	E	81/112 (72%)	77 (95%)	4 (5%)	25	58
2	B	63/81 (78%)	63 (100%)	0	100	100
2	F	66/81 (82%)	66 (100%)	0	100	100
3	C	82/102 (80%)	81 (99%)	1 (1%)	71	84
3	G	83/102 (81%)	82 (99%)	1 (1%)	71	84
4	D	79/107 (74%)	79 (100%)	0	100	100
4	H	77/107 (72%)	76 (99%)	1 (1%)	69	83
All	All	612/804 (76%)	601 (98%)	11 (2%)	59	79

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	117	VAL
1	E	120	MET
4	H	112	SER
3	G	71	ARG
3	C	74	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
4	D	63	ASN
1	E	93	GLN
3	G	104	GLN

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)

There are no ligands in this entry.

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	A	94/139 (67%)	0.71	8 (8%)	10	11	58, 80, 118, 144	0
1	E	95/139 (68%)	0.79	11 (11%)	4	4	60, 83, 115, 142	0
2	B	78/106 (73%)	0.72	6 (7%)	13	13	52, 75, 97, 102	0
2	F	80/106 (75%)	0.71	5 (6%)	20	21	51, 77, 103, 144	0
3	C	104/133 (78%)	0.51	3 (2%)	51	51	51, 75, 106, 114	0
3	G	104/133 (78%)	0.41	4 (3%)	40	39	54, 78, 109, 128	0
4	D	93/129 (72%)	0.51	3 (3%)	47	46	53, 76, 109, 136	0
4	H	91/129 (70%)	0.62	5 (5%)	25	26	54, 75, 100, 122	0
5	I	146/146 (100%)	-0.51	2 (1%)	75	75	119, 163, 204, 221	0
5	J	146/146 (100%)	-0.52	2 (1%)	75	75	115, 160, 200, 223	0
All	All	1031/1306 (78%)	0.29	49 (4%)	30	31	51, 86, 183, 223	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	22	LEU	5.5
1	E	119	ILE	5.0
2	F	44	LYS	4.2
1	E	44	GLY	4.0
1	E	118	THR	3.8

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.