



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 17, 2022 – 11:10 PM EDT

PDB ID : 4KUD
Title : Crystal structure of N-terminal acetylated Sir3 BAH domain D205N mutant in complex with yeast nucleosome core particle
Authors : Yang, D.; Fang, Q.; Wang, M.; Ren, R.; Wang, H.; He, M.; Sun, Y.; Yang, N.; Xu, R.M.
Deposited on : 2013-05-22
Resolution : 3.20 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 ⓘ 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.29
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) : 2.29

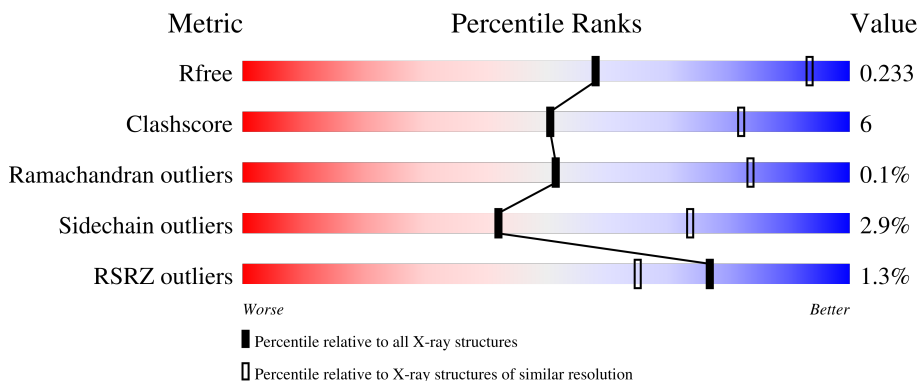
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 $\leq 5\%$. 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	136	 2% 61% 10% 29%
1	E	136	 2% 62% 10% 28%
2	B	103	 73% 13% 15%
2	F	103	 2% 67% 20% 13%
3	C	132	 2% 62% 14% 22%

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Mol	Chain	Length	Quality of chain
3	G	132	<p>2% 67% 12% 20%</p>
4	D	131	<p>% 56% 14% 29%</p>
4	H	131	<p>% 55% 16% 28%</p>
5	I	146	<p>3% 71% 26% .</p>
5	J	146	<p>2% 77% 21% .</p>
6	K	224	<p>79% 15% . 5%</p>
6	L	224	<p>75% 19% 5%</p>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 15732 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	96	790	502	151	137	0	0	0
1	E	98	808	514	155	139	0	0	0

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	88	709	446	142	121	0	0	0
2	F	90	717	450	144	123	0	0	0

- Molecule 3 is a protein called Histone H2A.2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	103	795	499	156	140	0	0	0
3	G	105	810	508	159	143	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ALA	SER	engineered mutation	UNP P04912
G	1	ALA	SER	engineered mutation	UNP P04912

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	93	724	455	125	143	1	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	94	Total	C	N	O	S	0	0	0
			735	461	129	144	1			

- Molecule 5 is a DNA chain called nucleosome DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	146	Total	C	N	O	P	0	0	0
			2990	1430	541	874	145			
5	J	146	Total	C	N	O	P	0	0	0
			2990	1430	541	874	145			

- Molecule 6 is a protein called Regulatory protein SIR3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	K	213	Total	C	N	O	S	0	0	0
			1799	1158	303	336	2			
6	L	213	Total	C	N	O	S	0	0	0
			1799	1158	303	336	2			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	205	ASN	ASP	engineered mutation	UNP P06701
K	220	HIS	-	expression tag	UNP P06701
K	221	HIS	-	expression tag	UNP P06701
K	222	HIS	-	expression tag	UNP P06701
K	223	HIS	-	expression tag	UNP P06701
K	224	HIS	-	expression tag	UNP P06701
K	225	HIS	-	expression tag	UNP P06701
L	205	ASN	ASP	engineered mutation	UNP P06701
L	220	HIS	-	expression tag	UNP P06701
L	221	HIS	-	expression tag	UNP P06701
L	222	HIS	-	expression tag	UNP P06701
L	223	HIS	-	expression tag	UNP P06701
L	224	HIS	-	expression tag	UNP P06701
L	225	HIS	-	expression tag	UNP P06701

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	6	Total	O	0	0
			6	6		

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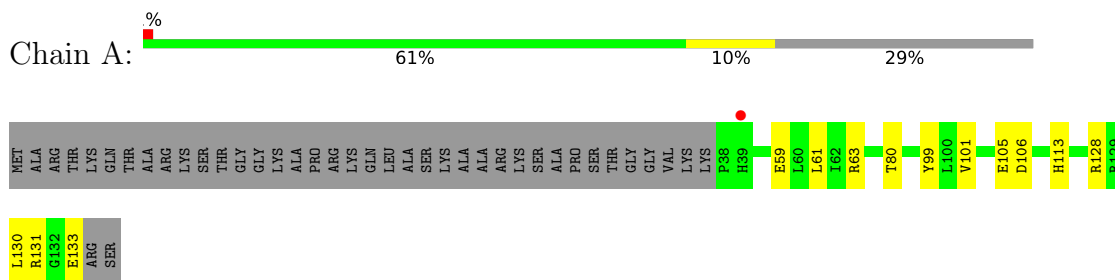
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	6	Total O 6 6	0	0
7	C	4	Total O 4 4	0	0
7	D	7	Total O 7 7	0	0
7	E	4	Total O 4 4	0	0
7	F	8	Total O 8 8	0	0
7	G	2	Total O 2 2	0	0
7	H	7	Total O 7 7	0	0
7	K	14	Total O 14 14	0	0
7	L	8	Total O 8 8	0	0

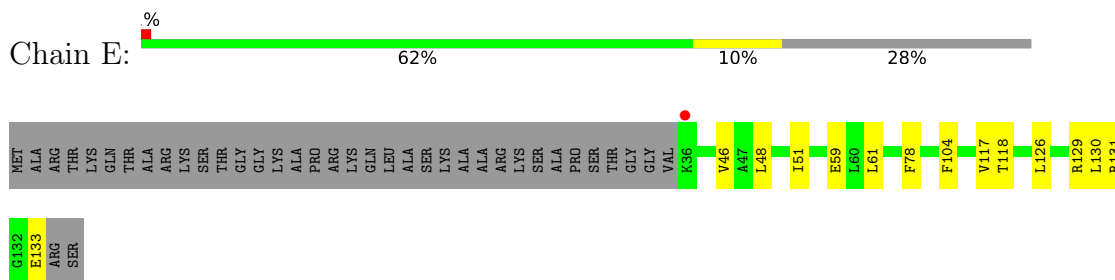
3 Residue-property plots [i](#)

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.

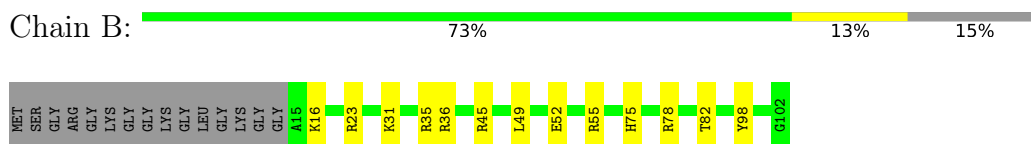
- Molecule 1: Histone H3



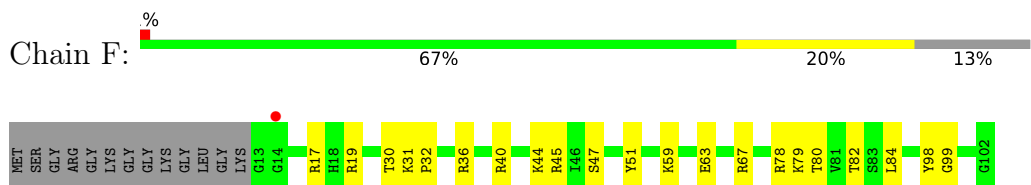
- Molecule 1: Histone H3



- Molecule 2: Histone H4

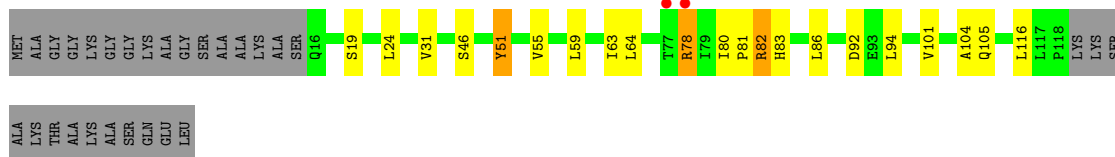


- Molecule 2: Histone H4

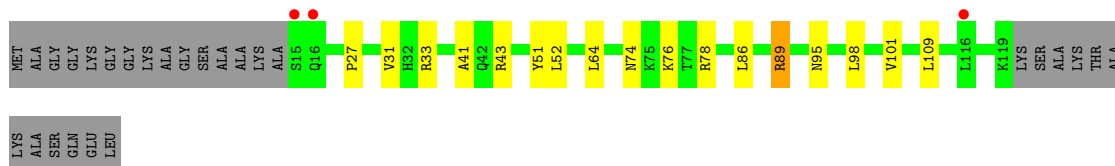


- Molecule 3: Histone H2A.2

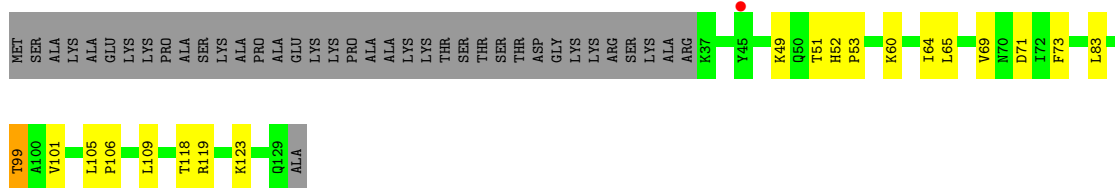




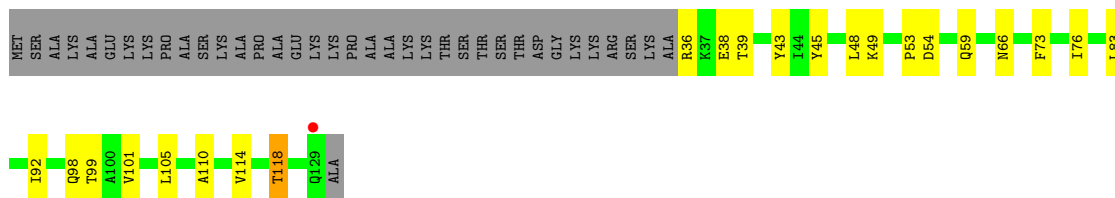
● Molecule 3: Histone H2A.2



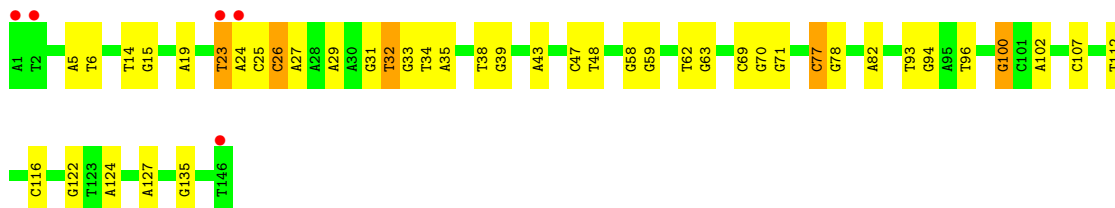
● Molecule 4: Histone H2B.1



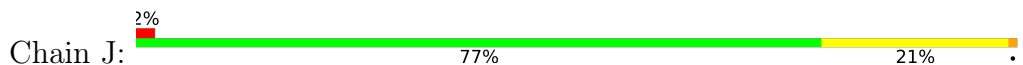
● Molecule 4: Histone H2B.1



● Molecule 5: nucleosome DNA



● Molecule 5: nucleosome DNA





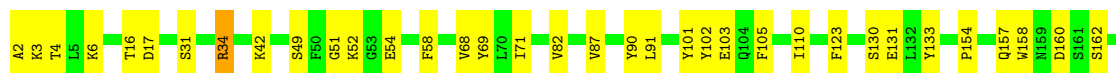
- Molecule 6: Regulatory protein SIR3

Chain K: 79% 15% 5%



- Molecule 6: Regulatory protein SIR3

Chain L: 75% 19% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	108.33Å 108.33Å 498.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.39 – 3.20 49.68 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.39-3.20) 99.5 (49.68-3.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 3.19Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.198 , 0.237 0.190 , 0.233	Depositor DCC
R_{free} test set	2758 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	77.1	Xtrriage
Anisotropy	0.277	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 38.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.057 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	15732	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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, 0.333 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: AYA

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	0.34	0/801	0.48	0/1072
1	E	0.36	0/819	0.49	0/1095
2	B	0.38	0/717	0.52	0/956
2	F	0.35	0/725	0.49	0/966
3	C	0.32	0/806	0.50	0/1091
3	G	0.34	0/821	0.50	0/1110
4	D	0.35	0/734	0.50	0/989
4	H	0.37	0/745	0.51	0/1003
5	I	0.51	0/3354	1.20	17/5175 (0.3%)
5	J	0.53	0/3354	1.23	18/5175 (0.3%)
6	K	0.35	0/1832	0.52	0/2475
6	L	0.35	0/1832	0.53	0/2475
All	All	0.42	0/16540	0.89	35/23582 (0.1%)

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	170	DA	O4'-C1'-N9	9.90	114.93	108.00
5	I	23	DT	O4'-C1'-N1	8.32	113.82	108.00
5	I	116	DC	O4'-C1'-N1	7.74	113.42	108.00
5	I	23	DT	O4'-C4'-C3'	-7.58	101.45	106.00
5	J	170	DA	C1'-O4'-C4'	-7.51	102.59	110.10

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	A	790	0	838	8	0
1	E	808	0	863	11	0
2	B	709	0	763	9	0
2	F	717	0	769	17	0
3	C	795	0	834	17	0
3	G	810	0	852	19	0
4	D	724	0	743	13	0
4	H	735	0	756	18	0
5	I	2990	0	1651	27	0
5	J	2990	0	1651	21	0
6	K	1799	0	1781	20	0
6	L	1799	0	1781	27	0
7	A	6	0	0	0	0
7	B	6	0	0	0	0
7	C	4	0	0	0	0
7	D	7	0	0	0	0
7	E	4	0	0	0	0
7	F	8	0	0	0	0
7	G	2	0	0	0	0
7	H	7	0	0	0	0
7	K	14	0	0	0	0
7	L	8	0	0	0	0
All	All	15732	0	13282	157	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 6.

The worst 5 of 157 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)
3:G:33:ARG:NH1	5:J:176:DA:OP1	2.17	0.77
3:C:46:SER:OG	5:J:257:DA:OP2	2.04	0.75
6:L:172:LEU:HD21	6:L:174:ARG:HD3	1.71	0.72
1:A:130:LEU:HD12	1:E:130:LEU:HD12	1.71	0.71
6:K:4:THR:HG22	6:K:6:LYS:H	1.56	0.70

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	94/136 (69%)	94 (100%)	0	0	100	100
1	E	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
2	B	86/103 (84%)	84 (98%)	2 (2%)	0	100	100
2	F	88/103 (85%)	86 (98%)	2 (2%)	0	100	100
3	C	101/132 (76%)	96 (95%)	5 (5%)	0	100	100
3	G	103/132 (78%)	99 (96%)	4 (4%)	0	100	100
4	D	91/131 (70%)	87 (96%)	4 (4%)	0	100	100
4	H	92/131 (70%)	89 (97%)	3 (3%)	0	100	100
6	K	211/224 (94%)	201 (95%)	9 (4%)	1 (0%)	29	67
6	L	211/224 (94%)	200 (95%)	11 (5%)	0	100	100
All	All	1173/1452 (81%)	1131 (96%)	41 (4%)	1 (0%)	51	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	K	160	ASP

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	84/113 (74%)	81 (96%)	3 (4%)	35	69
1	E	86/113 (76%)	83 (96%)	3 (4%)	36	69
2	B	74/81 (91%)	72 (97%)	2 (3%)	44	75
2	F	74/81 (91%)	72 (97%)	2 (3%)	44	75
3	C	82/98 (84%)	77 (94%)	5 (6%)	18	54
3	G	84/98 (86%)	83 (99%)	1 (1%)	71	88
4	D	81/109 (74%)	79 (98%)	2 (2%)	47	77
4	H	82/109 (75%)	80 (98%)	2 (2%)	49	77
6	K	200/210 (95%)	194 (97%)	6 (3%)	41	73
6	L	200/210 (95%)	196 (98%)	4 (2%)	55	80
All	All	1047/1222 (86%)	1017 (97%)	30 (3%)	42	74

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	129	ARG
6	L	130	SER
3	G	89	ARG
6	L	194	ARG
6	K	193	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	G	74	ASN
4	H	87	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](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	AYA	K	2	6	6,7,8	1.96	2 (33%)	5,8,10	1.01	0
6	AYA	L	2	6	6,7,8	1.79	2 (33%)	5,8,10	1.24	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	AYA	K	2	6	-	1/4/6/8	-
6	AYA	L	2	6	-	0/4/6/8	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	K	2	AYA	CA-N	-3.64	1.42	1.46
6	L	2	AYA	CA-N	-2.85	1.43	1.46
6	L	2	AYA	CT-N	2.66	1.43	1.34
6	K	2	AYA	CT-N	2.40	1.42	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	2	AYA	CM-CT-N	2.11	119.67	116.10

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	K	2	AYA	C-CA-N-CT

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	2	AYA	1	0

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	96/136 (70%)	-0.03	1 (1%) 82 72	47, 65, 107, 135	0
1	E	98/136 (72%)	-0.12	1 (1%) 82 72	48, 64, 107, 124	0
2	B	88/103 (85%)	-0.15	0 100 100	48, 61, 76, 83	0
2	F	90/103 (87%)	-0.22	1 (1%) 80 69	47, 60, 80, 92	0
3	C	103/132 (78%)	-0.16	2 (1%) 66 53	56, 68, 103, 112	0
3	G	105/132 (79%)	0.01	3 (2%) 51 36	49, 63, 98, 113	0
4	D	93/131 (70%)	-0.07	1 (1%) 80 69	49, 66, 98, 112	0
4	H	94/131 (71%)	-0.07	1 (1%) 80 69	47, 61, 86, 108	0
5	I	146/146 (100%)	0.04	5 (3%) 45 29	86, 128, 193, 202	0
5	J	146/146 (100%)	0.11	3 (2%) 63 49	86, 135, 194, 209	0
6	K	212/224 (94%)	-0.36	0 100 100	49, 62, 93, 107	1 (0%)
6	L	212/224 (94%)	-0.19	1 (0%) 91 86	47, 67, 104, 117	0
All	All	1483/1744 (85%)	-0.11	19 (1%) 77 65	47, 68, 162, 209	1 (0%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	16	GLN	4.0
5	I	146	DT	3.9
3	G	15	SER	3.4
1	A	39	HIS	3.1
5	J	292	DT	3.0

6.2 Non-standard residues in protein, DNA, RNA chains [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	AYA	K	2	8/9	0.97	0.20	56,59,63,63	0
6	AYA	L	2	8/9	0.98	0.22	55,56,60,60	0

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.