



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 8, 2017 – 10:02 PM EDT

PDB ID : 5OXV  
Title : Structure of the 4\_601\_157 tetranucleosome (C2 form)  
Authors : Ekundayo, B.; Schalch, T.  
Deposited on : unknown  
Resolution : 6.72 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030345

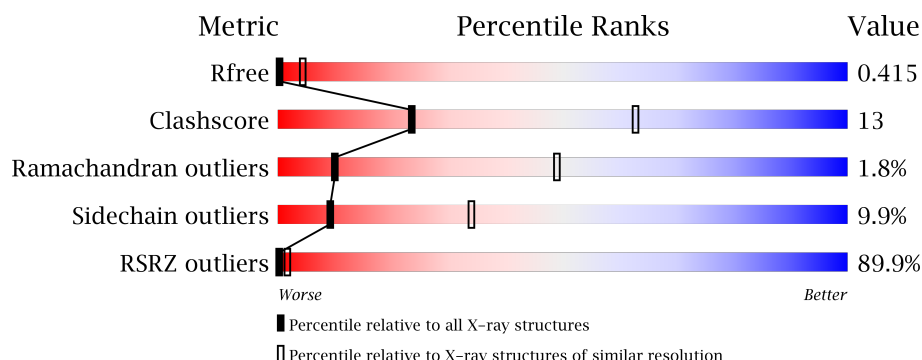
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 6.72 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))
$R_{free}$	100719	1099 (9.50-3.70)
Clashscore	112137	1033 (9.50-3.80)
Ramachandran outliers	110173	1002 (9.50-3.76)
Sidechain outliers	110143	1097 (9.50-3.70)
RSRZ outliers	101464	1002 (9.50-3.72)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	J	312	<div> <div>99%</div> <div> <div>44%</div> <div>44%</div> <div>12%</div> <div>.</div> </div> </div>
2	D	126	<div> <div>65%</div> <div> <div>43%</div> <div>27%</div> <div>5%</div> <div>.</div> <div>25%</div> </div> </div>
2	H	126	<div> <div>61%</div> <div> <div>44%</div> <div>27%</div> <div>.</div> <div>26%</div> </div> </div>
2	N	126	<div> <div>61%</div> <div> <div>44%</div> <div>26%</div> <div>5%</div> <div>.</div> <div>25%</div> </div> </div>
2	R	126	<div> <div>60%</div> <div> <div>44%</div> <div>26%</div> <div>.</div> <div>26%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	C	130	
3	G	130	
3	M	130	
3	Q	130	
4	B	102	
4	F	102	
4	L	102	
4	P	102	
5	A	135	
5	E	135	
5	K	135	
5	O	135	
6	I	313	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 24648 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 STRAND 1 (601-based sequence model).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	J	310	Total	C	N	O	P	0	0	0
			6394	3024	1203	1857	310			

- Molecule 2 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	93	Total	C	N	O	S	0	0	0
			726	457	130	137	2			
2	N	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			
2	H	93	Total	C	N	O	S	0	0	0
			726	457	130	137	2			
2	D	95	Total	C	N	O	S	0	0	0
			745	469	134	140	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	29	THR	SER	conflict	UNP P02281
N	29	THR	SER	conflict	UNP P02281
H	29	THR	SER	conflict	UNP P02281
D	29	THR	SER	conflict	UNP P02281

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	Q	105	Total	C	N	O	0	0	0
			809	510	158	141			
3	M	103	Total	C	N	O	0	0	0
			795	501	155	139			
3	G	105	Total	C	N	O	0	0	0
			809	510	158	141			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	103	Total	C	N	O	0	0	0
			795	501	155	139			

- Molecule 4 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	P	78	Total	C	N	O	S	0	0	0
			619	391	120	107	1			
4	L	83	Total	C	N	O	S	0	0	0
			662	418	129	114	1			
4	F	78	Total	C	N	O	S	0	0	0
			619	391	120	107	1			
4	B	83	Total	C	N	O	S	0	0	0
			662	418	129	114	1			

- Molecule 5 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	O	97	Total	C	N	O	S	0	0	0
			801	504	155	139	3			
5	K	97	Total	C	N	O	S	0	0	0
			802	506	155	138	3			
5	E	97	Total	C	N	O	S	0	0	0
			801	504	155	139	3			
5	A	97	Total	C	N	O	S	0	0	0
			802	506	155	138	3			

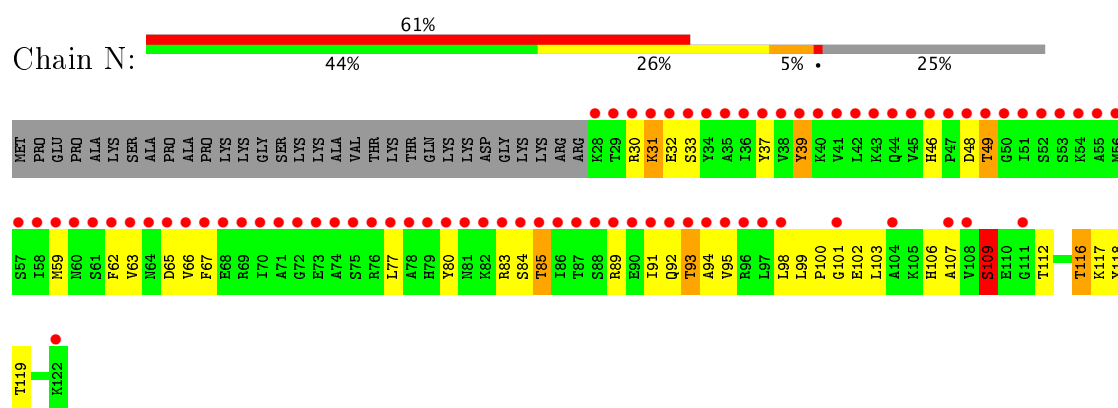
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	102	ALA	GLY	conflict	UNP P84233
K	102	ALA	GLY	conflict	UNP P84233
E	102	ALA	GLY	conflict	UNP P84233
A	102	ALA	GLY	conflict	UNP P84233

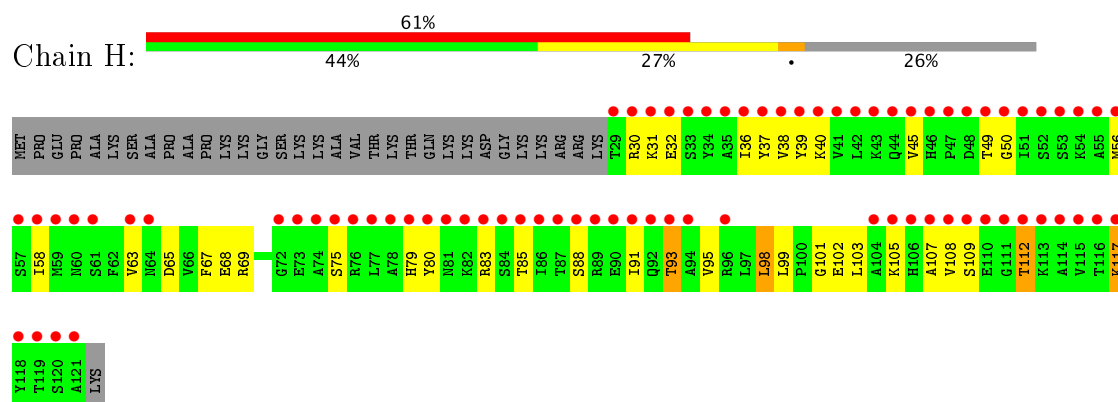
- Molecule 6 is a DNA chain called DNA STRAND 2 (601-based sequence model).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	I	311	Total	C	N	O	P	0	0	0
			6336	3009	1146	1870	311			

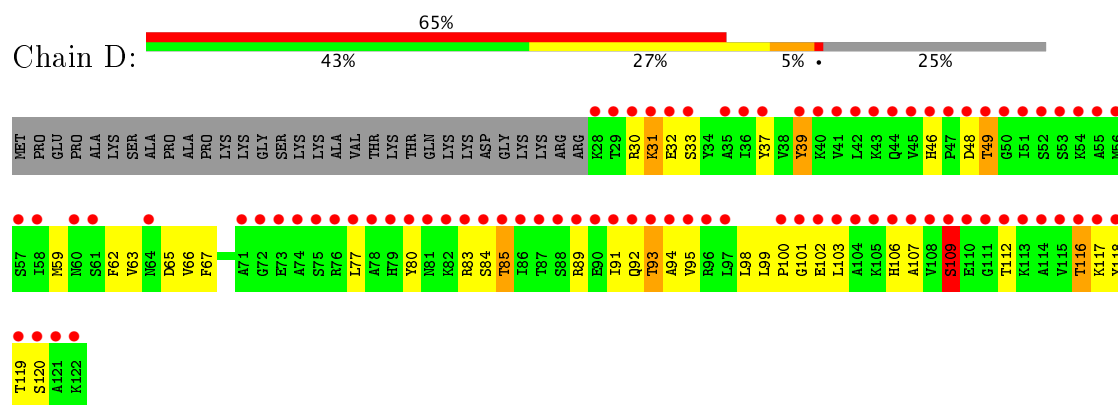




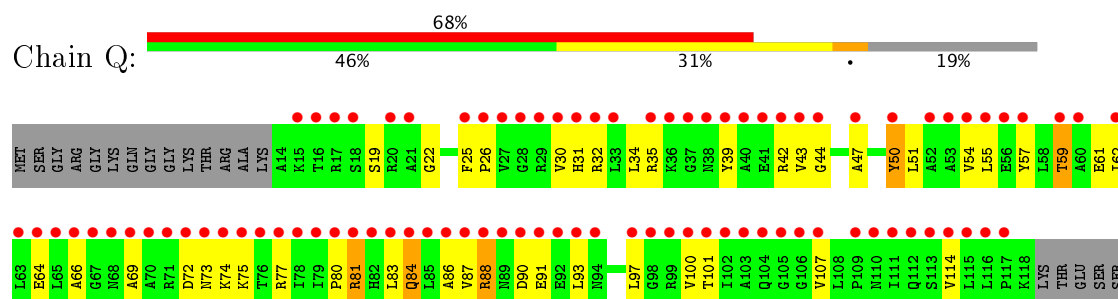
• Molecule 2: Histone H2B 1.1



• Molecule 2: Histone H2B 1.1

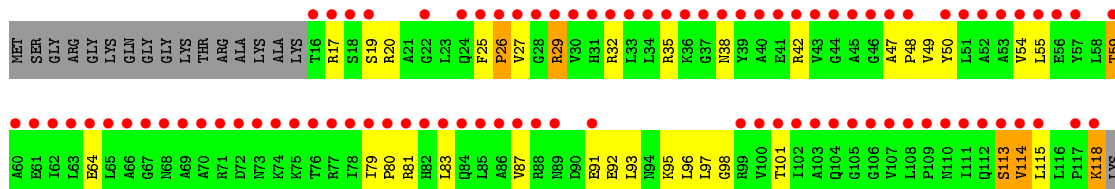


• Molecule 3: Histone H2A



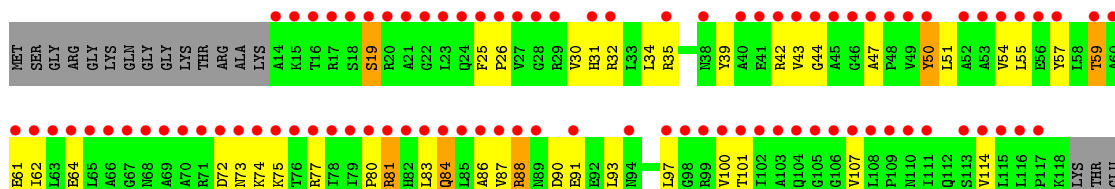
LYS  
SER  
ALA  
LYS  
SER  
LYS

• Molecule 3: Histone H2A



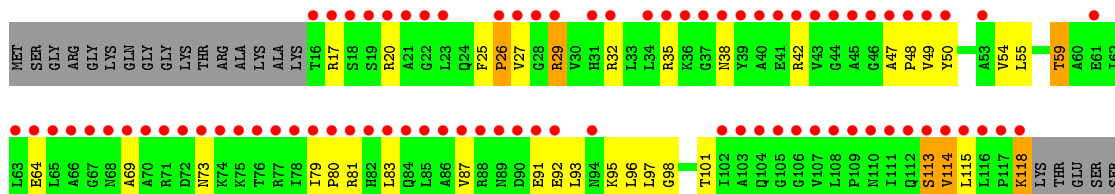
THR  
GLU  
SER  
SER  
LYS  
ALA  
LYS  
LYS

• Molecule 3: Histone H2A



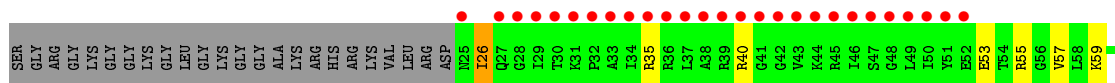
SER  
SER  
LYS  
LYS  
ALA  
SER  
LYS

• Molecule 3: Histone H2A

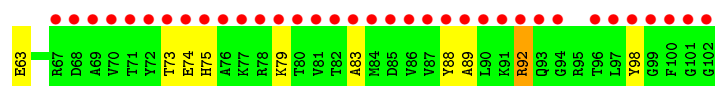


LYS  
SER  
ALA  
LYS  
SER  
LYS

• Molecule 4: Histone H4



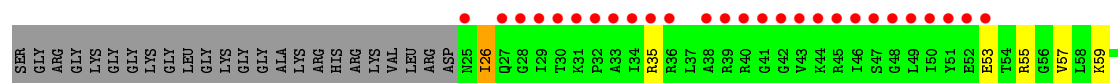




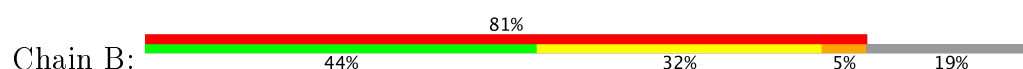
- Molecule 4: Histone H4



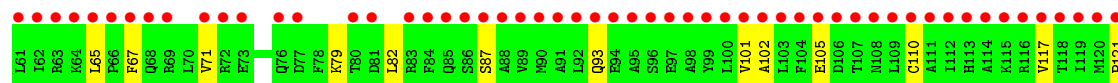
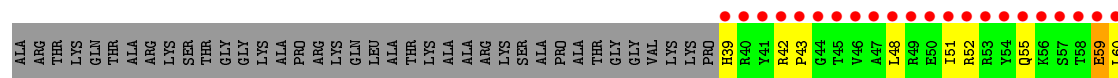
- Molecule 4: Histone H4



- Molecule 4: Histone H4

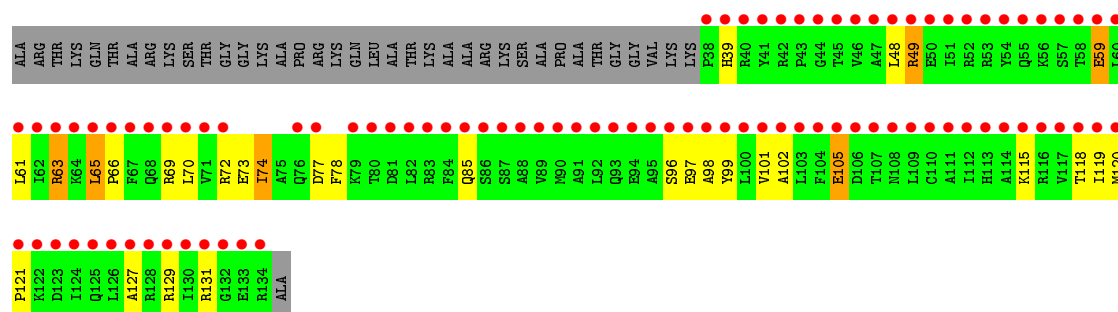


- Molecule 5: Histone H3.2

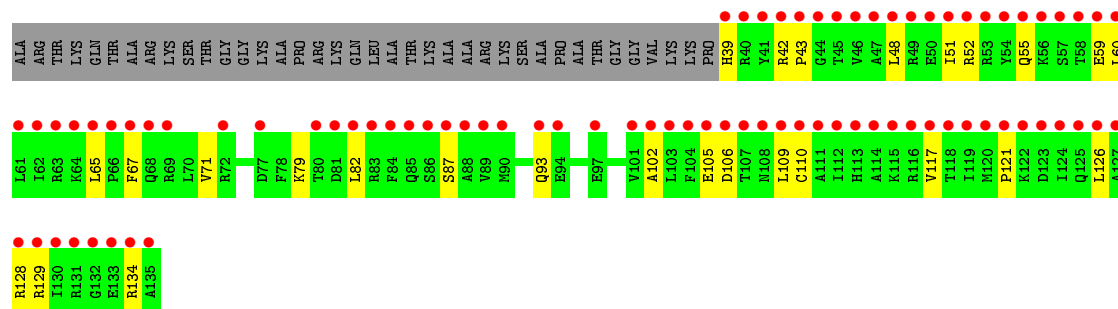


- Molecule 5: Histone H3.2

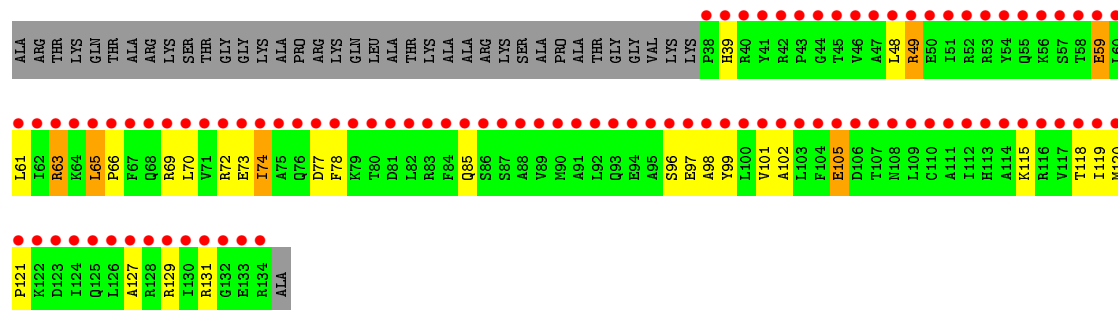
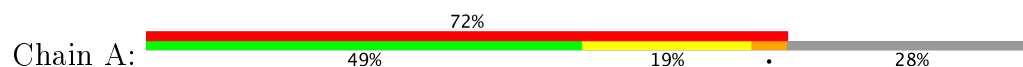




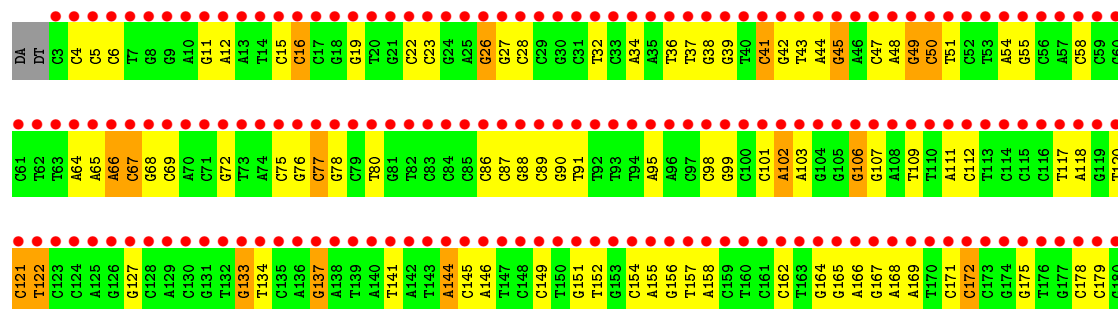
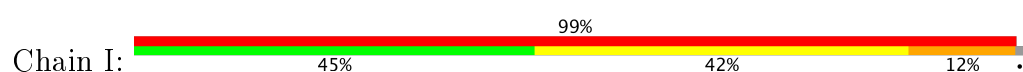
• Molecule 5: Histone H3.2



• Molecule 5: Histone H3.2



• Molecule 6: DNA STRAND 2 (601-based sequence model)



A181	G241	C301
G182	C242	A302
G183	C243	T303
C184	G244	C304
G185	C245	C305
G186	G246	T306
G187	T247	G307
T188	T248	T308
C189	T249	G309
A190	T250	C310
A191	A251	A311
T192	A252	G312
T193	C253	T313
G194	C254	
G195	G255	
T196	C256	
C197	C257	
G198	A258	
T199	A259	
A200	G260	
G201	G261	
A202	G262	
C203	G263	
A204	A264	
G205	T265	
C206	T266	
T207	A267	
C208	C268	
T209	T269	
A210	C270	
G211	C271	
C212	C272	
A213	T273	
C214	A274	
C215	G275	
G216	T276	
C217	C277	
T218	T278	
T219	C279	
A220	C280	
A221	A281	
A222	G282	
C223	G283	
G224	G284	
C225	A285	
A226	C286	
C227	G287	
G228	T288	
T229	G289	
A230	T290	
C231	C291	
G232	A292	
C233	G293	
G234	A294	
C235	T295	
T236	A296	
G237	T297	
T238	A298	
C239	T299	
C240	A300	

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	348.84Å 63.27Å 271.36Å 90.00° 124.74° 90.00°	Depositor
Resolution (Å)	71.67 – 6.72 222.99 – 6.72	Depositor EDS
% Data completeness (in resolution range)	87.8 (71.67-6.72) 82.3 (222.99-6.72)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.15 (at 6.74Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, $R_{free}$	0.317 , 0.352 0.366 , 0.415	Depositor DCC
$R_{free}$ test set	947 reflections (12.69%)	DCC
Wilson B-factor (Å <sup>2</sup> )	237.0	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.94 , -10.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.29$ , $\langle L^2 \rangle = 0.12$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.78	EDS
Total number of atoms	24648	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	637.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.55% 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 [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	J	0.74	2/7182 (0.0%)	1.47	96/11093 (0.9%)
2	D	0.49	0/756	0.64	0/1015
2	H	0.62	0/737	0.70	0/993
2	N	0.49	0/756	0.64	0/1015
2	R	0.62	0/737	0.70	0/993
3	C	0.42	0/805	0.61	0/1088
3	G	0.62	0/819	0.76	0/1106
3	M	0.43	0/805	0.61	0/1088
3	Q	0.63	0/819	0.76	0/1106
4	B	0.67	0/669	0.84	0/894
4	F	0.46	0/626	0.61	0/837
4	L	0.67	0/669	0.84	0/894
4	P	0.45	0/626	0.61	0/837
5	A	0.66	0/814	0.73	0/1092
5	E	0.41	0/812	0.58	0/1088
5	K	0.66	0/814	0.73	0/1092
5	O	0.41	0/812	0.58	0/1088
6	I	0.74	4/7098 (0.1%)	1.38	84/10943 (0.8%)
All	All	0.66	6/26356 (0.0%)	1.17	180/38262 (0.5%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	-310	DG	C1'-N9	-6.27	1.38	1.47
6	I	310	DC	C1'-N1	5.73	1.56	1.49
1	J	-305	DG	C1'-N9	-5.53	1.39	1.47
6	I	312	DG	C1'-N9	-5.43	1.39	1.47
6	I	308	DT	C1'-N1	5.30	1.56	1.49

The worst 5 of 180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	-163	DA	O3'-P-O5'	33.99	168.59	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	-163	DA	P-O3'-C3'	29.81	155.47	119.70
1	J	-163	DA	OP1-P-O3'	-20.17	60.83	105.20
6	I	162	DC	O3'-P-O5'	14.02	130.63	104.00
1	J	-163	DA	OP2-P-O3'	-12.28	78.18	105.20

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	J	6394	0	3474	141	2
2	D	745	0	773	37	2
2	H	726	0	747	36	1
2	N	745	0	773	36	2
2	R	726	0	747	35	2
3	C	795	0	846	25	0
3	G	809	0	864	43	1
3	M	795	0	846	26	1
3	Q	809	0	864	44	1
4	B	662	0	709	36	0
4	F	619	0	659	16	0
4	L	662	0	709	36	0
4	P	619	0	659	17	0
5	A	802	0	841	22	0
5	E	801	0	838	15	0
5	K	802	0	841	21	0
5	O	801	0	838	17	0
6	I	6336	0	3489	146	2
All	All	24648	0	19517	554	7

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 13.

The worst 5 of 554 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)
2:D:93:THR:HG21	4:B:75:HIS:CD2	1.58	1.37
2:N:93:THR:HG21	4:L:75:HIS:CD2	1.58	1.37
1:J:-306:DA:C2	6:I:307:DG:N2	1.97	1.32
1:J:-306:DA:H2	6:I:307:DG:C2	1.48	1.29
1:J:-306:DA:C2	6:I:307:DG:C2	2.28	1.21

The worst 5 of 7 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:-312:DC:P	6:I:313:DT:O3'[2_656]	1.61	0.59
1:J:-312:DC:OP2	6:I:313:DT:O3'[2_656]	1.79	0.41
2:H:117:LYS:CE	2:D:117:LYS:CE[1_545]	1.86	0.34
2:R:117:LYS:CE	2:N:117:LYS:NZ[1_565]	1.90	0.30
3:Q:22:GLY:CA	2:N:117:LYS:CE[1_565]	2.00	0.20

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	D	93/126 (74%)	82 (88%)	9 (10%)	2 (2%)	8	44
2	H	91/126 (72%)	79 (87%)	11 (12%)	1 (1%)	17	60
2	N	93/126 (74%)	81 (87%)	10 (11%)	2 (2%)	8	44
2	R	91/126 (72%)	80 (88%)	10 (11%)	1 (1%)	17	60
3	C	101/130 (78%)	88 (87%)	9 (9%)	4 (4%)	3	31
3	G	103/130 (79%)	88 (85%)	15 (15%)	0	100	100
3	M	101/130 (78%)	88 (87%)	9 (9%)	4 (4%)	3	31
3	Q	103/130 (79%)	88 (85%)	15 (15%)	0	100	100
4	B	81/102 (79%)	70 (86%)	8 (10%)	3 (4%)	4	33
4	F	76/102 (74%)	67 (88%)	9 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L	81/102 (79%)	70 (86%)	8 (10%)	3 (4%)	4	33
4	P	76/102 (74%)	67 (88%)	9 (12%)	0	100	100
5	A	95/135 (70%)	83 (87%)	9 (10%)	3 (3%)	5	36
5	E	95/135 (70%)	86 (90%)	9 (10%)	0	100	100
5	K	95/135 (70%)	83 (87%)	9 (10%)	3 (3%)	5	36
5	O	95/135 (70%)	86 (90%)	9 (10%)	0	100	100
All	All	1470/1972 (74%)	1286 (88%)	158 (11%)	26 (2%)	10	49

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	N	101	GLY
4	L	29	ILE
5	K	73	GLU
2	D	101	GLY
4	B	29	ILE

### 5.3.2 Protein sidechains ⓘ

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	D	81/106 (76%)	69 (85%)	12 (15%)	3	20
2	H	79/106 (74%)	67 (85%)	12 (15%)	3	19
2	N	81/106 (76%)	69 (85%)	12 (15%)	3	20
2	R	79/106 (74%)	67 (85%)	12 (15%)	3	19
3	C	82/102 (80%)	75 (92%)	7 (8%)	12	42
3	G	83/102 (81%)	74 (89%)	9 (11%)	7	31
3	M	82/102 (80%)	75 (92%)	7 (8%)	12	42
3	Q	83/102 (81%)	74 (89%)	9 (11%)	7	31
4	B	68/78 (87%)	63 (93%)	5 (7%)	16	48
4	F	63/78 (81%)	59 (94%)	4 (6%)	21	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	L	68/78 (87%)	63 (93%)	5 (7%)	16	48
4	P	63/78 (81%)	59 (94%)	4 (6%)	21	53
5	A	85/110 (77%)	77 (91%)	8 (9%)	10	36
5	E	84/110 (76%)	79 (94%)	5 (6%)	22	55
5	K	85/110 (77%)	77 (91%)	8 (9%)	10	36
5	O	84/110 (76%)	79 (94%)	5 (6%)	22	55
All	All	1250/1584 (79%)	1126 (90%)	124 (10%)	9	34

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	K	59	GLU
2	H	98	LEU
4	B	91	LYS
5	K	63	ARG
2	H	31	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
3	G	31	HIS
3	G	84	GLN
3	C	112	GLN
4	L	75	HIS
3	C	73	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates 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 ⓘ

### 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<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	J	310/312 (99%)	37.67	310 (100%) 0 0	341, 666, 716, 741	0
2	D	95/126 (75%)	11.59	82 (86%) 0 2	529, 585, 651, 667	0
2	H	93/126 (73%)	9.62	77 (82%) 0 2	534, 577, 613, 631	0
2	N	95/126 (75%)	19.80	77 (81%) 0 2	527, 585, 659, 665	0
2	R	93/126 (73%)	8.03	76 (81%) 0 2	517, 581, 620, 636	0
3	C	103/130 (79%)	7.62	81 (78%) 0 3	516, 610, 641, 662	0
3	G	105/130 (80%)	11.98	90 (85%) 0 2	551, 594, 649, 673	0
3	M	103/130 (79%)	18.39	89 (86%) 0 2	537, 625, 696, 724	0
3	Q	105/130 (80%)	5.86	88 (83%) 0 2	521, 586, 643, 659	0
4	B	83/102 (81%)	17.38	83 (100%) 0 0	539, 595, 652, 663	0
4	F	78/102 (76%)	7.42	48 (61%) 0 3	571, 623, 656, 664	0
4	L	83/102 (81%)	13.50	73 (87%) 0 2	516, 586, 644, 666	0
4	P	78/102 (76%)	14.35	62 (79%) 0 3	567, 652, 705, 715	0
5	A	97/135 (71%)	18.78	97 (100%) 0 0	558, 624, 666, 674	0
5	E	97/135 (71%)	17.80	82 (84%) 0 2	601, 641, 681, 698	0
5	K	97/135 (71%)	16.43	93 (95%) 0 1	563, 620, 659, 677	0
5	O	97/135 (71%)	13.63	90 (92%) 0 1	616, 671, 716, 724	0
6	I	311/313 (99%)	36.10	311 (100%) 0 0	329, 666, 717, 733	0
All	All	2123/2597 (81%)	20.16	1909 (89%) 0 2	329, 629, 704, 741	0

The worst 5 of 1909 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	-62	DA	173.8
1	J	-226	DT	146.4
2	N	49	THR	129.0

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Mol	Chain	Res	Type	RSRZ
1	J	-225	DG	126.9
1	J	-218	DA	119.0

## 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 carbohydrates 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.