W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 04:24 am BST

PDB ID	:	5J9U
Title	:	Crystal structure of the NuA4 core complex
Authors	:	Chen, Z.C.; Xu, P.
Deposited on	:	2016-04-11
Resolution	:	2.95 Å(reported)

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	:	2.11
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)	:	2.11

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 2.95 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.
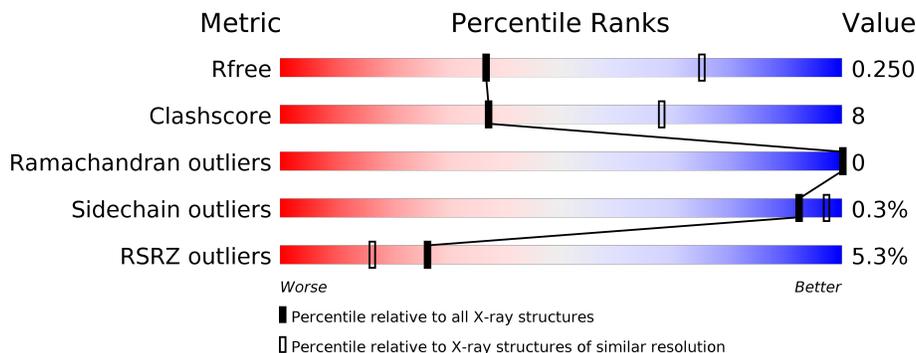
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 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	305	
1	E	305	
1	I	305	
2	B	113	
2	F	113	
2	J	113	

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Mol	Chain	Length	Quality of chain
3	C	351	6% / 67% / 16% / 16%
3	G	351	9% / 67% / 17% / 15%
3	N	351	5% / 62% / 22% / 16%
4	D	120	85% / 15%
4	H	120	4% / 84% / 16%
4	K	120	% / 84% / 16%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 19676 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 acetyltransferase ESA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	293	Total 2479	C 1601	N 419	O 448	S 11	0	0	0
1	A	292	Total 2470	C 1596	N 418	O 446	S 10	0	0	0
1	I	292	Total 2470	C 1596	N 418	O 446	S 10	0	0	0

- Molecule 2 is a protein called Chromatin modification-related protein EAF6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	75	Total 622	C 389	N 99	O 133	S 1	0	0	0
2	B	79	Total 660	C 413	N 108	O 138	S 1	0	0	0
2	J	76	Total 627	C 392	N 100	O 134	S 1	0	0	0

- Molecule 3 is a protein called Enhancer of polycomb-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	297	Total 2499	C 1577	N 443	O 471	S 8	0	0	0
3	N	295	Total 2475	C 1565	N 434	O 468	S 8	0	0	0
3	C	294	Total 2467	C 1560	N 431	O 468	S 8	0	0	0

- Molecule 4 is a protein called Chromatin modification-related protein YNG2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	120	Total 969	C 613	N 165	O 188	S 3	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	120	Total	C	N	O	S	0	0	0
			969	613	165	188	3			
4	K	120	Total	C	N	O	S	0	0	0
			969	613	165	188	3			

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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 acetyltransferase ESA1

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• Molecule 2: Chromatin modification-related protein EAF6

Chain F:

• Molecule 2: Chromatin modification-related protein EAF6

Chain B:

• Molecule 2: Chromatin modification-related protein EAF6

Chain J:

• Molecule 3: Enhancer of polycomb-like protein 1

Chain G:

● Molecule 3: Enhancer of polycomb-like protein 1

Chain N:

● Molecule 3: Enhancer of polycomb-like protein 1

Chain C:

● Molecule 4: Chromatin modification-related protein YNG2

Chain D:

● Molecule 4: Chromatin modification-related protein YNG2

Chain H:

● Molecule 4: Chromatin modification-related protein YNG2

Chain K:

4   Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	217.91Å 189.89Å 173.56Å 90.00° 113.61° 90.00°	Depositor
Resolution (Å)	29.69 – 2.95 45.87 – 2.93	Depositor EDS
% Data completeness (in resolution range)	78.8 (29.69-2.95) 77.4 (45.87-2.93)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.16 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.216 , 0.246 0.218 , 0.250	Depositor DCC
R_{free} test set	2000 reflections (1.86%)	wwPDB-VP
Wilson B-factor (Å^2)	55.4	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 32.7	EDS
L-test for twinning[2]	$<|L|> = 0.53$, $<L^2> = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	19676	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ALY

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	0.25	0/2523	0.46	0/3411
1	E	0.25	0/2532	0.45	0/3422
1	I	0.26	0/2523	0.45	0/3411
2	B	0.25	0/669	0.41	0/893
2	F	0.25	0/630	0.44	0/841
2	J	0.26	0/635	0.41	0/848
3	C	0.29	0/2518	0.45	0/3390
3	G	0.25	0/2551	0.44	0/3433
3	N	0.26	0/2526	0.47	1/3400 (0.0%)
4	D	0.26	0/981	0.41	0/1317
4	H	0.25	0/981	0.41	0/1317
4	K	0.24	0/981	0.40	0/1317
All	All	0.26	0/20050	0.44	1/27000 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	N	74	LEU	CA-CB-CG	5.14	127.11	115.30

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	A	2470	0	2444	48	0
1	E	2479	0	2456	50	0
1	I	2470	0	2444	44	0
2	B	660	0	619	10	0
2	F	622	0	579	15	0
2	J	627	0	581	18	0
3	C	2467	0	2427	59	0
3	G	2499	0	2462	57	0
3	N	2475	0	2436	70	0
4	D	969	0	1003	16	0
4	H	969	0	1003	19	0
4	K	969	0	1003	15	0
All	All	19676	0	19457	305	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 8.

The worst 5 of 305 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:407:GLU:HG3	3:N:63:LYS:HD3	1.52	0.92
2:J:41:THR:HG22	2:J:93:ARG:HH22	1.42	0.83
1:A:388:ALA:HB1	1:A:394:LEU:HD23	1.60	0.81
3:N:76:HIS:CD2	3:N:120:TYR:HA	2.17	0.80
1:I:391:LEU:HB2	1:I:393:ILE:HG12	1.66	0.76

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	289/305 (95%)	278 (96%)	11 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	290/305 (95%)	278 (96%)	12 (4%)	0	100	100
1	I	289/305 (95%)	278 (96%)	11 (4%)	0	100	100
2	B	73/113 (65%)	70 (96%)	3 (4%)	0	100	100
2	F	69/113 (61%)	67 (97%)	2 (3%)	0	100	100
2	J	70/113 (62%)	67 (96%)	3 (4%)	0	100	100
3	C	288/351 (82%)	280 (97%)	8 (3%)	0	100	100
3	G	291/351 (83%)	282 (97%)	9 (3%)	0	100	100
3	N	289/351 (82%)	280 (97%)	9 (3%)	0	100	100
4	D	118/120 (98%)	118 (100%)	0	0	100	100
4	H	118/120 (98%)	118 (100%)	0	0	100	100
4	K	118/120 (98%)	118 (100%)	0	0	100	100
All	All	2302/2667 (86%)	2234 (97%)	68 (3%)	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	270/283 (95%)	270 (100%)	0	100	100
1	E	272/283 (96%)	271 (100%)	1 (0%)	91	96
1	I	270/283 (95%)	270 (100%)	0	100	100
2	B	73/100 (73%)	73 (100%)	0	100	100
2	F	69/100 (69%)	69 (100%)	0	100	100
2	J	69/100 (69%)	69 (100%)	0	100	100
3	C	280/333 (84%)	278 (99%)	2 (1%)	84	93
3	G	283/333 (85%)	282 (100%)	1 (0%)	91	96
3	N	280/333 (84%)	277 (99%)	3 (1%)	73	89
4	D	111/111 (100%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H	111/111 (100%)	111 (100%)	0	100	100
4	K	111/111 (100%)	111 (100%)	0	100	100
All	All	2199/2481 (89%)	2192 (100%)	7 (0%)	92	97

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	N	215	LEU
3	C	311	CYS
3	N	311	CYS
3	G	311	CYS
3	C	63	LYS

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

Mol	Chain	Res	Type
2	F	33	GLN
4	D	12	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	#$|Z| > 2$
1	ALY	E	262	1	10,11,12	0.82	0	7,12,14	0.70	0
1	ALY	A	262	1	10,11,12	0.83	0	7,12,14	0.71	0
1	ALY	I	262	1	10,11,12	0.83	0	7,12,14	1.18	1 (14%)

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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	ALY	E	262	1	-	2/9/10/12	-
1	ALY	A	262	1	-	2/9/10/12	-
1	ALY	I	262	1	-	2/9/10/12	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	262	ALY	CE-NZ-CH	2.29	126.08	122.56

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	262	ALY	OH-CH-NZ-CE
1	E	262	ALY	CH3-CH-NZ-CE
1	A	262	ALY	OH-CH-NZ-CE
1	A	262	ALY	CH3-CH-NZ-CE
1	I	262	ALY	OH-CH-NZ-CE

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	262	ALY	1	0
1	A	262	ALY	2	0
1	I	262	ALY	1	0

5.5 Carbohydrates (i)

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 (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	291/305 (95%)	0.11	6 (2%)	63	46	23, 54, 102, 144	0
1	E	292/305 (95%)	0.25	6 (2%)	63	46	30, 63, 115, 127	0
1	I	291/305 (95%)	0.08	8 (2%)	54	38	27, 55, 95, 113	0
2	B	79/113 (69%)	0.90	15 (18%)	1	0	42, 76, 125, 149	0
2	F	75/113 (66%)	0.59	8 (10%)	6	3	60, 84, 123, 136	0
2	J	76/113 (67%)	0.52	7 (9%)	9	5	46, 73, 113, 138	0
3	C	294/351 (83%)	0.39	21 (7%)	16	9	30, 67, 116, 158	0
3	G	297/351 (84%)	0.67	31 (10%)	6	4	37, 79, 125, 152	0
3	N	295/351 (84%)	0.30	17 (5%)	23	14	36, 69, 122, 145	0
4	D	120/120 (100%)	0.00	0	100	100	31, 56, 79, 91	0
4	H	120/120 (100%)	0.53	5 (4%)	36	23	41, 72, 116, 119	0
4	K	120/120 (100%)	0.01	1 (0%)	86	73	31, 55, 80, 92	0
All	All	2350/2667 (88%)	0.32	125 (5%)	26	16	23, 65, 114, 158	0

The worst 5 of 125 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	86	SER	6.4
1	A	397	TYR	5.9
3	G	64	GLN	4.9
3	C	62	VAL	4.9
3	G	398	ARG	4.7

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
1	ALY	E	262	12/13	0.95	0.20	26,46,64,66	0
1	ALY	I	262	12/13	0.95	0.18	29,43,55,68	0
1	ALY	A	262	12/13	0.96	0.18	22,41,49,53	0

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.