



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:36 PM UTC

PDB ID : 3SWP / pdb_00003swp
Title : ANAC019 NAC domain in complex with DNA
Authors : Welner, D.; Lo Leggio, L.
Deposited on : 2011-07-14
Resolution : 4.11 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

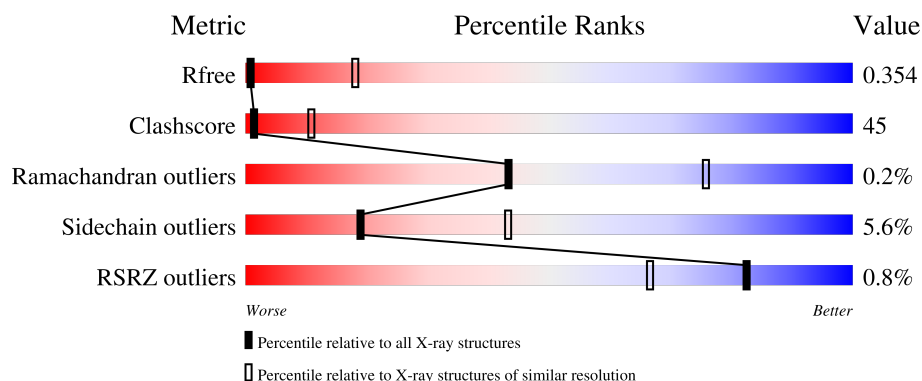
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.11 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}	180053	1249 (4.44-3.80)
Clashscore	190562	1031 (4.42-3.82)
Ramachandran outliers	187476	1211 (4.44-3.80)
Sidechain outliers	187428	1198 (4.44-3.80)
RSRZ outliers	180081	1246 (4.44-3.80)

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	174	25% 40% 15% • 19%
1	B	174	42% 31% 6% • 20%
1	C	174	26% 36% 14% • 22%
1	D	174	42% 34% • • 20%
2	E	26	92% 8%

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Mol	Chain	Length	Quality of chain
3	F	26	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a small green segment on the left, a large yellow segment in the middle, and a small orange segment on the right. Below the bar, the text '85%' is centered under the yellow segment, and '12%' is centered under the orange segment. A small black dot is visible at the start of the green segment.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5667 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 NAC domain-containing protein 19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1167	767	193	203	4			
1	B	140	Total	C	N	O	S	0	0	0
			1156	761	189	202	4			
1	C	135	Total	C	N	O	S	0	0	0
			1122	738	186	194	4			
1	D	140	Total	C	N	O	S	0	0	0
			1156	761	189	202	4			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP Q9C932
A	-4	HIS	-	expression tag	UNP Q9C932
A	-3	HIS	-	expression tag	UNP Q9C932
A	-2	HIS	-	expression tag	UNP Q9C932
A	-1	HIS	-	expression tag	UNP Q9C932
A	0	HIS	-	expression tag	UNP Q9C932
B	-5	HIS	-	expression tag	UNP Q9C932
B	-4	HIS	-	expression tag	UNP Q9C932
B	-3	HIS	-	expression tag	UNP Q9C932
B	-2	HIS	-	expression tag	UNP Q9C932
B	-1	HIS	-	expression tag	UNP Q9C932
B	0	HIS	-	expression tag	UNP Q9C932
C	-5	HIS	-	expression tag	UNP Q9C932
C	-4	HIS	-	expression tag	UNP Q9C932
C	-3	HIS	-	expression tag	UNP Q9C932
C	-2	HIS	-	expression tag	UNP Q9C932
C	-1	HIS	-	expression tag	UNP Q9C932
C	0	HIS	-	expression tag	UNP Q9C932
D	-5	HIS	-	expression tag	UNP Q9C932
D	-4	HIS	-	expression tag	UNP Q9C932
D	-3	HIS	-	expression tag	UNP Q9C932

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	HIS	-	expression tag	UNP Q9C932
D	-1	HIS	-	expression tag	UNP Q9C932
D	0	HIS	-	expression tag	UNP Q9C932

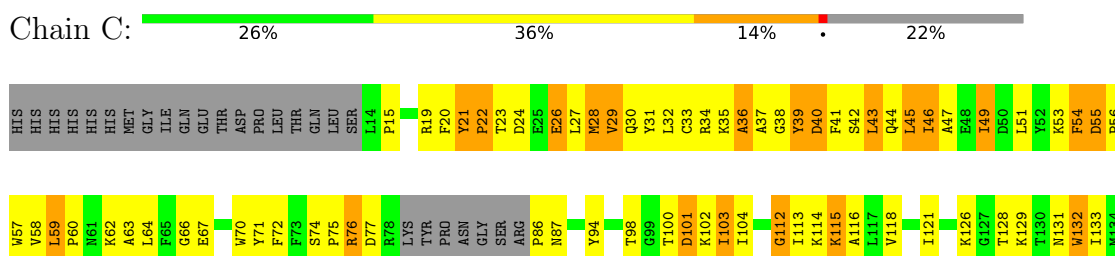
- Molecule 2 is a DNA chain called oligonucleotide forward.

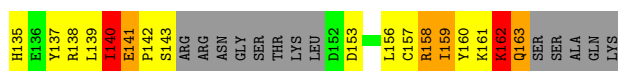
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	26	Total	C	N	O	P	0	0	0
			536	254	100	156	26			

- Molecule 3 is a DNA chain called oligonucleotide reverse.

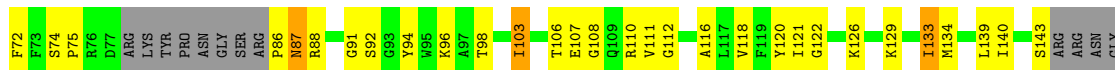
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	26	Total	C	N	O	P	0	0	0
			530	252	96	156	26			

- Molecule 1: NAC domain-containing protein 19

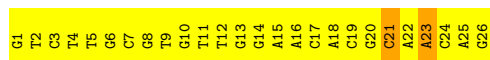




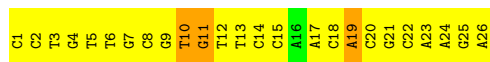
- Molecule 1: NAC domain-containing protein 19



- Molecule 2: oligonucleotide forward



- Molecule 3: oligonucleotide reverse



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.14Å 105.47Å 175.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.97 – 4.11 29.97 – 4.11	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.97-4.11) 98.8 (29.97-4.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 4.11Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.260 , 0.349 0.257 , 0.354	Depositor DCC
R_{free} test set	1035 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	174.1	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.19 , 141.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5667	wwPDB-VP
Average B, all atoms (Å ²)	263.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.41% 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](#)

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	1.16	4/1202 (0.3%)	1.95	49/1623 (3.0%)
1	B	0.81	2/1191 (0.2%)	1.63	33/1609 (2.1%)
1	C	1.08	3/1156 (0.3%)	1.89	46/1560 (2.9%)
1	D	0.76	1/1191 (0.1%)	1.55	25/1609 (1.6%)
2	E	0.37	0/601	1.18	2/926 (0.2%)
3	F	0.37	0/593	1.32	5/912 (0.5%)
All	All	0.88	10/5934 (0.2%)	1.66	160/8239 (1.9%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	10	THR	CA-C	9.88	1.69	1.52
1	B	10	THR	CA-C	9.85	1.69	1.52
1	C	66	GLY	CA-C	-6.49	1.47	1.52
1	B	21	TYR	CA-C	-6.35	1.46	1.52
1	A	49	ILE	CA-CB	-6.21	1.49	1.55

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	11	GLN	N-CA-C	-12.91	97.29	111.36
1	D	11	GLN	N-CA-C	-12.51	97.72	111.36
1	B	141	GLU	CA-C-N	11.94	134.77	119.84
1	B	141	GLU	C-N-CA	11.94	134.77	119.84
1	A	162	LYS	N-CA-C	11.85	127.41	110.23

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	1167	0	1163	119	0
1	B	1156	0	1150	73	0
1	C	1122	0	1113	90	0
1	D	1156	0	1150	60	0
2	E	536	0	293	120	0
3	F	530	0	293	112	0
All	All	5667	0	5162	478	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 45.

The worst 5 of 478 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:C:21:TYR:CD2	1:D:21:TYR:CD2	2.43	1.06
1:D:118:VAL:HG11	1:D:129:LYS:HE3	1.36	1.06
1:B:118:VAL:HG11	1:B:129:LYS:HE3	1.38	1.04
1:A:129:LYS:NZ	3:F:20:DC:P	2.31	1.03
1:A:129:LYS:HZ1	3:F:20:DC:P	1.82	1.01

There are no symmetry-related clashes.

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
1	A	135/174 (78%)	131 (97%)	3 (2%)	1 (1%)	18 55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	134/174 (77%)	130 (97%)	4 (3%)	0	100	100
1	C	129/174 (74%)	127 (98%)	2 (2%)	0	100	100
1	D	134/174 (77%)	130 (97%)	4 (3%)	0	100	100
All	All	532/696 (76%)	518 (97%)	13 (2%)	1 (0%)	43	76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	SER

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	
1	A	123/152 (81%)	116 (94%)	7 (6%)	18	43
1	B	122/152 (80%)	116 (95%)	6 (5%)	22	46
1	C	117/152 (77%)	110 (94%)	7 (6%)	17	42
1	D	122/152 (80%)	115 (94%)	7 (6%)	18	43
All	All	484/608 (80%)	457 (94%)	27 (6%)	19	43

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	43	LEU
1	C	143	SER
1	D	143	SER
1	C	140	ILE
1	C	162	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	131	ASN
1	C	163	GLN
1	D	131	ASN
1	D	30	GLN
1	B	30	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 oligosaccharides 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	141/174 (81%)	0.16	2 (1%) 73 56	127, 194, 305, 403	0
1	B	140/174 (80%)	0.21	2 (1%) 73 56	165, 269, 382, 579	0
1	C	135/174 (77%)	0.02	0 100 100	137, 209, 331, 529	0
1	D	140/174 (80%)	0.06	1 (0%) 84 69	163, 274, 354, 560	0
2	E	26/26 (100%)	0.14	0 100 100	249, 323, 393, 449	0
3	F	26/26 (100%)	0.24	0 100 100	230, 321, 445, 481	0
All	All	608/748 (81%)	0.12	5 (0%) 82 66	127, 243, 384, 579	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	97	ALA	4.6
1	A	100	THR	2.6
1	D	56	PRO	2.5
1	B	98	THR	2.4
1	A	136	GLU	2.2

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 oligosaccharides 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.