



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 03:44 am BST

PDB ID : 3SWM
Title : The NAC domain of ANAC019 in complex with DNA, gold derivative
Authors : Welner, D.; Lo Leggio, L.
Deposited on : 2011-07-14
Resolution : 4.25 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
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

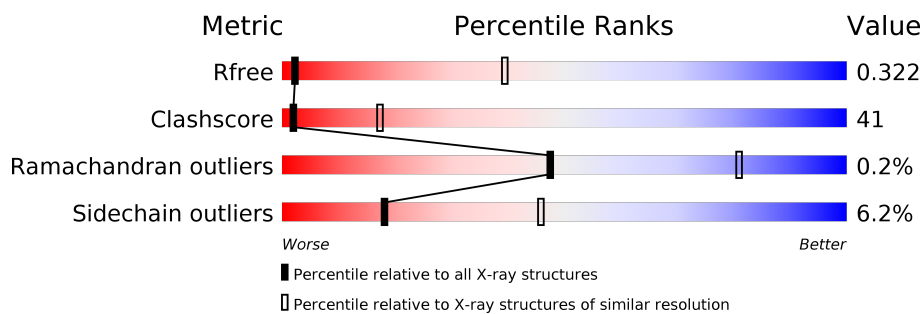
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.25 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	1017 (4.72-3.78)
Clashscore	141614	1059 (4.72-3.80)
Ramachandran outliers	138981	1014 (4.72-3.80)
Sidechain outliers	138945	1018 (4.72-3.78)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	174	<div> <div>35%</div> <div>38%</div> <div>7%</div> <div>•</div> <div>19%</div> </div>
1	B	174	<div> <div>47%</div> <div>32%</div> <div>•</div> <div>20%</div> </div>
1	C	174	<div> <div>33%</div> <div>39%</div> <div>6%</div> <div>22%</div> </div>
1	D	174	<div> <div>52%</div> <div>26%</div> <div>•</div> <div>20%</div> </div>
2	E	26	<div> <div>31%</div> <div>69%</div> </div>
3	F	26	<div> <div>23%</div> <div>77%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5676 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			

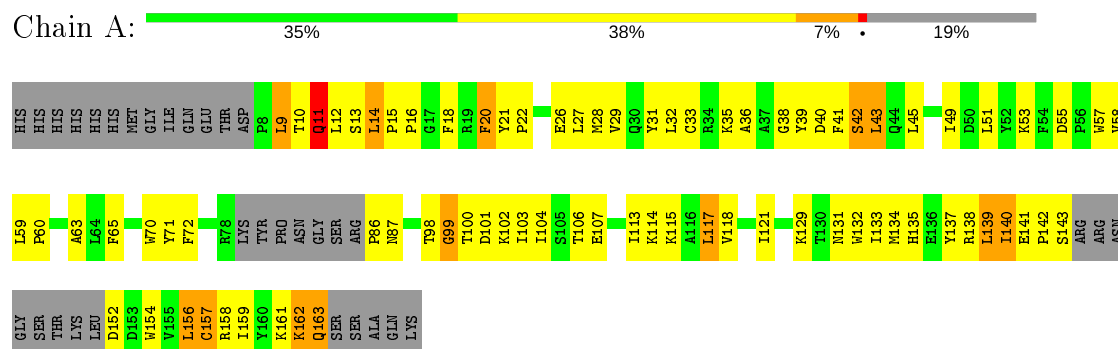
- Molecule 4 is GOLD ION (three-letter code: AU) (formula: Au).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Au	0	0
			1	1		
4	A	3	Total	Au	0	0
			3	3		
4	D	1	Total	Au	0	0
			1	1		
4	C	4	Total	Au	0	0
			4	4		

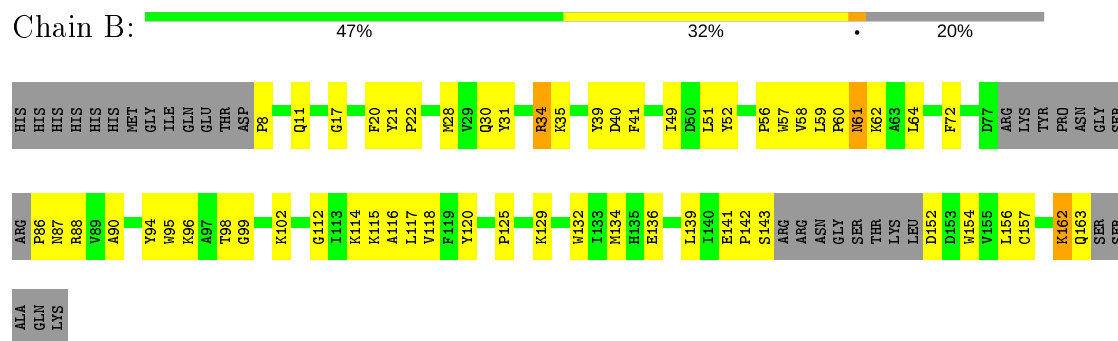
3 Residue-property plots

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. 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. 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.

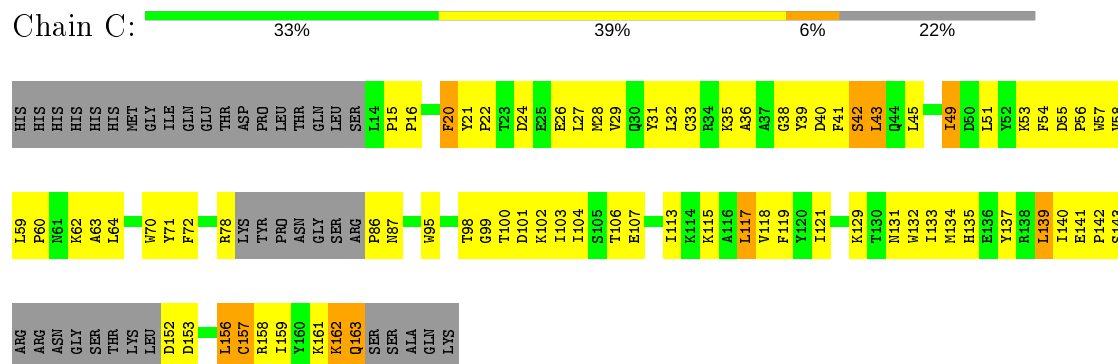
- Molecule 1: NAC domain-containing protein 19



- Molecule 1: NAC domain-containing protein 19



- Molecule 1: NAC domain-containing protein 19



- Molecule 1: NAC domain-containing protein 19

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.53Å 109.07Å 173.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.20 – 4.25 46.20 – 4.25	Depositor EDS
% Data completeness (in resolution range)	99.3 (46.20-4.25) 99.4 (46.20-4.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 4.28Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.250 , 0.309 0.264 , 0.322	Depositor DCC
R_{free} test set	960 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	167.1	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 203.7	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	0.86	EDS
Total number of atoms	5676	wwPDB-VP
Average B, all atoms (Å ²)	249.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.21% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.94	1/1202 (0.1%)	1.29	12/1623 (0.7%)
1	B	0.48	0/1191	0.88	0/1609
1	C	0.84	0/1156	1.26	12/1560 (0.8%)
1	D	0.48	0/1191	0.89	2/1609 (0.1%)
2	E	1.13	5/601 (0.8%)	2.15	45/926 (4.9%)
3	F	1.22	6/593 (1.0%)	2.07	34/912 (3.7%)
All	All	0.83	12/5934 (0.2%)	1.39	105/8239 (1.3%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	16	DA	C3'-O3'	-6.55	1.35	1.44
3	F	18	DC	C3'-O3'	-6.54	1.35	1.44
2	E	5	DT	C3'-O3'	-6.38	1.35	1.44
3	F	19	DA	P-O5'	-6.22	1.53	1.59
2	E	7	DC	C1'-N1	6.19	1.57	1.49

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	7	DC	O4'-C1'-C2'	-11.29	96.87	105.90
2	E	17	DC	O4'-C1'-N1	10.53	115.37	108.00
3	F	17	DA	O4'-C1'-N9	-10.21	100.85	108.00
3	F	19	DA	P-O5'-C5'	-10.19	104.60	120.90
3	F	9	DG	O4'-C1'-N9	-9.51	101.34	108.00

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	1162	110	0
1	B	1156	0	1150	88	0
1	C	1122	0	1111	69	0
1	D	1156	0	1149	63	0
2	E	536	0	293	112	0
3	F	530	0	293	107	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0
4	C	4	0	0	0	0
4	D	1	0	0	0	0
All	All	5676	0	5158	440	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 41.

The worst 5 of 440 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:A:86:PRO:CB	2:E:4:DT:H4'	1.71	1.21
1:A:86:PRO:HB2	2:E:4:DT:C4'	1.74	1.17
1:C:21:TYR:CG	1:D:21:TYR:HD2	1.65	1.14
1:D:56:PRO:HA	1:D:59:LEU:HD12	1.30	1.13
1:B:56:PRO:HA	1:B:59:LEU:HD12	1.31	1.12

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%)	130 (96%)	4 (3%)	1 (1%)	22	62
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%)	517 (97%)	14 (3%)	1 (0%)	47	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	GLN

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%)	112 (91%)	11 (9%)	9	33
1	B	122/152 (80%)	116 (95%)	6 (5%)	25	52
1	C	117/152 (77%)	109 (93%)	8 (7%)	16	43
1	D	122/152 (80%)	117 (96%)	5 (4%)	30	56
All	All	484/608 (80%)	454 (94%)	30 (6%)	18	46

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

Mol	Chain	Res	Type
1	B	61	ASN
1	B	163	GLN
1	D	143	SER
1	B	162	LYS
1	C	42	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	131	ASN
1	D	131	ASN
1	C	163	GLN
1	A	163	GLN
1	D	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](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.