



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2IF7
Title : Crystal Structure of NTB-A
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Almo, S.C.
Deposited on : unknown
Resolution : 3.00 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

<http://wwpdb.org/validation/2016/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)	:	1.9-1692
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

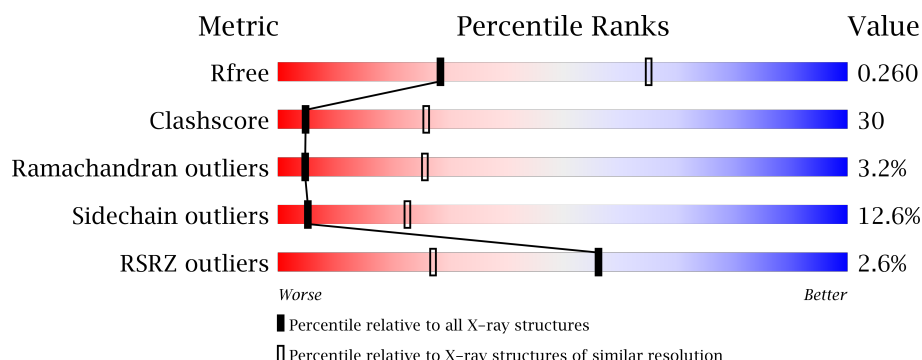
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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. 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	193	<div> <div>0.1%</div> <div>60% 31% 6% .</div> </div>
1	B	193	<div> <div>2%</div> <div>53% 37% 9% ..</div> </div>
1	C	193	<div> <div>5%</div> <div>37% 48% 11% .</div> </div>
1	D	193	<div> <div>2%</div> <div>54% 36% 9% .</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5966 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 SLAM family member 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1478	925	252	294	7			
1	B	191	Total	C	N	O	S	0	0	0
			1507	945	256	299	7			
1	C	186	Total	C	N	O	S	0	0	0
			1462	914	249	292	7			
1	D	192	Total	C	N	O	S	0	0	0
			1513	948	257	301	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP Q96DU3
B	1	MET	-	INITIATING METHIONINE	UNP Q96DU3
C	1	MET	-	INITIATING METHIONINE	UNP Q96DU3
D	1	MET	-	INITIATING METHIONINE	UNP Q96DU3

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Cl	0	0
			1	1		

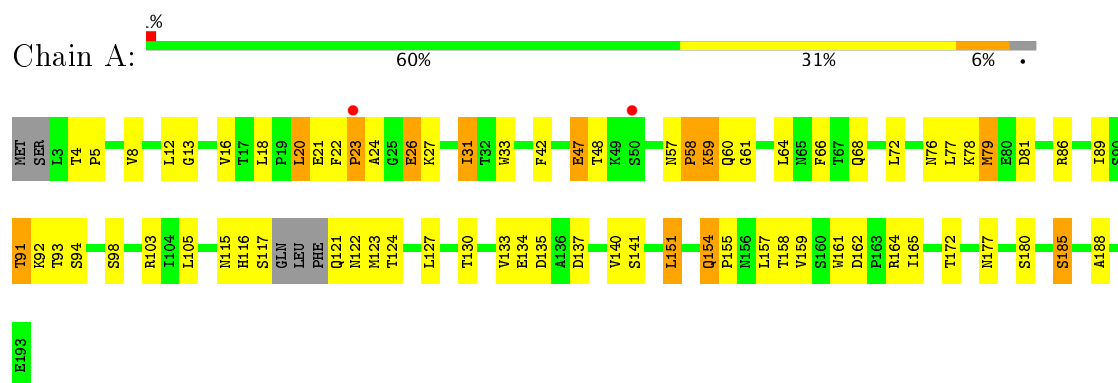
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	3	Total	O	0	0
			3	3		

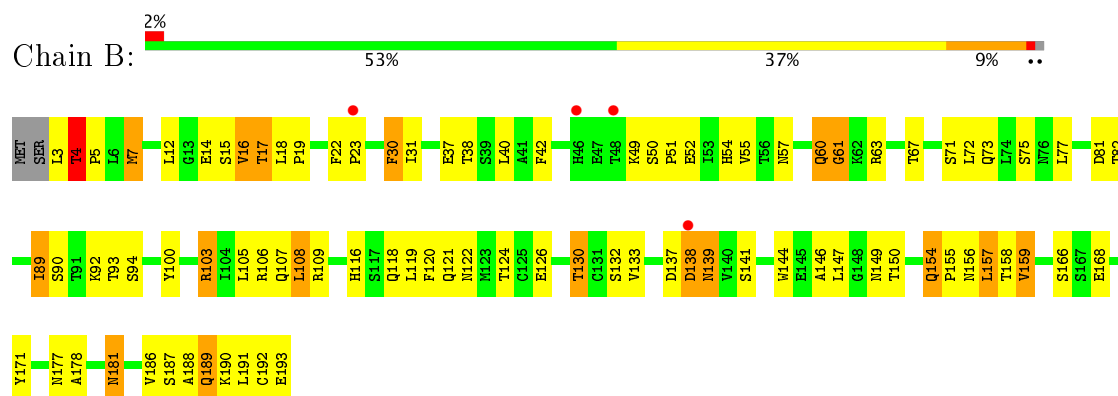
3 Residue-property plots [i](#)

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.

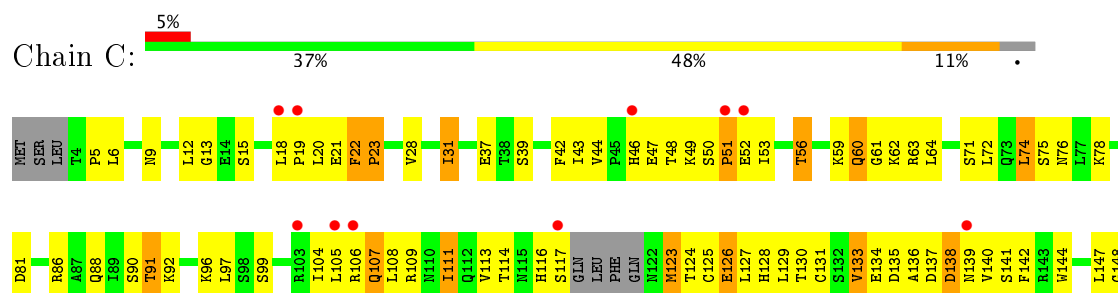
- Molecule 1: SLAM family member 6

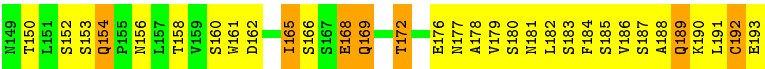


- Molecule 1: SLAM family member 6

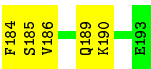


- Molecule 1: SLAM family member 6





● Molecule 1: SLAM family member 6



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	121.20Å 148.45Å 86.57Å 90.00° 112.86° 90.00°	Depositor
Resolution (Å)	40.00 – 3.00 39.89 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.00-3.00) 99.7 (39.89-3.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.213 , 0.266 0.208 , 0.260	Depositor DCC
R_{free} test set	1413 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	75.2	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 91.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5966	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.19% 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: CA, CL

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	0.41	0/1505	0.59	0/2045
1	B	0.40	0/1536	0.57	0/2087
1	C	0.30	0/1489	0.48	0/2022
1	D	0.43	0/1542	0.57	0/2095
All	All	0.39	0/6072	0.56	0/8249

There are no bond length outliers.

There are no bond angle outliers.

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	1478	0	1452	69	0
1	B	1507	0	1481	89	0
1	C	1462	0	1433	128	0
1	D	1513	0	1486	86	0
2	A	1	0	0	0	0
2	D	1	0	0	0	0
3	D	1	0	0	0	0
4	D	3	0	0	0	0
All	All	5966	0	5852	359	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 30.

The worst 5 of 359 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:125:CYS:HA	1:C:126:GLU:CB	1.56	1.25
1:A:47:GLU:OE1	1:A:48:THR:HG22	1.32	1.24
1:C:133:VAL:CG1	1:C:134:GLU:H	1.47	1.21
1:C:22:PHE:HB3	1:C:23:PRO:CD	1.73	1.15
1:C:133:VAL:HG12	1:C:134:GLU:H	1.00	1.14

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	184/193 (95%)	159 (86%)	20 (11%)	5 (3%)	6	30
1	B	189/193 (98%)	170 (90%)	17 (9%)	2 (1%)	17	56
1	C	182/193 (94%)	141 (78%)	28 (15%)	13 (7%)	1	6
1	D	190/193 (98%)	169 (89%)	17 (9%)	4 (2%)	8	38
All	All	745/772 (96%)	639 (86%)	82 (11%)	24 (3%)	5	26

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	PRO
1	A	59	LYS
1	B	4	THR
1	C	22	PHE
1	C	60	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	173/178 (97%)	156 (90%)	17 (10%)	9	34
1	B	176/178 (99%)	143 (81%)	33 (19%)	2	10
1	C	171/178 (96%)	156 (91%)	15 (9%)	12	41
1	D	177/178 (99%)	154 (87%)	23 (13%)	5	21
All	All	697/712 (98%)	609 (87%)	88 (13%)	5	23

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	139	ASN
1	B	190	LYS
1	D	125	CYS
1	B	141	SER
1	B	158	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	118	GLN
1	B	181	ASN
1	D	122	ASN
1	B	139	ASN
1	B	154	GLN

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

Of 3 ligands modelled in this entry, 3 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	188/193 (97%)	0.11	2 (1%) 80 55	61, 84, 102, 108	0
1	B	191/193 (98%)	0.13	4 (2%) 64 34	61, 83, 101, 109	0
1	C	186/193 (96%)	0.40	10 (5%) 26 11	57, 82, 104, 121	0
1	D	192/193 (99%)	0.07	4 (2%) 64 34	61, 82, 100, 123	0
All	All	757/772 (98%)	0.18	20 (2%) 56 27	57, 83, 102, 123	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	51	PRO	5.1
1	C	105	LEU	5.1
1	A	23	PRO	3.5
1	C	106	ARG	3.4
1	D	2	SER	3.3

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	CA	A	205	1/1	0.96	0.17	-	74,74,74,74	0
2	CA	D	204	1/1	0.98	0.03	-	62,62,62,62	0
3	CL	D	201	1/1	0.74	0.15	-	107,107,107,107	0

6.5 Other polymers [i](#)

There are no such residues in this entry.