



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 11, 2023 – 07:02 PM EDT

PDB ID : 4LTQ
Title : Bacterial sodium channel in low calcium, P42 space group
Authors : Shaya, D.; Findeisen, F.; Abderemane-Ali, F.; Arrigoni, C.; Wong, S.; Reddy
Nurva, S.; Loussouarn, G.; Minor, D.L.
Deposited on : 2013-07-23
Resolution : 5.50 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

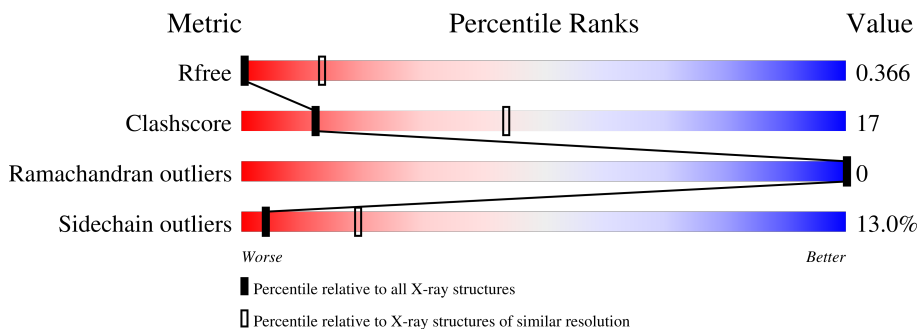
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.50 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	1019 (7.12-3.82)
Clashscore	141614	1010 (7.10-3.90)
Ramachandran outliers	138981	1014 (7.12-3.82)
Sidechain outliers	138945	1191 (7.20-3.80)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	152	54% (green), 32% (yellow), 11% (orange), 11% (grey)
1	B	152	53% (green), 34% (yellow), 11% (orange), 11% (grey)
1	C	152	57% (green), 29% (yellow), 11% (orange), 11% (grey)
1	D	152	53% (green), 32% (yellow), 11% (orange), 11% (grey)
1	H	152	55% (green), 31% (yellow), 11% (orange), 11% (grey)
1	I	152	56% (green), 30% (yellow), 11% (orange), 11% (grey)
1	J	152	55% (green), 29% (yellow), 5% (orange), 11% (grey)

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	K	152	 56% 30% 11%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 8086 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	136	1018	680	154	178	6	0	0	0
1	B	136	1014	680	153	175	6	0	0	0
1	C	136	1012	678	155	173	6	0	0	0
1	D	136	999	671	153	169	6	0	0	0
1	H	136	1018	680	154	178	6	0	0	0
1	I	136	1014	680	153	175	6	0	0	0
1	J	136	1012	678	155	173	6	0	0	0
1	K	136	999	671	153	169	6	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	137	GLY	-	expression tag	UNP Q0ABW0
A	138	PRO	-	expression tag	UNP Q0ABW0
A	139	SER	-	expression tag	UNP Q0ABW0
A	140	SER	-	expression tag	UNP Q0ABW0
A	141	PRO	-	expression tag	UNP Q0ABW0
A	142	SER	-	expression tag	UNP Q0ABW0
B	137	GLY	-	expression tag	UNP Q0ABW0
B	138	PRO	-	expression tag	UNP Q0ABW0
B	139	SER	-	expression tag	UNP Q0ABW0
B	140	SER	-	expression tag	UNP Q0ABW0
B	141	PRO	-	expression tag	UNP Q0ABW0
B	142	SER	-	expression tag	UNP Q0ABW0
C	137	GLY	-	expression tag	UNP Q0ABW0

Continued on next page...

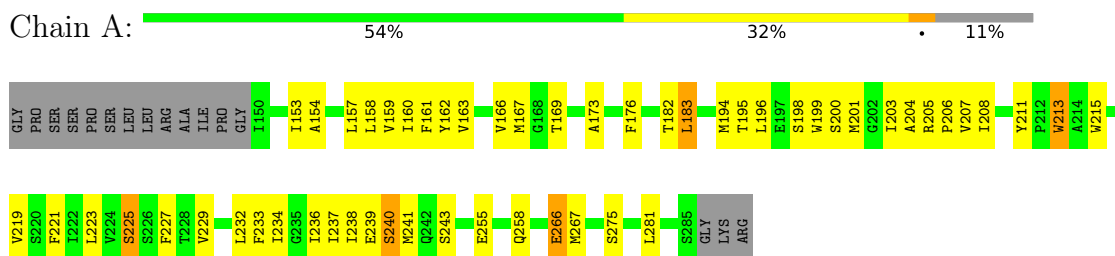
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	138	PRO	-	expression tag	UNP Q0ABW0
C	139	SER	-	expression tag	UNP Q0ABW0
C	140	SER	-	expression tag	UNP Q0ABW0
C	141	PRO	-	expression tag	UNP Q0ABW0
C	142	SER	-	expression tag	UNP Q0ABW0
D	137	GLY	-	expression tag	UNP Q0ABW0
D	138	PRO	-	expression tag	UNP Q0ABW0
D	139	SER	-	expression tag	UNP Q0ABW0
D	140	SER	-	expression tag	UNP Q0ABW0
D	141	PRO	-	expression tag	UNP Q0ABW0
D	142	SER	-	expression tag	UNP Q0ABW0
H	137	GLY	-	expression tag	UNP Q0ABW0
H	138	PRO	-	expression tag	UNP Q0ABW0
H	139	SER	-	expression tag	UNP Q0ABW0
H	140	SER	-	expression tag	UNP Q0ABW0
H	141	PRO	-	expression tag	UNP Q0ABW0
H	142	SER	-	expression tag	UNP Q0ABW0
I	137	GLY	-	expression tag	UNP Q0ABW0
I	138	PRO	-	expression tag	UNP Q0ABW0
I	139	SER	-	expression tag	UNP Q0ABW0
I	140	SER	-	expression tag	UNP Q0ABW0
I	141	PRO	-	expression tag	UNP Q0ABW0
I	142	SER	-	expression tag	UNP Q0ABW0
J	137	GLY	-	expression tag	UNP Q0ABW0
J	138	PRO	-	expression tag	UNP Q0ABW0
J	139	SER	-	expression tag	UNP Q0ABW0
J	140	SER	-	expression tag	UNP Q0ABW0
J	141	PRO	-	expression tag	UNP Q0ABW0
J	142	SER	-	expression tag	UNP Q0ABW0
K	137	GLY	-	expression tag	UNP Q0ABW0
K	138	PRO	-	expression tag	UNP Q0ABW0
K	139	SER	-	expression tag	UNP Q0ABW0
K	140	SER	-	expression tag	UNP Q0ABW0
K	141	PRO	-	expression tag	UNP Q0ABW0
K	142	SER	-	expression tag	UNP Q0ABW0

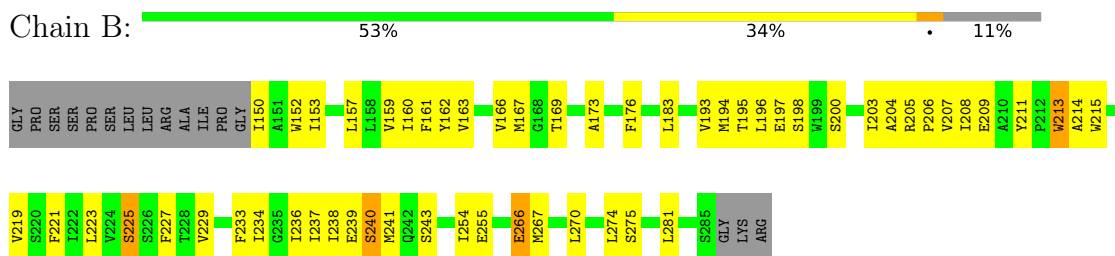
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

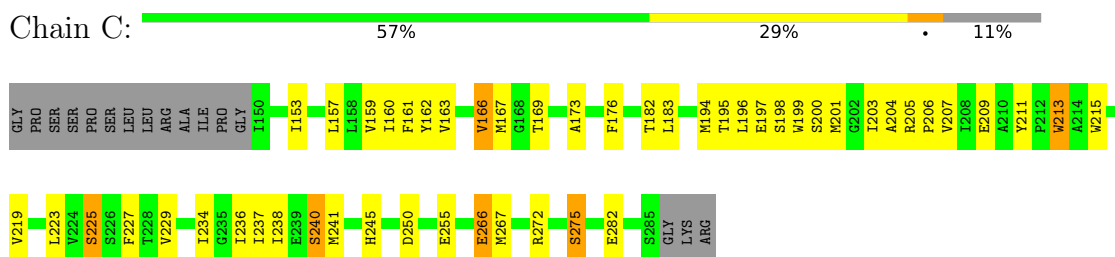
- Molecule 1: Ion transport protein



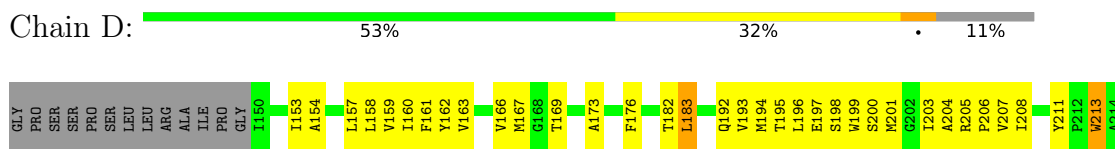
- Molecule 1: Ion transport protein



- Molecule 1: Ion transport protein

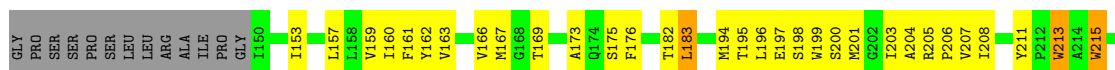


- Molecule 1: Ion transport protein





- Molecule 1: Ion transport protein



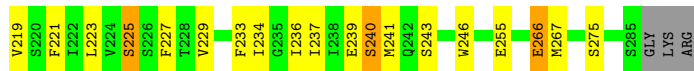
- Molecule 1: Ion transport protein



- Molecule 1: Ion transport protein



- Molecule 1: Ion transport protein



4 Data and refinement statistics i

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	181.14Å 181.14Å 94.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 5.50 128.08 – 5.50	Depositor EDS
% Data completeness (in resolution range)	96.9 (15.00-5.50) 96.6 (128.08-5.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 5.42Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.266 , 0.294 0.352 , 0.366	Depositor DCC
R_{free} test set	449 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å ²)	377.2	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 452.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.30$, $\langle L^2 \rangle = 0.14$	Xtriage
Estimated twinning fraction	0.326 for h,-k,-l	Xtriage
Reported twinning fraction	0.598 for H, K, L 0.402 for -H, K, -L	Depositor
Outliers	0 of 9776 reflections	Xtriage
F_o, F_c correlation	0.76	EDS
Total number of atoms	8086	wwPDB-VP
Average B, all atoms (Å ²)	292.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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	0.53	0/1045	0.62	0/1431
1	B	0.54	0/1041	0.62	0/1426
1	C	0.54	0/1040	0.62	0/1425
1	D	0.53	0/1026	0.61	0/1407
1	H	0.53	0/1045	0.62	0/1431
1	I	0.51	0/1041	0.60	0/1426
1	J	0.52	0/1040	0.60	0/1425
1	K	0.53	0/1026	0.61	0/1407
All	All	0.53	0/8304	0.61	0/11378

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 [i](#)

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	1018	0	946	44	0
1	B	1014	0	947	44	0
1	C	1012	0	939	38	0
1	D	999	0	926	45	0
1	H	1018	0	946	41	0
1	I	1014	0	947	40	0
1	J	1012	0	939	44	0
1	K	999	0	926	42	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8086	0	7516	265	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 17.

The worst 5 of 265 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:234:ILE:HD11	1:D:237:ILE:HA	1.50	0.92
1:J:245:HIS:CE1	1:K:246:TRP:CB	2.54	0.91
1:H:234:ILE:HD11	1:K:237:ILE:HA	1.52	0.90
1:J:195:THR:HB	1:K:196:LEU:HD13	1.54	0.89
1:C:195:THR:HB	1:D:196:LEU:HD13	1.56	0.87

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	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
1	B	134/152 (88%)	130 (97%)	4 (3%)	0	100	100
1	C	134/152 (88%)	128 (96%)	6 (4%)	0	100	100
1	D	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
1	H	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
1	I	134/152 (88%)	130 (97%)	4 (3%)	0	100	100
1	J	134/152 (88%)	128 (96%)	6 (4%)	0	100	100
1	K	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
All	All	1072/1216 (88%)	1032 (96%)	40 (4%)	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	95/131 (72%)	83 (87%)	12 (13%)	4	20
1	B	94/131 (72%)	84 (89%)	10 (11%)	6	25
1	C	93/131 (71%)	81 (87%)	12 (13%)	4	19
1	D	90/131 (69%)	78 (87%)	12 (13%)	4	19
1	H	95/131 (72%)	81 (85%)	14 (15%)	3	16
1	I	94/131 (72%)	81 (86%)	13 (14%)	3	18
1	J	93/131 (71%)	81 (87%)	12 (13%)	4	19
1	K	90/131 (69%)	78 (87%)	12 (13%)	4	19
All	All	744/1048 (71%)	647 (87%)	97 (13%)	4	19

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	275	SER
1	I	266	GLU
1	H	282	GLU
1	I	213	TRP
1	J	167	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	245	HIS

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 monosaccharides 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

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.