



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 04:59 am GMT

PDB ID : 3UQ4  
Title : X-ray structure of a pentameric ligand gated ion channel from *Erwinia chrysanthemi* (ELIC) mutant F247L (F16L)  
Authors : Gonzalez-Gutierrez, G.; Lukk, T.; Agarwal, V.; Papke, D.; Nair, S.K.; Grosman, C.  
Deposited on : 2011-11-19  
Resolution : 3.50 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](mailto: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.

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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	:	trunk28620
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)	:	recalc28949

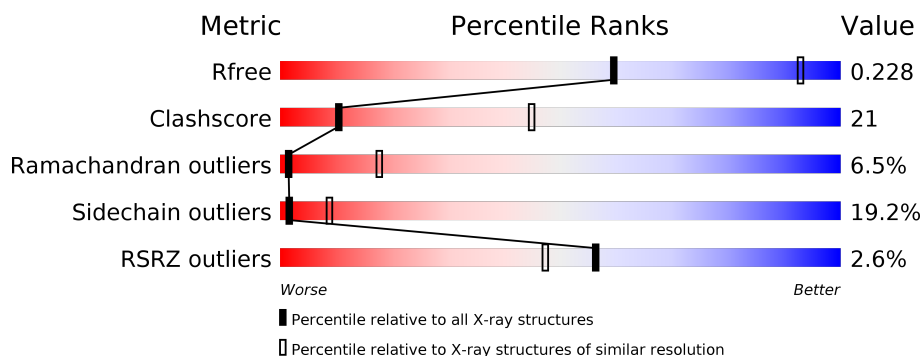
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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))
$R_{free}$	100719	1195 (3.60-3.40)
Clashscore	112137	1322 (3.60-3.40)
Ramachandran outliers	110173	1283 (3.60-3.40)
Sidechain outliers	110143	1284 (3.60-3.40)
RSRZ outliers	101464	1226 (3.60-3.40)

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  $\geq 3$ , 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	324	
1	B	324	
1	C	324	
1	D	324	
1	E	324	
1	F	324	

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Mol	Chain	Length	Quality of chain
1	G	324	<div><div><div></div><div></div><div></div><div></div><div></div></div><div><div>3%</div><div>46%</div><div>35%</div><div>11%</div><div>5%</div></div></div>
1	H	324	<div><div><div></div><div></div><div></div><div></div><div></div></div><div><div>2%</div><div>48%</div><div>35%</div><div>10%</div><div>5%</div></div></div>
1	I	324	<div><div><div></div><div></div><div></div><div></div><div></div></div><div><div>3%</div><div>45%</div><div>37%</div><div>11%</div><div>5%</div></div></div>
1	J	324	<div><div><div></div><div></div><div></div><div></div><div></div></div><div><div>3%</div><div>46%</div><div>39%</div><div>9%</div><div>5%</div></div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 25022 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 Gamma-aminobutyric-acid receptor subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	B	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	C	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	D	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	E	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	F	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	G	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	H	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	I	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	J	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
A	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
A	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
B	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
B	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
B	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
C	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
C	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
C	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
D	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
D	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
E	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
E	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
E	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
F	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
F	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
F	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
G	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
G	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
G	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
H	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
H	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
H	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
I	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
I	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
I	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4
J	-1	GLY	-	EXPRESSION TAG	UNP E0SJQ4
J	0	SER	-	EXPRESSION TAG	UNP E0SJQ4
J	247	LEU	PHE	ENGINEERED MUTATION	UNP E0SJQ4

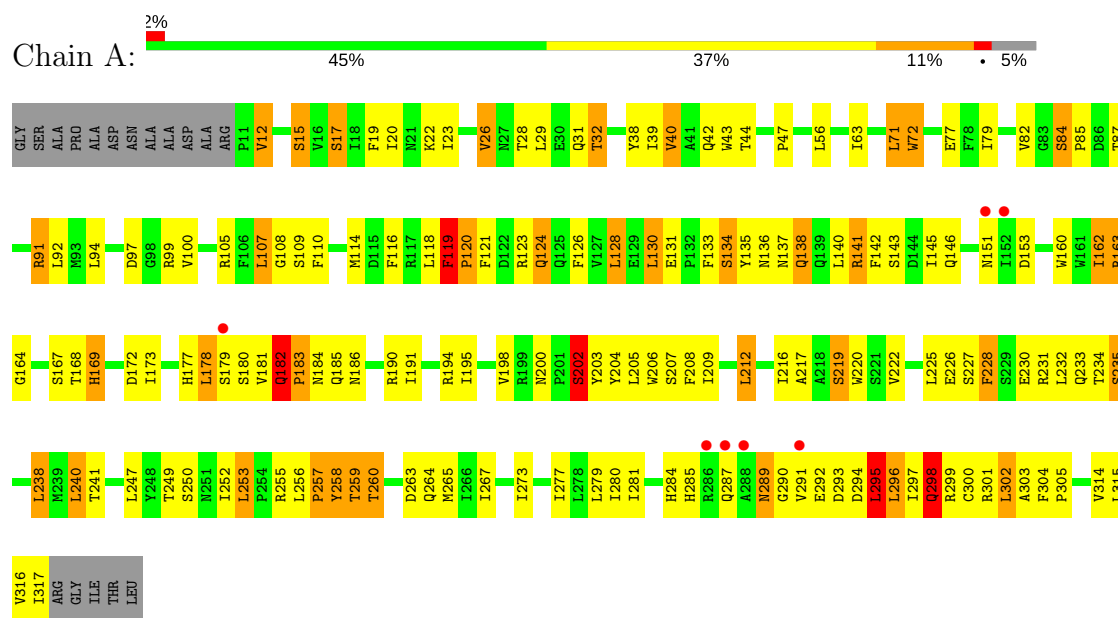
- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0
2	F	1	Total Na 1 1	0	0

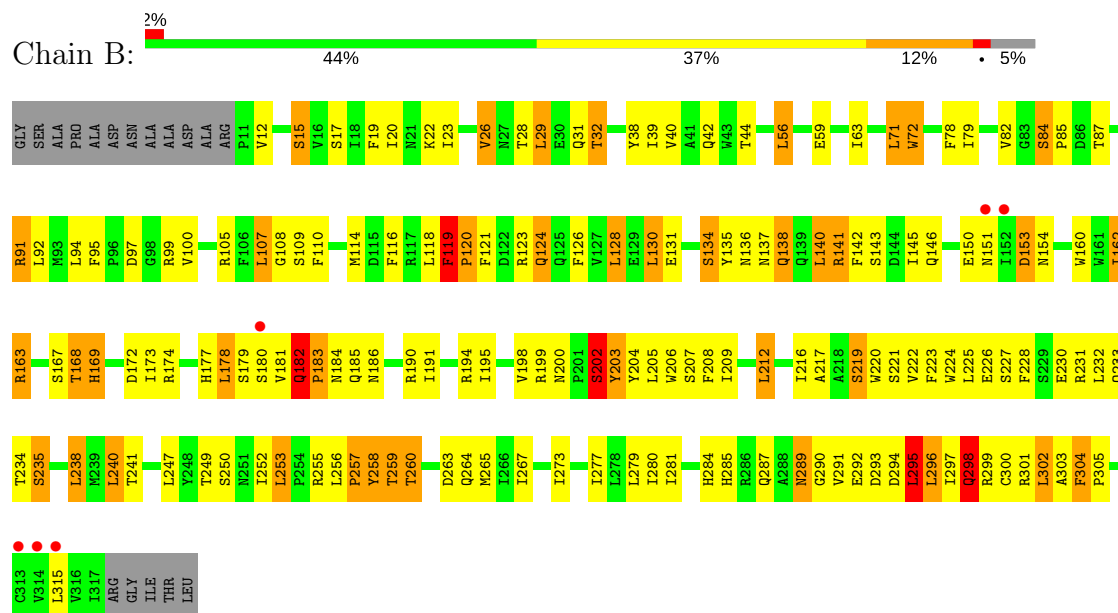
### 3 Residue-property plots

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.

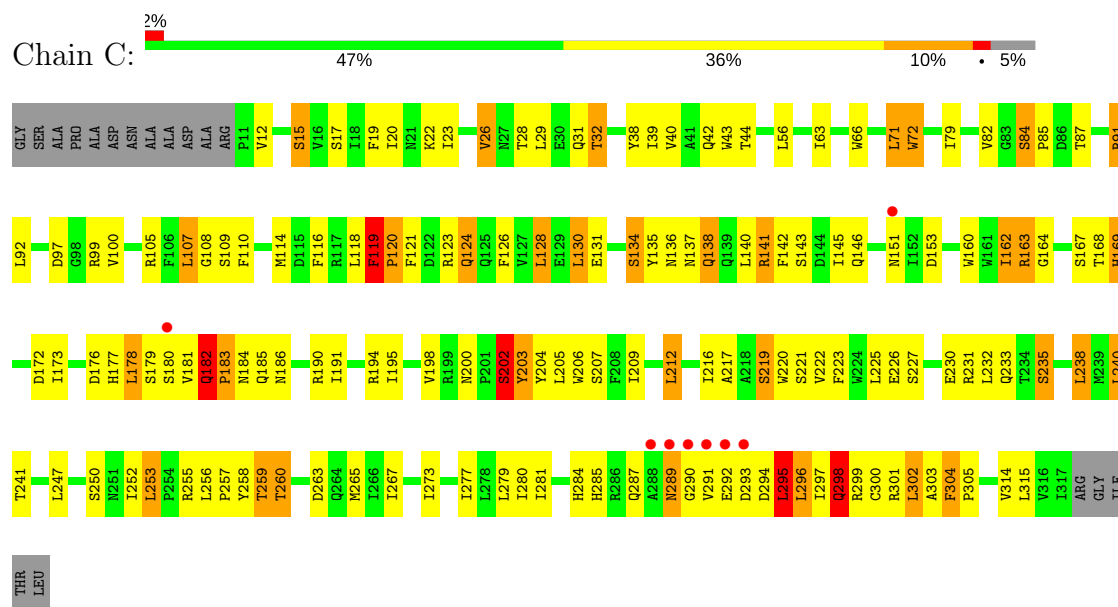
#### • Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



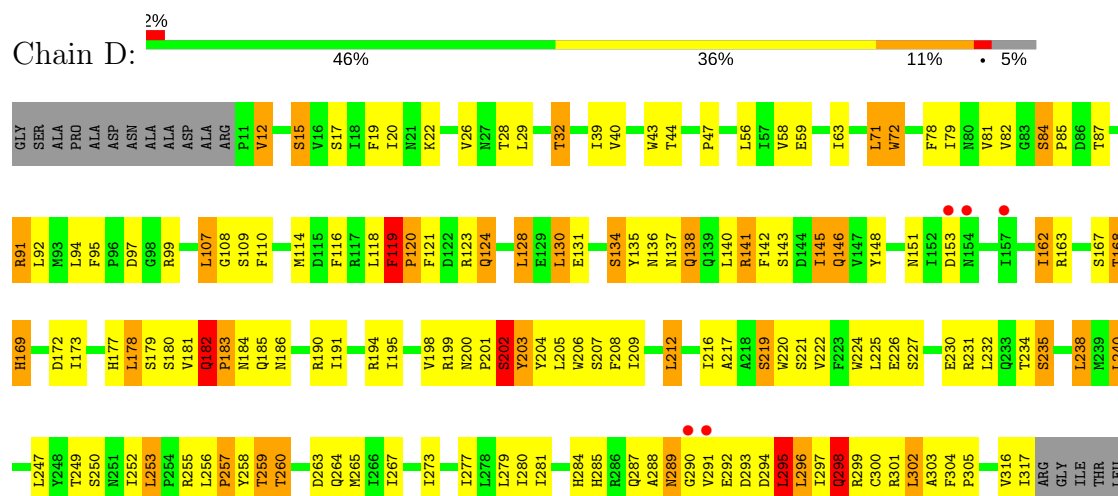
#### • Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



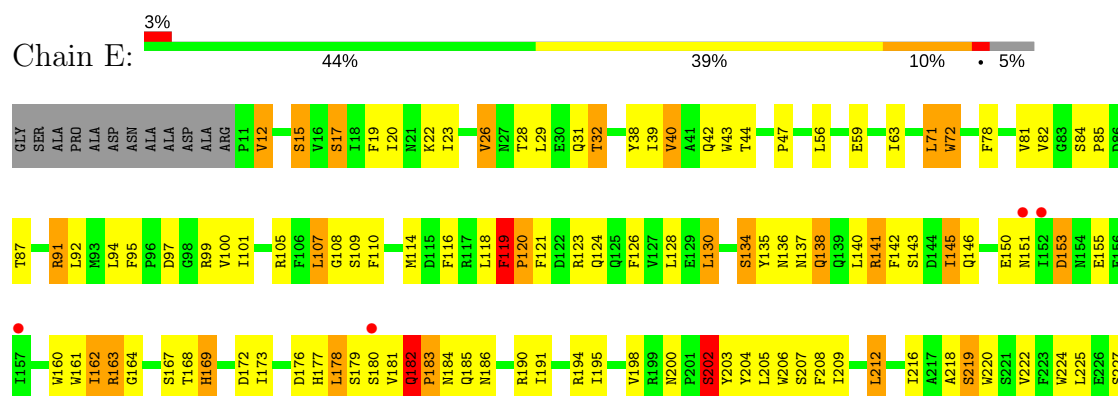
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

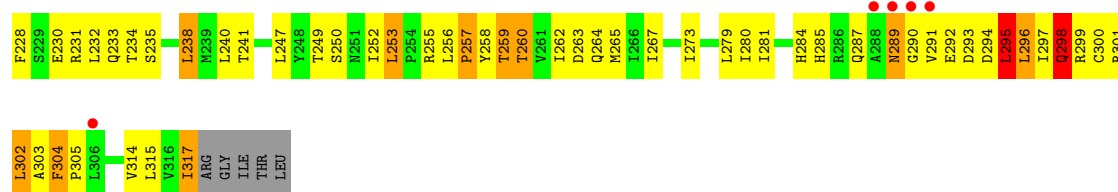


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

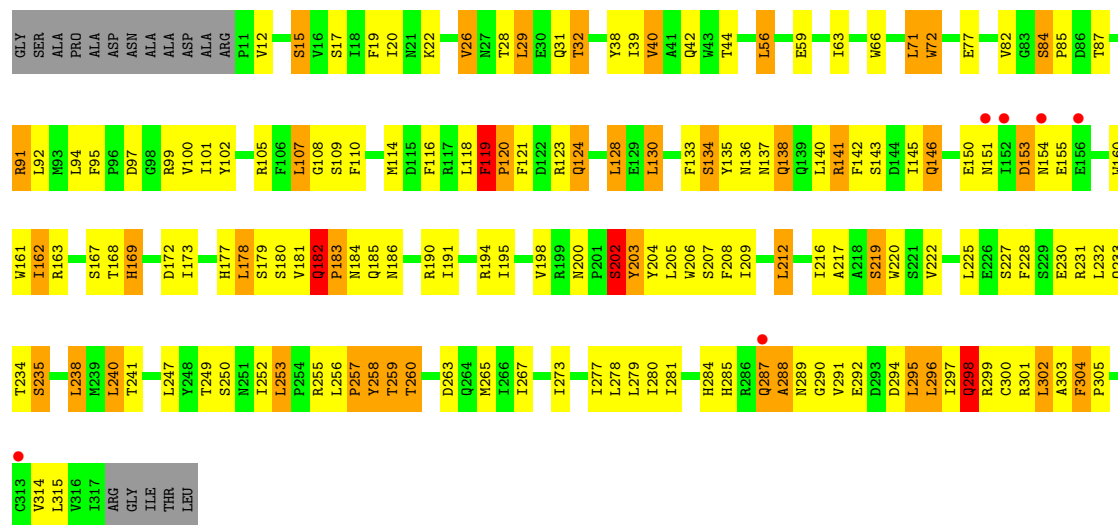
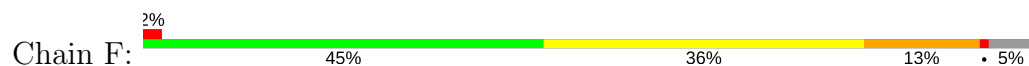


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

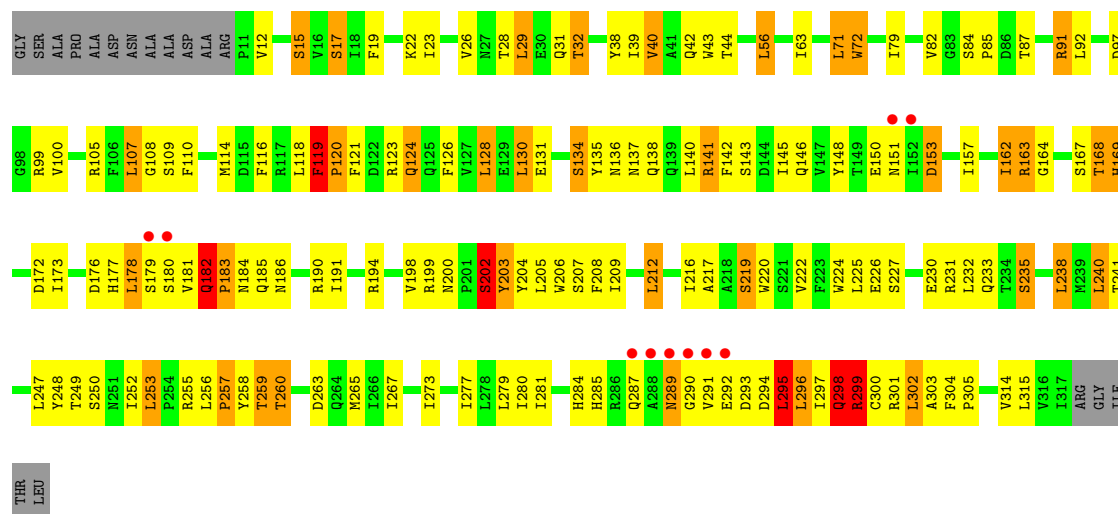




• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



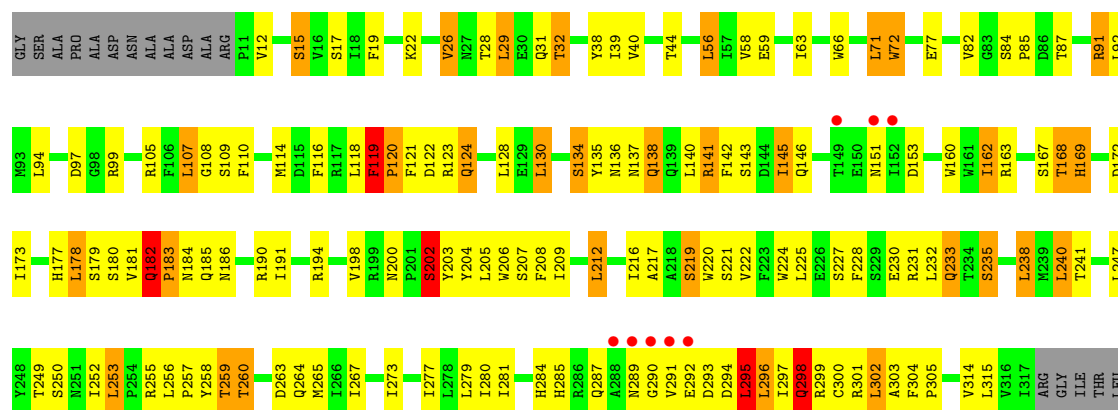
• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



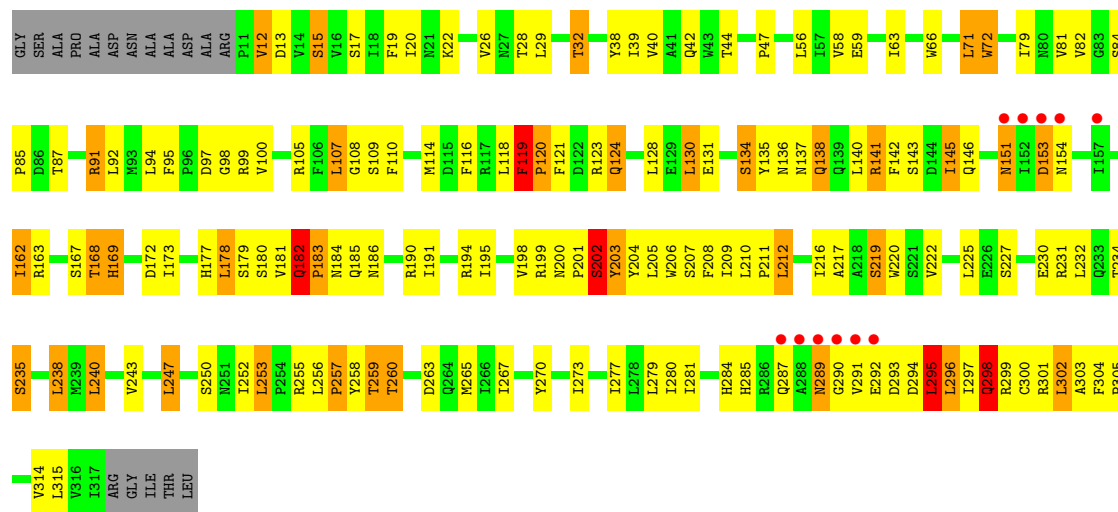
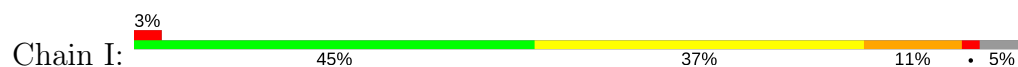
• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



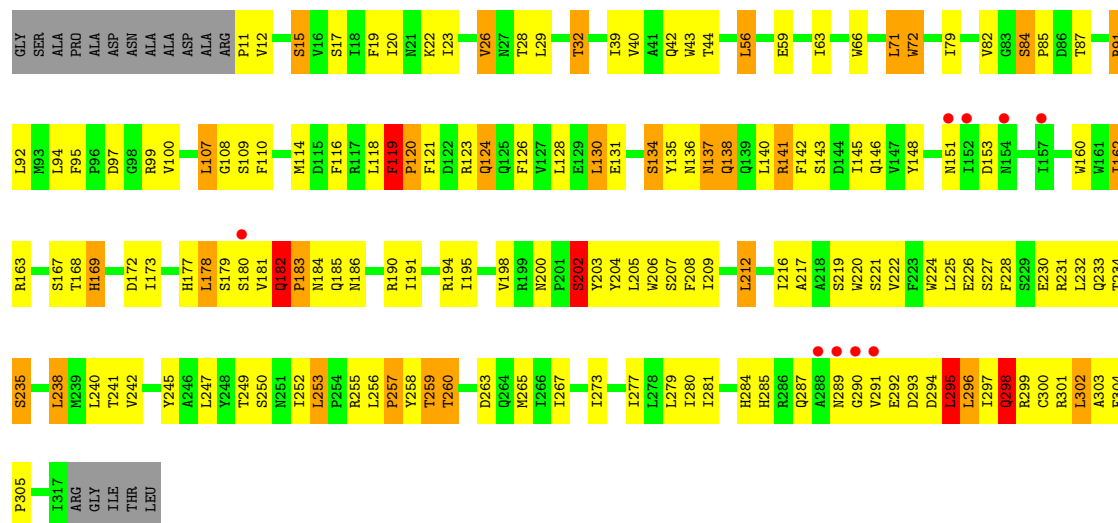




• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



• Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.35Å 266.94Å 110.84Å 90.00° 109.60° 90.00°	Depositor
Resolution (Å)	19.93 – 3.50 19.93 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.93-3.50) 99.8 (19.93-3.50)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.78 (at 3.52Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_897)	Depositor
R, $R_{free}$	0.215 , 0.239 0.202 , 0.228	Depositor DCC
$R_{free}$ test set	3593 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	97.4	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 64.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	25022	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NA

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	0.69	0/2569	0.85	2/3502 (0.1%)
1	B	0.70	0/2569	0.87	2/3502 (0.1%)
1	C	0.70	0/2569	0.84	1/3502 (0.0%)
1	D	0.73	0/2569	0.88	2/3502 (0.1%)
1	E	0.73	0/2569	0.85	2/3502 (0.1%)
1	F	0.69	0/2569	0.85	1/3502 (0.0%)
1	G	0.73	0/2569	1.02	4/3502 (0.1%)
1	H	0.71	1/2569 (0.0%)	0.85	2/3502 (0.1%)
1	I	0.71	0/2569	0.87	2/3502 (0.1%)
1	J	0.70	0/2569	0.85	1/3502 (0.0%)
All	All	0.71	1/25690 (0.0%)	0.87	19/35020 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
1	E	0	3
1	F	0	3
1	G	0	3
1	H	0	3
1	I	0	3
1	J	0	3
All	All	0	30

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	233	GLN	CG-CD	5.49	1.63	1.51

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	299	ARG	NE-CZ-NH1	-22.37	109.12	120.30
1	G	299	ARG	NE-CZ-NH2	21.64	131.12	120.30
1	G	299	ARG	CD-NE-CZ	10.27	137.97	123.60
1	J	119	PHE	C-N-CD	-9.47	99.76	120.60
1	D	119	PHE	C-N-CD	-9.39	99.95	120.60

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	PHE	Peptide
1	A	137	ASN	Peptide
1	A	298	GLN	Peptide
1	B	119	PHE	Peptide
1	B	137	ASN	Peptide

## 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	2502	0	2480	108	0
1	B	2502	0	2480	120	0
1	C	2502	0	2480	104	0
1	D	2502	0	2480	110	0
1	E	2502	0	2480	112	0
1	F	2502	0	2480	115	0
1	G	2502	0	2480	112	0
1	H	2502	0	2480	111	0
1	I	2502	0	2480	113	0
1	J	2502	0	2480	104	0
2	A	1	0	0	0	0
2	F	1	0	0	0	0
All	All	25022	0	24800	1031	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 21.

The worst 5 of 1031 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:I:300:CYS:HA	1:I:303:ALA:HB3	1.53	0.91
1:A:300:CYS:HA	1:A:303:ALA:HB3	1.54	0.89
1:F:205:LEU:HD23	1:F:209:ILE:HG13	1.54	0.89
1:I:205:LEU:HD23	1:I:209:ILE:HG13	1.55	0.88
1:D:205:LEU:HD23	1:D:209:ILE:HG13	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	305/324 (94%)	248 (81%)	38 (12%)	19 (6%)	2	19
1	B	305/324 (94%)	249 (82%)	36 (12%)	20 (7%)	1	17
1	C	305/324 (94%)	250 (82%)	33 (11%)	22 (7%)	1	15
1	D	305/324 (94%)	249 (82%)	33 (11%)	23 (8%)	1	13
1	E	305/324 (94%)	249 (82%)	36 (12%)	20 (7%)	1	17
1	F	305/324 (94%)	249 (82%)	37 (12%)	19 (6%)	2	19
1	G	305/324 (94%)	249 (82%)	36 (12%)	20 (7%)	1	17
1	H	305/324 (94%)	253 (83%)	34 (11%)	18 (6%)	2	20
1	I	305/324 (94%)	255 (84%)	31 (10%)	19 (6%)	2	19
1	J	305/324 (94%)	247 (81%)	39 (13%)	19 (6%)	2	19
All	All	3050/3240 (94%)	2498 (82%)	353 (12%)	199 (6%)	1	18

5 of 199 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	PRO
1	A	169	HIS
1	A	200	ASN
1	A	202	SER
1	B	120	PRO

### 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	275/285 (96%)	222 (81%)	53 (19%)	1	9
1	B	275/285 (96%)	220 (80%)	55 (20%)	1	8
1	C	275/285 (96%)	223 (81%)	52 (19%)	2	9
1	D	275/285 (96%)	221 (80%)	54 (20%)	1	8
1	E	275/285 (96%)	222 (81%)	53 (19%)	1	9
1	F	275/285 (96%)	222 (81%)	53 (19%)	1	9
1	G	275/285 (96%)	223 (81%)	52 (19%)	2	9
1	H	275/285 (96%)	224 (82%)	51 (18%)	2	10
1	I	275/285 (96%)	222 (81%)	53 (19%)	1	9
1	J	275/285 (96%)	224 (82%)	51 (18%)	2	10
All	All	2750/2850 (96%)	2223 (81%)	527 (19%)	1	9

5 of 527 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	167	SER
1	F	182	GLN
1	J	72	TRP
1	E	207	SER
1	F	12	VAL

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	125	GLN
1	J	125	GLN
1	I	125	GLN
1	A	285	HIS
1	I	151	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 2 ligands modelled in this entry, 2 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	307/324 (94%)	-0.52	7 (2%) 61 51	57, 94, 173, 216	0
1	B	307/324 (94%)	-0.53	6 (1%) 65 57	59, 92, 176, 210	0
1	C	307/324 (94%)	-0.43	8 (2%) 56 47	56, 92, 174, 216	0
1	D	307/324 (94%)	-0.52	5 (1%) 72 64	57, 90, 172, 215	0
1	E	307/324 (94%)	-0.50	9 (2%) 52 43	57, 93, 177, 215	0
1	F	307/324 (94%)	-0.56	6 (1%) 65 57	59, 93, 173, 210	0
1	G	307/324 (94%)	-0.50	10 (3%) 47 39	57, 91, 175, 216	0
1	H	307/324 (94%)	-0.54	8 (2%) 56 47	57, 91, 174, 214	0
1	I	307/324 (94%)	-0.46	11 (3%) 43 37	56, 91, 174, 217	0
1	J	307/324 (94%)	-0.52	9 (2%) 52 43	56, 93, 174, 217	0
All	All	3070/3240 (94%)	-0.51	79 (2%) 56 47	56, 92, 176, 217	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	151	ASN	8.6
1	C	289	ASN	7.0
1	G	289	ASN	7.0
1	G	291	VAL	6.7
1	C	291	VAL	6.5

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	NA	F	323	1/1	0.70	0.36	-	50,50,50,50	0
2	NA	A	323	1/1	0.59	0.41	-	48,48,48,48	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.