



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 3, 2016 – 09:25 PM EDT

PDB ID : 5JDJ
Title : Crystal structure of domain I10 from titin in space group P212121
Authors : Williams, R.; Bogomolovas, J.; Labiet, S.; Mayans, O.
Deposited on : 2016-04-16
Resolution : 1.74 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
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
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-20027939

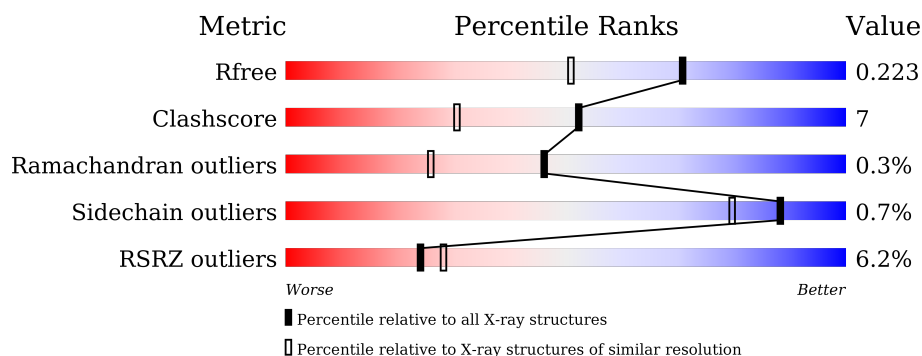
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.74 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.



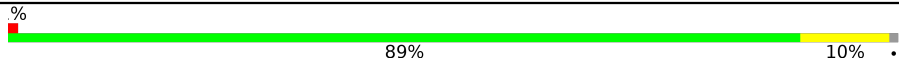
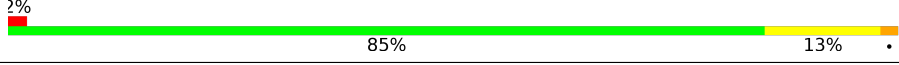
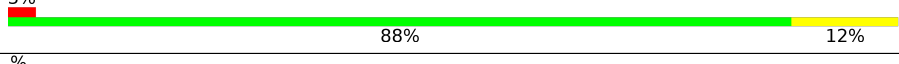


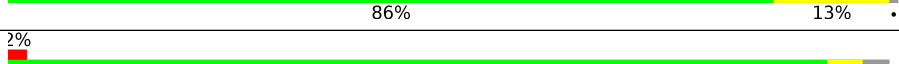
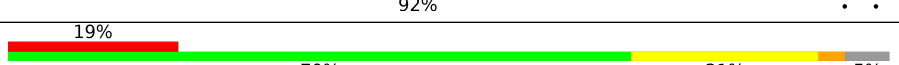
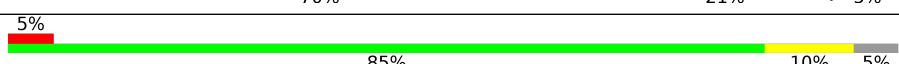
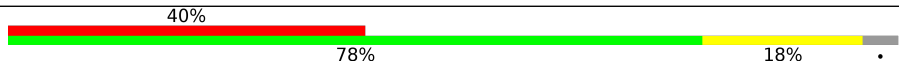

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2417 (1.76-1.72)
Clashscore	102246	2570 (1.76-1.72)
Ramachandran outliers	100387	2544 (1.76-1.72)
Sidechain outliers	100360	2544 (1.76-1.72)
RSRZ outliers	91569	2420 (1.76-1.72)

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	91	<div> <div>5%</div> <div>85%15%</div> </div>
1	B	91	<div> <div>7%</div> <div>82%16%</div> </div>
1	C	91	<div> <div>0%</div> <div>89%11%</div> </div>
1	D	91	<div> <div>2%</div> <div>85%14%</div> </div>
1	E	91	<div> <div>0%</div> <div>89%9%</div> </div>
1	F	91	<div> <div>2%</div> <div>82%16%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	91	
1	H	91	
1	I	91	
1	J	91	
1	K	91	
1	L	91	
1	M	91	
1	N	91	
1	O	91	
1	P	91	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CA	A	101	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12851 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 Titin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	91	Total	C	N	O	S	0	1	0
			712	448	113	143	8			
1	B	91	Total	C	N	O	S	0	1	0
			712	448	113	143	8			
1	C	91	Total	C	N	O	S	0	0	0
			709	446	113	143	7			
1	D	90	Total	C	N	O	S	0	2	0
			715	451	112	143	9			
1	E	89	Total	C	N	O	S	0	3	0
			711	448	113	144	6			
1	F	90	Total	C	N	O	S	0	0	0
			705	444	112	142	7			
1	G	90	Total	C	N	O	S	0	0	0
			702	442	112	142	6			
1	H	91	Total	C	N	O	S	0	5	0
			732	463	115	146	8			
1	I	91	Total	C	N	O	S	0	0	0
			706	444	113	143	6			
1	J	88	Total	C	N	O	S	0	2	0
			697	441	110	139	7			
1	K	89	Total	C	N	O	S	0	1	0
			702	442	111	143	6			
1	L	90	Total	C	N	O	S	0	1	0
			707	447	112	142	6			
1	M	88	Total	C	N	O	S	0	0	0
			692	436	110	140	6			
1	N	86	Total	C	N	O	S	0	1	0
			674	426	108	133	7			
1	O	86	Total	C	N	O	S	0	1	0
			678	429	108	135	6			
1	P	87	Total	C	N	O	S	0	1	0
			639	404	107	121	7			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q8WZ42
A	2	ALA	-	expression tag	UNP Q8WZ42
A	3	MET	-	expression tag	UNP Q8WZ42
B	1	GLY	-	expression tag	UNP Q8WZ42
B	2	ALA	-	expression tag	UNP Q8WZ42
B	3	MET	-	expression tag	UNP Q8WZ42
C	1	GLY	-	expression tag	UNP Q8WZ42
C	2	ALA	-	expression tag	UNP Q8WZ42
C	3	MET	-	expression tag	UNP Q8WZ42
D	1	GLY	-	expression tag	UNP Q8WZ42
D	2	ALA	-	expression tag	UNP Q8WZ42
D	3	MET	-	expression tag	UNP Q8WZ42
E	1	GLY	-	expression tag	UNP Q8WZ42
E	2	ALA	-	expression tag	UNP Q8WZ42
E	3	MET	-	expression tag	UNP Q8WZ42
F	1	GLY	-	expression tag	UNP Q8WZ42
F	2	ALA	-	expression tag	UNP Q8WZ42
F	3	MET	-	expression tag	UNP Q8WZ42
G	1	GLY	-	expression tag	UNP Q8WZ42
G	2	ALA	-	expression tag	UNP Q8WZ42
G	3	MET	-	expression tag	UNP Q8WZ42
H	1	GLY	-	expression tag	UNP Q8WZ42
H	2	ALA	-	expression tag	UNP Q8WZ42
H	3	MET	-	expression tag	UNP Q8WZ42
I	1	GLY	-	expression tag	UNP Q8WZ42
I	2	ALA	-	expression tag	UNP Q8WZ42
I	3	MET	-	expression tag	UNP Q8WZ42
J	1	GLY	-	expression tag	UNP Q8WZ42
J	2	ALA	-	expression tag	UNP Q8WZ42
J	3	MET	-	expression tag	UNP Q8WZ42
K	1	GLY	-	expression tag	UNP Q8WZ42
K	2	ALA	-	expression tag	UNP Q8WZ42
K	3	MET	-	expression tag	UNP Q8WZ42
L	1	GLY	-	expression tag	UNP Q8WZ42
L	2	ALA	-	expression tag	UNP Q8WZ42
L	3	MET	-	expression tag	UNP Q8WZ42
M	1	GLY	-	expression tag	UNP Q8WZ42
M	2	ALA	-	expression tag	UNP Q8WZ42
M	3	MET	-	expression tag	UNP Q8WZ42
N	1	GLY	-	expression tag	UNP Q8WZ42
N	2	ALA	-	expression tag	UNP Q8WZ42
N	3	MET	-	expression tag	UNP Q8WZ42

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Chain	Residue	Modelled	Actual	Comment	Reference
O	1	GLY	-	expression tag	UNP Q8WZ42
O	2	ALA	-	expression tag	UNP Q8WZ42
O	3	MET	-	expression tag	UNP Q8WZ42
P	1	GLY	-	expression tag	UNP Q8WZ42
P	2	ALA	-	expression tag	UNP Q8WZ42
P	3	MET	-	expression tag	UNP Q8WZ42

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	I	1	Total Ca 1 1	0	0
2	B	2	Total Ca 2 2	0	0
2	A	1	Total Ca 1 1	0	0
2	L	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	94	Total O 94 94	0	0
3	B	111	Total O 111 111	0	0
3	C	90	Total O 90 90	0	0
3	D	109	Total O 109 109	0	0
3	E	129	Total O 129 129	0	0
3	F	84	Total O 84 84	0	0
3	G	117	Total O 117 117	0	0
3	H	129	Total O 129 129	0	0
3	I	127	Total O 127 127	0	0

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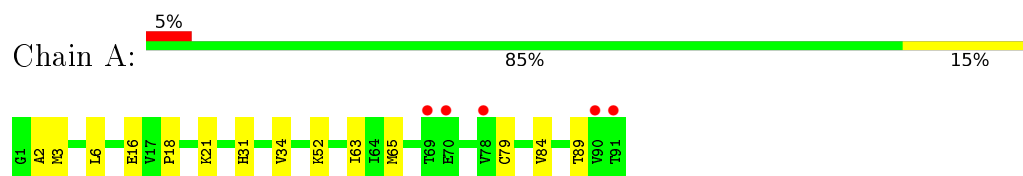
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	131	Total 131	O 131	0	0
3	K	111	Total 111	O 111	0	0
3	L	115	Total 115	O 115	0	0
3	M	132	Total 132	O 132	0	0
3	N	59	Total 59	O 59	0	0
3	O	70	Total 70	O 70	0	0
3	P	44	Total 44	O 44	0	0

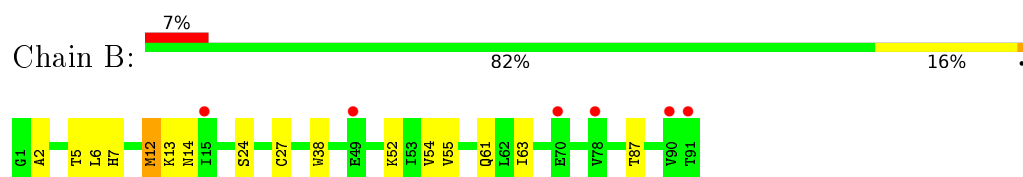
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

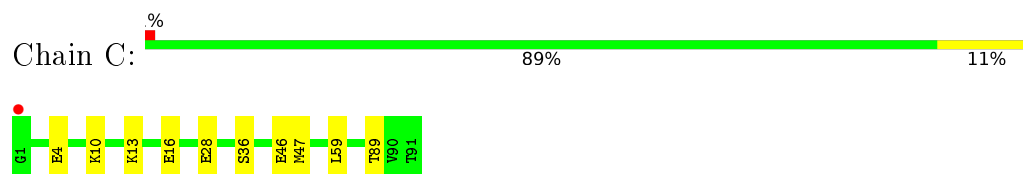
- Molecule 1: Titin



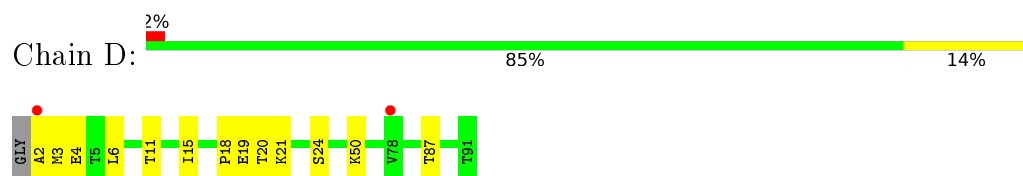
- Molecule 1: Titin



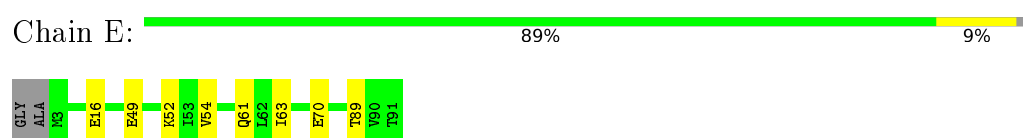
- Molecule 1: Titin



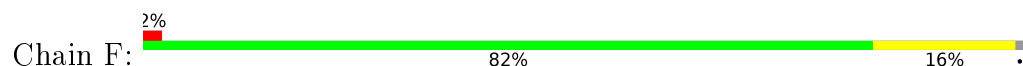
- Molecule 1: Titin



- Molecule 1: Titin

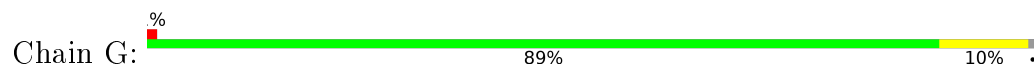


- Molecule 1: Titin

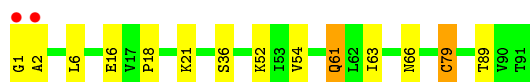
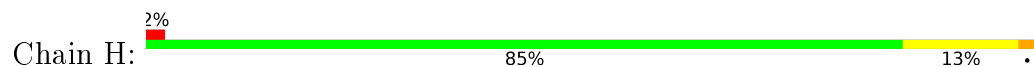




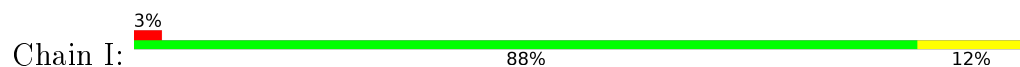
- Molecule 1: Titin



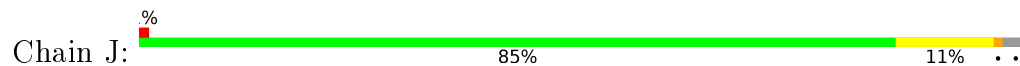
- Molecule 1: Titin



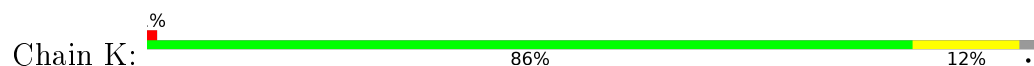
- Molecule 1: Titin



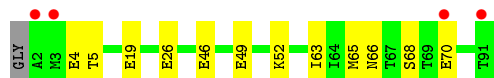
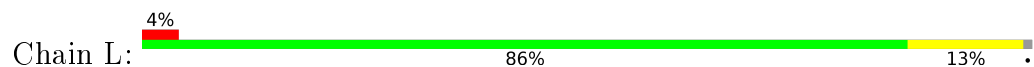
- Molecule 1: Titin



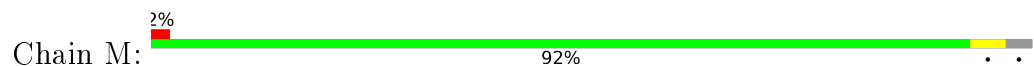
- Molecule 1: Titin

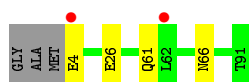


- Molecule 1: Titin

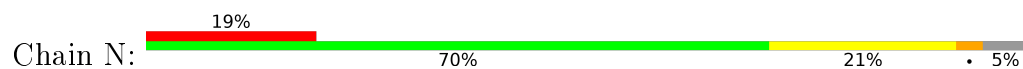


- Molecule 1: Titin

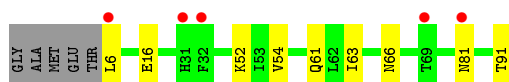
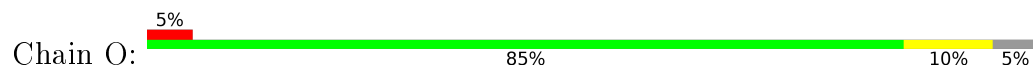




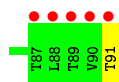
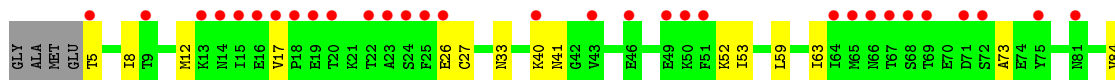
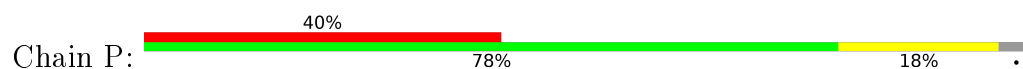
• Molecule 1: Titin



• Molecule 1: Titin



• Molecule 1: Titin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.64Å 136.24Å 140.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.65 – 1.74 29.65 – 1.74	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.65-1.74) 95.0 (29.65-1.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 1.74Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.186 , 0.224 0.185 , 0.223	Depositor DCC
R_{free} test set	1411 reflections (1.01%)	DCC
Wilson B-factor (Å ²)	16.6	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.027 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12851	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.54% 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

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	0.38	0/726	0.55	0/980
1	B	0.39	0/726	0.58	0/980
1	C	0.42	0/720	0.61	0/972
1	D	0.38	0/735	0.59	0/993
1	E	0.36	0/731	0.54	0/989
1	F	0.36	0/716	0.52	0/967
1	G	0.41	0/713	0.58	0/964
1	H	0.55	2/758 (0.3%)	0.64	0/1024
1	I	0.39	0/717	0.53	0/969
1	J	0.42	0/714	0.58	0/965
1	K	0.41	0/716	0.57	0/968
1	L	0.42	0/721	0.57	0/975
1	M	0.38	0/703	0.55	0/950
1	N	0.39	0/688	0.56	0/930
1	O	0.34	0/692	0.54	0/935
1	P	0.34	0/653	0.51	0/884
All	All	0.40	2/11429 (0.0%)	0.57	0/15445

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	79[A]	CYS	CB-SG	-6.61	1.71	1.82
1	H	79[B]	CYS	CB-SG	-6.61	1.71	1.82

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	712	0	711	13	0
1	B	712	0	710	15	0
1	C	709	0	706	10	0
1	D	715	0	717	13	0
1	E	711	0	707	5	0
1	F	705	0	700	12	0
1	G	702	0	693	7	0
1	H	732	0	743	15	0
1	I	706	0	699	5	0
1	J	697	0	698	9	0
1	K	702	0	692	8	0
1	L	707	0	704	10	0
1	M	692	0	686	5	0
1	N	674	0	666	17	0
1	O	678	0	675	8	0
1	P	639	0	584	13	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	E	1	0	0	0	0
2	I	1	0	0	0	0
2	L	1	0	0	0	0
3	A	94	0	0	1	0
3	B	111	0	0	4	0
3	C	90	0	0	5	0
3	D	109	0	0	5	1
3	E	129	0	0	2	1
3	F	84	0	0	5	0
3	G	117	0	0	2	0
3	H	129	0	0	3	1
3	I	127	0	0	0	3
3	J	131	0	0	4	2
3	K	111	0	0	4	1
3	L	115	0	0	5	1
3	M	132	0	0	4	3
3	N	59	0	0	3	1
3	O	70	0	0	4	2
3	P	44	0	0	2	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	12851	0	11091	149	9

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 7.

The worst 5 of 149 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:10:LYS:NZ	3:C:101:HOH:O	1.96	0.97
1:C:13:LYS:NZ	1:F:85:SER:O	2.05	0.90
1:A:3:MET:HG2	1:H:2:ALA:HB3	1.53	0.86
1:B:52:LYS:HB2	1:B:63:ILE:HB	1.62	0.81
1:D:2:ALA:HA	1:D:3:MET:HB2	1.64	0.79

The worst 5 of 9 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:302:HOH:O	3:N:109:HOH:O[4_566]	1.96	0.24
3:J:223:HOH:O	3:M:105:HOH:O[1_455]	2.01	0.19
3:L:204:HOH:O	3:M:166:HOH:O[4_465]	2.07	0.13
3:H:102:HOH:O	3:M:101:HOH:O[3_745]	2.11	0.09
3:O:130:HOH:O	3:P:105:HOH:O[3_745]	2.11	0.09

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	90/91 (99%)	86 (96%)	4 (4%)	0	100	100
1	B	90/91 (99%)	87 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
1	D	91/91 (100%)	86 (94%)	5 (6%)	0	100	100
1	E	90/91 (99%)	85 (94%)	5 (6%)	0	100	100
1	F	88/91 (97%)	86 (98%)	2 (2%)	0	100	100
1	G	88/91 (97%)	86 (98%)	2 (2%)	0	100	100
1	H	94/91 (103%)	89 (95%)	5 (5%)	0	100	100
1	I	89/91 (98%)	84 (94%)	4 (4%)	1 (1%)	17	4
1	J	88/91 (97%)	85 (97%)	2 (2%)	1 (1%)	17	4
1	K	88/91 (97%)	86 (98%)	2 (2%)	0	100	100
1	L	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
1	M	86/91 (94%)	83 (96%)	3 (4%)	0	100	100
1	N	85/91 (93%)	80 (94%)	3 (4%)	2 (2%)	7	1
1	O	85/91 (93%)	83 (98%)	2 (2%)	0	100	100
1	P	86/91 (94%)	83 (96%)	3 (4%)	0	100	100
All	All	1416/1456 (97%)	1362 (96%)	50 (4%)	4 (0%)	46	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	5	THR
1	N	20	THR
1	N	18	PRO
1	I	3	MET

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	84/83 (101%)	83 (99%)	1 (1%)	78	62
1	B	84/83 (101%)	83 (99%)	1 (1%)	78	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	83/83 (100%)	83 (100%)	0	100	100
1	D	86/83 (104%)	86 (100%)	0	100	100
1	E	85/83 (102%)	85 (100%)	0	100	100
1	F	83/83 (100%)	82 (99%)	1 (1%)	78	62
1	G	82/83 (99%)	81 (99%)	1 (1%)	78	62
1	H	88/83 (106%)	85 (97%)	3 (3%)	44	18
1	I	82/83 (99%)	81 (99%)	1 (1%)	78	62
1	J	83/83 (100%)	83 (100%)	0	100	100
1	K	83/83 (100%)	82 (99%)	1 (1%)	78	62
1	L	83/83 (100%)	83 (100%)	0	100	100
1	M	82/83 (99%)	82 (100%)	0	100	100
1	N	79/83 (95%)	78 (99%)	1 (1%)	76	60
1	O	80/83 (96%)	80 (100%)	0	100	100
1	P	64/83 (77%)	64 (100%)	0	100	100
All	All	1311/1328 (99%)	1301 (99%)	10 (1%)	88	77

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	36	SER
1	H	61[A]	GLN
1	I	37	MET
1	G	50	LYS
1	H	61[B]	GLN

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

Mol	Chain	Res	Type
1	E	7	HIS

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 6 ligands modelled in this entry, 6 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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	91/91 (100%)	0.39	5 (5%) 29 33	11, 22, 41, 48	0
1	B	91/91 (100%)	0.62	6 (6%) 22 26	16, 22, 34, 43	0
1	C	91/91 (100%)	0.22	1 (1%) 82 88	11, 18, 32, 36	0
1	D	90/91 (98%)	0.27	2 (2%) 65 72	10, 16, 34, 42	0
1	E	89/91 (97%)	-0.02	0 100 100	11, 17, 31, 41	0
1	F	90/91 (98%)	0.33	2 (2%) 65 72	15, 23, 39, 45	0
1	G	90/91 (98%)	0.12	1 (1%) 82 88	9, 18, 33, 53	0
1	H	91/91 (100%)	0.18	2 (2%) 65 72	9, 15, 26, 41	0
1	I	91/91 (100%)	0.39	3 (3%) 50 56	10, 18, 36, 75	0
1	J	88/91 (96%)	-0.12	1 (1%) 82 88	9, 15, 25, 50	0
1	K	89/91 (97%)	0.06	1 (1%) 82 88	11, 16, 30, 38	0
1	L	90/91 (98%)	0.23	4 (4%) 38 44	11, 20, 37, 72	0
1	M	88/91 (96%)	-0.01	2 (2%) 64 70	10, 16, 26, 52	0
1	N	86/91 (94%)	0.98	17 (19%) 1 2	17, 29, 60, 68	0
1	O	86/91 (94%)	0.58	5 (5%) 26 30	17, 28, 44, 52	0
1	P	87/91 (95%)	1.92	36 (41%) 0 0	22, 42, 85, 96	0
All	All	1428/1456 (98%)	0.38	88 (6%) 24 28	9, 20, 46, 96	0

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	2	ALA	14.4
1	L	2	ALA	11.1
1	P	17	VAL	8.5
1	H	1	GLY	8.2
1	I	1	GLY	7.2

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 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(Å ²)	Q<0.9
2	CA	A	101	1/1	0.97	0.18	5.22	42,42,42,42	0
2	CA	E	101	1/1	0.99	0.10	1.33	12,12,12,12	0
2	CA	B	101	1/1	0.93	0.09	-1.00	33,33,33,33	0
2	CA	I	101	1/1	0.98	0.08	-1.00	15,15,15,15	0
2	CA	L	101	1/1	1.00	0.06	-3.28	10,10,10,10	0
2	CA	B	102	1/1	0.99	0.18	-	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.