



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:29 PM GMT

PDB ID : 4F52  
Title : Structure of a Glomulin-RBX1-CUL1 complex  
Authors : Duda, D.M.; Olszewski, J.L.; Schulman, B.A.  
Deposited on : 2012-05-11  
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](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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

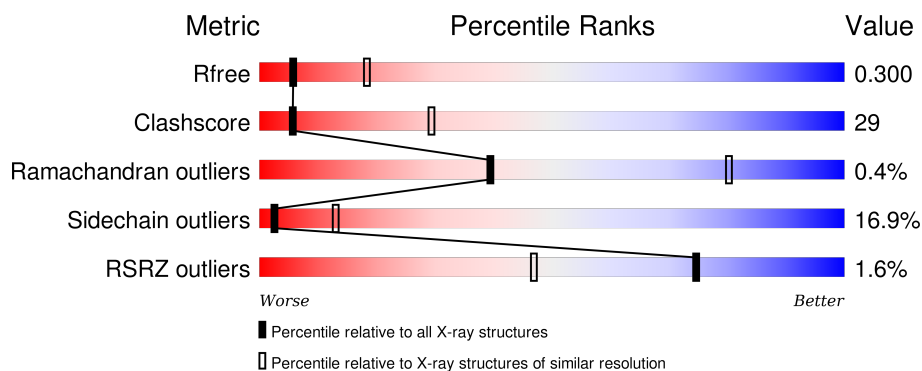
# 1 Overall quality at a glance ⓘ

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))
$R_{free}$	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (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  $\geq 3$ , 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	282	<div> <div>2%</div> <div>47% 35% 9% 9%</div> </div>
1	C	282	<div> <div>2%</div> <div>48% 35% 7% 10%</div> </div>
2	B	106	<div> <div>2%</div> <div>36% 40% • 21%</div> </div>
2	D	106	<div> <div></div> <div>37% 33% 10% 20%</div> </div>
3	E	596	<div> <div>2%</div> <div>40% 39% 8% 12%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	596	<div><div><div></div><div>%</div></div><div><div></div><div>33%</div><div>44%</div><div>9%</div><div>14%</div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13897 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 Cullin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			2103	1341	351	400	11			
1	C	254	Total	C	N	O	S	0	0	0
			2073	1326	345	392	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	409	GLY	-	EXPRESSION TAG	UNP Q13616
A	410	SER	-	EXPRESSION TAG	UNP Q13616
A	421	GLU	LEU	ENGINEERED MUTATION	UNP Q13616
A	451	GLU	VAL	ENGINEERED MUTATION	UNP Q13616
A	452	LYS	VAL	ENGINEERED MUTATION	UNP Q13616
A	455	LYS	TYR	ENGINEERED MUTATION	UNP Q13616
C	409	GLY	-	EXPRESSION TAG	UNP Q13616
C	410	SER	-	EXPRESSION TAG	UNP Q13616
C	421	GLU	LEU	ENGINEERED MUTATION	UNP Q13616
C	451	GLU	VAL	ENGINEERED MUTATION	UNP Q13616
C	452	LYS	VAL	ENGINEERED MUTATION	UNP Q13616
C	455	LYS	TYR	ENGINEERED MUTATION	UNP Q13616

- Molecule 2 is a protein called E3 ubiquitin-protein ligase RBX1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	84	Total	C	N	O	S	0	0	0
			692	438	127	118	9			
2	D	85	Total	C	N	O	S	0	0	0
			701	443	128	121	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	GLY	-	EXPRESSION TAG	UNP P62877
B	4	SER	-	EXPRESSION TAG	UNP P62877
D	3	GLY	-	EXPRESSION TAG	UNP P62877
D	4	SER	-	EXPRESSION TAG	UNP P62877

- Molecule 3 is a protein called Glomulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	523	Total	C	N	O	S	0	0	0
			4202	2720	685	772	25			
3	F	512	Total	C	N	O	S	0	0	0
			4120	2676	666	753	25			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	GLY	-	EXPRESSION TAG	UNP Q92990
E	0	SER	-	EXPRESSION TAG	UNP Q92990
F	-1	GLY	-	EXPRESSION TAG	UNP Q92990
F	0	SER	-	EXPRESSION TAG	UNP Q92990

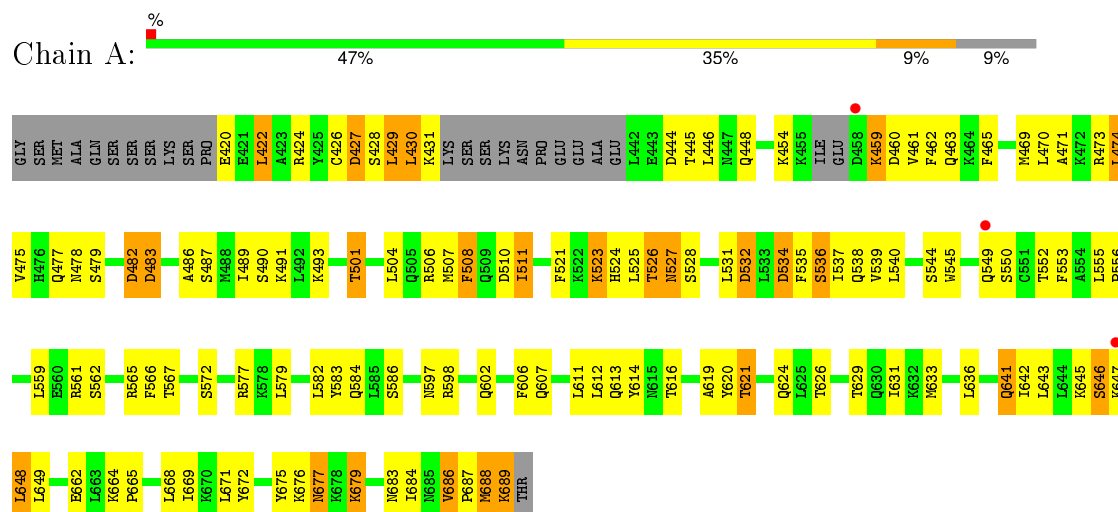
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total	Zn	0	0
			3	3		
4	D	3	Total	Zn	0	0
			3	3		

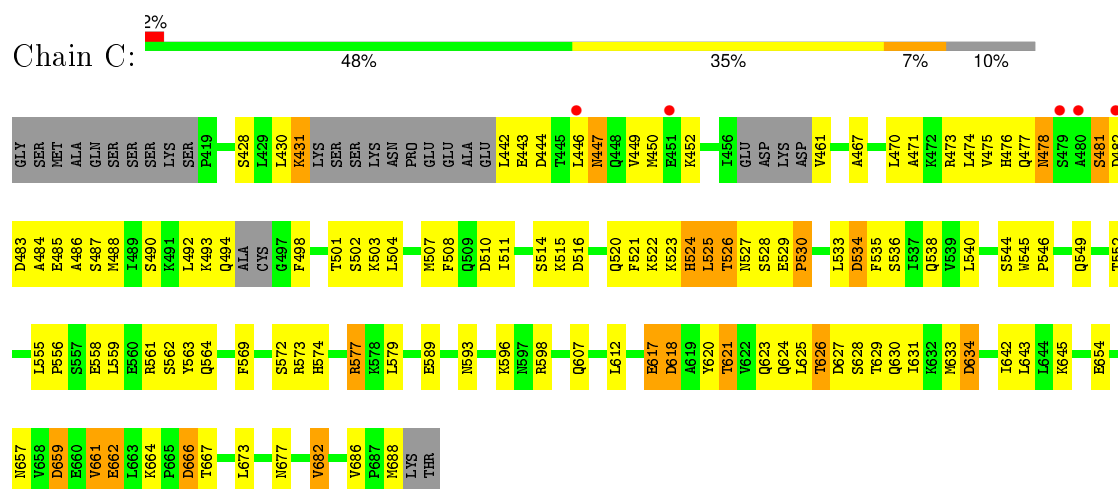
### 3 Residue-property plots

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

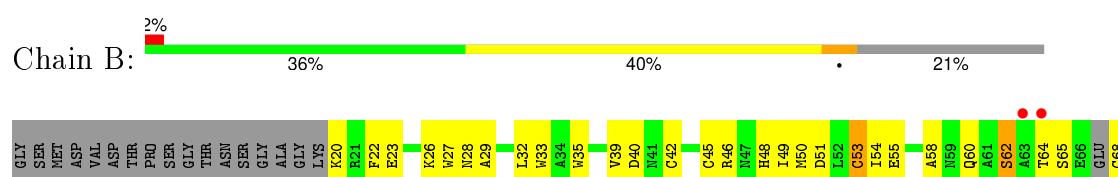
#### • Molecule 1: Cullin-1



#### • Molecule 1: Cullin-1

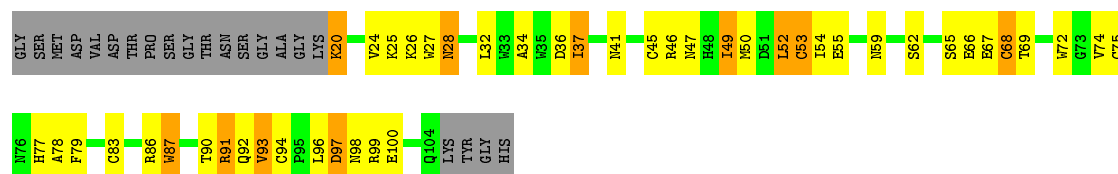


#### • Molecule 2: E3 ubiquitin-protein ligase RBX1

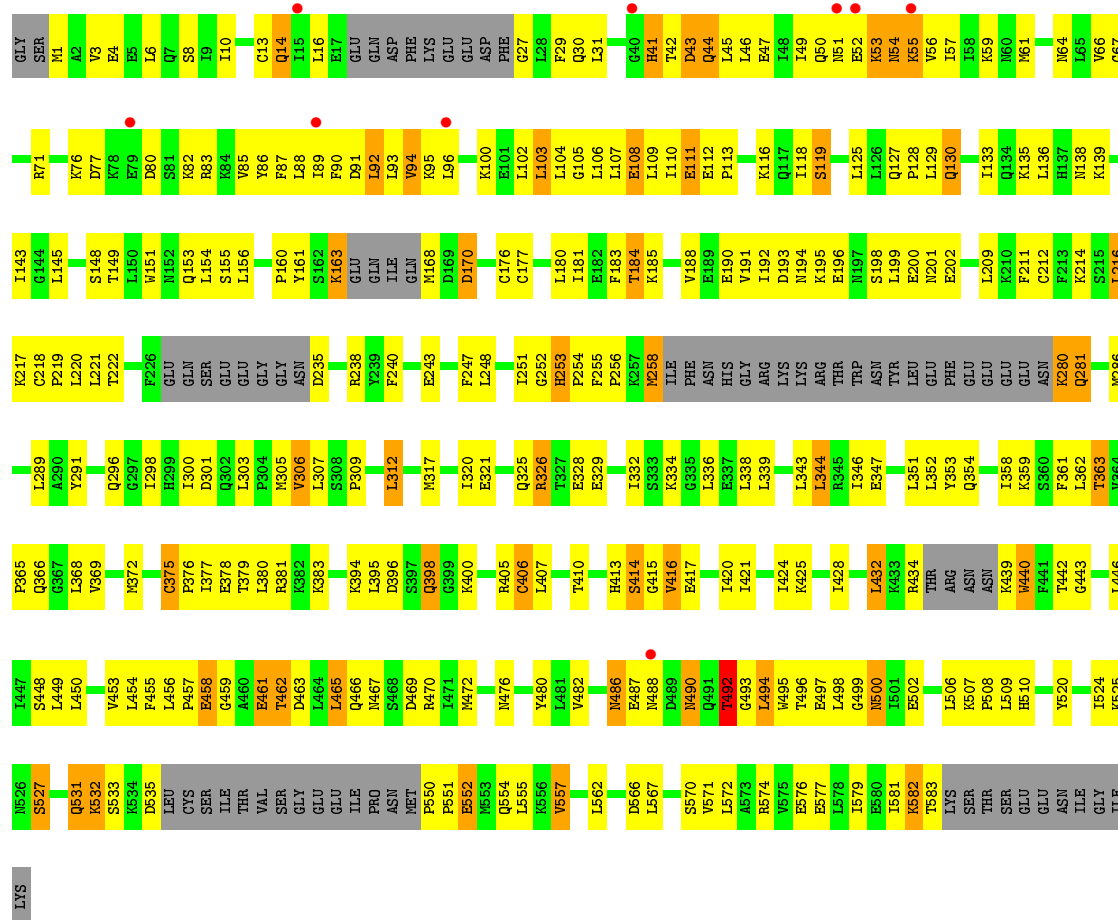




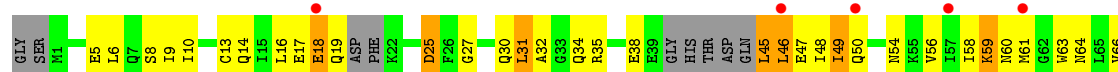
• Molecule 2: E3 ubiquitin-protein ligase RBX1



• Molecule 3: Glomulin



• Molecule 3: Glomulin







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.33Å 193.93Å 142.07Å 90.00° 98.81° 90.00°	Depositor
Resolution (Å)	37.39 – 3.00 45.83 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.8 (37.39-3.00) 98.8 (45.83-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.1_743)	Depositor
R, $R_{free}$	0.219 , 0.289 0.235 , 0.300	Depositor DCC
$R_{free}$ test set	2838 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	83.5	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 85.7	EDS
Estimated twinning fraction	0.033 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 56253 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13897	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN

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	0.46	0/2136	0.62	0/2870
1	C	0.43	0/2106	0.61	0/2830
2	B	0.47	0/711	0.68	0/965
2	D	0.44	0/721	0.66	0/980
3	E	0.44	0/4269	0.63	0/5753
3	F	0.39	0/4184	0.60	0/5639
All	All	0.43	0/14127	0.62	0/19037

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	1
3	E	0	4
3	F	0	4
All	All	0	9

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	501	THR	Peptide
3	E	111	GLU	Peptide
3	E	432	LEU	Peptide
3	E	492	THR	Peptide

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Mol	Chain	Res	Type	Group
3	E	493	GLY	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	2103	0	2127	117	0
1	C	2073	0	2101	118	0
2	B	692	0	647	48	0
2	D	701	0	654	44	0
3	E	4202	0	4360	271	0
3	F	4120	0	4271	277	0
4	B	3	0	0	0	0
4	D	3	0	0	0	0
All	All	13897	0	14160	820	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 29.

The worst 5 of 820 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:525:LEU:O	1:C:529:GLU:HB2	1.21	1.37
1:C:530:PRO:O	1:C:561:ARG:NH2	1.68	1.26
1:A:646:SER:OG	1:A:648:LEU:HD12	1.35	1.21
1:A:647:LYS:HB2	1:A:675:TYR:CE1	1.76	1.20
1:C:527:ASN:HD22	3:F:551:PRO:HB3	1.09	1.10

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	252/282 (89%)	225 (89%)	26 (10%)	1 (0%)	39	80
1	C	246/282 (87%)	228 (93%)	17 (7%)	1 (0%)	39	80
2	B	80/106 (76%)	72 (90%)	8 (10%)	0	100	100
2	D	83/106 (78%)	76 (92%)	6 (7%)	1 (1%)	16	56
3	E	509/596 (85%)	464 (91%)	44 (9%)	1 (0%)	52	88
3	F	492/596 (83%)	450 (92%)	40 (8%)	2 (0%)	39	80
All	All	1662/1968 (84%)	1515 (91%)	141 (8%)	6 (0%)	39	80

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	530	PRO
3	E	306	VAL
2	D	65	SER
3	F	113	PRO
1	A	489	ILE

### 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	237/258 (92%)	197 (83%)	40 (17%)	2	13
1	C	234/258 (91%)	199 (85%)	35 (15%)	3	17
2	B	74/90 (82%)	60 (81%)	14 (19%)	2	10
2	D	75/90 (83%)	59 (79%)	16 (21%)	1	6
3	E	481/548 (88%)	400 (83%)	81 (17%)	2	13
3	F	471/548 (86%)	391 (83%)	80 (17%)	2	13
All	All	1572/1792 (88%)	1306 (83%)	266 (17%)	2	13

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	77	ASP
3	E	326	ARG
3	F	454	LEU
3	E	102	LEU
3	E	184	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	467	ASN
3	F	50	GLN
3	F	486	ASN
3	F	14	GLN
3	F	60	ASN

### 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 [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	258/282 (91%)	-0.07	3 (1%) 81 55	51, 88, 168, 204	0
1	C	254/282 (90%)	0.03	5 (1%) 68 39	60, 99, 174, 207	0
2	B	84/106 (79%)	-0.03	2 (2%) 62 32	52, 114, 156, 217	0
2	D	85/106 (80%)	-0.15	0 100 100	69, 100, 152, 169	0
3	E	523/596 (87%)	-0.07	9 (1%) 73 45	49, 99, 165, 213	0
3	F	512/596 (85%)	-0.06	8 (1%) 74 47	54, 119, 170, 212	0
All	All	1716/1968 (87%)	-0.06	27 (1%) 74 47	49, 104, 169, 217	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	46	LEU	5.5
3	E	488	ASN	3.9
1	C	480	ALA	3.8
3	F	307	LEU	3.2
1	A	549	GLN	3.1

### 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(Å <sup>2</sup> )	Q<0.9
4	ZN	D	201	1/1	0.99	0.20	-0.18	79,79,79,79	0
4	ZN	B	202	1/1	0.99	0.18	-0.43	96,96,96,96	0
4	ZN	D	202	1/1	0.99	0.10	-1.40	120,120,120,120	0
4	ZN	D	203	1/1	0.99	0.19	-	101,101,101,101	0
4	ZN	B	203	1/1	0.98	0.14	-	112,112,112,112	0
4	ZN	B	201	1/1	0.96	0.21	-	91,91,91,91	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.