



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 26, 2026 – 09:30 PM UTC

PDB ID : 9NPG / pdb\_00009npg  
Title : X-ray crystal structure of recombinant Can f 1-C100S in complex with human IgE mAb 12F3 Fab  
Authors : Khatri, K.; Ball, A.; Smith, S.A.; Champan, M.D.; Pomes, A.; Chruszcz, M.  
Deposited on : 2025-03-11  
Resolution : 3.12 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

<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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

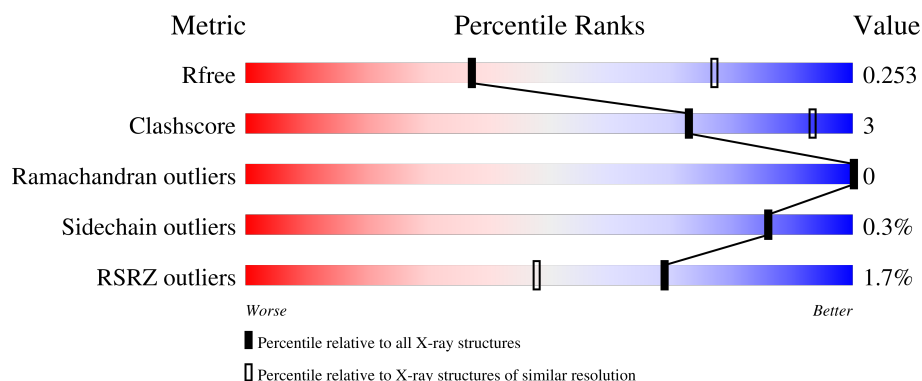
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.12 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))
$R_{free}$	180053	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	231	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>6%</div> <div>5%</div> </div> </div>
1	D	231	<div> <div>4%</div> <div> <div></div> <div>88%</div> <div>9%</div> <div>.</div> </div> </div>
1	G	231	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>6%</div> <div>5%</div> </div> </div>
1	K	231	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>.</div> </div> </div>
2	B	215	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>7%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	E	215	<div><div></div><div>91%</div><div>8%</div><div></div></div>
2	H	215	<div><div></div><div>89%</div><div>10%</div><div></div></div>
2	J	215	<div><div></div><div>93%</div><div>7%</div><div></div></div>
3	C	148	<div><div></div><div>%</div><div>87%</div><div>9%</div><div></div></div>
3	F	148	<div><div></div><div>%</div><div>86%</div><div>9%</div><div></div></div>
3	I	148	<div><div></div><div>2%</div><div>88%</div><div>8%</div><div></div></div>
3	L	148	<div><div></div><div>2%</div><div>91%</div><div>6%</div><div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17514 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 IgE 12F3 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1616	1020	263	327	6			
1	D	226	Total	C	N	O	S	0	0	0
			1661	1047	275	332	7			
1	G	220	Total	C	N	O	S	0	0	0
			1630	1028	268	328	6			
1	K	221	Total	C	N	O	S	0	0	0
			1621	1021	267	326	7			

- Molecule 2 is a protein called IgE 12F3 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1608	1007	270	327	4			
2	E	212	Total	C	N	O	S	0	0	0
			1618	1014	274	326	4			
2	H	214	Total	C	N	O	S	0	0	0
			1635	1025	278	328	4			
2	J	213	Total	C	N	O	S	0	0	0
			1626	1019	276	327	4			

- Molecule 3 is a protein called Major allergen Can f 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	143	Total	C	N	O	S	0	0	0
			1106	693	191	216	6			
3	F	142	Total	C	N	O	S	0	0	0
			1097	687	192	212	6			
3	L	143	Total	C	N	O	S	0	0	0
			1099	690	191	212	6			
3	I	142	Total	C	N	O	S	0	0	0
			1101	689	192	214	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	100	SER	CYS	engineered mutation	UNP O18873
F	100	SER	CYS	engineered mutation	UNP O18873
L	100	SER	CYS	engineered mutation	UNP O18873
I	100	SER	CYS	engineered mutation	UNP O18873

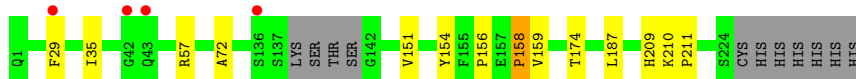
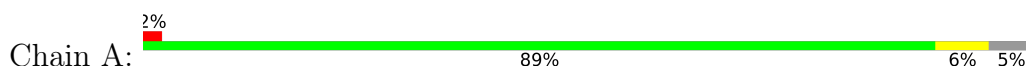
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	10	Total O 10 10	0	0
4	B	5	Total O 5 5	0	0
4	C	7	Total O 7 7	0	0
4	D	9	Total O 9 9	0	0
4	E	9	Total O 9 9	0	0
4	F	6	Total O 6 6	0	0
4	G	14	Total O 14 14	0	0
4	H	11	Total O 11 11	0	0
4	K	8	Total O 8 8	0	0
4	J	5	Total O 5 5	0	0
4	L	10	Total O 10 10	0	0
4	I	2	Total O 2 2	0	0

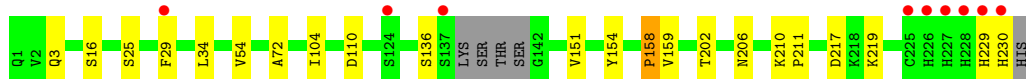
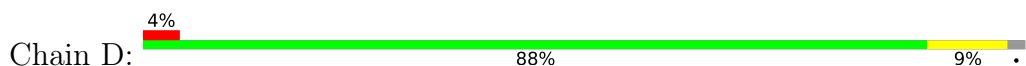
### 3 Residue-property plots [i](#)

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 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.

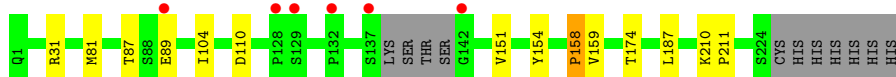
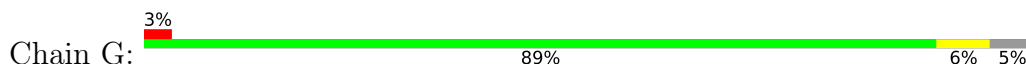
- Molecule 1: IgE 12F3 Fab heavy chain



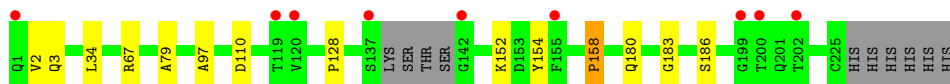
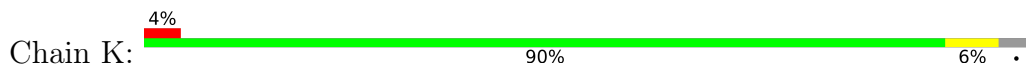
- Molecule 1: IgE 12F3 Fab heavy chain



- Molecule 1: IgE 12F3 Fab heavy chain



- Molecule 1: IgE 12F3 Fab heavy chain



- Molecule 2: IgE 12F3 Fab light chain




- Molecule 2: IgE 12F3 Fab light chain

Chain E:  91% 8%



• Molecule 2: IgE 12F3 Fab light chain

Chain H:  89% 10%




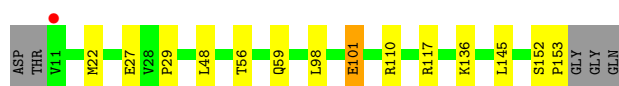
• Molecule 2: IgE 12F3 Fab light chain

Chain J:  93% 7%




• Molecule 3: Major allergen Can f 1

Chain C:  87% 9%




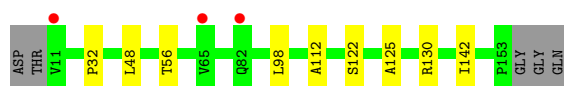
• Molecule 3: Major allergen Can f 1

Chain F:  86% 9%




• Molecule 3: Major allergen Can f 1

Chain L:  91% 6%



• Molecule 3: Major allergen Can f 1

Chain I:  88% 8%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.41Å 191.16Å 88.19Å 90.00° 102.91° 90.00°	Depositor
Resolution (Å)	39.67 – 3.12 39.67 – 3.12	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.67-3.12) 99.9 (39.67-3.12)	Depositor EDS
$R_{merge}$	0.26	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, $R_{free}$	0.203 , 0.245 0.213 , 0.253	Depositor DCC
$R_{free}$ test set	2298 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.8	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 66.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	17514	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.43 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.0083e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

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	0.55	0/1653	0.98	1/2261 (0.0%)
1	D	0.56	0/1699	0.98	1/2322 (0.0%)
1	G	0.56	0/1667	0.99	1/2277 (0.0%)
1	K	0.54	0/1658	0.98	2/2267 (0.1%)
2	B	0.53	0/1644	0.93	0/2242
2	E	0.56	0/1654	0.95	0/2252
2	H	0.53	0/1671	0.94	0/2272
2	J	0.54	0/1662	0.92	0/2261
3	C	0.53	0/1126	0.96	0/1524
3	F	0.53	0/1117	0.97	1/1511 (0.1%)
3	I	0.54	0/1121	0.95	0/1516
3	L	0.51	0/1119	0.93	0/1515
All	All	0.54	0/17791	0.96	6/24220 (0.0%)

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
1	D	0	1
1	K	0	1
2	B	0	2
2	E	0	2
2	H	0	2
2	J	0	1
3	F	0	1
3	I	0	2
All	All	0	13

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	158	PRO	N-CA-CB	-6.85	95.06	102.60
1	K	158	PRO	N-CA-CB	-6.75	95.18	102.60
1	D	158	PRO	N-CA-CB	-6.72	95.21	102.60
1	A	158	PRO	N-CA-CB	-6.39	95.57	102.60
3	F	73	PRO	N-CA-C	5.75	121.11	113.40

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	57	ARG	Sidechain
2	B	18	ARG	Sidechain
2	B	61	ARG	Sidechain
1	D	136	SER	Peptide
2	E	18	ARG	Sidechain

## 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	1616	0	1562	8	0
1	D	1661	0	1601	16	0
1	G	1630	0	1590	10	0
1	K	1621	0	1565	9	0
2	B	1608	0	1537	7	0
2	E	1618	0	1567	11	0
2	H	1635	0	1594	16	0
2	J	1626	0	1581	9	0
3	C	1106	0	1084	9	0
3	F	1097	0	1078	9	0
3	I	1101	0	1082	6	0
3	L	1099	0	1078	6	0
4	A	10	0	0	0	0
4	B	5	0	0	0	0
4	C	7	0	0	0	0
4	D	9	0	0	0	0
4	E	9	0	0	0	0
4	F	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	14	0	0	0	0
4	H	11	0	0	0	0
4	I	2	0	0	0	0
4	J	5	0	0	1	0
4	K	8	0	0	0	0
4	L	10	0	0	0	0
All	All	17514	0	16919	102	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 3.

The worst 5 of 102 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)
2:H:29:VAL:HG11	2:H:90:LEU:HD22	1.49	0.94
3:F:60:CYS:HG	3:F:151:CYS:HG	1.04	0.86
3:F:35:VAL:CG1	3:F:52:ILE:HD11	2.08	0.84
3:I:60:CYS:HG	3:I:151:CYS:HG	0.89	0.84
3:L:130:ARG:HA	3:L:142:ILE:HD11	1.67	0.77

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	216/231 (94%)	209 (97%)	7 (3%)	0	100	100
1	D	222/231 (96%)	215 (97%)	7 (3%)	0	100	100
1	G	216/231 (94%)	209 (97%)	7 (3%)	0	100	100
1	K	217/231 (94%)	212 (98%)	5 (2%)	0	100	100
2	B	211/215 (98%)	203 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	210/215 (98%)	203 (97%)	7 (3%)	0	100	100
2	H	212/215 (99%)	203 (96%)	9 (4%)	0	100	100
2	J	211/215 (98%)	204 (97%)	7 (3%)	0	100	100
3	C	141/148 (95%)	140 (99%)	1 (1%)	0	100	100
3	F	140/148 (95%)	138 (99%)	2 (1%)	0	100	100
3	I	140/148 (95%)	139 (99%)	1 (1%)	0	100	100
3	L	141/148 (95%)	138 (98%)	3 (2%)	0	100	100
All	All	2277/2376 (96%)	2213 (97%)	64 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	180/196 (92%)	179 (99%)	1 (1%)	78	81
1	D	183/196 (93%)	182 (100%)	1 (0%)	81	83
1	G	183/196 (93%)	182 (100%)	1 (0%)	81	83
1	K	180/196 (92%)	179 (99%)	1 (1%)	78	81
2	B	179/186 (96%)	179 (100%)	0	100	100
2	E	182/186 (98%)	182 (100%)	0	100	100
2	H	184/186 (99%)	184 (100%)	0	100	100
2	J	183/186 (98%)	183 (100%)	0	100	100
3	C	119/126 (94%)	118 (99%)	1 (1%)	73	80
3	F	117/126 (93%)	117 (100%)	0	100	100
3	I	118/126 (94%)	118 (100%)	0	100	100
3	L	117/126 (93%)	117 (100%)	0	100	100
All	All	1925/2032 (95%)	1920 (100%)	5 (0%)	86	86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	PRO
3	C	101	GLU
1	D	158	PRO
1	G	158	PRO
1	K	158	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	180	GLN
3	L	140	GLN
2	J	38	GLN
3	I	108	GLN
2	J	148	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 oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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, 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	220/231 (95%)	0.26	4 (1%) 67 46	48, 78, 122, 149	0
1	D	226/231 (97%)	0.37	9 (3%) 42 23	46, 79, 123, 179	0
1	G	220/231 (95%)	0.16	6 (2%) 56 35	51, 77, 110, 177	0
1	K	221/231 (95%)	0.37	9 (4%) 41 23	51, 81, 138, 162	0
2	B	213/215 (99%)	0.32	2 (0%) 81 63	59, 85, 150, 176	0
2	E	212/215 (98%)	-0.10	1 (0%) 87 73	44, 62, 88, 107	0
2	H	214/215 (99%)	0.11	0 100 100	45, 73, 102, 122	0
2	J	213/215 (99%)	0.06	0 100 100	49, 72, 98, 125	0
3	C	143/148 (96%)	0.22	1 (0%) 84 68	53, 92, 167, 209	0
3	F	142/148 (95%)	0.29	1 (0%) 84 68	51, 82, 131, 164	0
3	I	142/148 (95%)	0.40	3 (2%) 63 42	61, 95, 165, 202	0
3	L	143/148 (96%)	0.57	3 (2%) 63 42	58, 102, 179, 214	0
All	All	2309/2376 (97%)	0.24	39 (1%) 69 48	44, 79, 134, 214	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	11	VAL	3.3
1	G	129	SER	3.3
1	D	227	HIS	3.1
1	D	225	CYS	3.1
1	D	124	SER	3.0

### 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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

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

There are no such residues in this entry.