



# wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 12:54 AM GMT

PDB ID : 1U3H  
Title : Crystal structure of mouse TCR 172.10 complexed with MHC class II I-Au molecule at 2.4 Å  
Authors : Maynard, J.; Petersson, K.; Wilson, D.H.; Adams, E.J.; Blondelle, S.E.; Boulanger, M.J.; Wilson, D.B.; Garcia, K.C.  
Deposited on : 2004-07-21  
Resolution : 2.42 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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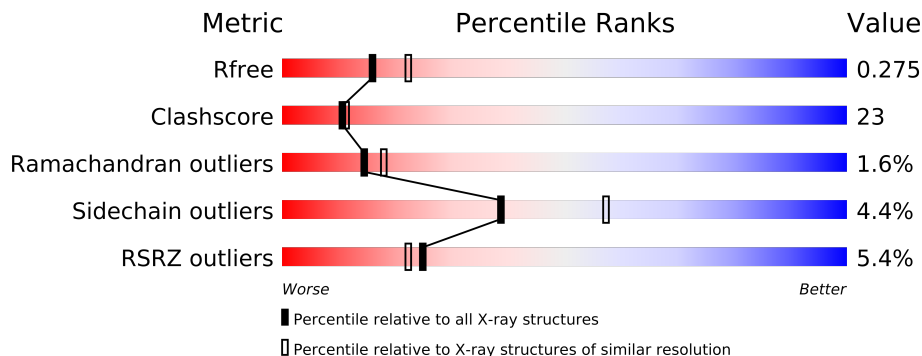
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.42 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))
$R_{free}$	66092	2496 (2.44-2.40)
Clashscore	79885	3124 (2.44-2.40)
Ramachandran outliers	78287	3067 (2.44-2.40)
Sidechain outliers	78261	3068 (2.44-2.40)
RSRZ outliers	66119	2499 (2.44-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	110	
1	E	110	
2	B	111	
2	F	111	
3	C	182	
3	G	182	
4	D	189	
4	H	189	
5	I	12	
5	P	12	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9909 atoms, of which 0 are hydrogen and 0 are deuterium.

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 T-cell receptor alpha-chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	110	Total	C	N	O	S	0	0	0
			869	554	144	169	2			
1	E	110	Total	C	N	O	S	0	0	0
			869	554	144	169	2			

- Molecule 2 is a protein called Mouse TCRVbeta 172.10, extracellular variable domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	111	Total	C	N	O	S	0	0	0
			853	528	148	174	3			
2	F	111	Total	C	N	O	S	0	0	0
			853	528	148	174	3			

- Molecule 3 is a protein called H-2 class II histocompatibility antigen, A-U alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	182	Total	C	N	O	S	0	0	0
			1464	946	233	282	3			
3	G	182	Total	C	N	O	S	0	0	0
			1464	946	233	282	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ILE	-	CLONING ARTIFACT	UNP P14438
C	2	GLU	-	CLONING ARTIFACT	UNP P14438
C	3	ALA	-	CLONING ARTIFACT	UNP P14438
G	1	ILE	-	CLONING ARTIFACT	UNP P14438
G	2	GLU	-	CLONING ARTIFACT	UNP P14438
G	3	ALA	-	CLONING ARTIFACT	UNP P14438

- Molecule 4 is a protein called H-2 class II histocompatibility antigen, A-U beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	189	Total	C	N	O	S	0	0	0
			1586	998	283	299	6			
4	H	189	Total	C	N	O	S	0	0	0
			1586	998	283	299	6			

- Molecule 5 is a protein called Myelin basic protein (MBP)-peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	P	12	Total	C	N	O	0	0	0
			91	52	20	19			
5	I	12	Total	C	N	O	0	0	0
			91	52	20	19			

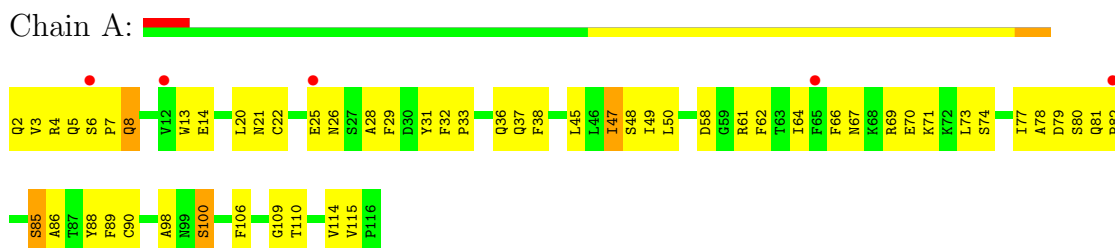
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total	O	0	0
			4	4		
6	B	4	Total	O	0	0
			4	4		
6	C	49	Total	O	0	0
			49	49		
6	D	42	Total	O	0	0
			42	42		
6	E	4	Total	O	0	0
			4	4		
6	F	3	Total	O	0	0
			3	3		
6	G	42	Total	O	0	0
			42	42		
6	H	30	Total	O	0	0
			30	30		
6	I	2	Total	O	0	0
			2	2		
6	P	3	Total	O	0	0
			3	3		

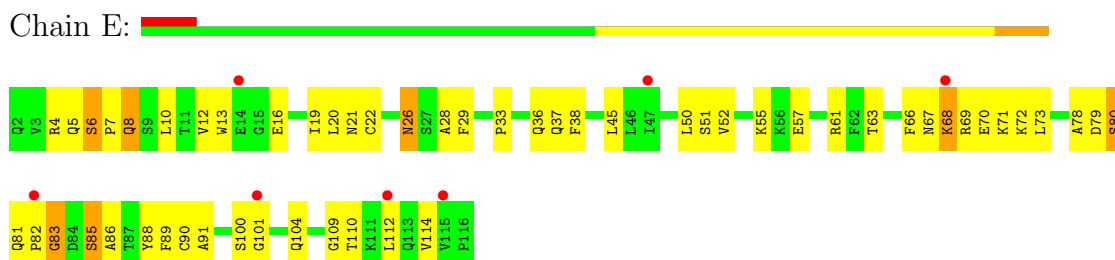
### 3 Residue-property plots

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.

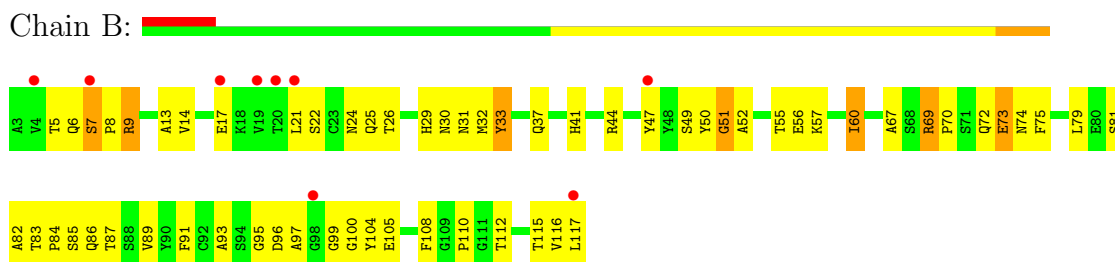
- Molecule 1: T-cell receptor alpha-chain



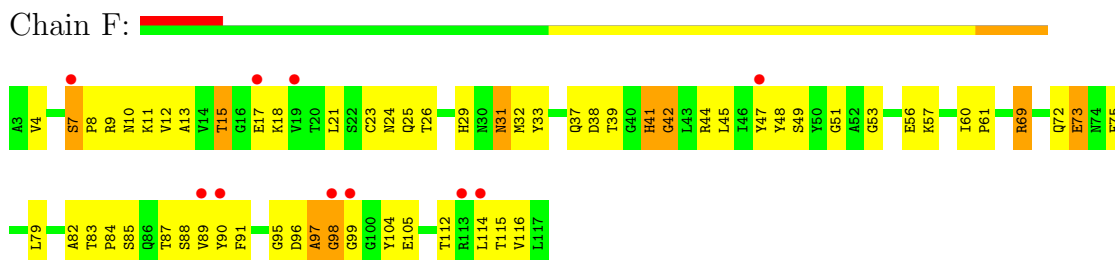
- Molecule 1: T-cell receptor alpha-chain



- Molecule 2: Mouse TCRVbeta 172.10, extracellular variable domain

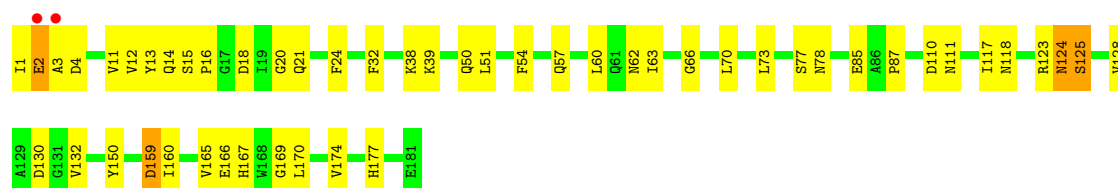


- Molecule 2: Mouse TCRVbeta 172.10, extracellular variable domain



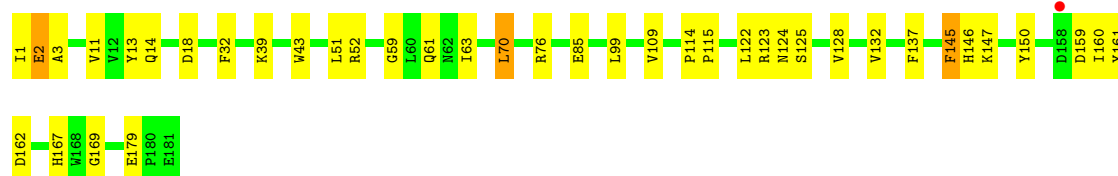
- Molecule 3: H-2 class II histocompatibility antigen, A-U alpha chain

Chain C: 



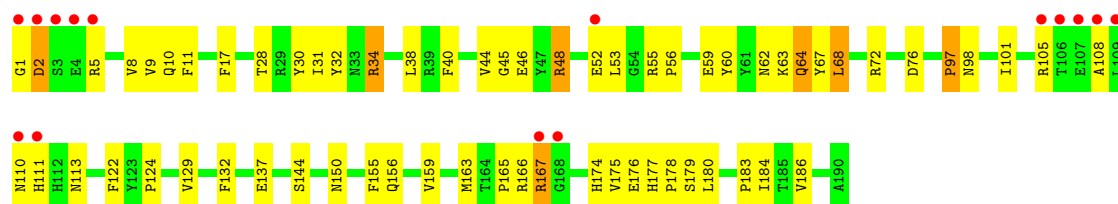
- Molecule 3: H-2 class II histocompatibility antigen, A-U alpha chain

Chain G: 



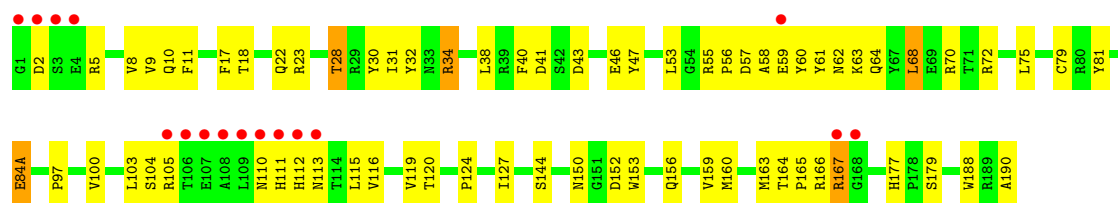
- Molecule 4: H-2 class II histocompatibility antigen, A-U beta chain

Chain D: 



- Molecule 4: H-2 class II histocompatibility antigen, A-U beta chain

Chain H: 



- Molecule 5: Myelin basic protein (MBP)-peptide

Chain P: 



- Molecule 5: Myelin basic protein (MBP)-peptide

Chain I: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.83Å 327.16Å 127.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.51 – 2.42 41.51 – 2.42	Depositor EDS
% Data completeness (in resolution range)	89.1 (41.51-2.42) 89.3 (41.51-2.42)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 2.42Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.232 , 0.274 0.235 , 0.275	Depositor DCC
$R_{free}$ test set	3205 reflections (5.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.1	Xtriage
Anisotropy	0.898	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 35.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 68519 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9909	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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	0.35	0/892	0.65	2/1208 (0.2%)
1	E	0.37	0/892	0.68	3/1208 (0.2%)
2	B	0.39	0/873	0.76	4/1184 (0.3%)
2	F	0.37	0/873	0.67	1/1184 (0.1%)
3	C	0.40	0/1509	0.69	1/2059 (0.0%)
3	G	0.42	0/1509	0.68	1/2059 (0.0%)
4	D	0.41	0/1625	0.70	1/2206 (0.0%)
4	H	0.42	0/1625	0.69	0/2206
5	I	0.41	0/92	0.69	0/120
5	P	0.43	0/92	0.68	0/120
All	All	0.40	0/9982	0.69	13/13554 (0.1%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	100	SER	C-N-CA	-7.21	107.17	122.30
2	F	53	GLY	N-CA-C	-6.52	96.79	113.10
2	B	52	ALA	CA-C-N	-6.26	103.68	116.20
1	E	100	SER	CA-C-N	6.21	128.61	116.20
2	B	52	ALA	C-N-CA	6.13	135.18	122.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the



chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	869	0	828	49	0
1	E	869	0	828	57	0
2	B	853	0	795	54	0
2	F	853	0	795	74	0
3	C	1464	0	1392	56	0
3	G	1464	0	1392	39	0
4	D	1586	0	1521	65	0
4	H	1586	0	1521	66	0
5	I	91	0	86	5	0
5	P	91	0	86	9	0
6	A	4	0	0	0	0
6	B	4	0	0	1	0
6	C	49	0	0	6	0
6	D	42	0	0	2	0
6	E	4	0	0	3	0
6	F	3	0	0	2	0
6	G	42	0	0	1	0
6	H	30	0	0	1	0
6	I	2	0	0	0	0
6	P	3	0	0	0	0
All	All	9909	0	9244	437	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 23.

The worst 5 of 437 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:1:ILE:CG2	6:C:230:HOH:O	1.78	1.26
2:F:60:ILE:HG22	6:F:120:HOH:O	1.41	1.17
3:C:124:ASN:O	3:C:125:SER:HB2	1.30	1.09
1:E:37:GLN:O	1:E:86:ALA:HB1	1.54	1.08
3:C:124:ASN:O	3:C:125:SER:CB	2.01	1.05

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	108/110 (98%)	90 (83%)	17 (16%)	1 (1%)	25	34
1	E	108/110 (98%)	89 (82%)	14 (13%)	5 (5%)	4	2
2	B	109/111 (98%)	94 (86%)	11 (10%)	4 (4%)	5	3
2	F	109/111 (98%)	89 (82%)	15 (14%)	5 (5%)	4	2
3	C	180/182 (99%)	169 (94%)	10 (6%)	1 (1%)	33	46
3	G	180/182 (99%)	174 (97%)	6 (3%)	0	100	100
4	D	187/189 (99%)	171 (91%)	14 (8%)	2 (1%)	21	28
4	H	187/189 (99%)	161 (86%)	25 (13%)	1 (0%)	38	52
5	I	10/12 (83%)	10 (100%)	0	0	100	100
5	P	10/12 (83%)	9 (90%)	1 (10%)	0	100	100
All	All	1188/1208 (98%)	1056 (89%)	113 (10%)	19 (2%)	14	18

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	80	SER
2	F	7	SER
2	F	42	GLY
2	F	97	ALA
1	A	80	SER

### 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	94/94 (100%)	91 (97%)	3 (3%)	51	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	94/94 (100%)	90 (96%)	4 (4%)	40	59
2	B	91/91 (100%)	84 (92%)	7 (8%)	18	28
2	F	91/91 (100%)	84 (92%)	7 (8%)	18	28
3	C	163/163 (100%)	159 (98%)	4 (2%)	60	79
3	G	163/163 (100%)	160 (98%)	3 (2%)	71	87
4	D	175/175 (100%)	166 (95%)	9 (5%)	33	50
4	H	175/175 (100%)	165 (94%)	10 (6%)	29	43
5	I	9/9 (100%)	9 (100%)	0	100	100
5	P	9/9 (100%)	9 (100%)	0	100	100
All	All	1064/1064 (100%)	1017 (96%)	47 (4%)	39	57

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	98	ASN
1	E	85	SER
4	H	97	PRO
1	E	8	GLN
2	F	9	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	5	GLN
1	E	76	HIS
4	H	174	HIS
1	E	26	ASN
1	E	81	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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 ⓘ

### 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, 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	110/110 (100%)	0.50	5 (4%) 32 29	47, 78, 102, 112	0
1	E	110/110 (100%)	0.56	7 (6%) 19 17	51, 80, 100, 110	0
2	B	111/111 (100%)	0.46	9 (8%) 12 10	48, 74, 92, 101	0
2	F	111/111 (100%)	0.60	10 (9%) 10 8	52, 78, 97, 104	0
3	C	182/182 (100%)	0.04	2 (1%) 77 77	27, 46, 79, 107	0
3	G	182/182 (100%)	-0.08	1 (0%) 88 88	28, 45, 74, 102	0
4	D	189/189 (100%)	0.50	15 (7%) 13 11	25, 49, 119, 154	0
4	H	189/189 (100%)	0.57	16 (8%) 11 9	24, 50, 120, 155	0
5	I	12/12 (100%)	0.61	0 100 100	45, 52, 83, 96	0
5	P	12/12 (100%)	0.30	0 100 100	38, 48, 71, 84	0
All	All	1208/1208 (100%)	0.37	65 (5%) 25 22	24, 60, 99, 155	0

The worst 5 of 65 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	106	THR	15.4
4	D	108	ALA	13.9
4	H	109	LEU	12.2
4	H	111	HIS	12.1
4	H	110	ASN	11.7

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.