



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 03:09 AM GMT

PDB ID : 3QRF
Title : Structure of a domain-swapped FOXP3 dimer
Authors : Bandukwala, H.S.; Wu, Y; Feurer, M; Chen, Y; Barbosa, B; Ghosh, S; Stroud, J.C.; Benoist, C.; Mathis, D.; Rao, A.; Chen, L.
Deposited on : 2011-02-17
Resolution : 2.80 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

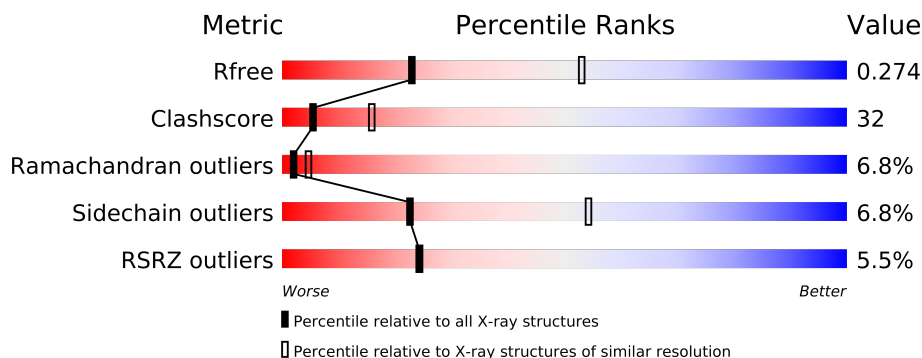
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.80 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	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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. 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	M	286	
1	N	286	
2	F	82	
2	G	82	
2	H	82	
2	I	82	
3	A	21	
3	C	21	
4	B	21	
4	D	21	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9105 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 Nuclear factor of activated T-cells, cytoplasmic 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	N	286	Total	C	N	O	S	0	0	0
			2264	1421	413	421	9			
1	M	286	Total	C	N	O	S	0	0	0
			2264	1421	413	421	9			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	393	SER	-	EXPRESSION TAG	UNP Q13469
N	394	SER	-	EXPRESSION TAG	UNP Q13469
N	395	VAL	-	EXPRESSION TAG	UNP Q13469
N	629	ALA	ASP	CONFLICT	UNP Q13469
N	630	ALA	LYS	CONFLICT	UNP Q13469
N	631	ALA	ASP	CONFLICT	UNP Q13469
N	632	ALA	LYS	CONFLICT	UNP Q13469
N	633	ALA	SER	CONFLICT	UNP Q13469
N	634	ALA	GLN	CONFLICT	UNP Q13469
M	393	SER	-	EXPRESSION TAG	UNP Q13469
M	394	SER	-	EXPRESSION TAG	UNP Q13469
M	395	VAL	-	EXPRESSION TAG	UNP Q13469
M	629	ALA	ASP	CONFLICT	UNP Q13469
M	630	ALA	LYS	CONFLICT	UNP Q13469
M	631	ALA	ASP	CONFLICT	UNP Q13469
M	632	ALA	LYS	CONFLICT	UNP Q13469
M	633	ALA	SER	CONFLICT	UNP Q13469
M	634	ALA	GLN	CONFLICT	UNP Q13469

- Molecule 2 is a protein called Forkhead box protein P3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	82	Total	C	N	O	S	0	0	0
			714	465	132	114	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	82	Total	C	N	O	S	0	0	0
			714	465	132	114	3			
2	H	82	Total	C	N	O	S	0	0	0
			714	465	132	114	3			
2	I	82	Total	C	N	O	S	0	0	0
			714	465	132	114	3			

- Molecule 3 is a DNA chain called human hARRE2 DNA (Plus Strand).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	21	Total	C	N	O	P	0	0	0
			431	209	76	126	20			
3	A	21	Total	C	N	O	P	0	0	0
			431	209	76	126	20			

- Molecule 4 is a DNA chain called human hARRE2 DNA (Minus Strand).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	21	Total	C	N	O	P	0	0	0
			424	206	76	122	20			
4	B	21	Total	C	N	O	P	0	0	0
			424	206	76	122	20			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Mg	0	0
			1	1		
5	G	1	Total	Mg	0	0
			1	1		
5	I	1	Total	Mg	0	0
			1	1		
5	F	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	N	1	Total	O	0	0
			1	1		
6	C	2	Total	O	0	0
			2	2		

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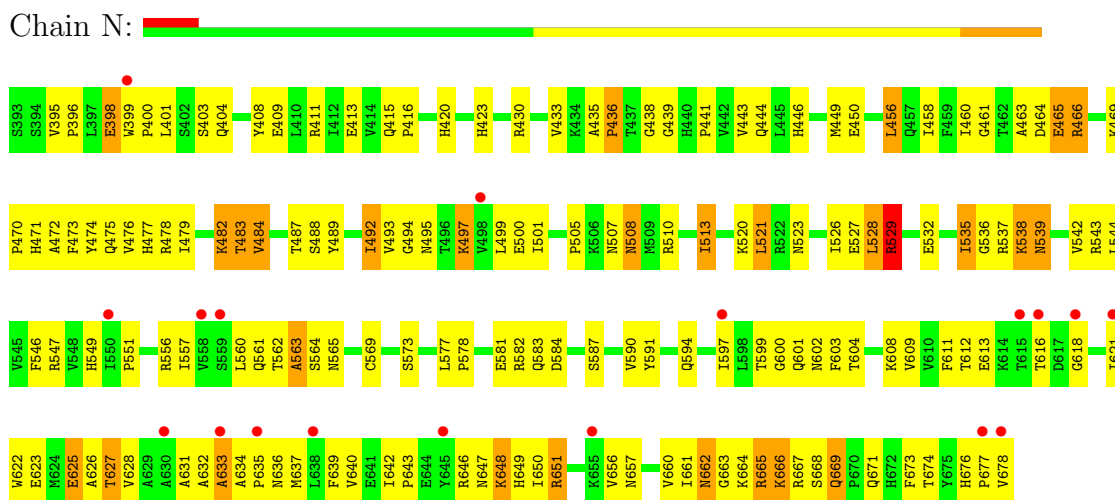
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	3	Total 3	O 3	0	0
6	B	1	Total 1	O 1	0	0

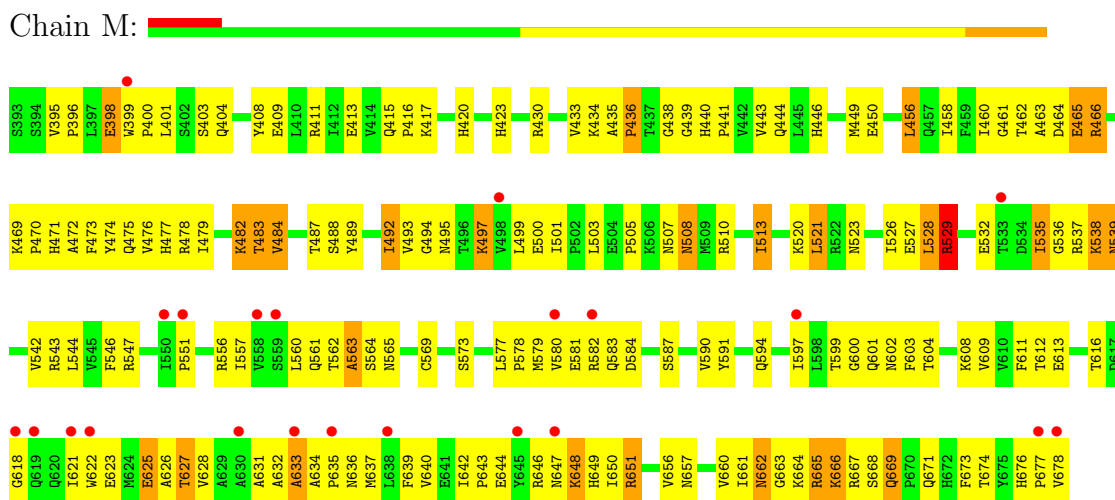
3 Residue-property plots

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

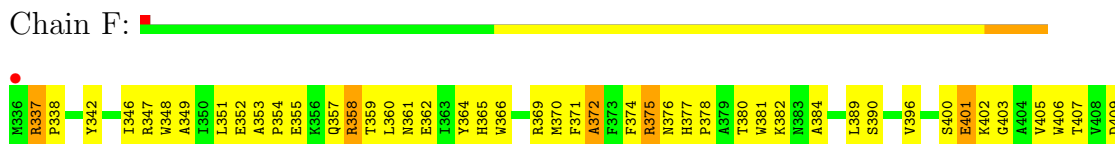
- Molecule 1: Nuclear factor of activated T-cells, cytoplasmic 2



- Molecule 1: Nuclear factor of activated T-cells, cytoplasmic 2



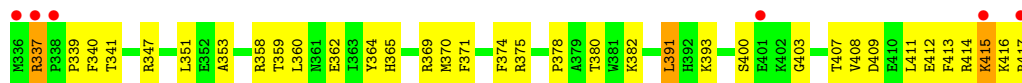
- Molecule 2: Forkhead box protein P3





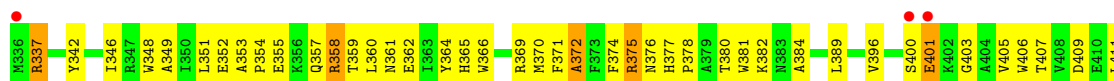
- Molecule 2: Forkhead box protein P3

Chain G:



- Molecule 2: Forkhead box protein P3

Chain H:



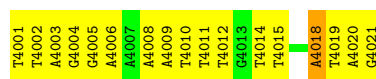
- Molecule 2: Forkhead box protein P3

Chain I:



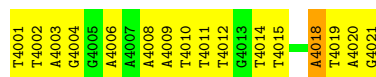
- Molecule 3: human hARRE2 DNA (Plus Strand)

Chain C:



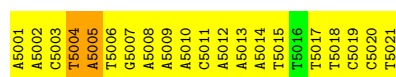
- Molecule 3: human hARRE2 DNA (Plus Strand)

Chain A:



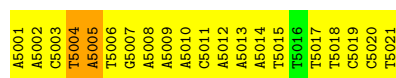
- Molecule 4: human hARRE2 DNA (Minus Strand)

Chain D:



- Molecule 4: human hARRE2 DNA (Minus Strand)

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.67Å 131.23Å 68.67Å 90.00° 89.95° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 19.93 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.80) 96.3 (19.93-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.79Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.248 , 0.283 0.245 , 0.274	Depositor DCC
R_{free} test set	3413 reflections (10.76%)	DCC
Wilson B-factor (Å ²)	63.7	Xtriage
Anisotropy	0.645	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 21.7	EDS
Estimated twinning fraction	0.480 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	2 of 36343 reflections (0.006%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9105	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	M	0.38	0/2314	0.65	0/3134
1	N	0.39	0/2314	0.65	0/3134
2	F	0.49	0/738	0.63	0/996
2	G	0.48	0/738	0.62	0/996
2	H	0.50	0/738	0.63	0/996
2	I	0.47	0/738	0.62	0/996
3	A	0.58	0/483	0.89	1/745 (0.1%)
3	C	0.53	0/483	0.88	1/745 (0.1%)
4	B	0.57	0/475	0.82	0/730
4	D	0.55	0/475	0.81	0/730
All	All	0.46	0/9496	0.69	2/13202 (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
3	A	0	1
3	C	0	1
4	B	0	2
4	D	0	2
All	All	0	6

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	4006	DA	N9-C1'-C2'	5.36	122.78	112.60
3	C	4006	DA	N9-C1'-C2'	5.25	122.56	112.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	4018	DA	Sidechain
4	B	5004	DT	Sidechain
3	C	4018	DA	Sidechain
4	D	5004	DT	Sidechain
4	D	5005	DA	Sidechain

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	M	2264	0	2271	168	0
1	N	2264	0	2271	161	0
2	F	714	0	708	51	0
2	G	714	0	708	38	0
2	H	714	0	708	48	0
2	I	714	0	708	38	0
3	A	431	0	242	24	0
3	C	431	0	242	25	0
4	B	424	0	240	24	0
4	D	424	0	240	25	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
5	I	1	0	0	0	0
6	B	1	0	0	0	0
6	C	2	0	0	0	0
6	D	3	0	0	0	0
6	N	1	0	0	0	0
All	All	9105	0	8338	563	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 32.

The worst 5 of 563 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:N:669:GLN:HE21	1:N:671:GLN:HE22	1.07	0.98
1:M:634:ALA:HB3	1:M:637:MET:HB2	1.44	0.98
3:A:4002:DT:H2"	3:A:4003:DA:H5"	1.44	0.98
1:N:475:GLN:HE22	1:N:497:LYS:H	1.04	0.98
3:C:4002:DT:H2"	3:C:4003:DA:H5"	1.45	0.97

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	M	284/286 (99%)	216 (76%)	42 (15%)	26 (9%)	1	2
1	N	284/286 (99%)	217 (76%)	41 (14%)	26 (9%)	1	2
2	F	80/82 (98%)	66 (82%)	10 (12%)	4 (5%)	3	10
2	G	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
2	H	80/82 (98%)	66 (82%)	10 (12%)	4 (5%)	3	10
2	I	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
All	All	888/900 (99%)	703 (79%)	125 (14%)	60 (7%)	2	5

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	465	GLU
1	N	563	ALA
1	N	583	GLN
1	N	604	THR
1	N	627	THR

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	M	250/250 (100%)	230 (92%)	20 (8%)	17	44
1	N	250/250 (100%)	230 (92%)	20 (8%)	17	44
2	F	74/74 (100%)	72 (97%)	2 (3%)	57	89
2	G	74/74 (100%)	69 (93%)	5 (7%)	22	54
2	H	74/74 (100%)	72 (97%)	2 (3%)	57	89
2	I	74/74 (100%)	69 (93%)	5 (7%)	22	54
All	All	796/796 (100%)	742 (93%)	54 (7%)	22	54

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	380	THR
1	M	436	PRO
2	I	337	ARG
2	G	391	LEU
1	M	395	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	365	HIS
1	M	457	GLN
2	I	357	GLN
2	G	377	HIS
1	M	423	HIS

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 ⓘ

Of 4 ligands modelled in this entry, 4 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.

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	M	286/286 (100%)	0.29	22 (7%) 13 12	36, 78, 110, 117	0
1	N	286/286 (100%)	0.28	18 (6%) 19 18	36, 78, 110, 117	0
2	F	82/82 (100%)	0.07	1 (1%) 75 76	31, 50, 82, 98	0
2	G	82/82 (100%)	0.19	6 (7%) 15 13	28, 52, 95, 100	0
2	H	82/82 (100%)	0.14	3 (3%) 39 39	31, 50, 81, 98	0
2	I	82/82 (100%)	0.19	4 (4%) 28 29	29, 52, 95, 100	0
3	A	21/21 (100%)	-0.53	0 100 100	32, 42, 65, 71	0
3	C	21/21 (100%)	-0.46	0 100 100	31, 42, 65, 71	0
4	B	21/21 (100%)	-0.32	0 100 100	32, 43, 68, 81	0
4	D	21/21 (100%)	-0.36	0 100 100	32, 43, 68, 81	0
All	All	984/984 (100%)	0.18	54 (5%) 24 24	28, 66, 105, 117	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	336	MET	5.5
1	N	618	GLY	4.8
2	H	336	MET	4.6
2	I	336	MET	4.2
1	M	399	TRP	3.9

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

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	MG	I	1	1/1	0.22	0.26	61,61,61,61	0
5	MG	G	1	1/1	0.19	-0.73	62,62,62,62	0
5	MG	F	1	1/1	0.08	-1.75	43,43,43,43	0
5	MG	H	1	1/1	0.09	-1.95	43,43,43,43	0

6.5 Other polymers

There are no such residues in this entry.