wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 04:47 PM GMT

PDB ID	:	4G59
Title	:	Crystal structure of the murine cytomegalovirus MHC-I homolog m152 with ligand RAE-1 gamma
Authors	:	Wang, R.; Natarajan, K.; Margulies, D.H.
Deposited on	:	2012-07-17
Resolution	:	2.44 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

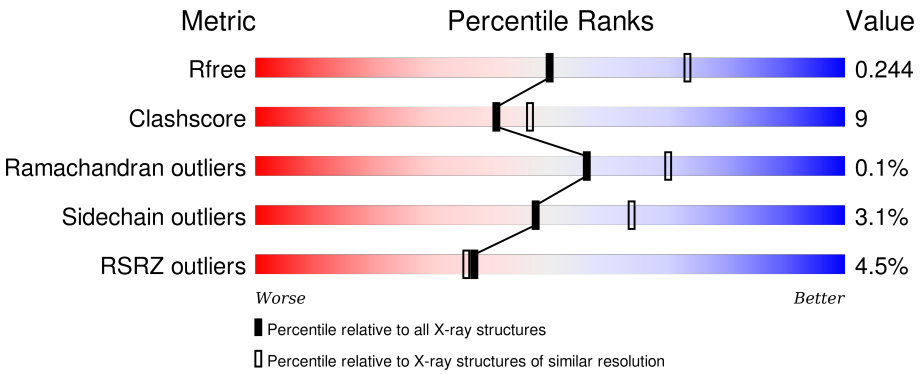
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 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	1003 (2.46-2.42)
Clashscore	102246	1071 (2.46-2.42)
Ramachandran outliers	100387	1065 (2.46-2.42)
Sidechain outliers	100360	1065 (2.46-2.42)
RSRZ outliers	91569	1005 (2.46-2.42)

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 <=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	205	5% 60% 17% • 21%
1	B	205	7% 59% 19% • 20%
2	C	321	2% 70% 12% 18%
2	D	321	2% 71% 11% 18%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7046 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 Retinoic acid early-inducible protein 1-gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	162	1312	828	222	254	8	0	0	0
1	B	163	1319	832	223	256	8	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	INITIATING METHIONINE	UNP O08604
B	-2	MET	-	INITIATING METHIONINE	UNP O08604

- Molecule 2 is a protein called M152 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	264	2142	1360	360	407	15	0	0	0
2	D	264	2142	1360	360	407	15	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	308	LEU	-	EXPRESSION TAG	UNP Q83156
C	309	VAL	-	EXPRESSION TAG	UNP Q83156
C	310	PRO	-	EXPRESSION TAG	UNP Q83156
C	311	ARG	-	EXPRESSION TAG	UNP Q83156
C	312	GLY	-	EXPRESSION TAG	UNP Q83156
C	313	SER	-	EXPRESSION TAG	UNP Q83156
C	314	HIS	-	EXPRESSION TAG	UNP Q83156
C	315	HIS	-	EXPRESSION TAG	UNP Q83156
C	316	HIS	-	EXPRESSION TAG	UNP Q83156
C	317	HIS	-	EXPRESSION TAG	UNP Q83156

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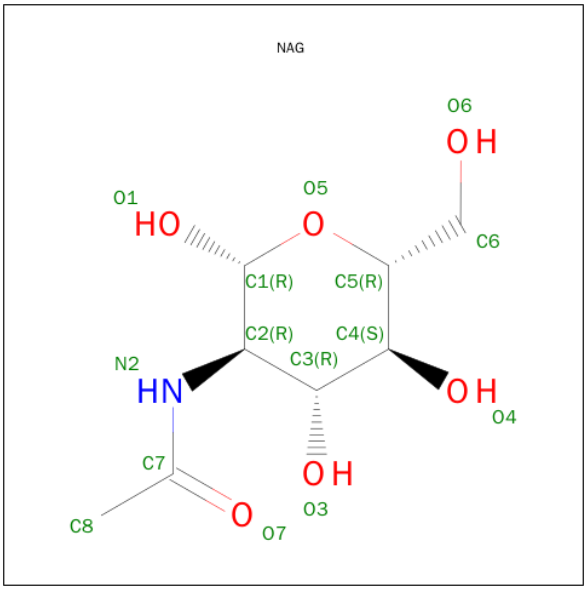
Chain	Residue	Modelled	Actual	Comment	Reference
C	318	HIS	-	EXPRESSION TAG	UNP Q83156
C	319	HIS	-	EXPRESSION TAG	UNP Q83156
D	308	LEU	-	EXPRESSION TAG	UNP Q83156
D	309	VAL	-	EXPRESSION TAG	UNP Q83156
D	310	PRO	-	EXPRESSION TAG	UNP Q83156
D	311	ARG	-	EXPRESSION TAG	UNP Q83156
D	312	GLY	-	EXPRESSION TAG	UNP Q83156
D	313	SER	-	EXPRESSION TAG	UNP Q83156
D	314	HIS	-	EXPRESSION TAG	UNP Q83156
D	315	HIS	-	EXPRESSION TAG	UNP Q83156
D	316	HIS	-	EXPRESSION TAG	UNP Q83156
D	317	HIS	-	EXPRESSION TAG	UNP Q83156
D	318	HIS	-	EXPRESSION TAG	UNP Q83156
D	319	HIS	-	EXPRESSION TAG	UNP Q83156

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	C	1	14	8	1	5	0	0
			Total	C	N	O		
3	C	1	14	8	1	5	0	0
			Total	C	N	O		
3	D	1	14	8	1	5	0	0
			Total	C	N	O		
3	D	1	14	8	1	5	0	0

- Molecule 4 is water.

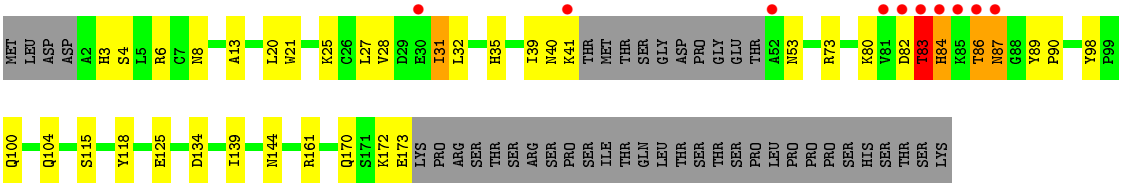
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	13	13	13	0	0
			Total	O		
4	C	26	26	26	0	0
			Total	O		
4	B	8	8	8	0	0
			Total	O		
4	D	28	28	28	0	0

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.

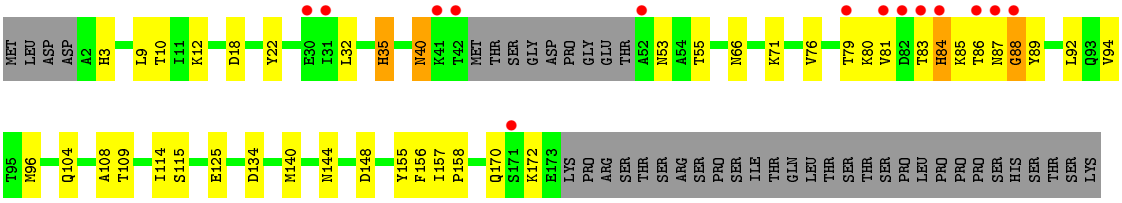
- Molecule 1: Retinoic acid early-inducible protein 1-gamma

Chain A:



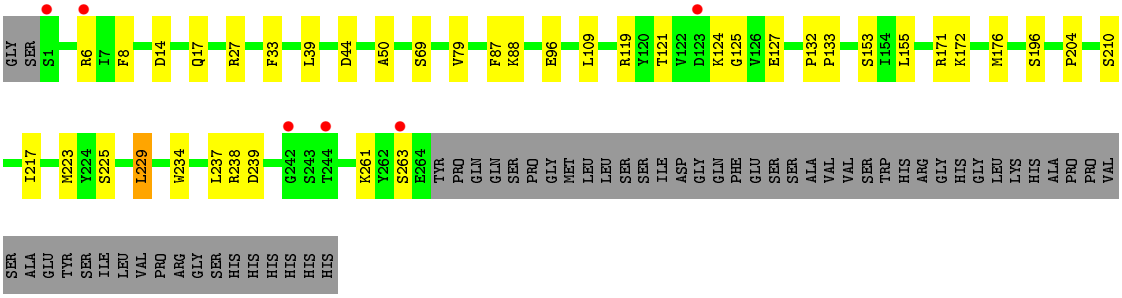
- Molecule 1: Retinoic acid early-inducible protein 1-gamma

Chain B:



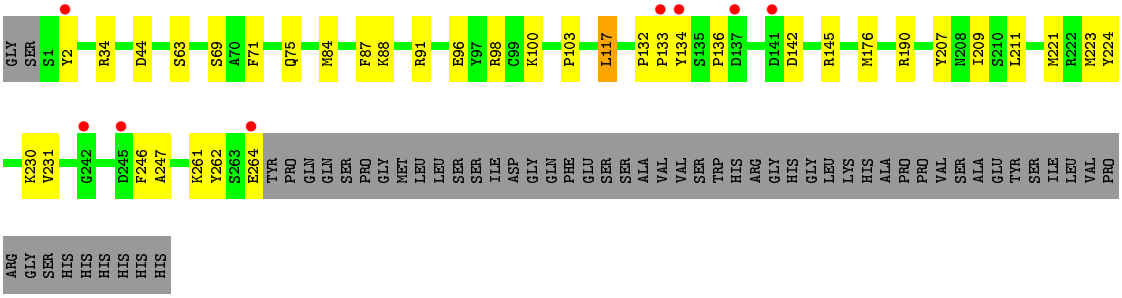
- Molecule 2: M152 protein

Chain C:



- Molecule 2: M152 protein

Chain D:


GLY
SER
S1
Y2
R34
D44
S63
S69
A70
F71
Q75
N84
F87
K88
R91
E96
Y97
R98
C99
K100
P103
I117
P132
P133
Y134
S135
P136
D137
D141
D142
R145
M176
R190
Y207
M208
I209
S210
L211
M221
K222
M223
Y224
K230
V231
G242
D245
F246
A247
K261
Y262
S263
E264
TYR PRO GLN GLN SER PRO GLY MET LEU LEU SER SER ILE ASP GLY GLN PHE GLU SER SER ALA VAL VAL SER TRP HIS ARG GLY HIS GLY LEU LYS HIS ALA PRO PRO VAL SER ALA GLU TYR SER ILE LEU VAL PRO
ARG
GLY
SER
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	193.44Å 99.80Å 68.61Å 90.00° 100.72° 90.00°	Depositor
Resolution (Å)	47.52 – 2.44 47.52 – 2.44	Depositor EDS
% Data completeness (in resolution range)	94.2 (47.52-2.44) 94.2 (47.52-2.44)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.00 (at 2.42Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.201 , 0.245 0.202 , 0.244	Depositor DCC
R_{free} test set	2245 reflections (4.96%)	DCC
Wilson B-factor (Å^2)	44.6	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 36.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 46945 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7046	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.45	0/1342	0.61	0/1821
1	B	0.41	0/1349	0.61	1/1831 (0.1%)
2	C	0.48	0/2194	0.65	2/2969 (0.1%)
2	D	0.54	2/2194 (0.1%)	0.62	0/2969
All	All	0.48	2/7079 (0.0%)	0.63	3/9590 (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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	207	TYR	CD2-CE2	-7.39	1.28	1.39
2	D	207	TYR	CD1-CE1	-6.61	1.29	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	88	GLY	N-CA-C	-8.74	91.26	113.10
2	C	239	ASP	N-CA-C	-6.09	94.55	111.00
2	C	229	LEU	CA-CB-CG	5.04	126.89	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	83	THR	Peptide

5.2 Too-close contacts (i)

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	1312	0	1266	33	0
1	B	1319	0	1273	31	0
2	C	2142	0	2050	26	0
2	D	2142	0	2050	26	0
3	C	28	0	26	3	0
3	D	28	0	26	2	0
4	A	13	0	0	0	0
4	B	8	0	0	0	0
4	C	26	0	0	1	0
4	D	28	0	0	1	0
All	All	7046	0	6691	118	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 9.

The worst 5 of 118 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:B:83:THR:OG1	1:B:86:THR:HG22	1.42	1.14
1:B:83:THR:CB	1:B:86:THR:HG22	1.85	1.07
2:C:237:LEU:O	2:C:238:ARG:HG2	1.63	0.99
1:A:20:LEU:HB2	1:A:39:ILE:HD11	1.47	0.93
1:A:40:ASN:O	1:A:41:LYS:HB2	1.66	0.93

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	158/205 (77%)	154 (98%)	3 (2%)	1 (1%)	30	36
1	B	159/205 (78%)	155 (98%)	4 (2%)	0	100	100
2	C	262/321 (82%)	253 (97%)	9 (3%)	0	100	100
2	D	262/321 (82%)	248 (95%)	14 (5%)	0	100	100
All	All	841/1052 (80%)	810 (96%)	30 (4%)	1 (0%)	56	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	ASN

5.3.2 Protein sidechains (i)

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	149/190 (78%)	142 (95%)	7 (5%)	32	45
1	B	150/190 (79%)	142 (95%)	8 (5%)	28	40
2	C	234/282 (83%)	229 (98%)	5 (2%)	61	76
2	D	234/282 (83%)	230 (98%)	4 (2%)	68	80
All	All	767/944 (81%)	743 (97%)	24 (3%)	47	64

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	155	LEU
1	B	40	ASN
2	D	117	LEU
2	C	225	SER
1	B	35	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	GLN
1	B	144	ASN
1	B	53	ASN
1	A	144	ASN
1	B	3	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	C	401	2	14,14,15	0.50	0	15,19,21	0.85	1 (6%)
3	NAG	C	402	2	14,14,15	0.50	0	15,19,21	0.89	1 (6%)
3	NAG	D	401	2	14,14,15	0.49	0	15,19,21	0.88	1 (6%)
3	NAG	D	402	2	14,14,15	0.64	0	15,19,21	1.24	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	401	2	-	0/6/23/26	0/1/1/1
3	NAG	C	402	2	-	0/6/23/26	0/1/1/1
3	NAG	D	401	2	-	0/6/23/26	0/1/1/1
3	NAG	D	402	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	402	NAG	C1-O5-C5	-3.89	107.31	112.25
3	C	402	NAG	C4-C3-C2	-2.31	107.64	111.23
3	D	401	NAG	C4-C3-C2	-2.26	107.72	111.23
3	C	401	NAG	C4-C3-C2	-2.21	107.80	111.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	NAG	3	0
3	D	402	NAG	2	0

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, 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	162/205 (79%)	-0.09	10 (6%)	24	22	30, 46, 100, 123	0
1	B	163/205 (79%)	0.28	14 (8%)	13	11	33, 53, 111, 124	0
2	C	264/321 (82%)	-0.20	6 (2%)	64	63	27, 44, 75, 114	0
2	D	264/321 (82%)	-0.09	8 (3%)	54	52	29, 48, 84, 119	0
All	All	853/1052 (81%)	-0.06	38 (4%)	37	36	27, 47, 90, 124	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	83	THR	6.2
1	B	88	GLY	5.6
1	A	81	VAL	5.3
2	D	134	TYR	5.0
1	B	42	THR	4.8

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
3	NAG	C	401	14/15	0.80	0.34	-	81,85,89,90	0
3	NAG	D	401	14/15	0.80	0.33	-	75,82,86,86	0
3	NAG	D	402	14/15	0.67	0.39	-	84,90,94,95	0
3	NAG	C	402	14/15	0.66	0.37	-	71,79,87,91	0

6.5 Other polymers (i)

There are no such residues in this entry.