



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:52 am BST

PDB ID : 6EWA
Title : Crystal structure of HLA-A2 in complex with LILRB1
Authors : Stones, D.H.; Willcox, B.E.; Mohammed, F.
Deposited on : 2017-11-03
Resolution : 2.39 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

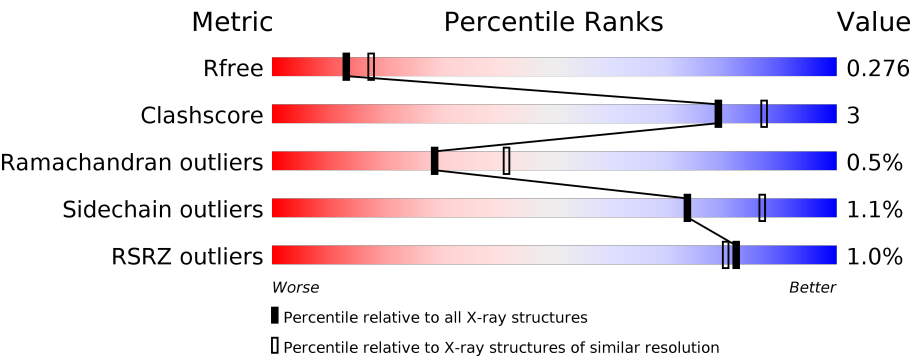
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 ≥ 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	276	<div><div>%</div><div><div></div><div>93%</div><div>7%</div></div><div>%</div></div>
1	E	276	<div><div>%</div><div><div></div><div>91%</div><div>8%</div><div></div></div><div>%</div></div>
2	B	99	<div><div>%</div><div><div></div><div>95%</div><div>5%</div></div><div>%</div></div>
2	F	99	<div><div>%</div><div><div></div><div>93%</div><div>6%</div><div></div></div><div>%</div></div>
3	C	9	<div><div></div><div>100%</div><div></div></div>
3	G	9	<div><div></div><div>89%</div><div>11%</div></div>

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Mol	Chain	Length	Quality of chain
4	D	195	<div><div></div><div>2%</div><div>78%</div><div>8%</div><div>•</div><div>13%</div></div>
4	H	195	<div><div></div><div>93%</div><div>•</div><div>•</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9148 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 HLA class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	67	0	0
			2254	1408	410	427	9			
1	E	274	Total	C	N	O	S	70	0	0
			2237	1398	408	422	9			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	29	0	0
			829	528	140	158	3			
2	F	99	Total	C	N	O	S	15	0	0
			829	528	140	158	3			

- Molecule 3 is a protein called Polypeptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	4	0	0
			70	46	12	12			
3	G	9	Total	C	N	O	3	0	0
			70	46	12	12			

- Molecule 4 is a protein called LIR-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	169	Total	C	N	O	S	40	0	0
			1337	857	228	246	6			
4	H	188	Total	C	N	O	S	44	0	0
			1477	938	255	278	6			

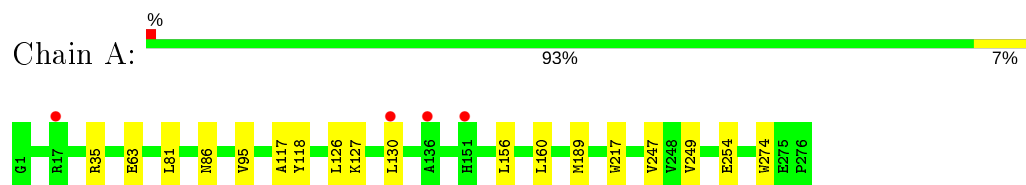
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	6	Total O 6 6	0	0
5	B	4	Total O 4 4	0	0
5	D	8	Total O 8 8	0	0
5	E	12	Total O 12 12	0	0
5	F	7	Total O 7 7	0	0
5	G	1	Total O 1 1	0	0
5	H	7	Total O 7 7	0	0

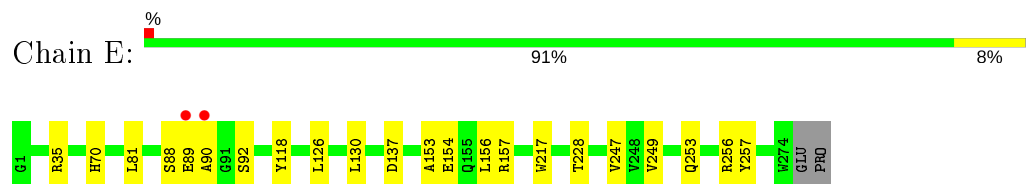
3 Residue-property plots [i](#)

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

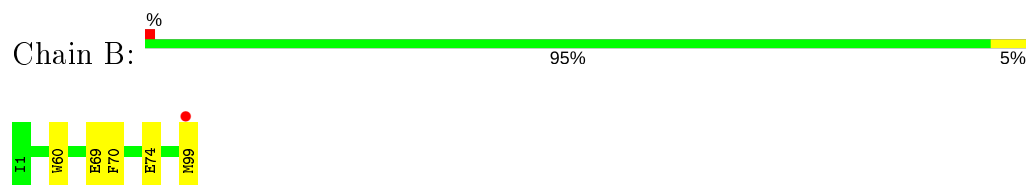
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



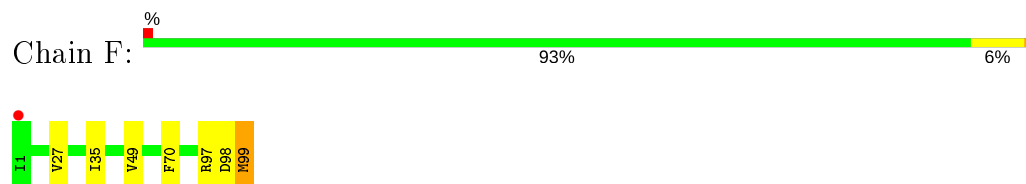
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: Polyprotein



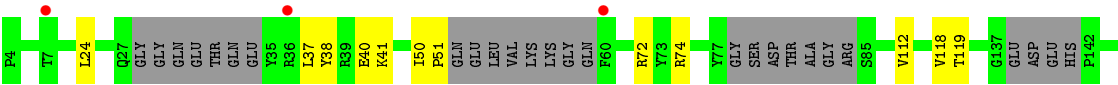
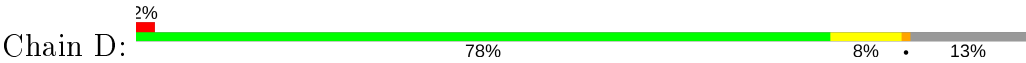
There are no outlier residues recorded for this chain.

- Molecule 3: Polyprotein

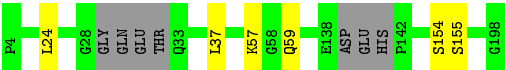




• Molecule 4: LIR-1



• Molecule 4: LIR-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.15Å 116.15Å 192.82Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.59 – 2.39 44.59 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.59-2.39) 99.7 (44.59-2.39)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.39Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.228 , 0.279 0.232 , 0.276	Depositor DCC
R_{free} test set	3020 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 26.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.037 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9148	wwPDB-VP
Average B, all atoms (Å ²)	37.0	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 24.37 % 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 3.8882e-03.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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	0/2320	0.68	0/3149
1	E	0.44	0/2302	0.66	0/3125
2	B	0.45	0/852	0.65	0/1152
2	F	0.48	0/852	0.66	0/1152
3	C	0.39	0/71	0.55	0/94
3	G	0.41	0/71	0.73	0/94
4	D	0.46	0/1378	0.61	0/1878
4	H	0.46	0/1520	0.68	0/2069
All	All	0.45	0/9366	0.66	0/12713

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	E	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	88	SER	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	2254	0	2103	13	0
1	E	2237	0	2090	18	0
2	B	829	0	794	1	0
2	F	829	0	794	3	0
3	C	70	0	78	0	0
3	G	70	0	78	1	0
4	D	1337	0	1296	10	0
4	H	1477	0	1432	3	0
5	A	6	0	0	0	0
5	B	4	0	0	0	0
5	D	8	0	0	0	0
5	E	12	0	0	0	0
5	F	7	0	0	0	0
5	G	1	0	0	0	0
5	H	7	0	0	0	0
All	All	9148	0	8665	47	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.

All (47) 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:E:81:LEU:HD13	1:E:118:TYR:CD1	1.96	0.99
1:A:81:LEU:HD13	1:A:118:TYR:CD1	1.97	0.99
1:A:81:LEU:HD13	1:A:118:TYR:CG	2.15	0.80
1:A:81:LEU:CD1	1:A:118:TYR:CD1	2.73	0.69
1:E:126:LEU:HD22	1:E:156:LEU:HD23	1.75	0.69
4:D:40:GLU:O	4:D:41:LYS:HB2	1.95	0.66
4:D:119:THR:HG23	4:D:158:ILE:HG23	1.78	0.65
4:H:57:LYS:O	4:H:59:GLN:HG3	1.97	0.64
1:E:217:TRP:CD1	1:E:247:VAL:HG13	2.34	0.62
1:E:126:LEU:HD22	1:E:156:LEU:CD2	2.30	0.61
4:D:119:THR:CG2	4:D:158:ILE:HG23	2.30	0.61
1:E:130:LEU:HD23	1:E:157:ARG:HB2	1.82	0.61
4:D:50:ILE:CG2	4:D:51:PRO:HD2	2.31	0.60
1:A:81:LEU:CD1	1:A:95:VAL:HG12	2.31	0.60
1:E:81:LEU:CD1	1:E:118:TYR:CD1	2.79	0.59
4:D:50:ILE:HG23	4:D:51:PRO:HD2	1.84	0.58
1:A:81:LEU:HD12	1:A:95:VAL:HG12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:LEU:HD12	1:A:95:VAL:CG1	2.36	0.56
1:A:189:MET:HE3	1:A:217:TRP:CH2	2.42	0.55
1:E:81:LEU:HD13	1:E:118:TYR:CG	2.42	0.54
1:E:228:THR:HG22	1:E:247:VAL:HG12	1.90	0.54
1:A:130:LEU:HD22	1:A:160:LEU:HD12	1.92	0.49
4:H:154:SER:O	4:H:155:SER:HB2	2.14	0.48
1:A:247:VAL:HG23	1:A:249:VAL:HG23	1.97	0.46
1:E:89:GLU:HG2	1:E:89:GLU:O	2.16	0.46
4:D:38:TYR:CE2	4:D:74:ARG:HB2	2.52	0.45
4:D:171:TRP:HB3	4:D:191:LEU:HD11	1.99	0.45
1:A:254:GLU:HB3	1:A:274:TRP:CD1	2.52	0.45
1:E:153:ALA:O	1:E:154:GLU:CB	2.65	0.44
1:E:217:TRP:CG	1:E:247:VAL:HG13	2.52	0.44
1:E:247:VAL:HG23	1:E:249:VAL:HG23	1.98	0.44
1:E:130:LEU:HD23	1:E:157:ARG:HA	2.01	0.43
4:H:24:LEU:HD12	4:H:37:LEU:HD21	1.99	0.43
4:D:112:VAL:HG11	4:D:118:VAL:HB	2.01	0.43
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.54	0.42
1:A:130:LEU:HD22	1:A:160:LEU:CD1	2.49	0.42
2:F:27:VAL:HG11	2:F:35:ILE:CD1	2.49	0.42
1:E:153:ALA:O	1:E:154:GLU:HB2	2.20	0.42
2:F:98:ASP:O	2:F:99:MET:HB2	2.20	0.42
4:D:24:LEU:HD12	4:D:37:LEU:HD21	2.01	0.41
4:D:151:ALA:O	4:D:152:ARG:C	2.59	0.41
2:F:97:ARG:NH1	2:F:97:ARG:HB3	2.35	0.41
1:E:217:TRP:CG	1:E:247:VAL:CG1	3.03	0.41
1:E:70:HIS:HA	3:G:6:VAL:HG21	2.03	0.41
1:A:126:LEU:HD22	1:A:156:LEU:HD13	2.04	0.40
1:E:249:VAL:HG22	1:E:257:TYR:CZ	2.56	0.40
1:E:253:GLN:HG2	1:E:256:ARG:HD3	2.02	0.40

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	274/276 (99%)	261 (95%)	11 (4%)	2 (1%)	22	32
1	E	272/276 (99%)	260 (96%)	10 (4%)	2 (1%)	22	32
2	B	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
2	F	97/99 (98%)	93 (96%)	3 (3%)	1 (1%)	15	23
3	C	7/9 (78%)	7 (100%)	0	0	100	100
3	G	7/9 (78%)	7 (100%)	0	0	100	100
4	D	159/195 (82%)	152 (96%)	6 (4%)	1 (1%)	25	36
4	H	182/195 (93%)	176 (97%)	6 (3%)	0	100	100
All	All	1095/1158 (95%)	1051 (96%)	38 (4%)	6 (0%)	29	41

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	90	ALA
2	F	49	VAL
1	A	127	LYS
1	A	86	ASN
4	D	152	ARG
1	E	92	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	232/232 (100%)	230 (99%)	2 (1%)	78	90
1	E	230/232 (99%)	228 (99%)	2 (1%)	78	90
2	B	94/94 (100%)	90 (96%)	4 (4%)	29	46
2	F	94/94 (100%)	92 (98%)	2 (2%)	53	72
3	C	8/8 (100%)	8 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	G	8/8 (100%)	8 (100%)	0	100	100
4	D	149/169 (88%)	148 (99%)	1 (1%)	84	92
4	H	163/169 (96%)	163 (100%)	0	100	100
All	All	978/1006 (97%)	967 (99%)	11 (1%)	73	87

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ARG
1	A	63	GLU
2	B	69	GLU
2	B	70	PHE
2	B	74	GLU
2	B	99	MET
4	D	72	ARG
1	E	35	ARG
1	E	137	ASP
2	F	70	PHE
2	F	99	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

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, 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	276/276 (100%)	-0.02	4 (1%) 75 73	20, 37, 57, 75	16 (5%)
1	E	274/276 (99%)	-0.08	2 (0%) 87 86	21, 37, 59, 88	16 (5%)
2	B	99/99 (100%)	-0.16	1 (1%) 82 80	20, 30, 48, 53	7 (7%)
2	F	99/99 (100%)	-0.21	1 (1%) 82 80	19, 27, 48, 53	4 (4%)
3	C	9/9 (100%)	0.24	0 100 100	36, 44, 48, 50	1 (11%)
3	G	9/9 (100%)	-0.15	0 100 100	29, 33, 38, 39	1 (11%)
4	D	169/195 (86%)	0.04	3 (1%) 68 66	20, 39, 74, 104	8 (4%)
4	H	188/195 (96%)	-0.11	0 100 100	18, 37, 57, 77	10 (5%)
All	All	1123/1158 (96%)	-0.07	11 (0%) 82 80	18, 36, 59, 104	63 (5%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	36	ARG	4.1
1	A	17	ARG	3.4
1	E	89	GLU	3.1
1	E	90	ALA	2.9
1	A	136	ALA	2.6
1	A	130	LEU	2.5
4	D	60	PHE	2.4
1	A	151	HIS	2.2
2	F	1	ILE	2.1
2	B	99	MET	2.0
4	D	7	THR	2.0

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 [i](#)

There are no carbohydrates 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.