Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 06:05 PM EDT

PDB ID	:	3ILA
Title	:	Crystal structure of rabbit ryanodine receptor 1 N-terminal domain (9-205)
Authors	:	Lobo, P.A.; Van Petegem, F.
Deposited on	:	2009-08-06
Resolution	:	2.90 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

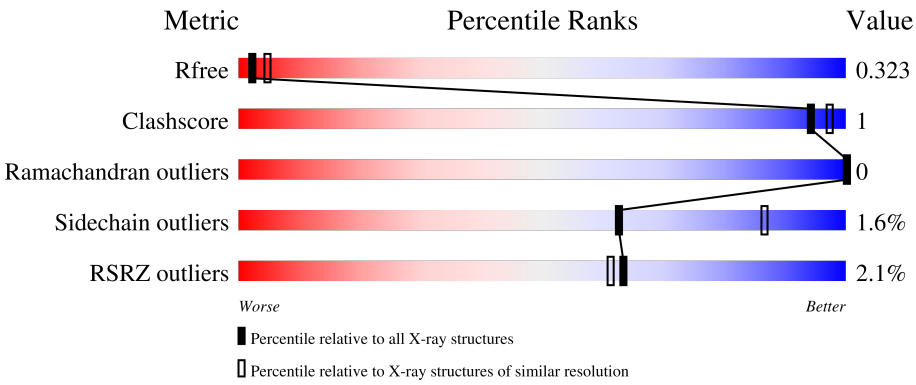
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 >=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 <=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	197	% 79% • 17%
1	B	197	2% 77% • 19%
1	C	197	% 77% 6% 18%
1	D	197	% 76% 7% 18%
1	E	197	74% 5% 21%

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Mol	Chain	Length	Quality of chain
1	F	197	2% 80% 18%
1	G	197	2% 79% 19%
1	H	197	2% 80% 19%
1	I	197	6% 54% 45%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 9944 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 Ryanodine receptor 1.

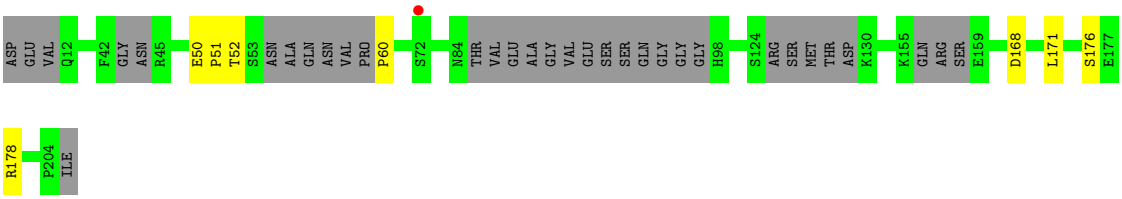
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	164	1180	748	198	222	12	0	0	0
1	B	160	1168	738	194	224	12	0	0	0
1	C	162	1160	731	193	225	11	0	0	0
1	D	162	1151	731	192	217	11	0	0	0
1	E	156	1127	715	187	213	12	0	0	0
1	F	162	1163	736	193	223	11	0	0	0
1	G	160	1133	722	186	214	11	0	0	0
1	H	159	1132	724	185	212	11	0	0	0
1	I	109	730	463	129	134	4	0	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.

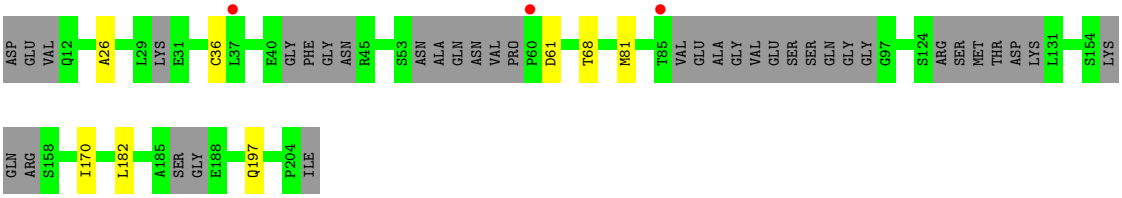
• Molecule 1: Ryanodine receptor 1

Chain A:



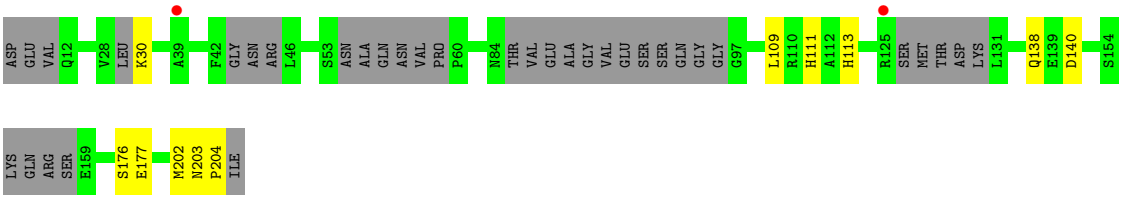
• Molecule 1: Ryanodine receptor 1

Chain B:



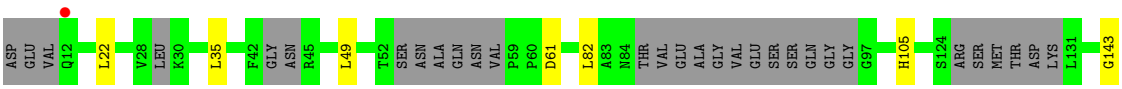
• Molecule 1: Ryanodine receptor 1

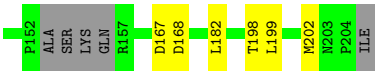
Chain C:



• Molecule 1: Ryanodine receptor 1

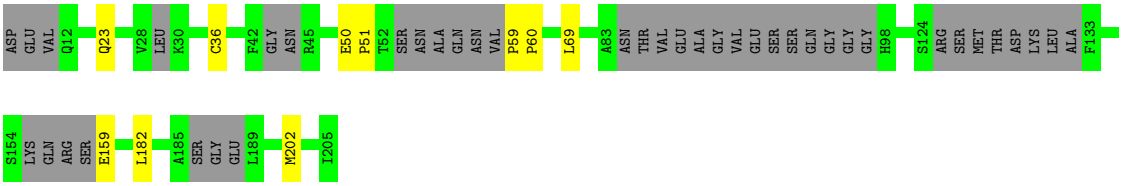
Chain D:





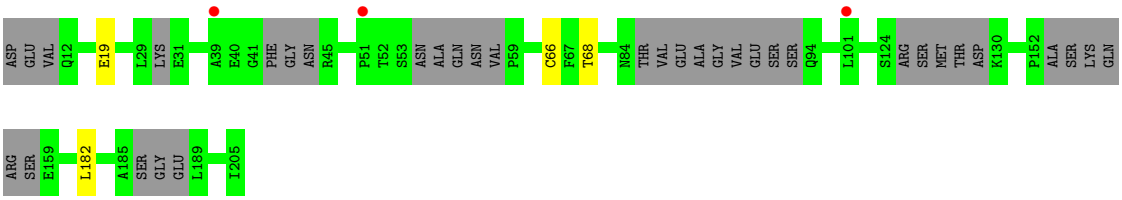
• Molecule 1: Ryanodine receptor 1

Chain E:



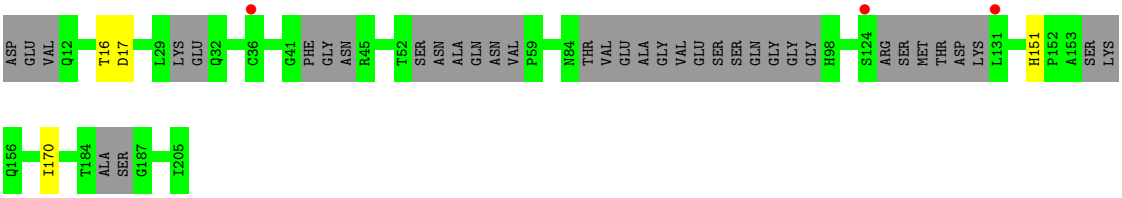
• Molecule 1: Ryanodine receptor 1

Chain F:



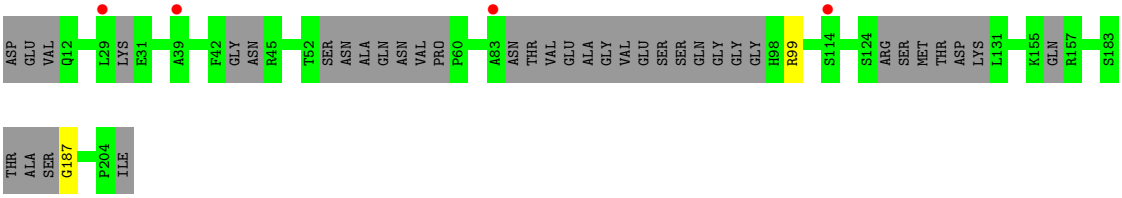
• Molecule 1: Ryanodine receptor 1

Chain G:



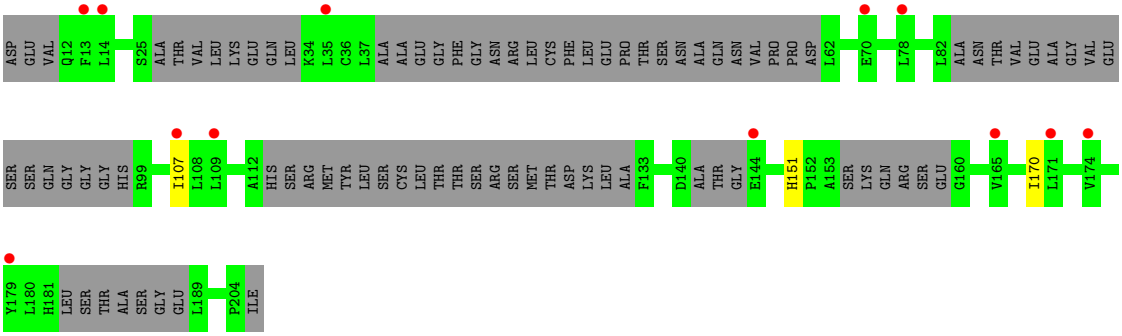
• Molecule 1: Ryanodine receptor 1

Chain H:



• Molecule 1: Ryanodine receptor 1

Chain I:


ASP
GLU
VAL
Q12
F13
L14
S25
ALA
THR
VAL
LEU
LYS
GLU
GLN
LEU
K34
L35
C36
L37
ALA
ALA
GLU
GLY
PHE
GLY
ASN
ARG
LEU
CYS
PHE
LEU
GLU
PRO
THR
SER
ASN
ALA
GLN
ASN
VAL
PRO
PRO
ASP
L62
E70
L78
L82
ALA
ASN
THR
VAL
GLU
ALA
GLY
VAL
GLU
SER
SER
GLN
GLY
GLY
GLY
HIS
R99
I107
L108
L109
A112
HIS
SER
ARG
MET
TYR
LEU
SER
CYS
LEU
THR
THR
SER
ARG
SER
MET
THR
ASP
LYS
LEU
ALA
F133
D140
ALA
THR
GLY
E144
H151
P152
A153
SER
LYS
GLN
ARG
SER
GLU
G160
V165
I170
L171
V174
Y179
L180
H181
LEU
SER
THR
ALA
SER
GLY
GLU
L189
P204
ILE

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	70.73Å 155.71Å 81.61Å 90.00° 110.63° 90.00°	Depositor
Resolution (Å)	48.51 – 2.90 48.49 – 2.90	Depositor EDS
% Data completeness (in resolution range)	93.1 (48.51-2.90) 73.5 (48.49-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$< I/\sigma(I) >$ [1]	3.16 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.274 , 0.320 0.275 , 0.323	Depositor DCC
R_{free} test set	1736 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	63.1	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 84.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	9944	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.66% 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, 0.333 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	0.29	0/1197	0.46	0/1627
1	B	0.28	0/1183	0.49	0/1606
1	C	0.28	0/1177	0.47	0/1598
1	D	0.29	0/1167	0.46	0/1587
1	E	0.29	0/1142	0.46	0/1551
1	F	0.29	0/1180	0.47	0/1603
1	G	0.28	0/1149	0.47	0/1565
1	H	0.29	0/1148	0.46	0/1559
1	I	0.28	0/736	0.42	0/1001
All	All	0.29	0/10079	0.46	0/13697

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1180	0	1083	3	0
1	B	1168	0	1071	2	0
1	C	1160	0	1035	5	0
1	D	1151	0	1043	5	0
1	E	1127	0	1027	4	0
1	F	1163	0	1044	2	0
1	G	1133	0	1014	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1132	0	1019	1	0
1	I	730	0	593	1	0
All	All	9944	0	8929	24	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 1.

All (24) 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:D:182:LEU:HB3	1:D:198:THR:HG21	1.79	0.63
1:E:69:LEU:HD21	1:E:202:MET:HE1	1.88	0.56
1:A:52:THR:HA	1:A:60:PRO:HG3	1.94	0.50
1:I:151:HIS:HB2	1:I:170:ILE:HB	1.96	0.48
1:A:176:SER:HB2	1:A:178:ARG:HE	1.79	0.48
1:D:168:ASP:HB3	1:D:199:LEU:HD22	1.96	0.48
1:B:26:ALA:HB2	1:B:182:LEU:HD21	1.96	0.47
1:G:151:HIS:HB2	1:G:170:ILE:HB	1.95	0.47
1:C:138:GLN:HE21	1:C:140:ASP:HB3	1.81	0.45
1:B:170:ILE:HD12	1:B:197:GLN:HB2	1.99	0.45
1:D:35:LEU:HB3	1:D:49:LEU:HB3	1.99	0.45
1:C:109:LEU:HD21	1:C:202:MET:HE3	1.99	0.45
1:D:82:LEU:HD22	1:D:143:GLY:H	1.82	0.44
1:A:50:GLU:HA	1:A:51:PRO:HD3	1.88	0.44
1:E:59:PRO:HA	1:E:60:PRO:HD3	1.90	0.43
1:C:176:SER:O	1:C:177:GLU:HB2	2.19	0.43
1:C:111:HIS:CE1	1:C:113:HIS:HB3	2.54	0.42
1:G:16:THR:O	1:G:17:ASP:HB2	2.18	0.42
1:E:23:GLN:HG2	1:E:36:CYS:HB3	2.01	0.42
1:F:66:CYS:HG	1:H:187:GLY:N	2.17	0.42
1:D:22:LEU:HG	1:D:202:MET:HG2	2.02	0.41
1:F:19:GLU:HG2	1:F:68:THR:HG22	2.03	0.41
1:E:50:GLU:HA	1:E:51:PRO:HD3	1.90	0.41
1:C:203:ASN:HA	1:C:204:PRO:HD3	1.95	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	152/197 (77%)	150 (99%)	2 (1%)	0	100	100
1	B	144/197 (73%)	143 (99%)	1 (1%)	0	100	100
1	C	148/197 (75%)	146 (99%)	2 (1%)	0	100	100
1	D	148/197 (75%)	145 (98%)	3 (2%)	0	100	100
1	E	140/197 (71%)	138 (99%)	2 (1%)	0	100	100
1	F	146/197 (74%)	144 (99%)	2 (1%)	0	100	100
1	G	144/197 (73%)	143 (99%)	1 (1%)	0	100	100
1	H	143/197 (73%)	138 (96%)	5 (4%)	0	100	100
1	I	93/197 (47%)	92 (99%)	1 (1%)	0	100	100
All	All	1258/1773 (71%)	1239 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	115/169 (68%)	113 (98%)	2 (2%)	60	86
1	B	117/169 (69%)	113 (97%)	4 (3%)	37	71
1	C	112/169 (66%)	111 (99%)	1 (1%)	78	93
1	D	110/169 (65%)	107 (97%)	3 (3%)	44	77
1	E	110/169 (65%)	108 (98%)	2 (2%)	59	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	113/169 (67%)	112 (99%)	1 (1%)	78	93
1	G	108/169 (64%)	108 (100%)	0	100	100
1	H	108/169 (64%)	107 (99%)	1 (1%)	78	93
1	I	56/169 (33%)	55 (98%)	1 (2%)	59	85
All	All	949/1521 (62%)	934 (98%)	15 (2%)	62	86

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	168	ASP
1	A	171	LEU
1	B	36	CYS
1	B	61	ASP
1	B	68	THR
1	B	81	MET
1	C	30	LYS
1	D	61	ASP
1	D	105	HIS
1	D	167	ASP
1	E	159	GLU
1	E	182	LEU
1	F	182	LEU
1	H	99	ARG
1	I	107	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	HIS
1	B	151	HIS
1	C	138	GLN
1	C	151	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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	164/197 (83%)	0.07	1 (0%)	89	89	55, 64, 76, 78	0
1	B	160/197 (81%)	0.09	3 (1%)	66	65	54, 62, 76, 79	0
1	C	162/197 (82%)	0.12	2 (1%)	79	79	58, 67, 79, 82	0
1	D	162/197 (82%)	0.13	1 (0%)	89	89	60, 71, 78, 81	0
1	E	156/197 (79%)	0.09	0	100	100	62, 73, 79, 84	0
1	F	162/197 (82%)	0.20	3 (1%)	66	65	67, 77, 85, 86	0
1	G	160/197 (81%)	0.17	3 (1%)	66	65	70, 79, 86, 90	0
1	H	159/197 (80%)	0.24	4 (2%)	57	55	56, 75, 95, 96	0
1	I	109/197 (55%)	0.65	12 (11%)	5	4	103, 117, 124, 125	0
All	All	1394/1773 (78%)	0.18	29 (2%)	63	61	54, 73, 117, 125	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	12	GLN	4.0
1	G	124	SER	3.8
1	H	83	ALA	3.6
1	I	78	LEU	3.4
1	A	72	SER	3.1
1	H	39	ALA	3.1
1	I	35	LEU	3.1
1	G	36	CYS	2.9
1	F	39	ALA	2.9
1	I	174	VAL	2.9
1	I	14	LEU	2.7
1	B	85	THR	2.7
1	I	179	TYR	2.7
1	G	131	LEU	2.6
1	H	114	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	I	171	LEU	2.5
1	H	29	LEU	2.4
1	B	60	PRO	2.4
1	I	70	GLU	2.4
1	F	101	LEU	2.4
1	I	144	GLU	2.3
1	I	13	PHE	2.3
1	C	125	ARG	2.3
1	I	107	ILE	2.2
1	I	165	VAL	2.2
1	B	37	LEU	2.1
1	F	51	PRO	2.1
1	C	39	ALA	2.0
1	I	109	LEU	2.0

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 monosaccharides 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.