



wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 01:44 am BST

PDB ID : 6N4F
Title : The crystal structure of hemagglutinin from A/canine/IL/11613/2015 (H3N2) influenza virus.
Authors : Yang, H.; Stevesn, J.
Deposited on : 2018-11-19
Resolution : 3.01 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

<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

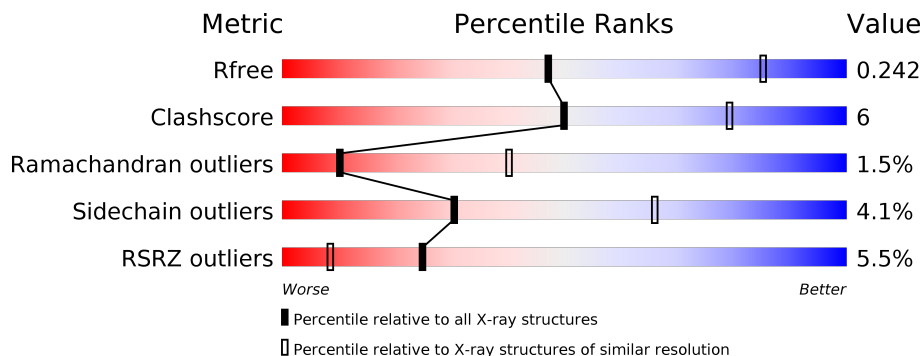
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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.



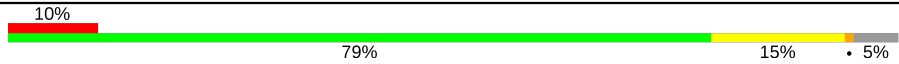
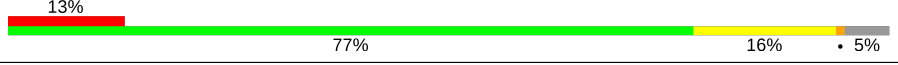
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)
RSRZ outliers	127900	2287 (3.04-3.00)

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	334	 2% 78% 16% • 5%
1	C	334	 2% 77% 17% • 5%
1	E	334	 % 79% 15% • 5%
1	G	334	 2% 78% 17% • 5%
2	B	182	 10% 77% 16% • 5%
2	D	182	 12% 78% 15% • 5%

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Mol	Chain	Length	Quality of chain
2	F	182	 <p>10% 79% 15% • 5%</p>
2	H	182	 <p>13% 77% 16% • 5%</p>

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 15352 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 Hemagglutinin HA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	317	2442	1526	434	468	14	0	0	0
1	C	317	2442	1526	434	468	14	0	0	0
1	E	317	2442	1526	434	468	14	0	0	0
1	G	317	2442	1526	434	468	14	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	ALA	-	expression tag	UNP A0A218KIQ1
A	-3	ASP	-	expression tag	UNP A0A218KIQ1
A	-2	LEU	-	expression tag	UNP A0A218KIQ1
A	-1	GLY	-	expression tag	UNP A0A218KIQ1
A	0	SER	-	expression tag	UNP A0A218KIQ1
C	-4	ALA	-	expression tag	UNP A0A218KIQ1
C	-3	ASP	-	expression tag	UNP A0A218KIQ1
C	-2	LEU	-	expression tag	UNP A0A218KIQ1
C	-1	GLY	-	expression tag	UNP A0A218KIQ1
C	0	SER	-	expression tag	UNP A0A218KIQ1
E	-4	ALA	-	expression tag	UNP A0A218KIQ1
E	-3	ASP	-	expression tag	UNP A0A218KIQ1
E	-2	LEU	-	expression tag	UNP A0A218KIQ1
E	-1	GLY	-	expression tag	UNP A0A218KIQ1
E	0	SER	-	expression tag	UNP A0A218KIQ1
G	-4	ALA	-	expression tag	UNP A0A218KIQ1
G	-3	ASP	-	expression tag	UNP A0A218KIQ1
G	-2	LEU	-	expression tag	UNP A0A218KIQ1
G	-1	GLY	-	expression tag	UNP A0A218KIQ1
G	0	SER	-	expression tag	UNP A0A218KIQ1

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	172	1396	863	248	279	6	0	0	0
2	D	172	1396	863	248	279	6	0	0	0
2	F	172	1396	863	248	279	6	0	0	0
2	H	172	1396	863	248	279	6	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	175	SER	-	expression tag	UNP A0A2U5FPI7
B	176	GLY	-	expression tag	UNP A0A2U5FPI7
B	177	ARG	-	expression tag	UNP A0A2U5FPI7
B	178	LEU	-	expression tag	UNP A0A2U5FPI7
B	179	VAL	-	expression tag	UNP A0A2U5FPI7
B	180	PRO	-	expression tag	UNP A0A2U5FPI7
B	181	ARG	-	expression tag	UNP A0A2U5FPI7
B	182	GLY	-	expression tag	UNP A0A2U5FPI7
D	175	SER	-	expression tag	UNP A0A2U5FPI7
D	176	GLY	-	expression tag	UNP A0A2U5FPI7
D	177	ARG	-	expression tag	UNP A0A2U5FPI7
D	178	LEU	-	expression tag	UNP A0A2U5FPI7
D	179	VAL	-	expression tag	UNP A0A2U5FPI7
D	180	PRO	-	expression tag	UNP A0A2U5FPI7
D	181	ARG	-	expression tag	UNP A0A2U5FPI7
D	182	GLY	-	expression tag	UNP A0A2U5FPI7
F	175	SER	-	expression tag	UNP A0A2U5FPI7
F	176	GLY	-	expression tag	UNP A0A2U5FPI7
F	177	ARG	-	expression tag	UNP A0A2U5FPI7
F	178	LEU	-	expression tag	UNP A0A2U5FPI7
F	179	VAL	-	expression tag	UNP A0A2U5FPI7
F	180	PRO	-	expression tag	UNP A0A2U5FPI7
F	181	ARG	-	expression tag	UNP A0A2U5FPI7
F	182	GLY	-	expression tag	UNP A0A2U5FPI7
H	175	SER	-	expression tag	UNP A0A2U5FPI7
H	176	GLY	-	expression tag	UNP A0A2U5FPI7
H	177	ARG	-	expression tag	UNP A0A2U5FPI7
H	178	LEU	-	expression tag	UNP A0A2U5FPI7
H	179	VAL	-	expression tag	UNP A0A2U5FPI7
H	180	PRO	-	expression tag	UNP A0A2U5FPI7

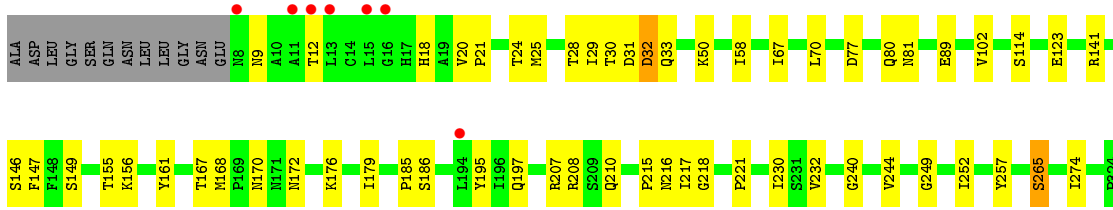
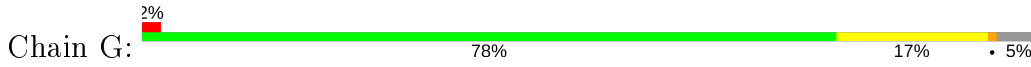
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Chain	Residue	Modelled	Actual	Comment	Reference
H	181	ARG	-	expression tag	UNP A0A2U5FPI7
H	182	GLY	-	expression tag	UNP A0A2U5FPI7

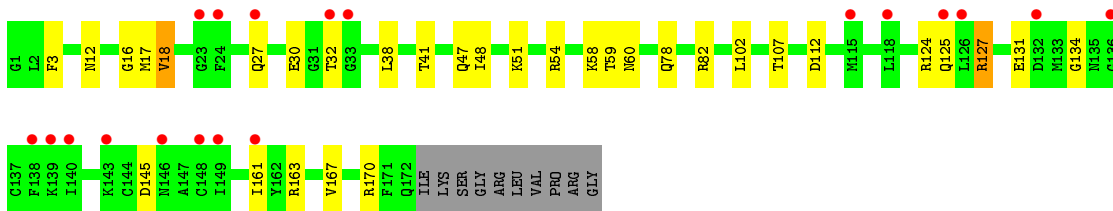
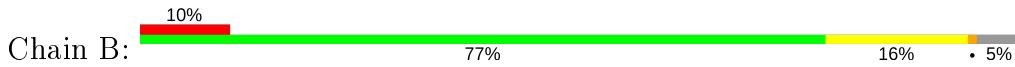
ARG

• Molecule 1: Hemagglutinin HA1

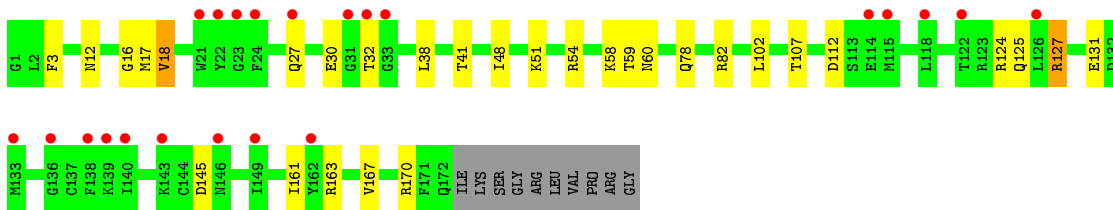
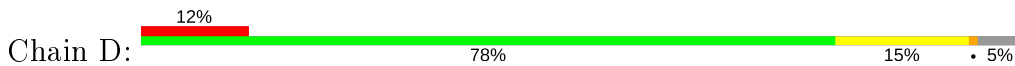


GLU
ARG
GLN
THR
ARG

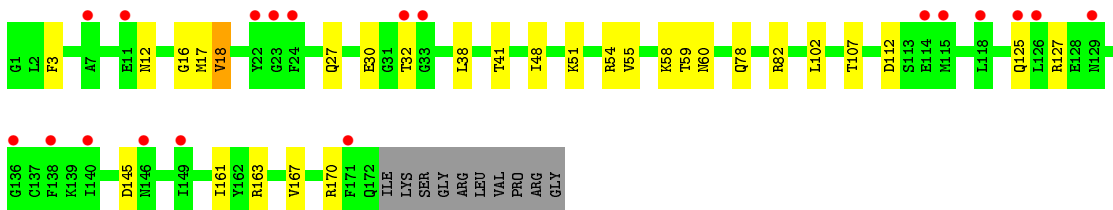
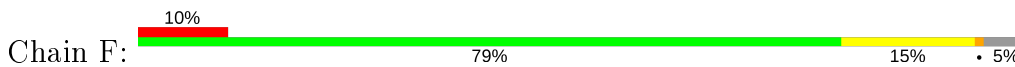
• Molecule 2: Hemagglutinin HA2




• Molecule 2: Hemagglutinin HA2

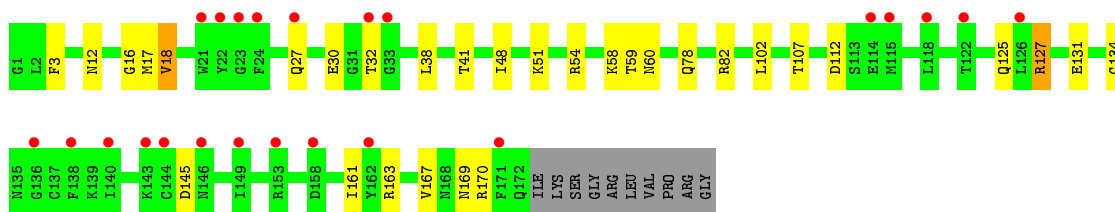


• Molecule 2: Hemagglutinin HA2



• Molecule 2: Hemagglutinin HA2

Chain H:  13% 77% 16% 5%



4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	241.15Å 241.15Å 147.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.01 45.61 – 3.01	Depositor EDS
% Data completeness (in resolution range)	98.9 (50.00-3.01) 98.6 (45.61-3.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.213 , 0.242 0.215 , 0.242	Depositor DCC
R_{free} test set	3188 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	84.5	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.009 for $-1/3^*h+1/3^*k+4/3^*l,-k,2/3^*h+1/3^*k+1/3^*l$ 0.009 for $-2/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+4/3^*l,-1/3^*h+1/3^*k+1/3^*l$ 0.005 for $-h,1/3^*h-1/3^*k-4/3^*l,-1/3^*h-2/3^*k+1/3^*l$ 0.428 for $-1/3^*h-2/3^*k+4/3^*l,-2/3^*h-1/3^*k-4/3^*l,1/3^*h-1/3^*k-1/3^*l$ 0.417 for $-h,2/3^*h+1/3^*k+4/3^*l,1/3^*h+2/3^*k-1/3^*l$ 0.428 for $1/3^*h+2/3^*k-4/3^*l,-k,-2/3^*h-1/3^*k-1/3^*l$ 0.010 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15352	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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	0.60	0/2497	0.79	0/3402
1	C	0.59	0/2497	0.79	0/3402
1	E	0.59	0/2497	0.78	0/3402
1	G	0.59	0/2497	0.79	0/3402
2	B	0.57	0/1419	0.69	0/1908
2	D	0.56	0/1419	0.69	0/1908
2	F	0.56	0/1419	0.69	0/1908
2	H	0.56	0/1419	0.69	0/1908
All	All	0.58	0/15664	0.75	0/21240

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	2442	0	2389	35	0
1	C	2442	0	2389	35	0
1	E	2442	0	2389	27	1
1	G	2442	0	2389	33	0
2	B	1396	0	1314	22	0
2	D	1396	0	1314	21	0
2	F	1396	0	1314	13	1
2	H	1396	0	1314	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	15352	0	14812	174	1

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 6.

The worst 5 of 174 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)
2:B:163:ARG:O	2:B:167:VAL:HG23	1.79	0.83
2:H:163:ARG:O	2:H:167:VAL:HG23	1.79	0.83
2:D:163:ARG:O	2:D:167:VAL:HG23	1.79	0.81
2:F:163:ARG:O	2:F:167:VAL:HG23	1.79	0.81
2:B:78:GLN:OE1	2:B:82:ARG:NH1	2.21	0.73

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:32:ASP:OD1	2:F:54:ARG:NH1[2_455]	2.18	0.02

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	315/334 (94%)	286 (91%)	29 (9%)	0	100	100
1	C	315/334 (94%)	284 (90%)	31 (10%)	0	100	100
1	E	315/334 (94%)	285 (90%)	30 (10%)	0	100	100
1	G	315/334 (94%)	285 (90%)	28 (9%)	2 (1%)	25	62
2	B	170/182 (93%)	150 (88%)	13 (8%)	7 (4%)	3	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	170/182 (93%)	150 (88%)	13 (8%)	7 (4%)	3	15
2	F	170/182 (93%)	150 (88%)	13 (8%)	7 (4%)	3	15
2	H	170/182 (93%)	150 (88%)	13 (8%)	7 (4%)	3	15
All	All	1940/2064 (94%)	1740 (90%)	170 (9%)	30 (2%)	10	40

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	17	MET
2	D	17	MET
2	F	17	MET
2	H	17	MET
2	B	59	THR

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	276/290 (95%)	264 (96%)	12 (4%)	29	64
1	C	276/290 (95%)	263 (95%)	13 (5%)	26	61
1	E	276/290 (95%)	264 (96%)	12 (4%)	29	64
1	G	276/290 (95%)	263 (95%)	13 (5%)	26	61
2	B	147/155 (95%)	142 (97%)	5 (3%)	37	72
2	D	147/155 (95%)	142 (97%)	5 (3%)	37	72
2	F	147/155 (95%)	142 (97%)	5 (3%)	37	72
2	H	147/155 (95%)	142 (97%)	5 (3%)	37	72
All	All	1692/1780 (95%)	1622 (96%)	70 (4%)	30	66

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	38	LEU

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Mol	Chain	Res	Type
1	E	50	LYS
1	G	265	SER
2	D	41	THR
1	E	12	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	116	ASN
1	E	75	HIS
2	H	60	ASN
1	E	8	ASN
1	E	197	GLN

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 [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	317/334 (94%)	0.04	6 (1%) 66 37	57, 84, 132, 199	0
1	C	317/334 (94%)	0.06	8 (2%) 57 28	57, 84, 132, 197	0
1	E	317/334 (94%)	0.05	4 (1%) 77 51	59, 86, 132, 189	0
1	G	317/334 (94%)	0.07	7 (2%) 62 32	59, 85, 135, 199	0
2	B	172/182 (94%)	0.47	19 (11%) 5 2	61, 135, 185, 202	0
2	D	172/182 (94%)	0.56	22 (12%) 3 1	59, 137, 186, 212	0
2	F	172/182 (94%)	0.51	19 (11%) 5 2	57, 137, 184, 203	0
2	H	172/182 (94%)	0.56	23 (13%) 3 1	55, 136, 191, 208	0
All	All	1956/2064 (94%)	0.22	108 (5%) 25 8	55, 92, 173, 212	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	15	LEU	6.9
2	B	138	PHE	6.8
2	H	138	PHE	6.7
2	D	136	GLY	6.6
2	D	138	PHE	5.9

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.