wwPDB X-ray Structure Validation Summary Report (i)

Jun 24, 2024 – 03:18 PM EDT

PDB ID	:	6QHD
Title	:	Lysine acetylated and tyrosine phosphorylated STAT3 in a complex with DNA
Authors	:	Arbely, E.; Belo, Y.; Shahar, A.; Zarivach, R.
Deposited on	:	2019-01-16
Resolution	:	2.85 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 (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 (i)) were used in the production of this report:

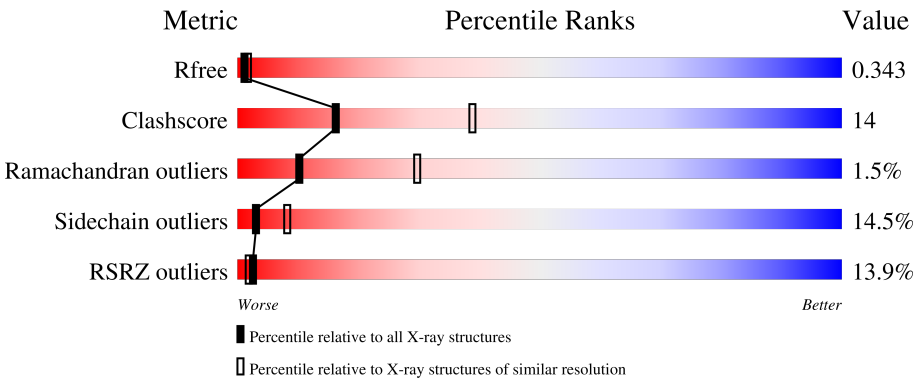
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	596	13%; 58%; 26%; 5% • 11%
1	B	596	13%; 59%; 24%; 6% • 11%
2	C	18	72%; 17%; 11%
3	D	18	67%; 22%; 11%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9454 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 Signal transducer and activator of transcription 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	530	4310	2756	728	796	1	29	0	1	0
1	B	532	4323	2767	731	797	1	27	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	631	SER	LYS	conflict	UNP P40763
B	631	SER	LYS	conflict	UNP P40763

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*AP*GP*AP*TP*TP*TP*AP*CP*GP*GP*GP*AP*AP*AP*TP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	18	372	178	74	103	17	0	0	0

- Molecule 3 is a DNA chain called DNA (5'-D(*TP*GP*CP*AP*TP*TP*TP*CP*CP*CP*GP*TP*AP*AP*AP*TP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	D	18	360	175	59	109	17	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	42	42	42	0	0
4	B	36	36	36	0	0

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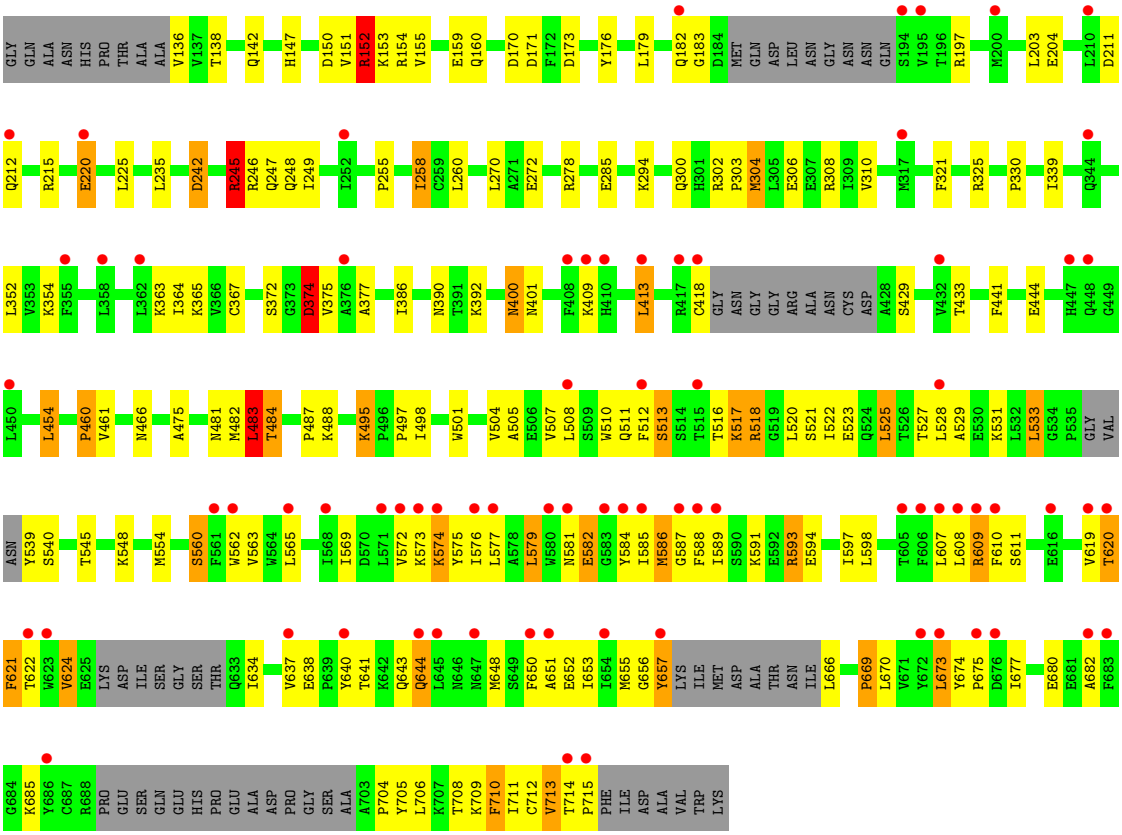
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	C	6	6	6	0	0
			Total	O		
4	D	5	5	5	0	0

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.

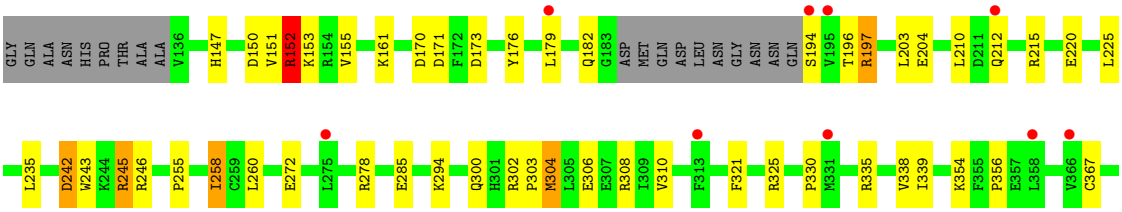
• Molecule 1: Signal transducer and activator of transcription 3

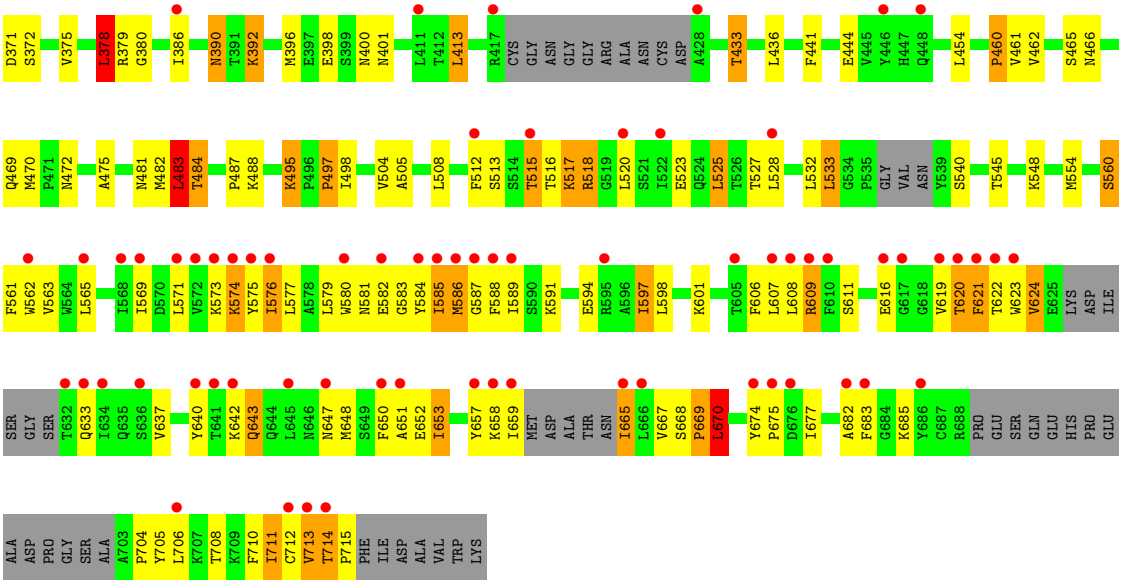
Chain A:



• Molecule 1: Signal transducer and activator of transcription 3

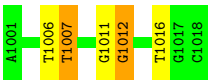
Chain B:





• Molecule 2: DNA (5'-D(*AP*AP*GP*AP*TP*TP*TP*AP*CP*GP*GP*GP*AP*AP*AP*TP*GP*C)-3')

Chain C: 72% 17% 11%



• Molecule 3: DNA (5'-D(*TP*GP*CP*AP*TP*TP*TP*CP*CP*CP*GP*TP*AP*AP*AP*TP*CP*T)-3')

Chain D: 67% 22% 11%

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α, β, γ	175.49Å 175.49Å 79.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.85 175.49 – 2.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.00-2.85) 100.0 (175.49-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.12 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.294 , 0.343 0.294 , 0.343	Depositor DCC
R_{free} test set	2781 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	75.5	Xtriage
Anisotropy	0.830	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 54.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.39$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	9454	wwPDB-VP
Average B, all atoms (Å^2)	109.0	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 98.07 % 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 5.6998e-11. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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)

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

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	0.98	2/4364 (0.0%)	1.11	21/5886 (0.4%)
1	B	0.99	2/4374 (0.0%)	1.08	15/5900 (0.3%)
2	C	0.99	1/419 (0.2%)	1.25	4/646 (0.6%)
3	D	0.88	0/401	1.32	7/616 (1.1%)
All	All	0.98	5/9558 (0.1%)	1.12	47/13048 (0.4%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	272	GLU	CD-OE2	6.47	1.32	1.25
1	B	272	GLU	CD-OE2	6.20	1.32	1.25
1	A	220	GLU	CD-OE1	5.85	1.32	1.25
2	C	1006	DT	O3'-P	-5.57	1.54	1.61
1	B	212	GLN	CG-CD	5.56	1.63	1.51

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	1007	DT	O5'-P-OP2	-8.89	97.70	105.70
1	B	152	ARG	NE-CZ-NH1	8.52	124.56	120.30
3	D	1007	DT	O5'-P-OP1	7.88	120.15	110.70
2	C	1012	DG	O5'-P-OP2	-7.19	99.23	105.70
1	A	152	ARG	NE-CZ-NH1	7.15	123.87	120.30

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	4310	0	4367	133	0
1	B	4323	0	4391	136	0
2	C	372	0	204	2	0
3	D	360	0	207	2	0
4	A	42	0	0	2	0
4	B	36	0	0	1	0
4	C	6	0	0	0	0
4	D	5	0	0	0	0
All	All	9454	0	9169	265	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 14.

The worst 5 of 265 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:A:517:LYS:HE2	1:A:577:LEU:CD2	1.70	1.20
1:A:656:GLY:O	1:A:711:ILE:CD1	1.96	1.13
1:A:711:ILE:HG12	1:A:713:VAL:HG13	1.33	1.10
1:A:517:LYS:HE2	1:A:577:LEU:HD23	1.19	1.09
1:B:505:ALA:HB1	1:B:525:LEU:HD11	1.46	0.96

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	515/596 (86%)	488 (95%)	20 (4%)	7 (1%)	11	31
1	B	516/596 (87%)	485 (94%)	23 (4%)	8 (2%)	9	28
All	All	1031/1192 (86%)	973 (94%)	43 (4%)	15 (2%)	10	30

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	183	GLY
1	A	669	PRO
1	A	704	PRO
1	B	497	PRO
1	B	669	PRO

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	483/532 (91%)	409 (85%)	74 (15%)	2	7
1	B	484/532 (91%)	418 (86%)	66 (14%)	3	9
All	All	967/1064 (91%)	827 (86%)	140 (14%)	3	8

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	565	LEU
1	B	586	MET
1	B	640	TYR
1	A	574	LYS
1	A	573	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	469	GLN

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Mol	Chain	Res	Type
1	B	581	ASN
1	B	647	ASN
1	B	567	ASN
1	B	205	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)

4 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	ALY	B	685	1	10,11,12	0.80	0	7,12,14	2.40	4 (57%)
1	PTR	B	705	1	15,16,17	2.61	7 (46%)	19,22,24	2.30	7 (36%)
1	PTR	A	705	1	15,16,17	2.70	8 (53%)	19,22,24	1.96	4 (21%)
1	ALY	A	685	1	10,11,12	0.87	0	7,12,14	2.22	3 (42%)

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
1	ALY	B	685	1	-	3/9/10/12	-
1	PTR	B	705	1	-	4/10/11/13	0/1/1/1
1	PTR	A	705	1	-	1/10/11/13	0/1/1/1
1	ALY	A	685	1	-	3/9/10/12	-

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	705	PTR	CE1-CD1	4.71	1.47	1.38
1	B	705	PTR	CE2-CD2	4.67	1.47	1.38
1	A	705	PTR	CE2-CD2	4.46	1.46	1.38
1	B	705	PTR	CE1-CD1	4.36	1.46	1.38
1	A	705	PTR	OH-CZ	4.04	1.49	1.40

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	705	PTR	CE2-CZ-CE1	-4.69	112.95	120.18
1	B	705	PTR	CG-CB-CA	4.49	123.20	114.10
1	B	705	PTR	CD1-CE1-CZ	4.21	124.88	119.73
1	A	705	PTR	CG-CB-CA	4.02	122.23	114.10
1	A	705	PTR	CE2-CZ-CE1	-3.82	114.30	120.18

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	705	PTR	O-C-CA-CB
1	B	705	PTR	O-C-CA-CB
1	A	685	ALY	OH-CH-NZ-CE
1	A	685	ALY	CH3-CH-NZ-CE
1	B	685	ALY	OH-CH-NZ-CE

There are no ring outliers.

No monomer is involved in short contacts.

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	528/596 (88%)	0.84	75 (14%)	2	2	70, 100, 170, 194	0
1	B	530/596 (88%)	0.84	77 (14%)	2	1	71, 100, 173, 225	0
2	C	18/18 (100%)	0.09	0	100	100	76, 92, 115, 119	0
3	D	18/18 (100%)	0.07	0	100	100	72, 89, 112, 116	0
All	All	1094/1228 (89%)	0.81	152 (13%)	2	2	70, 99, 171, 225	0

The worst 5 of 152 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	650	PHE	13.4
1	B	650	PHE	9.3
1	A	589	ILE	7.1
1	B	665	ILE	6.5
1	A	418	CYS	6.5

6.2 Non-standard residues in protein, DNA, RNA chains (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. 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	B-factors(Å^2)	Q<0.9
1	PTR	A	705	16/17	0.81	0.19	147,157,166,170	0
1	PTR	B	705	16/17	0.82	0.18	153,160,168,173	0
1	ALY	B	685	12/13	0.83	0.29	142,145,146,148	0
1	ALY	A	685	12/13	0.87	0.39	140,144,146,147	0

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.