



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:30 pm GMT

PDB ID : 4KB7
Title : HCV NS5B GT1B N316Y with CMPD 32
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Deposited on : 2013-04-23
Resolution : 1.85 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

<http://wwpdb.org/validation/2016/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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

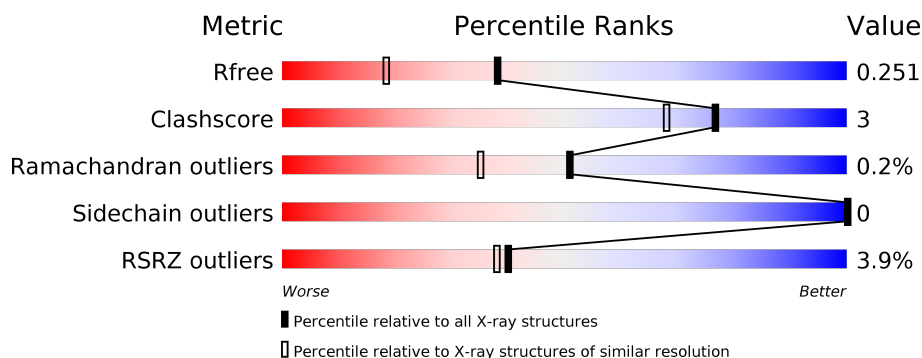
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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}	100719	1923 (1.86-1.86)
Clashscore	112137	2083 (1.86-1.86)
Ramachandran outliers	110173	2060 (1.86-1.86)
Sidechain outliers	110143	2060 (1.86-1.86)
RSRZ outliers	101464	1932 (1.86-1.86)

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 $\leq 5\%$. 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	580	
1	B	580	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9368 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 HCV Polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total	C	N	O	S	0	12	0
			4231	2675	731	790	35			
1	B	548	Total	C	N	O	S	0	10	0
			4237	2682	727	794	34			

There are 28 discrepancies between the modelled and reference sequences:

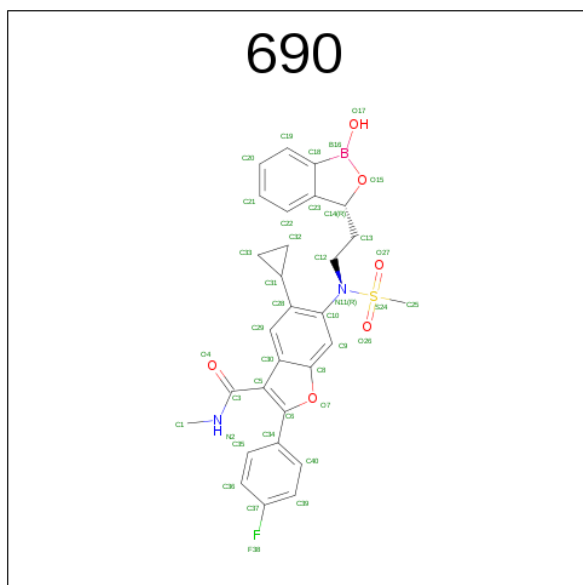
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP P26663
A	0	ALA	-	EXPRESSION TAG	UNP P26663
A	47	GLN	LEU	ENGINEERED MUTATION	UNP P26663
A	101	TYR	PHE	ENGINEERED MUTATION	UNP P26663
A	114	ARG	LYS	ENGINEERED MUTATION	UNP P26663
A	316	TYR	ASN	ENGINEERED MUTATION	UNP P26663
A	571	LEU	-	EXPRESSION TAG	UNP P26663
A	572	GLU	-	EXPRESSION TAG	UNP P26663
A	573	HIS	-	EXPRESSION TAG	UNP P26663
A	574	HIS	-	EXPRESSION TAG	UNP P26663
A	575	HIS	-	EXPRESSION TAG	UNP P26663
A	576	HIS	-	EXPRESSION TAG	UNP P26663
A	577	HIS	-	EXPRESSION TAG	UNP P26663
A	578	HIS	-	EXPRESSION TAG	UNP P26663
B	-1	MET	-	EXPRESSION TAG	UNP P26663
B	0	ALA	-	EXPRESSION TAG	UNP P26663
B	47	GLN	LEU	ENGINEERED MUTATION	UNP P26663
B	101	TYR	PHE	ENGINEERED MUTATION	UNP P26663
B	114	ARG	LYS	ENGINEERED MUTATION	UNP P26663
B	316	TYR	ASN	ENGINEERED MUTATION	UNP P26663
B	571	LEU	-	EXPRESSION TAG	UNP P26663
B	572	GLU	-	EXPRESSION TAG	UNP P26663
B	573	HIS	-	EXPRESSION TAG	UNP P26663
B	574	HIS	-	EXPRESSION TAG	UNP P26663
B	575	HIS	-	EXPRESSION TAG	UNP P26663

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Chain	Residue	Modelled	Actual	Comment	Reference
B	576	HIS	-	EXPRESSION TAG	UNP P26663
B	577	HIS	-	EXPRESSION TAG	UNP P26663
B	578	HIS	-	EXPRESSION TAG	UNP P26663

- Molecule 2 is 5-CYCLOPROPYL-2-(4-FLUOROPHENYL)-6-[{2-[(3R)-1-HYDROXY-1,3-DIHYDRO-2,1-BENZOXABOROL-3-YL]ETHYL}(METHYLSULFONYL)AMINO]-N-METHYL-1-BENZOFURAN-3-CARBOXAMIDE (three-letter code: 690) (formula: $C_{29}H_{28}BFN_2O_6S$).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	B	C	F	N	O	S		
2	A	1	Total 40	1	29	1	2	6	1	0	0
2	B	1	Total 40	1	29	1	2	6	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	424	Total 424 O 424	0	0
3	B	396	Total 396 O 396	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.03Å 106.62Å 126.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	81.53 – 1.85 45.98 – 1.85	Depositor EDS
% Data completeness (in resolution range)	92.4 (81.53-1.85) 92.4 (45.98-1.85)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.208 , 0.241 0.217 , 0.251	Depositor DCC
R_{free} test set	4626 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9368	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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 50.09 % 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 6.7967e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 690

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	0/4368	0.47	0/5937
1	B	0.29	0/4357	0.47	1/5925 (0.0%)
All	All	0.29	0/8725	0.47	1/11862 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	PRO	N-CA-CB	5.77	110.22	103.30

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	4231	0	4167	29	0
1	B	4237	0	4151	28	0
2	A	40	0	25	10	0
2	B	40	0	27	4	0
3	A	424	0	0	2	0
3	B	396	0	0	1	0
All	All	9368	0	8370	59	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 (59) 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:410:GLY:O	1:A:414[B]:MET:HE2	1.54	1.04
1:B:414[B]:MET:CE	1:B:414[B]:MET:HA	2.13	0.77
1:A:410:GLY:C	1:A:414[B]:MET:HE2	2.06	0.76
1:B:413:ILE:HG22	1:B:414[B]:MET:HE3	1.66	0.75
1:B:201[B]:VAL:HG12	1:B:384:LEU:HG	1.72	0.70
1:B:414[B]:MET:HA	1:B:414[B]:MET:HE2	1.80	0.62
1:B:413:ILE:HG22	1:B:414[B]:MET:CE	2.30	0.62
1:A:410:GLY:C	1:A:414[B]:MET:CE	2.70	0.60
1:B:414[B]:MET:HB3	2:B:601:690:H1	1.83	0.60
2:B:601:690:C31	2:B:601:690:H20	2.32	0.60
1:A:197:PRO:HG3	1:A:414[A]:MET:HE3	1.88	0.55
1:A:22:PRO:HG2	1:A:401:ARG:HG3	1.88	0.54
1:A:414[B]:MET:HG3	1:A:415:TYR:CD2	2.43	0.54
1:B:314:LEU:HG	2:B:601:690:H14	1.89	0.54
2:A:601:690:C31	2:A:601:690:H20	2.38	0.53
1:B:227:THR:HB	1:B:347[B]:SER:O	2.09	0.53
1:A:200:ARG:HD2	1:A:384:LEU:HD11	1.91	0.52
1:A:182:LEU:HD23	1:A:182:LEU:C	2.31	0.51
1:A:405:VAL:HG12	3:A:1100:HOH:O	2.10	0.50
1:B:414[B]:MET:CA	1:B:414[B]:MET:CE	2.86	0.50
1:B:46:GLY:HA2	1:B:49:GLN:HE21	1.77	0.50
1:A:219:TYR:HB3	1:A:320:LEU:HD23	1.94	0.50
1:A:414[B]:MET:HB2	2:A:601:690:H2	1.94	0.50
1:A:448:TYR:HE1	2:A:601:690:H3	1.75	0.50
1:B:160:ILE:HD12	1:B:282:SER:OG	2.12	0.50
1:B:144:VAL:HB	1:B:394:ARG:HG2	1.94	0.49
1:A:414[A]:MET:CE	2:A:601:690:C25	2.91	0.48
1:B:219:TYR:HB3	1:B:320:LEU:HD23	1.95	0.48
1:B:372:VAL:HG12	3:B:1052:HOH:O	2.12	0.48
1:B:22:PRO:HG2	1:B:401:ARG:HG3	1.96	0.48
1:B:138:ILE:HD11	1:B:159:LEU:HD13	1.95	0.48
1:B:52:VAL:HG12	1:B:223[A]:CYS:SG	2.54	0.47
1:A:141:LYS:CG	1:A:160:ILE:HG23	2.45	0.47
1:A:52:VAL:HG12	1:A:223[A]:CYS:SG	2.55	0.47
1:B:414[B]:MET:HE3	1:B:414[B]:MET:HA	1.95	0.46
1:B:414[B]:MET:HE3	1:B:414[B]:MET:CA	2.46	0.46
1:A:204:LEU:HD21	1:A:314:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:VAL:HG23	3:A:1123:HOH:O	2.16	0.44
2:A:601:690:C31	2:A:601:690:C12	2.95	0.44
1:A:414[A]:MET:HE2	2:A:601:690:C25	2.48	0.44
1:B:414[A]:MET:HB3	2:B:601:690:H1	2.00	0.44
1:A:336:LEU:HD22	1:A:356:PRO:HD3	2.00	0.43
1:A:172:LYS:HE3	1:A:560:ILE:HD13	1.99	0.43
1:B:172:LYS:HE3	1:B:560:ILE:HD13	2.01	0.43
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.99	0.42
1:A:314:LEU:HG	2:A:601:690:H14	2.02	0.42
2:A:601:690:H1	2:A:601:690:H19	1.75	0.42
1:B:182:LEU:HD12	1:B:243:CYS:SG	2.59	0.42
1:A:200:ARG:HD2	1:A:384:LEU:CD1	2.50	0.41
1:A:414[A]:MET:HE2	2:A:601:690:H3	2.01	0.41
1:A:59:VAL:CG1	1:B:59:VAL:CG1	2.99	0.41
1:A:414[B]:MET:HB2	2:A:601:690:C25	2.51	0.41
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.60	0.41
1:B:182:LEU:N	1:B:183:PRO:CD	2.83	0.41
1:A:59:VAL:CG1	1:B:59:VAL:HG13	2.50	0.40
1:A:187:MET:SD	1:A:292:THR:HG22	2.62	0.40
1:B:390:THR:HB	1:B:391:PRO:HD3	2.03	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	550/580 (95%)	543 (99%)	6 (1%)	1 (0%)	51 35
1	B	552/580 (95%)	543 (98%)	7 (1%)	2 (0%)	38 22
All	All	1102/1160 (95%)	1086 (98%)	13 (1%)	3 (0%)	51 29

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	347	SER
1	B	347[A]	SER
1	B	347[B]	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	456/494 (92%)	456 (100%)	0	100	100
1	B	451/494 (91%)	451 (100%)	0	100	100
All	All	907/988 (92%)	907 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
1	A	120	HIS
1	A	273	ASN
1	A	446	GLN
1	B	49	GLN
1	B	273	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 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	$\# Z > 2$
2	690	A	601	-	39,45,45	2.49	5 (12%)	48,68,68	2.55	12 (25%)
2	690	B	601	-	39,45,45	2.48	5 (12%)	48,68,68	2.45	14 (29%)

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
2	690	A	601	-	-	0/23/43/43	0/4/6/6
2	690	B	601	-	-	0/23/43/43	0/4/6/6

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	690	B16-C18	-4.80	1.48	1.55
2	A	601	690	B16-C18	-4.71	1.48	1.55
2	A	601	690	C23-C18	-4.40	1.37	1.40
2	B	601	690	C23-C18	-4.00	1.37	1.40
2	A	601	690	C25-S24	-3.97	1.65	1.75
2	B	601	690	C25-S24	-3.67	1.66	1.75
2	B	601	690	C29-C28	2.97	1.41	1.36
2	A	601	690	C29-C28	3.03	1.41	1.36
2	A	601	690	B16-O17	11.92	1.53	1.36
2	B	601	690	B16-O17	12.04	1.54	1.36

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	690	O27-S24-O26	-7.48	107.58	118.61
2	A	601	690	C9-C10-N11	-7.17	112.65	119.86
2	B	601	690	O27-S24-O26	-7.06	108.21	118.61
2	B	601	690	C9-C10-N11	-6.83	112.99	119.86
2	A	601	690	O17-B16-C18	-5.50	118.38	129.85
2	A	601	690	C33-C31-C28	-5.38	115.96	121.62
2	B	601	690	C33-C31-C28	-5.15	116.20	121.62
2	B	601	690	O17-B16-C18	-5.08	119.25	129.85
2	A	601	690	C5-C30-C8	-3.54	101.96	107.76
2	B	601	690	C5-C30-C8	-3.35	102.28	107.76
2	A	601	690	B16-C18-C19	-3.28	128.99	135.61
2	B	601	690	B16-C18-C19	-3.22	129.11	135.61
2	B	601	690	C20-C19-C18	-3.17	117.87	121.60
2	A	601	690	C30-C5-C3	-3.10	120.93	125.83
2	A	601	690	C20-C19-C18	-3.01	118.05	121.60
2	B	601	690	C30-C5-C3	-2.96	121.15	125.83
2	B	601	690	C12-N11-S24	-2.51	112.56	117.81
2	B	601	690	C39-C37-C36	-2.07	119.97	122.86
2	A	601	690	C19-C18-C23	2.64	122.04	119.07
2	B	601	690	C19-C18-C23	2.69	122.09	119.07
2	B	601	690	C5-C6-C34	3.18	131.65	127.16
2	A	601	690	C5-C6-C34	3.55	132.17	127.16
2	B	601	690	O26-S24-N11	4.52	112.17	107.57
2	B	601	690	C25-S24-N11	4.77	112.50	106.38
2	A	601	690	O26-S24-N11	4.84	112.49	107.57
2	A	601	690	C25-S24-N11	5.24	113.10	106.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	690	10	0
2	B	601	690	4	0

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	545/580 (93%)	0.31	16 (2%)	52	50	7, 17, 28, 40	2 (0%)
1	B	548/580 (94%)	0.36	27 (4%)	30	29	8, 19, 29, 43	2 (0%)
All	All	1093/1160 (94%)	0.34	43 (3%)	40	38	7, 18, 29, 43	4 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	556	SER	6.5
1	A	557	GLY	6.2
1	B	534	LEU	6.1
1	B	557	GLY	6.0
1	A	553	ALA	4.9
1	A	534	LEU	4.6
1	A	558	GLY	4.5
1	B	535	LYS	4.2
1	A	14	CYS	4.1
1	A	402	HIS	3.2
1	B	14	CYS	3.2
1	B	556	SER	3.2
1	B	551	PHE	3.2
1	B	352	ASP	3.0
1	B	213	ASN	3.0
1	A	552	VAL	3.0
1	B	448	TYR	2.9
1	A	449	GLY	2.8
1	B	35	ASN	2.8
1	A	414[A]	MET	2.8
1	A	532	THR	2.7
1	A	448	TYR	2.7
1	A	555	TYR	2.7
1	B	553	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	316[A]	TYR	2.6
1	A	195	TYR	2.5
1	A	35	ASN	2.5
1	B	483	ASN	2.5
1	B	178	VAL	2.3
1	B	329	THR	2.3
1	A	191	TYR	2.3
1	B	558	GLY	2.2
1	B	182	LEU	2.2
1	B	328	GLY	2.2
1	B	376	ALA	2.2
1	B	532	THR	2.1
1	B	330	GLN	2.1
1	B	15	ALA	2.1
1	B	239	ILE	2.1
1	B	554	GLY	2.1
1	B	149	PRO	2.1
1	B	353	PRO	2.1
1	B	533	LYS	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 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
2	690	B	601	40/40	0.79	0.20	0.86	33,36,40,40	0
2	690	A	601	40/40	0.86	0.19	0.76	21,25,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.