W O R L D W I D E
wwPDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 03:42 PM GMT

PDB ID   :   4C11
Title   :   Dengue virus RNA dependent RNA polymerase with residues from the NS5 linker region
Authors   :   Lim, S.P.; Lescar, J.
Deposited on   :   2013-08-09
Resolution   :   2.60 Å(reported)

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 2.60 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	Percentile Ranks	Value
Rfree		0.252
Clashscore		4
Ramachandran outliers		0.8%
Sidechain outliers		6.9%
RSRZ outliers		6.1%

Worse											Better

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
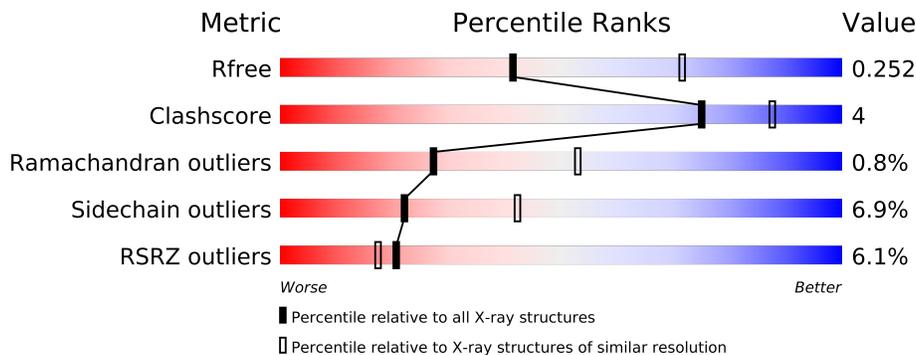
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	638	
2	B	638	

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 10134 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DENGUE VIRUS TYPE 3 RNA DEPENDENT RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	593	Total 4842	C 3057	N 872	O 882	S 31	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	374	GLU	GLY	CONFLICT	UNP Q6DLV0
A	454	LYS	MET	CONFLICT	UNP Q6DLV0

- Molecule 2 is a protein called DENGUE VIRUS TYPE 3 RNA DEPENDENT RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	603	Total 4864	C 3068	N 871	O 893	S 32	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	374	GLU	GLY	CONFLICT	UNP Q6DLV0
B	409	ALA	GLY	CONFLICT	UNP Q6DLV0
B	455	ALA	GLY	CONFLICT	UNP Q6DLV0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total 2	Zn 2	0	0
3	A	2	Total 2	Zn 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	236	Total O 236 236		0	0
4	B	188	Total O 188 188		0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: DENGUE VIRUS TYPE 3 RNA DEPENDENT RNA POLYMERASE

Chain A:
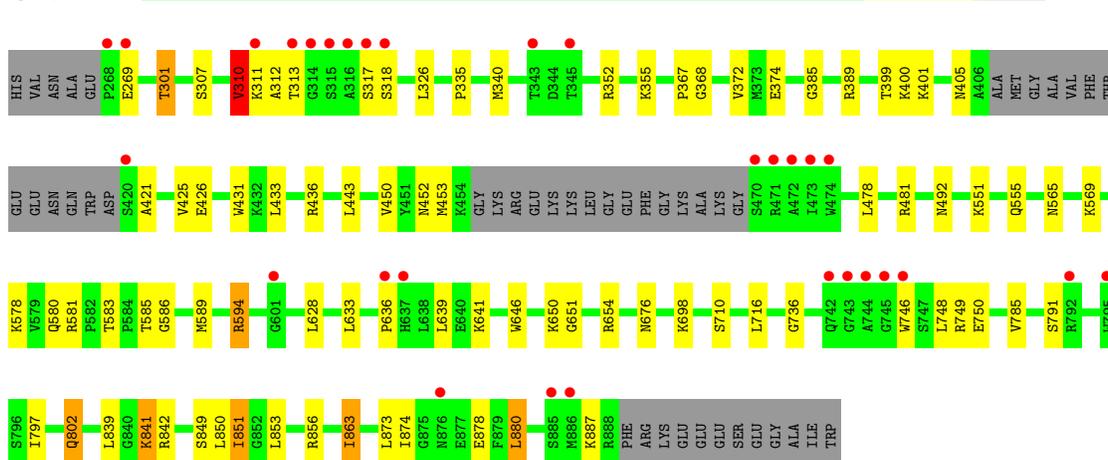
• Molecule 2: DENGUE VIRUS TYPE 3 RNA DEPENDENT RNA POLYMERASE

Chain B:
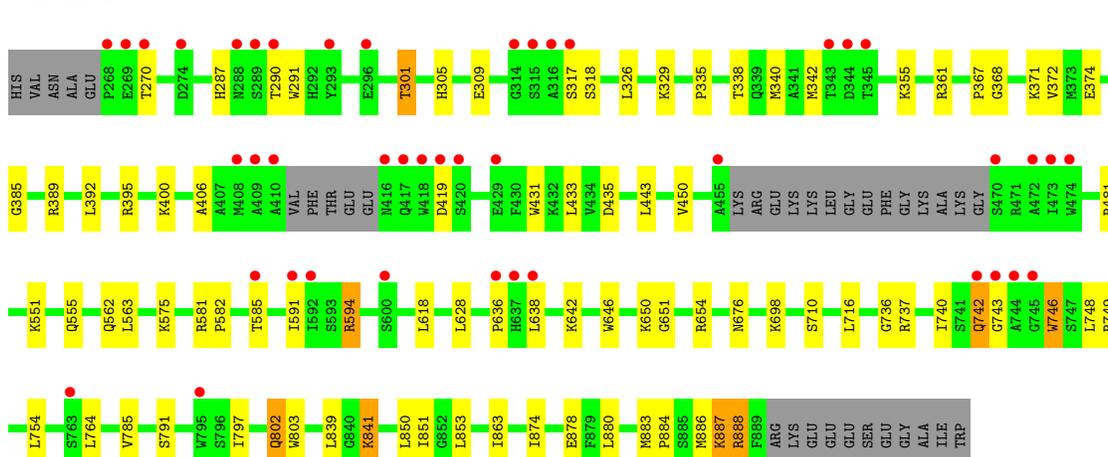
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	122.99Å 136.05Å 103.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.94 – 2.60 19.93 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.0 (19.94-2.60) 98.0 (19.93-2.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.53 (at 2.59Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.192 , 0.245 0.199 , 0.252	Depositor DCC
R_{free} test set	2676 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	56.2	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 60.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	1 of 52736 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	10134	wwPDB-VP
Average B, all atoms (Å^2)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.37% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.

5   Model quality ⓘ

5.1   Standard geometry ⓘ

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

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	0.52	0/4974	0.73	1/6737 (0.0%)
2	B	0.51	0/4987	0.72	3/6760 (0.0%)
All	All	0.51	0/9961	0.72	4/13497 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	886	MET	C-N-CA	6.74	138.54	121.70
1	A	310	VAL	C-N-CA	6.44	137.79	121.70
2	B	887	LYS	N-CA-C	5.61	126.14	111.00
2	B	746	TRP	N-CA-CB	5.12	119.81	110.60

There are no chirality outliers.

There are no planarity outliers.

5.2   Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4842	0	4748	43	0
2	B	4864	0	4723	35	0
3	A	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	2	0	0	0	0
4	A	236	0	0	1	0
4	B	188	0	0	1	0
All	All	10134	0	9471	77	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (77) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:311:LYS:HB2	1:A:312:ALA:HA	1.44	0.95
2:B:802:GLN:HE21	2:B:802:GLN:H	1.19	0.89
2:B:301:THR:CG2	2:B:594:ARG:HH12	1.88	0.87
1:A:802:GLN:H	1:A:802:GLN:HE21	1.19	0.87
1:A:301:THR:CG2	1:A:594:ARG:HH12	1.88	0.85
2:B:301:THR:HG23	2:B:594:ARG:HH12	1.49	0.77
1:A:313:THR:HB	1:A:580:GLN:HE22	1.49	0.76
1:A:301:THR:HG23	1:A:594:ARG:HH12	1.52	0.75
2:B:385:GLY:HA3	2:B:555:GLN:HE22	1.52	0.74
1:A:385:GLY:HA3	1:A:555:GLN:HE22	1.52	0.74
2:B:883:MET:HB3	2:B:888:ARG:HD3	1.68	0.74
2:B:716:LEU:HD21	2:B:839:LEU:HD23	1.71	0.73
1:A:452:ASN:HB3	1:A:578:LYS:HG2	1.78	0.66
1:A:310:VAL:HB	1:A:311:LYS:HA	1.79	0.65
1:A:716:LEU:HD21	1:A:839:LEU:HD23	1.79	0.65
1:A:311:LYS:CB	1:A:312:ALA:HA	2.25	0.62
1:A:797:ILE:H	1:A:797:ILE:HD12	1.66	0.61
2:B:301:THR:HG23	2:B:594:ARG:NH1	2.15	0.60
2:B:797:ILE:HD12	2:B:797:ILE:H	1.67	0.59
1:A:301:THR:HG23	1:A:594:ARG:NH1	2.16	0.59
2:B:368:GLY:O	2:B:372:VAL:HG23	2.03	0.59
2:B:737:ARG:HA	2:B:740:ILE:HD12	1.85	0.58
2:B:841:LYS:HG2	2:B:851:ILE:HD12	1.84	0.58
2:B:372:VAL:HG11	2:B:628:LEU:HD11	1.88	0.56
1:A:269:GLU:HG3	1:A:594:ARG:HA	1.87	0.55
1:A:335:PRO:HG3	2:B:335:PRO:HG3	1.89	0.54
1:A:421:ALA:O	1:A:425:VAL:HG23	2.07	0.54
1:A:785:VAL:HG11	1:A:880:LEU:HD13	1.89	0.54
1:A:372:VAL:HG11	1:A:628:LEU:HD11	1.88	0.54
1:A:802:GLN:H	1:A:802:GLN:NE2	1.99	0.52
1:A:849:SER:OG	1:A:851:ILE:HG13	2.09	0.52
2:B:340:MET:HG3	2:B:736:GLY:HA3	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:785:VAL:CG1	1:A:880:LEU:HB2	2.40	0.52
2:B:802:GLN:H	2:B:802:GLN:NE2	1.99	0.51
1:A:425:VAL:HG13	1:A:431:TRP:HZ2	1.76	0.51
1:A:583:THR:HG23	1:A:586:GLY:H	1.77	0.50
2:B:290:THR:HG21	2:B:309:GLU:HG2	1.94	0.50
2:B:371:LYS:HG2	2:B:638:LEU:HB3	1.94	0.50
2:B:785:VAL:HG11	2:B:880:LEU:HB2	1.93	0.49
2:B:748:LEU:HD21	2:B:874:ILE:HA	1.93	0.48
1:A:841:LYS:HD3	1:A:851:ILE:HD13	1.95	0.48
2:B:742:GLN:HG3	2:B:754:LEU:HD21	1.94	0.48
1:A:797:ILE:H	1:A:797:ILE:CD1	2.26	0.48
4:A:2231:HOH:O	2:B:582:PRO:HD2	2.14	0.47
2:B:392:LEU:HD21	2:B:563:LEU:HD12	1.96	0.47
1:A:583:THR:CG2	1:A:586:GLY:H	2.27	0.47
1:A:748:LEU:HD21	1:A:874:ILE:HA	1.96	0.47
2:B:287:HIS:O	2:B:291:TRP:HB2	2.15	0.47
1:A:367:PRO:HB2	1:A:636:PRO:HA	1.96	0.47
1:A:399:THR:HA	1:A:425:VAL:HG11	1.97	0.47
1:A:340:MET:HG3	1:A:736:GLY:HA3	1.97	0.47
1:A:746:TRP:HE3	1:A:750:GLU:HB3	1.79	0.47
2:B:841:LYS:HG2	2:B:851:ILE:CD1	2.46	0.46
2:B:367:PRO:HB2	2:B:636:PRO:HA	1.97	0.46
2:B:305:HIS:HB2	2:B:591:ILE:HG22	1.98	0.46
2:B:887:LYS:N	2:B:888:ARG:HA	2.31	0.46
1:A:628:LEU:HD13	1:A:633:LEU:HD21	1.97	0.46
2:B:797:ILE:CD1	2:B:797:ILE:H	2.28	0.45
1:A:565:ASN:O	1:A:569:LYS:HB2	2.16	0.45
1:A:785:VAL:HG11	1:A:880:LEU:HB2	1.97	0.45
2:B:850:LEU:O	2:B:853:LEU:HB2	2.16	0.44
1:A:850:LEU:O	1:A:853:LEU:HB2	2.16	0.44
1:A:401:LYS:O	1:A:405:ASN:HB2	2.17	0.43
1:A:310:VAL:HB	1:A:311:LYS:CA	2.48	0.43
2:B:764:LEU:HD12	2:B:803:TRP:HB3	2.01	0.43
2:B:395:ARG:HG3	2:B:431:TRP:CZ2	2.54	0.42
1:A:301:THR:CG2	1:A:594:ARG:NH1	2.68	0.42
2:B:884:PRO:HA	2:B:887:LYS:HA	2.01	0.42
1:A:646:TRP:CZ2	1:A:654:ARG:HG3	2.55	0.41
2:B:618:LEU:HA	2:B:618:LEU:HD23	1.96	0.41
1:A:307:SER:HA	1:A:589:MET:O	2.20	0.41
1:A:368:GLY:O	1:A:372:VAL:HG23	2.21	0.41
1:A:433:LEU:HD23	1:A:436:ARG:HE	1.86	0.41
1:A:863:ILE:HA	1:A:863:ILE:HD13	2.00	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:851:ILE:HG23	1:A:856:ARG:CZ	2.51	0.41
2:B:646:TRP:CZ2	2:B:654:ARG:HG3	2.56	0.41
2:B:562:GLN:HG3	4:B:2030:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	590/638 (92%)	564 (96%)	22 (4%)	4 (1%)	30	58
2	B	597/638 (94%)	576 (96%)	15 (2%)	6 (1%)	22	45
All	All	1187/1276 (93%)	1140 (96%)	37 (3%)	10 (1%)	27	53

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	742	GLN
1	A	310	VAL
1	A	651	GLY
2	B	651	GLY
2	B	743	GLY
1	A	551	LYS
2	B	551	LYS
2	B	791	SER
1	A	791	SER
2	B	406	ALA

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	520/555 (94%)	483 (93%)	37 (7%)	21	40
2	B	516/555 (93%)	481 (93%)	35 (7%)	22	43
All	All	1036/1110 (93%)	964 (93%)	72 (7%)	22	42

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	301	THR
1	A	310	VAL
1	A	317	SER
1	A	318	SER
1	A	326	LEU
1	A	352	ARG
1	A	355	LYS
1	A	374	GLU
1	A	389[A]	ARG
1	A	389[B]	ARG
1	A	400	LYS
1	A	426	GLU
1	A	443	LEU
1	A	450	VAL
1	A	453	MET
1	A	478	LEU
1	A	481	ARG
1	A	492	ASN
1	A	581	ARG
1	A	585	THR
1	A	594	ARG
1	A	639	LEU
1	A	641	LYS
1	A	650	LYS
1	A	676	ASN
1	A	698	LYS
1	A	710	SER
1	A	749	ARG
1	A	802	GLN
1	A	841	LYS
1	A	842	ARG
1	A	851	ILE
1	A	863	ILE
1	A	873	LEU
1	A	878	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	880	LEU
1	A	887	LYS
2	B	270	THR
2	B	301	THR
2	B	317	SER
2	B	318	SER
2	B	326	LEU
2	B	329	LYS
2	B	338	THR
2	B	342	MET
2	B	355	LYS
2	B	361	ARG
2	B	374	GLU
2	B	389	ARG
2	B	400	LYS
2	B	419	ASP
2	B	433	LEU
2	B	435	ASP
2	B	443	LEU
2	B	450	VAL
2	B	481	ARG
2	B	575	LYS
2	B	581	ARG
2	B	585	THR
2	B	594	ARG
2	B	642	LYS
2	B	650	LYS
2	B	676	ASN
2	B	698	LYS
2	B	710	SER
2	B	746	TRP
2	B	749	ARG
2	B	802	GLN
2	B	841	LYS
2	B	863	ILE
2	B	878	GLU
2	B	888	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	339	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	555	GLN
1	A	562	GLN
1	A	621	GLN
1	A	682	ASN
1	A	704	GLN
1	A	760	GLN
1	A	768	HIS
1	A	802	GLN
1	A	835	ASN
2	B	339	GLN
2	B	452	ASN
2	B	548	ASN
2	B	555	GLN
2	B	621	GLN
2	B	682	ASN
2	B	704	GLN
2	B	742	GLN
2	B	760	GLN
2	B	768	HIS
2	B	802	GLN
2	B	835	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers (i)

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	593/638 (92%)	-0.07	30 (5%)	27	23	28, 55, 98, 152	11 (1%)
2	B	603/638 (94%)	0.16	43 (7%)	16	12	32, 66, 118, 155	11 (1%)
All	All	1196/1276 (93%)	0.05	73 (6%)	21	17	28, 60, 111, 155	22 (1%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	455	ALA	11.6
2	B	470	SER	7.4
2	B	637	HIS	7.4
1	A	472	ALA	6.7
2	B	744	ALA	6.3
1	A	744	ALA	6.1
1	A	746	TRP	5.8
2	B	745	GLY	5.6
1	A	313	THR	5.3
2	B	316	ALA	5.1
1	A	474	TRP	5.1
2	B	317	SER	4.9
1	A	473	ILE	4.9
2	B	410	ALA	4.7
1	A	315	SER	4.7
2	B	473	ILE	4.7
2	B	638	LEU	4.5
2	B	743	GLY	4.3
2	B	472	ALA	4.3
2	B	636	PRO	4.2
1	A	316	ALA	4.2
2	B	417	GLN	4.2
2	B	268	PRO	4.1
1	A	745	GLY	4.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	317	SER	4.0
2	B	416	ASN	4.0
2	B	419	ASP	4.0
1	A	314	GLY	4.0
1	A	743	GLY	3.7
2	B	296	GLU	3.7
1	A	795	TRP	3.7
1	A	268	PRO	3.7
2	B	409	ALA	3.7
1	A	343	THR	3.6
1	A	470	SER	3.5
2	B	269	GLU	3.5
2	B	420	SER	3.4
2	B	585	THR	3.4
2	B	315	SER	3.3
2	B	314	GLY	3.2
2	B	288	ASN	3.2
2	B	345	THR	3.1
2	B	274	ASP	3.1
1	A	886	MET	3.0
2	B	591	ILE	3.0
2	B	474	TRP	2.9
2	B	763	SER	2.9
1	A	742	GLN	2.9
1	A	876	ASN	2.8
1	A	471	ARG	2.8
2	B	289	SER	2.8
2	B	293	TYR	2.8
2	B	600	SER	2.7
2	B	344	ASP	2.7
2	B	270	THR	2.7
1	A	637	HIS	2.6
2	B	343	THR	2.6
2	B	742	GLN	2.6
1	A	792	ARG	2.5
2	B	429	GLU	2.5
1	A	885	SER	2.5
1	A	636	PRO	2.5
1	A	601	GLY	2.4
2	B	795	TRP	2.3
1	A	269	GLU	2.2
2	B	418	TRP	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	408	MET	2.1
1	A	311	LYS	2.1
1	A	345	THR	2.1
1	A	318	SER	2.1
1	A	420	SER	2.0
2	B	592	ILE	2.0
2	B	290	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 ⓘ

There are no carbohydrates in this entry.

6.4   Ligands ⓘ

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	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	ZN	A	1890	1/1	0.09	-0.43	49,49,49,49	0
3	ZN	B	1891	1/1	0.05	-1.86	73,73,73,73	0
3	ZN	A	1889	1/1	0.04	-2.02	53,53,53,53	0
3	ZN	B	1890	1/1	0.06	-3.43	50,50,50,50	0

6.5   Other polymers ⓘ

There are no such residues in this entry.