



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 21, 2022 – 02:26 PM EDT

PDB ID : 7R73
Title : Crystal structure of llama VHH antibody D7 in complex with HIV-1 gp120 core
Authors : Zhou, T.; Kwong, P.D.
Deposited on : 2021-06-24
Resolution : 1.76 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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	:	2.27
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)	:	2.27

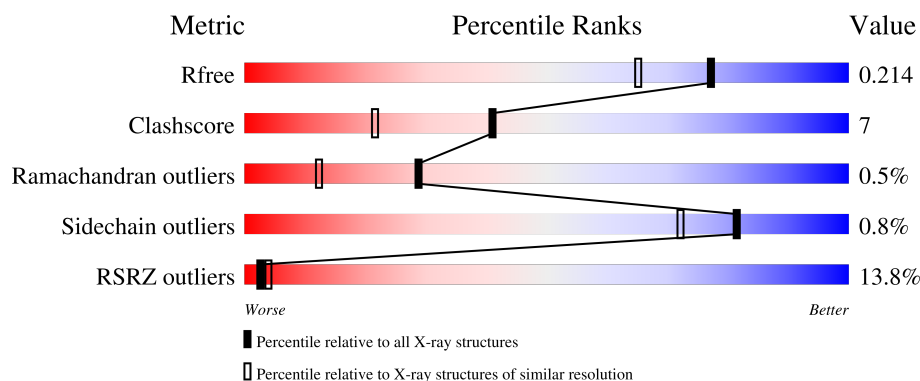
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 $\leq 5\%$. 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	G	358	
2	A	127	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	G	506	-	-	-	X
3	NAG	G	507	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6693 atoms, of which 3171 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.

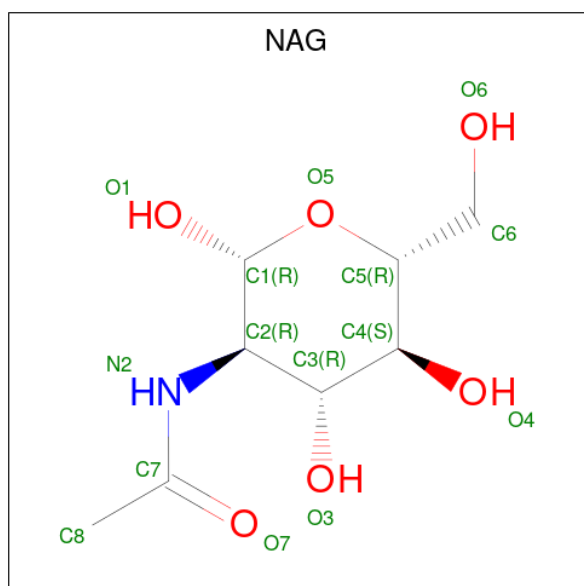
- Molecule 1 is a protein called Glycoprotein 120.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	G	287	Total	C	H	N	O	S	0	0	0
			4466	1433	2184	403	429	17			

- Molecule 2 is a protein called Llama antibody D7.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	126	Total	C	H	N	O	S	0	0	0
			1877	602	905	173	193	4			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	G	1	Total	C	H	N	O		0	0
			28	8	14	1	5			
3	G	1	Total	C	H	N	O		0	0
			28	8	14	1	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	G	1	Total	C	H	N	O	0	0
			26	8	12	1	5		
3	G	1	Total	C	N	O		0	0
			14	8	1	5			
3	G	1	Total	C	N	O		0	0
			14	8	1	5			

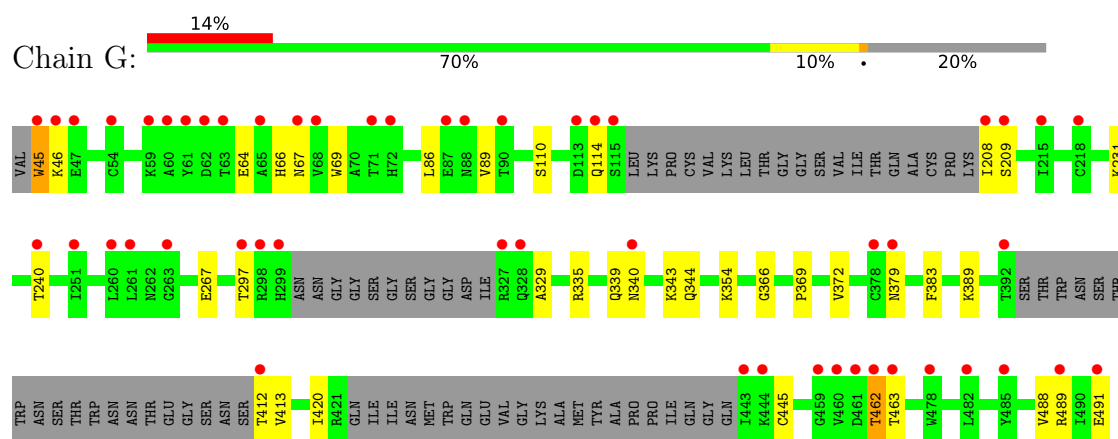
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	110	Total	O	0	0
			110	110		
4	A	46	Total	O	0	0
			46	46		

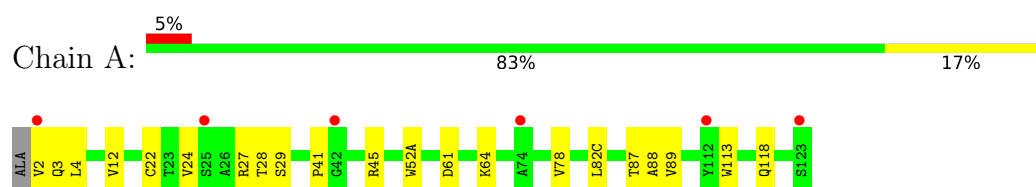
3 Residue-property plots [i](#)

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: Glycoprotein 120



• Molecule 2: Llama antibody D7



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	130.54Å 61.95Å 63.98Å 90.00° 108.16° 90.00°	Depositor
Resolution (Å)	31.44 – 1.76 31.44 – 1.76	Depositor EDS
% Data completeness (in resolution range)	91.7 (31.44-1.76) 91.7 (31.44-1.76)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 1.76Å)	Xtriage
Refinement program	PHENIX 1.19-4092	Depositor
R, R_{free}	0.179 , 0.215 0.178 , 0.214	Depositor DCC
R_{free} test set	2238 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6693	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.51% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5.1 Standard geometry

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

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	G	0.56	0/2328	0.72	0/3152
2	A	0.75	0/994	0.81	0/1347
All	All	0.63	0/3322	0.75	0/4499

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

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	G	2282	2184	2218	28	0
2	A	972	905	918	15	0
3	G	112	82	104	5	0
4	A	46	0	0	2	0
4	G	110	0	0	4	0
All	All	3522	3171	3240	47	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 7.

All (47) 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)
3:G:507:NAG:H83	3:G:507:NAG:H3	1.36	1.05
3:G:507:NAG:H3	3:G:507:NAG:C8	2.03	0.86
2:A:41:PRO:O	4:A:201:HOH:O	1.94	0.85
3:G:507:NAG:H83	3:G:507:NAG:C3	2.16	0.75
1:G:462:THR:HG22	1:G:463:THR:H	1.53	0.74
1:G:412:THR:HG23	1:G:413:VAL:H	1.52	0.73
2:A:28:THR:HG21	2:A:52(A):TRP:NE1	2.08	0.68
1:G:366:GLY:HA2	4:G:657:HOH:O	1.94	0.66
1:G:46:LYS:HE3	1:G:489:ARG:HH22	1.61	0.66
1:G:354:LYS:HB3	3:G:504:NAG:H82	1.80	0.63
1:G:64:GLU:OE1	1:G:67:ASN:ND2	2.34	0.61
1:G:110:SER:O	1:G:114:GLN:HG2	2.02	0.59
2:A:4:LEU:HD22	2:A:24:VAL:HG22	1.84	0.59
2:A:4:LEU:CD2	2:A:24:VAL:HG22	2.34	0.57
1:G:412:THR:HG23	1:G:413:VAL:N	2.19	0.57
1:G:369:PRO:O	1:G:372:VAL:HG22	2.06	0.56
1:G:462:THR:HG22	1:G:463:THR:N	2.19	0.55
3:G:503:NAG:N2	4:G:601:HOH:O	2.09	0.54
1:G:69:TRP:HD1	1:G:114:GLN:HG3	1.73	0.53
2:A:27:ARG:O	4:A:202:HOH:O	2.18	0.53
1:G:231:LYS:HE2	1:G:267:GLU:HB3	1.91	0.52
2:A:28:THR:HG21	2:A:52(A):TRP:HE1	1.73	0.51
1:G:335:ARG:NH2	4:G:606:HOH:O	2.44	0.51
1:G:45:TRP:HH2	1:G:86:LEU:CD1	2.25	0.50
1:G:89:VAL:O	1:G:240:THR:O	2.32	0.47
1:G:389:LYS:HG3	4:G:633:HOH:O	2.15	0.47
1:G:45:TRP:HD1	1:G:45:TRP:O	1.98	0.47
2:A:2:VAL:O	2:A:3:GLN:HB2	2.15	0.47
1:G:335:ARG:O	1:G:339:GLN:HG3	2.16	0.46
1:G:489:ARG:HG3	1:G:491:GLU:HG2	1.98	0.46
2:A:61:ASP:HA	2:A:64:LYS:HE3	1.98	0.46
2:A:28:THR:CG2	2:A:29:SER:N	2.79	0.45
1:G:383:PHE:CE2	1:G:420:ILE:HD11	2.52	0.45
1:G:45:TRP:O	1:G:45:TRP:CD1	2.71	0.44
1:G:297:THR:O	1:G:329:ALA:HB1	2.18	0.44
2:A:28:THR:CG2	2:A:52(A):TRP:NE1	2.80	0.43
1:G:64:GLU:OE2	1:G:66:HIS:HB2	2.18	0.43
2:A:12:VAL:HG21	2:A:82(C):LEU:HD13	2.01	0.43
1:G:45:TRP:HB2	1:G:488:VAL:HB	2.01	0.43
1:G:340:ASN:O	1:G:344:GLN:HG3	2.20	0.42
2:A:22:CYS:HB3	2:A:78:VAL:HG13	2.02	0.42
1:G:208:ILE:HD12	1:G:208:ILE:HA	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:87:THR:O	2:A:88:ALA:HB2	2.21	0.41
1:G:46:LYS:HE3	1:G:489:ARG:NH2	2.33	0.41
1:G:64:GLU:HG2	1:G:209:SER:O	2.21	0.40
2:A:89:VAL:HG22	2:A:118:GLN:OE1	2.22	0.40
2:A:45:ARG:HD3	2:A:113:TRP:CZ3	2.56	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	G	277/358 (77%)	266 (96%)	9 (3%)	2 (1%)	22	8
2	A	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
All	All	401/485 (83%)	388 (97%)	11 (3%)	2 (0%)	29	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	379	ASN
1	G	462	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	G	259/317 (82%)	256 (99%)	3 (1%)	71	56
2	A	104/104 (100%)	104 (100%)	0	100	100
All	All	363/421 (86%)	360 (99%)	3 (1%)	81	72

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	45	TRP
1	G	343	LYS
1	G	445	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	299	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](#)

8 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
3	NAG	G	508	1	14,14,15	0.31	0	17,19,21	0.40	0
3	NAG	G	502	1	14,14,15	0.23	0	17,19,21	0.72	1 (5%)
3	NAG	G	506	1	14,14,15	0.33	0	17,19,21	0.56	0
3	NAG	G	504	1	14,14,15	0.36	0	17,19,21	0.48	0
3	NAG	G	507	1	14,14,15	0.64	1 (7%)	17,19,21	1.12	2 (11%)
3	NAG	G	505	1	14,14,15	0.68	1 (7%)	17,19,21	0.70	0
3	NAG	G	503	1	14,14,15	0.33	0	17,19,21	0.42	0
3	NAG	G	501	1	14,14,15	0.91	1 (7%)	17,19,21	0.87	1 (5%)

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
3	NAG	G	508	1	-	0/6/23/26	0/1/1/1
3	NAG	G	502	1	-	0/6/23/26	0/1/1/1
3	NAG	G	506	1	-	3/6/23/26	0/1/1/1
3	NAG	G	504	1	-	0/6/23/26	0/1/1/1
3	NAG	G	507	1	-	5/6/23/26	0/1/1/1
3	NAG	G	505	1	-	0/6/23/26	0/1/1/1
3	NAG	G	503	1	-	0/6/23/26	0/1/1/1
3	NAG	G	501	1	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	501	NAG	O5-C1	3.14	1.48	1.43
3	G	505	NAG	O5-C1	2.41	1.47	1.43
3	G	507	NAG	C1-C2	2.30	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	507	NAG	C1-O5-C5	3.27	116.62	112.19
3	G	501	NAG	C1-O5-C5	3.08	116.36	112.19
3	G	502	NAG	C1-O5-C5	2.58	115.68	112.19
3	G	507	NAG	C2-N2-C7	2.27	126.14	122.90

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	507	NAG	C3-C2-N2-C7
3	G	507	NAG	C8-C7-N2-C2
3	G	507	NAG	O7-C7-N2-C2
3	G	506	NAG	O5-C5-C6-O6
3	G	501	NAG	O5-C5-C6-O6
3	G	506	NAG	C4-C5-C6-O6
3	G	506	NAG	C3-C2-N2-C7
3	G	501	NAG	C4-C5-C6-O6
3	G	507	NAG	O5-C5-C6-O6
3	G	507	NAG	C4-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	504	NAG	1	0
3	G	507	NAG	3	0
3	G	503	NAG	1	0

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

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	G	287/358 (80%)	1.06	51 (17%) 1 2	29, 52, 99, 119	0
2	A	126/127 (99%)	0.36	6 (4%) 30 36	28, 40, 69, 94	0
All	All	413/485 (85%)	0.85	57 (13%) 2 4	28, 48, 93, 119	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	443	ILE	15.9
1	G	208	ILE	15.7
1	G	460	VAL	14.5
2	A	2	VAL	8.9
1	G	61	TYR	8.8
1	G	461	ASP	6.9
1	G	328	GLN	6.7
1	G	463	THR	6.7
1	G	491	GLU	5.9
2	A	42	GLY	5.8
1	G	115	SER	5.5
1	G	63	THR	5.3
1	G	299	HIS	5.3
1	G	60	ALA	5.2
1	G	88	ASN	5.2
1	G	87	GLU	4.7
1	G	462	THR	4.7
1	G	459	GLY	4.5
1	G	62	ASP	4.4
1	G	72	HIS	4.1
1	G	327	ARG	3.8
1	G	45	TRP	3.6
1	G	59	LYS	3.6
1	G	444	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
1	G	240	THR	3.5
1	G	114	GLN	3.5
1	G	298	ARG	3.5
1	G	68	VAL	3.4
1	G	209	SER	3.1
1	G	71	THR	2.9
1	G	46	LYS	2.8
1	G	412	THR	2.8
2	A	112	TYR	2.4
1	G	90	THR	2.4
1	G	478	TRP	2.4
1	G	54	CYS	2.4
1	G	378	CYS	2.4
1	G	251	ILE	2.3
1	G	297	THR	2.3
1	G	260	LEU	2.3
1	G	482	LEU	2.2
1	G	65	ALA	2.2
1	G	379	ASN	2.2
1	G	261	LEU	2.2
1	G	215	ILE	2.2
1	G	113	ASP	2.2
1	G	218	CYS	2.1
2	A	74	ALA	2.1
1	G	340	ASN	2.1
1	G	485	TYR	2.1
1	G	489	ARG	2.1
2	A	123	SER	2.1
1	G	392	THR	2.1
1	G	263	GLY	2.1
1	G	67	ASN	2.1
2	A	25	SER	2.0
1	G	47	GLU	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 monosaccharides 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. 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
3	NAG	G	506	14/15	0.72	0.46	89,99,117,121	0
3	NAG	G	507	14/15	0.73	0.40	78,81,89,96	0
3	NAG	G	503	14/15	0.74	0.27	71,87,106,114	0
3	NAG	G	508	14/15	0.76	0.23	83,122,151,153	0
3	NAG	G	505	14/15	0.89	0.11	38,49,68,79	0
3	NAG	G	502	14/15	0.89	0.13	68,77,90,93	0
3	NAG	G	504	14/15	0.94	0.10	56,73,103,103	0
3	NAG	G	501	14/15	0.95	0.10	42,53,70,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.