



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 22, 2026 – 02:01 AM UTC

PDB ID : 7AMQ / pdb_00007amq
Title : Crystal structure of the complex of HuJovi-1 Fab with the human TRBC2
Authors : Ferrari, M.; Bulek, A.; Bughda, R.; Jha, R.; Welin, M.; Logan, D.T.; Sewell, A.; Onuoha, S.; Pule, M.
Deposited on : 2020-10-09
Resolution : 2.35 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

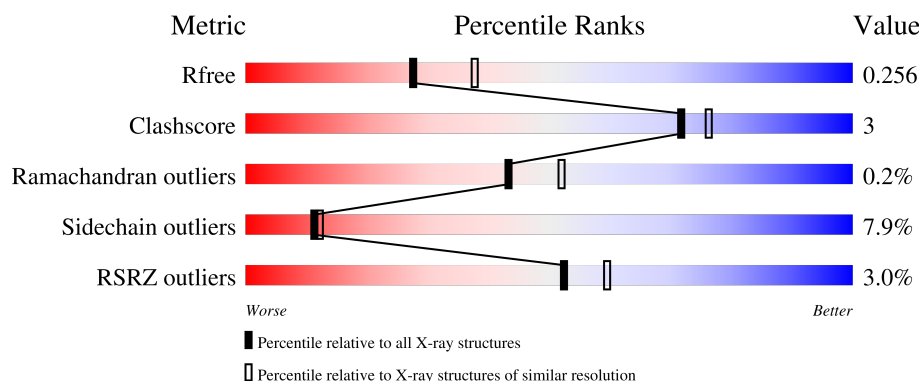
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	A	200	4% 82% 14% ..
2	B	246	4% 82% 13% ..
3	H	225	2% 84% 12% .
4	L	219	% 89% 7% ..

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7157 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 Human A6 T-cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	S	0	0	0
			1517	942	249	318	8			

- Molecule 2 is a protein called Human A6 T-cell receptor beta chain TRBC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	240	Total	C	N	O	S	0	0	0
			1902	1195	332	366	9			

- Molecule 3 is a protein called Human Jovi-1 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	218	Total	C	N	O	S	0	0	0
			1665	1054	283	319	9			

- Molecule 4 is a protein called Human Jovi-1 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	217	Total	C	N	O	S	0	0	0
			1684	1056	291	332	5			

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Zn	0	0
			1	1		
5	L	2	Total	Zn	0	0
			2	2		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	1	Total Cl 1 1	0	0
6	L	1	Total Cl 1 1	0	0

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	1	Total C O 6 3 3	0	0

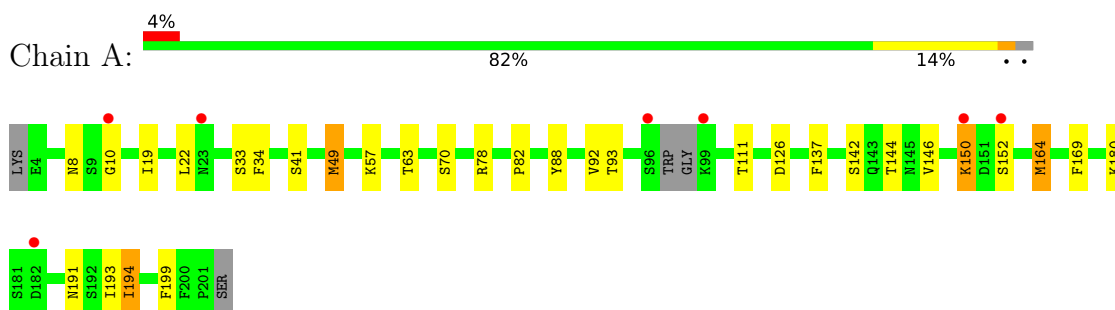
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	65	Total O 65 65	0	0
8	B	115	Total O 115 115	0	0
8	H	95	Total O 95 95	0	0
8	L	103	Total O 103 103	0	0

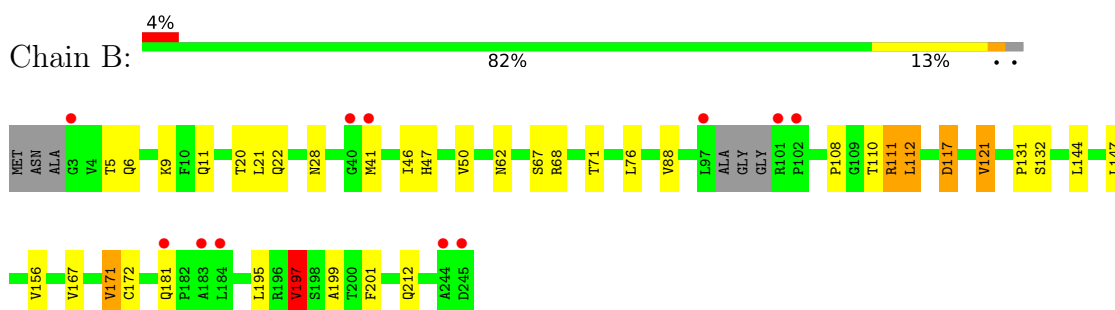
3 Residue-property plots [i](#)

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.

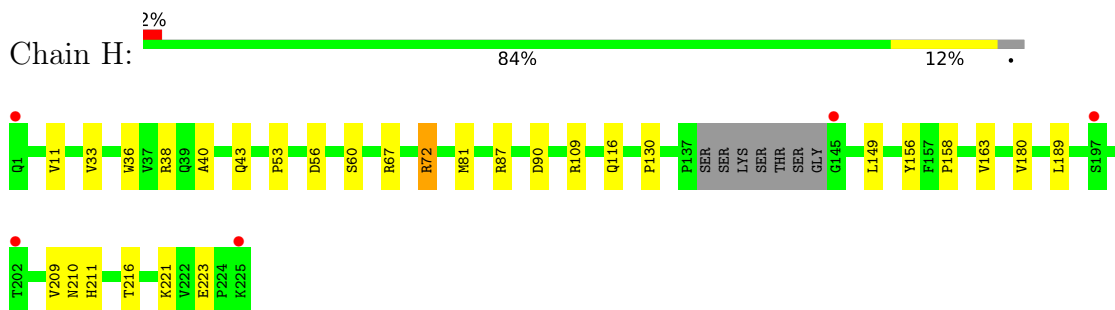
- Molecule 1: Human A6 T-cell receptor alpha chain



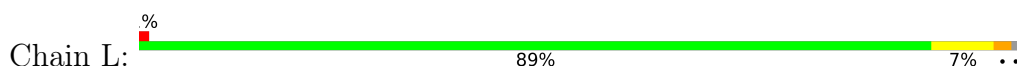
- Molecule 2: Human A6 T-cell receptor beta chain TRBC1

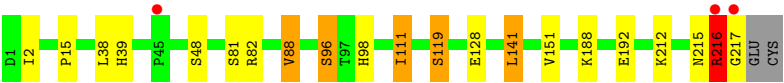


- Molecule 3: Human Jovi-1 Fab heavy chain



- Molecule 4: Human Jovi-1 Fab light chain





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	114.51Å 91.79Å 123.39Å 90.00° 94.62° 90.00°	Depositor
Resolution (Å)	47.84 – 2.35 47.84 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.84-2.35) 99.6 (47.84-2.35)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.34Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.201 , 0.249 0.204 , 0.256	Depositor DCC
R_{free} test set	2644 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.814	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7157	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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: CL, ZN, GOL

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	0.76	1/1547 (0.1%)	1.06	5/2098 (0.2%)
2	B	0.71	0/1954	1.05	5/2661 (0.2%)
3	H	0.71	0/1707	1.00	0/2320
4	L	0.72	0/1724	1.00	1/2343 (0.0%)
All	All	0.73	1/6932 (0.0%)	1.03	11/9422 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	164	MET	SD-CE	-6.09	1.64	1.79

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	126	ASP	CA-CB-CG	6.68	119.28	112.60
2	B	197	VAL	N-CA-CB	-6.34	100.63	112.36
2	B	121	VAL	N-CA-CB	6.25	117.34	110.53
1	A	8	ASN	CA-CB-CG	6.05	118.65	112.60
1	A	82	PRO	CA-C-N	5.59	128.33	120.28
1	A	82	PRO	C-N-CA	5.59	128.33	120.28
2	B	199	ALA	CA-C-N	5.47	127.61	120.28
2	B	199	ALA	C-N-CA	5.47	127.61	120.28
1	A	199	PHE	CA-CB-CG	5.20	119.00	113.80
4	L	119	SER	N-CA-C	-5.13	100.81	108.96
2	B	117	ASP	CA-CB-CG	5.08	117.67	112.60

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	A	1517	0	1423	13	0
2	B	1902	0	1803	9	0
3	H	1665	0	1617	11	0
4	L	1684	0	1646	12	0
5	H	1	0	0	0	0
5	L	2	0	0	0	0
6	H	1	0	0	0	0
6	L	1	0	0	0	0
7	L	6	0	8	0	0
8	A	65	0	0	0	1
8	B	115	0	0	0	0
8	H	95	0	0	0	0
8	L	103	0	0	1	0
All	All	7157	0	6497	44	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 3.

All (44) 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:H:11:VAL:HB	3:H:158:PRO:HG3	1.63	0.80
4:L:215:ASN:O	4:L:216:ARG:HB2	1.87	0.73
1:A:150:LYS:HD3	1:A:150:LYS:H	1.58	0.68
1:A:33:SER:HB2	1:A:93:THR:HG22	1.73	0.68
2:B:11:GLN:HB3	2:B:112:LEU:HD12	1.77	0.67
4:L:88:VAL:HG13	4:L:111:ILE:HG23	1.78	0.66
1:A:63:THR:OG1	1:A:78:ARG:NH1	2.23	0.62
3:H:109:ARG:HB3	4:L:96:SER:HB3	1.84	0.59
2:B:6:GLN:HB2	2:B:108:PRO:HD2	1.84	0.58
3:H:130:PRO:HD2	3:H:216:THR:HG21	1.88	0.56
1:A:19:ILE:HG12	1:A:78:ARG:HA	1.88	0.56
1:A:164:MET:HE3	1:A:169:PHE:HD1	1.71	0.54
1:A:150:LYS:H	1:A:150:LYS:CD	2.21	0.54
4:L:2:ILE:CD1	4:L:98:HIS:CD2	2.92	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:15:PRO:HG3	4:L:111:ILE:HD13	1.90	0.53
1:A:164:MET:HE3	1:A:169:PHE:CD1	2.45	0.51
2:B:21:LEU:HD22	2:B:110:THR:HG21	1.94	0.50
1:A:63:THR:HG1	1:A:78:ARG:HH12	1.53	0.50
3:H:211:HIS:HB3	3:H:216:THR:HB	1.94	0.50
2:B:197:VAL:HG13	2:B:201:PHE:HB3	1.94	0.50
1:A:111:THR:HB	1:A:142:SER:HB3	1.93	0.48
3:H:67:ARG:NH1	3:H:90:ASP:OD2	2.44	0.48
4:L:192:GLU:HA	4:L:217:GLY:C	2.39	0.48
3:H:36:TRP:CE2	3:H:81:MET:HB2	2.49	0.48
2:B:171:VAL:HG12	2:B:195:LEU:HD13	1.98	0.46
1:A:22:LEU:HD22	1:A:88:TYR:HB2	1.98	0.46
1:A:34:PHE:HD1	1:A:92:VAL:HG22	1.81	0.46
2:B:131:PRO:HD3	2:B:144:LEU:HG	1.97	0.46
1:A:49:MET:HE1	1:A:57:LYS:HG2	1.97	0.45
2:B:46:ILE:HG22	2:B:47:HIS:CD2	2.51	0.45
2:B:21:LEU:HD12	2:B:76:LEU:HD23	1.99	0.45
2:B:88:VAL:HG22	2:B:111:ARG:HG2	1.99	0.45
3:H:53:PRO:HA	3:H:72:ARG:HD2	1.99	0.45
3:H:109:ARG:HD3	8:L:633:HOH:O	2.17	0.44
4:L:2:ILE:HD11	4:L:98:HIS:CD2	2.53	0.44
4:L:39:HIS:HE2	4:L:96:SER:HB2	1.83	0.44
4:L:2:ILE:HD12	4:L:98:HIS:CD2	2.53	0.44
4:L:141:LEU:HD11	4:L:151:VAL:HG22	1.99	0.43
3:H:40:ALA:HB3	3:H:43:GLN:HG3	2.00	0.43
1:A:137:PHE:CZ	1:A:194:ILE:HG12	2.55	0.42
3:H:130:PRO:HB3	3:H:156:TYR:HB3	2.02	0.41
4:L:212:LYS:HD3	4:L:212:LYS:HA	1.93	0.41
3:H:163:VAL:HG22	3:H:209:VAL:HG22	2.03	0.40
4:L:2:ILE:HD12	4:L:98:HIS:HD2	1.86	0.40

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)
8:A:316:HOH:O	8:A:316:HOH:O[2_556]	0.95	1.25

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	192/200 (96%)	189 (98%)	2 (1%)	1 (0%)	24	27
2	B	236/246 (96%)	232 (98%)	4 (2%)	0	100	100
3	H	214/225 (95%)	209 (98%)	5 (2%)	0	100	100
4	L	215/219 (98%)	211 (98%)	3 (1%)	1 (0%)	24	27
All	All	857/890 (96%)	841 (98%)	14 (2%)	2 (0%)	43	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L	216	ARG
1	A	10	GLY

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	175/178 (98%)	164 (94%)	11 (6%)	16	19
2	B	208/210 (99%)	184 (88%)	24 (12%)	5	5
3	H	183/189 (97%)	170 (93%)	13 (7%)	13	15
4	L	194/196 (99%)	182 (94%)	12 (6%)	16	19
All	All	760/773 (98%)	700 (92%)	60 (8%)	11	12

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	SER
1	A	49	MET
1	A	70	SER
1	A	144	THR
1	A	146	VAL
1	A	150	LYS
1	A	152	SER
1	A	180	LYS
1	A	191	ASN
1	A	193	ILE
1	A	194	ILE
2	B	5	THR
2	B	9	LYS
2	B	20	THR
2	B	22	GLN
2	B	28	ASN
2	B	41	MET
2	B	50	VAL
2	B	62	ASN
2	B	67	SER
2	B	68	ARG
2	B	71	THR
2	B	111	ARG
2	B	112	LEU
2	B	117	ASP
2	B	121	VAL
2	B	132	SER
2	B	147	LEU
2	B	156	VAL
2	B	167	VAL
2	B	171	VAL
2	B	172	CYS
2	B	181	GLN
2	B	197	VAL
2	B	212	GLN
3	H	33	VAL
3	H	38	ARG
3	H	56	ASP
3	H	60	SER
3	H	72	ARG
3	H	87	ARG
3	H	116	GLN
3	H	149	LEU

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Mol	Chain	Res	Type
3	H	180	VAL
3	H	189	LEU
3	H	210	ASN
3	H	221	LYS
3	H	223	GLU
4	L	38	LEU
4	L	48	SER
4	L	81	SER
4	L	82	ARG
4	L	88	VAL
4	L	96	SER
4	L	111	ILE
4	L	119	SER
4	L	128	GLU
4	L	141	LEU
4	L	188	LYS
4	L	216	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	ASN
1	A	145	ASN
3	H	39	GLN
4	L	43	GLN
4	L	98	HIS
4	L	142	ASN
4	L	152	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
7	GOL	L	501	-	5,5,5	0.22	0	5,5,5	0.32	0

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
7	GOL	L	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	L	501	GOL	C1-C2-C3-O3
7	L	501	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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	196/200 (98%)	0.44	7 (3%) 46 52	42, 57, 78, 95	0
2	B	240/246 (97%)	0.32	11 (4%) 37 43	39, 55, 78, 94	0
3	H	218/225 (96%)	0.26	5 (2%) 61 66	41, 52, 72, 81	0
4	L	217/219 (99%)	0.07	3 (1%) 73 78	39, 50, 62, 72	0
All	All	871/890 (97%)	0.27	26 (2%) 52 59	39, 53, 76, 95	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	97	LEU	5.0
3	H	225	LYS	3.5
1	A	10	GLY	3.4
4	L	45	PRO	3.4
2	B	101	ARG	3.2
2	B	184	LEU	3.1
2	B	3	GLY	3.1
2	B	102	PRO	3.0
4	L	217	GLY	2.9
1	A	99	LYS	2.8
3	H	145	GLY	2.8
1	A	150	LYS	2.6
2	B	40	GLY	2.5
1	A	23	ASN	2.4
1	A	182	ASP	2.4
3	H	197	SER	2.4
4	L	216	ARG	2.3
2	B	181	GLN	2.3
3	H	202	THR	2.3
1	A	96	SER	2.2
3	H	1	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	152	SER	2.2
2	B	244	ALA	2.1
2	B	41	MET	2.0
2	B	183	ALA	2.0
2	B	245	ASP	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
6	CL	L	504	1/1	0.86	0.25	95,95,95,95	0
6	CL	H	302	1/1	0.92	0.19	79,79,79,79	0
7	GOL	L	501	6/6	0.92	0.12	53,53,53,53	0
5	ZN	H	301	1/1	0.99	0.05	51,51,51,51	0
5	ZN	L	502	1/1	0.99	0.07	52,52,52,52	0
5	ZN	L	503	1/1	0.99	0.18	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.