



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:35 PM UTC

PDB ID : 7NAB / pdb_00007nab
Title : Crystal structure of human neutralizing mAb CV3-25 binding to SARS-CoV-2 S MPER peptide 1140-1165
Authors : Chen, Y.; Tolbert, W.D.; Pazgier, M.
Deposited on : 2021-06-21
Resolution : 2.15 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

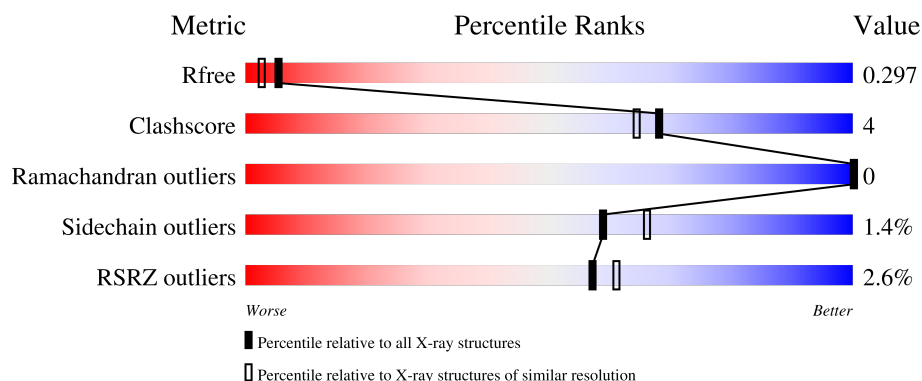
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	227	4% 87% 11% .
1	H	227	4% 91% 8%
2	B	213	92% 8%
2	L	213	% 92% 8%
3	C	27	7% 74% 22% .

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Mol	Chain	Length	Quality of chain
3	D	27	7% 74% 22%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7556 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 CV3-25 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	226	Total	C	N	O	S	0	1	0
			1719	1092	285	333	9			
1	A	226	Total	C	N	O	S	0	0	0
			1713	1089	284	331	9			

- Molecule 2 is a protein called CV3-25 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	0	0
			1627	1020	272	331	4			
2	B	213	Total	C	N	O	S	0	0	0
			1627	1020	272	331	4			

- Molecule 3 is a protein called Spike protein S2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	21	Total	C	N	O	0	0	1
			171	107	27	37			
3	C	21	Total	C	N	O	0	0	1
			171	107	27	37			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1166	NH2	-	amidation	UNP P0DTC2
C	1166	NH2	-	amidation	UNP P0DTC2

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

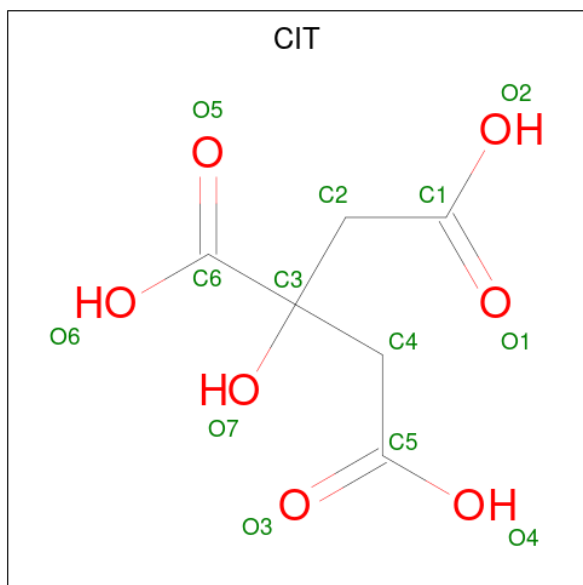
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	3	Total	Na	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	7	Total	Na	0	0
			7	7		
4	A	2	Total	Na	0	0
			2	2		
4	B	4	Total	Na	0	0
			4	4		

- Molecule 5 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	130	Total	O	0	0
			130	130		
6	L	130	Total	O	0	0
			130	130		
6	A	114	Total	O	0	0
			114	114		
6	B	112	Total	O	0	0
			112	112		
6	D	8	Total	O	0	0
			8	8		

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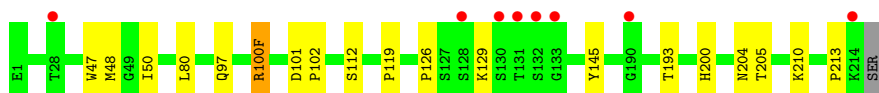
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	5	Total	O	0	0
			5	5		

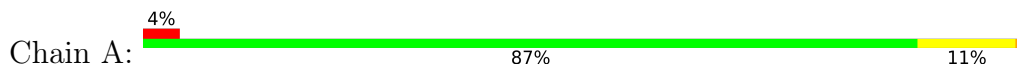
3 Residue-property plots [i](#)

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: CV3-25 Fab Heavy Chain



- Molecule 1: CV3-25 Fab Heavy Chain



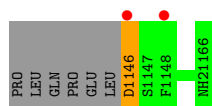
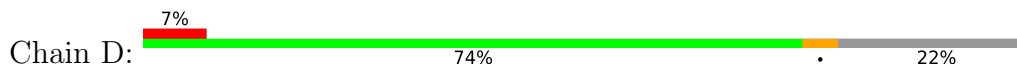
- Molecule 2: CV3-25 Fab Light Chain



- Molecule 2: CV3-25 Fab Light Chain

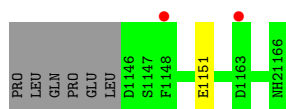


- Molecule 3: Spike protein S2



- Molecule 3: Spike protein S2

Chain C:  7% 74% 22%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.76Å 85.24Å 87.07Å 90.00° 114.77° 90.00°	Depositor
Resolution (Å)	38.56 – 2.15 38.56 – 2.15	Depositor EDS
% Data completeness (in resolution range)	95.9 (38.56-2.15) 93.4 (38.56-2.15)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.185 , 0.238 (Not available) , 0.297	Depositor DCC
R_{free} test set	2008 reflections (3.47%)	wwPDB-VP
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 34.5	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	0.96	EDS
Total number of atoms	7556	wwPDB-VP
Average B, all atoms (Å ²)	45.0	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 80.17 % 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 4.7443e-07. 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: NA, CIT, NH2

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	0/1761	0.97	10/2400 (0.4%)
1	H	0.45	0/1767	0.66	2/2408 (0.1%)
2	B	0.40	0/1663	0.59	2/2260 (0.1%)
2	L	0.42	0/1663	0.59	0/2260
3	C	0.26	0/174	0.41	0/233
3	D	0.35	0/174	0.49	0/233
All	All	0.52	0/7202	0.71	14/9794 (0.1%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	SER	N-CA-C	-12.28	99.09	113.21
1	A	130	SER	N-CA-C	-11.99	97.72	111.03
1	A	100(F)	ARG	N-CA-C	7.11	120.53	109.52
1	A	21	SER	N-CA-C	6.22	119.68	109.72
1	A	97	GLN	N-CA-C	6.18	118.81	109.23
1	H	100(F)	ARG	N-CA-C	6.07	119.09	109.50
1	A	35	GLY	N-CA-C	5.80	120.11	111.18
1	H	112	SER	N-CA-C	5.58	117.75	108.99
1	A	81	GLN	N-CA-C	5.42	118.29	109.24
2	B	58	VAL	CA-C-N	-5.32	114.76	120.03
2	B	58	VAL	C-N-CA	-5.32	114.76	120.03
1	A	133	GLY	N-CA-C	-5.20	106.66	115.34
1	A	100(H)	PHE	N-CA-C	5.12	117.05	107.99
1	A	79	TYR	N-CA-C	5.09	117.12	109.23

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	1713	0	1676	13	0
1	H	1719	0	1680	9	0
2	B	1627	0	1578	8	0
2	L	1627	0	1574	19	0
3	C	171	0	150	0	0
3	D	171	0	150	1	0
4	A	2	0	0	0	0
4	B	4	0	0	0	0
4	H	3	0	0	0	0
4	L	7	0	0	0	0
5	B	13	0	5	1	0
6	A	114	0	0	2	0
6	B	112	0	0	1	0
6	C	5	0	0	0	0
6	D	8	0	0	0	0
6	H	130	0	0	0	0
6	L	130	0	0	0	0
All	All	7556	0	6813	50	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 4.

All (50) 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)
2:L:21:ILE:HD11	2:L:102:THR:OG1	1.52	1.09
2:L:21:ILE:HD11	2:L:102:THR:CB	1.82	1.09
2:L:21:ILE:CD1	2:L:102:THR:CB	2.34	1.04
2:L:21:ILE:CD1	2:L:102:THR:HB	1.89	1.00
2:L:21:ILE:HD12	2:L:102:THR:HG21	1.41	0.99
2:L:21:ILE:HD12	2:L:102:THR:CG2	2.01	0.90
2:L:185:ASP:HA	2:L:188:LYS:HD2	1.68	0.75
1:A:131:THR:C	1:A:133:GLY:H	1.94	0.74
2:L:149:LYS:NZ	2:L:195:GLU:OE1	2.22	0.73
2:L:21:ILE:HD12	2:L:102:THR:CB	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ASN:HD21	1:A:206:LYS:HE2	1.57	0.69
2:B:183:LYS:NZ	2:B:187:GLU:OE2	2.23	0.67
2:L:21:ILE:CD1	2:L:102:THR:CG2	2.69	0.66
2:L:21:ILE:CD1	2:L:102:THR:HG21	2.22	0.65
2:B:188:LYS:HE3	6:B:432:HOH:O	2.01	0.61
2:L:21:ILE:HD11	2:L:102:THR:HG1	1.67	0.58
3:D:1146:ASP:OD1	3:D:1146:ASP:N	2.37	0.58
1:A:66:HIS:HE1	1:A:86:ASP:OD2	1.88	0.57
2:L:166:GLN:HG3	2:L:173:TYR:CZ	2.42	0.55
1:A:131:THR:C	1:A:133:GLY:N	2.59	0.54
1:A:39:GLN:HE22	2:B:38:GLN:HE22	1.54	0.53
1:A:126:PRO:HD3	1:A:138:LEU:HB3	1.91	0.53
2:L:142:ARG:HH11	2:L:142:ARG:HG2	1.74	0.52
1:A:178:LEU:HA	6:A:431:HOH:O	2.10	0.51
1:A:193:THR:HG23	1:A:210:LYS:HE3	1.91	0.51
1:A:87:THR:HG23	1:A:110:THR:HA	1.92	0.50
2:B:105:GLU:HG2	2:B:106:ILE:N	2.27	0.50
1:H:48:MET:HE1	1:H:80:LEU:HD21	1.94	0.50
1:H:193:THR:HG23	1:H:210:LYS:HE3	1.94	0.49
1:A:151:THR:HG22	1:A:199:ASN:HB3	1.95	0.48
2:L:182:SER:OG	2:L:185:ASP:OD1	2.32	0.47
2:L:78:LEU:HD11	2:L:104:LEU:HD21	1.97	0.47
5:B:305:CIT:O2	5:B:305:CIT:O7	2.30	0.47
1:A:120:SER:OG	6:A:401:HOH:O	2.21	0.46
2:B:142:ARG:CZ	2:B:163:VAL:HG21	2.47	0.45
2:L:151:ASP:OD1	2:L:191:VAL:HG12	2.17	0.45
2:L:24:ARG:HG2	2:L:70:ASP:OD1	2.17	0.45
1:A:199:ASN:ND2	1:A:206:LYS:HE2	2.29	0.44
2:B:186:TYR:HA	2:B:192:TYR:OH	2.18	0.43
1:H:129:LYS:HB3	1:H:129:LYS:HE2	1.72	0.43
2:B:12:SER:OG	2:B:105:GLU:OE2	2.36	0.43
1:H:97:GLN:HB3	1:H:100(F):ARG:HG2	2.01	0.42
2:B:105:GLU:HG3	2:B:173:TYR:OH	2.19	0.42
1:A:210:LYS:HE2	1:A:212:GLU:OE2	2.20	0.42
1:H:101:ASP:HA	1:H:102:PRO:HA	1.87	0.42
1:H:119:PRO:HB3	1:H:145:TYR:HB3	2.01	0.42
1:H:47:TRP:HE1	1:H:50:ILE:HG23	1.84	0.41
2:L:124:GLN:HG2	2:L:129:THR:O	2.21	0.41
1:H:200:HIS:HB3	1:H:205:THR:OG1	2.21	0.41
1:H:126:PRO:HG2	1:H:213:PRO:HB3	2.02	0.41

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	124/227 (55%)	121 (98%)	3 (2%)	0	100	100
2	B	181/213 (85%)	177 (98%)	4 (2%)	0	100	100
2	L	24/213 (11%)	24 (100%)	0	0	100	100
3	C	19/27 (70%)	19 (100%)	0	0	100	100
3	D	19/27 (70%)	18 (95%)	1 (5%)	0	100	100
All	All	367/707 (52%)	359 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	193/194 (100%)	189 (98%)	4 (2%)	47	52
1	H	194/194 (100%)	193 (100%)	1 (0%)	81	87
2	B	185/185 (100%)	182 (98%)	3 (2%)	55	61
2	L	185/185 (100%)	184 (100%)	1 (0%)	81	87
3	C	20/26 (77%)	19 (95%)	1 (5%)	22	18
3	D	20/26 (77%)	19 (95%)	1 (5%)	22	18
All	All	797/810 (98%)	786 (99%)	11 (1%)	59	66

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	204	ASN
2	L	78	LEU
1	A	62	SER
1	A	129	LYS
1	A	131	THR
1	A	151	THR
2	B	2	ILE
2	B	54	LEU
2	B	205	VAL
3	D	1146	ASP
3	C	1151	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	39	GLN
1	H	64	GLN
1	H	81	GLN
1	H	192	GLN
2	L	38	GLN
2	L	152	ASN
2	L	189	HIS
1	A	66	HIS
1	A	82(A)	ASN
1	A	199	ASN
2	B	38	GLN
2	B	92	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 17 ligands modelled in this entry, 16 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
5	CIT	B	305	-	12,12,12	1.05	0	17,17,17	1.43	2 (11%)

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
5	CIT	B	305	-	-	11/16/16/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	305	CIT	O6-C6-C3	3.69	120.22	113.14
5	B	305	CIT	O2-C1-C2	2.01	120.71	114.35

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	305	CIT	C2-C3-C6-O6
5	B	305	CIT	O7-C3-C6-O6
5	B	305	CIT	O2-C1-C2-C3
5	B	305	CIT	O1-C1-C2-C3
5	B	305	CIT	C4-C3-C6-O6
5	B	305	CIT	C1-C2-C3-C6
5	B	305	CIT	C2-C3-C6-O5
5	B	305	CIT	C4-C3-C6-O5

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Mol	Chain	Res	Type	Atoms
5	B	305	CIT	C1-C2-C3-O7
5	B	305	CIT	O7-C3-C6-O5
5	B	305	CIT	C1-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	305	CIT	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	A	226/227 (99%)	0.34	8 (3%) 47 51	29, 45, 72, 131	0
1	H	226/227 (99%)	0.14	8 (3%) 47 51	29, 42, 65, 141	1 (0%)
2	B	213/213 (100%)	0.09	1 (0%) 87 89	30, 42, 56, 70	0
2	L	213/213 (100%)	0.10	3 (1%) 73 77	29, 39, 57, 67	0
3	C	20/27 (74%)	0.67	2 (10%) 12 14	40, 58, 108, 118	0
3	D	20/27 (74%)	0.70	2 (10%) 12 14	35, 55, 96, 111	0
All	All	918/934 (98%)	0.19	24 (2%) 57 61	29, 42, 68, 141	1 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	131	THR	7.0
1	A	130	SER	5.9
1	H	131	THR	5.9
1	H	133	GLY	4.5
2	L	213	GLU	4.2
1	H	132	SER	3.9
1	H	214	LYS	3.3
3	C	1148	PHE	3.2
3	D	1146	ASP	3.1
1	A	129	LYS	3.1
1	A	207	VAL	2.9
1	H	128	SER	2.9
3	D	1148	PHE	2.8
2	L	21	ILE	2.8
2	L	24	ARG	2.7
2	B	1	GLU	2.7
1	A	132	SER	2.7
1	A	128	SER	2.5
1	A	213	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	133	GLY	2.5
1	H	28	THR	2.5
1	H	130	SER	2.4
3	C	1163	ASP	2.1
1	H	190	GLY	2.1

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
5	CIT	B	305	13/13	0.62	0.13	71,75,81,83	0
4	NA	L	307	1/1	0.79	0.20	30,30,30,30	0
4	NA	B	302	1/1	0.81	0.13	51,51,51,51	0
4	NA	B	303	1/1	0.82	0.54	30,30,30,30	0
4	NA	B	304	1/1	0.83	0.48	30,30,30,30	0
4	NA	H	303	1/1	0.84	0.39	30,30,30,30	0
4	NA	L	305	1/1	0.87	0.15	53,53,53,53	0
4	NA	A	301	1/1	0.87	0.47	30,30,30,30	0
4	NA	A	302	1/1	0.88	0.41	30,30,30,30	0
4	NA	L	304	1/1	0.89	0.17	51,51,51,51	0
4	NA	L	306	1/1	0.92	0.13	50,50,50,50	0
4	NA	B	301	1/1	0.92	0.11	52,52,52,52	0
4	NA	H	301	1/1	0.93	0.26	42,42,42,42	0
4	NA	L	303	1/1	0.94	0.28	50,50,50,50	0
4	NA	L	302	1/1	0.94	0.08	41,41,41,41	0
4	NA	H	302	1/1	0.95	0.08	46,46,46,46	0
4	NA	L	301	1/1	0.96	0.10	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.