



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:03 PM UTC

PDB ID : 9ATM / pdb_00009atm
Title : SARS-CoV-2 EG.5 RBD bound to the VIR-7229 and the S2H97 Fab fragments
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Deposited on : 2024-02-27
Resolution : 1.90 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

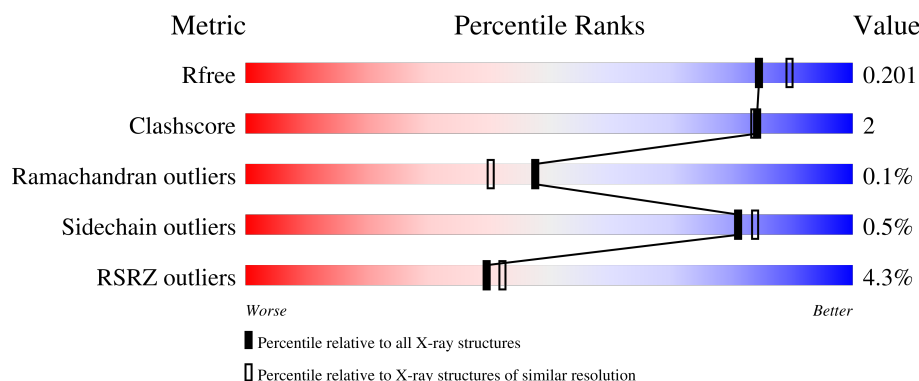
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	H	226	
2	I	223	
3	L	216	
4	M	218	
5	R	239	

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
8	CL	L	302	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 8689 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 VIR-7229 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	225	Total	C	N	O	S	0	1	0
			1685	1073	273	332	7			

- Molecule 2 is a protein called S2H97 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	214	Total	C	N	O	S	0	2	0
			1619	1039	264	309	7			

- Molecule 3 is a protein called VIR-7229 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	215	Total	C	N	O	S	0	0	0
			1590	1000	258	326	6			

- Molecule 4 is a protein called S2H97 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	M	216	Total	C	N	O	S	0	0	0
			1526	954	253	314	5			

- Molecule 5 is a protein called SARS-CoV-2 EG.5 RBD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	R	197	Total	C	N	O	S	0	2	0
			1557	1002	262	285	8			

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	I	1	Total	C	O	0	0
			4	2	2		
6	R	1	Total	C	O	0	0
			4	2	2		
6	R	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	L	1	Total	Ni	0	0
			1	1		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	L	1	Total	Cl	0	0
			1	1		

- Molecule 9 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	M	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	R	1	Total	C	N	O	0	0
			14	8	1	5		

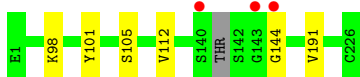
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	H	188	Total 188	O 188	0	0
11	I	99	Total 99	O 99	0	0
11	L	112	Total 112	O 112	0	0
11	M	128	Total 128	O 128	0	0
11	R	149	Total 149	O 149	0	0

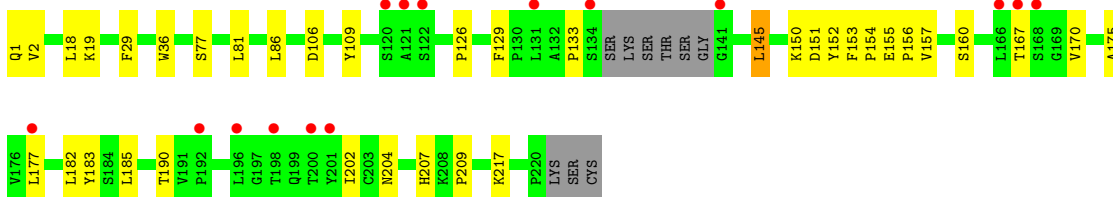
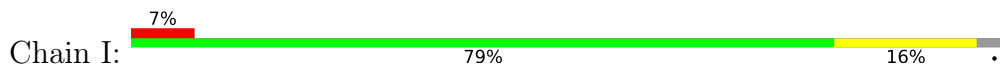
3 Residue-property plots [i](#)

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: VIR-7229 Fab heavy chain



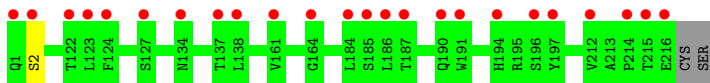
- Molecule 2: S2H97 Fab heavy chain



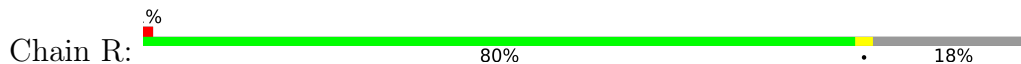
- Molecule 3: VIR-7229 Fab light chain



- Molecule 4: S2H97 Fab light chain



- Molecule 5: SARS-CoV-2 EG.5 RBD





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.73Å 149.70Å 167.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.78 – 1.90 46.78 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.78-1.90) 99.9 (46.78-1.90)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.194 , 0.227 (Not available) , 0.201	Depositor DCC
R_{free} test set	4870 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8689	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PCA, TRS, EDO, NAG, CL, NI

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	H	0.35	0/1730	0.54	0/2361
2	I	0.24	0/1662	0.42	0/2275
3	L	0.28	0/1625	0.55	0/2225
4	M	0.25	0/1565	0.49	0/2150
5	R	0.30	0/1611	0.50	0/2200
All	All	0.29	0/8193	0.50	0/11211

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 [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	H	1685	0	1623	3	0
2	I	1619	0	1520	19	0
3	L	1590	0	1502	8	0
4	M	1526	0	1394	1	0
5	R	1557	0	1474	3	0
6	I	4	0	6	0	0
6	R	8	0	12	1	0
7	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	1	0	0	3	1
9	M	8	0	12	0	0
10	R	14	0	13	0	0
11	H	188	0	0	0	1
11	I	99	0	0	1	1
11	L	112	0	0	2	0
11	M	128	0	0	1	0
11	R	149	0	0	3	1
All	All	8689	0	7556	36	2

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 2.

All (36) 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:L:192:HIS:NE2	8:L:302:CL:CL	2.09	1.22
8:L:302:CL:CL	11:L:444:HOH:O	1.95	1.22
8:L:302:CL:CL	11:L:506:HOH:O	2.47	0.68
6:R:603:EDO:O2	11:R:701:HOH:O	2.13	0.67
2:I:133:PRO:HG3	2:I:145:LEU:HB3	1.75	0.66
3:L:10:VAL:HG13	3:L:107:LEU:HD13	1.83	0.60
2:I:207:HIS:CE1	2:I:209:PRO:HG2	2.37	0.58
2:I:19:LYS:NZ	11:I:701:HOH:O	2.32	0.58
2:I:126:PRO:HB3	2:I:152:TYR:HB3	1.86	0.56
2:I:157:VAL:HG12	2:I:207:HIS:HB2	1.87	0.56
2:I:160:SER:HB2	2:I:204:ASN:HB2	1.86	0.56
2:I:155:GLU:HG2	2:I:156:PRO:HA	1.88	0.54
5:R:490:SER:OG	11:R:702:HOH:O	2.19	0.53
4:M:2:SER:HB3	11:M:488:HOH:O	2.10	0.52
3:L:136:LEU:HD12	3:L:182:LEU:HD23	1.94	0.48
5:R:478:LYS:NZ	11:R:704:HOH:O	2.39	0.47
2:I:129:PHE:CE1	2:I:150:LYS:HE2	2.49	0.47
1:H:98:LYS:HG2	1:H:112:VAL:HB	1.98	0.46
2:I:18:LEU:HB2	2:I:86:LEU:HD11	1.98	0.45
2:I:202:ILE:HG13	2:I:217:LYS:HA	1.99	0.45
2:I:151:ASP:HB3	2:I:182:LEU:HD13	1.99	0.44
2:I:129:PHE:HE1	2:I:150:LYS:HE2	1.83	0.44
1:H:191:VAL:HB	3:L:139:LEU:HD13	2.00	0.44
3:L:63:ARG:HB3	3:L:78:SER:O	2.18	0.43
2:I:175:ALA:HA	2:I:185:LEU:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:167:THR:O	2:I:170:VAL:HG22	2.18	0.43
3:L:136:LEU:HD21	3:L:189:TRP:CZ3	2.54	0.43
5:R:343:ASN:HB2	5:R:371:PHE:CD1	2.53	0.43
3:L:136:LEU:HB2	3:L:182:LEU:HB3	2.00	0.42
2:I:153:PHE:HA	2:I:154:PRO:HA	1.86	0.42
2:I:29:PHE:CD2	2:I:77:SER:HA	2.55	0.41
2:I:36:TRP:CG	2:I:81:LEU:HD13	2.56	0.41
2:I:2:VAL:HB	2:I:109:TYR:CE1	2.56	0.41
1:H:101:TYR:HB2	1:H:105:SER:OG	2.21	0.40
3:L:28:ASP:OD1	3:L:29:VAL:N	2.45	0.40
2:I:177:LEU:HD13	2:I:183:TYR:CZ	2.57	0.40

All (2) 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:L:302:CL:CL	11:R:765:HOH:O[2_655]	1.96	0.24
11:H:456:HOH:O	11:I:753:HOH:O[4_545]	2.17	0.03

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	H	222/226 (98%)	215 (97%)	6 (3%)	1 (0%)	24	16
2	I	212/223 (95%)	209 (99%)	3 (1%)	0	100	100
3	L	213/216 (99%)	209 (98%)	4 (2%)	0	100	100
4	M	214/218 (98%)	212 (99%)	2 (1%)	0	100	100
5	R	197/239 (82%)	194 (98%)	3 (2%)	0	100	100
All	All	1058/1122 (94%)	1039 (98%)	18 (2%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	144	GLY

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	H	185/191 (97%)	185 (100%)	0	100	100
2	I	170/191 (89%)	167 (98%)	3 (2%)	51	50
3	L	175/181 (97%)	175 (100%)	0	100	100
4	M	160/186 (86%)	160 (100%)	0	100	100
5	R	168/209 (80%)	167 (99%)	1 (1%)	78	81
All	All	858/958 (90%)	854 (100%)	4 (0%)	81	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	106	ASP
2	I	145	LEU
2	I	190	THR
5	R	382	VAL

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

Mol	Chain	Res	Type
1	H	39	GLN
3	L	40	GLN
4	M	55	ASN
4	M	81	GLN
4	M	203	HIS
5	R	334	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	PCA	I	1	2	7,8,9	2.62	3 (42%)	9,10,12	1.24	1 (11%)
3	PCA	L	1	3	7,8,9	2.53	2 (28%)	9,10,12	1.13	1 (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
2	PCA	I	1	2	-	0/0/11/13	0/1/1/1
3	PCA	L	1	3	-	0/0/11/13	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	1	PCA	CD-N	5.75	1.48	1.34
3	L	1	PCA	CD-N	5.59	1.48	1.34
2	I	1	PCA	CA-N	-2.40	1.43	1.46
2	I	1	PCA	OE-CD	-2.10	1.19	1.23
3	L	1	PCA	OE-CD	-2.04	1.19	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	1	PCA	O-C-CA	-2.16	119.20	124.77
3	L	1	PCA	CB-CG-CD	2.12	107.68	104.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	$\# Z > 2$
6	EDO	I	601	-	3,3,3	0.48	0	2,2,2	0.25	0
9	TRS	M	301	-	7,7,7	0.29	0	9,9,9	0.34	0
6	EDO	R	603	-	3,3,3	0.47	0	2,2,2	0.37	0
10	NAG	R	602	5	14,14,15	0.37	0	17,19,21	0.54	0
6	EDO	R	601	-	3,3,3	0.52	0	2,2,2	0.14	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
6	EDO	I	601	-	-	0/1/1/1	-
9	TRS	M	301	-	-	5/9/9/9	-
6	EDO	R	603	-	-	1/1/1/1	-
10	NAG	R	602	5	-	4/6/23/26	0/1/1/1
6	EDO	R	601	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	M	301	TRS	C1-C-C2-O2
9	M	301	TRS	C3-C-C2-O2
9	M	301	TRS	N-C-C2-O2
10	R	602	NAG	O5-C5-C6-O6
10	R	602	NAG	C4-C5-C6-O6
10	R	602	NAG	C8-C7-N2-C2
10	R	602	NAG	O7-C7-N2-C2
9	M	301	TRS	C2-C-C1-O1
9	M	301	TRS	N-C-C1-O1
6	R	603	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	603	EDO	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	H	225/226 (99%)	-0.19	3 (1%) 75 78	21, 38, 78, 136	1 (0%)
2	I	213/223 (95%)	0.44	15 (7%) 22 24	17, 57, 126, 159	2 (0%)
3	L	214/216 (99%)	0.07	1 (0%) 87 89	30, 47, 72, 143	0
4	M	216/218 (99%)	0.43	24 (11%) 10 11	32, 52, 132, 146	0
5	R	197/239 (82%)	-0.02	3 (1%) 72 75	26, 42, 79, 110	2 (1%)
All	All	1065/1122 (94%)	0.15	46 (4%) 40 42	17, 46, 119, 159	5 (0%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	140	SER	4.3
2	I	134	SER	4.1
4	M	185	SER	3.7
4	M	191	TRP	3.4
2	I	177	LEU	3.4
4	M	187	THR	3.2
2	I	122	SER	3.2
1	H	143	GLY	3.1
4	M	161	VAL	3.1
4	M	137	THR	3.1
4	M	212	VAL	3.0
4	M	216	GLU	3.0
4	M	127	SER	2.9
5	R	529	LYS	2.8
2	I	141	GLY	2.7
5	R	333	THR	2.7
2	I	196	LEU	2.7
4	M	122	THR	2.6
2	I	120	SER	2.6
2	I	192	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
4	M	184	LEU	2.6
4	M	190	GLN	2.6
4	M	215	THR	2.6
4	M	138	LEU	2.5
2	I	121	ALA	2.5
4	M	1	GLN	2.5
2	I	166	LEU	2.4
4	M	186	LEU	2.4
1	H	144	GLY	2.4
4	M	194	HIS	2.3
4	M	197	TYR	2.3
4	M	214	PRO	2.3
4	M	196	SER	2.2
4	M	164	GLY	2.2
4	M	124	PHE	2.2
3	L	215	CYS	2.2
2	I	131	LEU	2.2
4	M	123	LEU	2.2
2	I	200	THR	2.1
2	I	168	SER	2.1
2	I	198	THR	2.1
4	M	2	SER	2.1
5	R	371	PHE	2.1
2	I	167	THR	2.1
2	I	201	TYR	2.0
4	M	134	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	PCA	I	1	8/9	0.82	0.12	53,60,68,75	0
3	PCA	L	1	8/9	0.83	0.16	57,66,67,68	0

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(Å ²)	Q<0.9
10	NAG	R	602	14/15	0.39	0.15	77,83,87,88	14
9	TRS	M	301	8/8	0.77	0.13	73,81,87,91	0
6	EDO	R	603	4/4	0.79	0.15	61,62,62,62	0
7	NI	L	301	1/1	0.95	0.06	99,99,99,99	0
6	EDO	R	601	4/4	0.95	0.07	38,40,44,45	0
6	EDO	I	601	4/4	0.95	0.09	35,36,38,43	0
8	CL	L	302	1/1	0.97	0.16	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.