



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:06 PM UTC

PDB ID : 7SGM / pdb_00007sgm
Title : Crystal structure of a Fab variant containing a fluorescent noncanonical amino acid with blocked excited state proton transfer and in complex with its antigen, CD40L
Authors : Henderson, J.N.; Mills, J.H.; Simmons, C.R.
Deposited on : 2021-10-06
Resolution : 2.00 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:

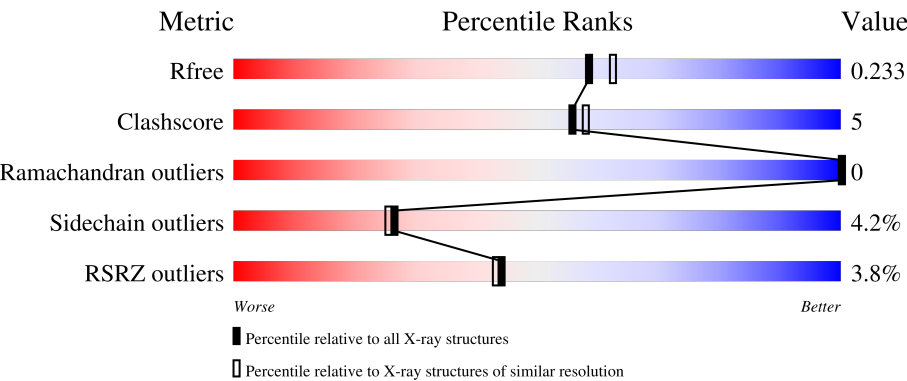
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	146	3% 72% 20% 6%
1	B	146	3% 77% 16%
1	C	146	4% 78% 12% 6%
2	H	226	11% 76% 16% 7%
2	K	226	2% 86% 8% 6%

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Mol	Chain	Length	Quality of chain
2	X	226	3% 84% 10% • 5%
3	L	218	3% 88% 8% 5%
3	M	218	3% 85% 13% •
3	Y	218	89% 9% ••

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14354 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 CD40 ligand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	137	Total	C	N	O	S	0	7	0
			1074	683	186	200	5			
1	B	140	Total	C	N	O	S	0	5	0
			1083	689	185	204	5			
1	C	137	Total	C	N	O	S	0	7	0
			1074	686	182	201	5			

- Molecule 2 is a protein called 5c8* Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	211	Total	C	N	O	S	0	5	0
			1566	990	251	317	8			
2	K	213	Total	C	N	O	S	0	1	0
			1574	991	254	321	8			
2	X	214	Total	C	N	O	S	0	3	0
			1590	1003	257	322	8			

- Molecule 3 is a protein called 5c8* Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	208	Total	C	N	O	S	0	3	0
			1606	1013	263	325	5			
3	M	217	Total	C	N	O	S	0	1	0
			1679	1054	279	341	5			
3	Y	216	Total	C	N	O	S	0	3	0
			1681	1055	280	340	6			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



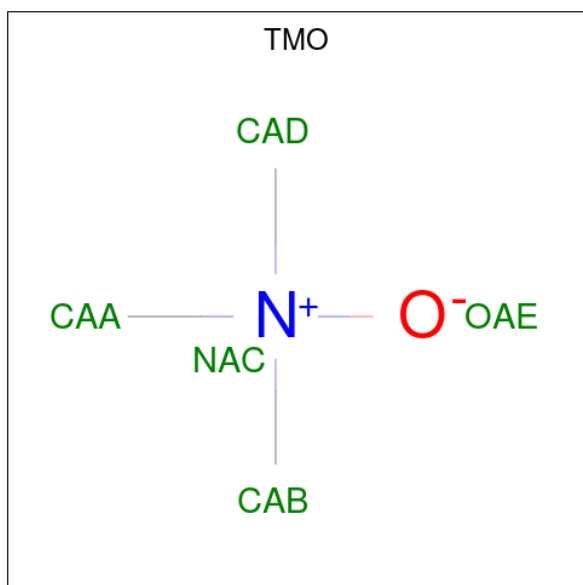
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	C	1	Total	C	O	0	0
			7	4	3		
6	H	1	Total	C	O	0	0
			5	3	2		
6	H	1	Total	C	O	0	0
			7	4	3		
6	L	1	Total	C	O	0	1
			7	4	3		
6	L	1	Total	C	O	0	0
			5	3	2		
6	L	1	Total	C	O	0	0
			7	4	3		
6	K	1	Total	C	O	0	0
			7	4	3		
6	M	1	Total	C	O	0	1
			7	4	3		
6	X	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	Y	1	Total	C	O	0	0
			6	4	2		
6	Y	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is trimethylamine oxide (CCD ID: TMO) (formula: C_3H_9NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	N	O	0	1
			5	3	1	1		
7	M	1	Total	C	N	O	0	1
			5	3	1	1		
7	Y	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	107	Total	O	0	9
			107	107		
8	B	99	Total	O	0	7
			99	99		
8	C	98	Total	O	0	6
			98	98		
8	H	97	Total	O	0	0
			97	97		

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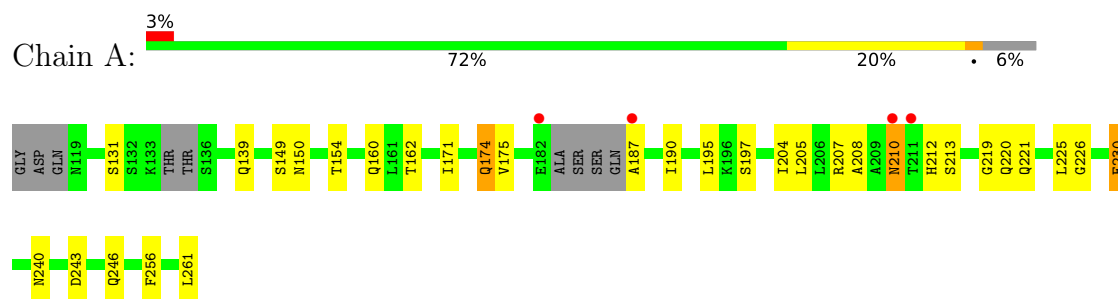
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	L	178	Total 178	O 178	0	1
8	K	160	Total 160	O 160	0	1
8	M	200	Total 200	O 200	0	0
8	X	150	Total 150	O 150	0	0
8	Y	187	Total 187	O 187	0	2

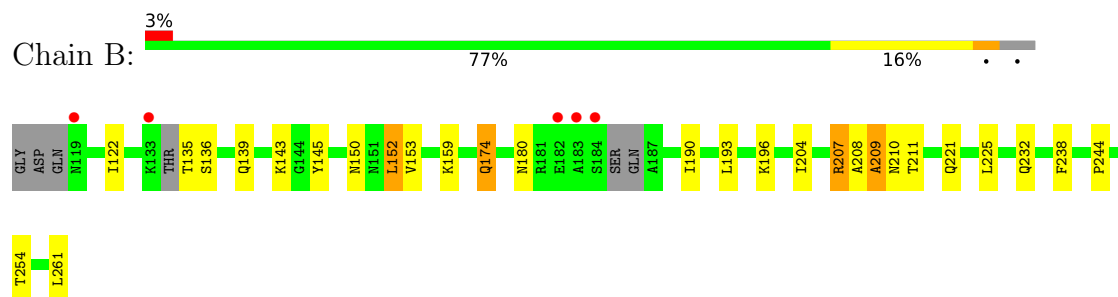
3 Residue-property plots [i](#)

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.

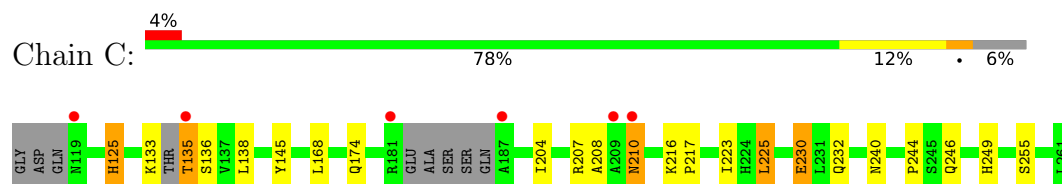
- Molecule 1: CD40 ligand



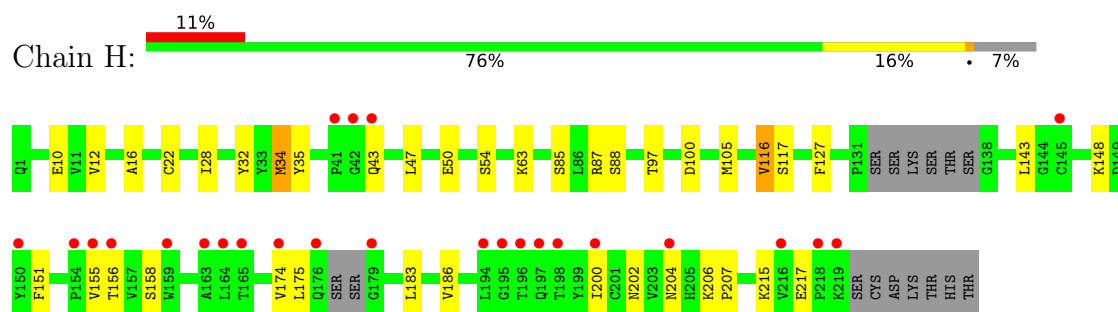
- Molecule 1: CD40 ligand



- Molecule 1: CD40 ligand



- Molecule 2: 5c8* Fab heavy chain



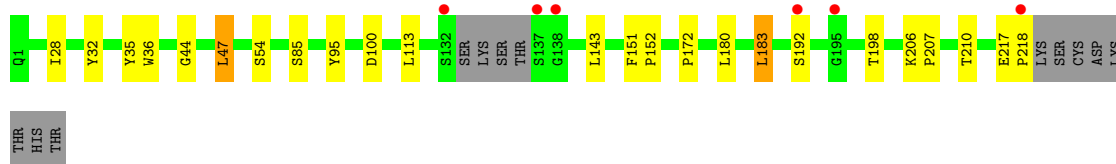
- Molecule 2: 5c8* Fab heavy chain

Chain K:  2% 86% 8% 6%



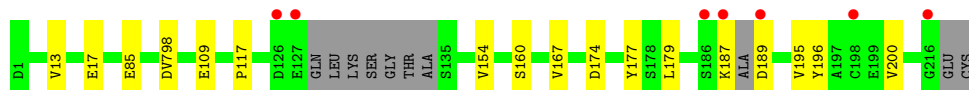
- Molecule 2: 5c8* Fab heavy chain

Chain X:  3% 84% 10% 5%



- Molecule 3: 5c8* Fab light chain

Chain L:  3% 88% 8% 5%



- Molecule 3: 5c8* Fab light chain

Chain M:  3% 85% 13% 0%



- Molecule 3: 5c8* Fab light chain

Chain Y:  0% 89% 9% 2%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	226.85Å 131.25Å 97.30Å 90.00° 109.10° 90.00°	Depositor
Resolution (Å)	48.42 – 2.00 48.42 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.6 (48.42-2.00) 97.6 (48.42-2.00)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.193 , 0.228 0.199 , 0.233	Depositor DCC
R_{free} test set	8919 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	20.0	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.9	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	0.94	EDS
Total number of atoms	14354	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% 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, TMO, DV7, PEG, TRS

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	1.14	2/1113 (0.2%)	1.37	7/1507 (0.5%)
1	B	1.20	2/1116 (0.2%)	1.28	3/1511 (0.2%)
1	C	1.17	3/1116 (0.3%)	1.35	4/1511 (0.3%)
2	H	1.11	1/1608 (0.1%)	1.36	1/2189 (0.0%)
2	K	1.14	1/1611 (0.1%)	1.34	5/2198 (0.2%)
2	X	1.12	2/1633 (0.1%)	1.33	2/2224 (0.1%)
3	L	1.12	1/1635 (0.1%)	1.31	1/2227 (0.0%)
3	M	1.20	2/1704 (0.1%)	1.34	3/2317 (0.1%)
3	Y	1.16	1/1709 (0.1%)	1.32	4/2323 (0.2%)
All	All	1.15	15/13245 (0.1%)	1.33	30/18007 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	H	0	1
2	X	0	1
3	L	0	1
3	M	0	1
All	All	0	4

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	202	HIS	C-O	5.98	1.31	1.23
1	C	138	LEU	C-O	5.93	1.31	1.23
1	B	143	LYS	C-O	-5.79	1.17	1.23
1	C	249	HIS	CE1-NE2	5.64	1.38	1.32
2	K	33	TYR	C-O	5.55	1.30	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	94	HIS	CE1-NE2	5.43	1.38	1.32
3	L	117	PRO	C-O	-5.40	1.17	1.23
2	H	28	ILE	C-O	5.39	1.30	1.23
1	B	209	ALA	C-O	5.35	1.30	1.23
1	A	243	ASP	CG-OD1	5.28	1.35	1.25
1	C	125	HIS	CE1-NE2	5.22	1.37	1.32
1	A	175	VAL	C-O	5.20	1.29	1.24
2	X	28	ILE	C-O	5.16	1.29	1.23
2	X	113	LEU	C-O	5.08	1.30	1.24
3	Y	44	PRO	C-O	-5.00	1.17	1.23

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Y	146	ARG	CG-CD-NE	-8.81	92.62	112.00
1	C	230	GLU	CB-CA-C	-7.50	99.01	110.26
1	A	210	ASN	CB-CA-C	7.15	121.97	109.89
3	Y	210	THR	CA-CB-OG1	-6.38	100.04	109.60
3	Y	136	VAL	CB-CA-C	6.10	119.92	110.83
2	X	198	THR	CA-CB-OG1	-6.08	100.48	109.60
2	K	186	VAL	N-CA-CB	-5.97	101.66	111.44
1	C	210	ASN	CB-CA-C	5.83	122.02	110.42
1	A	154	THR	CA-CB-OG1	-5.80	100.91	109.60
1	A	230	GLU	CB-CA-C	-5.75	101.64	110.26
2	X	210	THR	CB-CA-C	5.72	119.68	109.38
1	C	133	LYS	CA-C-O	-5.50	111.44	120.80
3	M	160	SER	CA-C-N	-5.44	113.03	122.83
3	M	160	SER	C-N-CA	-5.44	113.03	122.83
2	K	138	GLY	CA-C-N	5.32	126.79	120.14
2	K	138	GLY	C-N-CA	5.32	126.79	120.14
3	L	174	ASP	CA-CB-CG	5.30	117.90	112.60
2	K	186	VAL	CB-CA-C	5.29	118.65	110.50
1	A	150	ASN	CA-C-O	-5.26	115.51	121.25
1	A	162	THR	CA-CB-OG1	-5.25	101.73	109.60
1	A	240	ASN	CA-C-O	-5.21	115.22	121.11
2	K	61	ASN	CB-CA-C	5.18	117.62	110.16
1	C	240	ASN	CB-CA-C	-5.17	99.92	109.37
1	B	238	PHE	CA-CB-CG	5.12	118.92	113.80
1	B	180	ASN	CA-C-N	5.12	127.90	120.79
1	B	180	ASN	C-N-CA	5.12	127.90	120.79
3	M	32	SER	O-C-N	5.09	127.31	122.07
2	H	127	PHE	CB-CA-C	5.05	116.45	108.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	PHE	CA-CB-CG	5.02	118.82	113.80
3	Y	146	ARG	N-CA-C	5.01	117.39	111.33

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	43[B]	GLN	Peptide
3	L	160	SER	Peptide
3	M	161	GLY	Peptide
2	X	217	GLU	Peptide

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	1074	0	1056	20	0
1	B	1083	0	1060	18	0
1	C	1074	0	1064	19	0
2	H	1566	0	1503	19	0
2	K	1574	0	1513	8	0
2	X	1590	0	1546	9	0
3	L	1606	0	1488	8	0
3	M	1679	0	1582	17	0
3	Y	1681	0	1591	11	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
4	C	14	0	13	0	0
5	A	8	0	12	1	0
6	A	7	0	10	0	0
6	B	7	0	10	0	0
6	C	7	0	10	0	0
6	H	12	0	15	0	0
6	K	7	0	10	0	0
6	L	19	0	25	0	0
6	M	7	0	10	0	0
6	X	7	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Y	13	0	17	0	0
7	L	5	0	9	0	0
7	M	5	0	9	0	0
7	Y	5	0	9	0	0
8	A	107	0	0	3	0
8	B	99	0	0	1	0
8	C	98	0	0	2	0
8	H	97	0	0	1	0
8	K	160	0	0	1	0
8	L	178	0	0	2	0
8	M	200	0	0	0	0
8	X	150	0	0	0	0
8	Y	187	0	0	2	0
All	All	14354	0	12598	119	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 5.

All (119) 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:M:146[B]:ARG:HH11	3:M:146[B]:ARG:HG2	1.34	0.91
3:L:13[A]:VAL:HG13	3:L:17:GLU:HB3	1.63	0.80
1:C:232[B]:GLN:NE2	8:C:401:HOH:O	2.18	0.75
1:A:208:ALA:HB2	1:A:225:LEU:HD21	1.72	0.72
1:B:135:THR:O	1:B:244:PRO:HG2	1.89	0.71
2:H:87:ARG:O	2:H:116:VAL:HG11	1.94	0.68
1:A:210:ASN:OD1	1:A:221:GLN:NE2	2.27	0.68
1:A:174[B]:GLN:HG2	8:A:431:HOH:O	1.95	0.66
3:M:216:GLY:O	3:M:217:GLU:C	2.37	0.66
2:K:46:GLU:OE1	8:K:401:HOH:O	2.14	0.65
2:H:35:TYR:HB2	2:H:97:THR:CG2	2.28	0.64
1:B:232[B]:GLN:NE2	8:B:402:HOH:O	2.31	0.63
3:Y:112[A]:ARG:HD3	3:Y:113:THR:O	1.99	0.62
3:Y:146:ARG:NH2	8:Y:401[A]:HOH:O	2.31	0.62
1:A:225:LEU:HD23	1:C:174[A]:GLN:OE1	2.01	0.61
3:M:146[B]:ARG:HG2	3:M:146[B]:ARG:NH1	2.13	0.60
1:A:174[A]:GLN:HG3	8:A:431:HOH:O	2.00	0.60
1:B:208:ALA:HB2	1:B:225:LEU:HD21	1.84	0.60
1:C:135:THR:O	1:C:244:PRO:HG2	2.02	0.59
2:H:200:ILE:HD13	2:H:215:LYS:HA	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:117:SER:O	8:H:401:HOH:O	2.17	0.58
2:H:35:TYR:HB2	2:H:97:THR:HG22	1.84	0.58
1:C:204:ILE:HG21	1:C:207[B]:ARG:HG3	1.85	0.57
3:M:146[B]:ARG:HH11	3:M:146[B]:ARG:CG	2.12	0.57
2:H:88:SER:HA	2:H:116:VAL:HG13	1.86	0.57
1:C:208:ALA:HB2	1:C:225:LEU:CD1	2.36	0.56
3:Y:136:VAL:HG22	3:Y:152:TRP:CH2	2.41	0.56
3:Y:41:GLN:HB2	3:Y:51:LEU:HD11	1.88	0.55
2:X:183:LEU:HD12	2:X:183:LEU:C	2.31	0.55
3:M:192:LYS:CG	3:M:193:HIS:CE1	2.90	0.54
2:H:32:TYR:CE2	2:H:100:ASP:HB3	2.43	0.54
1:B:139:GLN:NE2	1:B:159:LYS:HG3	2.24	0.53
2:H:22:CYS:SG	2:H:34[A]:MET:HE1	2.48	0.53
1:B:150:ASN:OD1	1:B:152:LEU:HB2	2.08	0.53
2:H:117:SER:HB3	2:H:151:PHE:CZ	2.43	0.53
2:K:183:LEU:C	2:K:183:LEU:HD12	2.35	0.52
1:A:174[B]:GLN:HE22	1:B:225:LEU:HD23	1.75	0.52
2:H:156:THR:CG2	2:H:204:ASN:HB3	2.40	0.52
3:Y:128:GLN:HG2	3:Y:133:THR:O	2.10	0.52
1:B:190:ILE:HG21	1:B:207[B]:ARG:CZ	2.40	0.52
1:C:125:HIS:CE1	1:C:255:SER:HB2	2.45	0.52
1:B:190:ILE:HG21	1:B:207[B]:ARG:NH2	2.25	0.51
2:H:206:LYS:N	2:H:207:PRO:CD	2.73	0.51
1:A:149:SER:OG	8:A:401:HOH:O	2.19	0.51
2:X:44:GLY:HA3	8:Y:418:HOH:O	2.11	0.51
2:H:183:LEU:C	2:H:183:LEU:HD12	2.36	0.50
1:A:261:LEU:HA	5:A:302:TRS:H21	1.94	0.50
1:B:204:ILE:HG21	1:B:207[A]:ARG:HD2	1.94	0.50
2:H:200:ILE:CD1	2:H:215:LYS:HA	2.42	0.50
1:A:204:ILE:HG21	1:A:207[B]:ARG:HG3	1.94	0.49
1:C:232[B]:GLN:NE2	8:C:405:HOH:O	2.32	0.49
3:M:116:ALA:HB1	3:M:205:LEU:HD13	1.95	0.48
2:K:35:TYR:CD2	2:K:47:LEU:HD11	2.48	0.48
1:C:136:SER:HA	1:C:244:PRO:HG3	1.95	0.48
3:Y:136:VAL:HG22	3:Y:152:TRP:CZ3	2.49	0.48
1:B:204:ILE:HG21	1:B:207[A]:ARG:CD	2.43	0.48
3:M:205:LEU:HG	3:M:209:VAL:HG13	1.96	0.48
3:M:16:GLY:HA2	3:M:81:SER:OG	2.14	0.47
2:H:35:TYR:CE1	2:H:50:GLU:HB3	2.49	0.47
1:C:204:ILE:HG21	1:C:207[B]:ARG:CG	2.45	0.47
2:H:158:SER:HB3	2:H:202:ASN:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:ILE:HG21	1:A:207[B]:ARG:CG	2.45	0.47
2:H:97:THR:HG21	2:H:105:MET:SD	2.55	0.47
1:C:208:ALA:HB2	1:C:225:LEU:HD11	1.97	0.47
2:X:32:TYR:CE2	2:X:100:ASP:HB3	2.51	0.46
2:X:206:LYS:N	2:X:207:PRO:CD	2.79	0.46
1:C:216:LYS:HA	1:C:217:PRO:C	2.40	0.46
1:A:246[B]:GLN:HE22	2:H:54[B]:SER:HB2	1.79	0.46
1:A:187:ALA:O	1:A:212:HIS:CD2	2.69	0.46
1:B:208:ALA:CB	1:B:225:LEU:HD21	2.46	0.46
3:L:187:LYS:O	3:L:189:ASP:N	2.49	0.46
2:K:32:TYR:CE2	2:K:100:ASP:HB3	2.51	0.46
3:M:17:GLU:O	3:M:82:VAL:HG23	2.16	0.46
3:M:67:SER:O	3:M:77:LEU:HD12	2.16	0.45
3:M:146[B]:ARG:NH1	3:M:146[B]:ARG:CG	2.76	0.45
1:A:246[B]:GLN:HE22	2:H:54[B]:SER:CB	2.28	0.45
3:L:85[B]:GLU:CG	8:L:537:HOH:O	2.64	0.45
3:M:207:SER:HB2	3:M:208:PRO:CD	2.45	0.45
1:A:190:ILE:HG21	1:A:207[B]:ARG:NH1	2.31	0.45
1:B:145:TYR:OH	1:C:230:GLU:O	2.26	0.45
2:K:47:LEU:HD13	3:M:100:PRO:HD2	1.99	0.45
3:M:207:SER:HB2	3:M:208:PRO:HD2	1.99	0.45
1:A:195:LEU:HB2	1:A:205:LEU:HD11	1.99	0.45
2:X:35:TYR:CD1	2:X:47:LEU:HD11	2.52	0.45
3:Y:112[A]:ARG:HD2	3:Y:144:TYR:CG	2.52	0.45
1:C:246[B]:GLN:NE2	2:X:54:SER:OG	2.50	0.44
3:L:13[A]:VAL:HG13	3:L:17:GLU:CB	2.41	0.44
2:K:147:VAL:HG11	2:K:155:VAL:HG11	1.98	0.44
3:M:179:LEU:C	3:M:179:LEU:HD23	2.43	0.44
3:Y:144:TYR:CG	3:Y:145:PRO:HA	2.53	0.44
1:B:210:ASN:ND2	1:B:221:GLN:OE1	2.43	0.44
2:H:12:VAL:HG22	2:H:16:ALA:CB	2.47	0.44
1:A:220:GLN:HB3	1:B:209:ALA:HB3	2.00	0.43
3:Y:67:SER:O	3:Y:77:LEU:HD12	2.19	0.43
1:C:136:SER:HA	1:C:244:PRO:CG	2.49	0.43
3:M:116:ALA:HB1	3:M:205:LEU:CD1	2.49	0.43
3:L:154:VAL:HG22	3:L:196:TYR:CD1	2.54	0.43
3:Y:112[A]:ARG:HD2	3:Y:144:TYR:CB	2.48	0.43
1:B:174[A]:GLN:HE21	1:B:174[A]:GLN:HB2	1.59	0.42
2:K:206:LYS:N	2:K:207:PRO:CD	2.82	0.42
1:A:131:SER:CB	1:A:139[B]:GLN:NE2	2.82	0.42
1:C:174[B]:GLN:HE21	1:C:174[B]:GLN:HB2	1.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:ILE:HG23	1:B:153:VAL:HG23	2.01	0.42
1:C:232[A]:GLN:CD	1:C:232[A]:GLN:H	2.28	0.42
1:A:213:SER:OG	1:A:219:GLY:HA3	2.20	0.42
3:L:167:VAL:HG22	3:L:179:LEU:HD12	2.00	0.42
3:L:85[B]:GLU:HG3	8:L:537:HOH:O	2.20	0.42
2:K:35:TYR:CE2	2:K:50:GLU:HB3	2.54	0.41
2:X:36:TRP:HA	2:X:95:TYR:O	2.21	0.41
1:A:171:ILE:O	1:A:226:GLY:HA2	2.19	0.41
3:M:58:LEU:HD22	3:M:62:VAL:HB	2.03	0.41
3:L:109:GLU:OE2	3:L:177:TYR:OH	2.31	0.41
1:A:230:GLU:O	1:C:145:TYR:OH	2.36	0.41
1:C:174[A]:GLN:HG3	1:C:223:ILE:O	2.21	0.41
2:X:151:PHE:HA	2:X:152:PRO:HA	1.89	0.40
2:X:172:PRO:HD2	3:Y:166:SER:OG	2.20	0.40
1:B:174[B]:GLN:O	1:B:254:THR:HA	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	138/146 (94%)	134 (97%)	4 (3%)	0	100	100
1	B	139/146 (95%)	135 (97%)	4 (3%)	0	100	100
1	C	138/146 (94%)	132 (96%)	6 (4%)	0	100	100
2	H	210/226 (93%)	200 (95%)	10 (5%)	0	100	100
2	K	210/226 (93%)	205 (98%)	5 (2%)	0	100	100
2	X	213/226 (94%)	207 (97%)	6 (3%)	0	100	100
3	L	204/218 (94%)	195 (96%)	9 (4%)	0	100	100
3	M	215/218 (99%)	207 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Y	216/218 (99%)	211 (98%)	5 (2%)	0	100	100
All	All	1683/1770 (95%)	1626 (97%)	57 (3%)	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	116/122 (95%)	112 (97%)	4 (3%)	32	33
1	B	116/122 (95%)	106 (91%)	10 (9%)	10	6
1	C	117/122 (96%)	113 (97%)	4 (3%)	32	33
2	H	172/194 (89%)	158 (92%)	14 (8%)	11	7
2	K	176/194 (91%)	170 (97%)	6 (3%)	32	33
2	X	179/194 (92%)	172 (96%)	7 (4%)	28	28
3	L	176/191 (92%)	174 (99%)	2 (1%)	65	73
3	M	186/191 (97%)	178 (96%)	8 (4%)	26	25
3	Y	188/191 (98%)	179 (95%)	9 (5%)	23	21
All	All	1426/1521 (94%)	1362 (96%)	64 (4%)	26	23

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	160	GLN
1	A	174[A]	GLN
1	A	174[B]	GLN
1	A	197	SER
1	B	136	SER
1	B	152	LEU
1	B	174[A]	GLN
1	B	174[B]	GLN
1	B	193	LEU

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Mol	Chain	Res	Type
1	B	196	LYS
1	B	207[A]	ARG
1	B	207[B]	ARG
1	B	211	THR
1	B	261	LEU
1	C	135	THR
1	C	168	LEU
1	C	210	ASN
1	C	225	LEU
2	H	10	GLU
2	H	34[A]	MET
2	H	34[B]	MET
2	H	47	LEU
2	H	63	LYS
2	H	85	SER
2	H	116	VAL
2	H	143	LEU
2	H	148	LYS
2	H	155	VAL
2	H	174	VAL
2	H	175	LEU
2	H	186	VAL
2	H	217	GLU
3	L	195	VAL
3	L	200	VAL
2	K	85	SER
2	K	87	ARG
2	K	116	VAL
2	K	183	LEU
2	K	186	VAL
2	K	197	GLN
3	M	51	LEU
3	M	58	LEU
3	M	85	GLU
3	M	127	GLU
3	M	156	ASN
3	M	195	VAL
3	M	205	LEU
3	M	209	VAL
2	X	47	LEU
2	X	85	SER
2	X	143	LEU

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Mol	Chain	Res	Type
2	X	180	LEU
2	X	183	LEU
2	X	192	SER
2	X	218	PRO
3	Y	112[A]	ARG
3	Y	112[B]	ARG
3	Y	130	LYS
3	Y	136	VAL
3	Y	146	ARG
3	Y	151	GLN
3	Y	185	LEU
3	Y	195	VAL
3	Y	209	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	ASN
1	A	160	GLN
1	A	220	GLN
1	B	139	GLN
3	L	41	GLN
3	L	164	GLN
2	K	59	ASN
2	K	197	GLN
2	K	209	ASN
3	M	41	GLN
3	M	151	GLN
3	M	156	ASN
2	X	43	GLN
2	X	204	ASN
3	Y	41	GLN
3	Y	151	GLN
3	Y	164	GLN
3	Y	214	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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
3	DV7	Y	98	3	18,19,20	1.28	4 (22%)	21,26,28	1.72	4 (19%)
3	DV7	M	98	3	18,19,20	1.14	2 (11%)	21,26,28	1.48	4 (19%)
3	DV7	L	98	3	18,19,20	1.10	1 (5%)	21,26,28	1.44	4 (19%)

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	DV7	Y	98	3	-	1/6/7/9	0/2/2/2
3	DV7	M	98	3	-	2/6/7/9	0/2/2/2
3	DV7	L	98	3	-	2/6/7/9	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Y	98	DV7	CH1-CT	2.64	1.43	1.39
3	M	98	DV7	CH1-CT	2.49	1.42	1.39
3	Y	98	DV7	CG-CD	2.36	1.54	1.50
3	L	98	DV7	CH1-CT	2.27	1.42	1.39
3	M	98	DV7	CH2-CZ3	-2.23	1.35	1.38
3	Y	98	DV7	CB-CA	-2.10	1.50	1.53
3	Y	98	DV7	OH1-CZ2	2.06	1.41	1.38

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Y	98	DV7	CG-CD-CE2	3.91	123.00	118.68
3	Y	98	DV7	OH1-CZ2-CE2	-3.52	118.37	121.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	98	DV7	CH2-CT-CH1	-3.14	116.74	120.19
3	L	98	DV7	OH1-CZ2-CE2	-3.10	118.75	121.57
3	Y	98	DV7	OH1-CZ1-CE1	3.01	120.83	117.16
3	M	98	DV7	OH1-CZ2-CE2	-2.69	119.13	121.57
3	L	98	DV7	OH1-CZ1-CE1	2.59	120.31	117.16
3	M	98	DV7	CZ3-CH2-CT	2.38	122.40	119.88
3	L	98	DV7	CZ3-CH2-CT	2.38	122.39	119.88
3	Y	98	DV7	OH2-CZ1-CE1	-2.29	121.31	125.92
3	M	98	DV7	OH1-CZ2-CH1	2.09	118.80	115.83
3	L	98	DV7	CZ3-CE2-CZ2	-2.08	115.47	118.21

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L	98	DV7	O-C-CA-CB
3	L	98	DV7	CE2-CD-CG-CB
3	M	98	DV7	CA-CB-CG-CD
3	M	98	DV7	CE2-CD-CG-CB
3	Y	98	DV7	CE2-CD-CG-CB

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](#)

20 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
7	TMO	M	301[A]	-	4,4,4	0.94	0	6,6,6	0.05	0
6	PEG	A	303	-	6,6,6	0.16	0	5,5,5	0.11	0
6	PEG	L	303	-	4,4,6	0.27	0	3,3,5	0.21	0
6	PEG	M	302[B]	-	6,6,6	0.10	0	5,5,5	0.10	0
6	PEG	H	301	-	4,4,6	0.24	0	3,3,5	0.17	0
4	NAG	B	301	1	14,14,15	0.94	0	17,19,21	2.71	3 (17%)
6	PEG	Y	302	-	5,5,6	0.27	0	4,4,5	0.17	0
7	TMO	Y	301	-	4,4,4	0.97	0	6,6,6	0.07	0
6	PEG	K	301	-	6,6,6	0.15	0	5,5,5	0.06	0
7	TMO	L	301[B]	-	4,4,4	1.08	1 (25%)	6,6,6	0.08	0
5	TRS	A	302	-	7,7,7	0.13	0	9,9,9	0.42	0
6	PEG	C	302	-	6,6,6	0.25	0	5,5,5	0.19	0
6	PEG	L	302[A]	-	6,6,6	0.21	0	5,5,5	0.14	0
6	PEG	X	301	-	6,6,6	0.19	0	5,5,5	0.14	0
6	PEG	L	304	-	6,6,6	0.14	0	5,5,5	0.12	0
4	NAG	C	301	1	14,14,15	0.86	1 (7%)	17,19,21	2.10	3 (17%)
6	PEG	B	302	-	6,6,6	0.21	0	5,5,5	0.14	0
4	NAG	A	301	1	14,14,15	1.00	2 (14%)	17,19,21	2.06	4 (23%)
6	PEG	H	302	-	6,6,6	0.22	0	5,5,5	0.13	0
6	PEG	Y	303	-	6,6,6	0.16	0	5,5,5	0.08	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
4	NAG	B	301	1	-	2/6/23/26	0/1/1/1
4	NAG	A	301	1	-	2/6/23/26	0/1/1/1
6	PEG	C	302	-	-	2/4/4/4	-
6	PEG	L	302[A]	-	-	3/4/4/4	-
6	PEG	A	303	-	-	2/4/4/4	-
6	PEG	L	303	-	-	1/2/2/4	-
6	PEG	M	302[B]	-	-	2/4/4/4	-
6	PEG	X	301	-	-	3/4/4/4	-
6	PEG	H	302	-	-	3/4/4/4	-
6	PEG	K	301	-	-	2/4/4/4	-
6	PEG	H	301	-	-	2/2/2/4	-
6	PEG	Y	302	-	-	2/3/3/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	TRS	A	302	-	-	3/9/9/9	-
6	PEG	L	304	-	-	0/4/4/4	-
4	NAG	C	301	1	-	0/6/23/26	0/1/1/1
6	PEG	B	302	-	-	2/4/4/4	-
6	PEG	Y	303	-	-	2/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	301	NAG	C1-C2	2.14	1.55	1.52
7	L	301[B]	TMO	OAE-NAC	-2.11	1.39	1.42
4	A	301	NAG	O5-C1	2.09	1.47	1.43
4	C	301	NAG	C1-C2	2.04	1.55	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	301	NAG	C1-O5-C5	10.01	125.60	112.19
4	C	301	NAG	C1-O5-C5	7.10	121.71	112.19
4	A	301	NAG	C1-O5-C5	6.06	120.31	112.19
4	A	301	NAG	C1-C2-N2	3.43	115.84	110.43
4	C	301	NAG	O7-C7-C8	2.50	126.51	122.05
4	A	301	NAG	C6-C5-C4	-2.44	107.04	113.02
4	C	301	NAG	C6-C5-C4	-2.38	107.17	113.02
4	B	301	NAG	C6-C5-C4	-2.18	107.66	113.02
4	A	301	NAG	C8-C7-N2	-2.10	112.64	116.12
4	B	301	NAG	O5-C5-C4	2.07	115.86	110.83

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	302	TRS	C1-C-C3-O3
5	A	302	TRS	C2-C-C3-O3
6	K	301	PEG	O1-C1-C2-O2
6	A	303	PEG	O1-C1-C2-O2
6	B	302	PEG	O2-C3-C4-O4
6	H	302	PEG	O2-C3-C4-O4
4	A	301	NAG	C4-C5-C6-O6
4	B	301	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
6	H	302	PEG	O1-C1-C2-O2
6	K	301	PEG	O2-C3-C4-O4
6	C	302	PEG	O2-C3-C4-O4
6	Y	303	PEG	O2-C3-C4-O4
6	L	302[A]	PEG	O2-C3-C4-O4
6	X	301	PEG	O1-C1-C2-O2
6	X	301	PEG	O2-C3-C4-O4
4	A	301	NAG	O5-C5-C6-O6
6	Y	303	PEG	O1-C1-C2-O2
6	Y	302	PEG	C1-C2-O2-C3
6	L	303	PEG	C4-C3-O2-C2
5	A	302	TRS	N-C-C3-O3
6	M	302[B]	PEG	C4-C3-O2-C2
4	B	301	NAG	O5-C5-C6-O6
6	L	302[A]	PEG	C1-C2-O2-C3
6	Y	302	PEG	O2-C3-C4-O4
6	L	302[A]	PEG	O1-C1-C2-O2
6	A	303	PEG	C4-C3-O2-C2
6	X	301	PEG	C4-C3-O2-C2
6	H	301	PEG	C4-C3-O2-C2
6	C	302	PEG	C4-C3-O2-C2
6	H	302	PEG	C1-C2-O2-C3
6	B	302	PEG	O1-C1-C2-O2
6	M	302[B]	PEG	O1-C1-C2-O2
6	H	301	PEG	O2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	302	TRS	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	137/146 (93%)	-0.03	4 (2%)	53	52	9, 18, 38, 50	7 (5%)
1	B	140/146 (95%)	-0.04	5 (3%)	46	45	7, 18, 38, 53	5 (3%)
1	C	137/146 (93%)	-0.06	6 (4%)	39	38	9, 17, 35, 47	7 (5%)
2	H	211/226 (93%)	0.63	25 (11%)	9	8	11, 36, 65, 79	5 (2%)
2	K	213/226 (94%)	0.13	4 (1%)	66	66	11, 28, 41, 52	1 (0%)
2	X	214/226 (94%)	0.01	6 (2%)	55	54	10, 25, 40, 51	3 (1%)
3	L	207/218 (94%)	-0.02	7 (3%)	48	47	12, 21, 55, 72	3 (1%)
3	M	216/218 (99%)	-0.10	7 (3%)	50	49	11, 20, 43, 60	1 (0%)
3	Y	215/218 (98%)	-0.22	1 (0%)	87	87	11, 19, 44, 55	3 (1%)
All	All	1690/1770 (95%)	0.04	65 (3%)	44	43	7, 23, 48, 79	35 (2%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	42[A]	GLY	7.3
3	L	216	GLY	5.5
1	A	187	ALA	4.6
2	X	132	SER	4.1
2	X	137	SER	4.1
2	X	218	PRO	4.1
2	H	196	THR	3.7
2	H	194	LEU	3.4
2	K	195	GLY	3.3
2	H	198	THR	3.2
2	X	138	GLY	3.2
1	B	182	GLU	3.2
3	M	216	GLY	3.2
3	L	186	SER	3.1
1	A	211	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	182	GLU	3.1
1	C	181	ARG	3.0
3	L	187	LYS	3.0
3	L	127	GLU	2.9
1	C	119	ASN	2.9
2	K	196	THR	2.8
1	C	210	ASN	2.8
3	M	156	ASN	2.8
2	H	164	LEU	2.7
1	B	119	ASN	2.7
3	L	189	ASP	2.7
1	B	184	SER	2.6
1	C	209	ALA	2.6
2	H	195	GLY	2.5
2	H	200	ILE	2.5
2	H	145	CYS	2.4
3	L	198	CYS	2.4
2	K	137	SER	2.4
2	H	179	GLY	2.4
3	M	161	GLY	2.4
1	A	210	ASN	2.4
2	H	176	GLN	2.4
3	M	160	SER	2.4
1	C	187	ALA	2.4
2	H	154	PRO	2.4
2	H	159	TRP	2.4
2	H	218	PRO	2.4
3	Y	156	ASN	2.3
2	X	195	GLY	2.3
2	H	174	VAL	2.3
3	M	158	LEU	2.3
2	H	43[A]	GLN	2.3
2	H	163	ALA	2.3
2	X	192	SER	2.2
2	H	155	VAL	2.2
2	H	197	GLN	2.2
2	H	204	ASN	2.2
2	H	219	LYS	2.2
2	H	165	THR	2.2
3	M	191	GLU	2.1
2	K	204	ASN	2.1
2	H	150	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	135	THR	2.1
3	L	126	ASP	2.1
2	H	41	PRO	2.1
2	H	156	THR	2.1
3	M	198	CYS	2.0
1	B	133	LYS	2.0
2	H	216	VAL	2.0
1	B	183	ALA	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
3	DV7	M	98	18/19	0.94	0.09	18,20,21,22	0
3	DV7	L	98	18/19	0.95	0.09	18,21,23,23	0
3	DV7	Y	98	18/19	0.95	0.08	16,20,21,21	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
4	NAG	A	301	14/15	0.74	0.18	43,52,56,56	0
6	PEG	H	302	7/7	0.75	0.28	66,66,67,68	0
6	PEG	C	302	7/7	0.77	0.18	48,48,56,57	0
6	PEG	A	303	7/7	0.77	0.22	58,60,66,67	0
6	PEG	L	304	7/7	0.77	0.22	55,60,61,62	0
6	PEG	B	302	7/7	0.78	0.18	53,55,57,57	0
6	PEG	H	301	5/7	0.80	0.18	44,45,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	TMO	M	301[A]	5/5	0.82	0.37	27,28,29,31	5
6	PEG	Y	303	7/7	0.84	0.20	54,55,59,59	0
4	NAG	B	301	14/15	0.84	0.14	39,49,51,55	0
4	NAG	C	301	14/15	0.85	0.13	32,43,46,50	0
6	PEG	K	301	7/7	0.85	0.20	49,51,54,56	0
6	PEG	X	301	7/7	0.86	0.18	56,59,61,61	0
6	PEG	L	303	5/7	0.86	0.19	58,58,59,60	0
6	PEG	M	302[B]	7/7	0.86	0.30	21,23,25,27	7
6	PEG	L	302[A]	7/7	0.87	0.22	24,24,26,26	7
7	TMO	L	301[B]	5/5	0.87	0.40	24,24,25,25	5
5	TRS	A	302	8/8	0.87	0.16	50,53,56,58	0
6	PEG	Y	302	6/7	0.88	0.17	48,48,49,52	0
7	TMO	Y	301	5/5	0.89	0.20	60,61,61,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.