



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:34 PM UTC

PDB ID : 5AJI / pdb_00005aji
Title : MscS D67R1 high resolution
Authors : Naismith, J.H.; Pliotas, C.
Deposited on : 2015-02-24
Resolution : 2.99 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

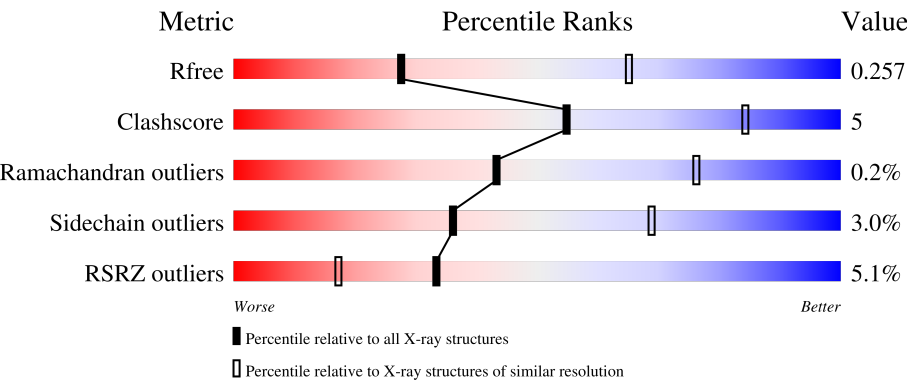
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	286	
1	B	286	
1	C	286	
1	D	286	
1	E	286	

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Mol	Chain	Length	Quality of chain
1	F	286	5% 78% 10% 10%
1	G	286	5% 76% 12% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13963 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.

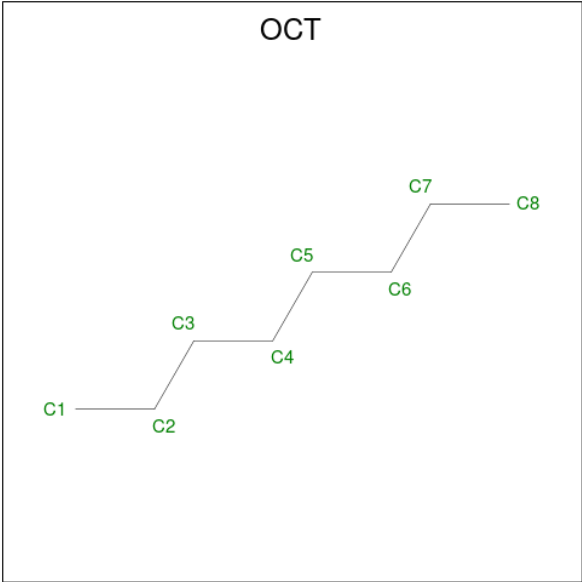
- Molecule 1 is a protein called SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	0	0
			2022	1300	353	361	8			
1	B	255	Total	C	N	O	S	0	0	0
			1956	1257	341	350	8			
1	C	255	Total	C	N	O	S	0	0	0
			1956	1257	341	350	8			
1	D	263	Total	C	N	O	S	0	0	0
			2014	1295	351	360	8			
1	E	262	Total	C	N	O	S	0	0	0
			2003	1289	347	359	8			
1	F	256	Total	C	N	O	S	0	0	0
			1963	1262	342	351	8			
1	G	254	Total	C	N	O	S	0	0	0
			1945	1251	337	349	8			

There are 7 discrepancies between the modelled and reference sequences:

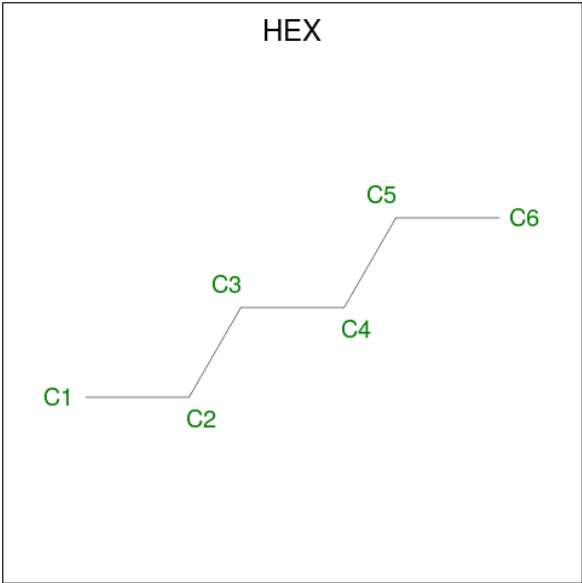
Chain	Residue	Modelled	Actual	Comment	Reference
A	67	R1A	ASP	engineered mutation	UNP P0C0S2
B	67	R1A	ASP	engineered mutation	UNP P0C0S2
C	67	R1A	ASP	engineered mutation	UNP P0C0S2
D	67	R1A	ASP	engineered mutation	UNP P0C0S2
E	67	R1A	ASP	engineered mutation	UNP P0C0S2
F	67	R1A	ASP	engineered mutation	UNP P0C0S2
G	67	R1A	ASP	engineered mutation	UNP P0C0S2

- Molecule 2 is N-OCTANE (CCD ID: OCT) (formula: C₈H₁₈).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	C	0	0
			8	8		
2	E	1	Total	C	0	0
			8	8		

- Molecule 3 is HEXANE (CCD ID: HEX) (formula: C₆H₁₄).



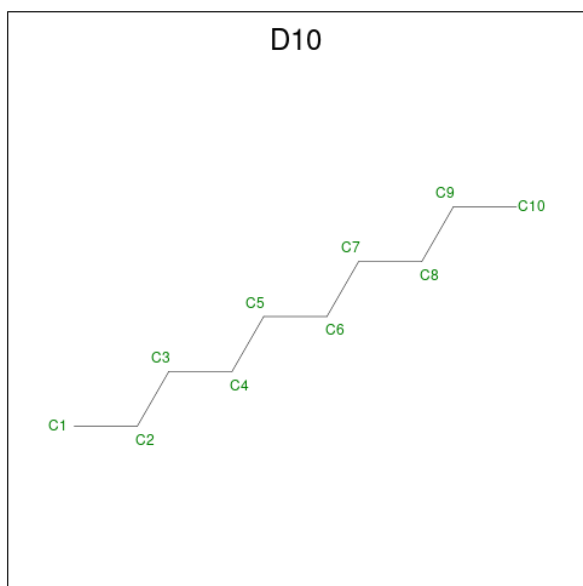
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C	0	0
			6	6		
3	B	1	Total	C	0	0
			6	6		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C 6 6	0	0
3	C	1	Total C 6 6	0	0
3	C	1	Total C 6 6	0	0
3	D	1	Total C 6 6	0	0
3	E	1	Total C 6 6	0	0
3	E	1	Total C 6 6	0	0
3	F	1	Total C 6 6	0	0
3	F	1	Total C 6 6	0	0

- Molecule 4 is DECANE (CCD ID: D10) (formula: $C_{10}H_{22}$).

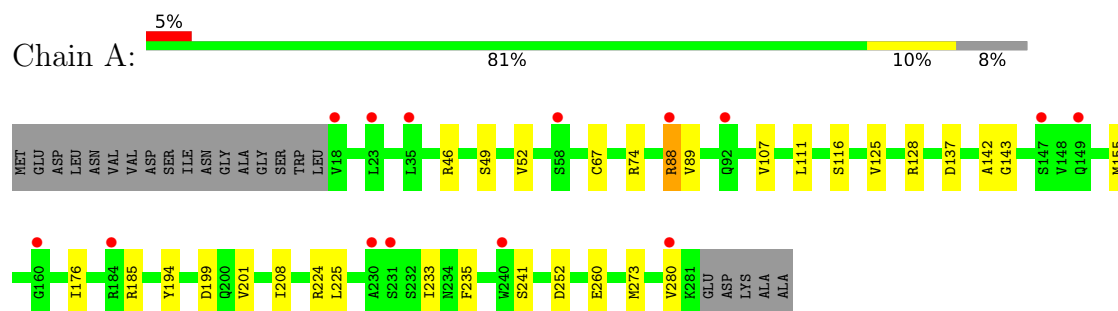


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C 8 8	0	0
4	D	1	Total C 10 10	0	0
4	G	1	Total C 10 10	0	0

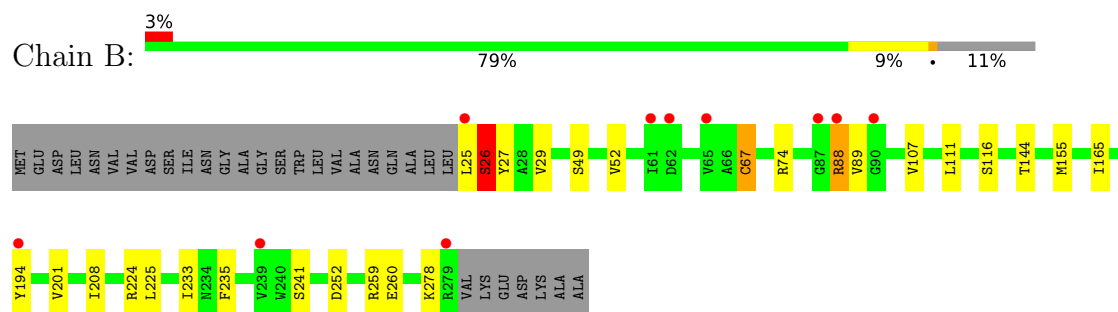
3 Residue-property plots

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.

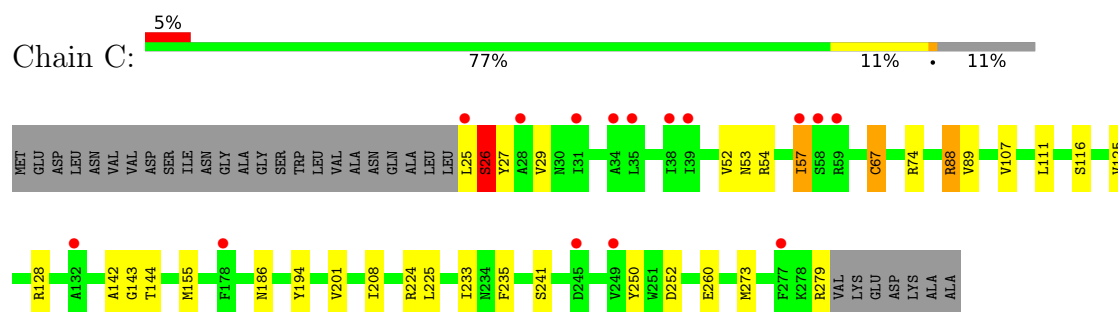
• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL



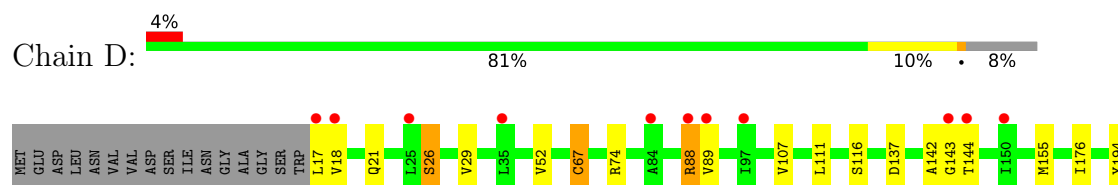
• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL



• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

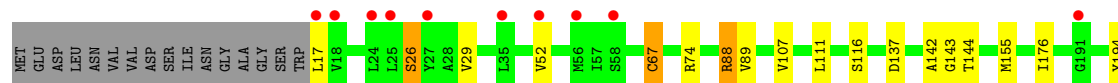
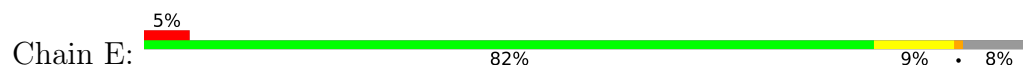


• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

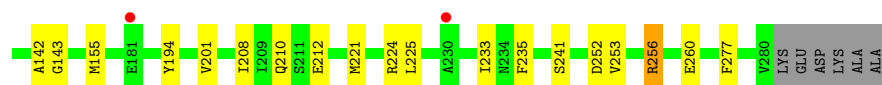
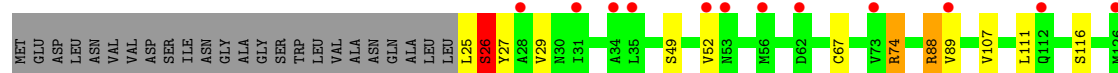
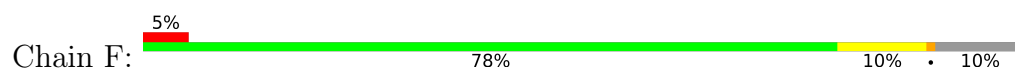




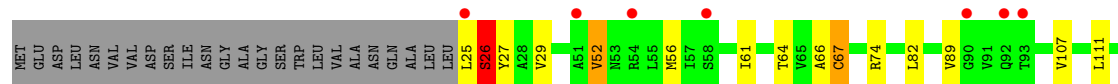
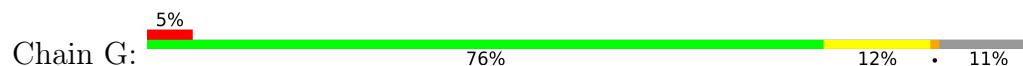
• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL



• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL



• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	126.33Å 149.09Å 173.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	68.51 – 2.99 68.51 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.6 (68.51-2.99) 99.6 (68.51-2.99)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.244 , 0.263 0.243 , 0.257	Depositor DCC
R_{free} test set	3401 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	90.8	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 69.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13963	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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: D10, OCT, HEX, R1A

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	0.57	0/2028	0.83	1/2748 (0.0%)
1	B	0.56	0/1962	0.80	0/2658
1	C	0.55	0/1962	0.83	2/2658 (0.1%)
1	D	0.57	2/2020 (0.1%)	0.80	0/2738
1	E	0.58	1/2009 (0.0%)	0.80	0/2724
1	F	0.59	1/1969 (0.1%)	0.83	2/2668 (0.1%)
1	G	0.52	0/1951	0.82	1/2644 (0.0%)
All	All	0.57	4/13901 (0.0%)	0.82	6/18838 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	89	VAL	CA-CB	6.62	1.62	1.54
1	D	279	ARG	C-O	5.52	1.34	1.23
1	D	26	SER	CA-C	5.41	1.60	1.52
1	E	26	SER	CA-C	5.36	1.59	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	256	ARG	CB-CG-CD	-6.51	96.33	111.30
1	A	185	ARG	CG-CD-NE	5.94	125.06	112.00
1	G	214	ARG	CG-CD-NE	5.76	124.68	112.00
1	C	57	ILE	N-CA-CB	5.63	118.19	110.54
1	C	88	ARG	CA-CB-CG	5.35	124.81	114.10
1	F	89	VAL	N-CA-C	-5.29	107.21	111.91

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	2022	0	2130	24	0
1	B	1956	0	2053	17	0
1	C	1956	0	2053	23	0
1	D	2014	0	2119	21	0
1	E	2003	0	2106	19	0
1	F	1963	0	2062	23	0
1	G	1945	0	2040	29	0
2	A	8	0	18	0	0
2	E	8	0	18	0	0
3	A	6	0	14	0	0
3	B	12	0	28	0	0
3	C	12	0	28	0	0
3	D	6	0	14	0	0
3	E	12	0	28	0	0
3	F	12	0	28	0	0
4	C	8	0	15	0	0
4	D	10	0	22	0	0
4	G	10	0	22	0	0
All	All	13963	0	14798	138	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 (138) 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)
1:G:185:ARG:NH1	1:G:238:ARG:HD3	1.88	0.87
1:A:273:MET:HB2	1:G:273:MET:HE2	1.66	0.76
1:A:224:ARG:NH2	1:B:252:ASP:OD1	2.18	0.75
1:F:49:SER:OG	1:F:74:ARG:HG2	1.87	0.75
1:E:224:ARG:NH2	1:F:252:ASP:OD1	2.22	0.73
1:F:49:SER:CB	1:F:74:ARG:HG2	2.23	0.69
1:C:224:ARG:NH2	1:D:252:ASP:OD1	2.28	0.67
1:C:25:LEU:O	1:C:27:TYR:N	2.30	0.64
1:G:25:LEU:O	1:G:27:TYR:N	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:LEU:O	1:B:27:TYR:N	2.31	0.64
1:G:56:MET:HG3	1:G:66:ALA:CB	2.28	0.63
1:F:25:LEU:O	1:F:27:TYR:N	2.31	0.63
1:B:224:ARG:NH2	1:C:252:ASP:OD1	2.34	0.61
1:D:224:ARG:NH2	1:E:252:ASP:OD1	2.34	0.61
1:A:194:TYR:HA	1:A:233:ILE:HD13	1.84	0.60
1:A:273:MET:CB	1:G:273:MET:HE2	2.32	0.59
1:D:194:TYR:HA	1:D:233:ILE:HD13	1.83	0.58
1:B:194:TYR:HA	1:B:233:ILE:HD13	1.85	0.58
1:F:194:TYR:HA	1:F:233:ILE:HD13	1.85	0.58
1:D:143:GLY:CA	1:D:155:MET:HE3	2.34	0.58
1:C:194:TYR:HA	1:C:233:ILE:HD13	1.85	0.57
1:E:194:TYR:HA	1:E:233:ILE:HD13	1.85	0.57
1:G:194:TYR:HA	1:G:233:ILE:HD13	1.84	0.57
1:C:143:GLY:CA	1:C:155:MET:HE3	2.35	0.57
1:C:225:LEU:HD13	1:C:233:ILE:HG23	1.87	0.57
1:E:143:GLY:CA	1:E:155:MET:HE3	2.34	0.57
1:B:225:LEU:HD13	1:B:233:ILE:HG23	1.87	0.57
1:G:225:LEU:HD13	1:G:233:ILE:HG23	1.87	0.57
1:D:67:R1A:O1	1:D:74:ARG:NH1	2.38	0.56
1:F:224:ARG:NH2	1:G:252:ASP:OD1	2.38	0.56
1:F:225:LEU:HD13	1:F:233:ILE:HG23	1.87	0.56
1:G:143:GLY:CA	1:G:155:MET:HE3	2.36	0.56
1:F:143:GLY:CA	1:F:155:MET:HE3	2.35	0.56
1:E:67:R1A:O1	1:E:74:ARG:NH1	2.40	0.55
1:E:225:LEU:HD13	1:E:233:ILE:HG23	1.87	0.55
1:A:143:GLY:CA	1:A:155:MET:HE3	2.35	0.55
1:D:225:LEU:HD13	1:D:233:ILE:HG23	1.88	0.55
1:B:67:R1A:O1	1:B:74:ARG:NH1	2.40	0.54
1:G:67:R1A:O1	1:G:74:ARG:NH1	2.40	0.54
1:C:273:MET:HE3	1:D:273:MET:CB	2.38	0.54
1:A:225:LEU:HD13	1:A:233:ILE:HG23	1.89	0.53
1:C:67:R1A:O1	1:C:74:ARG:NH1	2.40	0.53
1:A:252:ASP:OD1	1:G:224:ARG:NH2	2.41	0.52
1:E:201:VAL:HG11	1:E:235:PHE:CE1	2.44	0.52
1:F:212:GLU:OE1	1:F:256:ARG:NH2	2.43	0.51
1:G:56:MET:HG3	1:G:66:ALA:HB1	1.93	0.50
1:A:201:VAL:HG11	1:A:235:PHE:CE1	2.47	0.50
1:C:201:VAL:HG11	1:C:235:PHE:CE1	2.47	0.50
1:B:201:VAL:HG11	1:B:235:PHE:CE1	2.47	0.50
1:D:142:ALA:C	1:D:155:MET:CE	2.85	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:VAL:HG11	1:D:235:PHE:CE1	2.47	0.49
1:G:201:VAL:HG11	1:G:235:PHE:CE1	2.47	0.49
1:C:186:ASN:ND2	1:C:250:TYR:HB2	2.28	0.49
1:A:88:ARG:N	1:A:88:ARG:HD3	2.28	0.49
1:F:253:VAL:HA	1:F:256:ARG:HH11	1.78	0.49
1:C:142:ALA:C	1:C:155:MET:CE	2.86	0.48
1:E:107:VAL:HG12	1:E:111:LEU:HD12	1.95	0.48
1:A:142:ALA:C	1:A:155:MET:CE	2.86	0.48
1:C:107:VAL:HG12	1:C:111:LEU:HD12	1.96	0.48
1:D:26:SER:O	1:D:29:VAL:HG22	2.13	0.48
1:F:26:SER:O	1:F:29:VAL:HG22	2.14	0.48
1:B:49:SER:HA	1:B:52:VAL:HG22	1.96	0.48
1:B:88:ARG:N	1:B:88:ARG:HD3	2.29	0.48
1:C:225:LEU:CD1	1:C:233:ILE:HG23	2.44	0.48
1:A:107:VAL:HG12	1:A:111:LEU:HD12	1.96	0.48
1:F:201:VAL:HG11	1:F:235:PHE:CE1	2.48	0.48
1:E:225:LEU:CD1	1:E:233:ILE:HG23	2.44	0.48
1:A:49:SER:HA	1:A:52:VAL:HG22	1.95	0.47
1:D:88:ARG:N	1:D:88:ARG:HD3	2.29	0.47
1:G:26:SER:O	1:G:29:VAL:HG22	2.14	0.47
1:D:107:VAL:HG12	1:D:111:LEU:HD12	1.95	0.47
1:F:142:ALA:C	1:F:155:MET:CE	2.87	0.47
1:G:225:LEU:CD1	1:G:233:ILE:HG23	2.44	0.47
1:A:46:ARG:HD2	1:A:74:ARG:HH12	1.79	0.47
1:D:225:LEU:CD1	1:D:233:ILE:HG23	2.44	0.47
1:F:107:VAL:HG12	1:F:111:LEU:HD12	1.97	0.47
1:B:225:LEU:CD1	1:B:233:ILE:HG23	2.44	0.47
1:A:125:VAL:O	1:A:128:ARG:HG2	2.15	0.47
1:E:88:ARG:N	1:E:88:ARG:HD3	2.30	0.47
1:E:26:SER:O	1:E:29:VAL:HG12	2.15	0.46
1:G:107:VAL:HG12	1:G:111:LEU:HD12	1.96	0.46
1:D:143:GLY:N	1:D:155:MET:CE	2.78	0.46
1:F:225:LEU:CD1	1:F:233:ILE:HG23	2.45	0.46
1:A:199:ASP:OD1	1:B:259:ARG:NH2	2.48	0.46
1:A:143:GLY:N	1:A:155:MET:CE	2.79	0.46
1:A:225:LEU:CD1	1:A:233:ILE:HG23	2.45	0.46
1:E:142:ALA:C	1:E:155:MET:CE	2.89	0.46
1:F:88:ARG:N	1:F:88:ARG:HD3	2.31	0.46
1:B:107:VAL:HG12	1:B:111:LEU:HD12	1.97	0.46
1:C:279:ARG:HB3	1:D:277:PHE:HB2	1.98	0.46
1:C:54:ARG:HA	1:C:57:ILE:CG1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:125:VAL:O	1:C:128:ARG:HG2	2.16	0.45
1:E:143:GLY:HA3	1:E:155:MET:HE3	1.97	0.45
1:C:26:SER:O	1:C:29:VAL:HG12	2.15	0.45
1:C:143:GLY:N	1:C:155:MET:CE	2.79	0.45
1:G:142:ALA:C	1:G:155:MET:CE	2.89	0.45
1:A:280:VAL:HG11	1:B:278:LYS:HE2	1.98	0.45
1:F:143:GLY:HA3	1:F:155:MET:HE3	1.98	0.45
1:C:143:GLY:HA3	1:C:155:MET:HE3	1.99	0.45
1:B:26:SER:O	1:B:29:VAL:HG12	2.16	0.45
1:D:143:GLY:N	1:D:155:MET:HE3	2.32	0.44
1:A:143:GLY:N	1:A:155:MET:HE3	2.32	0.44
1:G:143:GLY:HA3	1:G:155:MET:HE3	2.00	0.44
1:D:143:GLY:HA3	1:D:155:MET:HE3	1.99	0.44
1:E:143:GLY:N	1:E:155:MET:CE	2.81	0.44
1:F:143:GLY:N	1:F:155:MET:CE	2.81	0.44
1:A:143:GLY:HA3	1:A:155:MET:HE3	1.99	0.43
1:C:143:GLY:N	1:C:155:MET:HE3	2.33	0.43
1:C:53:ASN:O	1:C:57:ILE:HG12	2.19	0.43
1:C:273:MET:HE3	1:D:273:MET:HB3	2.01	0.43
1:G:143:GLY:N	1:G:155:MET:CE	2.82	0.43
1:F:143:GLY:N	1:F:155:MET:HE3	2.34	0.42
1:A:273:MET:HE2	1:G:273:MET:CE	2.50	0.42
1:E:143:GLY:N	1:E:155:MET:HE3	2.35	0.42
1:G:137:ASP:HB3	1:G:176:ILE:HB	2.02	0.42
1:G:143:GLY:N	1:G:155:MET:HE3	2.35	0.42
1:C:208:ILE:HD11	1:C:260:GLU:HG3	2.02	0.42
1:F:208:ILE:HD11	1:F:260:GLU:HG3	2.02	0.42
1:A:208:ILE:HD11	1:A:260:GLU:HG3	2.02	0.42
1:D:18:VAL:O	1:D:21:GLN:CD	2.63	0.41
1:E:208:ILE:HD11	1:E:260:GLU:HG3	2.02	0.41
1:G:52:VAL:HG13	1:G:56:MET:CE	2.50	0.41
1:E:137:ASP:HB3	1:E:176:ILE:HB	2.02	0.41
1:E:277:PHE:CE1	1:F:277:PHE:HZ	2.38	0.41
1:A:273:MET:HB2	1:G:273:MET:CE	2.43	0.41
1:B:208:ILE:HD11	1:B:260:GLU:HG3	2.02	0.41
1:E:277:PHE:CE1	1:F:277:PHE:CZ	3.09	0.41
1:G:56:MET:HB2	1:G:61:ILE:HD12	2.03	0.41
1:F:210:GLN:NE2	1:F:221:MET:HE1	2.36	0.41
1:B:155:MET:HE3	1:B:165:ILE:CD1	2.51	0.41
1:G:56:MET:HG3	1:G:66:ALA:HB2	2.02	0.40
1:A:137:ASP:HB3	1:A:176:ILE:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:137:ASP:HB3	1:D:176:ILE:HB	2.03	0.40
1:D:208:ILE:HD11	1:D:260:GLU:HG3	2.03	0.40
1:G:64:THR:CG2	1:G:118:LEU:HD11	2.52	0.40
1:B:155:MET:HE3	1:B:165:ILE:HD12	2.04	0.40
1:G:56:MET:HB2	1:G:61:ILE:CD1	2.51	0.40
1:G:208:ILE:HD11	1:G:260:GLU:HG3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	261/286 (91%)	255 (98%)	6 (2%)	0	100	100
1	B	252/286 (88%)	247 (98%)	4 (2%)	1 (0%)	30	65
1	C	252/286 (88%)	247 (98%)	4 (2%)	1 (0%)	30	65
1	D	260/286 (91%)	253 (97%)	7 (3%)	0	100	100
1	E	259/286 (91%)	252 (97%)	7 (3%)	0	100	100
1	F	253/286 (88%)	248 (98%)	4 (2%)	1 (0%)	30	65
1	G	251/286 (88%)	245 (98%)	5 (2%)	1 (0%)	30	65
All	All	1788/2002 (89%)	1747 (98%)	37 (2%)	4 (0%)	43	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	26	SER
1	C	26	SER
1	F	26	SER
1	G	26	SER

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	213/230 (93%)	209 (98%)	4 (2%)	50	76
1	B	206/230 (90%)	200 (97%)	6 (3%)	37	70
1	C	206/230 (90%)	199 (97%)	7 (3%)	32	66
1	D	212/230 (92%)	205 (97%)	7 (3%)	33	67
1	E	211/230 (92%)	204 (97%)	7 (3%)	33	67
1	F	207/230 (90%)	201 (97%)	6 (3%)	37	70
1	G	205/230 (89%)	198 (97%)	7 (3%)	32	66
All	All	1460/1610 (91%)	1416 (97%)	44 (3%)	36	69

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	ARG
1	A	89	VAL
1	A	116	SER
1	A	241	SER
1	B	26	SER
1	B	88	ARG
1	B	89	VAL
1	B	116	SER
1	B	144	THR
1	B	241	SER
1	C	26	SER
1	C	52	VAL
1	C	88	ARG
1	C	89	VAL
1	C	116	SER
1	C	144	THR
1	C	241	SER
1	D	17	LEU
1	D	52	VAL
1	D	88	ARG

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Mol	Chain	Res	Type
1	D	89	VAL
1	D	116	SER
1	D	144	THR
1	D	241	SER
1	E	17	LEU
1	E	52	VAL
1	E	88	ARG
1	E	89	VAL
1	E	116	SER
1	E	144	THR
1	E	241	SER
1	F	26	SER
1	F	52	VAL
1	F	74	ARG
1	F	88	ARG
1	F	116	SER
1	F	241	SER
1	G	26	SER
1	G	52	VAL
1	G	82	LEU
1	G	89	VAL
1	G	116	SER
1	G	144	THR
1	G	241	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	GLN
1	A	247	GLN
1	A	272	GLN
1	B	272	GLN
1	B	276	ASN
1	C	203	GLN
1	C	207	ASN
1	C	272	GLN
1	D	272	GLN
1	E	276	ASN
1	F	210	GLN
1	G	149	GLN
1	G	272	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

7 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$
1	R1A	B	67	1	15,18,19	1.27	1 (6%)	15,27,29	2.85	3 (20%)
1	R1A	G	67	1	15,18,19	1.26	1 (6%)	15,27,29	2.82	3 (20%)
1	R1A	F	67	1	15,18,19	1.24	1 (6%)	15,27,29	3.17	3 (20%)
1	R1A	E	67	1	15,18,19	1.28	1 (6%)	15,27,29	3.16	3 (20%)
1	R1A	A	67	1	15,18,19	1.30	1 (6%)	15,27,29	3.09	3 (20%)
1	R1A	D	67	1	15,18,19	1.31	1 (6%)	15,27,29	2.83	3 (20%)
1	R1A	C	67	1	15,18,19	1.30	1 (6%)	15,27,29	2.79	3 (20%)

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
1	R1A	B	67	1	-	2/5/32/34	0/1/1/1
1	R1A	G	67	1	-	2/5/32/34	0/1/1/1
1	R1A	F	67	1	-	2/5/32/34	0/1/1/1
1	R1A	E	67	1	-	2/5/32/34	0/1/1/1
1	R1A	A	67	1	-	2/5/32/34	0/1/1/1
1	R1A	D	67	1	-	2/5/32/34	0/1/1/1
1	R1A	C	67	1	-	2/5/32/34	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	67	R1A	CE-SD	-4.03	1.76	1.82
1	D	67	R1A	CE-SD	-4.01	1.76	1.82
1	C	67	R1A	CE-SD	-4.00	1.76	1.82
1	G	67	R1A	CE-SD	-3.89	1.76	1.82
1	B	67	R1A	CE-SD	-3.86	1.76	1.82
1	E	67	R1A	CE-SD	-3.84	1.76	1.82
1	F	67	R1A	CE-SD	-3.80	1.76	1.82

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	67	R1A	CE-SD-SG	9.11	113.47	103.62
1	F	67	R1A	CE-SD-SG	9.07	113.42	103.62
1	C	67	R1A	CE-SD-SG	8.96	113.31	103.62
1	G	67	R1A	CE-SD-SG	8.94	113.28	103.62
1	D	67	R1A	CE-SD-SG	8.93	113.27	103.62
1	E	67	R1A	CE-SD-SG	8.81	113.15	103.62
1	A	67	R1A	CE-SD-SG	8.80	113.14	103.62
1	E	67	R1A	C7-C5-C4	-7.65	105.38	112.76
1	F	67	R1A	C7-C5-C4	-7.42	105.60	112.76
1	A	67	R1A	C7-C5-C4	-7.25	105.76	112.76
1	D	67	R1A	C6-C5-C4	-5.17	107.77	112.76
1	B	67	R1A	C6-C5-C4	-5.08	107.86	112.76
1	G	67	R1A	C6-C5-C4	-5.00	107.94	112.76
1	C	67	R1A	C6-C5-C4	-4.83	108.10	112.76
1	F	67	R1A	C5-C4-C3	-2.47	111.25	113.48
1	G	67	R1A	C5-C4-C3	-2.37	111.33	113.48
1	B	67	R1A	C5-C4-C3	-2.32	111.38	113.48
1	D	67	R1A	C5-C4-C3	-2.31	111.39	113.48
1	C	67	R1A	C5-C4-C3	-2.22	111.48	113.48
1	A	67	R1A	C5-C4-C3	-2.20	111.49	113.48
1	E	67	R1A	C5-C4-C3	-2.02	111.65	113.48

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	67	R1A	CE-SD-SG-CB
1	A	67	R1A	C3-CE-SD-SG
1	B	67	R1A	CE-SD-SG-CB
1	B	67	R1A	C3-CE-SD-SG
1	C	67	R1A	CE-SD-SG-CB

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Mol	Chain	Res	Type	Atoms
1	C	67	R1A	C3-CE-SD-SG
1	D	67	R1A	CE-SD-SG-CB
1	D	67	R1A	C3-CE-SD-SG
1	E	67	R1A	CE-SD-SG-CB
1	E	67	R1A	C3-CE-SD-SG
1	F	67	R1A	CE-SD-SG-CB
1	F	67	R1A	C3-CE-SD-SG
1	G	67	R1A	CE-SD-SG-CB
1	G	67	R1A	C3-CE-SD-SG

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	67	R1A	1	0
1	G	67	R1A	1	0
1	E	67	R1A	1	0
1	D	67	R1A	1	0
1	C	67	R1A	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

15 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	HEX	A	501	-	5,5,5	0.57	0	4,4,4	0.19	0
3	HEX	C	501	-	5,5,5	0.51	0	4,4,4	0.22	0
3	HEX	E	501	-	5,5,5	0.49	0	4,4,4	0.08	0
4	D10	G	408	-	9,9,9	0.33	0	8,8,8	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEX	C	500	-	5,5,5	0.43	0	4,4,4	0.22	0
2	OCT	E	406	-	7,7,7	0.48	0	6,6,6	0.21	0
3	HEX	F	501	-	5,5,5	0.42	0	4,4,4	0.08	0
3	HEX	B	501	-	5,5,5	0.45	0	4,4,4	0.26	0
3	HEX	B	500	-	5,5,5	0.51	0	4,4,4	0.29	0
2	OCT	A	401	-	7,7,7	0.41	0	6,6,6	0.28	0
3	HEX	F	500	-	5,5,5	0.48	0	4,4,4	0.28	0
4	D10	C	402	-	7,7,9	0.47	0	6,6,8	0.28	0
3	HEX	E	500	-	5,5,5	0.54	0	4,4,4	0.06	0
4	D10	D	404	-	9,9,9	0.38	0	8,8,8	0.40	0
3	HEX	D	501	-	5,5,5	0.40	0	4,4,4	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
3	HEX	A	501	-	-	3/3/3/3	-
3	HEX	C	501	-	-	1/3/3/3	-
3	HEX	E	501	-	-	3/3/3/3	-
4	D10	G	408	-	-	1/7/7/7	-
3	HEX	C	500	-	-	0/3/3/3	-
2	OCT	E	406	-	-	1/5/5/5	-
3	HEX	F	501	-	-	0/3/3/3	-
3	HEX	B	501	-	-	3/3/3/3	-
3	HEX	B	500	-	-	2/3/3/3	-
2	OCT	A	401	-	-	1/5/5/5	-
3	HEX	F	500	-	-	0/3/3/3	-
4	D10	C	402	-	-	0/5/5/7	-
3	HEX	E	500	-	-	2/3/3/3	-
4	D10	D	404	-	-	2/7/7/7	-
3	HEX	D	501	-	-	2/3/3/3	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	HEX	C2-C3-C4-C5
3	E	501	HEX	C2-C3-C4-C5
3	D	501	HEX	C2-C3-C4-C5
3	E	500	HEX	C2-C3-C4-C5
4	G	408	D10	C7-C8-C9-C10
3	E	501	HEX	C3-C4-C5-C6
3	B	501	HEX	C3-C4-C5-C6
4	D	404	D10	C7-C8-C9-C10
3	D	501	HEX	C3-C4-C5-C6
3	C	501	HEX	C3-C4-C5-C6
3	A	501	HEX	C3-C4-C5-C6
3	E	501	HEX	C1-C2-C3-C4
3	A	501	HEX	C1-C2-C3-C4
2	E	406	OCT	C3-C4-C5-C6
3	B	501	HEX	C1-C2-C3-C4
3	B	500	HEX	C1-C2-C3-C4
4	D	404	D10	C5-C6-C7-C8
3	A	501	HEX	C2-C3-C4-C5
3	B	500	HEX	C2-C3-C4-C5
3	E	500	HEX	C1-C2-C3-C4
2	A	401	OCT	C1-C2-C3-C4

There are no ring outliers.

No monomer is involved in short contacts.

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	263/286 (91%)	0.47	14 (5%) 32 16	80, 110, 171, 231	0
1	B	254/286 (88%)	0.36	10 (3%) 43 24	75, 105, 160, 215	0
1	C	254/286 (88%)	0.40	15 (5%) 28 14	76, 111, 159, 189	0
1	D	262/286 (91%)	0.27	11 (4%) 40 22	74, 106, 158, 216	0
1	E	261/286 (91%)	0.25	15 (5%) 29 15	72, 100, 162, 258	0
1	F	255/286 (89%)	0.37	14 (5%) 30 15	75, 108, 154, 170	0
1	G	253/286 (88%)	0.42	13 (5%) 33 17	80, 114, 166, 197	0
All	All	1802/2002 (90%)	0.36	92 (5%) 33 17	72, 108, 163, 258	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	58	SER	8.3
1	A	160	GLY	5.1
1	A	23	LEU	4.7
1	D	144	THR	4.6
1	E	276	ASN	4.4
1	F	56	MET	4.1
1	B	62	ASP	4.0
1	E	275	VAL	3.9
1	A	58	SER	3.8
1	G	58	SER	3.7
1	G	51	ALA	3.7
1	E	17	LEU	3.6
1	G	264	ALA	3.5
1	B	61	ILE	3.5
1	C	35	LEU	3.5
1	F	31	ILE	3.3
1	E	56	MET	3.3

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Mol	Chain	Res	Type	RSRZ
1	G	147	SER	3.3
1	A	240	TRP	3.2
1	D	89	VAL	3.1
1	D	97	ILE	3.1
1	A	35	LEU	3.1
1	A	88	ARG	3.1
1	C	245	ASP	3.0
1	A	149	GLN	3.0
1	A	92	GLN	3.0
1	B	25	LEU	3.0
1	A	18	VAL	3.0
1	E	52	VAL	3.0
1	B	279	ARG	2.9
1	F	34	ALA	2.9
1	E	191	GLY	2.9
1	C	178	PHE	2.9
1	C	277	PHE	2.9
1	E	278	LYS	2.8
1	B	65	VAL	2.8
1	B	90	GLY	2.8
1	D	17	LEU	2.8
1	G	25	LEU	2.8
1	G	266	ILE	2.8
1	G	93	THR	2.8
1	C	59	ARG	2.8
1	C	39	ILE	2.8
1	E	24	LEU	2.7
1	C	31	ILE	2.7
1	B	194	TYR	2.7
1	G	92	GLN	2.7
1	B	87	GLY	2.6
1	D	143	GLY	2.6
1	C	25	LEU	2.6
1	C	38	ILE	2.6
1	F	230	ALA	2.6
1	D	18	VAL	2.5
1	D	150	ILE	2.5
1	F	89	VAL	2.5
1	G	54	ARG	2.5
1	B	88	ARG	2.5
1	F	35	LEU	2.5
1	G	183	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	18	VAL	2.4
1	E	25	LEU	2.4
1	G	90	GLY	2.4
1	A	230	ALA	2.4
1	E	35	LEU	2.4
1	F	73	VAL	2.4
1	D	88	ARG	2.4
1	C	28	ALA	2.4
1	A	231	SER	2.4
1	F	53	ASN	2.3
1	G	181	GLU	2.3
1	D	35	LEU	2.3
1	A	147	SER	2.3
1	B	239	VAL	2.3
1	C	249	VAL	2.2
1	E	277	PHE	2.2
1	C	132	ALA	2.2
1	C	34	ALA	2.2
1	F	28	ALA	2.2
1	F	112	GLN	2.2
1	D	25	LEU	2.2
1	E	58	SER	2.2
1	A	184	ARG	2.1
1	F	62	ASP	2.1
1	E	268	PHE	2.1
1	C	57	ILE	2.1
1	D	84	ALA	2.1
1	E	27	TYR	2.1
1	F	52	VAL	2.0
1	G	182	PRO	2.0
1	F	181	GLU	2.0
1	F	126	MET	2.0
1	A	280	VAL	2.0

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

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
1	R1A	G	67	18/19	0.60	0.19	102,170,180,191	0
1	R1A	B	67	18/19	0.61	0.21	131,174,185,186	0
1	R1A	D	67	18/19	0.74	0.19	122,179,191,192	0
1	R1A	A	67	18/19	0.75	0.20	148,189,195,202	0
1	R1A	E	67	18/19	0.77	0.20	126,183,193,199	0
1	R1A	F	67	18/19	0.81	0.15	132,179,187,190	0
1	R1A	C	67	18/19	0.81	0.17	130,168,176,181	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($\text{\AA}^2$)	Q<0.9
3	HEX	A	501	6/6	0.66	0.26	88,91,93,94	0
4	D10	C	402	8/10	0.72	0.35	103,119,122,123	0
3	HEX	E	501	6/6	0.73	0.36	89,94,96,96	0
3	HEX	D	501	6/6	0.74	0.27	90,94,97,98	0
3	HEX	B	501	6/6	0.77	0.37	90,91,96,98	0
2	OCT	E	406	8/8	0.77	0.32	109,117,123,125	0
4	D10	D	404	10/10	0.79	0.25	112,114,118,118	0
3	HEX	E	500	6/6	0.80	0.34	83,85,87,87	0
3	HEX	F	500	6/6	0.81	0.17	88,92,94,95	0
3	HEX	C	501	6/6	0.82	0.28	95,98,103,105	0
3	HEX	B	500	6/6	0.83	0.23	81,85,86,87	0
3	HEX	F	501	6/6	0.84	0.28	97,103,105,105	0
2	OCT	A	401	8/8	0.87	0.23	102,111,114,115	0
4	D10	G	408	10/10	0.89	0.26	108,121,124,124	0
3	HEX	C	500	6/6	0.90	0.23	83,87,90,90	0

6.5 Other polymers [i](#)

There are no such residues in this entry.