



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:26 PM GMT

PDB ID : 1K9I
Title : Complex of DC-SIGN and GlcNAc2Man3
Authors : Feinberg, H.; Mitchell, D.A.; Drickamer, K.; Weis, W.I.
Deposited on : 2001-10-29
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

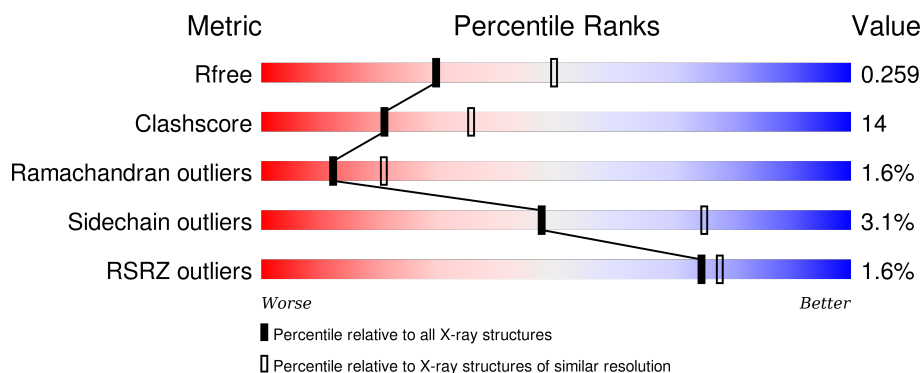
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	156	<div> <div>4%</div> <div>52%</div> <div>28%</div> <div>•</div> <div>18%</div> </div>
1	B	156	<div> <div>%</div> <div>61%</div> <div>20%</div> <div>•</div> <div>18%</div> </div>
1	C	156	<div> <div>61%</div> <div>19%</div> <div>•</div> <div>18%</div> </div>
1	D	156	<div> <div>67%</div> <div>18%</div> <div>15%</div> </div>
1	E	156	<div> <div>59%</div> <div>22%</div> <div>•</div> <div>18%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	156	<div><div><div>%</div><div><div></div><div>56%</div><div>24%</div><div>•</div><div>18%</div></div></div></div>
1	G	156	<div><div><div></div><div>59%</div><div>21%</div><div>•</div><div>18%</div></div></div>
1	H	156	<div><div><div>%</div><div><div></div><div>56%</div><div>24%</div><div>•</div><div>19%</div></div></div></div>
1	I	156	<div><div><div>%</div><div><div></div><div>50%</div><div>31%</div><div>•</div><div>18%</div></div></div></div>
1	J	156	<div><div><div>5%</div><div><div></div><div>54%</div><div>24%</div><div>•</div><div>18%</div></div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11035 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 mDC-SIGN1B type I isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			
1	B	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			
1	C	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			
1	D	132	Total	C	N	O	S	0	0	0
			1070	673	185	202	10			
1	E	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			
1	F	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			
1	G	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			
1	H	127	Total	C	N	O	S	0	0	0
			1037	655	178	196	8			
1	I	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			
1	J	128	Total	C	N	O	S	0	0	0
			1042	658	179	197	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	249	ALA	-	see remark 999	GB 15281089
B	249	ALA	-	see remark 999	GB 15281089
C	249	ALA	-	see remark 999	GB 15281089
D	249	ALA	-	see remark 999	GB 15281089
E	249	ALA	-	see remark 999	GB 15281089
F	249	ALA	-	see remark 999	GB 15281089
G	249	ALA	-	see remark 999	GB 15281089
H	249	ALA	-	see remark 999	GB 15281089
I	249	ALA	-	see remark 999	GB 15281089

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Chain	Residue	Modelled	Actual	Comment	Reference
J	249	ALA	-	see remark 999	GB 15281089

- Molecule 2 is a polymer of unknown type called SUGAR (NAG-MAN-MAN-MAN-NAG).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	5	Total	C	N	O	0	0
			62	34	2	26		
2	C	5	Total	C	N	O	0	0
			62	34	2	26		
2	D	5	Total	C	N	O	0	0
			62	34	2	26		
2	E	5	Total	C	N	O	0	0
			62	34	2	26		
2	H	5	Total	C	N	O	0	0
			62	34	2	26		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	3	Total	Ca	0	0
			3	3		
3	J	3	Total	Ca	0	0
			3	3		
3	D	3	Total	Ca	0	0
			3	3		
3	E	3	Total	Ca	0	0
			3	3		
3	H	3	Total	Ca	0	0
			3	3		
3	B	3	Total	Ca	0	0
			3	3		
3	I	3	Total	Ca	0	0
			3	3		
3	C	3	Total	Ca	0	0
			3	3		
3	A	3	Total	Ca	0	0
			3	3		
3	F	3	Total	Ca	0	0
			3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	13	Total 13	O 13	0	0
4	B	29	Total 29	O 29	0	0
4	C	36	Total 36	O 36	0	0
4	D	38	Total 38	O 38	0	0
4	E	31	Total 31	O 31	0	0
4	F	30	Total 30	O 30	0	0
4	G	25	Total 25	O 25	0	0
4	H	23	Total 23	O 23	0	0
4	I	15	Total 15	O 15	0	0
4	J	12	Total 12	O 12	0	0

ASP
GLU
GLN
GLN
PHE
LEU
SER
PRO
ALA
ALA
ALA
THR
ASN
PRO
PRO
PRO
PRO
ALA

• Molecule 1: mDC-SIGN1B type I isoform

Chain E:  59% 22% 18%

ALA GLU ARG LEU CYS HIS P255 W258 E259 F263 Y268 F269 M270 Q274 R275 N276 H278 T282 L291 V292 Q300 N301 F302 L303 Q304 Q306 N311 T314 L318 S319 D320 L321 N322 Q323 W327 P337 S338 V351 E354 D355 C356 A357 D366

P357 K368 L371 A372 K373 L376 A381 A382 SER CYS SER ARG ASP GLU GLN PHE LEU SER PRO ALA ALA THR ASN PRO PRO PRO PRO ALA

• Molecule 1: mDC-SIGN1B type I isoform

Chain F:  % 56% 24% 18%

ALA GLU ARG LEU HIS P255 C256 P257 W260 N272 R275 N276 T282 K285 Q290 L291 V292 V293 E298 E299 Q300 N301 F302 L303 Q304 L305 Q306 R309 R312 F313 S319 D320 W327 Q328 W329 P337 S338 F339 K340 Q341 Y342 N349 N350 V351 E354

D355 E358 N370 L371 F374 W375 A382 SER CYS SER ARG ASP GLU GLN PHE LEU SER PRO ALA ALA THR ASN PRO PRO PRO PRO ALA

• Molecule 1: mDC-SIGN1B type I isoform

Chain G:  59% 21% 18%

ALA GLU ARG LEU CYS HIS P255 C256 P257 W258 N260 F269 M270 S271 R275 H278 I281 L291 V292 E298 E299 Q300 N301 F302 L303 Q304 L305 Q306 T314 S319 D320 W327 S333 W343 P348 N349 N350 V351 E354 D355 D367 K368 C369 N370 L371

A372 W375 I376 A382 SER CYS SER ARG ASP GLU GLN PHE LEU SER PRO ALA ALA THR ASN PRO PRO PRO PRO ALA

• Molecule 1: mDC-SIGN1B type I isoform

Chain H:  % 56% 24% 19%

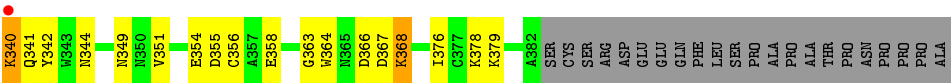
ALA GLU ARG LEU CYS HIS P255 C256 F262 F263 Q264 Y268 F269 M270 N276 A283 L291 V292 V293 I294 K295 E298 E299 Q300 N301 F302 Q306 S310 N311 R312 F313 T314 W315 M316 Q317 L318 S319 N322 W327 Q328 W329 V330 D331 P348 V351 D355

D366 D367 K368 L371 F374 W375 I376 K378 A381 ALA SER CYS SER ARG ASP GLU GLN PHE LEU SER PRO ALA ALA THR ASN PRO PRO PRO PRO ALA

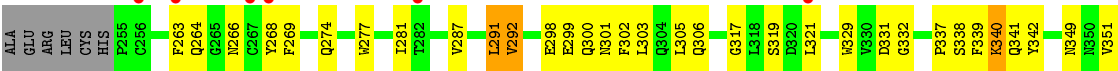
• Molecule 1: mDC-SIGN1B type I isoform

Chain I:  % 50% 31% 18%

ALA GLU ARG LEU CYS HIS P255 C256 P257 W260 F263 Y268 R275 N276 H277 S280 I281 T282 A283 V292 K295 S296 A297 E298 E299 Q300 N301 Q304 L305 S308 R309 F313 T314 S319 D320 Q323 T326 W327 Q328 W329 V330 D331 L336 P337 S338 F339



● Molecule 1: mDC-SIGN1B type I isoform



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.81Å 148.16Å 112.99Å 90.00° 91.03° 90.00°	Depositor
Resolution (Å)	26.68 – 2.50 48.61 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (26.68-2.50) 94.6 (48.61-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.27 (at 2.51Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.213 , 0.258 0.214 , 0.259	Depositor DCC
R_{free} test set	3585 reflections (6.65%)	DCC
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.480	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 41.8	EDS
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 59357 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11035	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, NAG, MAN

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	0.36	0/1075	0.57	0/1458
1	B	0.41	0/1075	0.63	0/1458
1	C	0.41	0/1075	0.59	0/1458
1	D	0.41	0/1104	0.62	0/1498
1	E	0.41	0/1075	0.60	0/1458
1	F	0.44	0/1075	0.64	0/1458
1	G	0.39	0/1075	0.59	0/1458
1	H	0.42	0/1070	0.62	0/1451
1	I	0.37	0/1075	0.56	0/1458
1	J	0.37	0/1075	0.57	0/1458
All	All	0.40	0/10774	0.60	0/14613

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

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	1042	0	945	36	0
1	B	1042	0	945	21	0
1	C	1042	0	945	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1070	0	964	20	0
1	E	1042	0	945	26	0
1	F	1042	0	945	31	0
1	G	1042	0	945	26	0
1	H	1037	0	940	29	0
1	I	1042	0	945	45	0
1	J	1042	0	945	37	0
2	A	62	0	52	1	0
2	C	62	0	51	2	0
2	D	62	0	50	3	0
2	E	62	0	50	2	0
2	H	62	0	51	1	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	0	0
3	H	3	0	0	0	0
3	I	3	0	0	0	0
3	J	3	0	0	0	0
4	A	13	0	0	0	0
4	B	29	0	0	0	0
4	C	36	0	0	2	0
4	D	38	0	0	5	0
4	E	31	0	0	0	0
4	F	30	0	0	1	0
4	G	25	0	0	1	0
4	H	23	0	0	1	0
4	I	15	0	0	4	0
4	J	12	0	0	0	0
All	All	11035	0	9718	296	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 14.

The worst 5 of 296 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:J:370:ASN:HD22	1:J:370:ASN:H	1.12	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:LYS:H	1:A:368:LYS:HD2	1.40	0.87
1:F:305:LEU:HD13	1:F:309:ARG:HH21	1.43	0.84
1:I:368:LYS:HD2	1:I:368:LYS:H	1.43	0.84
1:D:311:ASN:HA	2:D:5:NAG:O4	1.80	0.81

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	126/156 (81%)	110 (87%)	13 (10%)	3 (2%)	7	11
1	B	126/156 (81%)	117 (93%)	8 (6%)	1 (1%)	24	41
1	C	126/156 (81%)	116 (92%)	9 (7%)	1 (1%)	24	41
1	D	130/156 (83%)	126 (97%)	2 (2%)	2 (2%)	13	22
1	E	126/156 (81%)	119 (94%)	5 (4%)	2 (2%)	12	21
1	F	126/156 (81%)	121 (96%)	4 (3%)	1 (1%)	24	41
1	G	126/156 (81%)	116 (92%)	9 (7%)	1 (1%)	24	41
1	H	125/156 (80%)	119 (95%)	4 (3%)	2 (2%)	12	21
1	I	126/156 (81%)	115 (91%)	9 (7%)	2 (2%)	12	21
1	J	126/156 (81%)	109 (86%)	12 (10%)	5 (4%)	4	4
All	All	1263/1560 (81%)	1168 (92%)	75 (6%)	20 (2%)	12	21

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	381	ALA
1	I	292	VAL
1	A	292	VAL

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Mol	Chain	Res	Type
1	A	381	ALA
1	D	292	VAL

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	112/136 (82%)	110 (98%)	2 (2%)	66	88
1	B	112/136 (82%)	107 (96%)	5 (4%)	34	59
1	C	112/136 (82%)	107 (96%)	5 (4%)	34	59
1	D	116/136 (85%)	114 (98%)	2 (2%)	68	89
1	E	112/136 (82%)	108 (96%)	4 (4%)	42	69
1	F	112/136 (82%)	108 (96%)	4 (4%)	42	69
1	G	112/136 (82%)	107 (96%)	5 (4%)	34	59
1	H	112/136 (82%)	109 (97%)	3 (3%)	52	79
1	I	112/136 (82%)	110 (98%)	2 (2%)	66	88
1	J	112/136 (82%)	109 (97%)	3 (3%)	52	79
All	All	1124/1360 (83%)	1089 (97%)	35 (3%)	47	75

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	291	LEU
1	F	282	THR
1	J	291	LEU
1	E	322	ASN
1	E	368	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	370	ASN

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Mol	Chain	Res	Type
1	E	370	ASN
1	J	301	ASN
1	E	328	GLN
1	F	272	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 ⓘ

25 carbohydrates 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	NAG	A	1	3,2	14,14,15	0.51	0	15,19,21	0.82	0
2	MAN	A	2	3,2	11,11,12	0.49	0	14,15,17	0.86	1 (7%)
2	MAN	A	3	2	12,12,12	0.37	0	17,17,17	0.54	0
2	MAN	A	4	2	11,11,12	0.56	0	14,15,17	0.59	0
2	NAG	A	5	2	14,14,15	0.44	0	15,19,21	1.11	2 (13%)
2	NAG	C	1	3,2	14,14,15	0.53	0	15,19,21	1.03	1 (6%)
2	MAN	C	2	3,2	11,11,12	0.56	0	14,15,17	0.79	1 (7%)
2	MAN	C	3	2	12,12,12	0.44	0	17,17,17	0.52	0
2	MAN	C	4	2	11,11,12	0.60	0	14,15,17	0.70	0
2	NAG	C	5	2	14,14,15	0.48	0	15,19,21	0.72	1 (6%)
2	NAG	D	1	3,2	14,14,15	0.37	0	15,19,21	0.86	1 (6%)
2	MAN	D	2	3,2	11,11,12	0.52	0	14,15,17	0.72	1 (7%)
2	MAN	D	3	2	12,12,12	0.38	0	17,17,17	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	D	4	2	11,11,12	0.51	0	14,15,17	0.66	0
2	NAG	D	5	2	14,14,15	0.54	0	15,19,21	0.65	0
2	NAG	E	1	3,2	14,14,15	0.46	0	15,19,21	0.84	1 (6%)
2	MAN	E	2	3,2	11,11,12	0.48	0	14,15,17	0.77	1 (7%)
2	MAN	E	3	2	12,12,12	0.56	0	17,17,17	0.62	0
2	MAN	E	4	2	11,11,12	0.43	0	14,15,17	0.83	1 (7%)
2	NAG	E	5	2	14,14,15	0.51	0	15,19,21	0.86	1 (6%)
2	NAG	H	1	3,2	14,14,15	0.42	0	15,19,21	0.77	0
2	MAN	H	2	3,2	11,11,12	0.50	0	14,15,17	0.72	1 (7%)
2	MAN	H	3	2	12,12,12	0.38	0	17,17,17	0.53	0
2	MAN	H	4	2	11,11,12	0.53	0	14,15,17	0.76	1 (7%)
2	NAG	H	5	2	14,14,15	0.48	0	15,19,21	0.79	1 (6%)

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	NAG	A	1	3,2	-	0/6/23/26	0/1/1/1
2	MAN	A	2	3,2	-	0/2/19/22	0/1/1/1
2	MAN	A	3	2	-	0/2/22/22	0/1/1/1
2	MAN	A	4	2	-	0/2/19/22	0/1/1/1
2	NAG	A	5	2	-	0/6/23/26	0/1/1/1
2	NAG	C	1	3,2	-	0/6/23/26	0/1/1/1
2	MAN	C	2	3,2	-	0/2/19/22	0/1/1/1
2	MAN	C	3	2	-	0/2/22/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	NAG	C	5	2	-	0/6/23/26	0/1/1/1
2	NAG	D	1	3,2	-	0/6/23/26	0/1/1/1
2	MAN	D	2	3,2	-	0/2/19/22	0/1/1/1
2	MAN	D	3	2	-	0/2/22/22	0/1/1/1
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1
2	NAG	D	5	2	-	0/6/23/26	0/1/1/1
2	NAG	E	1	3,2	-	0/6/23/26	0/1/1/1
2	MAN	E	2	3,2	-	0/2/19/22	0/1/1/1
2	MAN	E	3	2	-	0/2/22/22	0/1/1/1
2	MAN	E	4	2	-	0/2/19/22	0/1/1/1
2	NAG	E	5	2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	3,2	-	0/6/23/26	0/1/1/1
2	MAN	H	2	3,2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	H	3	2	-	0/2/22/22	0/1/1/1
2	MAN	H	4	2	-	0/2/19/22	0/1/1/1
2	NAG	H	5	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C2-N2-C7	-2.84	119.39	123.04
2	E	1	NAG	C2-N2-C7	-2.80	119.44	123.04
2	A	5	NAG	C2-N2-C7	-2.69	119.58	123.04
2	A	5	NAG	C4-C3-C2	-2.64	107.13	111.23
2	E	5	NAG	C2-N2-C7	-2.59	119.72	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5	NAG	1	0
2	C	2	MAN	1	0
2	C	5	NAG	1	0
2	D	1	NAG	2	0
2	D	5	NAG	1	0
2	E	2	MAN	1	0
2	E	5	NAG	1	0
2	H	5	NAG	1	0

5.6 Ligand geometry

Of 30 ligands modelled in this entry, 30 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	128/156 (82%)	0.44	7 (5%) 29 32	39, 66, 81, 87	0
1	B	128/156 (82%)	-0.08	1 (0%) 87 89	27, 43, 59, 77	0
1	C	128/156 (82%)	-0.01	0 100 100	26, 42, 56, 68	0
1	D	132/156 (84%)	0.02	0 100 100	25, 43, 57, 74	0
1	E	128/156 (82%)	0.11	0 100 100	26, 44, 57, 67	0
1	F	128/156 (82%)	0.00	1 (0%) 87 89	26, 38, 54, 69	0
1	G	128/156 (82%)	-0.07	0 100 100	30, 45, 64, 83	0
1	H	127/156 (81%)	0.17	1 (0%) 87 89	31, 47, 60, 68	0
1	I	128/156 (82%)	0.28	2 (1%) 74 78	43, 62, 81, 84	0
1	J	128/156 (82%)	0.40	8 (6%) 23 26	43, 62, 76, 83	0
All	All	1283/1560 (82%)	0.13	20 (1%) 74 78	25, 48, 74, 87	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	382	ALA	3.8
1	A	256	CYS	3.4
1	A	292	VAL	3.3
1	A	267	CYS	3.1
1	J	321	LEU	3.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	A	5	14/15	0.89	0.22	1.92	68,71,73,73	0
2	MAN	D	3	12/12	0.95	0.17	0.93	31,39,42,48	0
2	MAN	C	4	11/12	0.96	0.19	0.54	47,49,51,55	0
2	NAG	A	1	14/15	0.96	0.17	0.52	48,50,52,52	0
2	MAN	D	2	11/12	0.98	0.15	0.45	23,27,30,33	0
2	MAN	A	3	12/12	0.93	0.14	0.35	49,55,59,62	0
2	NAG	H	1	14/15	0.95	0.15	0.19	33,38,46,47	0
2	NAG	C	1	14/15	0.96	0.15	0.14	41,42,46,50	0
2	MAN	E	4	11/12	0.96	0.17	-0.02	39,44,46,47	0
2	MAN	D	4	11/12	0.97	0.16	-0.04	36,38,40,42	0
2	NAG	C	5	14/15	0.95	0.17	-0.08	42,46,48,49	0
2	NAG	E	5	14/15	0.93	0.16	-0.08	47,49,51,54	0
2	MAN	C	2	11/12	0.97	0.15	-0.20	30,37,41,45	0
2	NAG	D	5	14/15	0.94	0.16	-0.25	32,41,42,43	0
2	MAN	E	3	12/12	0.93	0.16	-0.26	38,41,44,45	0
2	MAN	A	2	11/12	0.95	0.13	-0.27	39,45,49,50	0
2	NAG	E	1	14/15	0.97	0.15	-0.42	31,35,39,42	0
2	NAG	D	1	14/15	0.98	0.14	-0.64	25,27,31,34	0
2	NAG	H	5	14/15	0.92	0.14	-0.76	51,52,54,54	0
2	MAN	E	2	11/12	0.98	0.15	-0.85	29,33,38,39	0
2	MAN	H	2	11/12	0.97	0.14	-0.92	28,33,36,36	0
2	MAN	A	4	11/12	0.94	0.11	-1.53	61,63,66,66	0
2	MAN	H	4	11/12	0.95	0.12	-3.74	42,46,48,53	0
2	MAN	H	3	12/12	0.97	0.12	-5.21	35,40,42,44	0
2	MAN	C	3	12/12	0.96	0.15	-	44,48,50,50	0

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	CA	A	406	1/1	0.98	0.15	0.51	41,41,41,41	0
3	CA	H	1101	1/1	0.98	0.17	0.13	37,37,37,37	0
3	CA	I	1202	1/1	0.98	0.14	-0.02	43,43,43,43	0
3	CA	E	802	1/1	0.99	0.16	-0.15	31,31,31,31	0
3	CA	E	801	1/1	0.99	0.16	-0.28	33,33,33,33	0
3	CA	D	702	1/1	0.99	0.13	-0.36	32,32,32,32	0
3	CA	H	1102	1/1	0.97	0.15	-0.54	33,33,33,33	0
3	CA	F	901	1/1	0.99	0.12	-0.68	29,29,29,29	0
3	CA	C	602	1/1	0.98	0.12	-0.75	34,34,34,34	0
3	CA	B	501	1/1	0.99	0.13	-0.76	32,32,32,32	0
3	CA	J	1302	1/1	0.99	0.14	-0.84	39,39,39,39	0
3	CA	G	1002	1/1	0.99	0.12	-0.87	30,30,30,30	0
3	CA	B	502	1/1	0.99	0.13	-1.05	27,27,27,27	0
3	CA	D	701	1/1	0.99	0.11	-1.11	37,37,37,37	0
3	CA	J	1303	1/1	0.93	0.06	-1.12	53,53,53,53	0
3	CA	F	902	1/1	0.99	0.12	-1.37	28,28,28,28	0
3	CA	G	1001	1/1	0.96	0.11	-1.73	32,32,32,32	0
3	CA	J	1301	1/1	0.98	0.10	-1.76	46,46,46,46	0
3	CA	I	1201	1/1	0.97	0.10	-2.24	44,44,44,44	0
3	CA	A	405	1/1	0.96	0.09	-3.80	56,56,56,56	0
3	CA	C	601	1/1	0.96	0.08	-4.92	54,54,54,54	0
3	CA	D	703	1/1	0.97	0.08	-	50,50,50,50	0
3	CA	F	903	1/1	0.96	0.09	-	48,48,48,48	0
3	CA	A	407	1/1	0.91	0.13	-	64,64,64,64	0
3	CA	I	1203	1/1	0.98	0.13	-	56,56,56,56	0
3	CA	G	1003	1/1	0.96	0.13	-	43,43,43,43	0
3	CA	B	503	1/1	0.99	0.07	-	49,49,49,49	0
3	CA	E	803	1/1	0.98	0.09	-	40,40,40,40	0
3	CA	H	1103	1/1	0.99	0.20	-	51,51,51,51	0
3	CA	C	603	1/1	0.97	0.12	-	59,59,59,59	0

6.5 Other polymers

There are no such residues in this entry.