

wwPDB EM Validation Summary Report (i)

Jun 20, 2024 – 11:22 AM EDT

PDB ID	:	9B37
EMDB ID	:	EMD-44130
Title	:	Open state of kainate receptor GluK2 in complex with agonist glutamate and
		positive allosteric modulator BPAM344 bound to one concanavalin A dimer.
		Composite map.
Authors	:	Nadezhdin, K.D.; Gangwar, S.P.; Sobolevsky, A.I.
Deposited on	:	2024-03-18
Resolution	:	6.66 Å(reported)

This is a wwPDB EM Validation Summary 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/EMValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 6.66 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.



Motrie	Whole archive	EM structures
wiethc	$(\# { m Entries})$	$(\# { m Entries})$
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain		
1	А	912	78%	14%	• 8%
1	В	912	77%	15%	8%
1	С	912	78%	14%	• 8%
1	D	912	78%	15%	8%
2	Е	237	73%	25%	•
2	F	237	70%	29%	•
3	G	2	50% 50%		
3	J	2	50% 50%		



Mol	Chain	Length	Quality of cha	ain
3	Κ	2	50%	50%
3	L	2	100%	
3	М	2	100%	
3	Q	2	100%	
3	R	2	100%	
3	Т	2	100%	
3	U	2	50%	50%
3	V	2	100%	
3	Х	2	50%	50%
3	Ζ	2	50%	50%
3	b	2	50%	50%
3	е	2	100%	
3	g	2	100%	
4	Н	3	33%	67%
4	Y	3	67%	33%
4	d	3	100%	
5	Ι	8	75%	25%
5	W	8	25% 62%	12%
6	N	7	86%	14%
6	О	7	14% 71%	14%
7	Р	6	17% 83%	
8	S	4	100%	
8	f	4	100%	
9	a	4	50%	50%
10	C C	7	20%	71%
	5	•	25/0	



The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	NAG	S	1	X	-	-	-



2 Entry composition (i)

There are 17 unique types of molecules in this entry. The entry contains 32654 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Δ	842	Total	С	Ν	Ο	\mathbf{S}	2	0
1	Л	042	6684	4283	1117	1244	40	2	0
1	Р	849	Total	С	Ν	Ο	S	1	0
	D	042	6680	4280	1117	1243	40	L	0
1	C	849	Total	С	Ν	Ο	S	2	0
		042	6684	4283	1117	1244	40	2	0
1 D	842	Total	С	Ν	Ο	S	1	0	
) 842	6680	4280	1117	1243	40		U	

• Molecule 1 is a protein called Glutamate receptor ionotropic, kainate 2.

There are 24	discrepancies	between	the modelled	and	reference	sequences:
Incre are 21	unsereparteres	Detween	une moueneu	ana	renerence	bequeinces.

Chain	Residue	Modelled	Actual	Comment	Reference
А	567	VAL	ILE	conflict	UNP P42260
А	571	CYS	TYR	conflict	UNP P42260
А	909	LEU	-	expression tag	UNP P42260
А	910	VAL	-	expression tag	UNP P42260
А	911	PRO	-	expression tag	UNP P42260
А	912	ARG	-	expression tag	UNP P42260
В	567	VAL	ILE	conflict	UNP P42260
В	571	CYS	TYR	conflict	UNP P42260
В	909	LEU	-	expression tag	UNP P42260
В	910	VAL	-	expression tag	UNP P42260
В	911	PRO	-	expression tag	UNP P42260
В	912	ARG	-	expression tag	UNP P42260
С	567	VAL	ILE	conflict	UNP P42260
С	571	CYS	TYR	conflict	UNP P42260
С	909	LEU	-	expression tag	UNP P42260
С	910	VAL	-	expression tag	UNP P42260
С	911	PRO	-	expression tag	UNP P42260
С	912	ARG	-	expression tag	UNP P42260
D	567	VAL	ILE	conflict	UNP P42260
D	571	CYS	TYR	conflict	UNP P42260
D	909	LEU	-	expression tag	UNP P42260
D	910	VAL	-	expression tag	UNP P42260



Chain	Residue	Modelled	Actual	Comment	Reference
D	911	PRO	-	expression tag	UNP P42260
D	912	ARG	-	expression tag	UNP P42260

• Molecule 2 is a protein called Concanavalin A.

Mol	Chain	Residues	Atoms				AltConf	Trace	
2	F	237	Total	С	Ν	0	S	0	0
	201	1806	1140	302	362	2	0	0	
2	F	227	Total	С	Ν	0	S	0	0
Z F	231	1809	1141	302	364	2	0	0	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Е	58	ASP	GLY	conflict	UNP C0HJY1
Е	70	ALA	GLY	conflict	UNP C0HJY1
Е	129	MET	VAL	conflict	UNP C0HJY1
Е	192	GLU	ASP	conflict	UNP C0HJY1
F	58	ASP	GLY	conflict	UNP C0HJY1
F	70	ALA	GLY	conflict	UNP C0HJY1
F	129	MET	VAL	conflict	UNP C0HJY1
F	192	GLU	ASP	conflict	UNP C0HJY1

• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	AltConf	Trace
2	С	2	Total C N O	0	0
0	G	2	28 16 2 10	0	0
3	т	9	Total C N O	0	0
0	J	2	28 16 2 10	U	0
3	K	9	Total C N O	0	0
0	п	2	28 16 2 10	0	
2	т	2	Total C N O	0	0
0		2	28 16 2 10	0	0
3	М	9	Total C N O	0	0
ა	IVI	2	28 16 2 10	0	0



Mol	Chain	Residues	Atoms	AltConf	Trace
3	0	9	Total C N O	0	0
0	Ŷ	2	28 16 2 10	0	0
3	В	9	Total C N O	0	0
0	п	Δ	28 16 2 10	0	0
3	Т	9	Total C N O	0	0
0	T	2	28 16 2 10	0	0
3	TT	2	Total C N O	0	0
0	U		28 16 2 10	0	0
3	V	2	Total C N O	0	0
0	v	2	28 16 2 10	V	0
3	x	2	Total C N O	0	0
0			28 16 2 10	0	0
3	Z	2	Total C N O	0	0
0		2	28 16 2 10	0	0
3	h	2	Total C N O	0	0
0	D		28 16 2 10	0	0
3	е	2	Total C N O	0	0
o e	Č.	2	28 16 2 10	0	0
3	σ	2	Total C N O	0	0
ა	g		28 16 2 10	0	0

• Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	AltConf	Trace
4	Н	3	Total C N O 39 22 2 15	0	0
4	Y	3	Total C N O 39 22 2 15	0	0
4	d	3	Total C N O 39 22 2 15	0	0

• Molecule 5 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-gluc opyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.





Mol	Chain	Residues	Atoms	AltConf	Trace
5	Ι	8	Total C N O 100 56 4 40	0	0
5	W	8	Total C N O 100 56 4 40	0	0

• Molecule 6 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]be ta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetami



Mol	Chain	Residues	Atoms				AltConf	Trace
6	Ν	7	Total 86	C 48	N 3	O 35	0	0
6	О	7	Total 86	C 48	N 3	O 35	0	0

• Molecule 7 is an oligosaccharide called Cyclic 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)]alpha-D-mannopyr anose.



Mol	Chain	Residues	Atoms				AltConf	Trace
7	Р	6	Total 75	C 42	N 3	O 30	0	0

• Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranos e-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-gluco pyranose.





Mol	Chain	Residues	Atoms	AltConf	Trace
8	S	4	Total C N O 50 28 2 20	0	0
8	f	4	Total C N O 50 28 2 20	0	0

• Molecule 9 is an oligosaccharide called beta-D-mannopyranose-(1-3)-beta-D-mannopyranose -(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	I	Atoms			AltConf	Trace
9	я	4	Total	С	Ν	Ο	0	0
	a	T	50	28	2	20	0	0

• Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-al pha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-ma nnopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose -(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			AltConf	Trace	
10	С	7	Total 89	C 50	N 4	O 35	0	0

• Molecule 11 is 4-cyclopropyl-7-fluoro-3,4-dihydro-2H-1,2,4-benzothiadiazine 1,1dioxide (three-letter code: 2J9) (formula: C₁₀H₁₁FN₂O₂S) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms						AltConf
11	Λ	1	Total	С	F	Ν	0	S	0
	A	1	16	10	1	2	2	1	0
11	Р	1	Total	С	F	Ν	0	S	0
	D	1	16	10	1	2	2	1	0
11	С	1	Total	С	F	Ν	0	S	0
	U	1	16	10	1	2	2	1	0
11	Л	1	Total	С	F	Ν	0	S	0
	D		16	10	1	2	2	1	

• Molecule 12 is GLUTAMIC ACID (three-letter code: GLU) (formula: $C_5H_9NO_4$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	AltConf
12	Δ	1	Total C N O	0
14	11	I	10 5 1 4	0
12	В	1	Total C N O	0
14	D	1	10 5 1 4	0
19	С	1	Total C N O	0
12	U	I	10 5 1 4	0
19	р	1	Total C N O	0
12	D	1	10 5 1 4	0

• Molecule 13 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylam monio)ethyl phosphate (three-letter code: POV) (formula: $C_{42}H_{82}NO_8P$).



Mol	Chain	Residues		Ato	oms			AltConf	
12	Δ	1	Total	С	Ν	0	Р	0	
10	Л	1	52	42	1	8	1	0	
13	Δ	1	Total	С	Ν	Ο	Р	0	
10	Λ	1	52	42	1	8	1	0	
13	Δ	1	Total	С	Ν	Ο	Р	0	
10	Λ	1	52	42	1	8	1	0	
13	Δ	1	Total	С	Ν	Ο	Р	0	
10	Π	1	52	42	1	8	1	0	
13	B	1	Total	С	Ν	Ο	Р	0	
10	D	I	52	42	1	8	1	0	
13	B	1	Total	С	Ν	Ο	Р	0	
10	D	1	52	42	1	8	1	0	
13	B	1	Total	С	Ν	0	Р	0	
19	D	В	1	52	42	1	8	1	0



Mol	Chain	Residues		Ato	oms			AltConf
19	С	1	Total	С	Ν	Ο	Р	0
10	U	L	52	42	1	8	1	0
12	С	1	Total	С	Ν	0	Р	0
10	U	L	52	42	1	8	1	0
12	С	1	Total	С	Ν	Ο	Р	0
10	U	L	52	42	1	8	1	0
13	С	1	Total	С	Ν	0	Р	0
10	U	T	52	42	1	8	1	0
13	Л	1	Total	С	Ν	0	Р	0
10	D	T	52	42	1	8	1	0
13	Л	1	Total	С	Ν	0	Р	0
10	D	T	52	42	1	8	1	0
13	р	1	Total	С	N	0	Р	0
10	D	L	52	42	1	8	1	0

Continued from previous page...

• Molecule 14 is CHOLESTEROL (three-letter code: CLR) (formula: $C_{27}H_{46}O$).



Mol	Chain	Residues	Atoms	AltConf
14	А	1	Total C O 28 27 1	0
14	А	1	Total C O 28 27 1	0
14	А	1	Total C O 28 27 1	0
14	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 28 & 27 & 1 \end{array}$	0



Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf
14	В	1	Total C O 28 27 1	0
14	С	1	Total C O 28 27 1	0
14	С	1	Total C O 28 27 1	0
14	С	1	Total C O 28 27 1	0

• Molecule 15 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	А	tor	ns		AltConf
15	В	1	Total	С	Ν	Ο	0
10	D	1	14	8	1	5	0
15	С	1	Total	С	Ν	Ο	0
15	U	T	14	8	1	5	0

• Molecule 16 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
16	Е	1	Total Zn 1 1	0
16	F	1	Total Zn 1 1	0



• Molecule 17 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	AltConf
17	Е	1	Total Ca 1 1	0
17	F	1	Total Ca 1 1	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.







LT 91 LT 91 LT 92 LT 92

PRO GLY CLYS CLYS GLU THR MET ALA LEU VAL VAL PRO ARG

 \bullet Molecule 1: Glutamate receptor ionotropic, kainate 2



• Molecule 1: Glutamate receptor ionotropic, kainate 2

Cl	ha	in	D	: '															78	%																15	%			8	%	-			
MET I VS	ILE	ILE	PRO	VAL	SER	ASN	LEU	PHE	SER	ARG	SER	TLE	VAL	LEU	LEU	CYS I EII	LEU	TRP	ILE	GLY	TYK	GLN	GLY	THR T33	201	G 39	G40	E54		R66 W67	10 M	L71		180 081	K82		L85	F89		K94	098		1106	L125	
Q131	K135	11 60	COT M	V172 T172	0/11	G181	D1 O1	L185		A191	P192	1.1 99		E223		K240	T257	T258	L259			V289		W296	R300	L301	q 302	K306	P307	D308	T318	-	L322	<u>A326</u>		<mark>0335</mark>	HO 11	1041	L345	<mark>0346</mark>	R349	L L L	F355	K364	
L371	F377	N378	T380	N381	S427	L428	S429	N400	V435	T436	1 420	L439	D465	L466	L467	R468	L482		Y488		N495	M501		E504	L512	A513	V514	1519		D528	5530 S530	K531	P532	1.541	Y542	R543	TE AO	1 04 0 N 5 4 9		L556	L559		W564	V574	
V577	R583		1092	C595 ME 06	OFCN	D600	V601	N604	NGO5	F606	T607	1.609	N610		q622	TEAE	E023 L626		K629	A630	L631 S630	T633		W641	R663		I668	L674		A684	R712	R7 13			L729		L752	1755		G771	R775		n/ 86	L791	H792
1206		N802	A812	101	G816		N819 Teco	1020 G821	G822	1823	a Con	07870	<mark>6830</mark>		E853	K854 Defe		C858	<mark>8859</mark>	A860	E864		R874	LEU I VS	HIS	LYS	PRO	ALA	PRO	VAL	VAL	LYS	THR	GLU	VAL	ILE	ASN	HIS	THR	PHE	ASP	ARG	ARG LEU	PRO	GLY
CT II	THR	MET	LEU	VAL	ARG																																								



• Molecule 2:	Concanavalin A		
Chain E:	73%	25%	•
A1 111 712 713 713 813 813 618 618 618	Y22 127 127 127 127 440 440 440 440 440 440 440 450 856 856 866 866 866 866	L85 P86 890 991 991 991 692 1112 1112 1113 1113 8116 8117 8118 8118 8118	H127 4132
K135 D136 Q137 Q137 D139 D145 G149	V159 V159 V159 V156 F165 F175 F175 F175 F175 F175 F175 F175 F17	F195 F197 F197 F197 F197 F126 F1210 F210 F210 F214 F210 F218 F210 F218 F220 F220 F220 F220 F220 F220 F220 F22	11237
• Molecule 2:	Concanavalin A		
Chain F:	70%	29%	
A1 14 18 11 11 11 11 125	834 V47 C48 C48 C48 A50 A50 A50 B55 E61 B66 N65 N67 N75 N75 N75 N75 N75 N77 N77 N77	L81 L85 F86 F87 F86 F89 F89 A95 S96 A95 S96 A95 F100 F100 F100 F103 T103 T103	1106 111 1112
L115 N118 S119 H127 M129 M129 Q132	N162 9166 8169 8173 8173 8175 8175 8175 8177 8176 8177 8187 8183 8184 8183 8185 8185 8185 8186 8186 8187 8188 8188 8188 8188 8188	F195 F195 L198 1199 X200 X200 X200 X200 X211 F212 F212 F212 F212 F212 F222 F222	1229 1230 1233 1233 1233
• Molecule 3: opyranose	2-acetamido-2-deoxy-beta-D-gluc	opyranose-(1-4)-2-acetamic	lo-2-deoxy-beta-D-gluc
Chain G:	50%	50%	•
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy-beta-D-gluc	copyranose-(1-4)-2-acetamic	lo-2-deoxy-beta-D-gluc
Chain J:	50%	50%	
NAG2 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy-beta-D-gluc	copyranose-(1-4)-2-acetamic	lo-2-deoxy-beta-D-gluc

Chain K: 50% 50%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:

100%



NAG1 NAG2

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:	100%		
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy-beta-D-glucopyrar	nose-(1-4)-2-acetamide	o-2-deoxy-beta-D-gluc
Chain Q:	100%		
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy-beta-D-glucopyrar	nose-(1-4)-2-acetamide	o-2-deoxy-beta-D-gluc
Chain R:	100%		
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy-beta-D-glucopyrar	nose-(1-4)-2-acetamide	o-2-deoxy-beta-D-gluc
Chain T:	100%		
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy-beta-D-glucopyrar	nose-(1-4)-2-acetamide	o-2-deoxy-beta-D-gluc
Chain U:	50%	50%	

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-gluc opyranose

Chain V:

100%

NAG1 NAG2

NAG1 NAG2



• Molecule 3: opyranose	2-acetamido-2-deoxy	r-beta-D-glucopyranose-(1-4)-2-ace	tamido-2-deoxy-beta-D-gluc
Chain X:	50%	50%	
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy	r-beta-D-glucopyranose-(1-4)-2-ace	tamido-2-deoxy-beta-D-gluc
Chain Z:	50%	50%	
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy	r-beta-D-glucopyranose-(1-4)-2-ace	tamido-2-deoxy-beta-D-gluc
Chain b:	50%	50%	
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy	r-beta-D-glucopyranose-(1-4)-2-ace	tamido-2-deoxy-beta-D-gluc
Chain e:		100%	
NAG1 NAG2			
• Molecule 3: opyranose	2-acetamido-2-deoxy	r-beta-D-glucopyranose-(1-4)-2-ace	tamido-2-deoxy-beta-D-gluc
Chain g:		100%	
NAG1 NAG2			
• Molecule 4: etamido-2-dec	beta-D-mannopyrano oxy-beta-D-glucopyran	ose-(1-4)-2-acetamido-2-deoxy-beta nose	a-D-glucopyranose-(1-4)-2-ac
Chain H:	33%	67%	

NAG1 NAG2 BMA3

• Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:

33%



NAG1 NAG2 BMA3

• Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:

100%

NAG1 NAG2 BMA3

 $\label{eq:constraint} \bullet \mbox{Molecule 5: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetami$

Chain I:	75%	25%
NAG1 NAG2 BM33 MAN4 NAG5 GAL6 GAL6 MAN7 NAG8		

 $\label{eq:main_optimal_states} \bullet \mbox{Molecule 5: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-$

Chain W:	25%	62%	12%
NAG1 NAG2 BMA3 MAG5 CAL6 MAN7 NAG8 NAG8			

 $\label{eq:manopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-ac$

Chain N:	86%	14%
NAG1 NAG2 BMA3 MAN4 NAG5 GAL6 MAN7		

 $\label{eq:manopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-ac$



 $\bullet \ Molecule \ 7: \ Cyclic \ 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-$



 $\label{eq:2-deoxy-beta-D-glucopyranose-(1-2)] alpha-D-mannopyranose} 2-deoxy-beta-D-glucopyranose-(1-2)] alpha-D-mannopyranose and alpha-D-mannopy$

Chain P: 17% 83%

 $\bullet \ Molecule \ 8: \ alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose \\ eta-D-glucopyranose \ (1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose \ (1-4)-2-acetamido-2-deoxy-beta-D-glucopyra$

Chain S: 100%

 $\bullet \ Molecule \ 8: \ alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose$

Chain f:	100%	
NAG1 NAG2 BMA3 MAN4 MAN4		
• Molecule	9. heta-D-mannonyranose-(1-3)-beta-D-mannonyranose-(1-4)-2	P-acetamido-2-deoxy-be

 $\bullet \ Molecule \ 9: \ beta-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose \\ ta-D-glucopyranose \ (1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose \ (1-4)-2-acetamido-2-deoxy-beta-D-glucopyrano$

Chain a: 50% 50%

NAG1 NAG2 BMA3 BMA4

 $\label{eq:constraint} \bullet \mbox{Molecule 10: } 2\mbox{-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2 -acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)] beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-$

Chain c:	29%	71%





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	77567	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	52.113	Depositor
Minimum map value	-34.369	Depositor
Average map value	0.016	Depositor
Map value standard deviation	1.197	Depositor
Recommended contour level	1.3487	Depositor
Map size (Å)	345.2672, 345.2672, 345.2672	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3487, 1.3487, 1.3487	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CLR, MAN, ZN, GAL, 2J9, POV, CA, BMA, NAG

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	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.32	0/6840	0.57	3/9258~(0.0%)
1	В	0.31	0/6833	0.56	2/9248~(0.0%)
1	С	0.32	0/6840	0.57	2/9258~(0.0%)
1	D	0.31	0/6833	0.57	3/9248~(0.0%)
2	Е	0.38	0/1848	0.79	2/2518~(0.1%)
2	F	0.39	0/1851	0.79	3/2522~(0.1%)
All	All	0.33	0/31045	0.60	15/42052~(0.0%)

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
1	А	0	6
1	В	0	5
1	С	0	6
1	D	0	3
2	Е	0	10
2	F	0	8
All	All	0	38

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	Е	48	GLY	N-CA-C	9.40	136.60	113.10
2	F	48	GLY	N-CA-C	9.15	135.99	113.10
2	Е	230	LEU	CA-CB-CG	6.62	130.52	115.30
1	С	85	LEU	CA-CB-CG	6.21	129.58	115.30



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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	D	85	LEU	CA-CB-CG	6.19	129.53	115.30

There are no chirality outliers.

5 of 38 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	191	ALA	Peptide
1	А	416	SER	Peptide
1	А	431	ARG	Peptide
1	А	495	ASN	Peptide
1	А	592	PRO	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	6684	0	6666	74	0
1	В	6680	0	6658	75	0
1	С	6684	0	6667	72	0
1	D	6680	0	6656	76	0
2	Ε	1806	0	1753	30	0
2	F	1809	0	1755	36	0
3	G	28	0	25	1	0
3	J	28	0	25	1	0
3	Κ	28	0	25	0	0
3	L	28	0	25	0	0
3	М	28	0	25	0	0
3	Q	28	0	25	0	0
3	R	28	0	25	0	0
3	Т	28	0	25	0	0
3	U	28	0	25	1	0
3	V	28	0	25	0	0
3	Х	28	0	25	0	0
3	Ζ	28	0	25	0	0
3	b	28	0	25	0	0
3	е	28	0	25	0	0
3	g	28	0	25	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Н	39	0	34	0	0
4	Y	39	0	34	0	0
4	d	39	0	34	0	0
5	Ι	100	0	85	2	0
5	W	100	0	85	1	0
6	N	86	0	73	1	0
6	0	86	0	73	1	0
7	Р	75	0	63	0	0
8	S	50	0	43	0	0
8	f	50	0	43	0	0
9	a	50	0	43	0	0
10	с	89	0	76	0	0
11	А	16	0	10	0	0
11	В	16	0	10	0	0
11	С	16	0	10	0	0
11	D	16	0	10	1	0
12	А	10	0	5	1	0
12	В	10	0	5	0	0
12	С	10	0	5	1	0
12	D	10	0	5	0	0
13	А	208	0	328	9	0
13	В	156	0	246	5	0
13	С	208	0	328	7	0
13	D	156	0	246	7	0
14	А	112	0	184	1	0
14	В	28	0	46	1	0
14	С	84	0	138	0	0
15	В	14	0	13	0	0
15	С	14	0	13	0	0
16	Е	1	0	0	0	0
16	F	1	0	0	0	0
17	Е	1	0	0	0	0
17	F	1	0	0	0	0
All	All	32654	0	32818	366	0

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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 6.

The worst 5 of 366 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:D:71:LEU:H	1:D:335:GLN:HE21	1.39	0.71
1:C:71:LEU:H	1:C:335:GLN:HE21	1.39	0.71
1:D:181:GLY:HA2	1:D:184:ARG:HE	1.56	0.70
1:A:181:GLY:HA2	1:A:184:ARG:HE	1.56	0.69
1:A:71:LEU:H	1:A:335:GLN:HE21	1.39	0.69

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 PDB entries followed by that with respect to all EM entries.

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	Perce	entiles
1	А	842/912~(92%)	757~(90%)	82 (10%)	3 (0%)	34	72
1	В	841/912 (92%)	746 (89%)	93 (11%)	2 (0%)	47	81
1	С	842/912~(92%)	753~(89%)	85 (10%)	4 (0%)	29	69
1	D	841/912 (92%)	749 (89%)	90 (11%)	2 (0%)	47	81
2	Е	235/237~(99%)	178 (76%)	54 (23%)	3 (1%)	12	48
2	F	235/237~(99%)	176 (75%)	55 (23%)	4 (2%)	9	42
All	All	3836/4122 (93%)	3359 (88%)	459 (12%)	18 (0%)	32	69

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Ε	186	ALA
2	F	186	ALA
1	А	427	SER
1	В	631	LEU
1	D	631	LEU



5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	А	735/798~(92%)	720~(98%)	15~(2%)	55 74		
1	В	734/798~(92%)	726~(99%)	8 (1%)	73 84		
1	С	735/798~(92%)	719~(98%)	16 (2%)	52 71		
1	D	734/798~(92%)	726~(99%)	8 (1%)	73 84		
2	Ε	202/203~(100%)	199~(98%)	3~(2%)	65 80		
2	F	203/203~(100%)	200~(98%)	3~(2%)	65 80		
All	All	3343/3598~(93%)	3290 (98%)	53 (2%)	66 79		

 $5~{\rm of}~53$ residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	С	471[A]	SER
1	С	712	ARG
2	Е	162	ASN
1	С	471[B]	SER
1	С	596	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	С	423	ASN
1	D	335	GLN
1	С	596	ASN
1	С	802	ASN
1	D	430	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

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

5.5 Carbohydrates (i)

94 monosaccharides 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	Dec	Tiple	Bo	ond leng	$_{\rm ths}$	Bond angles		
IVIOI	туре	Unain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	1	1,3	14,14,15	1.76	2 (14%)	17,19,21	2.68	4 (23%)
3	NAG	G	2	3	14,14,15	0.41	0	17,19,21	0.39	0
4	NAG	Н	1	4	14,14,15	0.75	1 (7%)	17,19,21	1.05	1(5%)
4	NAG	Н	2	4	14,14,15	0.26	0	17,19,21	0.54	0
4	BMA	Н	3	4	11,11,12	1.23	2 (18%)	$15,\!15,\!17$	1.64	2 (13%)
5	NAG	Ι	1	1,5	$14,\!14,\!15$	0.51	0	17,19,21	0.84	1 (5%)
5	NAG	Ι	2	5	14,14,15	0.68	1 (7%)	17,19,21	1.24	2 (11%)
5	BMA	Ι	3	5	11,11,12	1.33	2 (18%)	$15,\!15,\!17$	1.85	3 (20%)
5	MAN	Ι	4	5	11,11,12	1.14	1 (9%)	15,15,17	1.19	2 (13%)
5	NAG	Ι	5	5	14,14,15	0.64	0	17,19,21	1.30	3 (17%)
5	GAL	Ι	6	5	11,11,12	1.05	0	15,15,17	1.13	1 (6%)
5	MAN	Ι	7	5	11,11,12	0.93	0	15,15,17	1.11	2 (13%)
5	NAG	Ι	8	5	14,14,15	0.52	0	17,19,21	1.03	2 (11%)
3	NAG	J	1	1,3	14,14,15	1.18	1 (7%)	17,19,21	1.44	1 (5%)
3	NAG	J	2	3	14,14,15	2.55	2 (14%)	17,19,21	2.39	2 (11%)
3	NAG	K	1	1,3	14,14,15	0.33	0	17,19,21	0.54	0
3	NAG	К	2	3	14,14,15	1.04	1 (7%)	17,19,21	1.95	1 (5%)
3	NAG	L	1	1,3	14,14,15	1.73	2 (14%)	17,19,21	1.74	2 (11%)
3	NAG	L	2	3	14,14,15	0.55	0	17,19,21	0.74	1 (5%)
3	NAG	М	1	1,3	14,14,15	0.54	0	17,19,21	0.74	0
3	NAG	М	2	3	14,14,15	0.52	0	17,19,21	0.64	0
6	NAG	Ν	1	1,6	$14,\!14,\!15$	1.24	1 (7%)	$17,\!19,\!21$	1.26	2(11%)
6	NAG	N	2	6	14,14,15	1.08	1 (7%)	17,19,21	1.55	3 (17%)



Mal	Tune	Chain	Dec	Tiple	Bond lengths		Bond angles			
	туре	Chan	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
6	BMA	Ν	3	6	11,11,12	1.20	2 (18%)	$15,\!15,\!17$	1.23	3 (20%)
6	MAN	Ν	4	6	11,11,12	1.41	2 (18%)	$15,\!15,\!17$	1.57	4 (26%)
6	NAG	Ν	5	6	14,14,15	0.56	0	17,19,21	1.62	3 (17%)
6	GAL	Ν	6	6	11,11,12	1.34	3 (27%)	15, 15, 17	1.37	3 (20%)
6	MAN	Ν	7	6	11,11,12	1.09	1 (9%)	15,15,17	1.96	3 (20%)
6	NAG	0	1	1,6	14,14,15	0.44	0	17,19,21	1.21	1 (5%)
6	NAG	0	2	6	14,14,15	0.50	0	17,19,21	0.52	0
6	BMA	0	3	6	11,11,12	0.86	0	$15,\!15,\!17$	1.14	1 (6%)
6	MAN	0	4	6	11,11,12	1.58	2 (18%)	15,15,17	2.08	4 (26%)
6	NAG	0	5	6	14,14,15	1.39	1 (7%)	17,19,21	1.51	1 (5%)
6	GAL	0	6	6	11,11,12	0.81	0	15,15,17	1.11	1 (6%)
6	MAN	0	7	6	11,11,12	1.12	0	15,15,17	1.49	2 (13%)
7	MAN	Р	1	7	11,11,12	1.68	3 (27%)	15,15,17	1.89	4 (26%)
7	NAG	Р	2	7	14,14,15	0.39	0	17,19,21	1.13	1 (5%)
7	BMA	Р	3	7	11,11,12	3.81	5 (45%)	15,15,17	2.08	3 (20%)
7	MAN	Р	4	7	11,11,12	1.12	2 (18%)	15,15,17	1.50	3 (20%)
7	NAG	Р	5	7	14,14,15	2.12	2 (14%)	17,19,21	1.93	2 (11%)
7	NAG	Р	6	7	14,14,15	0.34	0	17,19,21	0.83	0
3	NAG	Q	1	1,3	14,14,15	0.44	0	17,19,21	0.68	0
3	NAG	Q	2	3	14,14,15	0.66	0	17,19,21	0.48	0
3	NAG	R	1	1,3	14,14,15	1.17	1 (7%)	$17,\!19,\!21$	1.80	1 (5%)
3	NAG	R	2	3	14,14,15	0.90	1 (7%)	$17,\!19,\!21$	1.77	2 (11%)
8	NAG	S	1	8,1	14,14,15	1.04	1 (7%)	17,19,21	1.61	4 (23%)
8	NAG	S	2	8	14,14,15	0.79	0	17,19,21	1.68	4 (23%)
8	BMA	S	3	8	11,11,12	1.71	3 (27%)	$15,\!15,\!17$	2.62	3 (20%)
8	MAN	S	4	8	11,11,12	0.91	0	15,15,17	1.24	2 (13%)
3	NAG	Т	1	1,3	14,14,15	1.63	2 (14%)	17,19,21	1.33	1 (5%)
3	NAG	Т	2	3	14,14,15	0.68	0	17,19,21	0.98	1 (5%)
3	NAG	U	1	1,3	14,14,15	1.71	2 (14%)	17,19,21	1.58	2 (11%)
3	NAG	U	2	3	14,14,15	0.48	0	17,19,21	0.41	0
3	NAG	V	1	3	14,14,15	0.82	1 (7%)	17,19,21	1.04	2 (11%)
3	NAG	V	2	3	14,14,15	0.31	0	17,19,21	0.61	1 (5%)
5	NAG	W	1	1,5	14,14,15	0.74	1 (7%)	17,19,21	0.77	1 (5%)
5	NAG	W	2	5	14,14,15	0.90	1 (7%)	17,19,21	1.11	1 (5%)
5	BMA	W	3	5	11,11,12	1.33	2 (18%)	15,15,17	2.24	4 (26%)
5	MAN	W	4	5	11,11,12	1.91	2 (18%)	15,15,17	2.14	5 (33%)



Mal	Tune	Chain	Dec	Tink	Bo	ond leng	Bond lengths		Bond angles		
IVIOI	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
5	NAG	W	5	5	14,14,15	0.34	0	17,19,21	0.87	0	
5	GAL	W	6	5	11,11,12	0.87	0	15,15,17	0.81	0	
5	MAN	W	7	5	11,11,12	1.07	1 (9%)	$15,\!15,\!17$	1.21	3 (20%)	
5	NAG	W	8	5	14,14,15	0.68	1 (7%)	17,19,21	0.86	1 (5%)	
3	NAG	Х	1	1,3	14,14,15	1.98	1 (7%)	17,19,21	2.39	1 (5%)	
3	NAG	Х	2	3	14,14,15	0.53	0	17,19,21	0.54	0	
4	NAG	Y	1	1,4	14,14,15	0.35	0	17,19,21	0.51	0	
4	NAG	Y	2	4	14,14,15	0.42	0	17,19,21	0.63	0	
4	BMA	Y	3	4	11,11,12	0.90	0	$15,\!15,\!17$	1.09	1 (6%)	
3	NAG	Z	1	1,3	14,14,15	0.40	0	17,19,21	1.95	3 (17%)	
3	NAG	Z	2	3	14,14,15	0.57	0	17,19,21	0.46	0	
9	NAG	a	1	1,9	14,14,15	0.86	1 (7%)	17,19,21	1.09	2 (11%)	
9	NAG	a	2	9	14,14,15	0.64	0	17,19,21	1.32	4 (23%)	
9	BMA	a	3	9	11,11,12	0.77	0	15,15,17	0.92	0	
9	BMA	a	4	9	11,11,12	0.83	0	$15,\!15,\!17$	0.80	0	
3	NAG	b	1	1,3	14,14,15	0.40	0	17,19,21	1.09	1 (5%)	
3	NAG	b	2	3	14,14,15	0.42	0	17,19,21	0.40	0	
10	NAG	с	1	1,10	14,14,15	0.86	1 (7%)	17,19,21	0.96	1 (5%)	
10	NAG	с	2	10	14,14,15	0.50	0	17,19,21	0.54	0	
10	BMA	с	3	10	11,11,12	1.73	4 (36%)	$15,\!15,\!17$	1.76	5 (33%)	
10	MAN	с	4	10	11,11,12	2.15	3 (27%)	$15,\!15,\!17$	1.47	2 (13%)	
10	NAG	с	5	10	14,14,15	0.63	1 (7%)	17,19,21	0.66	0	
10	MAN	с	6	10	11,11,12	1.10	1 (9%)	15,15,17	1.20	1 (6%)	
10	NAG	с	7	10	14,14,15	0.47	0	17,19,21	0.48	0	
4	NAG	d	1	1,4	14,14,15	0.71	1 (7%)	17,19,21	0.72	0	
4	NAG	d	2	4	14,14,15	0.91	1 (7%)	17,19,21	1.72	3 (17%)	
4	BMA	d	3	4	11,11,12	1.15	1 (9%)	15,15,17	1.06	1 (6%)	
3	NAG	е	1	1,3	14,14,15	0.49	0	17,19,21	0.74	1(5%)	
3	NAG	е	2	3	14,14,15	1.45	2 (14%)	17,19,21	1.42	1 (5%)	
8	NAG	f	1	8,1	14,14,15	1.55	1 (7%)	17,19,21	2.07	4 (23%)	
8	NAG	f	2	8	14,14,15	1.52	2 (14%)	17,19,21	1.36	1 (5%)	
8	BMA	f	3	8	11,11,12	0.84	0	15,15,17	1.26	1 (6%)	
8	MAN	f	4	8	11,11,12	1.28	3 (27%)	15,15,17	1.26	2 (13%)	
3	NAG	g	1	1,3	14,14,15	0.93	1 (7%)	17,19,21	1.95	1 (5%)	
3	NAG	g	2	3	14,14,15	0.58	0	17,19,21	0.88	1 (5%)	

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	1	1,3	-	5/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
4	NAG	Н	1	4	-	2/6/23/26	0/1/1/1
4	NAG	Н	2	4	-	2/6/23/26	0/1/1/1
4	BMA	Н	3	4	-	0/2/19/22	0/1/1/1
5	NAG	Ι	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	Ι	2	5	-	2/6/23/26	0/1/1/1
5	BMA	Ι	3	5	-	1/2/19/22	0/1/1/1
5	MAN	Ι	4	5	-	0/2/19/22	1/1/1/1
5	NAG	Ι	5	5	-	3/6/23/26	0/1/1/1
5	GAL	Ι	6	5	-	2/2/19/22	0/1/1/1
5	MAN	Ι	7	5	-	2/2/19/22	0/1/1/1
5	NAG	Ι	8	5	-	1/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	3/6/23/26	0/1/1/1
3	NAG	K	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	K	2	3	-	4/6/23/26	0/1/1/1
3	NAG	L	1	1,3	_	4/6/23/26	0/1/1/1
3	NAG	L	2	3	-	1/6/23/26	0/1/1/1
3	NAG	М	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	М	2	3	-	2/6/23/26	0/1/1/1
6	NAG	N	1	1,6	_	2/6/23/26	0/1/1/1
6	NAG	N	2	6	_	2/6/23/26	0/1/1/1
6	BMA	N	3	6	_	0/2/19/22	0/1/1/1
6	MAN	N	4	6	_	$\frac{2}{2}/\frac{2}{19}/22$	0/1/1/1
6	NAG	N	5	6	_	3/6/23/26	0/1/1/1
6	GAL	N	6	6	_	1/2/19/22	0/1/1/1
6	MAN	N	7	6	-	$\frac{2}{2}/\frac{2}{19}/22$	0/1/1/1
6	NAG	Ο	1	1,6	-	3/6/23/26	0/1/1/1
6	NAG	Ο	2	6	_	4/6/23/26	0/1/1/1
6	BMA	Ο	3	6	_	2/2/19/22	0/1/1/1
6	MAN	0	4	6	-	1/2/19/22	0/1/1/1
6	NAG	Ο	5	6	-	3/6/23/26	0/1/1/1
6	GAL	Ο	6	6	_	2/2/19/22	0/1/1/1

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	0	7	6	-	0/2/19/22	1/1/1/1
7	MAN	Р	1	7	-	2/2/19/22	0/1/1/1
7	NAG	Р	2	7	-	2/6/23/26	0/1/1/1
7	BMA	Р	3	7	-	2/2/19/22	0/1/1/1
7	MAN	Р	4	7	-	2/2/19/22	1/1/1/1
7	NAG	Р	5	7	-	3/6/23/26	0/1/1/1
7	NAG	Р	6	7	-	4/6/23/26	0/1/1/1
3	NAG	Q	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	4/6/23/26	0/1/1/1
3	NAG	R	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	R	2	3	-	2/6/23/26	0/1/1/1
8	NAG	S	1	8,1	1/1/5/7	3/6/23/26	0/1/1/1
8	NAG	S	2	8	-	3/6/23/26	0/1/1/1
8	BMA	S	3	8	-	2/2/19/22	0/1/1/1
8	MAN	S	4	8	-	2/2/19/22	0/1/1/1
3	NAG	Т	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	Т	2	3	-	3/6/23/26	0/1/1/1
3	NAG	U	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	U	2	3	-	0/6/23/26	0/1/1/1
3	NAG	V	1	3	-	2/6/23/26	0/1/1/1
3	NAG	V	2	3	-	2/6/23/26	0/1/1/1
5	NAG	W	1	1,5	-	3/6/23/26	0/1/1/1
5	NAG	W	2	5	-	2/6/23/26	0/1/1/1
5	BMA	W	3	5	-	2/2/19/22	0/1/1/1
5	MAN	W	4	5	-	2/2/19/22	0/1/1/1
5	NAG	W	5	5	-	4/6/23/26	0/1/1/1
5	GAL	W	6	5	-	0/2/19/22	0/1/1/1
5	MAN	W	7	5	-	2/2/19/22	0/1/1/1
5	NAG	W	8	5	-	3/6/23/26	0/1/1/1
3	NAG	Х	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	Х	2	3	-	4/6/23/26	0/1/1/1
4	NAG	Y	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	Y	2	4	-	2/6/23/26	0/1/1/1
4	BMA	Y	3	4	-	0/2/19/22	0/1/1/1
3	NAG	Z	1	1,3	-	4/6/23/26	0/1/1/1



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	Z	2	3	-	2/6/23/26	0/1/1/1
9	NAG	a	1	1,9	-	1/6/23/26	0/1/1/1
9	NAG	a	2	9	-	3/6/23/26	0/1/1/1
9	BMA	a	3	9	-	2/2/19/22	0/1/1/1
9	BMA	a	4	9	-	1/2/19/22	0/1/1/1
3	NAG	b	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	b	2	3	-	0/6/23/26	0/1/1/1
10	NAG	с	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	с	2	10	-	0/6/23/26	0/1/1/1
10	BMA	с	3	10	-	2/2/19/22	0/1/1/1
10	MAN	с	4	10	-	2/2/19/22	0/1/1/1
10	NAG	с	5	10	-	0/6/23/26	0/1/1/1
10	MAN	с	6	10	-	1/2/19/22	0/1/1/1
10	NAG	с	7	10	-	4/6/23/26	0/1/1/1
4	NAG	d	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	d	2	4	-	1/6/23/26	0/1/1/1
4	BMA	d	3	4	-	1/2/19/22	0/1/1/1
3	NAG	е	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	е	2	3	-	2/6/23/26	0/1/1/1
8	NAG	f	1	8,1	-	2/6/23/26	0/1/1/1
8	NAG	f	2	8	-	2/6/23/26	0/1/1/1
8	BMA	f	3	8	-	0/2/19/22	0/1/1/1
8	MAN	f	4	8	-	2/2/19/22	1/1/1/1
3	NAG	g	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	g	2	3	-	4/6/23/26	0/1/1/1

The worst 5 of 83 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
3	J	2	NAG	O5-C1	9.01	1.58	1.43
7	Р	3	BMA	C1-C2	8.29	1.71	1.52
7	Р	3	BMA	C2-C3	7.32	1.63	1.52
3	Х	1	NAG	O5-C1	7.28	1.55	1.43
7	Р	5	NAG	O5-C1	6.81	1.54	1.43

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	Х	1	NAG	C1-O5-C5	9.50	125.07	112.19



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	J	2	NAG	C1-O5-C5	9.07	124.48	112.19
3	G	1	NAG	C2-N2-C7	8.22	134.60	122.90
8	S	3	BMA	C1-O5-C5	7.96	122.98	112.19
3	Κ	2	NAG	C1-O5-C5	7.48	122.32	112.19

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	S	1	NAG	C1

5 of 196 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	Ζ	1	NAG	C4-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
5	Ι	7	MAN	O5-C5-C6-O6
3	U	1	NAG	C4-C5-C6-O6
9	a	2	NAG	O5-C5-C6-O6

All (4) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	Ι	4	MAN	C1-C2-C3-C4-C5-O5
8	f	4	MAN	C1-C2-C3-C4-C5-O5
6	0	7	MAN	C1-C2-C3-C4-C5-O5
7	Р	4	MAN	C1-C2-C3-C4-C5-O5

8 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	U	1	NAG	1	0
3	G	1	NAG	1	0
3	J	1	NAG	1	0
6	0	1	NAG	1	0
5	W	8	NAG	1	0
5	Ι	1	NAG	1	0
6	Ν	7	MAN	1	0
5	Ι	8	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.




























































































5.6 Ligand geometry (i)

Of 36 ligands modelled in this entry, 4 are monoatomic - leaving 32 for Mogul analysis.

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

	Turne	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain Da	Dec Link		Bond lengths			Bond angles		
IVIOI	Moi Type Chain	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2												
13	POV	В	1005	-	51,51,51	1.08	3 (5%)	57,59,59	0.93	4 (7%)												
12	GLU	В	1003	-	8,9,9	1.07	1 (12%)	10,11,11	1.41	2 (20%)												



Mal	True	Chain	Dec	Timle	Bo	Bond lengths		Bond angles		
	Type	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	CLR	С	1009	-	31,31,31	0.19	0	48,48,48	0.41	0
13	POV	А	1004	-	51,51,51	1.06	3 (5%)	57, 59, 59	0.93	3 (5%)
12	GLU	А	1002	-	8,9,9	1.09	1 (12%)	10,11,11	1.31	2 (20%)
13	POV	С	1001	-	51,51,51	1.08	3 (5%)	57,59,59	0.92	3 (5%)
14	CLR	А	1006	-	31,31,31	0.15	0	48,48,48	0.35	0
11	2J9	С	1002	-	17,18,18	7.25	8 (47%)	23,28,28	5.89	7 (30%)
13	POV	С	1004	-	51,51,51	1.06	3 (5%)	57,59,59	0.91	3 (5%)
11	2J9	А	1001	-	17,18,18	7.21	8 (47%)	23,28,28	<mark>5.76</mark>	7 (30%)
13	POV	А	1005	-	51,51,51	1.08	2 (3%)	57,59,59	0.97	3 (5%)
13	POV	А	1010	-	51,51,51	1.07	3 (5%)	57,59,59	0.92	3 (5%)
13	POV	В	1004	-	51,51,51	1.07	3 (5%)	57,59,59	0.93	3 (5%)
15	NAG	В	1006	1	14,14,15	0.57	1 (7%)	17,19,21	0.37	0
12	GLU	С	1003	-	8,9,9	1.10	1 (12%)	10,11,11	1.31	2 (20%)
14	CLR	А	1007	-	31,31,31	0.18	0	48,48,48	0.32	0
14	CLR	В	1007	-	31,31,31	0.14	0	48,48,48	0.34	0
11	2J9	В	1002	-	17,18,18	7.29	8 (47%)	$23,\!28,\!28$	6.07	6 (26%)
13	POV	В	1001	-	51,51,51	1.07	3 (5%)	57,59,59	0.93	4 (7%)
13	POV	С	1006	-	51,51,51	1.08	2 (3%)	57,59,59	0.96	3 (5%)
11	2J9	D	1002	-	17,18,18	7.33	8 (47%)	23,28,28	<mark>5.89</mark>	6 (26%)
13	POV	D	1001	-	51,51,51	1.07	3 (5%)	57, 59, 59	0.93	4 (7%)
14	CLR	А	1009	-	31,31,31	0.18	0	48,48,48	0.30	0
15	NAG	С	1008	1	14,14,15	1.77	2 (14%)	17,19,21	1.58	1 (5%)
14	CLR	С	1007	-	31,31,31	0.19	0	48,48,48	0.33	0
12	GLU	D	1003	-	8,9,9	1.05	1 (12%)	10,11,11	1.40	2 (20%)
13	POV	А	1003	-	51,51,51	1.05	3 (5%)	57,59,59	0.95	4 (7%)
13	POV	D	1005	-	51,51,51	1.07	3 (5%)	57,59,59	0.93	3 (5%)
13	POV	С	1005	-	51,51,51	1.07	3 (5%)	57,59,59	0.90	3 (5%)
14	CLR	С	1010	-	31,31,31	0.18	0	48,48,48	0.31	0
13	POV	D	1004	-	51,51,51	1.07	3 (5%)	57,59,59	0.93	3 (5%)
14	CLR	A	1008	-	31,31,31	0.20	0	48,48,48	0.41	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
13	POV	В	1005	-	-	26/55/55/55	-
12	GLU	В	1003	-	-	0/9/9/9	-
14	CLR	С	1009	-	-	2/10/68/68	0/4/4/4
13	POV	А	1004	-	-	22/55/55/55	-
12	GLU	А	1002	-	-	2/9/9/9	-
13	POV	С	1001	-	-	30/55/55/55	-
14	CLR	А	1006	-	-	7/10/68/68	0/4/4/4
11	2J9	С	1002	-	-	2/4/22/22	0/3/3/3
13	POV	С	1004	-	-	34/55/55/55	-
11	2J9	А	1001	-	-	1/4/22/22	0/3/3/3
13	POV	А	1005	-	-	33/55/55/55	-
13	POV	А	1010	-	-	28/55/55/55	-
13	POV	В	1004	-	-	31/55/55/55	-
15	NAG	В	1006	1	-	0/6/23/26	0/1/1/1
12	GLU	С	1003	-	-	2/9/9/9	-
14	CLR	А	1007	-	-	7/10/68/68	0/4/4/4
14	CLR	В	1007	-	-	7/10/68/68	0/4/4/4
11	2J9	В	1002	_	-	0/4/22/22	0/3/3/3
13	POV	В	1001	-	-	28/55/55/55	-
13	POV	С	1006	-	-	30/55/55/55	-
11	2J9	D	1002	-	-	0/4/22/22	0/3/3/3
13	POV	D	1001	-	-	29/55/55/55	-
14	CLR	А	1009	-	-	6/10/68/68	0/4/4/4
15	NAG	С	1008	1	-	4/6/23/26	0/1/1/1
14	CLR	С	1007	-	-	7/10/68/68	0/4/4/4
12	GLU	D	1003	-	-	0/9/9/9	-
13	POV	А	1003	-	-	28/55/55/55	-
13	POV	D	1005	-	-	27/55/55/55	-
13	POV	С	1005	-	-	31/55/55/55	-
14	CLR	С	1010	-	-	6/10/68/68	0/4/4/4
13	POV	D	1004	-	-	28/55/55/55	-
14	CLR	А	1008	-	-	2/10/68/68	0/4/4/4

The worst 5 of 79 bond length outliers are listed below:

IVIOI	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(A)
11	D	1002	2J9	OAA-SAP	20.02	1.66	1.43

Continued on next page...



0 0											
Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)				
11	В	1002	2J9	OAA-SAP	19.94	1.66	1.43				
11	С	1002	2J9	OAA-SAP	19.83	1.66	1.43				
11	А	1001	2J9	OAA-SAP	19.76	1.66	1.43				
11	D	1002	2J9	OAB-SAP	19.37	1.65	1.43				

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The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
11	В	1002	2J9	CAI-NAO-CAL	25.52	121.67	110.25
11	D	1002	2J9	CAI-NAO-CAL	25.14	121.50	110.25
11	С	1002	2J9	CAI-NAO-CAL	24.08	121.03	110.25
11	А	1001	2J9	CAI-NAO-CAL	23.07	120.58	110.25
11	А	1001	2J9	CAM-SAP-NAJ	10.67	110.81	102.37

There are no chirality outliers.

5 of 460 torsion outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms
11	А	1001	2J9	CAG-CAN-NAO-CAL
11	С	1002	2J9	CAG-CAN-NAO-CAL
11	С	1002	2J9	CAH-CAN-NAO-CAI
13	А	1003	POV	C1-O11-P-O13
13	А	1003	POV	C1-O11-P-O14

There are no ring outliers.

19 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	В	1005	POV	2	0
13	А	1004	POV	3	0
12	А	1002	GLU	1	0
13	С	1001	POV	3	0
14	А	1006	CLR	1	0
13	С	1004	POV	2	0
13	А	1005	POV	1	0
13	А	1010	POV	4	0
13	В	1004	POV	4	0
12	С	1003	GLU	1	0
14	В	1007	CLR	1	0
13	В	1001	POV	1	0
13	С	1006	POV	1	0

Continued on next page...



	v	1	1 0		
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	D	1002	2J9	1	0
13	D	1001	POV	3	0
13	А	1003	POV	2	0
13	D	1005	POV	2	0
13	С	1005	POV	2	0
13	D	1004	POV	4	0

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The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and similar rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.






















































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 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-44130. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map



The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 134

Y Index: 127

Z Index: 121

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.3487. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



7.2 Volume estimate (i)



The volume at the recommended contour level is 1440 nm^3 ; this corresponds to an approximate mass of 1300 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.150 ${\rm \AA^{-1}}$



8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-44130 and PDB model 9B37. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 1.3487 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Q-score mapped to coordinate model (i)



The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.3487).



9.4 Atom inclusion (i)



At the recommended contour level, 100% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (1.3487) and Q-score for the entire model and for each chain.

\mathbf{Chain}	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.9690	0.3690
А	0.9770	0.3720
В	0.9790	0.4020
С	0.9770	0.3750
D	0.9730	0.3940
Е	0.9310	0.2840
F	0.9100	0.2860
G	1.0000	0.3410
Н	1.0000	0.3950
Ι	0.8900	0.2220
J	1.0000	0.2140
К	1.0000	0.1060
L	0.8210	0.0550
М	1.0000	-0.0130
Ν	0.9880	0.3050
О	0.8950	0.1830
Р	0.9070	0.2800
Q	0.9640	0.1450
R	1.0000	0.2520
S	0.9800	0.2440
Т	1.0000	0.1920
U	0.9640	0.3550
V	1.0000	0.4300
W	0.9600	0.2970
Х	1.0000	0.1300
Y	0.9230	0.0950
Ζ	1.0000	0.2800
a	1.0000	0.3770
b	1.0000	0.3750
с	0.9550	0.2580
d	1.0000	0.1680
е	0.9640	0.1710
f	0.9200	0.3050
g	1.0000	0.1590

