



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 12:03 AM UTC

PDB ID : 8WYR / pdb_00008wyr
EMDB ID : EMD-37936
Title : Cryo-EM structure of human CD5L bound to IgM-Fc/J
Authors : Wang, Y.X.; Su, C.; Xiao, J.Y.
Deposited on : 2023-10-31
Resolution : 3.39 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 ⓘ 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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

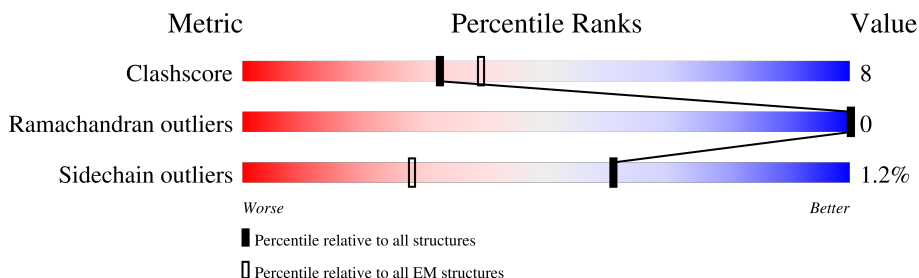
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.39 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.



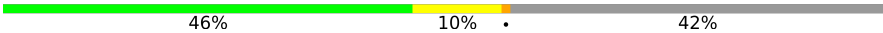
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	403	44% 13% 42%
1	B	403	43% 14% 43%
1	C	403	42% 14% 44%
1	D	403	43% 12% 44%
1	E	403	44% 12% 44%
1	F	403	43% 12% 44%
1	G	403	39% 16% 44%
1	H	403	46% 11% 42%
1	K	403	46% 11% 42%

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Mol	Chain	Length	Quality of chain
1	L	403	 46% 10% 42%
2	J	168	 60% 14% 24%
3	M	359	 49% 10% 41%
4	I	2	 50% 50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20612 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.

- Molecule 1 is a protein called Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	232	Total	C	N	O	S	0	0
			1798	1132	304	353	9		
1	B	230	Total	C	N	O	S	0	0
			1780	1120	302	350	8		
1	C	226	Total	C	N	O	S	0	0
			1757	1107	298	344	8		
1	D	227	Total	C	N	O	S	0	0
			1764	1111	299	346	8		
1	E	226	Total	C	N	O	S	0	0
			1757	1107	298	344	8		
1	F	227	Total	C	N	O	S	0	0
			1764	1111	299	346	8		
1	G	225	Total	C	N	O	S	0	0
			1749	1103	297	341	8		
1	H	232	Total	C	N	O	S	0	0
			1798	1132	304	353	9		
1	K	232	Total	C	N	O	S	0	0
			1798	1132	304	353	9		
1	L	232	Total	C	N	O	S	0	0
			1798	1132	304	353	9		

There are 340 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	SER	-	linker	UNP P60568
A	196	ALA	-	linker	UNP P60568
A	197	TRP	-	linker	UNP P60568
A	198	SER	-	linker	UNP P60568
A	199	HIS	-	linker	UNP P60568
A	200	PRO	-	linker	UNP P60568
A	201	GLN	-	linker	UNP P60568
A	202	PHE	-	linker	UNP P60568
A	203	GLU	-	linker	UNP P60568
A	204	LYS	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
A	205	GLY	-	linker	UNP P60568
A	206	GLY	-	linker	UNP P60568
A	207	GLY	-	linker	UNP P60568
A	208	SER	-	linker	UNP P60568
A	209	GLY	-	linker	UNP P60568
A	210	GLY	-	linker	UNP P60568
A	211	GLY	-	linker	UNP P60568
A	212	SER	-	linker	UNP P60568
A	213	GLY	-	linker	UNP P60568
A	214	GLY	-	linker	UNP P60568
A	215	SER	-	linker	UNP P60568
A	216	ALA	-	linker	UNP P60568
A	217	TRP	-	linker	UNP P60568
A	218	SER	-	linker	UNP P60568
A	219	HIS	-	linker	UNP P60568
A	220	PRO	-	linker	UNP P60568
A	221	GLN	-	linker	UNP P60568
A	222	PHE	-	linker	UNP P60568
A	223	GLU	-	linker	UNP P60568
A	224	LYS	-	linker	UNP P60568
A	225	ILE	-	linker	UNP P60568
A	226	ASP	-	linker	UNP P60568
A	227	THR	-	linker	UNP P60568
A	228	THR	-	linker	UNP P60568
B	195	SER	-	linker	UNP P60568
B	196	ALA	-	linker	UNP P60568
B	197	TRP	-	linker	UNP P60568
B	198	SER	-	linker	UNP P60568
B	199	HIS	-	linker	UNP P60568
B	200	PRO	-	linker	UNP P60568
B	201	GLN	-	linker	UNP P60568
B	202	PHE	-	linker	UNP P60568
B	203	GLU	-	linker	UNP P60568
B	204	LYS	-	linker	UNP P60568
B	205	GLY	-	linker	UNP P60568
B	206	GLY	-	linker	UNP P60568
B	207	GLY	-	linker	UNP P60568
B	208	SER	-	linker	UNP P60568
B	209	GLY	-	linker	UNP P60568
B	210	GLY	-	linker	UNP P60568
B	211	GLY	-	linker	UNP P60568
B	212	SER	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
B	213	GLY	-	linker	UNP P60568
B	214	GLY	-	linker	UNP P60568
B	215	SER	-	linker	UNP P60568
B	216	ALA	-	linker	UNP P60568
B	217	TRP	-	linker	UNP P60568
B	218	SER	-	linker	UNP P60568
B	219	HIS	-	linker	UNP P60568
B	220	PRO	-	linker	UNP P60568
B	221	GLN	-	linker	UNP P60568
B	222	PHE	-	linker	UNP P60568
B	223	GLU	-	linker	UNP P60568
B	224	LYS	-	linker	UNP P60568
B	225	ILE	-	linker	UNP P60568
B	226	ASP	-	linker	UNP P60568
B	227	THR	-	linker	UNP P60568
B	228	THR	-	linker	UNP P60568
C	195	SER	-	linker	UNP P60568
C	196	ALA	-	linker	UNP P60568
C	197	TRP	-	linker	UNP P60568
C	198	SER	-	linker	UNP P60568
C	199	HIS	-	linker	UNP P60568
C	200	PRO	-	linker	UNP P60568
C	201	GLN	-	linker	UNP P60568
C	202	PHE	-	linker	UNP P60568
C	203	GLU	-	linker	UNP P60568
C	204	LYS	-	linker	UNP P60568
C	205	GLY	-	linker	UNP P60568
C	206	GLY	-	linker	UNP P60568
C	207	GLY	-	linker	UNP P60568
C	208	SER	-	linker	UNP P60568
C	209	GLY	-	linker	UNP P60568
C	210	GLY	-	linker	UNP P60568
C	211	GLY	-	linker	UNP P60568
C	212	SER	-	linker	UNP P60568
C	213	GLY	-	linker	UNP P60568
C	214	GLY	-	linker	UNP P60568
C	215	SER	-	linker	UNP P60568
C	216	ALA	-	linker	UNP P60568
C	217	TRP	-	linker	UNP P60568
C	218	SER	-	linker	UNP P60568
C	219	HIS	-	linker	UNP P60568
C	220	PRO	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
C	221	GLN	-	linker	UNP P60568
C	222	PHE	-	linker	UNP P60568
C	223	GLU	-	linker	UNP P60568
C	224	LYS	-	linker	UNP P60568
C	225	ILE	-	linker	UNP P60568
C	226	ASP	-	linker	UNP P60568
C	227	THR	-	linker	UNP P60568
C	228	THR	-	linker	UNP P60568
D	195	SER	-	linker	UNP P60568
D	196	ALA	-	linker	UNP P60568
D	197	TRP	-	linker	UNP P60568
D	198	SER	-	linker	UNP P60568
D	199	HIS	-	linker	UNP P60568
D	200	PRO	-	linker	UNP P60568
D	201	GLN	-	linker	UNP P60568
D	202	PHE	-	linker	UNP P60568
D	203	GLU	-	linker	UNP P60568
D	204	LYS	-	linker	UNP P60568
D	205	GLY	-	linker	UNP P60568
D	206	GLY	-	linker	UNP P60568
D	207	GLY	-	linker	UNP P60568
D	208	SER	-	linker	UNP P60568
D	209	GLY	-	linker	UNP P60568
D	210	GLY	-	linker	UNP P60568
D	211	GLY	-	linker	UNP P60568
D	212	SER	-	linker	UNP P60568
D	213	GLY	-	linker	UNP P60568
D	214	GLY	-	linker	UNP P60568
D	215	SER	-	linker	UNP P60568
D	216	ALA	-	linker	UNP P60568
D	217	TRP	-	linker	UNP P60568
D	218	SER	-	linker	UNP P60568
D	219	HIS	-	linker	UNP P60568
D	220	PRO	-	linker	UNP P60568
D	221	GLN	-	linker	UNP P60568
D	222	PHE	-	linker	UNP P60568
D	223	GLU	-	linker	UNP P60568
D	224	LYS	-	linker	UNP P60568
D	225	ILE	-	linker	UNP P60568
D	226	ASP	-	linker	UNP P60568
D	227	THR	-	linker	UNP P60568
D	228	THR	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
E	195	SER	-	linker	UNP P60568
E	196	ALA	-	linker	UNP P60568
E	197	TRP	-	linker	UNP P60568
E	198	SER	-	linker	UNP P60568
E	199	HIS	-	linker	UNP P60568
E	200	PRO	-	linker	UNP P60568
E	201	GLN	-	linker	UNP P60568
E	202	PHE	-	linker	UNP P60568
E	203	GLU	-	linker	UNP P60568
E	204	LYS	-	linker	UNP P60568
E	205	GLY	-	linker	UNP P60568
E	206	GLY	-	linker	UNP P60568
E	207	GLY	-	linker	UNP P60568
E	208	SER	-	linker	UNP P60568
E	209	GLY	-	linker	UNP P60568
E	210	GLY	-	linker	UNP P60568
E	211	GLY	-	linker	UNP P60568
E	212	SER	-	linker	UNP P60568
E	213	GLY	-	linker	UNP P60568
E	214	GLY	-	linker	UNP P60568
E	215	SER	-	linker	UNP P60568
E	216	ALA	-	linker	UNP P60568
E	217	TRP	-	linker	UNP P60568
E	218	SER	-	linker	UNP P60568
E	219	HIS	-	linker	UNP P60568
E	220	PRO	-	linker	UNP P60568
E	221	GLN	-	linker	UNP P60568
E	222	PHE	-	linker	UNP P60568
E	223	GLU	-	linker	UNP P60568
E	224	LYS	-	linker	UNP P60568
E	225	ILE	-	linker	UNP P60568
E	226	ASP	-	linker	UNP P60568
E	227	THR	-	linker	UNP P60568
E	228	THR	-	linker	UNP P60568
F	195	SER	-	linker	UNP P60568
F	196	ALA	-	linker	UNP P60568
F	197	TRP	-	linker	UNP P60568
F	198	SER	-	linker	UNP P60568
F	199	HIS	-	linker	UNP P60568
F	200	PRO	-	linker	UNP P60568
F	201	GLN	-	linker	UNP P60568
F	202	PHE	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
F	203	GLU	-	linker	UNP P60568
F	204	LYS	-	linker	UNP P60568
F	205	GLY	-	linker	UNP P60568
F	206	GLY	-	linker	UNP P60568
F	207	GLY	-	linker	UNP P60568
F	208	SER	-	linker	UNP P60568
F	209	GLY	-	linker	UNP P60568
F	210	GLY	-	linker	UNP P60568
F	211	GLY	-	linker	UNP P60568
F	212	SER	-	linker	UNP P60568
F	213	GLY	-	linker	UNP P60568
F	214	GLY	-	linker	UNP P60568
F	215	SER	-	linker	UNP P60568
F	216	ALA	-	linker	UNP P60568
F	217	TRP	-	linker	UNP P60568
F	218	SER	-	linker	UNP P60568
F	219	HIS	-	linker	UNP P60568
F	220	PRO	-	linker	UNP P60568
F	221	GLN	-	linker	UNP P60568
F	222	PHE	-	linker	UNP P60568
F	223	GLU	-	linker	UNP P60568
F	224	LYS	-	linker	UNP P60568
F	225	ILE	-	linker	UNP P60568
F	226	ASP	-	linker	UNP P60568
F	227	THR	-	linker	UNP P60568
F	228	THR	-	linker	UNP P60568
G	195	SER	-	linker	UNP P60568
G	196	ALA	-	linker	UNP P60568
G	197	TRP	-	linker	UNP P60568
G	198	SER	-	linker	UNP P60568
G	199	HIS	-	linker	UNP P60568
G	200	PRO	-	linker	UNP P60568
G	201	GLN	-	linker	UNP P60568
G	202	PHE	-	linker	UNP P60568
G	203	GLU	-	linker	UNP P60568
G	204	LYS	-	linker	UNP P60568
G	205	GLY	-	linker	UNP P60568
G	206	GLY	-	linker	UNP P60568
G	207	GLY	-	linker	UNP P60568
G	208	SER	-	linker	UNP P60568
G	209	GLY	-	linker	UNP P60568
G	210	GLY	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
G	211	GLY	-	linker	UNP P60568
G	212	SER	-	linker	UNP P60568
G	213	GLY	-	linker	UNP P60568
G	214	GLY	-	linker	UNP P60568
G	215	SER	-	linker	UNP P60568
G	216	ALA	-	linker	UNP P60568
G	217	TRP	-	linker	UNP P60568
G	218	SER	-	linker	UNP P60568
G	219	HIS	-	linker	UNP P60568
G	220	PRO	-	linker	UNP P60568
G	221	GLN	-	linker	UNP P60568
G	222	PHE	-	linker	UNP P60568
G	223	GLU	-	linker	UNP P60568
G	224	LYS	-	linker	UNP P60568
G	225	ILE	-	linker	UNP P60568
G	226	ASP	-	linker	UNP P60568
G	227	THR	-	linker	UNP P60568
G	228	THR	-	linker	UNP P60568
H	195	SER	-	linker	UNP P60568
H	196	ALA	-	linker	UNP P60568
H	197	TRP	-	linker	UNP P60568
H	198	SER	-	linker	UNP P60568
H	199	HIS	-	linker	UNP P60568
H	200	PRO	-	linker	UNP P60568
H	201	GLN	-	linker	UNP P60568
H	202	PHE	-	linker	UNP P60568
H	203	GLU	-	linker	UNP P60568
H	204	LYS	-	linker	UNP P60568
H	205	GLY	-	linker	UNP P60568
H	206	GLY	-	linker	UNP P60568
H	207	GLY	-	linker	UNP P60568
H	208	SER	-	linker	UNP P60568
H	209	GLY	-	linker	UNP P60568
H	210	GLY	-	linker	UNP P60568
H	211	GLY	-	linker	UNP P60568
H	212	SER	-	linker	UNP P60568
H	213	GLY	-	linker	UNP P60568
H	214	GLY	-	linker	UNP P60568
H	215	SER	-	linker	UNP P60568
H	216	ALA	-	linker	UNP P60568
H	217	TRP	-	linker	UNP P60568
H	218	SER	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
H	219	HIS	-	linker	UNP P60568
H	220	PRO	-	linker	UNP P60568
H	221	GLN	-	linker	UNP P60568
H	222	PHE	-	linker	UNP P60568
H	223	GLU	-	linker	UNP P60568
H	224	LYS	-	linker	UNP P60568
H	225	ILE	-	linker	UNP P60568
H	226	ASP	-	linker	UNP P60568
H	227	THR	-	linker	UNP P60568
H	228	THR	-	linker	UNP P60568
K	195	SER	-	linker	UNP P60568
K	196	ALA	-	linker	UNP P60568
K	197	TRP	-	linker	UNP P60568
K	198	SER	-	linker	UNP P60568
K	199	HIS	-	linker	UNP P60568
K	200	PRO	-	linker	UNP P60568
K	201	GLN	-	linker	UNP P60568
K	202	PHE	-	linker	UNP P60568
K	203	GLU	-	linker	UNP P60568
K	204	LYS	-	linker	UNP P60568
K	205	GLY	-	linker	UNP P60568
K	206	GLY	-	linker	UNP P60568
K	207	GLY	-	linker	UNP P60568
K	208	SER	-	linker	UNP P60568
K	209	GLY	-	linker	UNP P60568
K	210	GLY	-	linker	UNP P60568
K	211	GLY	-	linker	UNP P60568
K	212	SER	-	linker	UNP P60568
K	213	GLY	-	linker	UNP P60568
K	214	GLY	-	linker	UNP P60568
K	215	SER	-	linker	UNP P60568
K	216	ALA	-	linker	UNP P60568
K	217	TRP	-	linker	UNP P60568
K	218	SER	-	linker	UNP P60568
K	219	HIS	-	linker	UNP P60568
K	220	PRO	-	linker	UNP P60568
K	221	GLN	-	linker	UNP P60568
K	222	PHE	-	linker	UNP P60568
K	223	GLU	-	linker	UNP P60568
K	224	LYS	-	linker	UNP P60568
K	225	ILE	-	linker	UNP P60568
K	226	ASP	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
K	227	THR	-	linker	UNP P60568
K	228	THR	-	linker	UNP P60568
L	195	SER	-	linker	UNP P60568
L	196	ALA	-	linker	UNP P60568
L	197	TRP	-	linker	UNP P60568
L	198	SER	-	linker	UNP P60568
L	199	HIS	-	linker	UNP P60568
L	200	PRO	-	linker	UNP P60568
L	201	GLN	-	linker	UNP P60568
L	202	PHE	-	linker	UNP P60568
L	203	GLU	-	linker	UNP P60568
L	204	LYS	-	linker	UNP P60568
L	205	GLY	-	linker	UNP P60568
L	206	GLY	-	linker	UNP P60568
L	207	GLY	-	linker	UNP P60568
L	208	SER	-	linker	UNP P60568
L	209	GLY	-	linker	UNP P60568
L	210	GLY	-	linker	UNP P60568
L	211	GLY	-	linker	UNP P60568
L	212	SER	-	linker	UNP P60568
L	213	GLY	-	linker	UNP P60568
L	214	GLY	-	linker	UNP P60568
L	215	SER	-	linker	UNP P60568
L	216	ALA	-	linker	UNP P60568
L	217	TRP	-	linker	UNP P60568
L	218	SER	-	linker	UNP P60568
L	219	HIS	-	linker	UNP P60568
L	220	PRO	-	linker	UNP P60568
L	221	GLN	-	linker	UNP P60568
L	222	PHE	-	linker	UNP P60568
L	223	GLU	-	linker	UNP P60568
L	224	LYS	-	linker	UNP P60568
L	225	ILE	-	linker	UNP P60568
L	226	ASP	-	linker	UNP P60568
L	227	THR	-	linker	UNP P60568
L	228	THR	-	linker	UNP P60568

- Molecule 2 is a protein called Immunoglobulin J chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	127	Total	C	N	O	S	0	0
			1010	622	176	203	9		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	137	TYR	-	expression tag	UNP P01591
J	138	PRO	-	expression tag	UNP P01591
J	139	TYR	-	expression tag	UNP P01591
J	140	ASP	-	expression tag	UNP P01591
J	141	VAL	-	expression tag	UNP P01591
J	142	PRO	-	expression tag	UNP P01591
J	143	ASP	-	expression tag	UNP P01591
J	144	TYR	-	expression tag	UNP P01591
J	145	ALA	-	expression tag	UNP P01591

- Molecule 3 is a protein called Interleukin-2,CD5 antigen-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	213	Total	C	N	O	S	0	0
			1669	1026	315	309	19		

There are 10 discrepancies between the modelled and reference sequences:

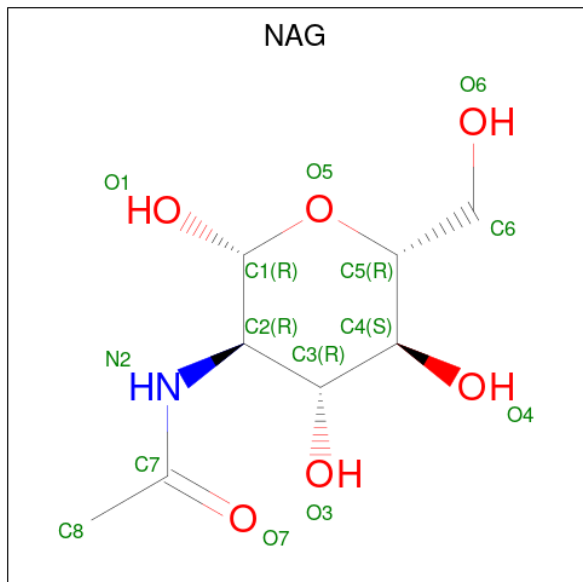
Chain	Residue	Modelled	Actual	Comment	Reference
M	10	ARG	-	linker	UNP P60568
M	11	ILE	-	linker	UNP P60568
M	12	HIS	-	linker	UNP P60568
M	13	HIS	-	linker	UNP P60568
M	14	HIS	-	linker	UNP P60568
M	15	HIS	-	linker	UNP P60568
M	16	HIS	-	linker	UNP P60568
M	17	HIS	-	linker	UNP P60568
M	18	HIS	-	linker	UNP P60568
M	19	HIS	-	linker	UNP P60568

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



Mol	Chain	Residues	Atoms				AltConf	Trace
4	I	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

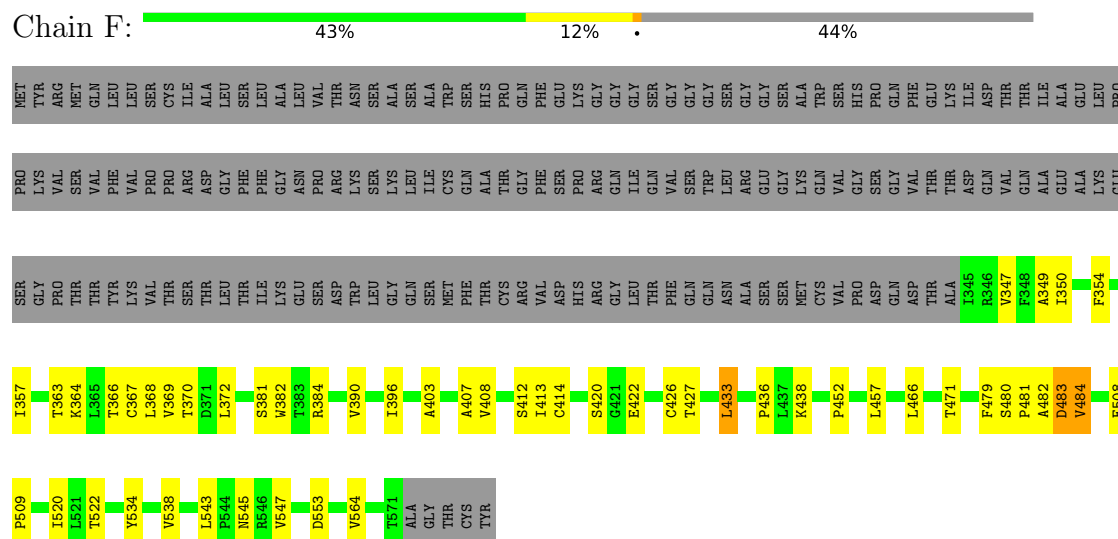


Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	D	1	Total	C	N	O	0
			14	8	1	5	
5	E	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	G	1	Total	C	N	O	0
			14	8	1	5	
5	H	1	Total	C	N	O	0
			14	8	1	5	
5	K	1	Total	C	N	O	0
			14	8	1	5	
5	L	1	Total	C	N	O	0
			14	8	1	5	

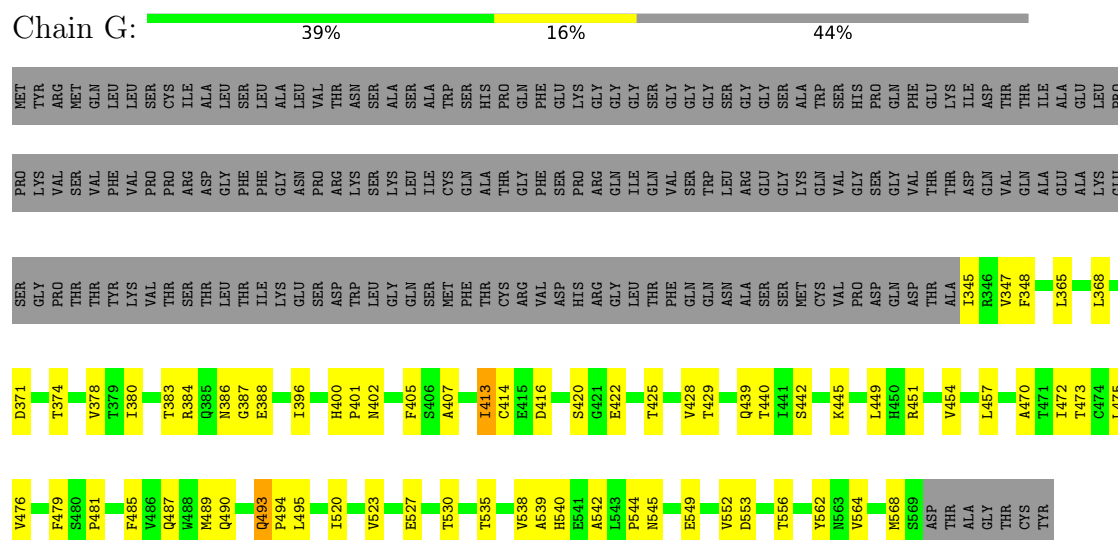
- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	M	2	Total	Ca	0
			2	2	

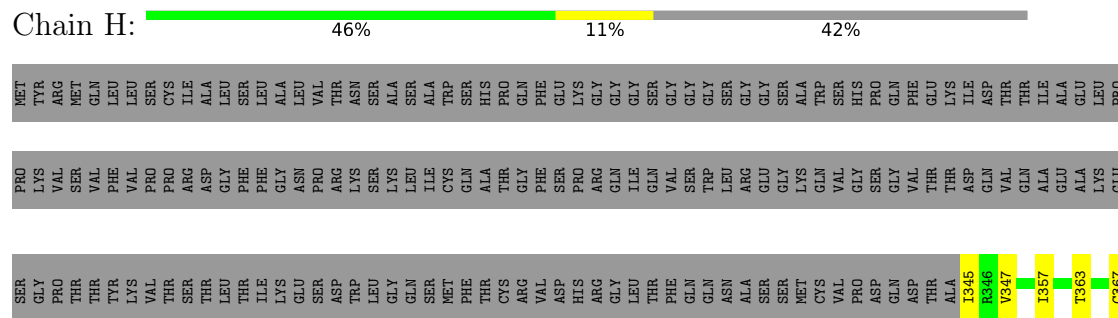
● Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu

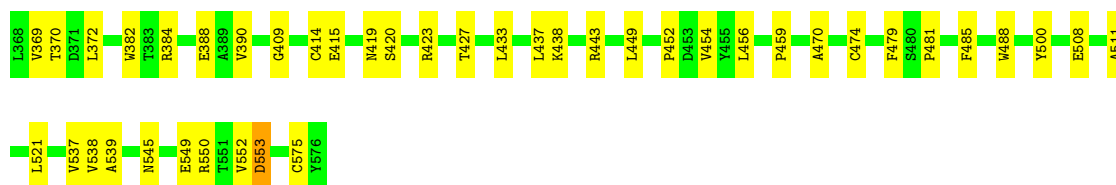


● Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu



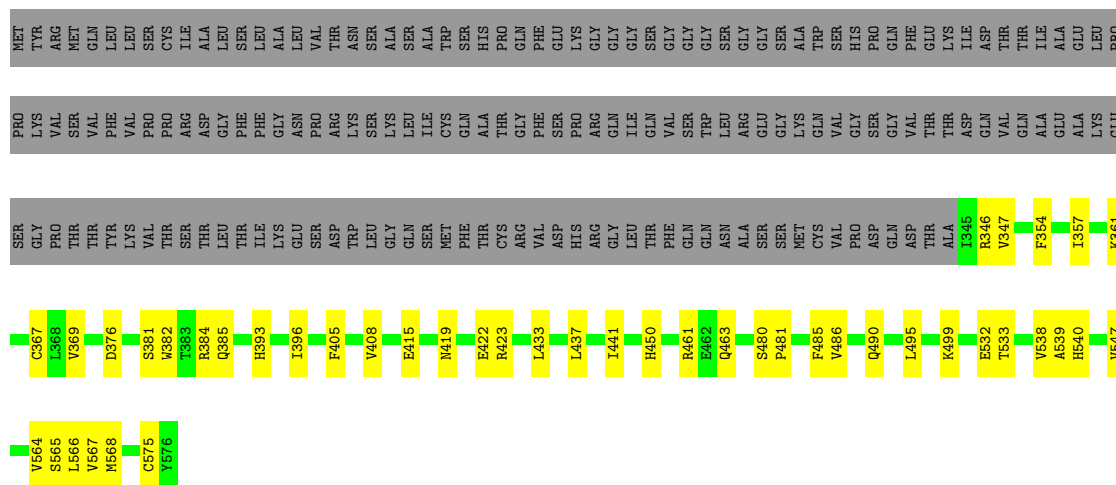
● Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu





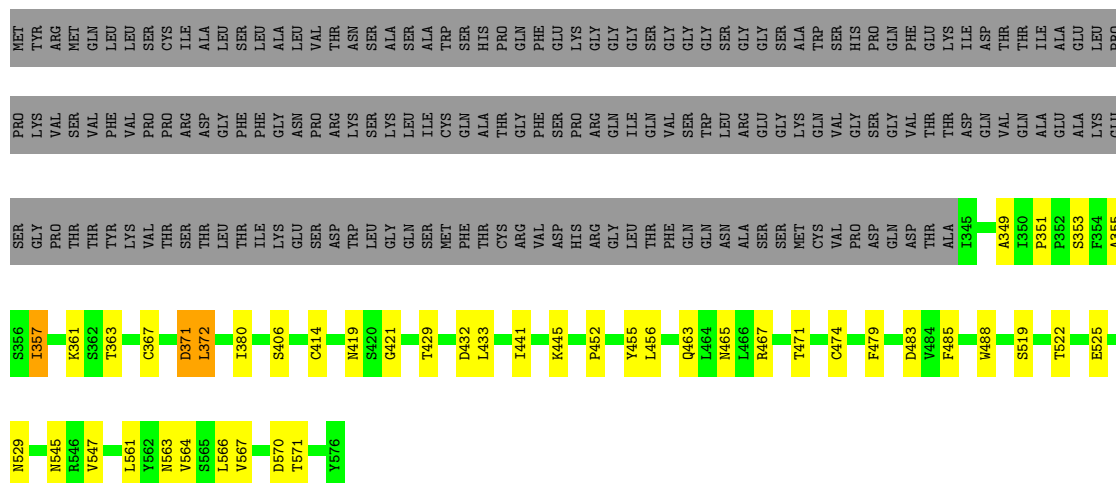
- Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu

Chain K: 46% 11% 42%



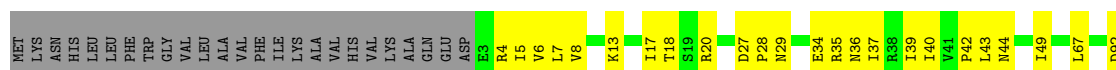
- Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu

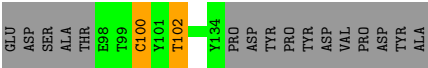
Chain L: 46% 10% 42%



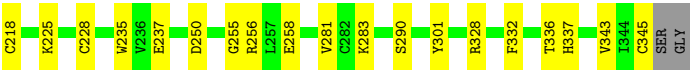
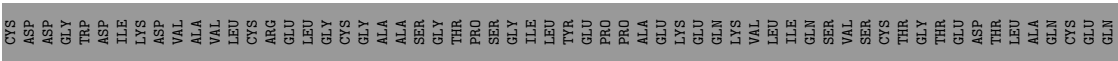
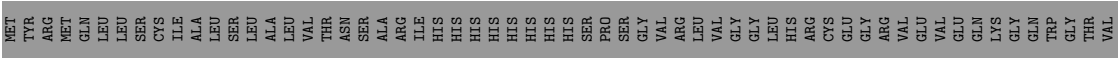
- Molecule 2: Immunoglobulin J chain

Chain J: 60% 14% 24%





● Molecule 3: Interleukin-2,CD5 antigen-like



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	381470	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

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

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	0.32	0/1844	0.58	0/2526
1	B	0.34	0/1825	0.58	1/2500 (0.0%)
1	C	0.51	0/1802	0.64	0/2468
1	D	0.44	0/1809	0.68	3/2478 (0.1%)
1	E	0.38	0/1802	0.61	1/2468 (0.0%)
1	F	0.50	0/1809	0.82	7/2478 (0.3%)
1	G	0.33	0/1794	0.64	1/2457 (0.0%)
1	H	0.28	0/1844	0.56	0/2526
1	K	0.26	0/1844	0.52	0/2526
1	L	0.34	0/1844	0.64	3/2526 (0.1%)
2	J	0.33	0/1023	0.60	0/1390
3	M	0.24	0/1710	0.61	0/2311
All	All	0.37	0/20950	0.63	16/28654 (0.1%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	480	SER	N-CA-C	-9.69	97.52	109.83
1	E	483	ASP	N-CA-C	8.55	123.36	109.76
1	D	483	ASP	N-CA-C	8.49	121.28	110.24
1	F	479	PHE	N-CA-C	7.57	120.58	109.07
1	F	482	ALA	N-CA-C	-7.41	105.12	112.97

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	1798	0	1752	34	0
1	B	1780	0	1738	37	0
1	C	1757	0	1716	36	0
1	D	1764	0	1723	33	0
1	E	1757	0	1716	36	0
1	F	1764	0	1724	34	0
1	G	1749	0	1713	41	0
1	H	1798	0	1751	27	0
1	K	1798	0	1750	31	0
1	L	1798	0	1751	33	0
2	J	1010	0	993	21	0
3	M	1669	0	1570	22	0
4	I	28	0	25	0	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
5	C	14	0	13	0	0
5	D	14	0	13	0	0
5	E	14	0	13	0	0
5	F	14	0	13	0	0
5	G	14	0	13	0	0
5	H	14	0	13	0	0
5	K	14	0	13	1	0
5	L	14	0	13	0	0
6	M	2	0	0	0	0
All	All	20612	0	20052	343	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 8.

The worst 5 of 343 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:F:547:VAL:HG11	1:G:545:ASN:HD21	1.53	0.72
1:B:472:ILE:HG21	1:B:552:VAL:HG11	1.72	0.72
1:A:454:VAL:HG12	1:A:476:VAL:HG22	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:537:VAL:HG12	1:B:549:GLU:HG2	1.72	0.71
1:B:454:VAL:HG21	1:B:538:VAL:HG11	1.73	0.71

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	Percentiles	
1	A	230/403 (57%)	217 (94%)	13 (6%)	0	100	100
1	B	228/403 (57%)	216 (95%)	12 (5%)	0	100	100
1	C	224/403 (56%)	209 (93%)	15 (7%)	0	100	100
1	D	225/403 (56%)	210 (93%)	15 (7%)	0	100	100
1	E	224/403 (56%)	211 (94%)	13 (6%)	0	100	100
1	F	225/403 (56%)	203 (90%)	22 (10%)	0	100	100
1	G	223/403 (55%)	214 (96%)	9 (4%)	0	100	100
1	H	230/403 (57%)	208 (90%)	22 (10%)	0	100	100
1	K	230/403 (57%)	216 (94%)	14 (6%)	0	100	100
1	L	230/403 (57%)	212 (92%)	18 (8%)	0	100	100
2	J	123/168 (73%)	119 (97%)	4 (3%)	0	100	100
3	M	211/359 (59%)	191 (90%)	20 (10%)	0	100	100
All	All	2603/4557 (57%)	2426 (93%)	177 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	A	206/349 (59%)	204 (99%)	2 (1%)	68	75
1	B	204/349 (58%)	203 (100%)	1 (0%)	81	81
1	C	202/349 (58%)	198 (98%)	4 (2%)	48	65
1	D	203/349 (58%)	202 (100%)	1 (0%)	81	81
1	E	202/349 (58%)	201 (100%)	1 (0%)	81	81
1	F	203/349 (58%)	198 (98%)	5 (2%)	42	62
1	G	201/349 (58%)	198 (98%)	3 (2%)	57	69
1	H	206/349 (59%)	205 (100%)	1 (0%)	81	81
1	K	206/349 (59%)	206 (100%)	0	100	100
1	L	206/349 (59%)	200 (97%)	6 (3%)	37	60
2	J	120/155 (77%)	116 (97%)	4 (3%)	33	57
3	M	182/304 (60%)	181 (100%)	1 (0%)	81	81
All	All	2341/3949 (59%)	2312 (99%)	29 (1%)	61	72

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	378	VAL
1	L	561	LEU
1	H	553	ASP
1	L	372	LEU
1	G	429	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	465	ASN
1	K	529	ASN
1	G	490	GLN
1	K	419	ASN

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Mol	Chain	Res	Type
1	F	540	HIS

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 ⓘ

2 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	I	1	2,4	14,14,15	0.20	0	17,19,21	0.65	1 (5%)
4	NAG	I	2	4	14,14,15	0.35	0	17,19,21	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	I	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	1	NAG	C1-O5-C5	2.21	115.15	112.19

There are no chirality outliers.

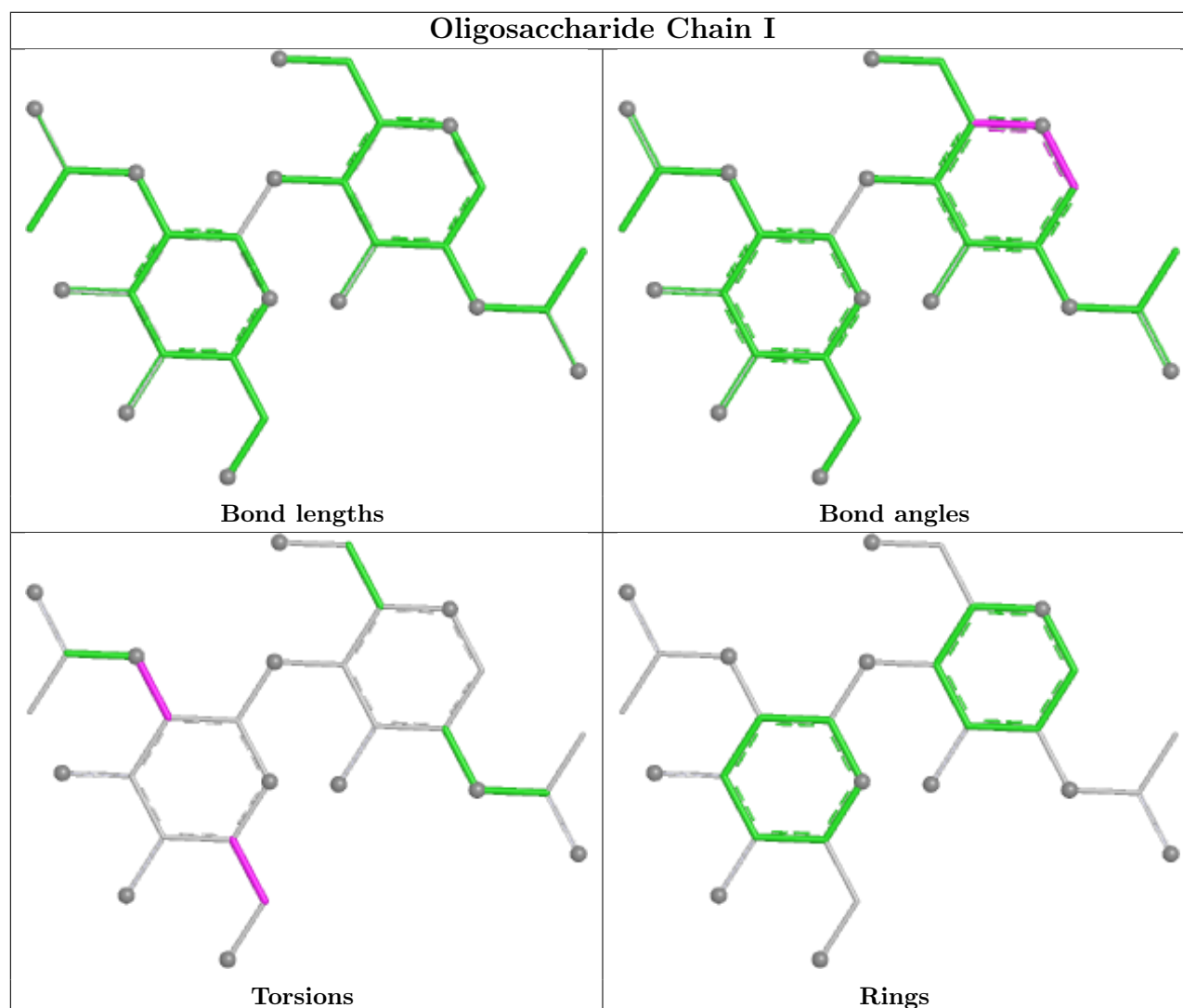
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	2	NAG	C4-C5-C6-O6
4	I	2	NAG	O5-C5-C6-O6
4	I	2	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	G	601	1	14,14,15	0.43	0	17,19,21	0.50	0
5	NAG	H	601	1	14,14,15	0.45	0	17,19,21	0.78	1 (5%)
5	NAG	A	601	1	14,14,15	0.42	0	17,19,21	0.59	1 (5%)
5	NAG	K	601	1	14,14,15	0.48	0	17,19,21	0.51	0
5	NAG	C	601	1	14,14,15	0.47	0	17,19,21	0.47	0
5	NAG	D	601	1	14,14,15	0.29	0	17,19,21	0.45	0
5	NAG	F	601	1	14,14,15	0.39	0	17,19,21	0.51	0
5	NAG	B	601	1	14,14,15	0.44	0	17,19,21	0.57	0
5	NAG	E	601	1	14,14,15	0.29	0	17,19,21	0.48	0
5	NAG	L	601	1	14,14,15	0.48	0	17,19,21	0.62	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
5	NAG	G	601	1	-	2/6/23/26	0/1/1/1
5	NAG	H	601	1	-	2/6/23/26	0/1/1/1
5	NAG	A	601	1	-	2/6/23/26	0/1/1/1
5	NAG	K	601	1	-	2/6/23/26	0/1/1/1
5	NAG	C	601	1	-	4/6/23/26	0/1/1/1
5	NAG	D	601	1	-	2/6/23/26	0/1/1/1
5	NAG	F	601	1	-	2/6/23/26	0/1/1/1
5	NAG	B	601	1	-	0/6/23/26	0/1/1/1
5	NAG	E	601	1	-	2/6/23/26	0/1/1/1
5	NAG	L	601	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	601	NAG	C1-O5-C5	2.73	115.84	112.19
5	A	601	NAG	C1-O5-C5	2.03	114.90	112.19

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	601	NAG	C4-C5-C6-O6
5	H	601	NAG	O5-C5-C6-O6
5	C	601	NAG	O5-C5-C6-O6
5	F	601	NAG	O5-C5-C6-O6
5	H	601	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	K	601	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-37936. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.