Full wwPDB EM Validation Report (i)

Nov 12, 2022 – 06:23 PM EST

PDB ID	:	6V4O
EMDB ID	:	EMD-21043
Title	:	Structure of human 2E01 Fab in complex with influenza virus neuraminidase from B/Phuket/3073/2013
Authors	:	Dai, Y.N.; Fremont, D.H.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2019-11-28
Resolution	:	2.80 Å(reported)
Based on initial model	:	6V4N

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/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 (i)) were used in the production of this report:

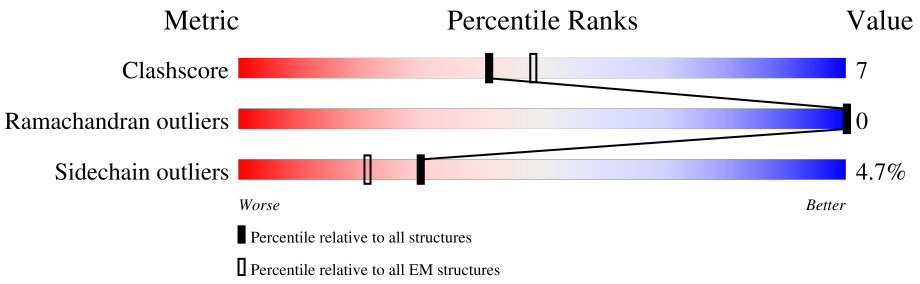
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 2.80 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	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	I	448	71% 9% • 19%
1	M	448	72% 8% • 19%
1	N	448	72% 8% • 19%
1	W	448	71% 9% • 19%
2	A	249	• 70% 19% 10%
2	C	249	• 70% 19% 10%
2	D	249	• 70% 19% 10%
2	H	249	• 71% 18% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	B	215	6% 71% 26%
3	E	215	6% 71% 27%
3	G	215	7% 70% 27%
3	L	215	6% 72% 25%
4	F	2	100%
4	J	2	100%
4	K	2	100%
4	O	2	100%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 24796 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 Neuraminidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	I	364	2830	1779	495	528	28	0	0
1	M	364	2830	1779	495	528	28	0	0
1	N	364	2830	1779	495	528	28	0	0
1	W	364	2830	1779	495	528	28	0	0

There are 244 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	19	ALA	-	expression tag	UNP A0A4P8YQ63
I	20	ASP	-	expression tag	UNP A0A4P8YQ63
I	21	PRO	-	expression tag	UNP A0A4P8YQ63
I	22	HIS	-	expression tag	UNP A0A4P8YQ63
I	23	HIS	-	expression tag	UNP A0A4P8YQ63
I	24	HIS	-	expression tag	UNP A0A4P8YQ63
I	25	HIS	-	expression tag	UNP A0A4P8YQ63
I	26	HIS	-	expression tag	UNP A0A4P8YQ63
I	27	HIS	-	expression tag	UNP A0A4P8YQ63
I	28	SER	-	expression tag	UNP A0A4P8YQ63
I	29	SER	-	expression tag	UNP A0A4P8YQ63
I	30	SER	-	expression tag	UNP A0A4P8YQ63
I	31	ASP	-	expression tag	UNP A0A4P8YQ63
I	32	TYR	-	expression tag	UNP A0A4P8YQ63
I	33	SER	-	expression tag	UNP A0A4P8YQ63
I	34	ASP	-	expression tag	UNP A0A4P8YQ63
I	35	LEU	-	expression tag	UNP A0A4P8YQ63
I	36	GLN	-	expression tag	UNP A0A4P8YQ63
I	37	ARG	-	expression tag	UNP A0A4P8YQ63
I	38	VAL	-	expression tag	UNP A0A4P8YQ63
I	39	LYS	-	expression tag	UNP A0A4P8YQ63
I	40	GLN	-	expression tag	UNP A0A4P8YQ63

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	41	GLU	-	expression tag	UNP A0A4P8YQ63
I	42	LEU	-	expression tag	UNP A0A4P8YQ63
I	43	LEU	-	expression tag	UNP A0A4P8YQ63
I	44	GLU	-	expression tag	UNP A0A4P8YQ63
I	45	GLU	-	expression tag	UNP A0A4P8YQ63
I	46	VAL	-	expression tag	UNP A0A4P8YQ63
I	47	LYS	-	expression tag	UNP A0A4P8YQ63
I	48	LYS	-	expression tag	UNP A0A4P8YQ63
I	49	GLU	-	expression tag	UNP A0A4P8YQ63
I	50	LEU	-	expression tag	UNP A0A4P8YQ63
I	51	GLN	-	expression tag	UNP A0A4P8YQ63
I	52	LYS	-	expression tag	UNP A0A4P8YQ63
I	53	VAL	-	expression tag	UNP A0A4P8YQ63
I	54	LYS	-	expression tag	UNP A0A4P8YQ63
I	55	GLU	-	expression tag	UNP A0A4P8YQ63
I	56	GLU	-	expression tag	UNP A0A4P8YQ63
I	57	ILE	-	expression tag	UNP A0A4P8YQ63
I	58	ILE	-	expression tag	UNP A0A4P8YQ63
I	59	GLU	-	expression tag	UNP A0A4P8YQ63
I	60	ALA	-	expression tag	UNP A0A4P8YQ63
I	61	PHE	-	expression tag	UNP A0A4P8YQ63
I	62	VAL	-	expression tag	UNP A0A4P8YQ63
I	63	GLN	-	expression tag	UNP A0A4P8YQ63
I	64	GLU	-	expression tag	UNP A0A4P8YQ63
I	65	LEU	-	expression tag	UNP A0A4P8YQ63
I	66	ARG	-	expression tag	UNP A0A4P8YQ63
I	67	LYS	-	expression tag	UNP A0A4P8YQ63
I	68	ARG	-	expression tag	UNP A0A4P8YQ63
I	69	GLY	-	expression tag	UNP A0A4P8YQ63
I	70	SER	-	expression tag	UNP A0A4P8YQ63
I	71	LEU	-	expression tag	UNP A0A4P8YQ63
I	72	VAL	-	expression tag	UNP A0A4P8YQ63
I	73	PRO	-	expression tag	UNP A0A4P8YQ63
I	74	ARG	-	expression tag	UNP A0A4P8YQ63
I	75	GLY	-	expression tag	UNP A0A4P8YQ63
I	76	SER	-	expression tag	UNP A0A4P8YQ63
I	77	PRO	-	expression tag	UNP A0A4P8YQ63
I	78	SER	-	expression tag	UNP A0A4P8YQ63
I	79	ARG	-	expression tag	UNP A0A4P8YQ63
M	19	ALA	-	expression tag	UNP A0A4P8YQ63
M	20	ASP	-	expression tag	UNP A0A4P8YQ63
M	21	PRO	-	expression tag	UNP A0A4P8YQ63

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
M	22	HIS	-	expression tag	UNP A0A4P8YQ63
M	23	HIS	-	expression tag	UNP A0A4P8YQ63
M	24	HIS	-	expression tag	UNP A0A4P8YQ63
M	25	HIS	-	expression tag	UNP A0A4P8YQ63
M	26	HIS	-	expression tag	UNP A0A4P8YQ63
M	27	HIS	-	expression tag	UNP A0A4P8YQ63
M	28	SER	-	expression tag	UNP A0A4P8YQ63
M	29	SER	-	expression tag	UNP A0A4P8YQ63
M	30	SER	-	expression tag	UNP A0A4P8YQ63
M	31	ASP	-	expression tag	UNP A0A4P8YQ63
M	32	TYR	-	expression tag	UNP A0A4P8YQ63
M	33	SER	-	expression tag	UNP A0A4P8YQ63
M	34	ASP	-	expression tag	UNP A0A4P8YQ63
M	35	LEU	-	expression tag	UNP A0A4P8YQ63
M	36	GLN	-	expression tag	UNP A0A4P8YQ63
M	37	ARG	-	expression tag	UNP A0A4P8YQ63
M	38	VAL	-	expression tag	UNP A0A4P8YQ63
M	39	LYS	-	expression tag	UNP A0A4P8YQ63
M	40	GLN	-	expression tag	UNP A0A4P8YQ63
M	41	GLU	-	expression tag	UNP A0A4P8YQ63
M	42	LEU	-	expression tag	UNP A0A4P8YQ63
M	43	LEU	-	expression tag	UNP A0A4P8YQ63
M	44	GLU	-	expression tag	UNP A0A4P8YQ63
M	45	GLU	-	expression tag	UNP A0A4P8YQ63
M	46	VAL	-	expression tag	UNP A0A4P8YQ63
M	47	LYS	-	expression tag	UNP A0A4P8YQ63
M	48	LYS	-	expression tag	UNP A0A4P8YQ63
M	49	GLU	-	expression tag	UNP A0A4P8YQ63
M	50	LEU	-	expression tag	UNP A0A4P8YQ63
M	51	GLN	-	expression tag	UNP A0A4P8YQ63
M	52	LYS	-	expression tag	UNP A0A4P8YQ63
M	53	VAL	-	expression tag	UNP A0A4P8YQ63
M	54	LYS	-	expression tag	UNP A0A4P8YQ63
M	55	GLU	-	expression tag	UNP A0A4P8YQ63
M	56	GLU	-	expression tag	UNP A0A4P8YQ63
M	57	ILE	-	expression tag	UNP A0A4P8YQ63
M	58	ILE	-	expression tag	UNP A0A4P8YQ63
M	59	GLU	-	expression tag	UNP A0A4P8YQ63
M	60	ALA	-	expression tag	UNP A0A4P8YQ63
M	61	PHE	-	expression tag	UNP A0A4P8YQ63
M	62	VAL	-	expression tag	UNP A0A4P8YQ63
M	63	GLN	-	expression tag	UNP A0A4P8YQ63

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
M	64	GLU	-	expression tag	UNP A0A4P8YQ63
M	65	LEU	-	expression tag	UNP A0A4P8YQ63
M	66	ARG	-	expression tag	UNP A0A4P8YQ63
M	67	LYS	-	expression tag	UNP A0A4P8YQ63
M	68	ARG	-	expression tag	UNP A0A4P8YQ63
M	69	GLY	-	expression tag	UNP A0A4P8YQ63
M	70	SER	-	expression tag	UNP A0A4P8YQ63
M	71	LEU	-	expression tag	UNP A0A4P8YQ63
M	72	VAL	-	expression tag	UNP A0A4P8YQ63
M	73	PRO	-	expression tag	UNP A0A4P8YQ63
M	74	ARG	-	expression tag	UNP A0A4P8YQ63
M	75	GLY	-	expression tag	UNP A0A4P8YQ63
M	76	SER	-	expression tag	UNP A0A4P8YQ63
M	77	PRO	-	expression tag	UNP A0A4P8YQ63
M	78	SER	-	expression tag	UNP A0A4P8YQ63
M	79	ARG	-	expression tag	UNP A0A4P8YQ63
N	19	ALA	-	expression tag	UNP A0A4P8YQ63
N	20	ASP	-	expression tag	UNP A0A4P8YQ63
N	21	PRO	-	expression tag	UNP A0A4P8YQ63
N	22	HIS	-	expression tag	UNP A0A4P8YQ63
N	23	HIS	-	expression tag	UNP A0A4P8YQ63
N	24	HIS	-	expression tag	UNP A0A4P8YQ63
N	25	HIS	-	expression tag	UNP A0A4P8YQ63
N	26	HIS	-	expression tag	UNP A0A4P8YQ63
N	27	HIS	-	expression tag	UNP A0A4P8YQ63
N	28	SER	-	expression tag	UNP A0A4P8YQ63
N	29	SER	-	expression tag	UNP A0A4P8YQ63
N	30	SER	-	expression tag	UNP A0A4P8YQ63
N	31	ASP	-	expression tag	UNP A0A4P8YQ63
N	32	TYR	-	expression tag	UNP A0A4P8YQ63
N	33	SER	-	expression tag	UNP A0A4P8YQ63
N	34	ASP	-	expression tag	UNP A0A4P8YQ63
N	35	LEU	-	expression tag	UNP A0A4P8YQ63
N	36	GLN	-	expression tag	UNP A0A4P8YQ63
N	37	ARG	-	expression tag	UNP A0A4P8YQ63
N	38	VAL	-	expression tag	UNP A0A4P8YQ63
N	39	LYS	-	expression tag	UNP A0A4P8YQ63
N	40	GLN	-	expression tag	UNP A0A4P8YQ63
N	41	GLU	-	expression tag	UNP A0A4P8YQ63
N	42	LEU	-	expression tag	UNP A0A4P8YQ63
N	43	LEU	-	expression tag	UNP A0A4P8YQ63
N	44	GLU	-	expression tag	UNP A0A4P8YQ63

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
N	45	GLU	-	expression tag	UNP A0A4P8YQ63
N	46	VAL	-	expression tag	UNP A0A4P8YQ63
N	47	LYS	-	expression tag	UNP A0A4P8YQ63
N	48	LYS	-	expression tag	UNP A0A4P8YQ63
N	49	GLU	-	expression tag	UNP A0A4P8YQ63
N	50	LEU	-	expression tag	UNP A0A4P8YQ63
N	51	GLN	-	expression tag	UNP A0A4P8YQ63
N	52	LYS	-	expression tag	UNP A0A4P8YQ63
N	53	VAL	-	expression tag	UNP A0A4P8YQ63
N	54	LYS	-	expression tag	UNP A0A4P8YQ63
N	55	GLU	-	expression tag	UNP A0A4P8YQ63
N	56	GLU	-	expression tag	UNP A0A4P8YQ63
N	57	ILE	-	expression tag	UNP A0A4P8YQ63
N	58	ILE	-	expression tag	UNP A0A4P8YQ63
N	59	GLU	-	expression tag	UNP A0A4P8YQ63
N	60	ALA	-	expression tag	UNP A0A4P8YQ63
N	61	PHE	-	expression tag	UNP A0A4P8YQ63
N	62	VAL	-	expression tag	UNP A0A4P8YQ63
N	63	GLN	-	expression tag	UNP A0A4P8YQ63
N	64	GLU	-	expression tag	UNP A0A4P8YQ63
N	65	LEU	-	expression tag	UNP A0A4P8YQ63
N	66	ARG	-	expression tag	UNP A0A4P8YQ63
N	67	LYS	-	expression tag	UNP A0A4P8YQ63
N	68	ARG	-	expression tag	UNP A0A4P8YQ63
N	69	GLY	-	expression tag	UNP A0A4P8YQ63
N	70	SER	-	expression tag	UNP A0A4P8YQ63
N	71	LEU	-	expression tag	UNP A0A4P8YQ63
N	72	VAL	-	expression tag	UNP A0A4P8YQ63
N	73	PRO	-	expression tag	UNP A0A4P8YQ63
N	74	ARG	-	expression tag	UNP A0A4P8YQ63
N	75	GLY	-	expression tag	UNP A0A4P8YQ63
N	76	SER	-	expression tag	UNP A0A4P8YQ63
N	77	PRO	-	expression tag	UNP A0A4P8YQ63
N	78	SER	-	expression tag	UNP A0A4P8YQ63
N	79	ARG	-	expression tag	UNP A0A4P8YQ63
W	19	ALA	-	expression tag	UNP A0A4P8YQ63
W	20	ASP	-	expression tag	UNP A0A4P8YQ63
W	21	PRO	-	expression tag	UNP A0A4P8YQ63
W	22	HIS	-	expression tag	UNP A0A4P8YQ63
W	23	HIS	-	expression tag	UNP A0A4P8YQ63
W	24	HIS	-	expression tag	UNP A0A4P8YQ63
W	25	HIS	-	expression tag	UNP A0A4P8YQ63

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
W	26	HIS	-	expression tag	UNP A0A4P8YQ63
W	27	HIS	-	expression tag	UNP A0A4P8YQ63
W	28	SER	-	expression tag	UNP A0A4P8YQ63
W	29	SER	-	expression tag	UNP A0A4P8YQ63
W	30	SER	-	expression tag	UNP A0A4P8YQ63
W	31	ASP	-	expression tag	UNP A0A4P8YQ63
W	32	TYR	-	expression tag	UNP A0A4P8YQ63
W	33	SER	-	expression tag	UNP A0A4P8YQ63
W	34	ASP	-	expression tag	UNP A0A4P8YQ63
W	35	LEU	-	expression tag	UNP A0A4P8YQ63
W	36	GLN	-	expression tag	UNP A0A4P8YQ63
W	37	ARG	-	expression tag	UNP A0A4P8YQ63
W	38	VAL	-	expression tag	UNP A0A4P8YQ63
W	39	LYS	-	expression tag	UNP A0A4P8YQ63
W	40	GLN	-	expression tag	UNP A0A4P8YQ63
W	41	GLU	-	expression tag	UNP A0A4P8YQ63
W	42	LEU	-	expression tag	UNP A0A4P8YQ63
W	43	LEU	-	expression tag	UNP A0A4P8YQ63
W	44	GLU	-	expression tag	UNP A0A4P8YQ63
W	45	GLU	-	expression tag	UNP A0A4P8YQ63
W	46	VAL	-	expression tag	UNP A0A4P8YQ63
W	47	LYS	-	expression tag	UNP A0A4P8YQ63
W	48	LYS	-	expression tag	UNP A0A4P8YQ63
W	49	GLU	-	expression tag	UNP A0A4P8YQ63
W	50	LEU	-	expression tag	UNP A0A4P8YQ63
W	51	GLN	-	expression tag	UNP A0A4P8YQ63
W	52	LYS	-	expression tag	UNP A0A4P8YQ63
W	53	VAL	-	expression tag	UNP A0A4P8YQ63
W	54	LYS	-	expression tag	UNP A0A4P8YQ63
W	55	GLU	-	expression tag	UNP A0A4P8YQ63
W	56	GLU	-	expression tag	UNP A0A4P8YQ63
W	57	ILE	-	expression tag	UNP A0A4P8YQ63
W	58	ILE	-	expression tag	UNP A0A4P8YQ63
W	59	GLU	-	expression tag	UNP A0A4P8YQ63
W	60	ALA	-	expression tag	UNP A0A4P8YQ63
W	61	PHE	-	expression tag	UNP A0A4P8YQ63
W	62	VAL	-	expression tag	UNP A0A4P8YQ63
W	63	GLN	-	expression tag	UNP A0A4P8YQ63
W	64	GLU	-	expression tag	UNP A0A4P8YQ63
W	65	LEU	-	expression tag	UNP A0A4P8YQ63
W	66	ARG	-	expression tag	UNP A0A4P8YQ63
W	67	LYS	-	expression tag	UNP A0A4P8YQ63

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
W	68	ARG	-	expression tag	UNP A0A4P8YQ63
W	69	GLY	-	expression tag	UNP A0A4P8YQ63
W	70	SER	-	expression tag	UNP A0A4P8YQ63
W	71	LEU	-	expression tag	UNP A0A4P8YQ63
W	72	VAL	-	expression tag	UNP A0A4P8YQ63
W	73	PRO	-	expression tag	UNP A0A4P8YQ63
W	74	ARG	-	expression tag	UNP A0A4P8YQ63
W	75	GLY	-	expression tag	UNP A0A4P8YQ63
W	76	SER	-	expression tag	UNP A0A4P8YQ63
W	77	PRO	-	expression tag	UNP A0A4P8YQ63
W	78	SER	-	expression tag	UNP A0A4P8YQ63
W	79	ARG	-	expression tag	UNP A0A4P8YQ63

- Molecule 2 is a protein called Antibody Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	223	1695	1084	276	329	6	0	0
2	C	223	1695	1084	276	329	6	0	0
2	D	223	1695	1084	276	329	6	0	0
2	H	223	1695	1084	276	329	6	0	0

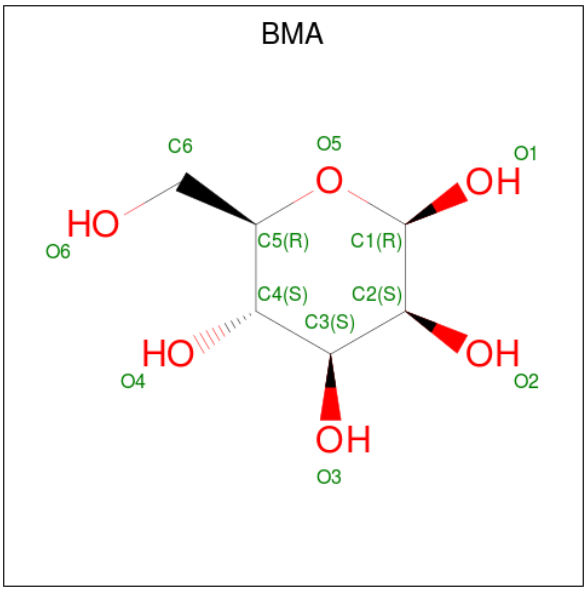
- Molecule 3 is a protein called Antibody Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	214	1634	1022	282	326	4	0	0
3	E	214	1634	1022	282	326	4	0	0
3	G	214	1634	1022	282	326	4	0	0
3	L	214	1634	1022	282	326	4	0	0

- 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	F	2	Total	C	N	O	0	0
			28	16	2	10		
4	J	2	Total	C	N	O	0	0
			28	16	2	10		
4	K	2	Total	C	N	O	0	0
			28	16	2	10		
4	O	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is beta-D-mannopyranose (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			AltConf
5	I	1	Total	C	O	0
			11	6	5	
5	M	1	Total	C	O	0
			11	6	5	
5	N	1	Total	C	O	0
			11	6	5	
5	W	1	Total	C	O	0
			11	6	5	

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

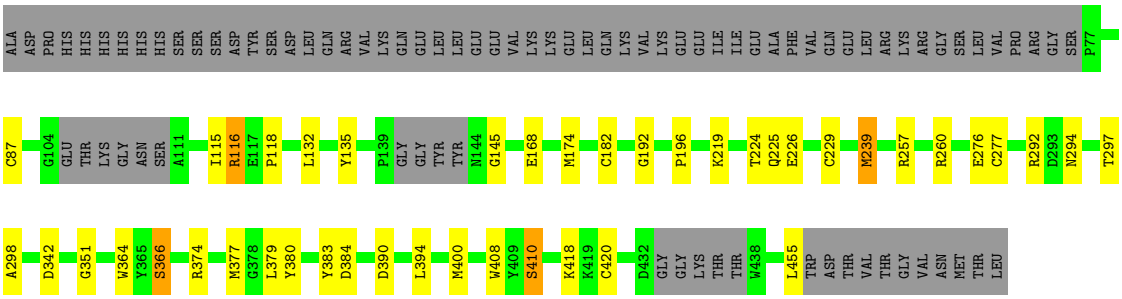
Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
6	I	1	1	1	0
6	M	1	1	1	0
6	N	1	1	1	0
6	W	1	1	1	0

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.

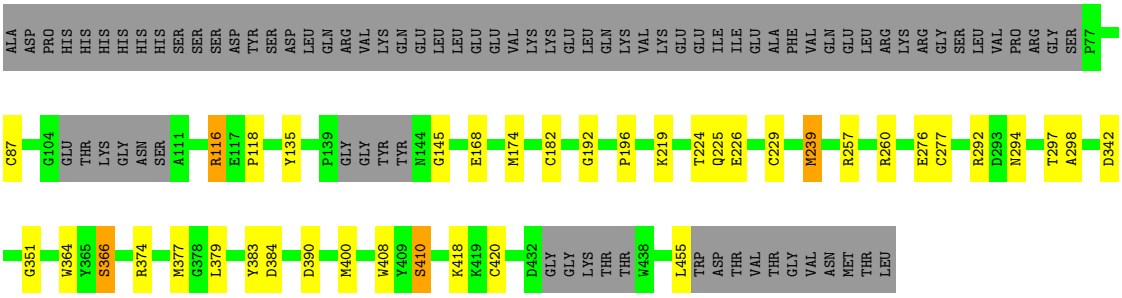
- Molecule 1: Neuraminidase

Chain I: 71% 9% • 19%



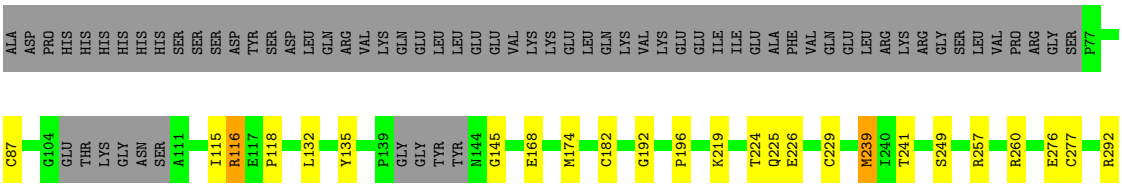
- Molecule 1: Neuraminidase

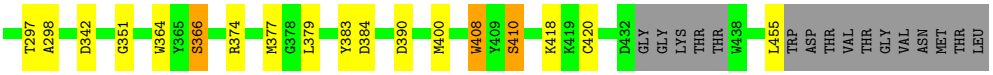
Chain M: 72% 8% • 19%



- Molecule 1: Neuraminidase

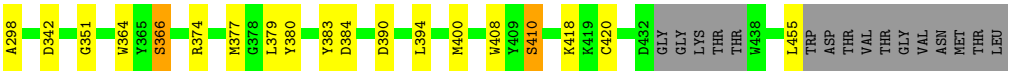
Chain N: 72% 8% • 19%





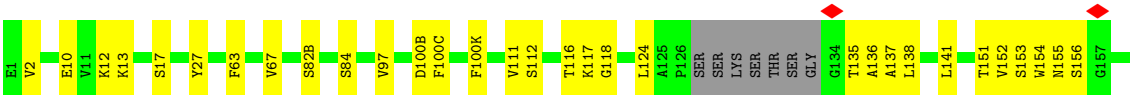
- Molecule 1: Neuraminidase

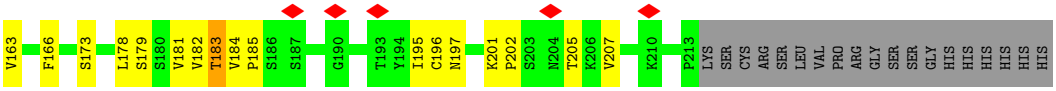
Chain W:



- Molecule 2: Antibody Fab heavy chain

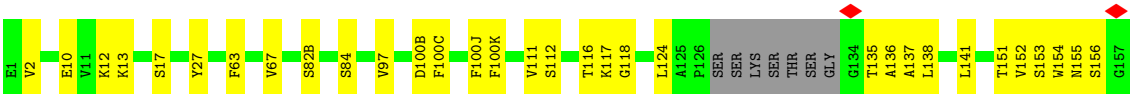
Chain A:

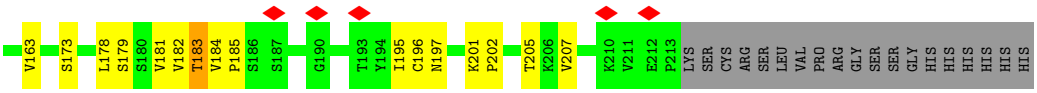




- Molecule 2: Antibody Fab heavy chain

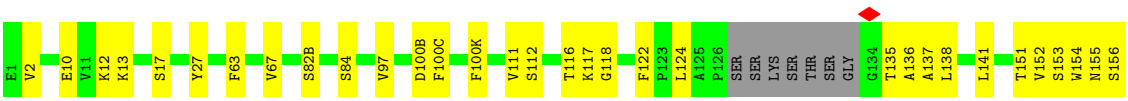
Chain C:

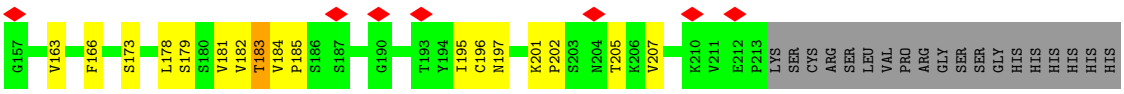




- Molecule 2: Antibody Fab heavy chain

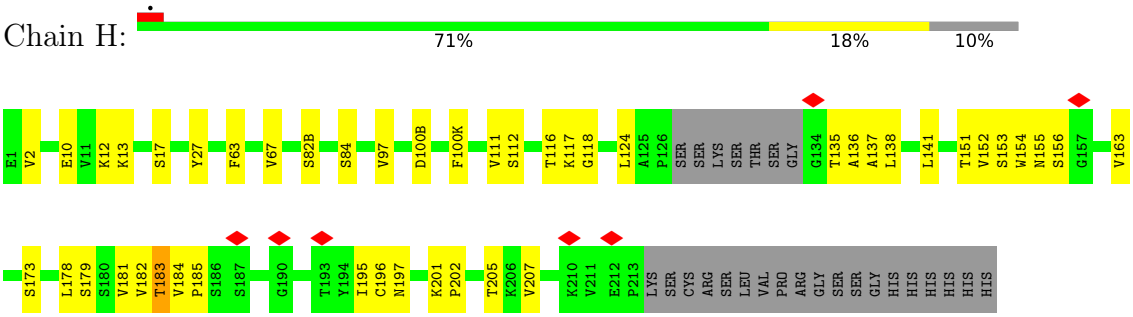
Chain D:





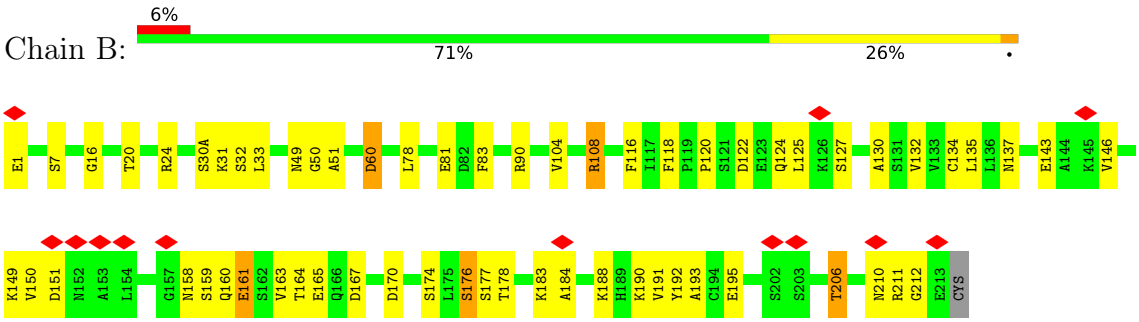
- Molecule 2: Antibody Fab heavy chain

Chain H:



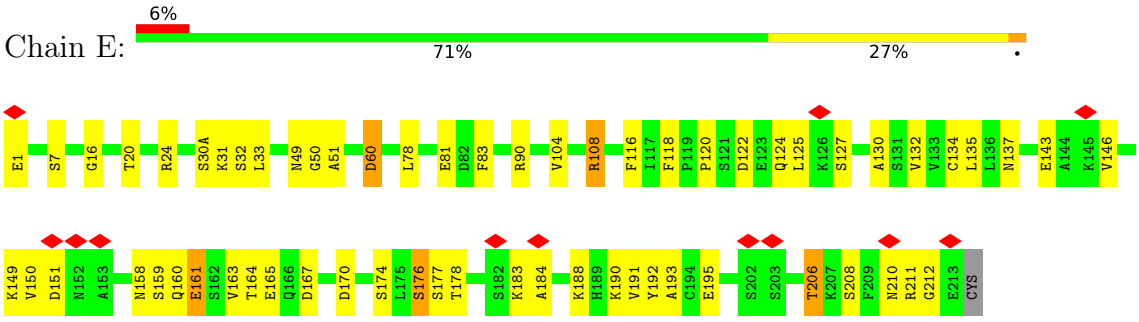
- Molecule 3: Antibody Fab light chain

Chain B:



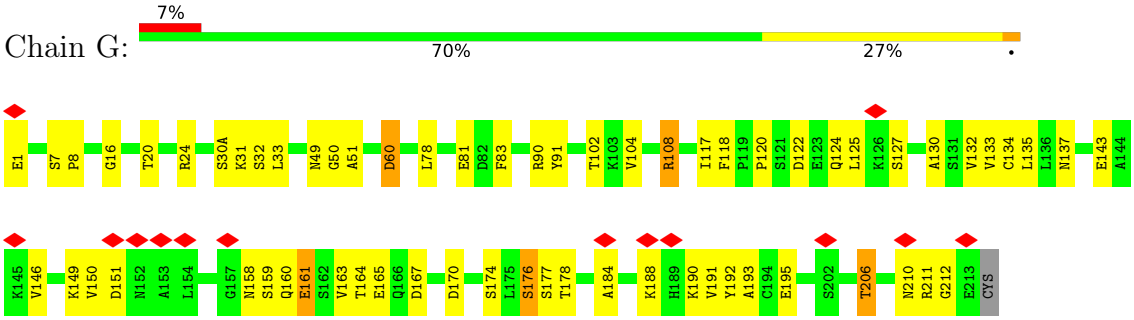
- Molecule 3: Antibody Fab light chain

Chain E:



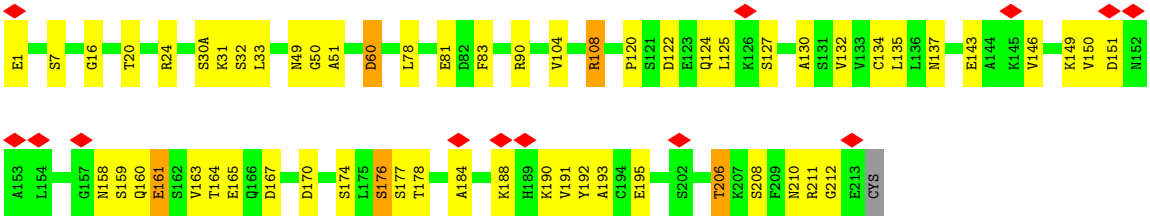
- Molecule 3: Antibody Fab light chain

Chain G:



- Molecule 3: Antibody Fab light chain

Chain L:



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

Chain F: 100%

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

Chain J: 100%

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

Chain K: 100%

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

Chain O: 100%

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	150730	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	66	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.144	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0123	Depositor
Map size (Å)	275.0, 275.0, 275.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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: 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	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	I	0.63	0/2897	0.55	2/3907 (0.1%)
1	M	0.63	0/2897	0.55	2/3907 (0.1%)
1	N	0.63	0/2897	0.55	2/3907 (0.1%)
1	W	0.62	0/2897	0.55	2/3907 (0.1%)
2	A	0.41	0/1739	0.51	0/2372
2	C	0.41	0/1739	0.51	0/2372
2	D	0.41	0/1739	0.51	0/2372
2	H	0.41	0/1739	0.51	0/2372
3	B	0.37	0/1669	0.52	0/2264
3	E	0.37	0/1669	0.52	0/2264
3	G	0.37	0/1669	0.52	0/2264
3	L	0.37	0/1669	0.52	0/2264
All	All	0.51	0/25220	0.53	8/34172 (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
2	A	0	1
2	C	0	1
2	D	0	1
2	H	0	1
All	All	0	4

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	408	TRP	C-N-CA	5.45	135.33	121.70
1	M	408	TRP	C-N-CA	5.44	135.30	121.70
1	W	408	TRP	C-N-CA	5.44	135.30	121.70
1	N	408	TRP	C-N-CA	5.43	135.28	121.70
1	I	145	GLY	C-N-CA	5.04	134.29	121.70
1	M	145	GLY	C-N-CA	5.02	134.25	121.70
1	N	145	GLY	C-N-CA	5.00	134.21	121.70
1	W	145	GLY	C-N-CA	5.00	134.21	121.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	183	THR	Peptide
2	C	183	THR	Peptide
2	D	183	THR	Peptide
2	H	183	THR	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	I	2830	0	2751	23	0
1	M	2830	0	2751	21	0
1	N	2830	0	2751	23	0
1	W	2830	0	2751	22	0
2	A	1695	0	1660	38	0
2	C	1695	0	1660	37	0
2	D	1695	0	1660	45	0
2	H	1695	0	1660	32	0
3	B	1634	0	1600	39	0
3	E	1634	0	1600	46	0
3	G	1634	0	1600	39	0
3	L	1634	0	1600	35	0
4	F	28	0	24	0	0
4	J	28	0	24	0	0
4	K	28	0	24	0	0
4	O	28	0	24	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	11	0	10	0	0
5	M	11	0	10	0	0
5	N	11	0	10	0	0
5	W	11	0	10	0	0
6	I	1	0	0	0	0
6	M	1	0	0	0	0
6	N	1	0	0	0	0
6	W	1	0	0	0	0
All	All	24796	0	24180	362	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 7.

All (362) 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)
2:A:135:THR:OG1	2:A:184:VAL:O	1.60	1.19
2:H:135:THR:OG1	2:H:184:VAL:O	1.60	1.18
2:D:135:THR:OG1	2:D:184:VAL:O	1.60	1.18
2:C:135:THR:OG1	2:C:184:VAL:O	1.60	1.15
3:G:184:ALA:O	3:G:188:LYS:NZ	2.02	0.93
3:E:184:ALA:O	3:E:188:LYS:NZ	2.02	0.92
3:L:184:ALA:O	3:L:188:LYS:NZ	2.02	0.92
3:B:184:ALA:O	3:B:188:LYS:NZ	2.02	0.91
1:M:374:ARG:NH1	2:C:100(B):ASP:OD2	2.13	0.82
3:E:124:GLN:O	3:E:127:SER:OG	2.00	0.80
1:N:374:ARG:NH1	2:H:100(B):ASP:OD2	2.14	0.79
2:D:137:ALA:HB2	3:E:116:PHE:CD2	2.18	0.79
3:B:124:GLN:O	3:B:127:SER:OG	2.00	0.78
3:L:124:GLN:O	3:L:127:SER:OG	2.00	0.77
1:W:374:ARG:NH1	2:D:100(B):ASP:OD2	2.17	0.77
3:G:124:GLN:O	3:G:127:SER:OG	2.00	0.76
3:L:108:ARG:NH1	3:L:170:ASP:O	2.19	0.76
3:G:108:ARG:NH1	3:G:170:ASP:O	2.19	0.76
3:B:108:ARG:NH1	3:B:170:ASP:O	2.19	0.75
3:E:108:ARG:NH1	3:E:170:ASP:O	2.19	0.75
1:W:116:ARG:NH1	2:D:100(B):ASP:OD1	2.22	0.72
1:N:116:ARG:NH1	2:H:100(B):ASP:OD1	2.24	0.71
3:G:167:ASP:OD2	3:G:170:ASP:N	2.24	0.71
1:M:168:GLU:N	1:M:168:GLU:OE1	2.24	0.71
3:B:167:ASP:OD2	3:B:170:ASP:N	2.24	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:12:LYS:O	2:C:112:SER:N	2.25	0.70
1:N:168:GLU:OE1	1:N:168:GLU:N	2.24	0.70
2:H:12:LYS:O	2:H:112:SER:N	2.25	0.70
1:W:168:GLU:N	1:W:168:GLU:OE1	2.24	0.70
3:E:167:ASP:OD2	3:E:170:ASP:N	2.24	0.69
2:D:12:LYS:O	2:D:112:SER:N	2.25	0.69
2:D:166:PHE:CD2	3:E:176:SER:HB2	2.27	0.69
1:I:168:GLU:N	1:I:168:GLU:OE1	2.24	0.69
2:A:12:LYS:O	2:A:112:SER:N	2.25	0.69
3:L:167:ASP:OD2	3:L:170:ASP:N	2.24	0.69
1:M:116:ARG:NH1	2:C:100(B):ASP:OD1	2.26	0.67
1:I:116:ARG:NH1	2:A:100(B):ASP:OD1	2.27	0.67
2:D:166:PHE:HD2	3:E:176:SER:HB2	1.59	0.65
3:G:1:GLU:OE1	3:G:1:GLU:N	2.25	0.64
1:M:342:ASP:OD2	3:G:31:LYS:N	2.30	0.63
3:L:151:ASP:H	3:L:191:VAL:HG22	1.63	0.63
3:E:151:ASP:H	3:E:191:VAL:HG22	1.63	0.63
3:E:158:ASN:OD1	3:E:159:SER:N	2.32	0.63
3:B:151:ASP:H	3:B:191:VAL:HG22	1.63	0.63
3:B:158:ASN:OD1	3:B:159:SER:N	2.32	0.62
3:L:158:ASN:OD1	3:L:159:SER:N	2.32	0.62
3:G:151:ASP:H	3:G:191:VAL:HG22	1.63	0.62
1:I:374:ARG:NH1	2:A:100(B):ASP:OD2	2.30	0.62
3:G:158:ASN:OD1	3:G:159:SER:N	2.32	0.62
3:L:149:LYS:HB2	3:L:193:ALA:HB3	1.82	0.61
2:A:155:ASN:N	2:A:195:ILE:O	2.32	0.61
3:E:149:LYS:HB2	3:E:193:ALA:HB3	1.83	0.60
3:E:1:GLU:OE1	3:E:1:GLU:N	2.26	0.60
3:G:149:LYS:HB2	3:G:193:ALA:HB3	1.82	0.60
1:W:276:GLU:OE1	1:W:292:ARG:NH1	2.33	0.60
2:H:155:ASN:N	2:H:195:ILE:O	2.32	0.59
1:N:366:SER:OG	1:N:377:MET:SD	2.61	0.59
1:W:366:SER:OG	1:W:377:MET:SD	2.61	0.59
2:D:155:ASN:N	2:D:195:ILE:O	2.32	0.59
3:B:191:VAL:HA	3:B:210:ASN:HA	1.85	0.59
3:E:191:VAL:HA	3:E:210:ASN:HA	1.85	0.59
3:B:149:LYS:HB2	3:B:193:ALA:HB3	1.83	0.59
3:G:191:VAL:HA	3:G:210:ASN:HA	1.85	0.59
1:M:276:GLU:OE1	1:M:292:ARG:NH1	2.33	0.59
3:L:1:GLU:OE1	3:L:1:GLU:N	2.25	0.59
2:C:155:ASN:N	2:C:195:ILE:O	2.32	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:10:GLU:OE1	2:H:10:GLU:N	2.36	0.58
2:D:10:GLU:N	2:D:10:GLU:OE1	2.36	0.58
3:B:1:GLU:OE1	3:B:1:GLU:N	2.26	0.58
2:C:10:GLU:OE1	2:C:10:GLU:N	2.36	0.58
2:A:10:GLU:N	2:A:10:GLU:OE1	2.36	0.58
1:I:276:GLU:OE1	1:I:292:ARG:NH1	2.33	0.58
1:I:366:SER:OG	1:I:377:MET:SD	2.61	0.58
1:M:351:GLY:N	1:M:410:SER:OG	2.37	0.58
1:N:276:GLU:OE1	1:N:292:ARG:NH1	2.33	0.58
1:N:351:GLY:N	1:N:410:SER:OG	2.37	0.58
1:W:351:GLY:N	1:W:410:SER:OG	2.37	0.58
3:E:132:VAL:O	3:E:178:THR:HA	2.04	0.57
3:E:195:GLU:HB3	3:E:206:THR:OG1	2.04	0.57
1:W:342:ASP:OD2	3:E:31:LYS:N	2.36	0.57
3:L:191:VAL:HA	3:L:210:ASN:HA	1.85	0.57
3:L:195:GLU:HB3	3:L:206:THR:OG1	2.04	0.57
1:M:366:SER:OG	1:M:377:MET:SD	2.61	0.57
1:I:351:GLY:N	1:I:410:SER:OG	2.37	0.57
3:B:195:GLU:HB3	3:B:206:THR:OG1	2.04	0.57
3:G:195:GLU:HB3	3:G:206:THR:OG1	2.04	0.57
1:M:364:TRP:CE3	1:M:379:LEU:HD21	2.40	0.57
2:C:12:LYS:O	2:C:112:SER:OG	2.23	0.57
3:L:132:VAL:O	3:L:178:THR:HA	2.04	0.57
1:I:364:TRP:CE3	1:I:379:LEU:HD21	2.40	0.57
2:H:12:LYS:O	2:H:112:SER:OG	2.23	0.57
2:A:12:LYS:O	2:A:112:SER:OG	2.23	0.57
2:D:12:LYS:O	2:D:112:SER:OG	2.23	0.56
3:B:132:VAL:O	3:B:178:THR:HA	2.04	0.56
1:W:364:TRP:CE3	1:W:379:LEU:HD21	2.40	0.56
3:G:132:VAL:O	3:G:178:THR:HA	2.04	0.56
1:N:364:TRP:CE3	1:N:379:LEU:HD21	2.40	0.56
2:D:137:ALA:HB3	3:E:118:PHE:CZ	2.41	0.55
3:L:161:GLU:HB2	3:L:176:SER:O	2.07	0.54
3:B:161:GLU:HB2	3:B:176:SER:O	2.07	0.54
3:E:146:VAL:HA	3:E:195:GLU:O	2.08	0.54
1:I:342:ASP:OD2	3:B:31:LYS:N	2.40	0.54
3:G:146:VAL:HA	3:G:195:GLU:O	2.08	0.54
1:M:364:TRP:HE3	1:M:379:LEU:HD21	1.73	0.54
2:C:2:VAL:HG13	2:C:27:TYR:CD1	2.43	0.54
1:N:342:ASP:OD2	3:L:31:LYS:N	2.39	0.54
2:A:2:VAL:HG13	2:A:27:TYR:CD1	2.43	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:161:GLU:HB2	3:G:176:SER:O	2.07	0.53
3:B:146:VAL:HA	3:B:195:GLU:O	2.08	0.53
2:C:156:SER:N	2:C:197:ASN:OD1	2.40	0.53
2:A:117:LYS:NZ	2:A:118:GLY:O	2.39	0.53
3:E:161:GLU:HB2	3:E:176:SER:O	2.07	0.53
1:I:455:LEU:HD11	1:M:196:PRO:HD2	1.91	0.53
1:N:364:TRP:HE3	1:N:379:LEU:HD21	1.73	0.53
1:I:294:ASN:HD21	2:A:100(C):PHE:HB2	1.73	0.53
2:D:2:VAL:HG13	2:D:27:TYR:CD1	2.43	0.53
2:H:2:VAL:HG13	2:H:27:TYR:CD1	2.43	0.52
3:B:151:ASP:N	3:B:191:VAL:HG22	2.25	0.52
3:E:81:GLU:N	3:E:81:GLU:OE1	2.43	0.52
2:A:138:LEU:O	2:A:182:VAL:O	2.28	0.52
3:L:146:VAL:HA	3:L:195:GLU:O	2.08	0.52
3:G:151:ASP:N	3:G:191:VAL:HG22	2.24	0.52
1:I:364:TRP:HE3	1:I:379:LEU:HD21	1.73	0.52
1:W:364:TRP:HE3	1:W:379:LEU:HD21	1.73	0.52
2:A:137:ALA:HB3	3:B:118:PHE:CZ	2.45	0.52
2:C:138:LEU:O	2:C:182:VAL:O	2.28	0.52
2:D:156:SER:N	2:D:197:ASN:OD1	2.40	0.52
3:G:81:GLU:N	3:G:81:GLU:OE1	2.43	0.52
3:B:81:GLU:N	3:B:81:GLU:OE1	2.43	0.52
3:E:151:ASP:N	3:E:191:VAL:HG22	2.25	0.52
3:L:81:GLU:N	3:L:81:GLU:OE1	2.43	0.52
2:C:153:SER:O	2:C:196:CYS:HB2	2.10	0.51
2:D:138:LEU:O	2:D:182:VAL:O	2.28	0.51
2:H:156:SER:N	2:H:197:ASN:OD1	2.40	0.51
2:A:84:SER:HA	2:A:111:VAL:HG21	1.93	0.51
2:A:137:ALA:HB1	2:A:183:THR:HG22	1.92	0.51
2:H:138:LEU:O	2:H:182:VAL:O	2.28	0.51
2:A:153:SER:O	2:A:196:CYS:HB2	2.10	0.51
2:H:153:SER:O	2:H:196:CYS:HB2	2.10	0.51
2:A:137:ALA:HB3	3:B:118:PHE:HZ	1.75	0.51
2:D:84:SER:HA	2:D:111:VAL:HG21	1.93	0.51
2:H:137:ALA:HB1	2:H:183:THR:HG22	1.92	0.51
3:L:151:ASP:N	3:L:191:VAL:HG22	2.25	0.51
2:C:84:SER:HA	2:C:111:VAL:HG21	1.93	0.51
3:L:120:PRO:HG3	3:L:130:ALA:HB1	1.93	0.51
3:E:120:PRO:HG3	3:E:130:ALA:HB1	1.93	0.50
2:A:156:SER:N	2:A:197:ASN:OD1	2.40	0.50
2:D:153:SER:O	2:D:196:CYS:HB2	2.10	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:137:ALA:HB1	2:C:183:THR:HG22	1.92	0.50
2:D:181:VAL:HG11	3:E:135:LEU:CD1	2.41	0.50
3:E:190:LYS:NZ	3:E:212:GLY:O	2.45	0.50
2:H:84:SER:HA	2:H:111:VAL:HG21	1.93	0.50
3:G:190:LYS:NZ	3:G:212:GLY:O	2.45	0.50
3:G:120:PRO:HG3	3:G:130:ALA:HB1	1.93	0.50
2:D:117:LYS:NZ	2:D:118:GLY:O	2.39	0.49
2:D:137:ALA:HB1	2:D:183:THR:HG22	1.92	0.49
3:B:120:PRO:HG3	3:B:130:ALA:HB1	1.93	0.49
3:B:190:LYS:NZ	3:B:212:GLY:O	2.45	0.49
1:I:294:ASN:HD21	2:A:100(C):PHE:CB	2.25	0.49
2:C:117:LYS:NZ	2:C:118:GLY:O	2.39	0.49
3:G:134:CYS:O	3:G:177:SER:HB3	2.13	0.49
3:L:190:LYS:NZ	3:L:212:GLY:O	2.45	0.49
1:W:379:LEU:HD12	1:W:400:MET:CE	2.43	0.48
1:M:225:GLN:O	1:M:226:GLU:HB2	2.14	0.48
2:H:117:LYS:NZ	2:H:118:GLY:O	2.39	0.48
3:E:134:CYS:O	3:E:177:SER:HB3	2.13	0.48
2:D:138:LEU:HA	3:E:118:PHE:CE2	2.48	0.48
2:D:154:TRP:CE2	2:D:182:VAL:HG23	2.48	0.48
1:M:379:LEU:HD12	1:M:400:MET:CE	2.43	0.48
1:N:379:LEU:HD12	1:N:400:MET:CE	2.43	0.48
2:A:137:ALA:CB	2:A:183:THR:HG22	2.44	0.48
3:L:134:CYS:O	3:L:177:SER:HB3	2.13	0.48
2:A:137:ALA:HB2	3:B:116:PHE:CD2	2.49	0.48
2:A:154:TRP:CE2	2:A:182:VAL:HG23	2.48	0.48
2:C:138:LEU:O	2:C:181:VAL:HG13	2.14	0.48
1:I:196:PRO:HD2	1:W:455:LEU:HD11	1.94	0.48
1:N:225:GLN:O	1:N:226:GLU:HB2	2.14	0.48
2:D:136:ALA:C	2:D:184:VAL:HG22	2.35	0.48
2:D:137:ALA:CB	2:D:183:THR:HG22	2.44	0.48
2:C:154:TRP:CE2	2:C:182:VAL:HG23	2.49	0.48
2:H:138:LEU:O	2:H:181:VAL:HG13	2.14	0.48
3:B:135:LEU:HD21	3:B:137:ASN:HB2	1.96	0.48
1:I:379:LEU:HD12	1:I:400:MET:CE	2.43	0.47
3:B:134:CYS:O	3:B:177:SER:HB3	2.13	0.47
3:G:135:LEU:HD21	3:G:137:ASN:HB2	1.96	0.47
2:D:63:PHE:O	2:D:67:VAL:HG12	2.14	0.47
2:D:137:ALA:HB2	3:E:116:PHE:HD2	1.74	0.47
1:I:239:MET:SD	1:I:277:CYS:SG	3.12	0.47
1:M:239:MET:SD	1:M:277:CYS:SG	3.12	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:138:LEU:O	2:A:181:VAL:HG13	2.14	0.47
2:C:136:ALA:C	2:C:184:VAL:HG22	2.34	0.47
2:H:136:ALA:C	2:H:184:VAL:HG22	2.35	0.47
1:N:239:MET:SD	1:N:277:CYS:SG	3.12	0.47
2:H:154:TRP:CE2	2:H:182:VAL:HG23	2.48	0.47
1:W:225:GLN:O	1:W:226:GLU:HB2	2.14	0.47
2:A:63:PHE:O	2:A:67:VAL:HG12	2.14	0.47
2:A:136:ALA:C	2:A:184:VAL:HG22	2.35	0.47
2:D:138:LEU:O	2:D:181:VAL:HG13	2.14	0.47
2:H:137:ALA:CB	2:H:183:THR:HG22	2.44	0.47
3:E:135:LEU:HD21	3:E:137:ASN:HB2	1.96	0.47
3:L:135:LEU:HD21	3:L:137:ASN:HB2	1.95	0.47
2:C:151:THR:HG22	2:C:152:VAL:N	2.30	0.47
2:H:63:PHE:O	2:H:67:VAL:HG12	2.14	0.47
2:D:138:LEU:HA	3:E:118:PHE:HE2	1.80	0.47
2:H:151:THR:HG22	2:H:152:VAL:N	2.30	0.47
1:W:239:MET:SD	1:W:277:CYS:SG	3.12	0.47
2:A:163:VAL:HA	2:A:182:VAL:HG22	1.97	0.47
2:C:137:ALA:CB	2:C:183:THR:HG22	2.44	0.47
1:I:225:GLN:O	1:I:226:GLU:HB2	2.14	0.46
2:A:166:PHE:CD2	3:B:176:SER:HB2	2.50	0.46
2:C:163:VAL:HA	2:C:182:VAL:HG22	1.97	0.46
2:D:151:THR:HG22	2:D:152:VAL:N	2.30	0.46
2:D:201:LYS:N	2:D:202:PRO:CD	2.78	0.46
2:H:201:LYS:N	2:H:202:PRO:CD	2.78	0.46
2:A:201:LYS:N	2:A:202:PRO:CD	2.78	0.46
2:C:201:LYS:N	2:C:202:PRO:CD	2.79	0.46
2:C:63:PHE:O	2:C:67:VAL:HG12	2.14	0.46
2:C:137:ALA:HB3	3:G:118:PHE:HZ	1.81	0.46
3:E:16:GLY:N	3:E:78:LEU:O	2.49	0.46
2:A:151:THR:HG22	2:A:152:VAL:N	2.30	0.46
3:G:16:GLY:N	3:G:78:LEU:O	2.49	0.46
1:N:241:THR:HG1	1:N:249:SER:HG	1.63	0.46
1:N:455:LEU:HD11	1:W:196:PRO:HD2	1.97	0.46
2:D:2:VAL:HG13	2:D:27:TYR:HD1	1.80	0.46
2:D:163:VAL:HA	2:D:182:VAL:HG22	1.97	0.46
1:M:455:LEU:HD11	1:N:196:PRO:HD2	1.97	0.46
2:D:122:PHE:CD1	3:E:124:GLN:HB3	2.51	0.46
2:D:13:LYS:HA	2:D:112:SER:H	1.82	0.45
2:D:181:VAL:HG11	3:E:135:LEU:HD13	1.98	0.45
2:A:2:VAL:HG13	2:A:27:TYR:HD1	1.80	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:100(J):PHE:O	3:G:91:TYR:O	2.34	0.45
3:L:16:GLY:N	3:L:78:LEU:O	2.49	0.45
2:H:163:VAL:HA	2:H:182:VAL:HG22	1.97	0.45
2:H:13:LYS:HA	2:H:112:SER:H	1.82	0.45
2:H:2:VAL:HG13	2:H:27:TYR:HD1	1.80	0.45
3:E:60:ASP:OD1	3:E:60:ASP:N	2.50	0.45
2:A:124:LEU:HD21	2:A:141:LEU:HB2	1.99	0.45
2:H:124:LEU:HD21	2:H:141:LEU:HB2	1.99	0.45
3:B:60:ASP:OD1	3:B:60:ASP:N	2.50	0.45
2:C:124:LEU:HD21	2:C:141:LEU:HB2	1.99	0.45
3:B:16:GLY:N	3:B:78:LEU:O	2.49	0.45
3:L:83:PHE:HA	3:L:104:VAL:HG23	1.99	0.45
3:E:151:ASP:H	3:E:191:VAL:CG2	2.30	0.45
3:G:83:PHE:HA	3:G:104:VAL:HG23	1.99	0.45
3:L:124:GLN:C	3:L:127:SER:HG	2.08	0.45
2:C:13:LYS:HA	2:C:112:SER:H	1.82	0.44
3:B:164:THR:HG21	3:B:174:SER:HB2	1.99	0.44
3:L:164:THR:HG21	3:L:174:SER:HB2	1.99	0.44
2:D:124:LEU:HD21	2:D:141:LEU:HB2	1.99	0.44
3:E:164:THR:HG21	3:E:174:SER:HB2	1.99	0.44
2:D:205:THR:HG22	2:D:207:VAL:HG23	1.99	0.44
3:G:60:ASP:OD1	3:G:60:ASP:N	2.50	0.44
2:A:13:LYS:HA	2:A:112:SER:H	1.82	0.44
3:L:60:ASP:OD1	3:L:60:ASP:N	2.50	0.44
2:C:205:THR:HG22	2:C:207:VAL:HG23	1.99	0.44
2:C:2:VAL:HG13	2:C:27:TYR:HD1	1.80	0.44
3:G:164:THR:HG21	3:G:174:SER:HB2	1.99	0.44
2:D:153:SER:OG	2:D:154:TRP:N	2.51	0.43
3:E:83:PHE:HA	3:E:104:VAL:HG23	1.99	0.43
3:L:151:ASP:H	3:L:191:VAL:CG2	2.30	0.43
1:N:379:LEU:HD12	1:N:400:MET:HE3	1.99	0.43
2:A:153:SER:OG	2:A:154:TRP:N	2.51	0.43
2:H:116:THR:HG22	2:H:117:LYS:N	2.34	0.43
3:B:83:PHE:HA	3:B:104:VAL:HG23	1.99	0.43
3:L:192:TYR:O	3:L:208:SER:OG	2.31	0.43
2:A:116:THR:HG22	2:A:117:LYS:N	2.34	0.43
2:A:178:LEU:HD23	2:A:179:SER:N	2.34	0.43
3:G:50:GLY:O	3:G:51:ALA:HB3	2.19	0.43
3:L:50:GLY:O	3:L:51:ALA:HB3	2.19	0.43
3:L:192:TYR:CE1	3:L:211:ARG:HD2	2.54	0.43
2:C:116:THR:HG22	2:C:117:LYS:N	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:205:THR:HG22	2:H:207:VAL:HG23	1.99	0.43
2:D:116:THR:HG22	2:D:117:LYS:N	2.34	0.43
3:E:159:SER:OG	3:E:160:GLN:N	2.52	0.43
3:E:192:TYR:O	3:E:208:SER:OG	2.31	0.43
2:A:205:THR:HG22	2:A:207:VAL:HG23	1.99	0.43
2:C:178:LEU:HD23	2:C:179:SER:N	2.34	0.43
2:D:178:LEU:HD23	2:D:179:SER:N	2.34	0.43
3:B:192:TYR:CE1	3:B:211:ARG:HD2	2.54	0.43
3:G:159:SER:OG	3:G:160:GLN:N	2.52	0.43
3:E:50:GLY:O	3:E:51:ALA:HB3	2.19	0.43
2:H:153:SER:OG	2:H:154:TRP:N	2.51	0.43
3:G:192:TYR:CE1	3:G:211:ARG:HD2	2.54	0.43
3:B:50:GLY:O	3:B:51:ALA:HB3	2.19	0.42
2:A:136:ALA:O	2:A:183:THR:HB	2.19	0.42
3:B:159:SER:OG	3:B:160:GLN:N	2.52	0.42
3:L:159:SER:OG	3:L:160:GLN:N	2.52	0.42
1:M:379:LEU:HD12	1:M:400:MET:HE3	2.00	0.42
1:I:297:THR:OG1	1:I:298:ALA:N	2.53	0.42
1:M:294:ASN:HD21	2:C:100(C):PHE:HB2	1.84	0.42
1:M:297:THR:OG1	1:M:298:ALA:N	2.53	0.42
1:N:297:THR:OG1	1:N:298:ALA:N	2.53	0.42
3:L:163:VAL:HG12	3:L:164:THR:N	2.34	0.42
2:C:153:SER:OG	2:C:154:TRP:N	2.51	0.42
2:H:136:ALA:O	2:H:183:THR:HB	2.19	0.42
3:E:192:TYR:CE1	3:E:211:ARG:HD2	2.54	0.42
3:G:151:ASP:H	3:G:191:VAL:CG2	2.30	0.42
1:I:383:TYR:O	1:I:384:ASP:C	2.58	0.42
2:D:136:ALA:O	2:D:183:THR:HB	2.19	0.42
3:B:163:VAL:HG12	3:B:164:THR:N	2.34	0.42
3:G:124:GLN:C	3:G:127:SER:HG	2.12	0.42
2:C:136:ALA:O	2:C:183:THR:HB	2.19	0.42
2:H:178:LEU:HD23	2:H:179:SER:N	2.34	0.42
3:B:125:LEU:C	3:B:183:LYS:HZ1	2.22	0.42
3:E:20:THR:HG23	3:E:20:THR:O	2.20	0.42
3:G:190:LYS:O	3:G:191:VAL:HG13	2.20	0.42
1:N:383:TYR:O	1:N:384:ASP:C	2.58	0.42
1:W:294:ASN:HD21	2:D:100(C):PHE:HB2	1.84	0.42
2:D:135:THR:OG1	2:D:185:PRO:HA	2.20	0.42
3:B:124:GLN:C	3:B:127:SER:HG	2.10	0.42
3:G:151:ASP:N	3:G:191:VAL:CG2	2.83	0.42
3:L:20:THR:HG23	3:L:20:THR:O	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:224:THR:OG1	1:M:225:GLN:N	2.52	0.41
3:E:151:ASP:N	3:E:191:VAL:CG2	2.83	0.41
3:G:163:VAL:HG12	3:G:164:THR:N	2.34	0.41
1:I:224:THR:OG1	1:I:225:GLN:N	2.52	0.41
2:A:135:THR:OG1	2:A:185:PRO:HA	2.20	0.41
3:B:151:ASP:N	3:B:191:VAL:CG2	2.83	0.41
1:W:297:THR:OG1	1:W:298:ALA:N	2.53	0.41
3:B:122:ASP:O	3:B:125:LEU:HB2	2.20	0.41
1:W:224:THR:OG1	1:W:225:GLN:N	2.52	0.41
3:E:190:LYS:O	3:E:191:VAL:HG13	2.20	0.41
2:A:97:VAL:HG21	2:A:100(K):PHE:CG	2.56	0.41
3:B:190:LYS:O	3:B:191:VAL:HG13	2.20	0.41
3:E:163:VAL:HG12	3:E:164:THR:N	2.34	0.41
2:C:137:ALA:HB3	3:G:118:PHE:CZ	2.56	0.41
2:D:137:ALA:HB3	3:E:118:PHE:HZ	1.82	0.41
2:H:135:THR:OG1	2:H:185:PRO:HA	2.20	0.41
3:E:122:ASP:O	3:E:125:LEU:HB2	2.20	0.41
1:M:116:ARG:O	1:M:118:PRO:HD3	2.21	0.41
2:H:97:VAL:HG21	2:H:100(K):PHE:CG	2.55	0.41
3:E:125:LEU:C	3:E:183:LYS:HZ1	2.23	0.41
1:W:383:TYR:O	1:W:384:ASP:C	2.58	0.41
2:C:97:VAL:HG21	2:C:100(K):PHE:CG	2.56	0.41
2:D:97:VAL:HG21	2:D:100(K):PHE:CG	2.56	0.41
1:I:116:ARG:O	1:I:118:PRO:HD3	2.21	0.41
1:M:383:TYR:O	1:M:384:ASP:C	2.58	0.41
1:N:116:ARG:O	1:N:118:PRO:HD3	2.21	0.41
1:N:224:THR:OG1	1:N:225:GLN:N	2.52	0.41
2:C:135:THR:OG1	2:C:185:PRO:HA	2.20	0.41
3:B:20:THR:HG23	3:B:20:THR:O	2.20	0.41
3:B:151:ASP:H	3:B:191:VAL:CG2	2.30	0.41
3:G:8:PRO:O	3:G:102:THR:HG22	2.21	0.41
3:G:20:THR:O	3:G:20:THR:HG23	2.20	0.41
3:L:122:ASP:O	3:L:125:LEU:HB2	2.20	0.41
1:I:174:MET:SD	1:I:192:GLY:HA3	2.61	0.41
1:N:174:MET:SD	1:N:192:GLY:HA3	2.61	0.41
1:W:174:MET:SD	1:W:192:GLY:HA3	2.61	0.41
3:L:151:ASP:N	3:L:191:VAL:CG2	2.83	0.41
3:L:190:LYS:O	3:L:191:VAL:HG13	2.20	0.41
1:I:380:TYR:HB3	1:I:394:LEU:HB3	2.03	0.40
1:I:115:ILE:HA	1:I:132:LEU:O	2.21	0.40
1:N:115:ILE:HA	1:N:132:LEU:O	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:380:TYR:HB3	1:W:394:LEU:HB3	2.03	0.40
3:G:122:ASP:O	3:G:125:LEU:HB2	2.20	0.40
1:W:116:ARG:O	1:W:118:PRO:HD3	2.21	0.40
1:M:174:MET:SD	1:M:192:GLY:HA3	2.61	0.40
1:N:408:TRP:N	1:N:408:TRP:CD1	2.90	0.40
2:C:153:SER:O	2:C:154:TRP:CG	2.75	0.40
2:D:153:SER:O	2:D:154:TRP:CG	2.75	0.40
3:G:117:ILE:HG13	3:G:133:VAL:O	2.22	0.40
1:W:115:ILE:HA	1:W:132:LEU:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	I	356/448 (80%)	327 (92%)	29 (8%)	0	100	100
1	M	356/448 (80%)	327 (92%)	29 (8%)	0	100	100
1	N	356/448 (80%)	327 (92%)	29 (8%)	0	100	100
1	W	356/448 (80%)	327 (92%)	29 (8%)	0	100	100
2	A	219/249 (88%)	189 (86%)	30 (14%)	0	100	100
2	C	219/249 (88%)	187 (85%)	32 (15%)	0	100	100
2	D	219/249 (88%)	189 (86%)	30 (14%)	0	100	100
2	H	219/249 (88%)	188 (86%)	31 (14%)	0	100	100
3	B	212/215 (99%)	194 (92%)	18 (8%)	0	100	100
3	E	212/215 (99%)	194 (92%)	18 (8%)	0	100	100
3	G	212/215 (99%)	194 (92%)	18 (8%)	0	100	100
3	L	212/215 (99%)	194 (92%)	18 (8%)	0	100	100
All	All	3148/3648 (86%)	2837 (90%)	311 (10%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	I	305/379 (80%)	291 (95%)	14 (5%)	27	60
1	M	305/379 (80%)	291 (95%)	14 (5%)	27	60
1	N	305/379 (80%)	291 (95%)	14 (5%)	27	60
1	W	305/379 (80%)	291 (95%)	14 (5%)	27	60
2	A	189/212 (89%)	186 (98%)	3 (2%)	62	88
2	C	189/212 (89%)	186 (98%)	3 (2%)	62	88
2	D	189/212 (89%)	186 (98%)	3 (2%)	62	88
2	H	189/212 (89%)	186 (98%)	3 (2%)	62	88
3	B	183/184 (100%)	168 (92%)	15 (8%)	11	33
3	E	183/184 (100%)	168 (92%)	15 (8%)	11	33
3	G	183/184 (100%)	168 (92%)	15 (8%)	11	33
3	L	183/184 (100%)	168 (92%)	15 (8%)	11	33
All	All	2708/3100 (87%)	2580 (95%)	128 (5%)	30	59

All (128) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	87	CYS
1	I	116	ARG
1	I	135	TYR
1	I	182	CYS
1	I	219	LYS
1	I	229	CYS
1	I	239	MET
1	I	257	ARG
1	I	260	ARG
1	I	366	SER
1	I	390	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	I	410	SER
1	I	418	LYS
1	I	420	CYS
1	M	87	CYS
1	M	116	ARG
1	M	135	TYR
1	M	182	CYS
1	M	219	LYS
1	M	229	CYS
1	M	239	MET
1	M	257	ARG
1	M	260	ARG
1	M	366	SER
1	M	390	ASP
1	M	410	SER
1	M	418	LYS
1	M	420	CYS
1	N	87	CYS
1	N	116	ARG
1	N	135	TYR
1	N	182	CYS
1	N	219	LYS
1	N	229	CYS
1	N	239	MET
1	N	257	ARG
1	N	260	ARG
1	N	366	SER
1	N	390	ASP
1	N	410	SER
1	N	418	LYS
1	N	420	CYS
1	W	87	CYS
1	W	116	ARG
1	W	135	TYR
1	W	182	CYS
1	W	219	LYS
1	W	229	CYS
1	W	239	MET
1	W	257	ARG
1	W	260	ARG
1	W	366	SER
1	W	390	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	W	410	SER
1	W	418	LYS
1	W	420	CYS
2	A	17	SER
2	A	82(B)	SER
2	A	173	SER
2	C	17	SER
2	C	82(B)	SER
2	C	173	SER
2	D	17	SER
2	D	82(B)	SER
2	D	173	SER
2	H	17	SER
2	H	82(B)	SER
2	H	173	SER
3	B	7	SER
3	B	24	ARG
3	B	30(A)	SER
3	B	32	SER
3	B	33	LEU
3	B	49	ASN
3	B	60	ASP
3	B	90	ARG
3	B	108	ARG
3	B	143	GLU
3	B	150	VAL
3	B	161	GLU
3	B	165	GLU
3	B	176	SER
3	B	206	THR
3	E	7	SER
3	E	24	ARG
3	E	30(A)	SER
3	E	32	SER
3	E	33	LEU
3	E	49	ASN
3	E	60	ASP
3	E	90	ARG
3	E	108	ARG
3	E	143	GLU
3	E	150	VAL
3	E	161	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	E	165	GLU
3	E	176	SER
3	E	206	THR
3	G	7	SER
3	G	24	ARG
3	G	30(A)	SER
3	G	32	SER
3	G	33	LEU
3	G	49	ASN
3	G	60	ASP
3	G	90	ARG
3	G	108	ARG
3	G	143	GLU
3	G	150	VAL
3	G	161	GLU
3	G	165	GLU
3	G	176	SER
3	G	206	THR
3	L	7	SER
3	L	24	ARG
3	L	30(A)	SER
3	L	32	SER
3	L	33	LEU
3	L	49	ASN
3	L	60	ASP
3	L	90	ARG
3	L	108	ARG
3	L	143	GLU
3	L	150	VAL
3	L	161	GLU
3	L	165	GLU
3	L	176	SER
3	L	206	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	I	225	GLN
1	I	431	HIS
1	M	225	GLN
1	M	431	HIS
1	N	225	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	N	431	HIS
1	W	225	GLN
1	W	431	HIS
2	A	204	ASN
2	C	204	ASN
2	D	164	HIS
2	D	204	ASN
2	H	204	ASN
3	G	38	HIS
3	L	38	HIS

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)

8 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	F	1	4,1	14,14,15	0.46	0	17,19,21	0.37	0
4	NAG	F	2	4	14,14,15	0.23	0	17,19,21	0.38	0
4	NAG	J	1	4,1	14,14,15	0.45	0	17,19,21	0.38	0
4	NAG	J	2	4	14,14,15	0.23	0	17,19,21	0.38	0
4	NAG	K	1	4,1	14,14,15	0.45	0	17,19,21	0.38	0
4	NAG	K	2	4	14,14,15	0.24	0	17,19,21	0.38	0
4	NAG	O	1	4,1	14,14,15	0.45	0	17,19,21	0.38	0
4	NAG	O	2	4	14,14,15	0.22	0	17,19,21	0.38	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	F	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	0/1/1/1
4	NAG	K	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	0/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

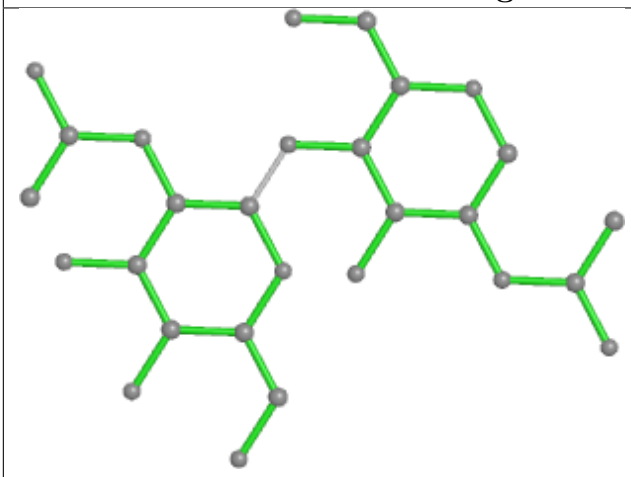
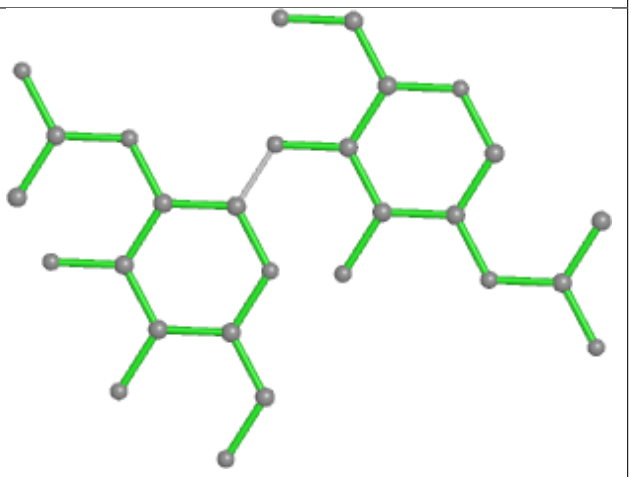
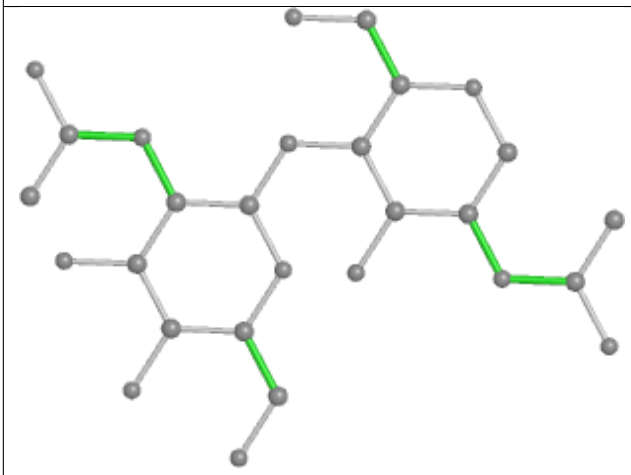
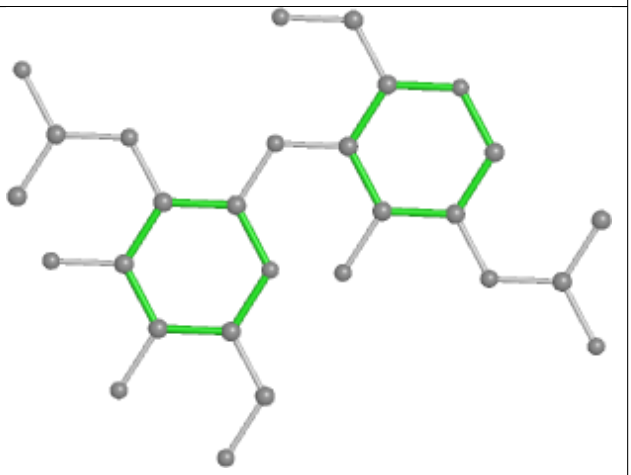
There are no chirality outliers.

There are no torsion outliers.

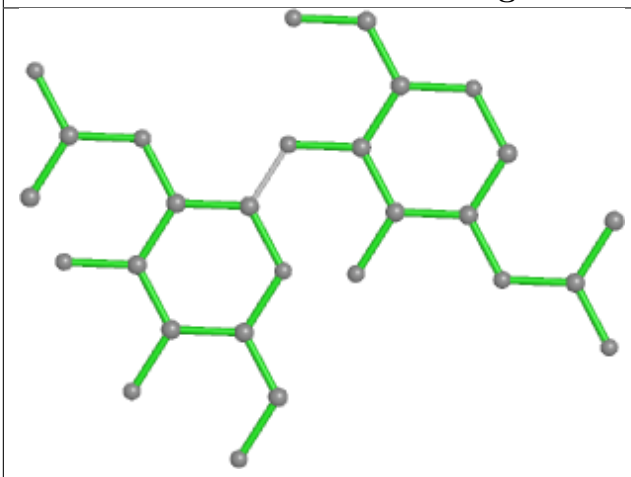
There are no ring outliers.

No monomer is involved in short contacts.

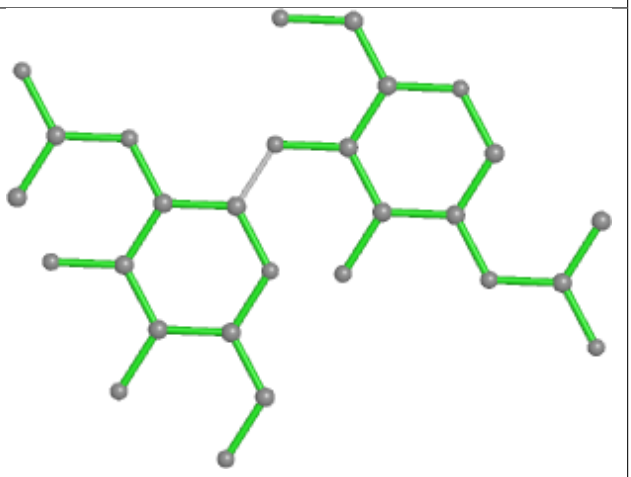
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

Oligosaccharide Chain F	
 Bond lengths	 Bond angles
 Torsions	 Rings

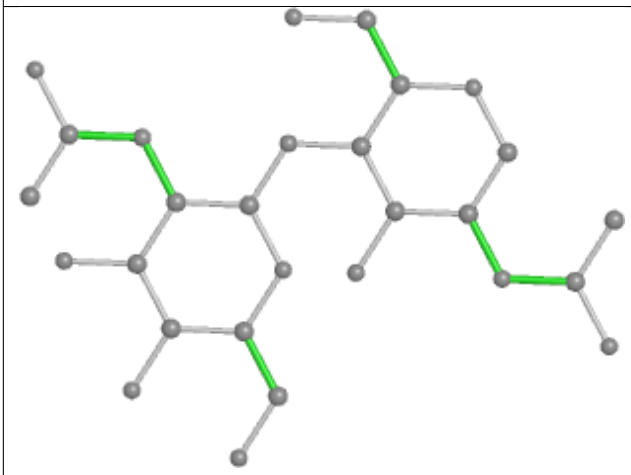
Oligosaccharide Chain J



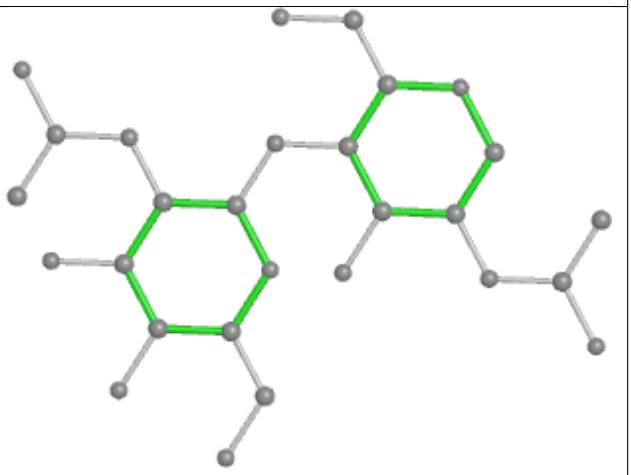
Bond lengths



Bond angles

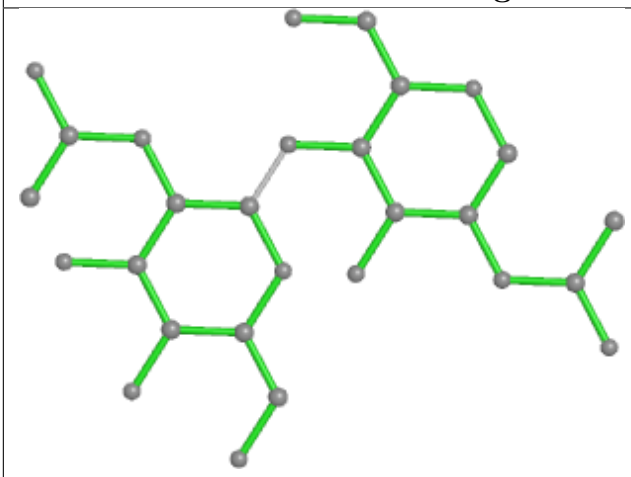


Torsions

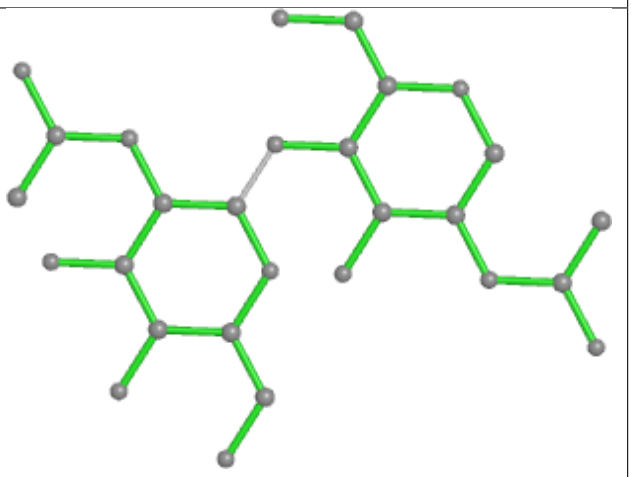


Rings

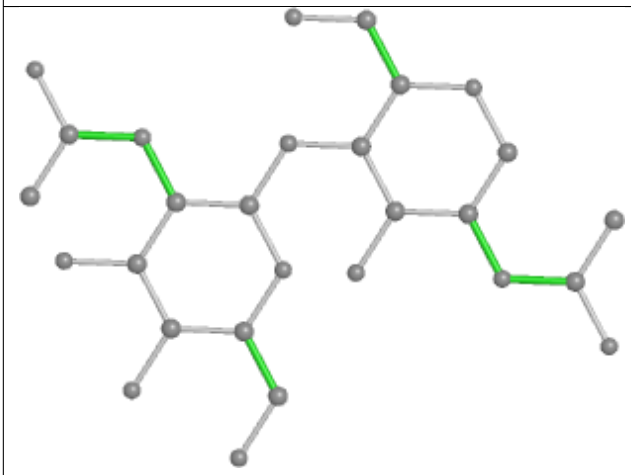
Oligosaccharide Chain K



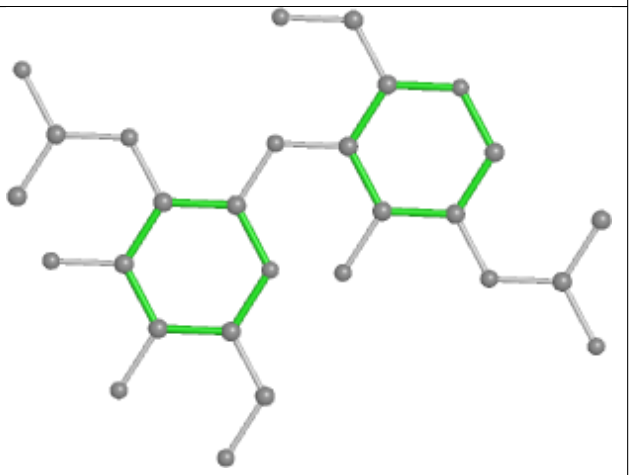
Bond lengths



Bond angles

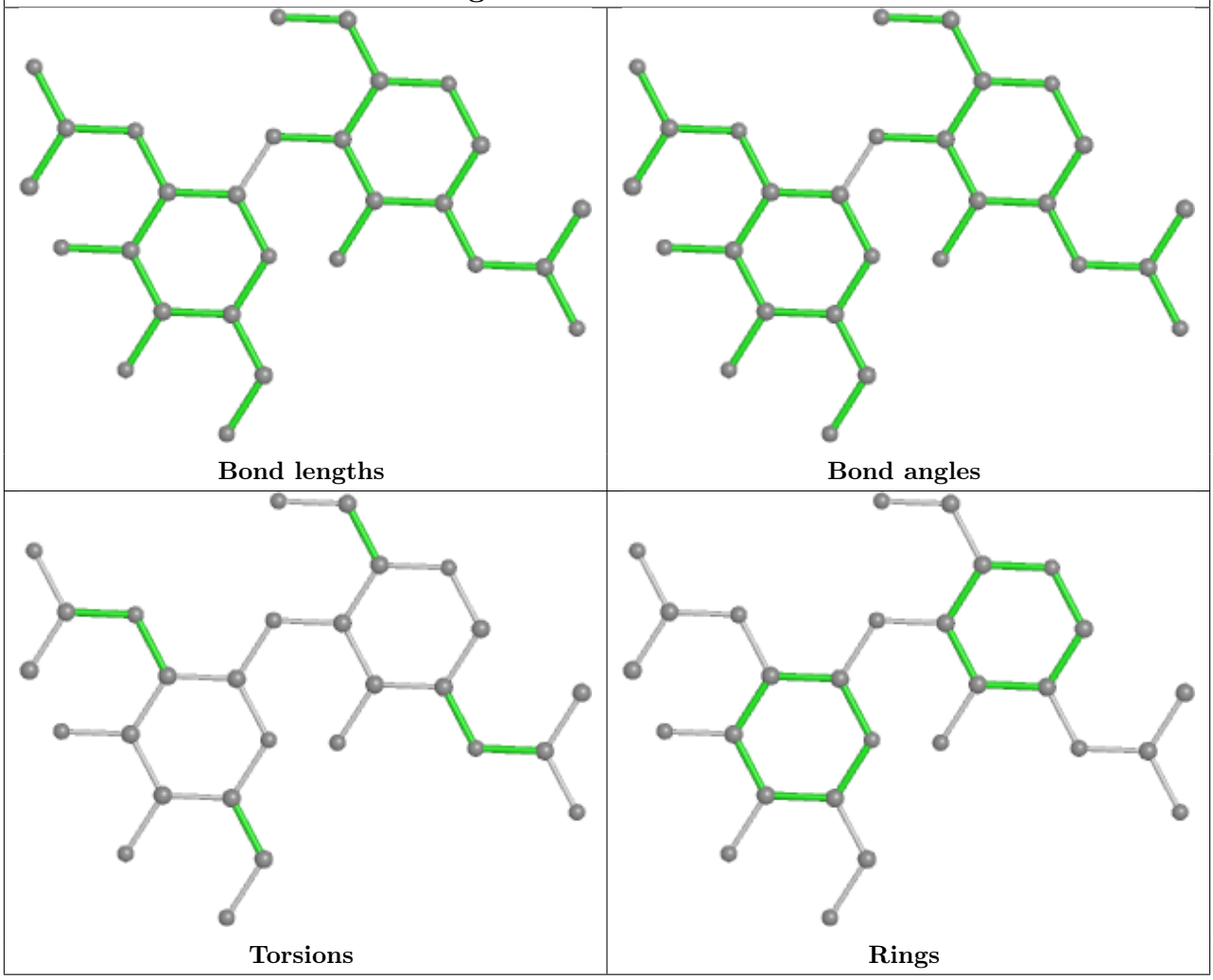


Torsions



Rings

Oligosaccharide Chain O



5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	BMA	W	503	-	11,11,12	0.59	0	15,15,17	0.77	0
5	BMA	I	503	-	11,11,12	0.60	0	15,15,17	0.77	0
5	BMA	N	503	-	11,11,12	0.60	0	15,15,17	0.77	0
5	BMA	M	503	-	11,11,12	0.60	0	15,15,17	0.76	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	BMA	W	503	-	-	2/2/19/22	0/1/1/1
5	BMA	I	503	-	-	2/2/19/22	0/1/1/1
5	BMA	N	503	-	-	2/2/19/22	0/1/1/1
5	BMA	M	503	-	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	N	503	BMA	C4-C5-C6-O6
5	I	503	BMA	C4-C5-C6-O6
5	M	503	BMA	C4-C5-C6-O6
5	W	503	BMA	C4-C5-C6-O6
5	M	503	BMA	O5-C5-C6-O6
5	N	503	BMA	O5-C5-C6-O6
5	W	503	BMA	O5-C5-C6-O6
5	I	503	BMA	O5-C5-C6-O6

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.

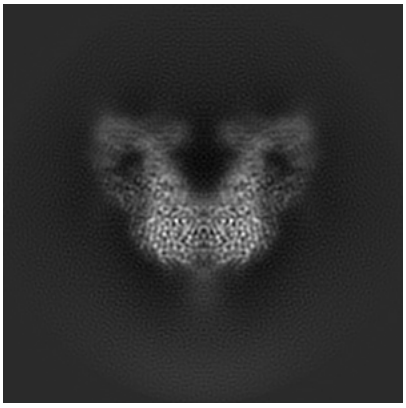
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-21043. These allow visual inspection of the internal detail of the map and identification of artifacts.

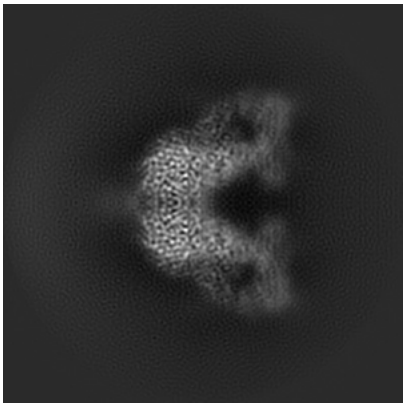
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

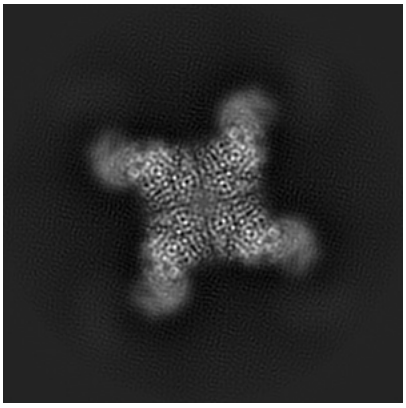
6.1.1 Primary map



X



Y

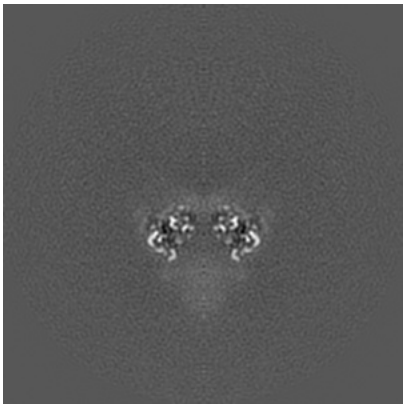


Z

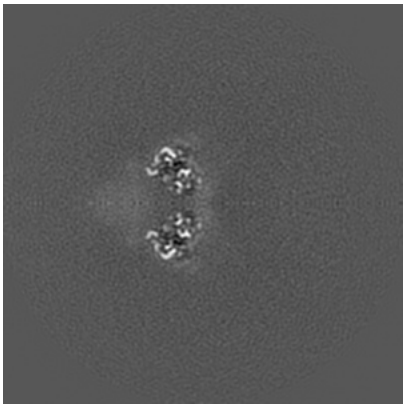
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

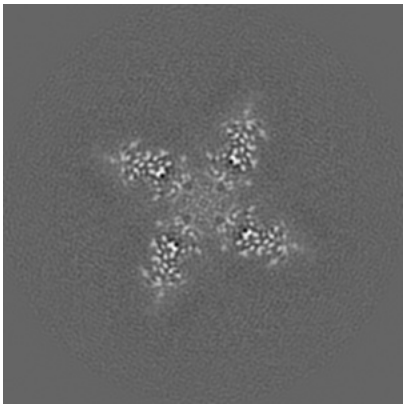
6.2.1 Primary map



X Index: 125



Y Index: 125

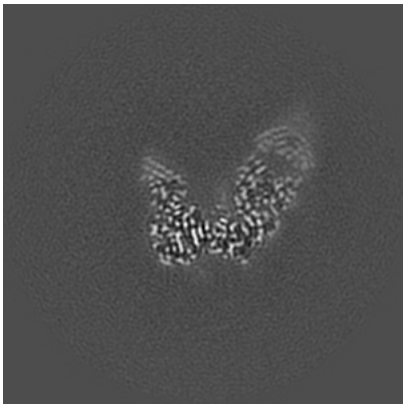


Z Index: 125

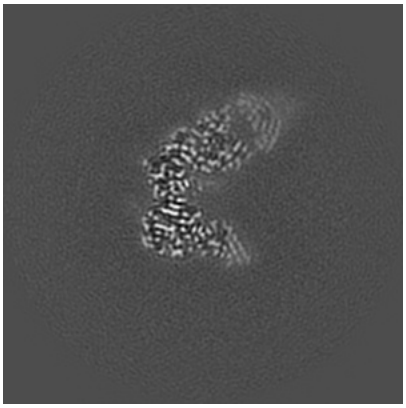
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

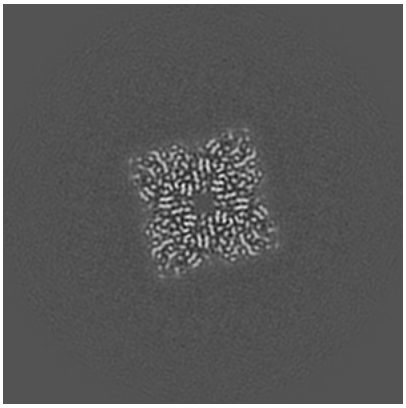
6.3.1 Primary map



X Index: 150



Y Index: 100



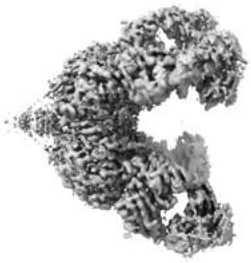
Z Index: 109

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.0123. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

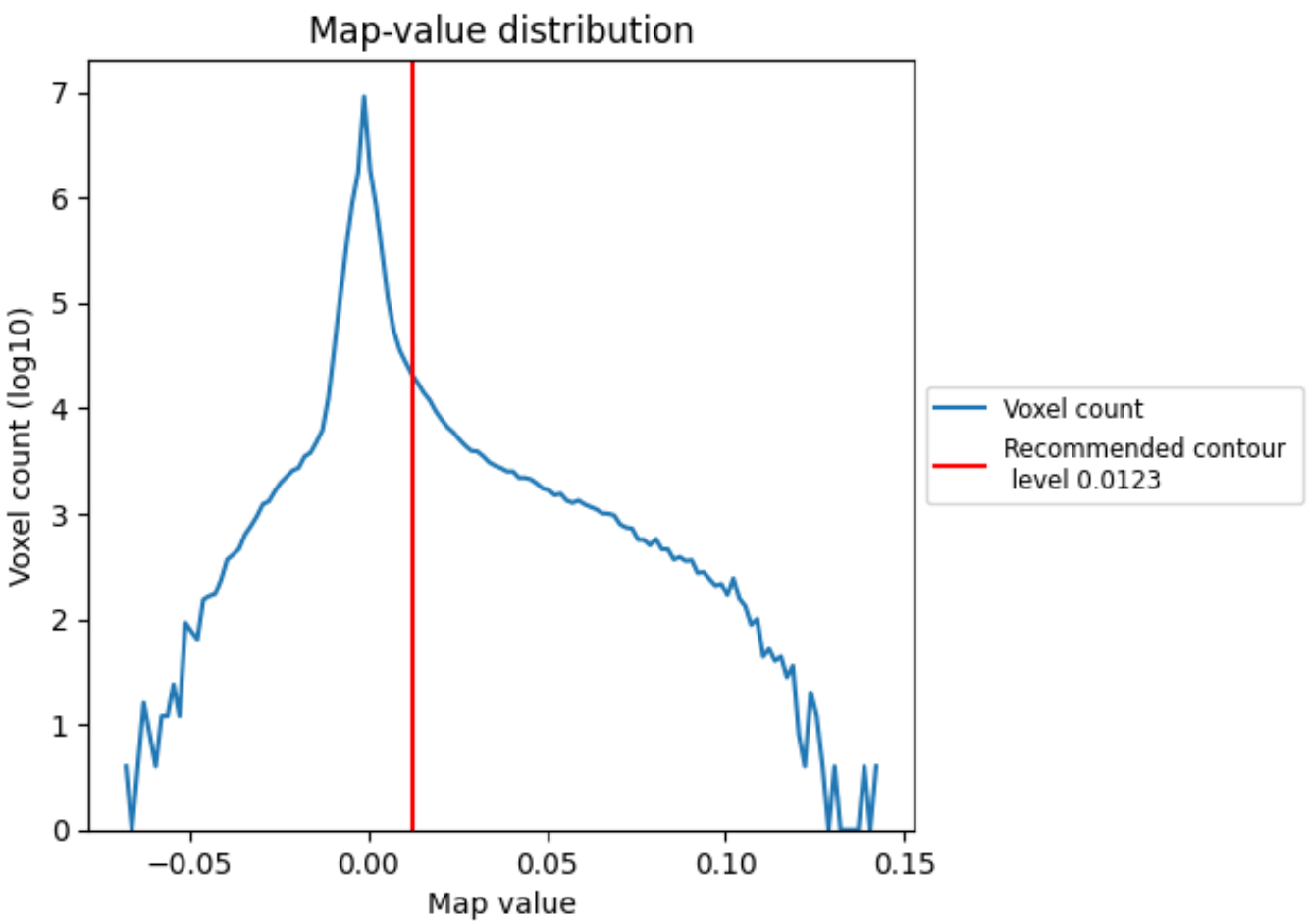
6.5 Mask visualisation (i)

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

7 Map analysis (i)

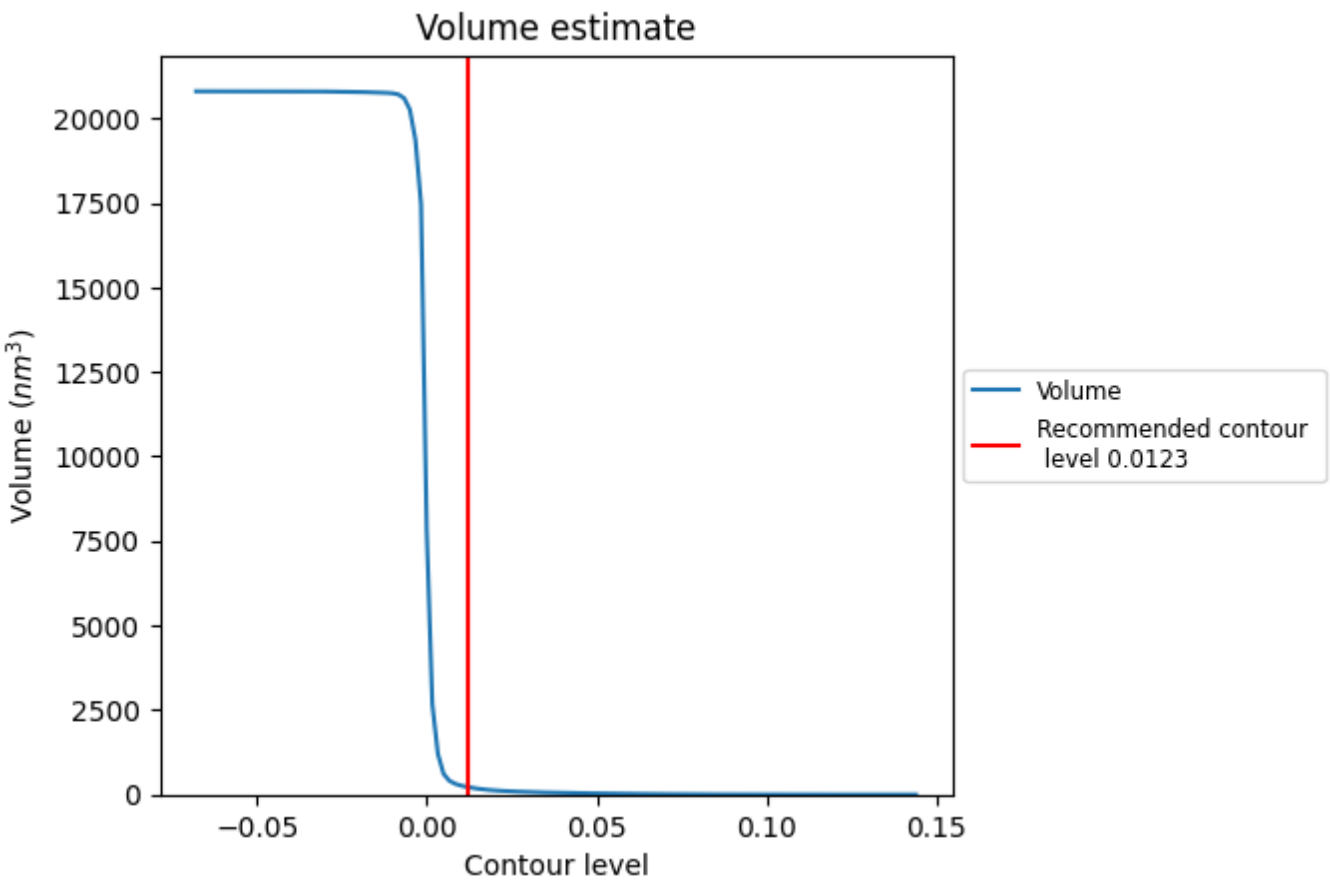
This section contains the results of statistical analysis of the map.

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.

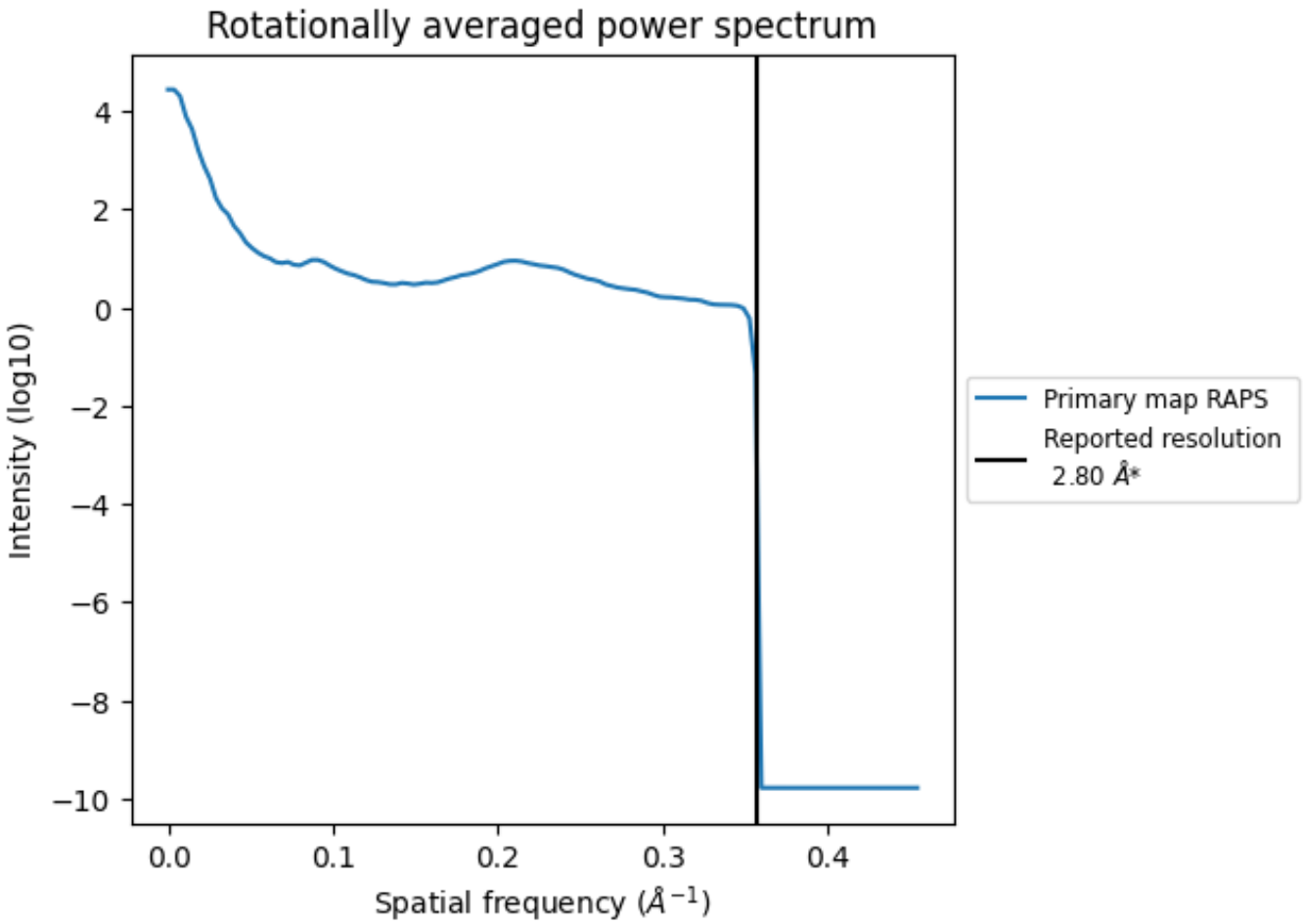
7.2 Volume estimate (i)



The volume at the recommended contour level is 215 nm^3; this corresponds to an approximate mass of 195 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)

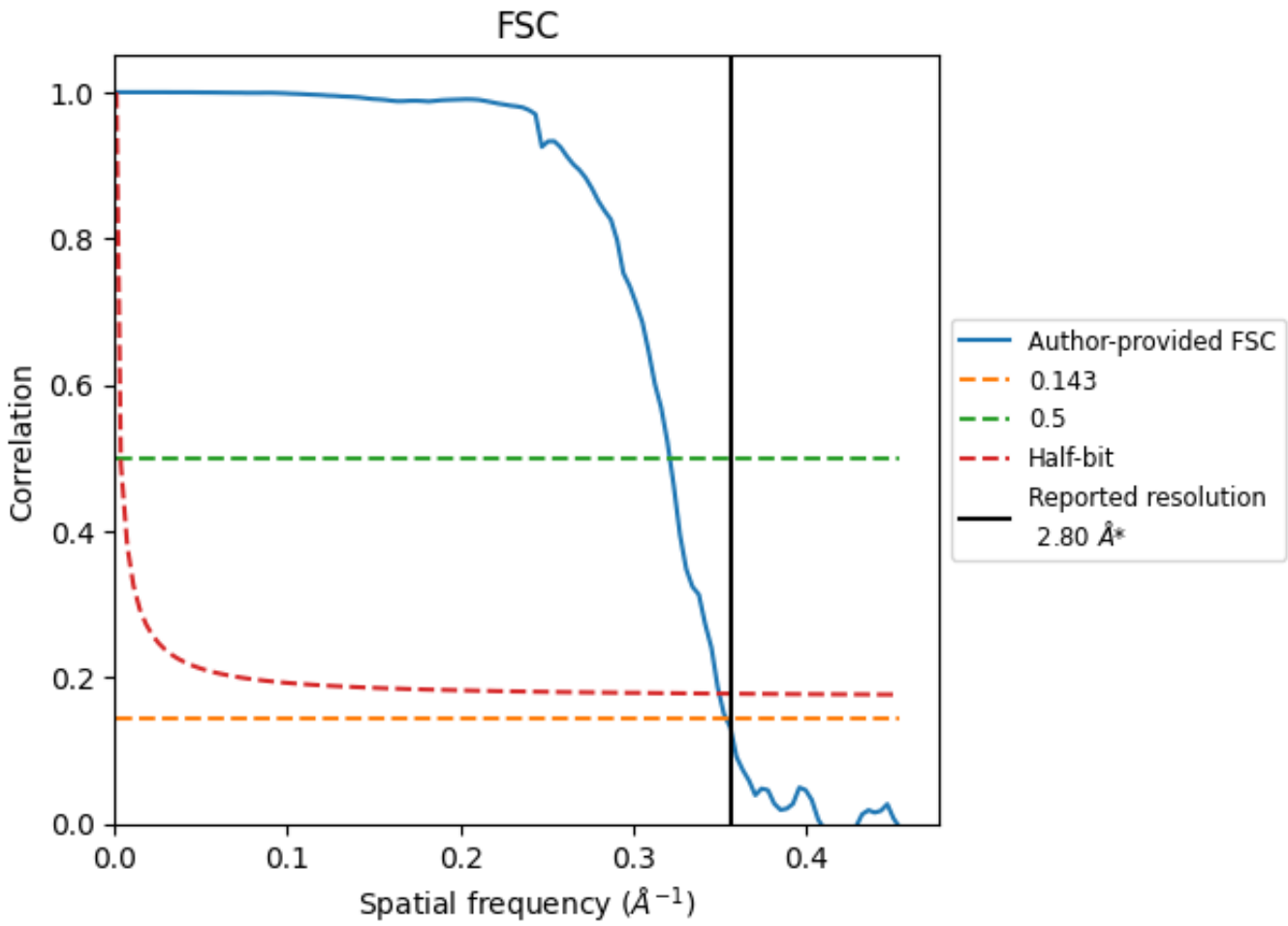


*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8.2 Resolution estimates (i)

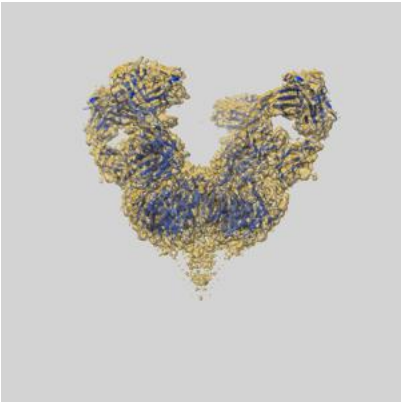
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.82	3.11	2.86
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

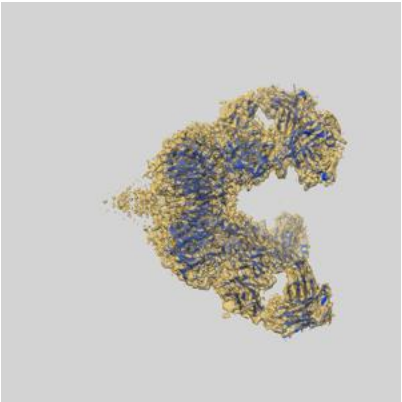
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-21043 and PDB model 6V4O. Per-residue inclusion information can be found in section 3 on page 13.

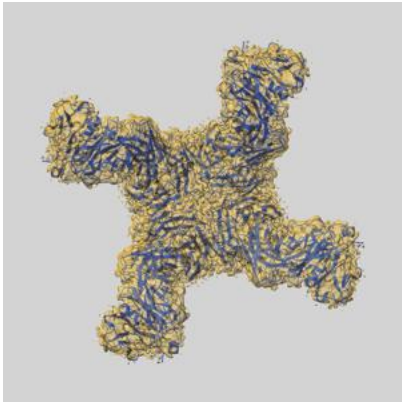
9.1 Map-model overlay (i)



X



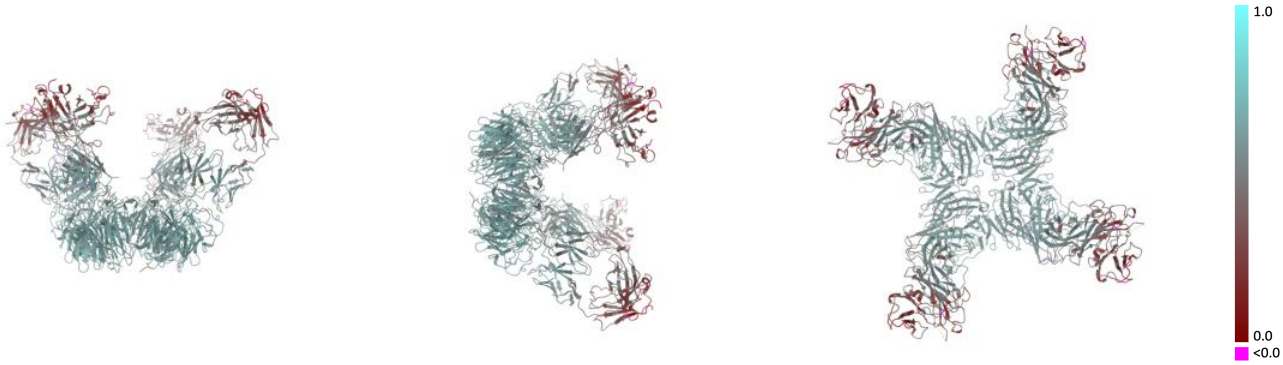
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0123 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.

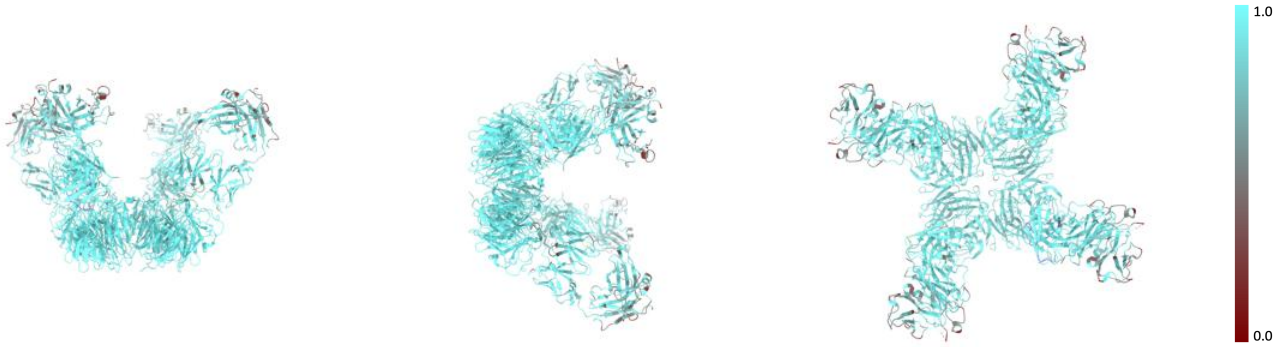
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

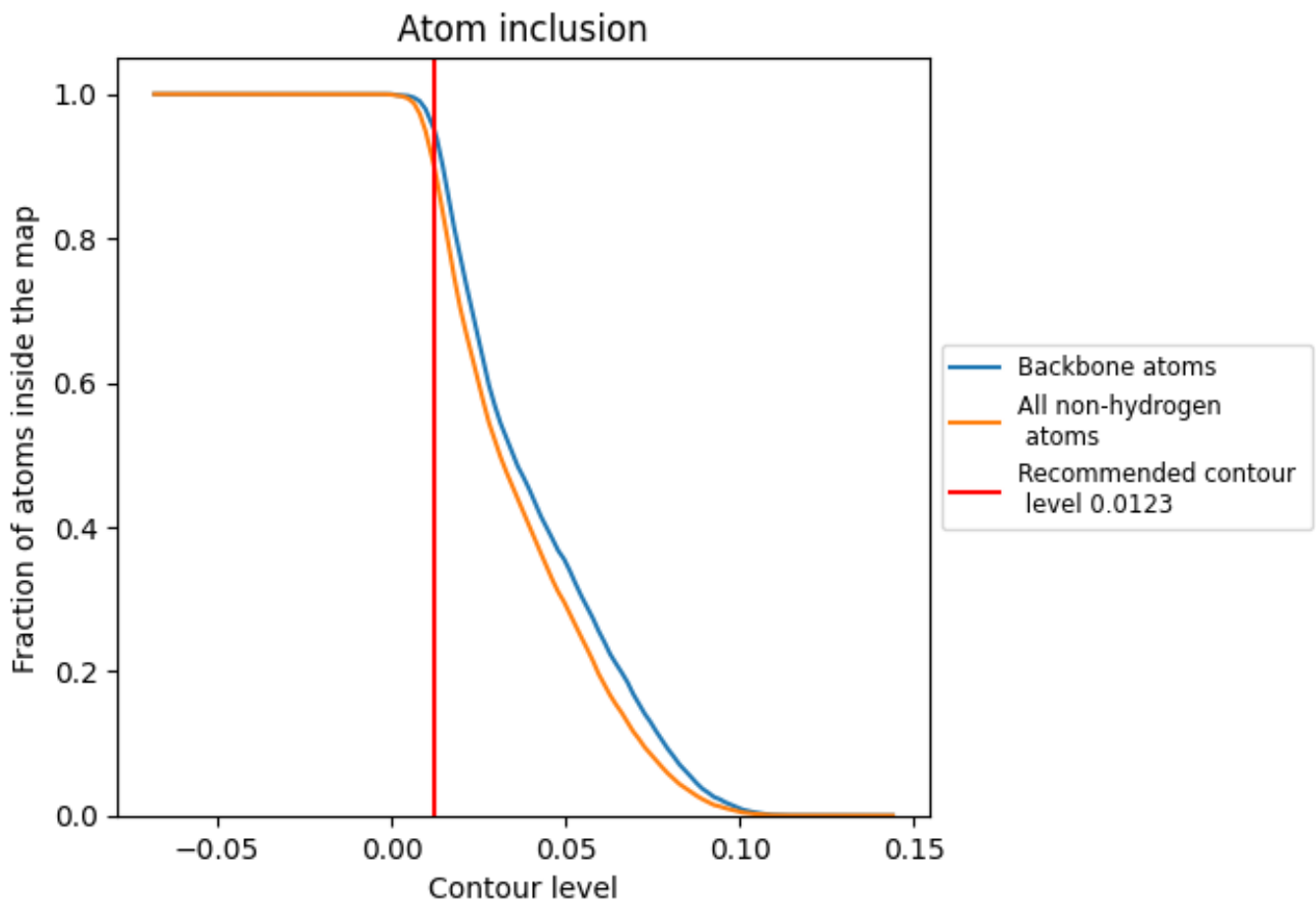
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0123).

9.4 Atom inclusion (i)



At the recommended contour level, 95% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0123) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9000	0.5250
A	0.8568	0.4780
B	0.8186	0.4400
C	0.8580	0.4800
D	0.8592	0.4830
E	0.8173	0.4340
F	0.9643	0.5560
G	0.8229	0.4380
H	0.8580	0.4820
I	0.9708	0.6010
J	0.9643	0.5520
K	0.9643	0.5680
L	0.8254	0.4370
M	0.9694	0.6000
N	0.9701	0.6000
O	0.9643	0.5650
W	0.9701	0.6010