



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 11:45 AM UTC

PDB ID : 7WO4 / pdb_00007wo4
EMDB ID : EMD-32638
Title : SARS-CoV-2 Spike in complex with IgG 553-15 (S-553-15 dimer trimer)
Authors : Zhan, W.Q.; Zhang, X.; Chen, Z.G.; Sun, L.
Deposited on : 2022-01-20
Resolution : 4.47 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 : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

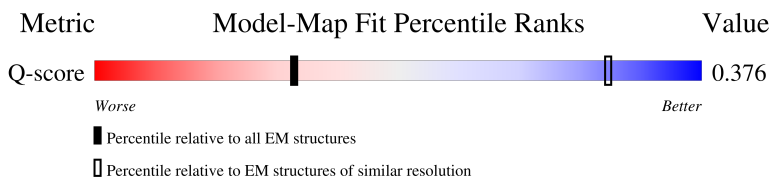
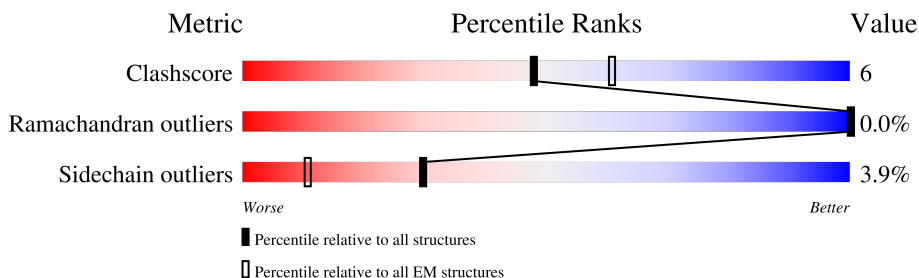
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.47 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.



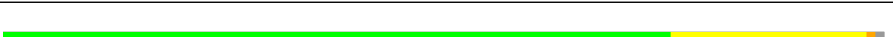
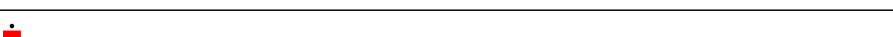
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2963 (3.97 - 4.97)

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 $\leq 5\%$. 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	A	1288	70% 13% • 16%
1	B	1288	70% 12% • 16%
1	C	1288	70% 13% • 16%
1	J	1288	70% 13% • 16%

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Mol	Chain	Length	Quality of chain
1	K	1288	
1	L	1288	
2	D	225	
2	F	225	
2	H	225	
2	M	225	
2	O	225	
2	Q	225	
3	E	218	
3	G	218	
3	I	218	
3	N	218	
3	P	218	
3	R	218	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 71208 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1076	Total	C	N	O	S	0	0
			8338	5318	1396	1586	38		
1	B	1076	Total	C	N	O	S	0	0
			8338	5318	1396	1586	38		
1	C	1076	Total	C	N	O	S	0	0
			8338	5318	1396	1586	38		
1	J	1076	Total	C	N	O	S	0	0
			8338	5318	1396	1586	38		
1	K	1076	Total	C	N	O	S	0	0
			8338	5318	1396	1586	38		
1	L	1076	Total	C	N	O	S	0	0
			8338	5318	1396	1586	38		

There are 516 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	614	GLY	ASP	variant	UNP P0DTC2
A	682	GLY	ARG	conflict	UNP P0DTC2
A	683	SER	ARG	conflict	UNP P0DTC2
A	685	SER	ARG	conflict	UNP P0DTC2
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	SER	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2
A	1212	TYR	-	expression tag	UNP P0DTC2
A	1213	ILE	-	expression tag	UNP P0DTC2
A	1214	PRO	-	expression tag	UNP P0DTC2
A	1215	GLU	-	expression tag	UNP P0DTC2
A	1216	ALA	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	ARG	-	expression tag	UNP P0DTC2
A	1219	ASP	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	ALA	-	expression tag	UNP P0DTC2
A	1223	TYR	-	expression tag	UNP P0DTC2
A	1224	VAL	-	expression tag	UNP P0DTC2
A	1225	ARG	-	expression tag	UNP P0DTC2
A	1226	LYS	-	expression tag	UNP P0DTC2
A	1227	ASP	-	expression tag	UNP P0DTC2
A	1228	GLY	-	expression tag	UNP P0DTC2
A	1229	GLU	-	expression tag	UNP P0DTC2
A	1230	TRP	-	expression tag	UNP P0DTC2
A	1231	VAL	-	expression tag	UNP P0DTC2
A	1232	PHE	-	expression tag	UNP P0DTC2
A	1233	LEU	-	expression tag	UNP P0DTC2
A	1234	SER	-	expression tag	UNP P0DTC2
A	1235	THR	-	expression tag	UNP P0DTC2
A	1236	PHE	-	expression tag	UNP P0DTC2
A	1237	LEU	-	expression tag	UNP P0DTC2
A	1238	SER	-	expression tag	UNP P0DTC2
A	1239	GLY	-	expression tag	UNP P0DTC2
A	1240	LEU	-	expression tag	UNP P0DTC2
A	1241	GLU	-	expression tag	UNP P0DTC2
A	1242	VAL	-	expression tag	UNP P0DTC2
A	1243	LEU	-	expression tag	UNP P0DTC2
A	1244	PHE	-	expression tag	UNP P0DTC2
A	1245	GLN	-	expression tag	UNP P0DTC2
A	1246	GLY	-	expression tag	UNP P0DTC2
A	1247	PRO	-	expression tag	UNP P0DTC2
A	1248	GLY	-	expression tag	UNP P0DTC2
A	1249	GLY	-	expression tag	UNP P0DTC2
A	1250	TRP	-	expression tag	UNP P0DTC2
A	1251	SER	-	expression tag	UNP P0DTC2
A	1252	HIS	-	expression tag	UNP P0DTC2
A	1253	PRO	-	expression tag	UNP P0DTC2
A	1254	GLN	-	expression tag	UNP P0DTC2
A	1255	PHE	-	expression tag	UNP P0DTC2
A	1256	GLU	-	expression tag	UNP P0DTC2
A	1257	LYS	-	expression tag	UNP P0DTC2
A	1258	GLY	-	expression tag	UNP P0DTC2
A	1259	GLY	-	expression tag	UNP P0DTC2
A	1260	GLY	-	expression tag	UNP P0DTC2
A	1261	SER	-	expression tag	UNP P0DTC2
A	1262	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1263	GLY	-	expression tag	UNP P0DTC2
A	1264	GLY	-	expression tag	UNP P0DTC2
A	1265	SER	-	expression tag	UNP P0DTC2
A	1266	GLY	-	expression tag	UNP P0DTC2
A	1267	GLY	-	expression tag	UNP P0DTC2
A	1268	SER	-	expression tag	UNP P0DTC2
A	1269	ALA	-	expression tag	UNP P0DTC2
A	1270	TRP	-	expression tag	UNP P0DTC2
A	1271	SER	-	expression tag	UNP P0DTC2
A	1272	HIS	-	expression tag	UNP P0DTC2
A	1273	PRO	-	expression tag	UNP P0DTC2
A	1274	GLN	-	expression tag	UNP P0DTC2
A	1275	PHE	-	expression tag	UNP P0DTC2
A	1276	GLU	-	expression tag	UNP P0DTC2
A	1277	LYS	-	expression tag	UNP P0DTC2
A	1278	GLY	-	expression tag	UNP P0DTC2
A	1279	GLY	-	expression tag	UNP P0DTC2
A	1280	SER	-	expression tag	UNP P0DTC2
A	1281	HIS	-	expression tag	UNP P0DTC2
A	1282	HIS	-	expression tag	UNP P0DTC2
A	1283	HIS	-	expression tag	UNP P0DTC2
A	1284	HIS	-	expression tag	UNP P0DTC2
A	1285	HIS	-	expression tag	UNP P0DTC2
A	1286	HIS	-	expression tag	UNP P0DTC2
A	1287	HIS	-	expression tag	UNP P0DTC2
A	1288	HIS	-	expression tag	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	682	GLY	ARG	conflict	UNP P0DTC2
B	683	SER	ARG	conflict	UNP P0DTC2
B	685	SER	ARG	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	TYR	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	GLU	-	expression tag	UNP P0DTC2
B	1216	ALA	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1219	ASP	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2
B	1223	TYR	-	expression tag	UNP P0DTC2
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2
B	1228	GLY	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	PHE	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	SER	-	expression tag	UNP P0DTC2
B	1239	GLY	-	expression tag	UNP P0DTC2
B	1240	LEU	-	expression tag	UNP P0DTC2
B	1241	GLU	-	expression tag	UNP P0DTC2
B	1242	VAL	-	expression tag	UNP P0DTC2
B	1243	LEU	-	expression tag	UNP P0DTC2
B	1244	PHE	-	expression tag	UNP P0DTC2
B	1245	GLN	-	expression tag	UNP P0DTC2
B	1246	GLY	-	expression tag	UNP P0DTC2
B	1247	PRO	-	expression tag	UNP P0DTC2
B	1248	GLY	-	expression tag	UNP P0DTC2
B	1249	GLY	-	expression tag	UNP P0DTC2
B	1250	TRP	-	expression tag	UNP P0DTC2
B	1251	SER	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2
B	1253	PRO	-	expression tag	UNP P0DTC2
B	1254	GLN	-	expression tag	UNP P0DTC2
B	1255	PHE	-	expression tag	UNP P0DTC2
B	1256	GLU	-	expression tag	UNP P0DTC2
B	1257	LYS	-	expression tag	UNP P0DTC2
B	1258	GLY	-	expression tag	UNP P0DTC2
B	1259	GLY	-	expression tag	UNP P0DTC2
B	1260	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1261	SER	-	expression tag	UNP P0DTC2
B	1262	GLY	-	expression tag	UNP P0DTC2
B	1263	GLY	-	expression tag	UNP P0DTC2
B	1264	GLY	-	expression tag	UNP P0DTC2
B	1265	SER	-	expression tag	UNP P0DTC2
B	1266	GLY	-	expression tag	UNP P0DTC2
B	1267	GLY	-	expression tag	UNP P0DTC2
B	1268	SER	-	expression tag	UNP P0DTC2
B	1269	ALA	-	expression tag	UNP P0DTC2
B	1270	TRP	-	expression tag	UNP P0DTC2
B	1271	SER	-	expression tag	UNP P0DTC2
B	1272	HIS	-	expression tag	UNP P0DTC2
B	1273	PRO	-	expression tag	UNP P0DTC2
B	1274	GLN	-	expression tag	UNP P0DTC2
B	1275	PHE	-	expression tag	UNP P0DTC2
B	1276	GLU	-	expression tag	UNP P0DTC2
B	1277	LYS	-	expression tag	UNP P0DTC2
B	1278	GLY	-	expression tag	UNP P0DTC2
B	1279	GLY	-	expression tag	UNP P0DTC2
B	1280	SER	-	expression tag	UNP P0DTC2
B	1281	HIS	-	expression tag	UNP P0DTC2
B	1282	HIS	-	expression tag	UNP P0DTC2
B	1283	HIS	-	expression tag	UNP P0DTC2
B	1284	HIS	-	expression tag	UNP P0DTC2
B	1285	HIS	-	expression tag	UNP P0DTC2
B	1286	HIS	-	expression tag	UNP P0DTC2
B	1287	HIS	-	expression tag	UNP P0DTC2
B	1288	HIS	-	expression tag	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	682	GLY	ARG	conflict	UNP P0DTC2
C	683	SER	ARG	conflict	UNP P0DTC2
C	685	SER	ARG	conflict	UNP P0DTC2
C	986	PRO	LYS	conflict	UNP P0DTC2
C	987	PRO	VAL	conflict	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
C	1224	VAL	-	expression tag	UNP P0DTC2
C	1225	ARG	-	expression tag	UNP P0DTC2
C	1226	LYS	-	expression tag	UNP P0DTC2
C	1227	ASP	-	expression tag	UNP P0DTC2
C	1228	GLY	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2
C	1230	TRP	-	expression tag	UNP P0DTC2
C	1231	VAL	-	expression tag	UNP P0DTC2
C	1232	PHE	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	SER	-	expression tag	UNP P0DTC2
C	1235	THR	-	expression tag	UNP P0DTC2
C	1236	PHE	-	expression tag	UNP P0DTC2
C	1237	LEU	-	expression tag	UNP P0DTC2
C	1238	SER	-	expression tag	UNP P0DTC2
C	1239	GLY	-	expression tag	UNP P0DTC2
C	1240	LEU	-	expression tag	UNP P0DTC2
C	1241	GLU	-	expression tag	UNP P0DTC2
C	1242	VAL	-	expression tag	UNP P0DTC2
C	1243	LEU	-	expression tag	UNP P0DTC2
C	1244	PHE	-	expression tag	UNP P0DTC2
C	1245	GLN	-	expression tag	UNP P0DTC2
C	1246	GLY	-	expression tag	UNP P0DTC2
C	1247	PRO	-	expression tag	UNP P0DTC2
C	1248	GLY	-	expression tag	UNP P0DTC2
C	1249	GLY	-	expression tag	UNP P0DTC2
C	1250	TRP	-	expression tag	UNP P0DTC2
C	1251	SER	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	PRO	-	expression tag	UNP P0DTC2
C	1254	GLN	-	expression tag	UNP P0DTC2
C	1255	PHE	-	expression tag	UNP P0DTC2
C	1256	GLU	-	expression tag	UNP P0DTC2
C	1257	LYS	-	expression tag	UNP P0DTC2
C	1258	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1259	GLY	-	expression tag	UNP P0DTC2
C	1260	GLY	-	expression tag	UNP P0DTC2
C	1261	SER	-	expression tag	UNP P0DTC2
C	1262	GLY	-	expression tag	UNP P0DTC2
C	1263	GLY	-	expression tag	UNP P0DTC2
C	1264	GLY	-	expression tag	UNP P0DTC2
C	1265	SER	-	expression tag	UNP P0DTC2
C	1266	GLY	-	expression tag	UNP P0DTC2
C	1267	GLY	-	expression tag	UNP P0DTC2
C	1268	SER	-	expression tag	UNP P0DTC2
C	1269	ALA	-	expression tag	UNP P0DTC2
C	1270	TRP	-	expression tag	UNP P0DTC2
C	1271	SER	-	expression tag	UNP P0DTC2
C	1272	HIS	-	expression tag	UNP P0DTC2
C	1273	PRO	-	expression tag	UNP P0DTC2
C	1274	GLN	-	expression tag	UNP P0DTC2
C	1275	PHE	-	expression tag	UNP P0DTC2
C	1276	GLU	-	expression tag	UNP P0DTC2
C	1277	LYS	-	expression tag	UNP P0DTC2
C	1278	GLY	-	expression tag	UNP P0DTC2
C	1279	GLY	-	expression tag	UNP P0DTC2
C	1280	SER	-	expression tag	UNP P0DTC2
C	1281	HIS	-	expression tag	UNP P0DTC2
C	1282	HIS	-	expression tag	UNP P0DTC2
C	1283	HIS	-	expression tag	UNP P0DTC2
C	1284	HIS	-	expression tag	UNP P0DTC2
C	1285	HIS	-	expression tag	UNP P0DTC2
C	1286	HIS	-	expression tag	UNP P0DTC2
C	1287	HIS	-	expression tag	UNP P0DTC2
C	1288	HIS	-	expression tag	UNP P0DTC2
J	614	GLY	ASP	variant	UNP P0DTC2
J	682	GLY	ARG	conflict	UNP P0DTC2
J	683	SER	ARG	conflict	UNP P0DTC2
J	685	SER	ARG	conflict	UNP P0DTC2
J	986	PRO	LYS	conflict	UNP P0DTC2
J	987	PRO	VAL	conflict	UNP P0DTC2
J	1209	GLY	-	expression tag	UNP P0DTC2
J	1210	SER	-	expression tag	UNP P0DTC2
J	1211	GLY	-	expression tag	UNP P0DTC2
J	1212	TYR	-	expression tag	UNP P0DTC2
J	1213	ILE	-	expression tag	UNP P0DTC2
J	1214	PRO	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1215	GLU	-	expression tag	UNP P0DTC2
J	1216	ALA	-	expression tag	UNP P0DTC2
J	1217	PRO	-	expression tag	UNP P0DTC2
J	1218	ARG	-	expression tag	UNP P0DTC2
J	1219	ASP	-	expression tag	UNP P0DTC2
J	1220	GLY	-	expression tag	UNP P0DTC2
J	1221	GLN	-	expression tag	UNP P0DTC2
J	1222	ALA	-	expression tag	UNP P0DTC2
J	1223	TYR	-	expression tag	UNP P0DTC2
J	1224	VAL	-	expression tag	UNP P0DTC2
J	1225	ARG	-	expression tag	UNP P0DTC2
J	1226	LYS	-	expression tag	UNP P0DTC2
J	1227	ASP	-	expression tag	UNP P0DTC2
J	1228	GLY	-	expression tag	UNP P0DTC2
J	1229	GLU	-	expression tag	UNP P0DTC2
J	1230	TRP	-	expression tag	UNP P0DTC2
J	1231	VAL	-	expression tag	UNP P0DTC2
J	1232	PHE	-	expression tag	UNP P0DTC2
J	1233	LEU	-	expression tag	UNP P0DTC2
J	1234	SER	-	expression tag	UNP P0DTC2
J	1235	THR	-	expression tag	UNP P0DTC2
J	1236	PHE	-	expression tag	UNP P0DTC2
J	1237	LEU	-	expression tag	UNP P0DTC2
J	1238	SER	-	expression tag	UNP P0DTC2
J	1239	GLY	-	expression tag	UNP P0DTC2
J	1240	LEU	-	expression tag	UNP P0DTC2
J	1241	GLU	-	expression tag	UNP P0DTC2
J	1242	VAL	-	expression tag	UNP P0DTC2
J	1243	LEU	-	expression tag	UNP P0DTC2
J	1244	PHE	-	expression tag	UNP P0DTC2
J	1245	GLN	-	expression tag	UNP P0DTC2
J	1246	GLY	-	expression tag	UNP P0DTC2
J	1247	PRO	-	expression tag	UNP P0DTC2
J	1248	GLY	-	expression tag	UNP P0DTC2
J	1249	GLY	-	expression tag	UNP P0DTC2
J	1250	TRP	-	expression tag	UNP P0DTC2
J	1251	SER	-	expression tag	UNP P0DTC2
J	1252	HIS	-	expression tag	UNP P0DTC2
J	1253	PRO	-	expression tag	UNP P0DTC2
J	1254	GLN	-	expression tag	UNP P0DTC2
J	1255	PHE	-	expression tag	UNP P0DTC2
J	1256	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1257	LYS	-	expression tag	UNP P0DTC2
J	1258	GLY	-	expression tag	UNP P0DTC2
J	1259	GLY	-	expression tag	UNP P0DTC2
J	1260	GLY	-	expression tag	UNP P0DTC2
J	1261	SER	-	expression tag	UNP P0DTC2
J	1262	GLY	-	expression tag	UNP P0DTC2
J	1263	GLY	-	expression tag	UNP P0DTC2
J	1264	GLY	-	expression tag	UNP P0DTC2
J	1265	SER	-	expression tag	UNP P0DTC2
J	1266	GLY	-	expression tag	UNP P0DTC2
J	1267	GLY	-	expression tag	UNP P0DTC2
J	1268	SER	-	expression tag	UNP P0DTC2
J	1269	ALA	-	expression tag	UNP P0DTC2
J	1270	TRP	-	expression tag	UNP P0DTC2
J	1271	SER	-	expression tag	UNP P0DTC2
J	1272	HIS	-	expression tag	UNP P0DTC2
J	1273	PRO	-	expression tag	UNP P0DTC2
J	1274	GLN	-	expression tag	UNP P0DTC2
J	1275	PHE	-	expression tag	UNP P0DTC2
J	1276	GLU	-	expression tag	UNP P0DTC2
J	1277	LYS	-	expression tag	UNP P0DTC2
J	1278	GLY	-	expression tag	UNP P0DTC2
J	1279	GLY	-	expression tag	UNP P0DTC2
J	1280	SER	-	expression tag	UNP P0DTC2
J	1281	HIS	-	expression tag	UNP P0DTC2
J	1282	HIS	-	expression tag	UNP P0DTC2
J	1283	HIS	-	expression tag	UNP P0DTC2
J	1284	HIS	-	expression tag	UNP P0DTC2
J	1285	HIS	-	expression tag	UNP P0DTC2
J	1286	HIS	-	expression tag	UNP P0DTC2
J	1287	HIS	-	expression tag	UNP P0DTC2
J	1288	HIS	-	expression tag	UNP P0DTC2
K	614	GLY	ASP	variant	UNP P0DTC2
K	682	GLY	ARG	conflict	UNP P0DTC2
K	683	SER	ARG	conflict	UNP P0DTC2
K	685	SER	ARG	conflict	UNP P0DTC2
K	986	PRO	LYS	conflict	UNP P0DTC2
K	987	PRO	VAL	conflict	UNP P0DTC2
K	1209	GLY	-	expression tag	UNP P0DTC2
K	1210	SER	-	expression tag	UNP P0DTC2
K	1211	GLY	-	expression tag	UNP P0DTC2
K	1212	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
K	1213	ILE	-	expression tag	UNP P0DTC2
K	1214	PRO	-	expression tag	UNP P0DTC2
K	1215	GLU	-	expression tag	UNP P0DTC2
K	1216	ALA	-	expression tag	UNP P0DTC2
K	1217	PRO	-	expression tag	UNP P0DTC2
K	1218	ARG	-	expression tag	UNP P0DTC2
K	1219	ASP	-	expression tag	UNP P0DTC2
K	1220	GLY	-	expression tag	UNP P0DTC2
K	1221	GLN	-	expression tag	UNP P0DTC2
K	1222	ALA	-	expression tag	UNP P0DTC2
K	1223	TYR	-	expression tag	UNP P0DTC2
K	1224	VAL	-	expression tag	UNP P0DTC2
K	1225	ARG	-	expression tag	UNP P0DTC2
K	1226	LYS	-	expression tag	UNP P0DTC2
K	1227	ASP	-	expression tag	UNP P0DTC2
K	1228	GLY	-	expression tag	UNP P0DTC2
K	1229	GLU	-	expression tag	UNP P0DTC2
K	1230	TRP	-	expression tag	UNP P0DTC2
K	1231	VAL	-	expression tag	UNP P0DTC2
K	1232	PHE	-	expression tag	UNP P0DTC2
K	1233	LEU	-	expression tag	UNP P0DTC2
K	1234	SER	-	expression tag	UNP P0DTC2
K	1235	THR	-	expression tag	UNP P0DTC2
K	1236	PHE	-	expression tag	UNP P0DTC2
K	1237	LEU	-	expression tag	UNP P0DTC2
K	1238	SER	-	expression tag	UNP P0DTC2
K	1239	GLY	-	expression tag	UNP P0DTC2
K	1240	LEU	-	expression tag	UNP P0DTC2
K	1241	GLU	-	expression tag	UNP P0DTC2
K	1242	VAL	-	expression tag	UNP P0DTC2
K	1243	LEU	-	expression tag	UNP P0DTC2
K	1244	PHE	-	expression tag	UNP P0DTC2
K	1245	GLN	-	expression tag	UNP P0DTC2
K	1246	GLY	-	expression tag	UNP P0DTC2
K	1247	PRO	-	expression tag	UNP P0DTC2
K	1248	GLY	-	expression tag	UNP P0DTC2
K	1249	GLY	-	expression tag	UNP P0DTC2
K	1250	TRP	-	expression tag	UNP P0DTC2
K	1251	SER	-	expression tag	UNP P0DTC2
K	1252	HIS	-	expression tag	UNP P0DTC2
K	1253	PRO	-	expression tag	UNP P0DTC2
K	1254	GLN	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
K	1255	PHE	-	expression tag	UNP P0DTC2
K	1256	GLU	-	expression tag	UNP P0DTC2
K	1257	LYS	-	expression tag	UNP P0DTC2
K	1258	GLY	-	expression tag	UNP P0DTC2
K	1259	GLY	-	expression tag	UNP P0DTC2
K	1260	GLY	-	expression tag	UNP P0DTC2
K	1261	SER	-	expression tag	UNP P0DTC2
K	1262	GLY	-	expression tag	UNP P0DTC2
K	1263	GLY	-	expression tag	UNP P0DTC2
K	1264	GLY	-	expression tag	UNP P0DTC2
K	1265	SER	-	expression tag	UNP P0DTC2
K	1266	GLY	-	expression tag	UNP P0DTC2
K	1267	GLY	-	expression tag	UNP P0DTC2
K	1268	SER	-	expression tag	UNP P0DTC2
K	1269	ALA	-	expression tag	UNP P0DTC2
K	1270	TRP	-	expression tag	UNP P0DTC2
K	1271	SER	-	expression tag	UNP P0DTC2
K	1272	HIS	-	expression tag	UNP P0DTC2
K	1273	PRO	-	expression tag	UNP P0DTC2
K	1274	GLN	-	expression tag	UNP P0DTC2
K	1275	PHE	-	expression tag	UNP P0DTC2
K	1276	GLU	-	expression tag	UNP P0DTC2
K	1277	LYS	-	expression tag	UNP P0DTC2
K	1278	GLY	-	expression tag	UNP P0DTC2
K	1279	GLY	-	expression tag	UNP P0DTC2
K	1280	SER	-	expression tag	UNP P0DTC2
K	1281	HIS	-	expression tag	UNP P0DTC2
K	1282	HIS	-	expression tag	UNP P0DTC2
K	1283	HIS	-	expression tag	UNP P0DTC2
K	1284	HIS	-	expression tag	UNP P0DTC2
K	1285	HIS	-	expression tag	UNP P0DTC2
K	1286	HIS	-	expression tag	UNP P0DTC2
K	1287	HIS	-	expression tag	UNP P0DTC2
K	1288	HIS	-	expression tag	UNP P0DTC2
L	614	GLY	ASP	variant	UNP P0DTC2
L	682	GLY	ARG	conflict	UNP P0DTC2
L	683	SER	ARG	conflict	UNP P0DTC2
L	685	SER	ARG	conflict	UNP P0DTC2
L	986	PRO	LYS	conflict	UNP P0DTC2
L	987	PRO	VAL	conflict	UNP P0DTC2
L	1209	GLY	-	expression tag	UNP P0DTC2
L	1210	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
L	1211	GLY	-	expression tag	UNP P0DTC2
L	1212	TYR	-	expression tag	UNP P0DTC2
L	1213	ILE	-	expression tag	UNP P0DTC2
L	1214	PRO	-	expression tag	UNP P0DTC2
L	1215	GLU	-	expression tag	UNP P0DTC2
L	1216	ALA	-	expression tag	UNP P0DTC2
L	1217	PRO	-	expression tag	UNP P0DTC2
L	1218	ARG	-	expression tag	UNP P0DTC2
L	1219	ASP	-	expression tag	UNP P0DTC2
L	1220	GLY	-	expression tag	UNP P0DTC2
L	1221	GLN	-	expression tag	UNP P0DTC2
L	1222	ALA	-	expression tag	UNP P0DTC2
L	1223	TYR	-	expression tag	UNP P0DTC2
L	1224	VAL	-	expression tag	UNP P0DTC2
L	1225	ARG	-	expression tag	UNP P0DTC2
L	1226	LYS	-	expression tag	UNP P0DTC2
L	1227	ASP	-	expression tag	UNP P0DTC2
L	1228	GLY	-	expression tag	UNP P0DTC2
L	1229	GLU	-	expression tag	UNP P0DTC2
L	1230	TRP	-	expression tag	UNP P0DTC2
L	1231	VAL	-	expression tag	UNP P0DTC2
L	1232	PHE	-	expression tag	UNP P0DTC2
L	1233	LEU	-	expression tag	UNP P0DTC2
L	1234	SER	-	expression tag	UNP P0DTC2
L	1235	THR	-	expression tag	UNP P0DTC2
L	1236	PHE	-	expression tag	UNP P0DTC2
L	1237	LEU	-	expression tag	UNP P0DTC2
L	1238	SER	-	expression tag	UNP P0DTC2
L	1239	GLY	-	expression tag	UNP P0DTC2
L	1240	LEU	-	expression tag	UNP P0DTC2
L	1241	GLU	-	expression tag	UNP P0DTC2
L	1242	VAL	-	expression tag	UNP P0DTC2
L	1243	LEU	-	expression tag	UNP P0DTC2
L	1244	PHE	-	expression tag	UNP P0DTC2
L	1245	GLN	-	expression tag	UNP P0DTC2
L	1246	GLY	-	expression tag	UNP P0DTC2
L	1247	PRO	-	expression tag	UNP P0DTC2
L	1248	GLY	-	expression tag	UNP P0DTC2
L	1249	GLY	-	expression tag	UNP P0DTC2
L	1250	TRP	-	expression tag	UNP P0DTC2
L	1251	SER	-	expression tag	UNP P0DTC2
L	1252	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
L	1253	PRO	-	expression tag	UNP P0DTC2
L	1254	GLN	-	expression tag	UNP P0DTC2
L	1255	PHE	-	expression tag	UNP P0DTC2
L	1256	GLU	-	expression tag	UNP P0DTC2
L	1257	LYS	-	expression tag	UNP P0DTC2
L	1258	GLY	-	expression tag	UNP P0DTC2
L	1259	GLY	-	expression tag	UNP P0DTC2
L	1260	GLY	-	expression tag	UNP P0DTC2
L	1261	SER	-	expression tag	UNP P0DTC2
L	1262	GLY	-	expression tag	UNP P0DTC2
L	1263	GLY	-	expression tag	UNP P0DTC2
L	1264	GLY	-	expression tag	UNP P0DTC2
L	1265	SER	-	expression tag	UNP P0DTC2
L	1266	GLY	-	expression tag	UNP P0DTC2
L	1267	GLY	-	expression tag	UNP P0DTC2
L	1268	SER	-	expression tag	UNP P0DTC2
L	1269	ALA	-	expression tag	UNP P0DTC2
L	1270	TRP	-	expression tag	UNP P0DTC2
L	1271	SER	-	expression tag	UNP P0DTC2
L	1272	HIS	-	expression tag	UNP P0DTC2
L	1273	PRO	-	expression tag	UNP P0DTC2
L	1274	GLN	-	expression tag	UNP P0DTC2
L	1275	PHE	-	expression tag	UNP P0DTC2
L	1276	GLU	-	expression tag	UNP P0DTC2
L	1277	LYS	-	expression tag	UNP P0DTC2
L	1278	GLY	-	expression tag	UNP P0DTC2
L	1279	GLY	-	expression tag	UNP P0DTC2
L	1280	SER	-	expression tag	UNP P0DTC2
L	1281	HIS	-	expression tag	UNP P0DTC2
L	1282	HIS	-	expression tag	UNP P0DTC2
L	1283	HIS	-	expression tag	UNP P0DTC2
L	1284	HIS	-	expression tag	UNP P0DTC2
L	1285	HIS	-	expression tag	UNP P0DTC2
L	1286	HIS	-	expression tag	UNP P0DTC2
L	1287	HIS	-	expression tag	UNP P0DTC2
L	1288	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called mAb15 VH.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	225	Total	C	N	O	S	0	0
			1704	1077	289	331	7		

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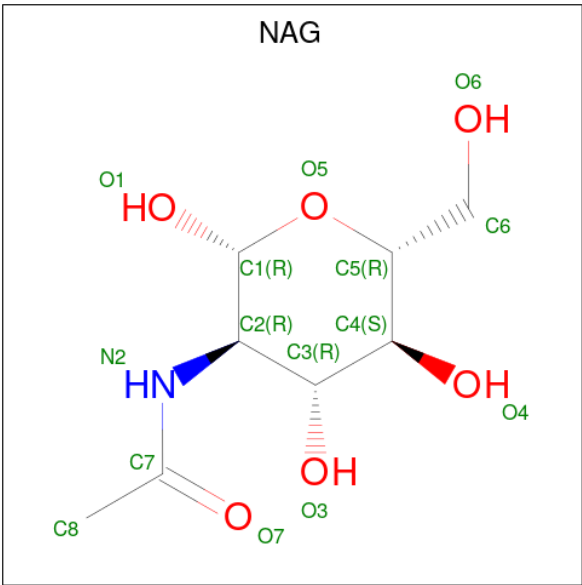
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	225	Total	C	N	O	S	0	0
			1704	1077	289	331	7		
2	H	225	Total	C	N	O	S	0	0
			1704	1077	289	331	7		
2	M	225	Total	C	N	O	S	0	0
			1704	1077	289	331	7		
2	O	225	Total	C	N	O	S	0	0
			1704	1077	289	331	7		
2	Q	225	Total	C	N	O	S	0	0
			1704	1077	289	331	7		

- Molecule 3 is a protein called mAb15 VL.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	215	Total	C	N	O	S	0	0
			1616	999	270	342	5		
3	G	215	Total	C	N	O	S	0	0
			1616	999	270	342	5		
3	I	215	Total	C	N	O	S	0	0
			1616	999	270	342	5		
3	N	215	Total	C	N	O	S	0	0
			1616	999	270	342	5		
3	P	215	Total	C	N	O	S	0	0
			1616	999	270	342	5		
3	R	215	Total	C	N	O	S	0	0
			1616	999	270	342	5		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	C	1	Total 14	C 8	N 1	O 5	0
4	C	1	Total 14	C 8	N 1	O 5	0
4	C	1	Total 14	C 8	N 1	O 5	0
4	C	1	Total 14	C 8	N 1	O 5	0
4	C	1	Total 14	C 8	N 1	O 5	0

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Mol	Chain	Residues	Atoms				AltConf
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	J	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	K	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	

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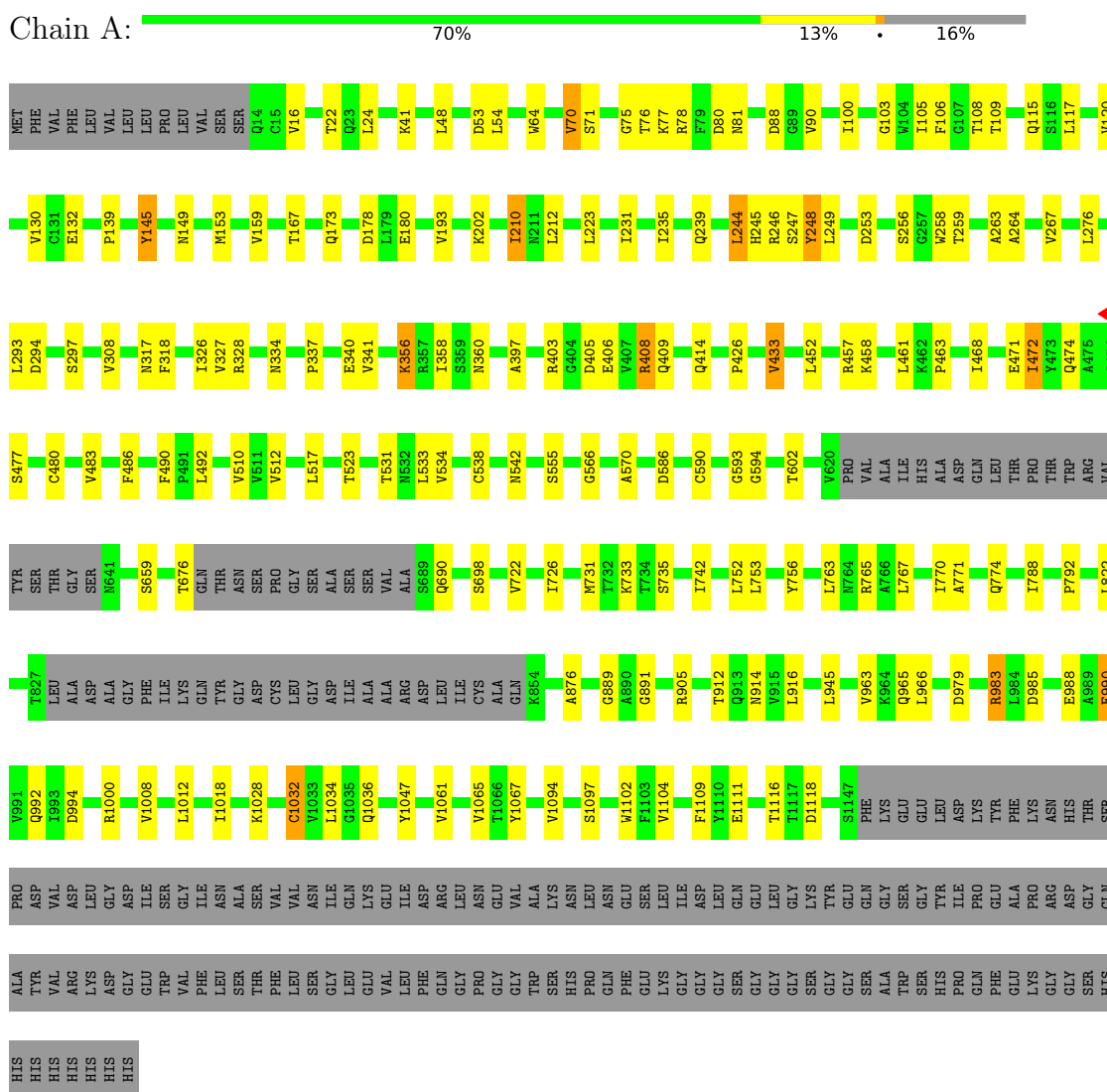
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Mol	Chain	Residues	Atoms				AltConf
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	
4	L	1	Total	C	N	O	0
			14	8	1	5	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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: Spike glycoprotein



• Molecule 1: Spike glycoprotein

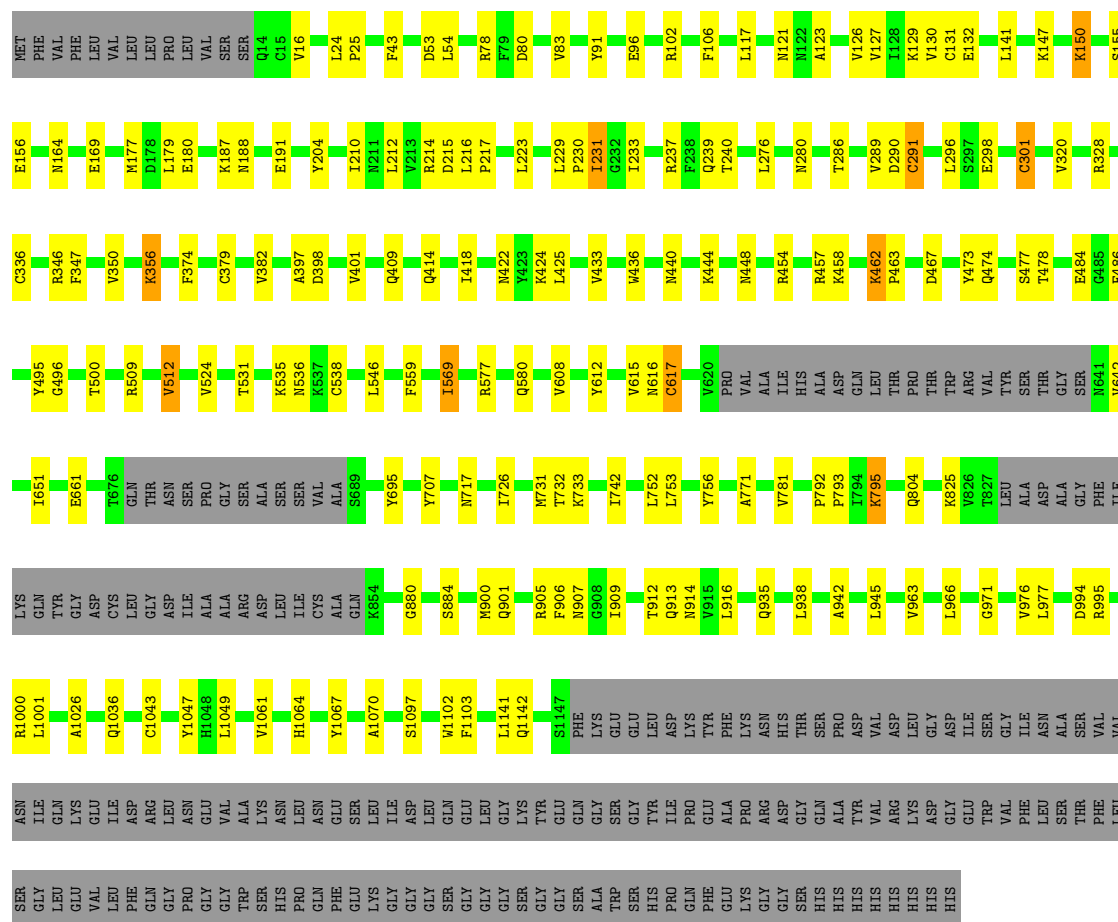


VAL	LEU	ILE	GLU	Q1036	Q1036	ILE	ALA	ALA	SER	K535	V350	N164	MET
PHE	ASP	GLY	ARG	C1043	C1043	ASP	ALA	GLY	PRO	K536	K356	E169	PHE
GLN	GLY	LEU	ARG	Y1047	Y1047	ASP	ALA	SER	ALA	C538	F374	E180	LEU
PRO	ASN	ASN	ASN	H1048	H1048	LEU	LEU	SER	SER	L546	A397	K187	VAL
GLY	GLY	GLU	GLU	L1049	L1049	ILE	ILE	SER	VAL	D398	D398		LEU
GLY	VAL	VAL	VAL	V1061	V1061	CYS	CYS	VAL	ALA	F559	Y204		LEU
TRP	ALA	ALA	ALA			ALA	ALA	ALA	ALA	Q409	Y204		PRO
SER	LYS	LYS	LYS			GLN	GLN	S689	S689	I569	Q409		LEU
HIS	ASN	ASN	ASN	H1064	H1064	K954	K954	Y695	Y695	R577	Q414	T210	VAL
PRO	PRO	LEU	ASN	Y1067	Y1067	G880	G880				Q414	N211	SER
GLN	ASN	ASN	ASN					Y707	Y707	Q580	I418	L212	SER
PHE	GLU	GLU	GLU	V1094	V1094	S884	S884	I726	I726	V608	M422	R214	Q14
GLU	SER	SER	SER	F1095	F1095					Y423	M422	D215	C15
LYS	LEU	LEU	LEU	V1096	V1096	M900	M900	M731	M731	K424	L425	L216	V16
GLY	ILE	ILE	ILE	S1097	S1097	Q901	Q901	T732	T732	Y612	L425	P217	M17
GLY	ASP	ASP	ASP					K733	K733	V615	V433	L223	P25
GLY	GLY	GLY	GLY	W1102	W1102	R905	R905	I742	I742	M616	V433		
GLY	GLY	GLY	GLY	F1103	F1103	F906	F906			C617	W436	I231	P39
GLY	GLY	GLY	GLY			N907	N907	L752	L752	V620	N440	G232	F43
GLY	SER	SER	SER	L1141	L1141	G908	G908	L763	L763	PRD	N440	I235	L48
GLY	LYS	LYS	LYS	Q1142	Q1142	I909	I909			VAL	K444	Q239	F55
GLY	TYR	TYR	TYR	S1147	S1147	T912	T912	Y756	Y756	ALA	K444	T240	
GLY	GLU	GLU	GLU	PHE	PHE	Q913	Q913	G757	G757	ILE	N448		
GLY	GLY	GLY	GLY	LYS	LYS	N914	N914	S758	S758	HIS			
GLY	GLY	GLY	GLY	GLU	GLU	V915	V915	L916	L916	ALA	R454	S255	R78
GLY	TRP	HIS	HIS	LEU	LEU	LEU	LEU	A771	A771	ASP	F456	V267	F79
PRO	PRO	ILE	ILE	ASP	ASP	Q935	Q935			GLN	R457		D80
GLN	GLN	PRO	PRO	LYS	LYS			V781	V781	LEU	K458		V90
PHE	PHE	GLU	GLU	TYR	TYR	L938	L938			THR	R457	L276	
GLU	GLU	ALA	ALA	PHE	PHE	ALA	ALA	P792	P792	THR	K458		
LYS	LYS	PRO	PRO	LYS	LYS	A942	A942	P793	P793	PRO	N280		R102
GLY	GLY	ARG	ARG	ASN	ASN			I794	I794	THR	P463	T286	G107
GLY	GLY	ASP	ASP	HIS	HIS	L945	L945	K795	K795	TRP			T108
SER	SER	GLY	GLY	THR	THR					ARG	D467		
HIS	HIS	GLN	GLN	SER	SER	V963	V963	Q804	Q804	VAL			
HIS	HIS	ALA	ALA	PRO	PRO					TYR	V289	N121	
HIS	HIS	TYR	TYR	ASP	ASP	L966	L966	K825	K825	SER	D290	N122	
HIS	HIS	VAL	VAL	VAL	VAL	V826	V826	V826	V826	THR	Y473		
HIS	HIS	ARG	ARG	ASP	ASP	ASP	ASP	G971	G971	GLY	L293	V126	
HIS	HIS	LYS	LYS	LEU	LEU	LEU	LEU			SER	T478		
HIS	HIS	ASP	ASP	GLY	GLY	V976	V976	N641	N641	ALA	L296	K129	
HIS	HIS	GLY	GLY	ASP	ASP	L977	L977	V642	V642	ASP	C488	V130	
		GLU	GLU	ILE	ILE	ALA	ALA			ALA	C301	C131	
		TRP	TRP	SER	SER	E988	E988	I651	I651	GLY	F490	E132	
		VAL	VAL	GLY	GLY			PHE	PHE	PHE	P491	F306	
		PHE	PHE	ILE	ILE	Q992	Q992	V656	V656	ILE	G496	L141	
		LEU	LEU	ASN	ASN	I993	I993	N657	N657	LYS	T500	K147	
		SER	SER	ALA	ALA	D994	D994	N658	N658	GLN	V320	N148	
		THR	THR	SER	SER	R995	R995			TYR	R328	N149	
		PHE	PHE	VAL	VAL			GLY	GLY	GLY	V512	K150	
		LEU	LEU	VAL	VAL	R1000	R1000	ASP	ASP	CYS	C336		
		SER	SER	ASN	ASN	L1001	L1001			LEU	V524	S155	
		GLY	GLY	ILE	ILE			GLN	GLN	THR	F347	E156	
		LEU	LEU	LYS	LYS	A1026	A1026	ASN	ASN	ASN	T531		

● Molecule 1: Spike glycoprotein

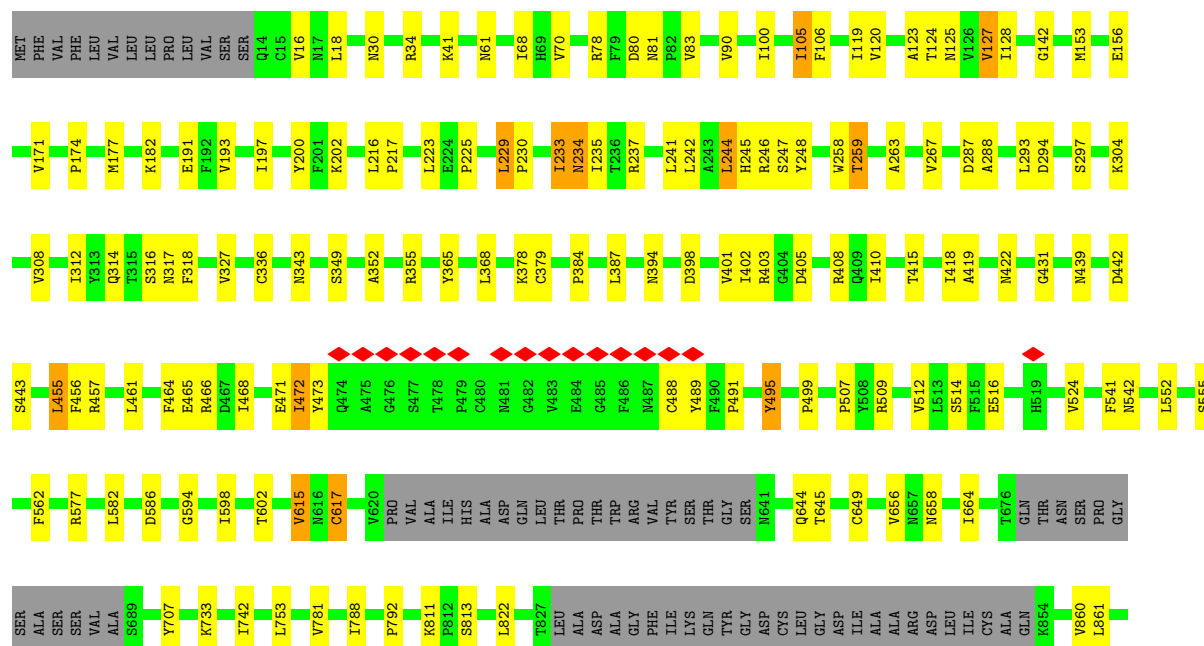


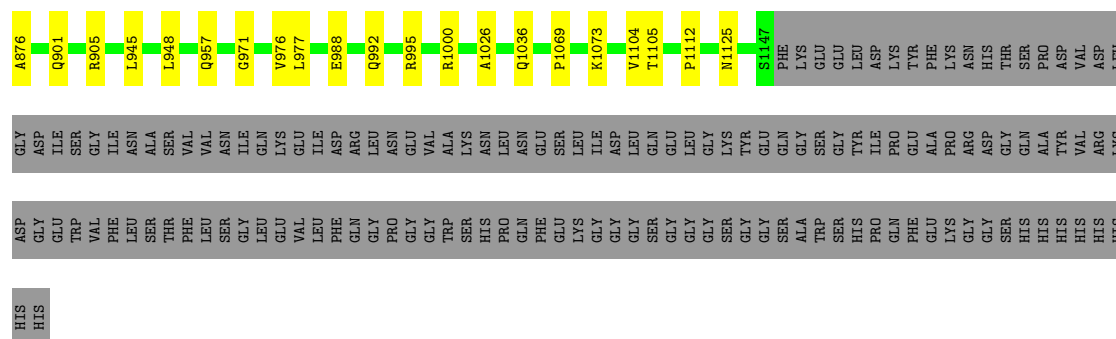
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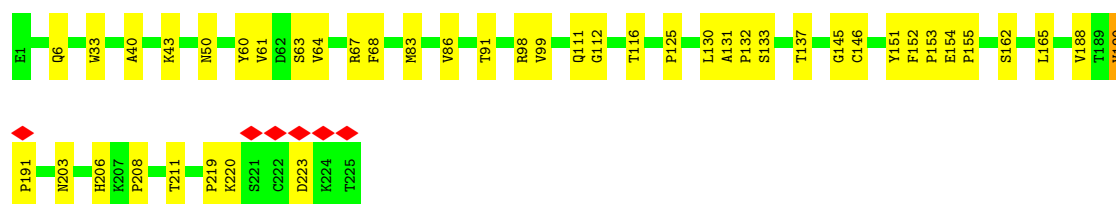
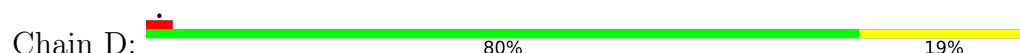
• Molecule 1: Spike glycoprotein

Chain L: 70% 12% 16%

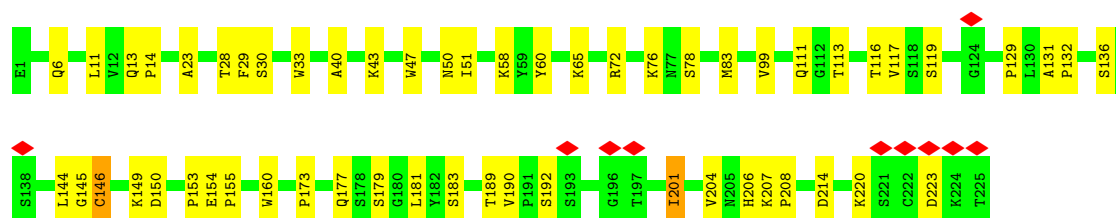
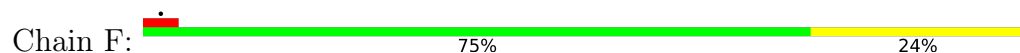




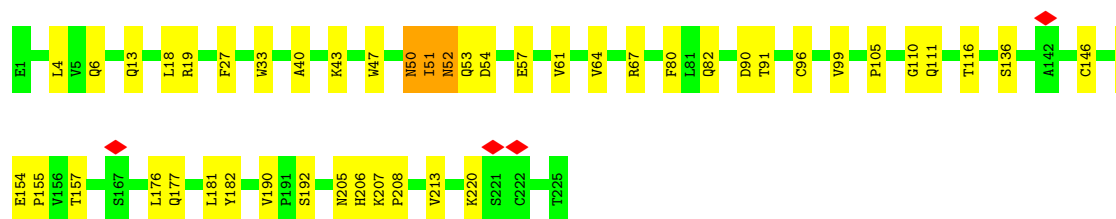
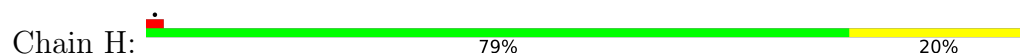
• Molecule 2: mAb15 VH



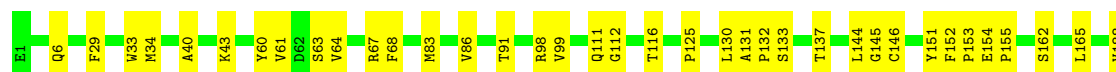
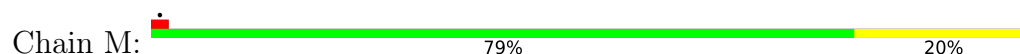
• Molecule 2: mAb15 VH



• Molecule 2: mAb15 VH

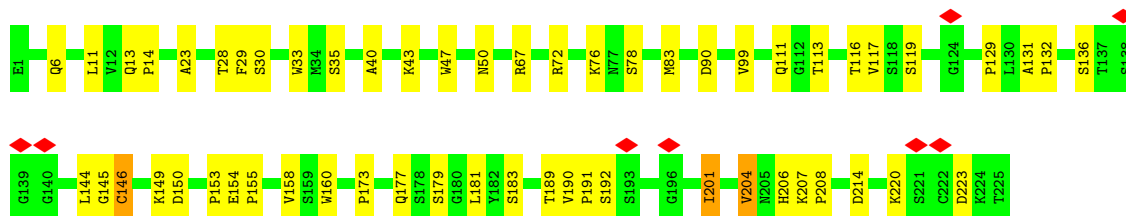
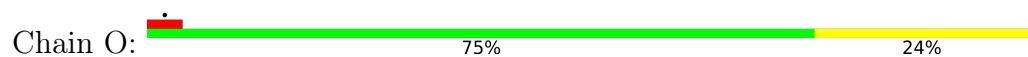


• Molecule 2: mAb15 VH

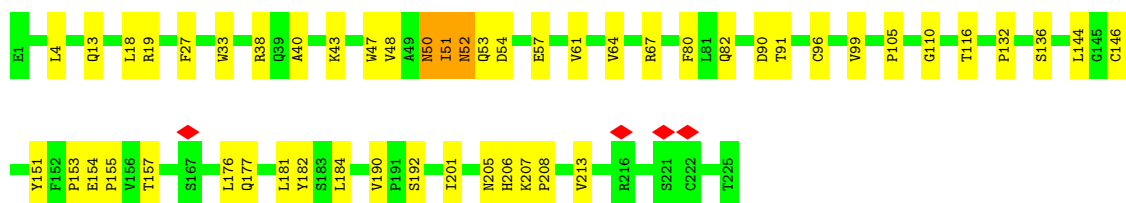
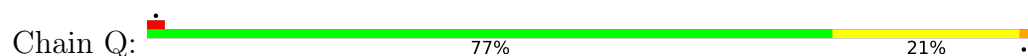




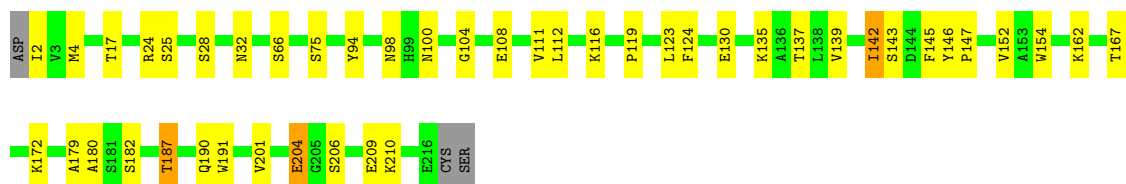
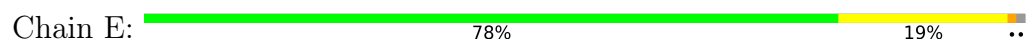
- Molecule 2: mAb15 VH



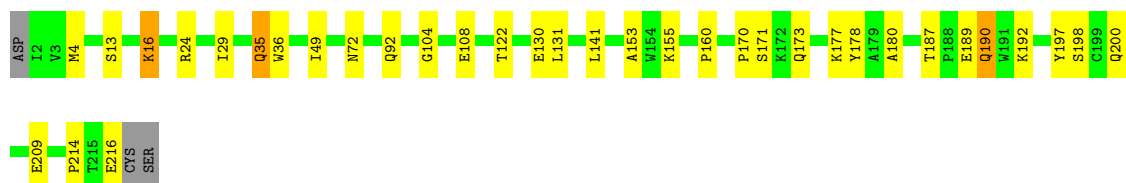
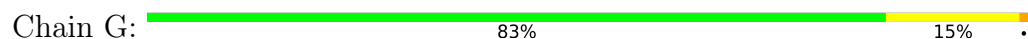
- Molecule 2: mAb15 VH



- Molecule 3: mAb15 VL

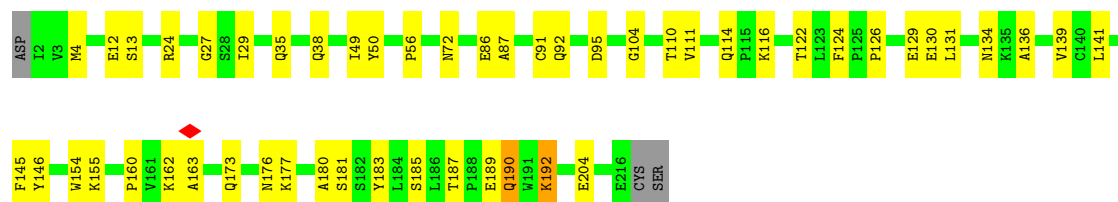


- Molecule 3: mAb15 VL



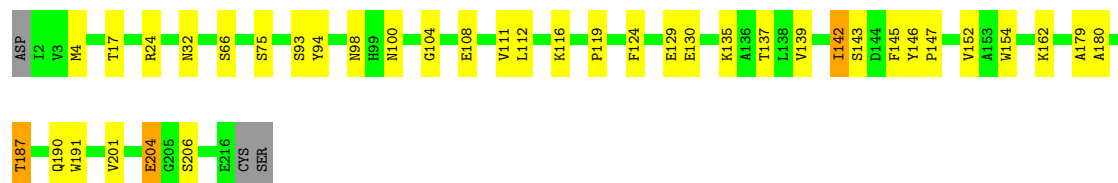
- Molecule 3: mAb15 VL





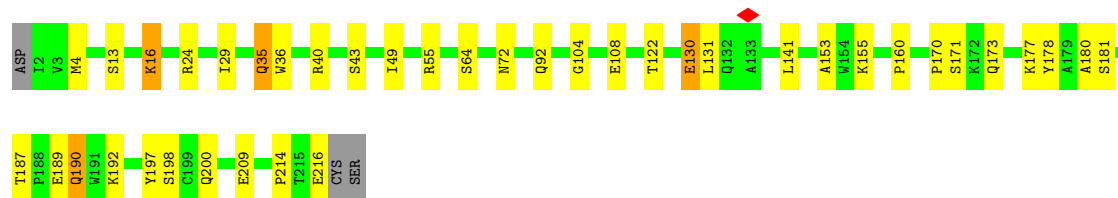
• Molecule 3: mAb15 VL

Chain N: 81% 16% ..



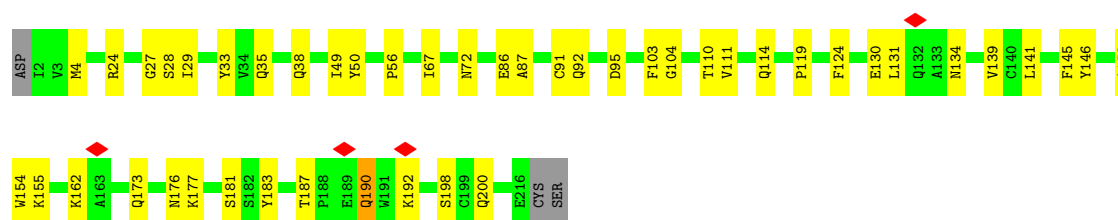
• Molecule 3: mAb15 VL

Chain P: 80% 17% ..



• Molecule 3: mAb15 VL

Chain R: 78% 21% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	188942	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 ($e^-/\text{\AA}^2$)	61	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	513.60004, 513.60004, 513.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.09	0/8534	0.25	0/11626
1	B	0.11	0/8534	0.28	1/11626 (0.0%)
1	C	0.11	0/8534	0.26	1/11626 (0.0%)
1	J	0.11	0/8534	0.26	0/11626
1	K	0.11	0/8534	0.26	0/11626
1	L	0.12	0/8534	0.27	0/11626
2	D	0.10	0/1748	0.29	0/2379
2	F	0.10	0/1748	0.26	0/2379
2	H	0.10	0/1748	0.26	0/2379
2	M	0.10	0/1748	0.29	0/2379
2	O	0.10	0/1748	0.26	0/2379
2	Q	0.10	0/1748	0.26	0/2379
3	E	0.08	0/1654	0.25	0/2260
3	G	0.08	0/1654	0.23	0/2260
3	I	0.08	0/1654	0.24	0/2260
3	N	0.08	0/1654	0.24	0/2260
3	P	0.08	0/1654	0.24	0/2260
3	R	0.08	0/1654	0.24	0/2260
All	All	0.10	0/71616	0.26	2/97590 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	293	LEU	N-CA-C	-7.45	105.09	114.56
1	C	613	GLN	N-CA-C	5.50	117.68	109.59

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	8338	0	8069	95	0
1	B	8338	0	8065	86	0
1	C	8338	0	8065	91	0
1	J	8338	0	8069	92	0
1	K	8338	0	8065	90	0
1	L	8338	0	8065	93	0
2	D	1704	0	1657	24	0
2	F	1704	0	1657	30	0
2	H	1704	0	1657	26	0
2	M	1704	0	1657	27	0
2	O	1704	0	1657	33	0
2	Q	1704	0	1657	30	0
3	E	1616	0	1538	22	0
3	G	1616	0	1538	16	0
3	I	1616	0	1538	27	0
3	N	1616	0	1538	20	0
3	P	1616	0	1538	21	0
3	R	1616	0	1538	24	0
4	A	210	0	195	1	0
4	B	210	0	195	1	0
4	C	210	0	195	5	0
4	J	210	0	195	1	0
4	K	210	0	195	2	0
4	L	210	0	195	6	0
All	All	71208	0	68738	819	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 6.

The worst 5 of 819 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:K:477:SER:HB2	1:K:486:PHE:CE2	2.17	0.80
2:D:206:HIS:HB3	2:D:211:THR:HB	1.71	0.73
2:M:206:HIS:HB3	2:M:211:THR:HB	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:LYS:HB2	1:B:397:ALA:HB3	1.73	0.71
2:H:52:ASN:HD22	2:H:53:GLN:H	1.38	0.71

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	A	1068/1288 (83%)	1019 (95%)	49 (5%)	0	100	100
1	B	1068/1288 (83%)	1018 (95%)	50 (5%)	0	100	100
1	C	1068/1288 (83%)	1020 (96%)	48 (4%)	0	100	100
1	J	1068/1288 (83%)	1017 (95%)	50 (5%)	1 (0%)	48	83
1	K	1068/1288 (83%)	1022 (96%)	46 (4%)	0	100	100
1	L	1068/1288 (83%)	1017 (95%)	51 (5%)	0	100	100
2	D	223/225 (99%)	202 (91%)	21 (9%)	0	100	100
2	F	223/225 (99%)	195 (87%)	28 (13%)	0	100	100
2	H	223/225 (99%)	199 (89%)	24 (11%)	0	100	100
2	M	223/225 (99%)	202 (91%)	21 (9%)	0	100	100
2	O	223/225 (99%)	195 (87%)	28 (13%)	0	100	100
2	Q	223/225 (99%)	199 (89%)	24 (11%)	0	100	100
3	E	213/218 (98%)	196 (92%)	17 (8%)	0	100	100
3	G	213/218 (98%)	195 (92%)	18 (8%)	0	100	100
3	I	213/218 (98%)	194 (91%)	19 (9%)	0	100	100
3	N	213/218 (98%)	198 (93%)	15 (7%)	0	100	100
3	P	213/218 (98%)	195 (92%)	18 (8%)	0	100	100
3	R	213/218 (98%)	193 (91%)	20 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9024/10386 (87%)	8476 (94%)	547 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	292	ALA

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	922/1111 (83%)	891 (97%)	31 (3%)	32	54
1	B	922/1111 (83%)	885 (96%)	37 (4%)	28	49
1	C	922/1111 (83%)	889 (96%)	33 (4%)	31	52
1	J	922/1111 (83%)	890 (96%)	32 (4%)	32	53
1	K	922/1111 (83%)	887 (96%)	35 (4%)	29	51
1	L	922/1111 (83%)	889 (96%)	33 (4%)	31	52
2	D	189/189 (100%)	180 (95%)	9 (5%)	23	45
2	F	189/189 (100%)	181 (96%)	8 (4%)	26	48
2	H	189/189 (100%)	180 (95%)	9 (5%)	23	45
2	M	189/189 (100%)	181 (96%)	8 (4%)	26	48
2	O	189/189 (100%)	181 (96%)	8 (4%)	26	48
2	Q	189/189 (100%)	180 (95%)	9 (5%)	23	45
3	E	188/191 (98%)	178 (95%)	10 (5%)	20	42
3	G	188/191 (98%)	179 (95%)	9 (5%)	23	45
3	I	188/191 (98%)	181 (96%)	7 (4%)	30	51
3	N	188/191 (98%)	180 (96%)	8 (4%)	26	48
3	P	188/191 (98%)	179 (95%)	9 (5%)	23	45
3	R	188/191 (98%)	180 (96%)	8 (4%)	26	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7794/8946 (87%)	7491 (96%)	303 (4%)	30 50

5 of 303 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	234	ASN
2	Q	13	GLN
1	L	378	LYS
2	M	220	LYS
3	R	134	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 222 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	360	ASN
3	R	200	GLN
1	K	280	ASN
3	R	175	ASN
2	O	206	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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

90 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	A	1313	1	14,14,15	0.21	0	17,19,21	0.42	0
4	NAG	C	1306	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	B	1304	1	14,14,15	0.22	0	17,19,21	0.45	0
4	NAG	K	1307	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	B	1312	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	B	1301	1	14,14,15	0.25	0	17,19,21	0.46	0
4	NAG	A	1312	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	B	1303	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	A	1314	1	14,14,15	0.22	0	17,19,21	0.46	0
4	NAG	A	1307	1	14,14,15	0.35	0	17,19,21	0.42	0
4	NAG	K	1302	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	L	1301	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	C	1308	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	L	1306	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	B	1315	1	14,14,15	0.22	0	17,19,21	0.42	0
4	NAG	K	1315	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	A	1305	1	14,14,15	0.36	0	17,19,21	0.43	0
4	NAG	A	1301	1	14,14,15	0.27	0	17,19,21	0.45	0
4	NAG	K	1304	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	J	1301	1	14,14,15	0.27	0	17,19,21	0.45	0
4	NAG	A	1303	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	A	1306	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	C	1304	1	14,14,15	0.28	0	17,19,21	0.55	0
4	NAG	J	1306	1	14,14,15	0.34	0	17,19,21	0.42	0
4	NAG	L	1302	1	14,14,15	0.25	0	17,19,21	0.40	0
4	NAG	C	1314	1	14,14,15	0.22	0	17,19,21	0.45	0
4	NAG	C	1315	1	14,14,15	0.49	0	17,19,21	1.34	2 (11%)
4	NAG	C	1302	1	14,14,15	0.24	0	17,19,21	0.39	0
4	NAG	K	1303	1	14,14,15	0.22	0	17,19,21	0.45	0
4	NAG	B	1310	1	14,14,15	0.42	0	17,19,21	1.26	1 (5%)
4	NAG	B	1314	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	L	1308	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	L	1304	1	14,14,15	0.27	0	17,19,21	0.55	0
4	NAG	C	1312	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	L	1315	1	14,14,15	0.48	0	17,19,21	1.34	2 (11%)
4	NAG	A	1309	1	14,14,15	0.29	0	17,19,21	0.56	0
4	NAG	C	1303	1	14,14,15	0.28	0	17,19,21	0.55	0
4	NAG	C	1310	1	14,14,15	0.23	0	17,19,21	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	L	1312	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	C	1309	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	J	1311	1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	J	1307	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	A	1302	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	J	1302	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	L	1307	1	14,14,15	0.21	0	17,19,21	0.45	0
4	NAG	K	1301	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	K	1312	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	J	1315	1	14,14,15	0.33	0	17,19,21	0.71	0
4	NAG	K	1305	1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	C	1307	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	B	1308	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	K	1306	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	J	1308	1	14,14,15	0.28	0	17,19,21	0.56	0
4	NAG	J	1304	1	14,14,15	0.35	0	17,19,21	0.43	0
4	NAG	B	1309	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	L	1305	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	C	1311	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	C	1305	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	K	1308	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	K	1310	1	14,14,15	0.42	0	17,19,21	1.26	1 (5%)
4	NAG	L	1313	1	14,14,15	0.41	0	17,19,21	0.39	0
4	NAG	A	1308	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	J	1310	1	14,14,15	0.21	0	17,19,21	0.43	0
4	NAG	C	1313	1	14,14,15	0.41	0	17,19,21	0.40	0
4	NAG	L	1310	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	J	1312	1	14,14,15	0.21	0	17,19,21	0.43	0
4	NAG	K	1314	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	B	1306	1	14,14,15	0.22	0	17,19,21	0.42	0
4	NAG	C	1301	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	K	1311	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	J	1305	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	J	1303	1	14,14,15	0.28	0	17,19,21	0.57	0
4	NAG	B	1302	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	A	1311	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	K	1309	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	L	1309	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	B	1311	1	14,14,15	0.21	0	17,19,21	0.43	0
4	NAG	J	1313	1	14,14,15	0.22	0	17,19,21	0.47	0
4	NAG	L	1314	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	B	1305	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	A	1315	1	14,14,15	0.20	0	17,19,21	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	J	1314	1	14,14,15	0.21	0	17,19,21	0.47	0
4	NAG	A	1310	1	14,14,15	0.26	0	17,19,21	0.56	0
4	NAG	A	1304	1	14,14,15	0.28	0	17,19,21	0.56	0
4	NAG	L	1303	1	14,14,15	0.26	0	17,19,21	0.56	0
4	NAG	J	1309	1	14,14,15	0.28	0	17,19,21	0.55	0
4	NAG	B	1307	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	L	1311	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	B	1313	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	K	1313	1	14,14,15	0.22	0	17,19,21	0.43	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	A	1313	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	K	1307	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1312	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1312	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1303	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1314	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1307	1	-	0/6/23/26	0/1/1/1
4	NAG	K	1302	1	-	0/6/23/26	0/1/1/1
4	NAG	L	1301	1	-	3/6/23/26	0/1/1/1
4	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1306	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1315	1	-	0/6/23/26	0/1/1/1
4	NAG	K	1315	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
4	NAG	K	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1301	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1303	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1304	1	-	4/6/23/26	0/1/1/1
4	NAG	J	1306	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	L	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1314	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1315	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	K	1303	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1310	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1314	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1308	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1304	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1312	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1315	1	-	6/6/23/26	0/1/1/1
4	NAG	A	1309	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1303	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1310	1	-	0/6/23/26	0/1/1/1
4	NAG	L	1312	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1309	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1311	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1307	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1307	1	-	2/6/23/26	0/1/1/1
4	NAG	K	1301	1	-	0/6/23/26	0/1/1/1
4	NAG	K	1312	1	-	1/6/23/26	0/1/1/1
4	NAG	J	1315	1	-	0/6/23/26	0/1/1/1
4	NAG	K	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1307	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1308	1	-	1/6/23/26	0/1/1/1
4	NAG	K	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	J	1308	1	-	4/6/23/26	0/1/1/1
4	NAG	J	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1309	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1311	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	K	1308	1	-	2/6/23/26	0/1/1/1
4	NAG	K	1310	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	L	1313	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1310	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1313	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1310	1	-	0/6/23/26	0/1/1/1
4	NAG	J	1312	1	-	0/6/23/26	0/1/1/1
4	NAG	K	1314	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1301	1	-	4/6/23/26	0/1/1/1
4	NAG	K	1311	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1305	1	-	0/6/23/26	0/1/1/1
4	NAG	J	1303	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1311	1	-	0/6/23/26	0/1/1/1
4	NAG	K	1309	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1309	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1311	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1313	1	-	0/6/23/26	0/1/1/1
4	NAG	L	1314	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1315	1	-	2/6/23/26	0/1/1/1
4	NAG	J	1314	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1310	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1303	1	-	3/6/23/26	0/1/1/1
4	NAG	J	1309	1	-	3/6/23/26	0/1/1/1
4	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
4	NAG	L	1311	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1313	1	-	4/6/23/26	0/1/1/1
4	NAG	K	1313	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1310	NAG	C1-O5-C5	4.79	118.61	112.19
4	K	1310	NAG	C1-O5-C5	4.79	118.61	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	1315	NAG	C2-N2-C7	4.58	129.04	122.90
4	C	1315	NAG	C2-N2-C7	4.58	129.04	122.90
4	L	1315	NAG	C1-C2-N2	2.16	113.84	110.43

There are no chirality outliers.

5 of 153 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1307	NAG	O5-C5-C6-O6
4	A	1302	NAG	O5-C5-C6-O6
4	C	1305	NAG	O5-C5-C6-O6
4	L	1305	NAG	O5-C5-C6-O6
4	C	1302	NAG	C4-C5-C6-O6

There are no ring outliers.

13 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	K	1302	NAG	1	0
4	C	1314	NAG	2	0
4	C	1315	NAG	1	0
4	C	1312	NAG	1	0
4	L	1315	NAG	1	0
4	L	1312	NAG	1	0
4	L	1307	NAG	1	0
4	C	1307	NAG	1	0
4	J	1312	NAG	1	0
4	K	1314	NAG	1	0
4	B	1302	NAG	1	0
4	L	1314	NAG	3	0
4	A	1315	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.

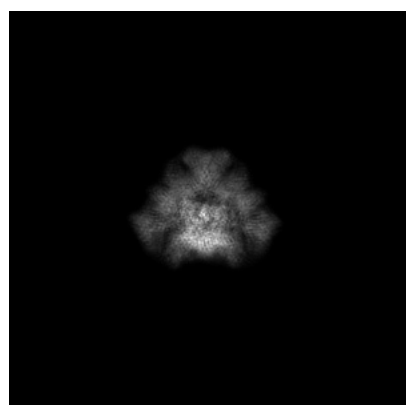
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32638. These allow visual inspection of the internal detail of the map and identification of artifacts.

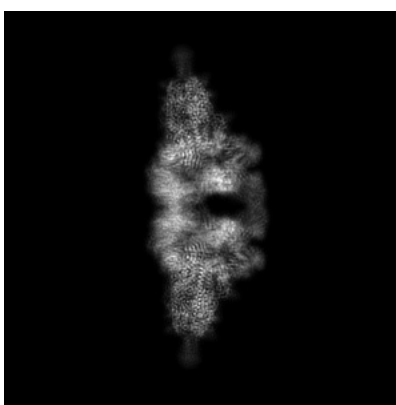
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

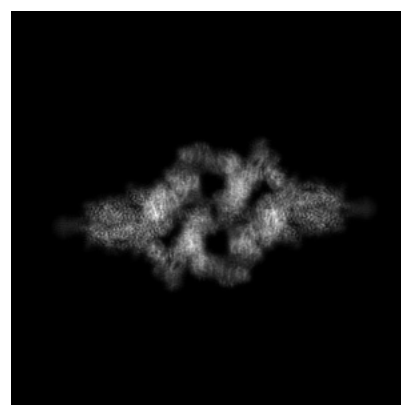
6.1.1 Primary map



X



Y

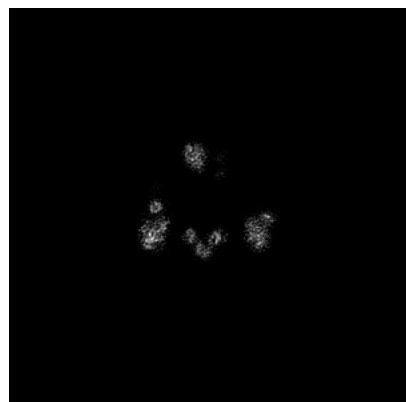


Z

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

6.2 Central slices [i](#)

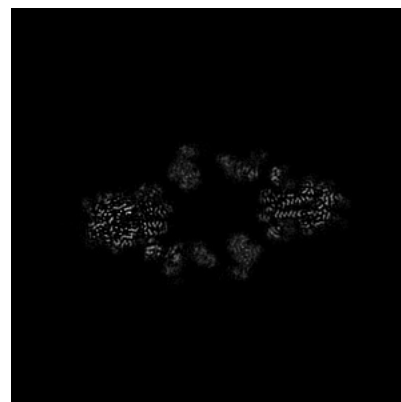
6.2.1 Primary map



X Index: 240



Y Index: 240

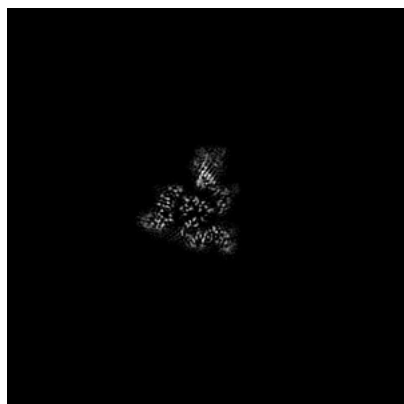


Z Index: 240

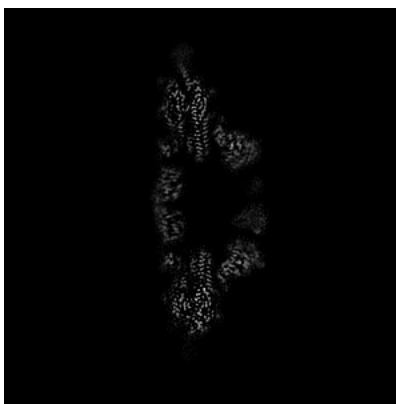
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

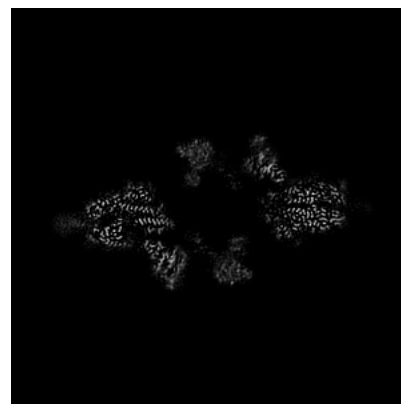
6.3.1 Primary map



X Index: 174



Y Index: 234

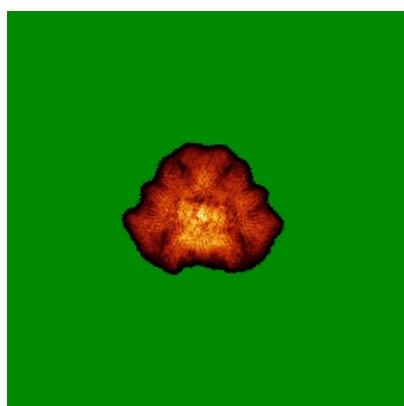


Z Index: 228

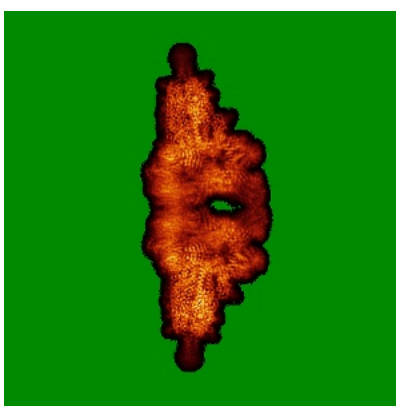
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

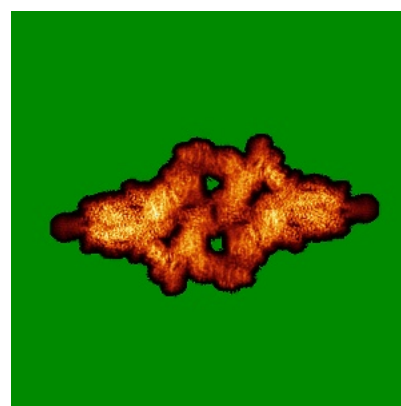
6.4.1 Primary map



X



Y

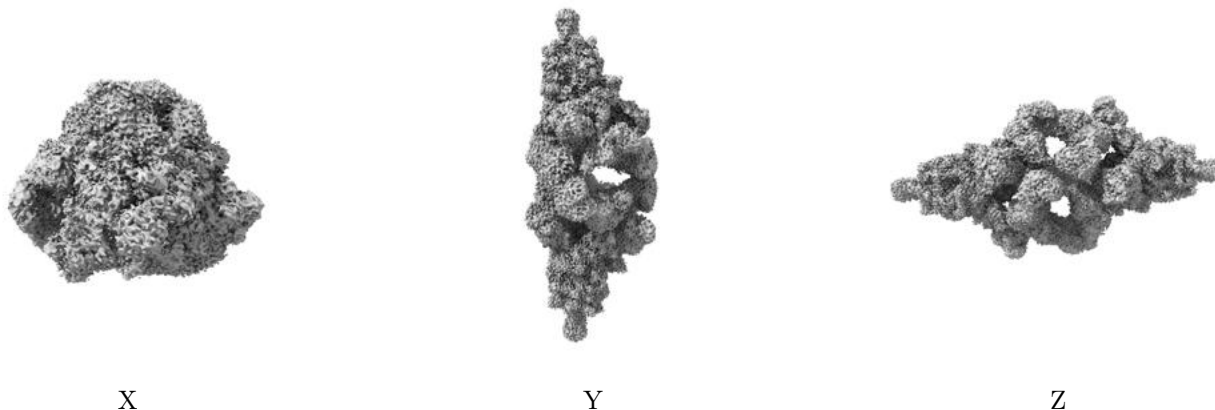


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

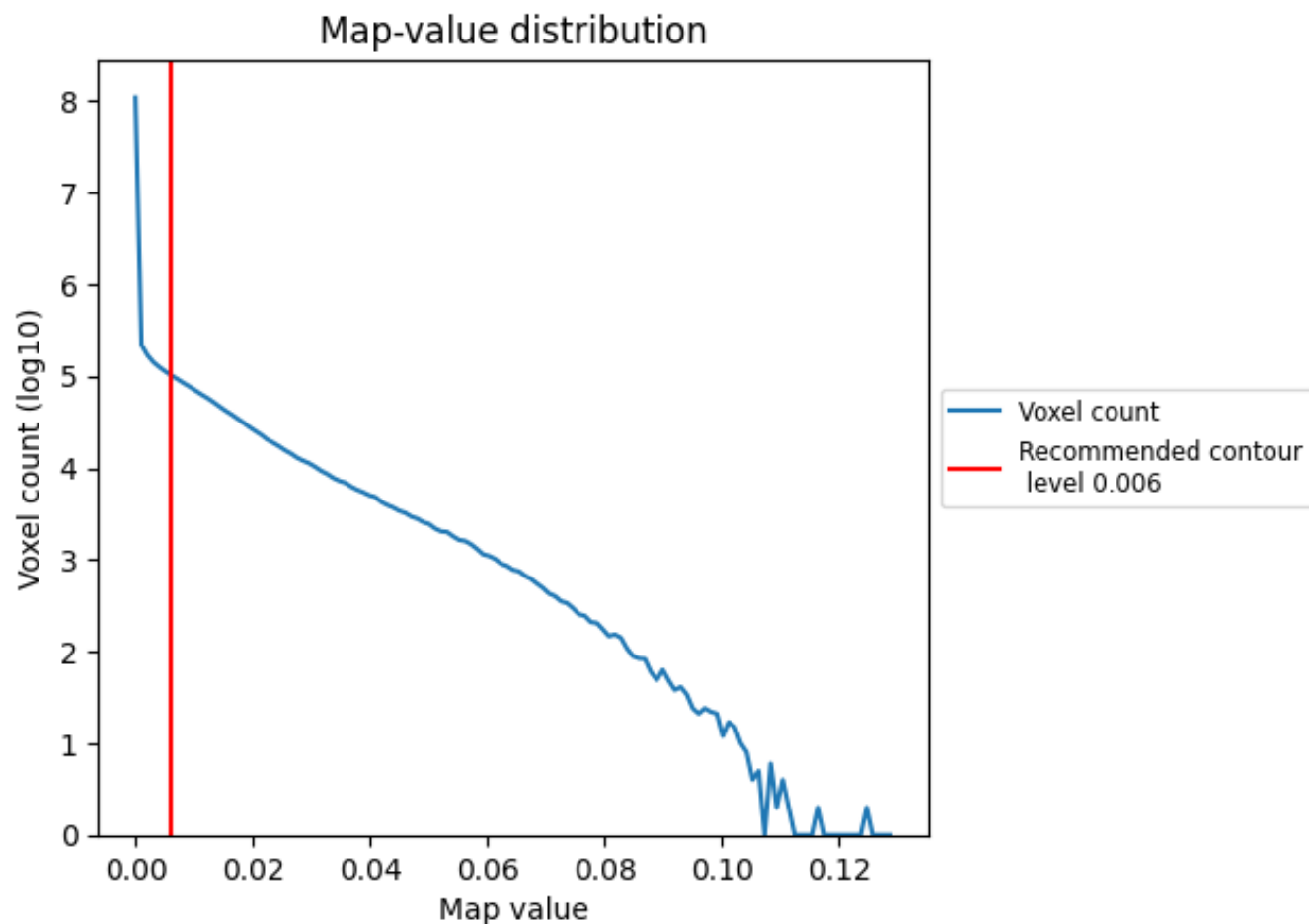
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

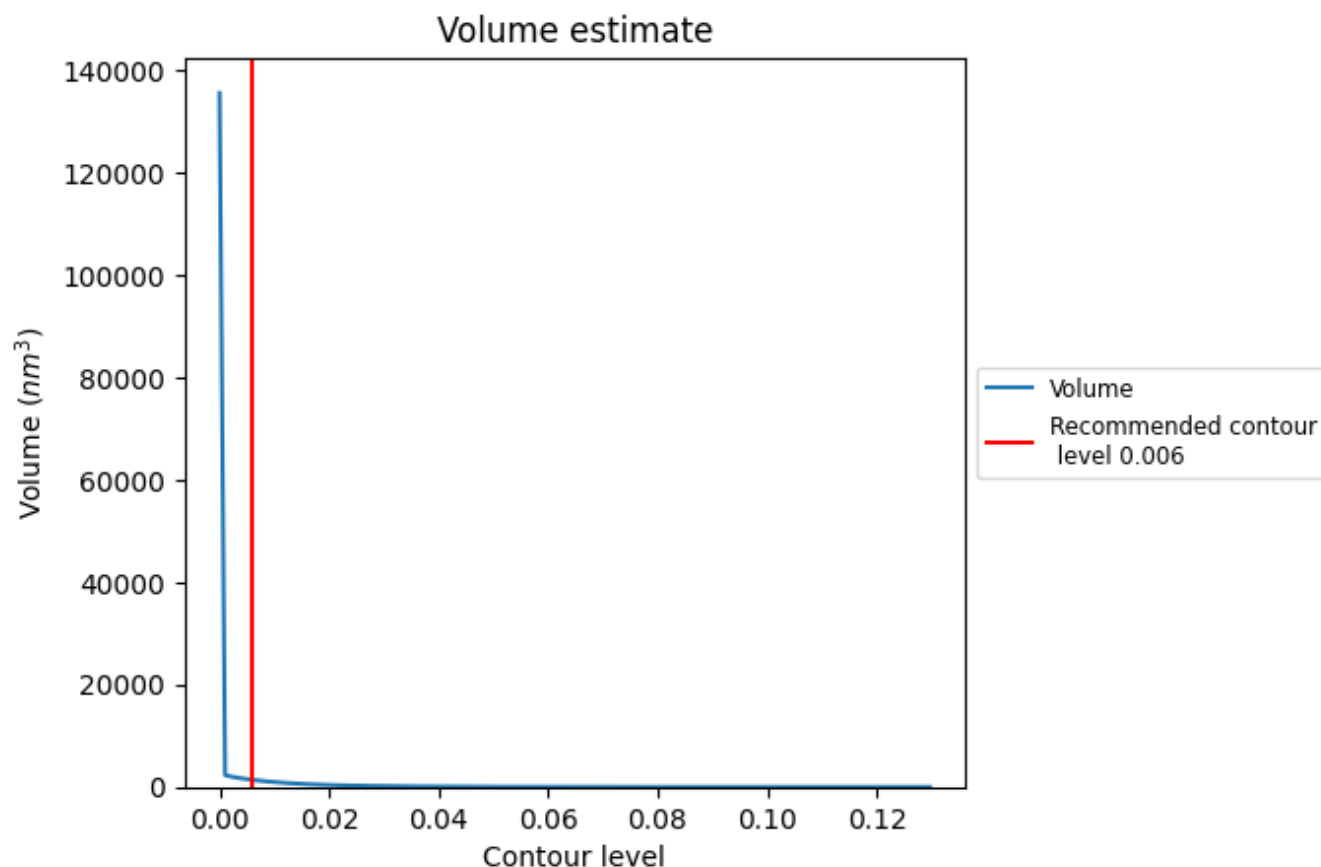
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

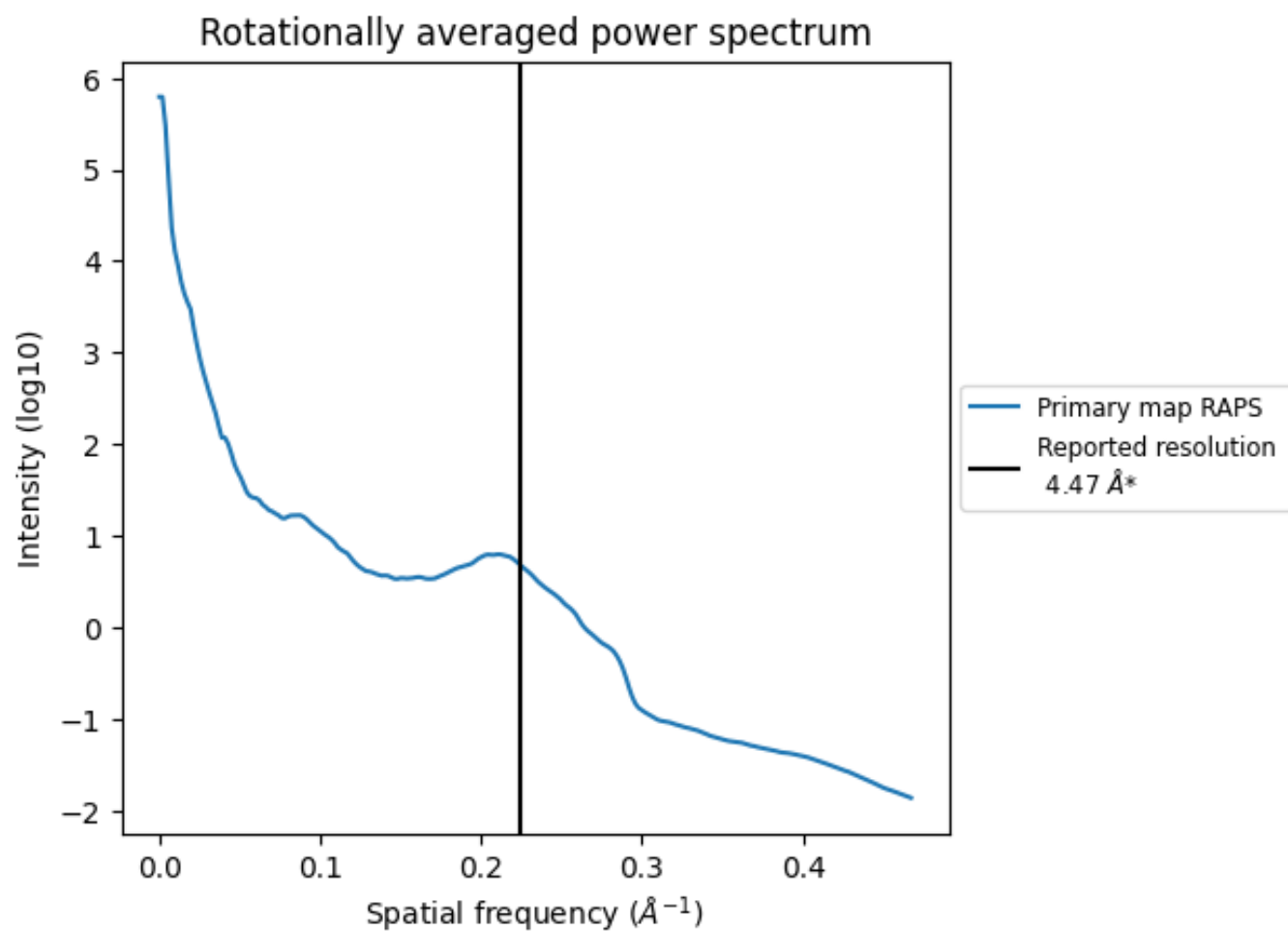
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1388 nm^3 ; this corresponds to an approximate mass of 1254 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.224 Å⁻¹

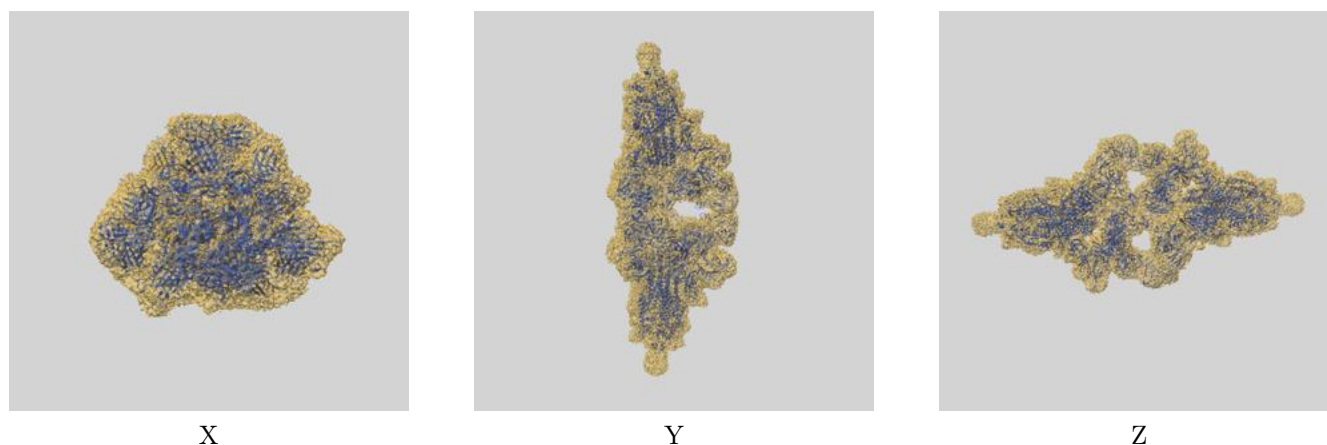
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

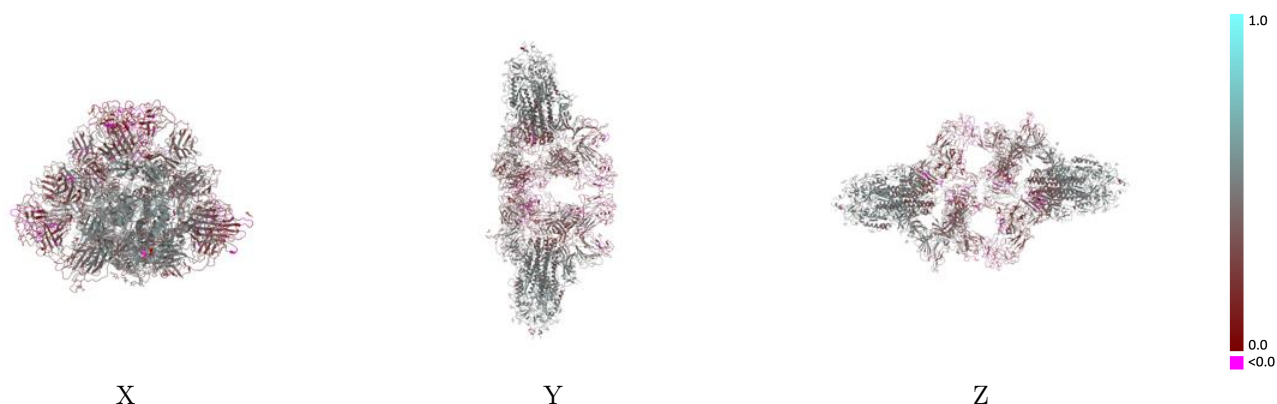
This section contains information regarding the fit between EMDB map EMD-32638 and PDB model 7WO4. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



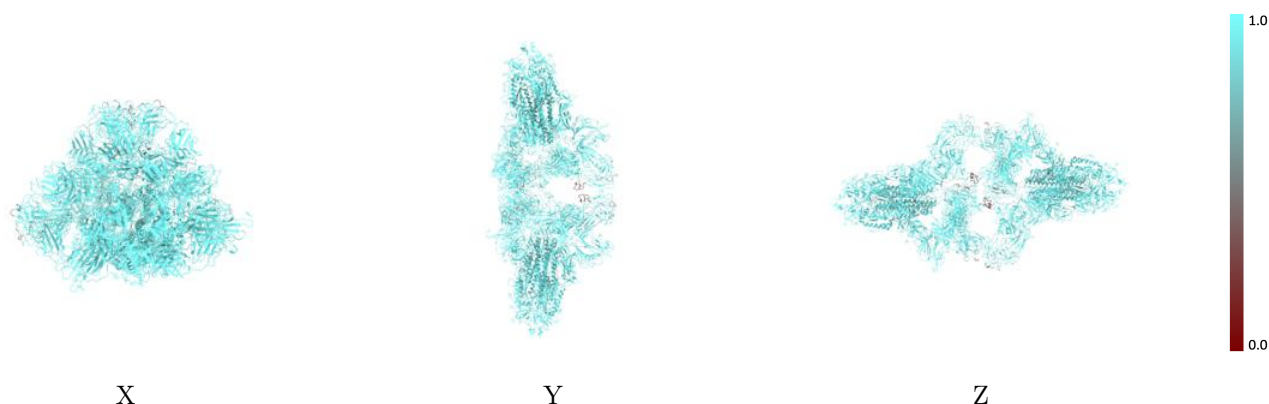
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



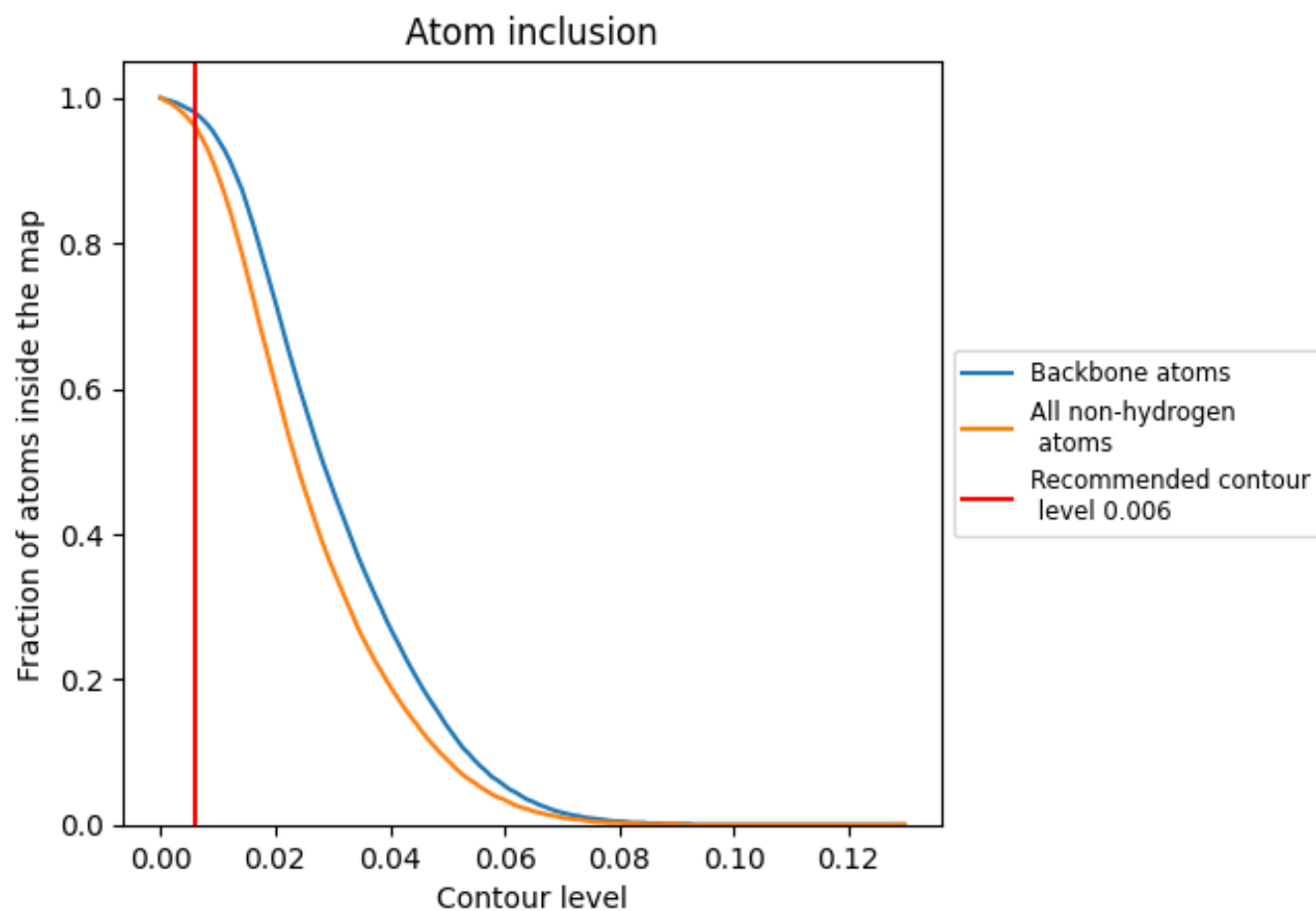
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9610	 0.3760
A	 0.9710	 0.4270
B	 0.9690	 0.4360
C	 0.9580	 0.4100
D	 0.9430	 0.3080
E	 0.9590	 0.3050
F	 0.9240	 0.2840
G	 0.9720	 0.2940
H	 0.9600	 0.2710
I	 0.9440	 0.2310
J	 0.9690	 0.3980
K	 0.9650	 0.4100
L	 0.9570	 0.3940
M	 0.9430	 0.3090
N	 0.9500	 0.3090
O	 0.9430	 0.2900
P	 0.9770	 0.2910
Q	 0.9490	 0.2580
R	 0.9420	 0.2120

