



# Full wwPDB EM Validation Report (i)

Nov 21, 2022 – 12:36 PM EST

PDB ID : 7R8N  
EMDB ID : EMD-24319  
Title : Structure of the SARS-CoV-2 S 6P trimer in complex with neutralizing antibody C051  
Authors : Barnes, C.O.; Bjorkman, P.J.  
Deposited on : 2021-06-26  
Resolution : 3.55 Å(reported)  
Based on initial model : 7K90

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

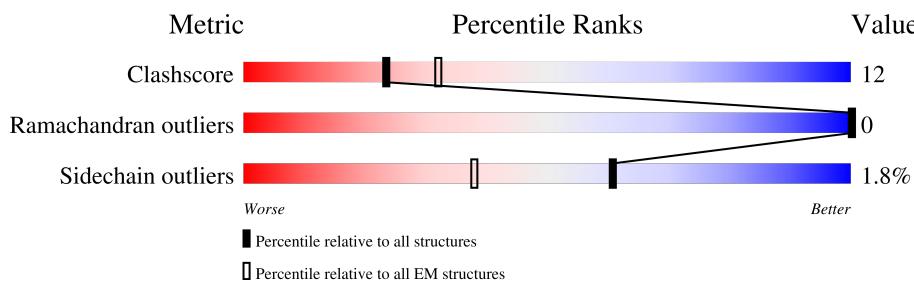
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 1 Overall quality at a glance

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

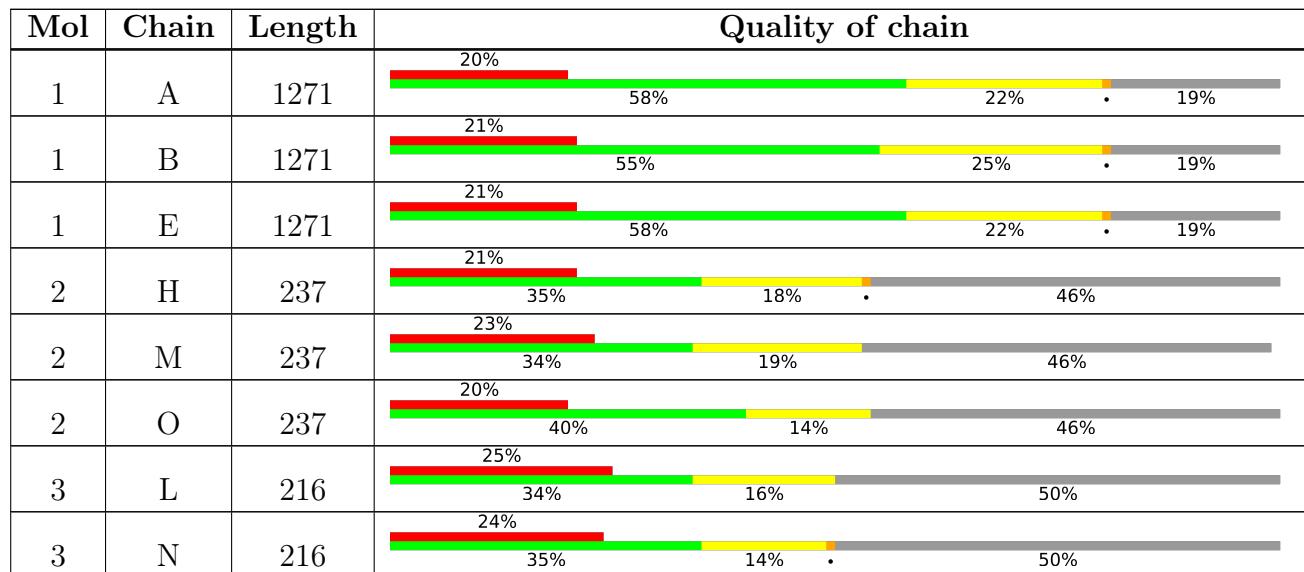
The reported resolution of this entry is 3.55 Å.

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.



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Mol	Chain	Length	Quality of chain			
3	P	216	25%	32%	17%	50%
4	C	2	50%	100%	50%	50%
4	D	2	50%	50%	50%	50%
4	F	2	50%	100%	50%	50%
4	G	2	50%	50%	50%	50%

## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 29719 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	1034	Total	C 7945	N 5082	O 1325	S 1499	39	0
1	B	1034	Total	C 7945	N 5082	O 1325	S 1499	39	0
1	E	1034	Total	C 7945	N 5082	O 1325	S 1499	39	0

There are 213 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP P0DTC2
A	?	-	ARG	deletion	UNP P0DTC2
A	?	-	ALA	deletion	UNP P0DTC2
A	685	ALA	ARG	conflict	UNP P0DTC2
A	817	PRO	PHE	conflict	UNP P0DTC2
A	892	PRO	ALA	conflict	UNP P0DTC2
A	899	PRO	ALA	conflict	UNP P0DTC2
A	942	PRO	ALA	conflict	UNP P0DTC2
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
A	1214	SER	-	expression tag	UNP P0DTC2
A	1215	GLY	-	expression tag	UNP P0DTC2
A	1216	ARG	-	expression tag	UNP P0DTC2
A	1217	LEU	-	expression tag	UNP P0DTC2
A	1218	VAL	-	expression tag	UNP P0DTC2
A	1219	PRO	-	expression tag	UNP P0DTC2
A	1220	ARG	-	expression tag	UNP P0DTC2
A	1221	GLY	-	expression tag	UNP P0DTC2
A	1222	SER	-	expression tag	UNP P0DTC2
A	1223	PRO	-	expression tag	UNP P0DTC2
A	1224	GLY	-	expression tag	UNP P0DTC2
A	1225	SER	-	expression tag	UNP P0DTC2
A	1226	GLY	-	expression tag	UNP P0DTC2
A	1227	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1228	ILE	-	expression tag	UNP P0DTC2
A	1229	PRO	-	expression tag	UNP P0DTC2
A	1230	GLU	-	expression tag	UNP P0DTC2
A	1231	ALA	-	expression tag	UNP P0DTC2
A	1232	PRO	-	expression tag	UNP P0DTC2
A	1233	ARG	-	expression tag	UNP P0DTC2
A	1234	ASP	-	expression tag	UNP P0DTC2
A	1235	GLY	-	expression tag	UNP P0DTC2
A	1236	GLN	-	expression tag	UNP P0DTC2
A	1237	ALA	-	expression tag	UNP P0DTC2
A	1238	TYR	-	expression tag	UNP P0DTC2
A	1239	VAL	-	expression tag	UNP P0DTC2
A	1240	ARG	-	expression tag	UNP P0DTC2
A	1241	LYS	-	expression tag	UNP P0DTC2
A	1242	ASP	-	expression tag	UNP P0DTC2
A	1243	GLY	-	expression tag	UNP P0DTC2
A	1244	GLU	-	expression tag	UNP P0DTC2
A	1245	TRP	-	expression tag	UNP P0DTC2
A	1246	VAL	-	expression tag	UNP P0DTC2
A	1247	LEU	-	expression tag	UNP P0DTC2
A	1248	LEU	-	expression tag	UNP P0DTC2
A	1249	SER	-	expression tag	UNP P0DTC2
A	1250	THR	-	expression tag	UNP P0DTC2
A	1251	PHE	-	expression tag	UNP P0DTC2
A	1252	LEU	-	expression tag	UNP P0DTC2
A	1253	GLY	-	expression tag	UNP P0DTC2
A	1254	HIS	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	HIS	-	expression tag	UNP P0DTC2
A	1257	HIS	-	expression tag	UNP P0DTC2
A	1258	HIS	-	expression tag	UNP P0DTC2
A	1259	HIS	-	expression tag	UNP P0DTC2
A	1260	GLY	-	expression tag	UNP P0DTC2
A	1261	LEU	-	expression tag	UNP P0DTC2
A	1262	ASN	-	expression tag	UNP P0DTC2
A	1263	ASP	-	expression tag	UNP P0DTC2
A	1264	ILE	-	expression tag	UNP P0DTC2
A	1265	PHE	-	expression tag	UNP P0DTC2
A	1266	GLU	-	expression tag	UNP P0DTC2
A	1267	ALA	-	expression tag	UNP P0DTC2
A	1268	GLN	-	expression tag	UNP P0DTC2
A	1269	LYS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1270	ILE	-	expression tag	UNP P0DTC2
A	1271	GLU	-	expression tag	UNP P0DTC2
A	1272	TRP	-	expression tag	UNP P0DTC2
A	1273	HIS	-	expression tag	UNP P0DTC2
A	1274	GLU	-	expression tag	UNP P0DTC2
B	?	-	ARG	deletion	UNP P0DTC2
B	?	-	ARG	deletion	UNP P0DTC2
B	?	-	ALA	deletion	UNP P0DTC2
B	685	ALA	ARG	conflict	UNP P0DTC2
B	817	PRO	PHE	conflict	UNP P0DTC2
B	892	PRO	ALA	conflict	UNP P0DTC2
B	899	PRO	ALA	conflict	UNP P0DTC2
B	942	PRO	ALA	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
B	1214	SER	-	expression tag	UNP P0DTC2
B	1215	GLY	-	expression tag	UNP P0DTC2
B	1216	ARG	-	expression tag	UNP P0DTC2
B	1217	LEU	-	expression tag	UNP P0DTC2
B	1218	VAL	-	expression tag	UNP P0DTC2
B	1219	PRO	-	expression tag	UNP P0DTC2
B	1220	ARG	-	expression tag	UNP P0DTC2
B	1221	GLY	-	expression tag	UNP P0DTC2
B	1222	SER	-	expression tag	UNP P0DTC2
B	1223	PRO	-	expression tag	UNP P0DTC2
B	1224	GLY	-	expression tag	UNP P0DTC2
B	1225	SER	-	expression tag	UNP P0DTC2
B	1226	GLY	-	expression tag	UNP P0DTC2
B	1227	TYR	-	expression tag	UNP P0DTC2
B	1228	ILE	-	expression tag	UNP P0DTC2
B	1229	PRO	-	expression tag	UNP P0DTC2
B	1230	GLU	-	expression tag	UNP P0DTC2
B	1231	ALA	-	expression tag	UNP P0DTC2
B	1232	PRO	-	expression tag	UNP P0DTC2
B	1233	ARG	-	expression tag	UNP P0DTC2
B	1234	ASP	-	expression tag	UNP P0DTC2
B	1235	GLY	-	expression tag	UNP P0DTC2
B	1236	GLN	-	expression tag	UNP P0DTC2
B	1237	ALA	-	expression tag	UNP P0DTC2
B	1238	TYR	-	expression tag	UNP P0DTC2
B	1239	VAL	-	expression tag	UNP P0DTC2
B	1240	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1241	LYS	-	expression tag	UNP P0DTC2
B	1242	ASP	-	expression tag	UNP P0DTC2
B	1243	GLY	-	expression tag	UNP P0DTC2
B	1244	GLU	-	expression tag	UNP P0DTC2
B	1245	TRP	-	expression tag	UNP P0DTC2
B	1246	VAL	-	expression tag	UNP P0DTC2
B	1247	LEU	-	expression tag	UNP P0DTC2
B	1248	LEU	-	expression tag	UNP P0DTC2
B	1249	SER	-	expression tag	UNP P0DTC2
B	1250	THR	-	expression tag	UNP P0DTC2
B	1251	PHE	-	expression tag	UNP P0DTC2
B	1252	LEU	-	expression tag	UNP P0DTC2
B	1253	GLY	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	HIS	-	expression tag	UNP P0DTC2
B	1259	HIS	-	expression tag	UNP P0DTC2
B	1260	GLY	-	expression tag	UNP P0DTC2
B	1261	LEU	-	expression tag	UNP P0DTC2
B	1262	ASN	-	expression tag	UNP P0DTC2
B	1263	ASP	-	expression tag	UNP P0DTC2
B	1264	ILE	-	expression tag	UNP P0DTC2
B	1265	PHE	-	expression tag	UNP P0DTC2
B	1266	GLU	-	expression tag	UNP P0DTC2
B	1267	ALA	-	expression tag	UNP P0DTC2
B	1268	GLN	-	expression tag	UNP P0DTC2
B	1269	LYS	-	expression tag	UNP P0DTC2
B	1270	ILE	-	expression tag	UNP P0DTC2
B	1271	GLU	-	expression tag	UNP P0DTC2
B	1272	TRP	-	expression tag	UNP P0DTC2
B	1273	HIS	-	expression tag	UNP P0DTC2
B	1274	GLU	-	expression tag	UNP P0DTC2
E	?	-	ARG	deletion	UNP P0DTC2
E	?	-	ARG	deletion	UNP P0DTC2
E	?	-	ALA	deletion	UNP P0DTC2
E	685	ALA	ARG	conflict	UNP P0DTC2
E	817	PRO	PHE	conflict	UNP P0DTC2
E	892	PRO	ALA	conflict	UNP P0DTC2
E	899	PRO	ALA	conflict	UNP P0DTC2
E	942	PRO	ALA	conflict	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	986	PRO	LYS	conflict	UNP P0DTC2
E	987	PRO	VAL	conflict	UNP P0DTC2
E	1214	SER	-	expression tag	UNP P0DTC2
E	1215	GLY	-	expression tag	UNP P0DTC2
E	1216	ARG	-	expression tag	UNP P0DTC2
E	1217	LEU	-	expression tag	UNP P0DTC2
E	1218	VAL	-	expression tag	UNP P0DTC2
E	1219	PRO	-	expression tag	UNP P0DTC2
E	1220	ARG	-	expression tag	UNP P0DTC2
E	1221	GLY	-	expression tag	UNP P0DTC2
E	1222	SER	-	expression tag	UNP P0DTC2
E	1223	PRO	-	expression tag	UNP P0DTC2
E	1224	GLY	-	expression tag	UNP P0DTC2
E	1225	SER	-	expression tag	UNP P0DTC2
E	1226	GLY	-	expression tag	UNP P0DTC2
E	1227	TYR	-	expression tag	UNP P0DTC2
E	1228	ILE	-	expression tag	UNP P0DTC2
E	1229	PRO	-	expression tag	UNP P0DTC2
E	1230	GLU	-	expression tag	UNP P0DTC2
E	1231	ALA	-	expression tag	UNP P0DTC2
E	1232	PRO	-	expression tag	UNP P0DTC2
E	1233	ARG	-	expression tag	UNP P0DTC2
E	1234	ASP	-	expression tag	UNP P0DTC2
E	1235	GLY	-	expression tag	UNP P0DTC2
E	1236	GLN	-	expression tag	UNP P0DTC2
E	1237	ALA	-	expression tag	UNP P0DTC2
E	1238	TYR	-	expression tag	UNP P0DTC2
E	1239	VAL	-	expression tag	UNP P0DTC2
E	1240	ARG	-	expression tag	UNP P0DTC2
E	1241	LYS	-	expression tag	UNP P0DTC2
E	1242	ASP	-	expression tag	UNP P0DTC2
E	1243	GLY	-	expression tag	UNP P0DTC2
E	1244	GLU	-	expression tag	UNP P0DTC2
E	1245	TRP	-	expression tag	UNP P0DTC2
E	1246	VAL	-	expression tag	UNP P0DTC2
E	1247	LEU	-	expression tag	UNP P0DTC2
E	1248	LEU	-	expression tag	UNP P0DTC2
E	1249	SER	-	expression tag	UNP P0DTC2
E	1250	THR	-	expression tag	UNP P0DTC2
E	1251	PHE	-	expression tag	UNP P0DTC2
E	1252	LEU	-	expression tag	UNP P0DTC2
E	1253	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1254	HIS	-	expression tag	UNP P0DTC2
E	1255	HIS	-	expression tag	UNP P0DTC2
E	1256	HIS	-	expression tag	UNP P0DTC2
E	1257	HIS	-	expression tag	UNP P0DTC2
E	1258	HIS	-	expression tag	UNP P0DTC2
E	1259	HIS	-	expression tag	UNP P0DTC2
E	1260	GLY	-	expression tag	UNP P0DTC2
E	1261	LEU	-	expression tag	UNP P0DTC2
E	1262	ASN	-	expression tag	UNP P0DTC2
E	1263	ASP	-	expression tag	UNP P0DTC2
E	1264	ILE	-	expression tag	UNP P0DTC2
E	1265	PHE	-	expression tag	UNP P0DTC2
E	1266	GLU	-	expression tag	UNP P0DTC2
E	1267	ALA	-	expression tag	UNP P0DTC2
E	1268	GLN	-	expression tag	UNP P0DTC2
E	1269	LYS	-	expression tag	UNP P0DTC2
E	1270	ILE	-	expression tag	UNP P0DTC2
E	1271	GLU	-	expression tag	UNP P0DTC2
E	1272	TRP	-	expression tag	UNP P0DTC2
E	1273	HIS	-	expression tag	UNP P0DTC2
E	1274	GLU	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called C051 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	129	Total	C	N	O	S	0	0
			999	630	170	195	4		
2	M	129	Total	C	N	O	S	0	0
			999	630	170	195	4		
2	O	129	Total	C	N	O	S	0	0
			999	630	170	195	4		

- Molecule 3 is a protein called C051 Fab Light Chain.

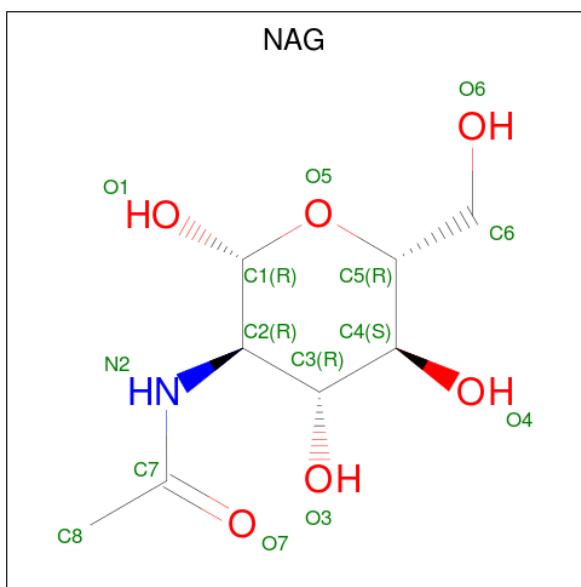
Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	108	Total	C	N	O	S	0	0
			799	497	131	169	2		
3	N	108	Total	C	N	O	S	0	0
			799	497	131	169	2		
3	P	108	Total	C	N	O	S	0	0
			799	497	131	169	2		

- 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	C	2	Total C N O 28 16 2 10	0	0
4	D	2	Total C N O 28 16 2 10	0	0
4	F	2	Total C N O 28 16 2 10	0	0
4	G	2	Total C N O 28 16 2 10	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms	AltConf
5	A	1	Total C N O 112 64 8 40	0
5	A	1	Total C N O 112 64 8 40	0
5	A	1	Total C N O 112 64 8 40	0
5	A	1	Total C N O 112 64 8 40	0

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Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			112	64	8	40	
5	A	1	Total	C	N	O	0
			112	64	8	40	
5	A	1	Total	C	N	O	0
			112	64	8	40	
5	A	1	Total	C	N	O	0
			112	64	8	40	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	B	1	Total	C	N	O	0
			126	72	9	45	
5	E	1	Total	C	N	O	0
			140	80	10	50	
5	E	1	Total	C	N	O	0
			140	80	10	50	
5	E	1	Total	C	N	O	0
			140	80	10	50	
5	E	1	Total	C	N	O	0
			140	80	10	50	
5	E	1	Total	C	N	O	0
			140	80	10	50	
5	E	1	Total	C	N	O	0
			140	80	10	50	
5	E	1	Total	C	N	O	0
			140	80	10	50	
5	E	1	Total	C	N	O	0
			140	80	10	50	

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Mol	Chain	Residues	Atoms				AltConf
5	E	1	Total	C	N	O	0
			140	80	10	50	

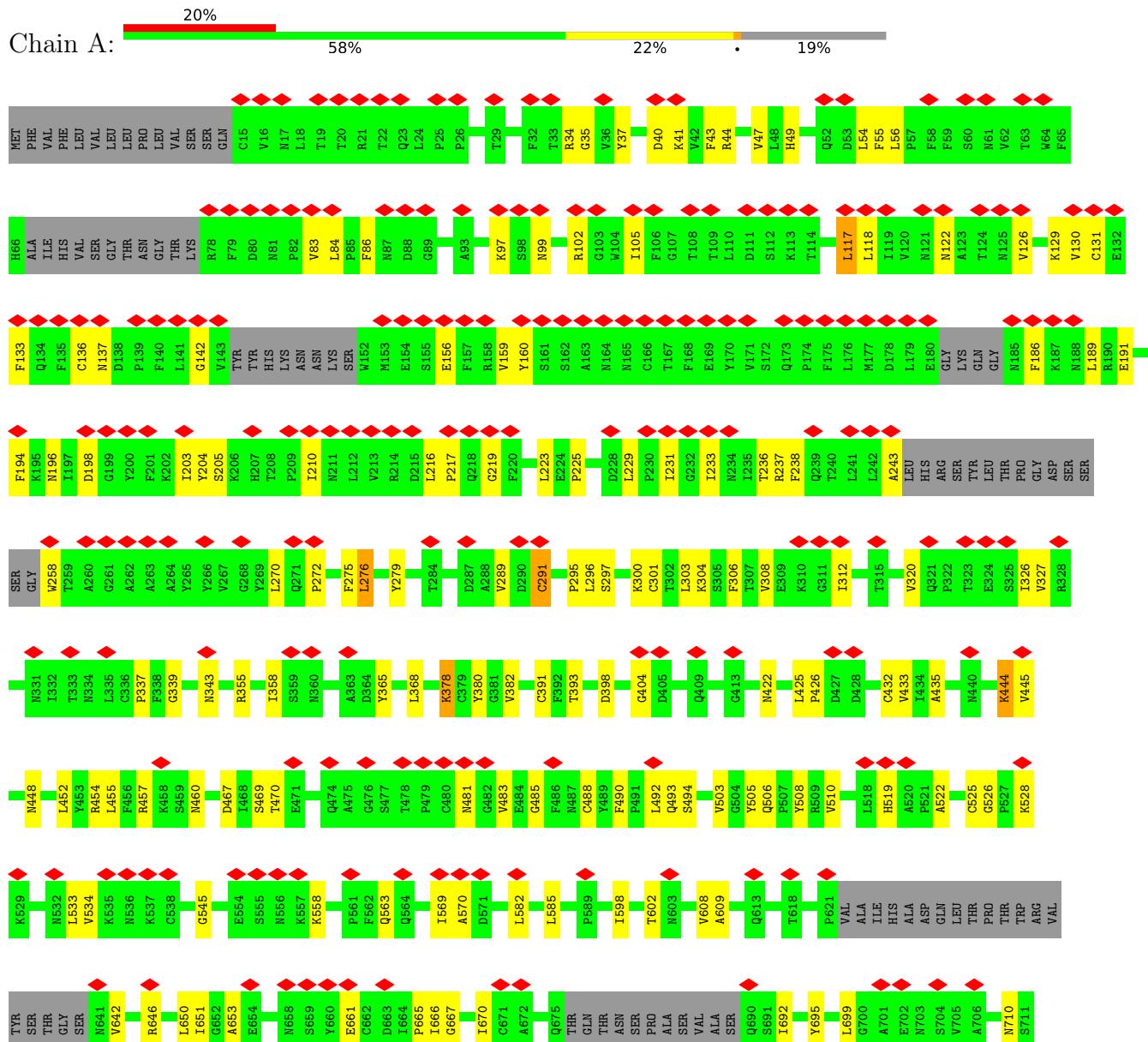
  

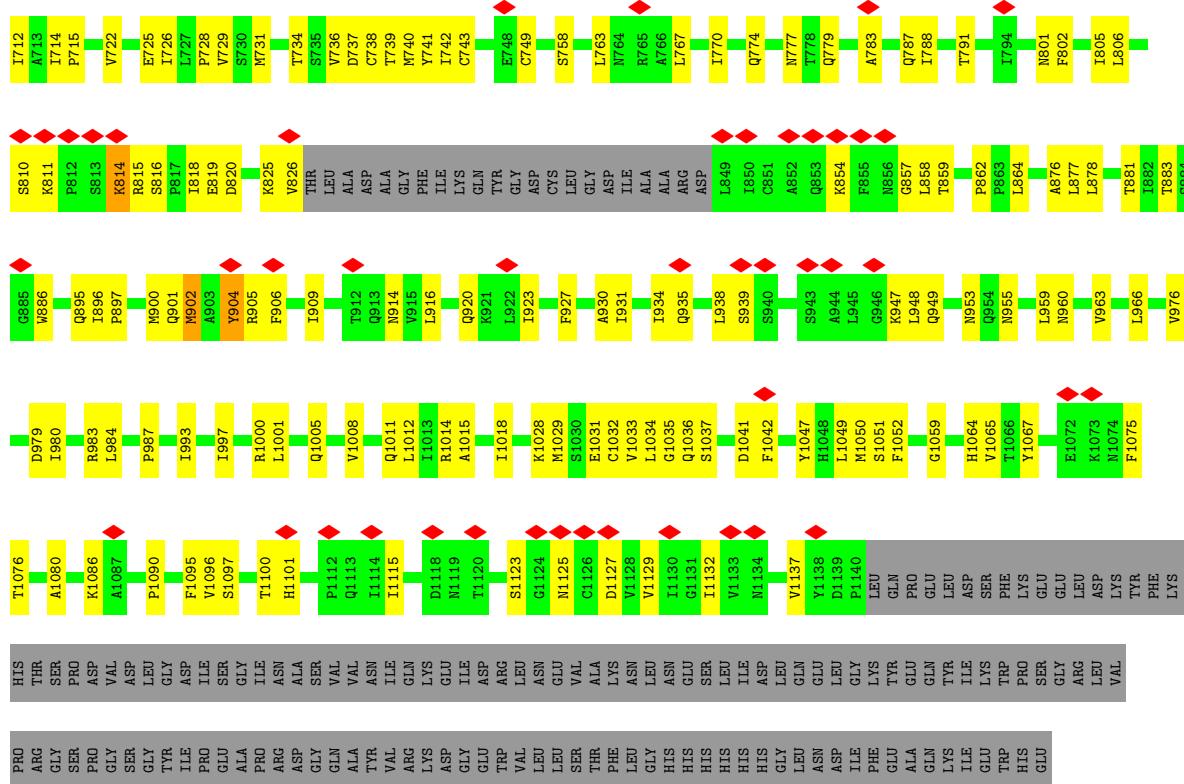
Mol	Chain	Residues	Atoms				AltConf
5	E	1	Total	C	N	O	0
			140	80	10	50	

### 3 Residue-property plots [\(i\)](#)

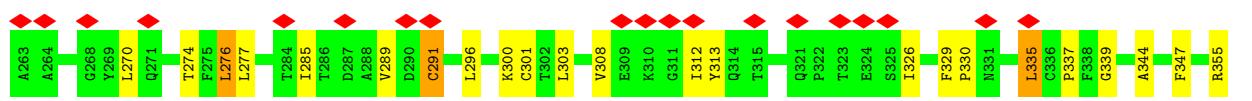
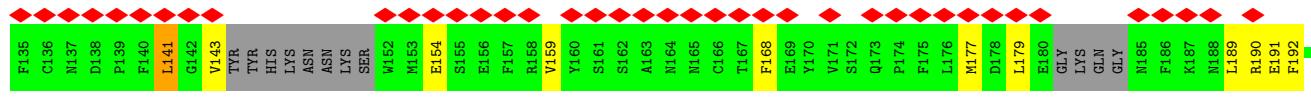
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

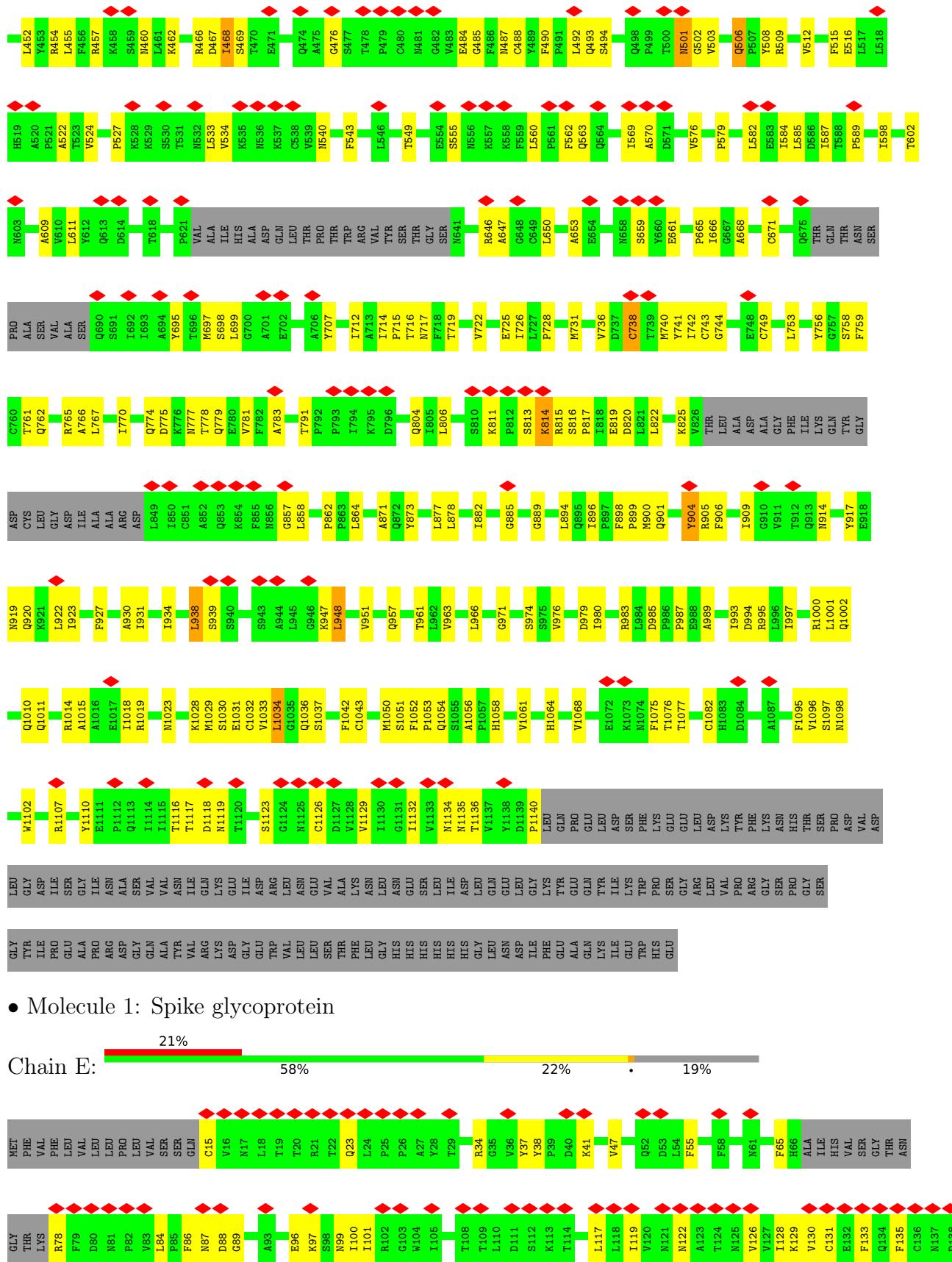
- Molecule 1: Spike glycoprotein

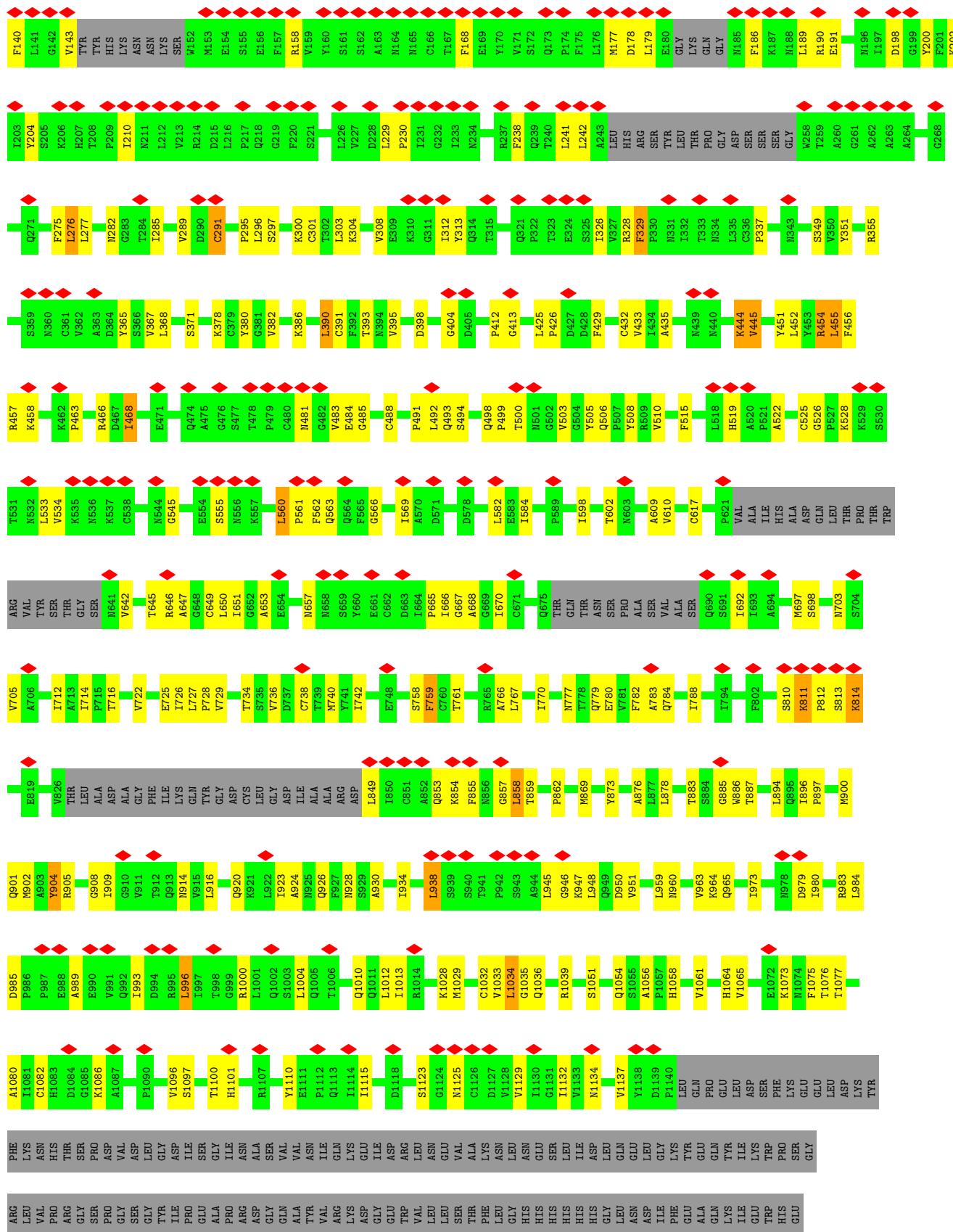




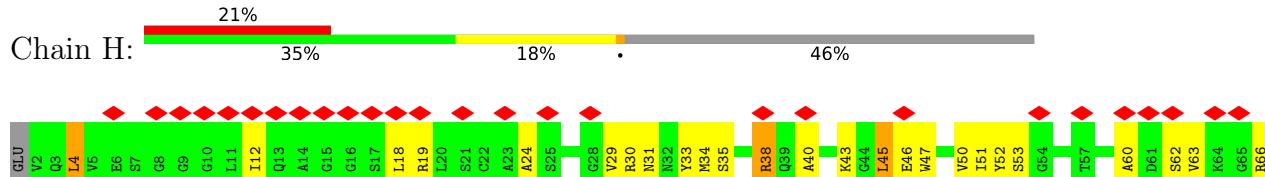
- Molecule 1: Spike glycoprotein



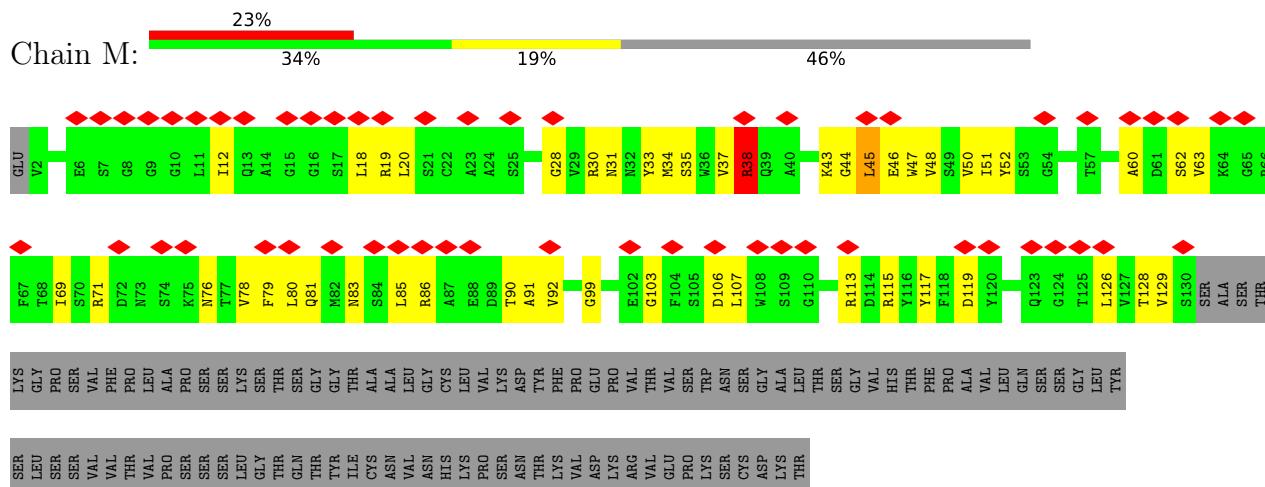




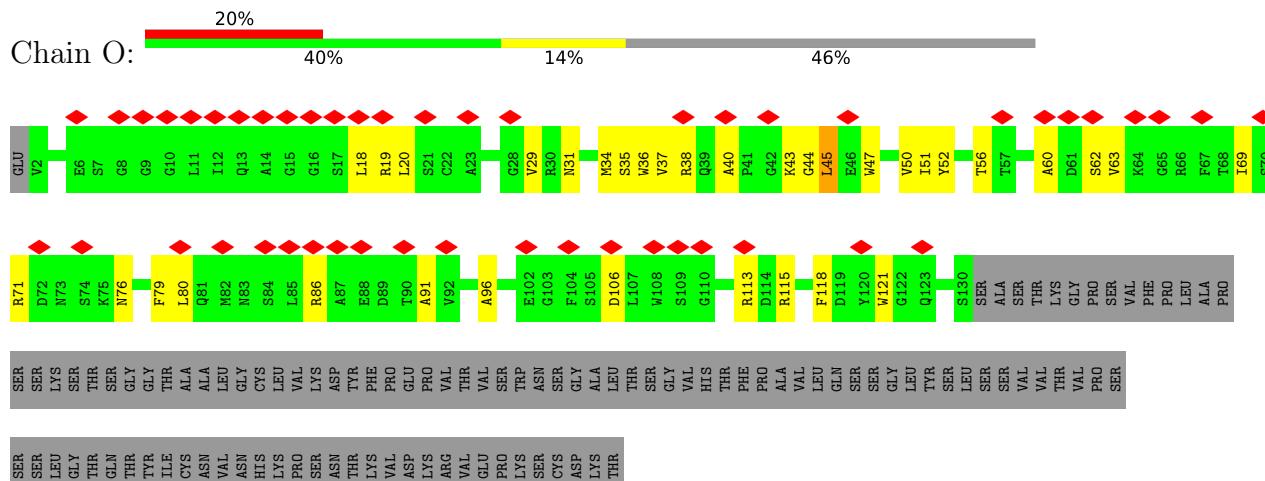
- Molecule 2: C051 Fab Heavy Chain



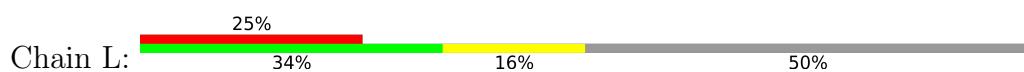
- Molecule 2: C051 Fab Heavy Chain

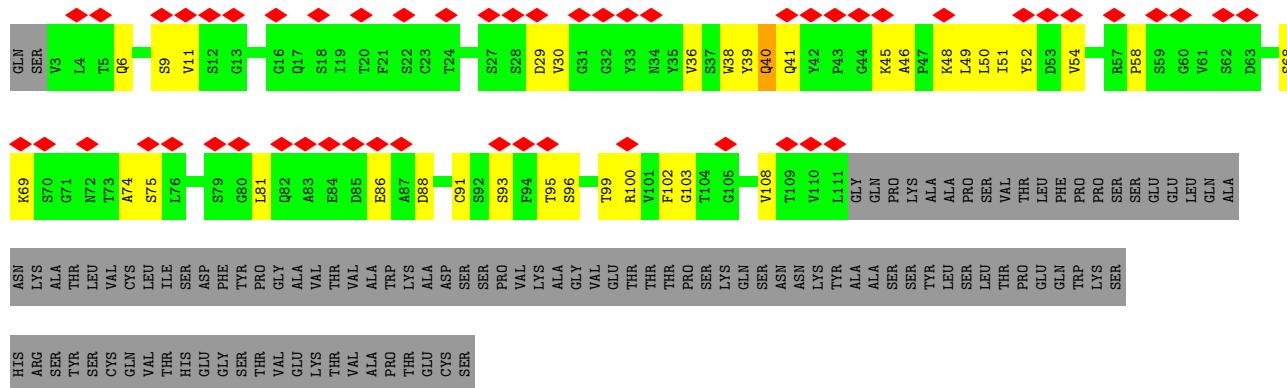


- Molecule 2: C051 Fab Heavy Chain

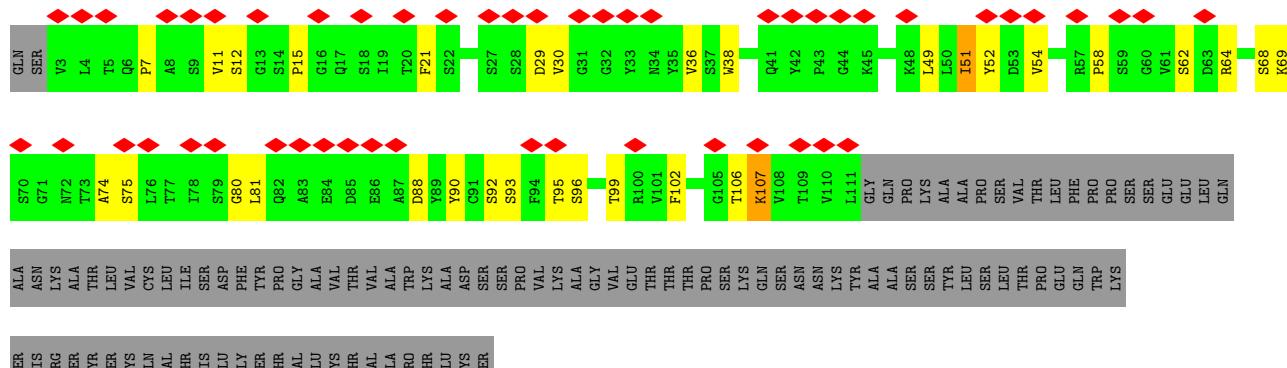
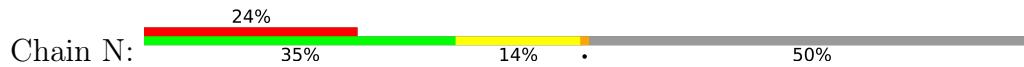


- Molecule 3: C051 Fab Light Chain

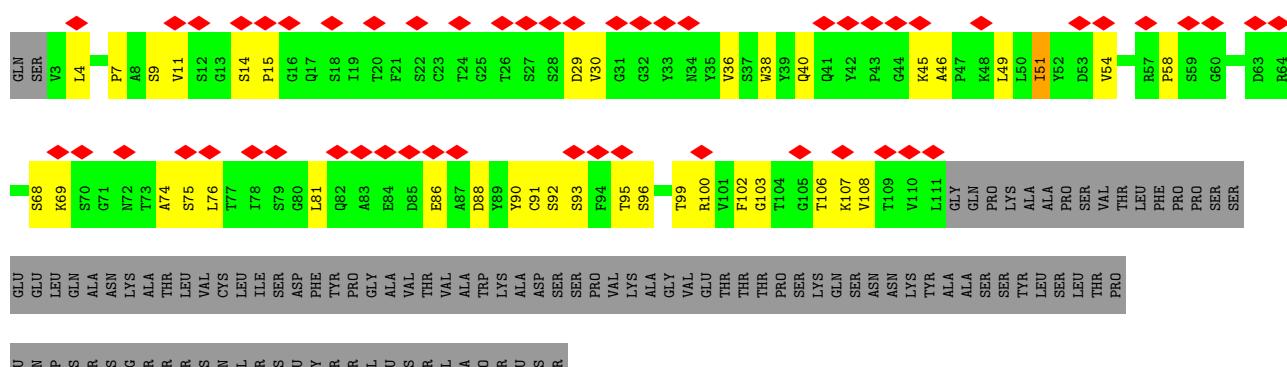
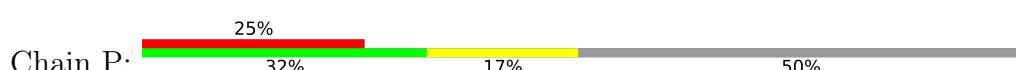




- Molecule 3: C051 Fab Light Chain



#### • Molecule 3: C051 Fab Light Chain



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





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



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



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



## 4 Experimental information i

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	134506	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	45000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.774	Depositor
Minimum map value	-0.435	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	375.40802, 375.40802, 375.40802	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.869, 0.869, 0.869	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:  
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	0.40	0/8130	0.84	18/11081 (0.2%)
1	B	0.41	0/8130	0.85	17/11081 (0.2%)
1	E	0.40	0/8130	0.85	22/11081 (0.2%)
2	H	0.41	0/1022	0.85	2/1384 (0.1%)
2	M	0.39	0/1022	0.91	4/1384 (0.3%)
2	O	0.35	0/1022	0.86	2/1384 (0.1%)
3	L	0.42	0/816	0.77	1/1111 (0.1%)
3	N	0.40	0/816	0.72	0/1111
3	P	0.44	0/816	0.77	0/1111
All	All	0.40	0/29904	0.84	66/40728 (0.2%)

There are no bond length outliers.

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	45	LEU	CA-CB-CG	10.89	140.34	115.30
1	B	948	LEU	CA-CB-CG	10.64	139.78	115.30
1	A	272	PRO	CA-N-CD	-9.24	98.56	111.50
1	E	1034	LEU	CB-CG-CD2	-8.73	96.17	111.00
1	B	1034	LEU	CB-CG-CD2	-8.65	96.29	111.00
1	A	858	LEU	CA-CB-CG	8.28	134.35	115.30
1	A	291	CYS	CA-CB-SG	8.17	128.70	114.00
1	E	560	LEU	CA-CB-CG	7.96	133.62	115.30
1	B	858	LEU	CA-CB-CG	7.78	133.18	115.30
1	E	291	CYS	CA-CB-SG	7.68	127.82	114.00
1	E	858	LEU	CA-CB-CG	7.43	132.38	115.30
1	B	291	CYS	CA-CB-SG	7.35	127.23	114.00
1	B	276	LEU	CA-CB-CG	7.29	132.08	115.30
1	E	563	GLN	CA-CB-CG	6.95	128.70	113.40
1	A	198	ASP	CB-CG-OD1	6.88	124.50	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	390	LEU	CB-CG-CD2	-6.69	99.63	111.00
1	B	198	ASP	CB-CG-OD1	6.53	124.17	118.30
1	A	878	LEU	CA-CB-CG	6.46	130.15	115.30
1	E	996	LEU	CA-CB-CG	6.37	129.94	115.30
1	E	198	ASP	CB-CG-OD1	6.30	123.97	118.30
1	B	15	CYS	CA-CB-SG	6.11	124.99	114.00
1	B	904	TYR	CA-CB-CG	6.10	124.99	113.40
1	E	432	CYS	CA-CB-SG	6.09	124.96	114.00
1	B	1043	CYS	CA-CB-SG	6.04	124.87	114.00
1	B	738	CYS	CA-CB-SG	5.96	124.72	114.00
1	B	118	LEU	CA-CB-CG	5.95	128.99	115.30
1	E	1034	LEU	CA-CB-CG	5.95	128.98	115.30
2	O	45	LEU	CA-CB-CG	5.93	128.93	115.30
1	A	904	TYR	CA-CB-CG	5.91	124.62	113.40
1	B	229	LEU	CA-CB-CG	5.86	128.77	115.30
1	E	938	LEU	CB-CG-CD1	5.81	120.87	111.00
1	A	117	LEU	CA-CB-CG	5.74	128.49	115.30
1	A	938	LEU	CB-CG-CD1	5.71	120.70	111.00
1	A	320	VAL	C-N-CA	-5.70	107.46	121.70
1	A	276	LEU	CB-CG-CD1	-5.66	101.37	111.00
1	B	141	LEU	CA-CB-CG	5.64	128.27	115.30
1	B	900	MET	CG-SD-CE	-5.61	91.22	100.20
1	E	878	LEU	CA-CB-CG	5.61	128.20	115.30
1	E	276	LEU	CB-CG-CD1	-5.56	101.55	111.00
1	E	582	LEU	CA-CB-CG	5.56	128.08	115.30
1	E	117	LEU	CA-CB-CG	5.52	127.99	115.30
1	A	229	LEU	CA-CB-CG	5.50	127.94	115.30
1	A	563	GLN	CA-CB-CG	5.49	125.47	113.40
1	E	904	TYR	CA-CB-CG	5.41	123.68	113.40
1	A	432	CYS	CA-CB-SG	5.41	123.73	114.00
1	E	301	CYS	CA-CB-SG	5.37	123.67	114.00
1	E	945	LEU	CA-CB-CG	5.36	127.62	115.30
1	B	938	LEU	CB-CG-CD1	5.34	120.09	111.00
1	E	996	LEU	CB-CG-CD1	5.33	120.07	111.00
2	H	45	LEU	CA-CB-CG	5.30	127.49	115.30
1	A	585	LEU	CA-CB-CG	5.29	127.47	115.30
1	A	118	LEU	CA-CB-CG	5.29	127.45	115.30
1	B	468	ILE	CG1-CB-CG2	-5.24	99.86	111.40
1	E	337	PRO	CA-N-CD	-5.24	104.17	111.50
3	L	81	LEU	CA-CB-CG	5.22	127.30	115.30
1	B	582	LEU	CA-CB-CG	5.21	127.29	115.30
2	O	18	LEU	CA-CB-CG	5.21	127.29	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	582	LEU	CA-CB-CG	5.20	127.25	115.30
2	M	18	LEU	CA-CB-CG	5.19	127.24	115.30
2	M	38	ARG	CA-CB-CG	5.18	124.79	113.40
2	M	107	LEU	CA-CB-CG	5.15	127.14	115.30
1	A	1127	ASP	CB-CG-OD1	5.11	122.90	118.30
1	A	902	MET	CB-CG-SD	-5.08	97.15	112.40
1	E	468	ILE	CG1-CB-CG2	-5.08	100.23	111.40
2	H	4	LEU	CB-CG-CD2	-5.04	102.44	111.00
1	E	229	LEU	CB-CG-CD1	-5.01	102.48	111.00

There are no chirality outliers.

There are no planarity outliers.

## 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	A	7945	0	7635	188	0
1	B	7945	0	7633	226	0
1	E	7945	0	7633	191	0
2	H	999	0	935	37	0
2	M	999	0	935	33	0
2	O	999	0	935	24	0
3	L	799	0	760	23	0
3	N	799	0	760	26	0
3	P	799	0	760	25	0
4	C	28	0	25	1	0
4	D	28	0	25	0	0
4	F	28	0	25	0	0
4	G	28	0	25	0	0
5	A	112	0	104	0	0
5	B	126	0	117	4	0
5	E	140	0	130	3	0
All	All	29719	0	28437	709	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 12.

All (709) 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)
3:N:11:VAL:HG11	3:N:21:PHE:HZ	1.35	0.90
1:A:339:GLY:O	1:A:343:ASN:HB2	1.75	0.86
1:A:452:LEU:HD12	1:A:492:LEU:HB3	1.59	0.83
1:B:452:LEU:HD12	1:B:492:LEU:HB3	1.61	0.81
1:E:276:LEU:HD11	1:E:304:LYS:HA	1.62	0.80
1:A:276:LEU:HD11	1:A:304:LYS:HA	1.61	0.80
1:E:312:ILE:HD11	1:E:665:PRO:HG2	1.64	0.78
1:E:726:ILE:HG21	1:E:948:LEU:HB2	1.64	0.77
1:A:1029:MET:O	1:A:1033:VAL:HB	1.84	0.77
1:A:312:ILE:HD11	1:A:665:PRO:HG2	1.67	0.76
2:H:34:MET:HG2	2:H:78:VAL:HG11	1.68	0.76
2:H:19:ARG:HE	2:H:79:PHE:HB3	1.51	0.75
1:A:47:VAL:HG12	1:E:569:ILE:HD13	1.69	0.75
1:A:130:VAL:HG11	1:A:231:ILE:HG12	1.67	0.74
1:B:726:ILE:HB	1:B:947:LYS:HB2	1.68	0.74
3:N:11:VAL:HG11	3:N:21:PHE:CZ	2.21	0.73
1:B:1029:MET:O	1:B:1033:VAL:HB	1.89	0.73
1:A:83:VAL:HB	1:A:237:ARG:HH22	1.54	0.73
1:E:886:TRP:HB3	1:E:1035:GLY:HA2	1.71	0.72
1:B:1107:ARG:HH21	1:E:887:THR:HG23	1.54	0.71
1:B:452:LEU:HD13	1:B:494:SER:HB3	1.73	0.71
1:A:391:CYS:HA	1:A:525:CYS:HB3	1.73	0.70
1:B:393:THR:HA	1:B:522:ALA:HA	1.74	0.70
1:B:476:GLY:HA3	1:B:487:ASN:HD22	1.56	0.70
1:E:452:LEU:HD12	1:E:492:LEU:HB3	1.73	0.69
1:A:485:GLY:H	1:A:488:CYS:HB2	1.56	0.69
1:B:1054:GLN:HB2	1:B:1061:VAL:HB	1.75	0.69
1:B:312:ILE:HD11	1:B:665:PRO:HG2	1.73	0.69
1:B:437:ASN:C	1:B:437:ASN:HD22	1.94	0.69
2:M:38:ARG:NH1	2:M:46:GLU:OE2	2.26	0.68
1:E:277:LEU:HD23	1:E:285:ILE:HD13	1.74	0.68
1:E:973:ILE:HD11	1:E:984:LEU:HD11	1.76	0.68
1:A:791:THR:HG21	1:A:806:LEU:HD11	1.74	0.68
1:A:897:PRO:HG2	1:A:900:MET:HE2	1.74	0.68
1:E:452:LEU:HA	1:E:494:SER:HA	1.76	0.68
2:M:52:TYR:O	2:M:71:ARG:NH2	2.27	0.68
1:E:452:LEU:HD13	1:E:494:SER:HB3	1.76	0.67
2:M:33:TYR:HE1	2:M:113:ARG:HG2	1.58	0.67
1:A:886:TRP:HB3	1:A:1035:GLY:HA2	1.77	0.67
1:B:202:LYS:NZ	1:B:228:ASP:OD1	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:38:TRP:HE1	3:P:91:CYS:HG	1.43	0.67
1:A:196:ASN:ND2	1:A:233:ILE:O	2.24	0.66
2:O:19:ARG:HE	2:O:79:PHE:HB3	1.60	0.66
2:O:52:TYR:O	2:O:71:ARG:NH2	2.28	0.66
1:B:598:ILE:HB	1:B:609:ALA:HB3	1.78	0.66
1:B:457:ARG:NH1	1:B:460:ASN:O	2.29	0.65
1:E:617:CYS:N	1:E:649:CYS:SG	2.68	0.65
1:E:887:THR:HG21	1:E:894:LEU:HD22	1.77	0.65
1:E:901:GLN:HA	1:E:904:TYR:HD2	1.61	0.65
1:B:393:THR:OG1	1:B:516:GLU:O	2.15	0.65
3:L:95:THR:O	3:L:99:THR:N	2.28	0.65
1:B:569:ILE:HD13	1:E:47:VAL:HG12	1.78	0.65
1:E:99:ASN:HD22	1:E:178:ASP:H	1.45	0.65
1:E:391:CYS:HA	1:E:525:CYS:HB3	1.79	0.64
1:A:726:ILE:HG21	1:A:948:LEU:HB2	1.78	0.64
1:A:779:GLN:HG3	1:A:783:ALA:HB3	1.78	0.64
3:N:95:THR:O	3:N:99:THR:N	2.27	0.64
1:B:485:GLY:H	1:B:488:CYS:HB2	1.61	0.64
2:M:103:GLY:H	2:M:115:ARG:HH12	1.44	0.64
1:A:901:GLN:HA	1:A:904:TYR:HD2	1.63	0.63
1:E:96:GLU:OE2	1:E:190:ARG:NH1	2.31	0.63
1:A:816:SER:O	1:A:820:ASP:HB2	1.99	0.63
1:A:976:VAL:HG13	1:A:979:ASP:HB2	1.80	0.63
1:B:96:GLU:OE2	1:B:190:ARG:NH1	2.30	0.63
3:P:38:TRP:HB2	3:P:51:ILE:HG13	1.80	0.63
1:B:931:ILE:HD12	1:B:934:ILE:HD12	1.80	0.63
1:A:326:ILE:HD12	1:A:534:VAL:HG22	1.80	0.63
1:B:562:PHE:O	1:E:41:LYS:NZ	2.30	0.63
1:E:485:GLY:H	1:E:488:CYS:HB2	1.64	0.63
1:A:326:ILE:HD11	1:A:533:LEU:HA	1.79	0.63
1:E:722:VAL:HG22	1:E:930:ALA:HB1	1.81	0.63
1:E:905:ARG:O	1:E:1036:GLN:NE2	2.31	0.63
1:E:1029:MET:O	1:E:1033:VAL:HB	1.98	0.63
1:A:598:ILE:HB	1:A:609:ALA:HB3	1.81	0.62
1:E:454:ARG:HG3	1:E:492:LEU:HD23	1.81	0.62
1:E:1033:VAL:HG22	1:E:1051:SER:HB3	1.80	0.62
2:M:20:LEU:HD12	2:M:80:LEU:HD23	1.81	0.62
2:H:12:ILE:HG21	2:H:18:LEU:HD21	1.82	0.62
1:A:204:TYR:HB3	1:A:223:LEU:HB3	1.82	0.62
1:B:329:PHE:HB3	1:B:330:PRO:HD2	1.82	0.62
1:B:699:LEU:HD11	1:E:869:MET:HG2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:738:CYS:SG	1:A:739:THR:N	2.74	0.61
1:B:433:VAL:HG12	1:B:512:VAL:HG22	1.82	0.61
2:H:103:GLY:HA3	2:H:115:ARG:HH21	1.64	0.61
1:A:715:PRO:HD3	1:B:894:LEU:HD21	1.82	0.61
1:B:435:ALA:HB1	1:B:508:TYR:HB3	1.81	0.61
1:B:901:GLN:HA	1:B:904:TYR:HD2	1.65	0.61
1:A:1047:TYR:HB2	1:A:1067:TYR:HB3	1.83	0.61
1:E:99:ASN:OD1	1:E:190:ARG:NH1	2.29	0.61
1:A:1012:LEU:HB3	1:E:1013:ILE:HG21	1.81	0.61
1:B:715:PRO:HD3	1:E:894:LEU:HD21	1.82	0.60
1:B:976:VAL:HG13	1:B:979:ASP:HB2	1.83	0.60
1:A:1033:VAL:HG22	1:A:1051:SER:HB3	1.82	0.60
1:E:425:LEU:HD12	1:E:426:PRO:HD2	1.84	0.60
1:A:909:ILE:HG12	1:A:1047:TYR:HB3	1.84	0.60
1:B:484:GLU:HG3	2:O:56:THR:HG22	1.82	0.60
2:H:35:SER:HA	2:H:50:VAL:HA	1.82	0.60
1:B:339:GLY:HA3	5:B:1308:NAG:H82	1.83	0.60
1:E:854:LYS:HG3	1:E:859:THR:HG22	1.84	0.60
1:A:770:ILE:HD11	1:A:1012:LEU:HD23	1.84	0.60
1:B:948:LEU:HD11	1:B:1056:ALA:HB1	1.83	0.60
1:E:1028:LYS:O	1:E:1032:CYS:HB2	2.01	0.60
1:A:40:ASP:OD1	1:A:41:LYS:N	2.30	0.59
1:A:558:LYS:HG2	5:B:1303:NAG:H82	1.83	0.59
1:A:877:LEU:HD11	1:A:1034:LEU:HD11	1.83	0.59
1:B:296:LEU:HD21	1:B:602:THR:HG22	1.83	0.59
1:B:791:THR:HG21	1:B:806:LEU:HD11	1.83	0.59
1:A:236:THR:HG21	4:C:1:NAG:H5	1.84	0.59
1:A:457:ARG:NH1	1:A:460:ASN:O	2.35	0.59
1:A:758:SER:OG	1:E:965:GLN:NE2	2.26	0.59
1:B:130:VAL:HG11	1:B:231:ILE:HG12	1.83	0.59
3:N:11:VAL:HG22	3:N:12:SER:H	1.67	0.59
3:P:95:THR:O	3:P:99:THR:N	2.30	0.59
1:E:393:THR:HA	1:E:522:ALA:HA	1.84	0.59
1:A:296:LEU:HD21	1:A:602:THR:HG22	1.84	0.59
1:A:425:LEU:HD12	1:A:426:PRO:HD2	1.84	0.59
1:A:97:LYS:HE2	1:A:186:PHE:HA	1.84	0.59
1:E:598:ILE:HB	1:E:609:ALA:HB3	1.85	0.59
3:N:15:PRO:HA	3:N:81:LEU:HB2	1.85	0.59
1:B:1028:LYS:O	1:B:1032:CYS:HB2	2.03	0.59
1:B:494:SER:O	2:O:31:ASN:ND2	2.36	0.58
1:E:989:ALA:HB1	1:E:993:ILE:HD12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:34:MET:HG2	2:M:78:VAL:HG11	1.84	0.58
2:M:47:TRP:HZ2	2:M:50:VAL:HG12	1.69	0.58
1:E:493:GLN:HG2	2:M:31:ASN:HA	1.85	0.58
1:A:570:ALA:HB1	1:B:963:VAL:HG11	1.86	0.58
1:A:422:ASN:ND2	1:A:454:ARG:O	2.36	0.58
2:O:37:VAL:HG11	2:O:45:LEU:HD12	1.84	0.58
1:E:329:PHE:HE2	1:E:528:LYS:HZ2	1.51	0.57
2:H:62:SER:O	2:H:86:ARG:NH2	2.37	0.57
1:A:642:VAL:HG22	1:A:651:ILE:HG22	1.87	0.57
1:B:1036:GLN:NE2	1:B:1037:SER:O	2.37	0.57
1:A:862:PRO:HB3	1:E:646:ARG:HH11	1.68	0.57
2:H:47:TRP:HZ2	2:H:50:VAL:HG12	1.68	0.57
1:A:337:PRO:HD2	1:A:358:ILE:HG23	1.87	0.57
1:B:726:ILE:H	1:B:947:LYS:HE2	1.69	0.57
2:H:118:PHE:HB3	2:H:121:TRP:HE1	1.69	0.57
3:L:52:TYR:CE2	3:L:58:PRO:HG3	2.40	0.57
1:A:122:ASN:HB3	1:A:126:VAL:HG22	1.86	0.57
1:B:1116:THR:OG1	1:B:1119:ASN:ND2	2.38	0.57
1:B:985:ASP:O	1:B:989:ALA:CB	2.53	0.57
1:A:481:ASN:H	1:A:483:VAL:HG12	1.70	0.56
1:A:802:PHE:HD1	1:A:805:ILE:HD11	1.70	0.56
1:A:1028:LYS:NZ	1:A:1042:PHE:O	2.38	0.56
1:B:533:LEU:HD11	1:B:585:LEU:HD11	1.86	0.56
1:E:779:GLN:HG3	1:E:783:ALA:HB3	1.86	0.56
1:B:659:SER:HB2	1:B:698:SER:HB3	1.87	0.56
1:E:326:ILE:HD12	1:E:534:VAL:HG22	1.86	0.56
1:E:404:GLY:H	1:E:505:TYR:HA	1.70	0.56
2:O:106:ASP:OD2	2:O:115:ARG:NH1	2.35	0.56
1:A:740:MET:HG3	1:A:857:GLY:HA3	1.87	0.56
1:A:914:ASN:HD22	1:E:1123:SER:HB2	1.69	0.56
1:B:192:PHE:HD2	1:B:203:ILE:HD11	1.71	0.56
1:A:722:VAL:HG22	1:A:930:ALA:HB1	1.88	0.56
2:M:20:LEU:HB2	2:M:80:LEU:HB3	1.88	0.56
3:N:52:TYR:CE2	3:N:58:PRO:HG3	2.41	0.56
1:E:555:SER:HB3	1:E:584:ILE:HG22	1.87	0.56
3:P:92:SER:HB2	3:P:102:PHE:CZ	2.40	0.56
1:A:494:SER:H	2:H:30:ARG:HB3	1.70	0.56
3:N:68:SER:OG	3:N:75:SER:OG	2.24	0.56
1:B:712:ILE:HB	1:B:1077:THR:HB	1.88	0.56
1:A:736:VAL:H	1:A:767:LEU:HD13	1.70	0.55
2:H:24:ALA:O	2:H:76:ASN:ND2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:398:ASP:HB2	1:B:512:VAL:HB	1.88	0.55
1:E:926:GLN:NE2	5:E:1306:NAG:O6	2.38	0.55
1:B:102:ARG:HB3	1:B:141:LEU:HD13	1.87	0.55
1:E:481:ASN:H	1:E:483:VAL:HG12	1.70	0.55
1:E:308:VAL:HG22	1:E:602:THR:HG23	1.88	0.55
3:N:49:LEU:HD21	3:N:52:TYR:HD2	1.72	0.55
1:A:1129:VAL:HB	1:A:1132:ILE:HD11	1.89	0.55
2:M:115:ARG:NH2	2:M:117:TYR:OH	2.39	0.55
1:E:412:PRO:HB3	1:E:429:PHE:HB3	1.89	0.55
1:B:330:PRO:HA	1:B:579:PRO:HB2	1.87	0.55
3:N:11:VAL:CG1	3:N:21:PHE:HZ	2.14	0.55
1:A:729:VAL:HG22	1:A:1059:GLY:HA2	1.88	0.54
1:A:1041:ASP:HB3	1:B:1030:SER:HB3	1.89	0.54
1:B:1117:THR:HG22	1:B:1140:PRO:HD2	1.87	0.54
1:A:34:ARG:NH2	1:A:219:GLY:O	2.40	0.54
1:A:728:PRO:HB2	1:A:1018:ILE:HD12	1.89	0.54
1:B:570:ALA:HB1	1:E:963:VAL:HG11	1.90	0.54
3:L:49:LEU:HD21	3:L:52:TYR:HD2	1.72	0.54
1:B:779:GLN:HG3	1:B:783:ALA:HB3	1.89	0.54
1:E:122:ASN:HB3	1:E:126:VAL:HG22	1.89	0.54
2:M:62:SER:O	2:M:86:ARG:NH2	2.41	0.54
3:N:11:VAL:HG13	3:N:12:SER:N	2.21	0.54
1:A:189:LEU:HD11	1:A:210:ILE:HB	1.90	0.54
1:B:122:ASN:HB3	1:B:126:VAL:HG22	1.90	0.54
2:M:103:GLY:HA3	2:M:115:ARG:HH22	1.73	0.54
1:B:1123:SER:HB2	1:E:914:ASN:HD22	1.72	0.54
1:B:756:TYR:HB3	1:B:759:PHE:HD2	1.72	0.54
1:E:996:LEU:HD23	1:E:1000:ARG:HH12	1.73	0.54
1:A:854:LYS:HG3	1:A:859:THR:HG22	1.90	0.54
1:A:920:GLN:HA	1:A:923:ILE:HG22	1.88	0.54
1:E:119:ILE:HG12	1:E:128:ILE:HG13	1.90	0.54
2:H:52:TYR:O	2:H:71:ARG:NH2	2.41	0.54
1:A:1011:GLN:O	1:A:1015:ALA:HB2	2.08	0.54
1:B:308:VAL:HG22	1:B:602:THR:HG23	1.90	0.54
1:A:433:VAL:HG23	1:A:510:VAL:HG13	1.89	0.54
1:E:811:LYS:HE2	1:E:812:PRO:HD2	1.90	0.54
1:B:555:SER:HB3	1:B:584:ILE:HG12	1.88	0.53
1:E:716:THR:HA	1:E:1110:TYR:HB3	1.90	0.53
2:O:40:ALA:HB3	2:O:43:LYS:HB2	1.90	0.53
1:B:738:CYS:HB3	1:B:753:LEU:HD21	1.89	0.53
1:E:326:ILE:HD11	1:E:533:LEU:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:69:LYS:HA	3:L:74:ALA:HA	1.90	0.53
1:A:949:GLN:O	1:A:953:ASN:HB2	2.08	0.53
1:A:731:MET:H	1:A:774:GLN:HG2	1.72	0.53
2:H:45:LEU:HB2	3:L:102:PHE:CD1	2.44	0.53
1:A:646:ARG:HH11	1:B:862:PRO:HB3	1.71	0.53
1:B:274:THR:OG1	1:B:291:CYS:SG	2.63	0.53
1:B:1031:GLU:HG2	1:B:1037:SER:HB2	1.89	0.53
3:P:68:SER:OG	3:P:75:SER:OG	2.27	0.53
1:B:277:LEU:HD23	1:B:285:ILE:HD13	1.91	0.53
1:B:1028:LYS:NZ	1:B:1042:PHE:O	2.42	0.53
1:A:729:VAL:O	1:A:777:ASN:ND2	2.42	0.53
1:A:1028:LYS:O	1:A:1032:CYS:HB2	2.09	0.52
1:B:671:CYS:SG	1:B:697:MET:HG3	2.49	0.52
1:A:303:LEU:HD12	1:A:308:VAL:HG12	1.92	0.52
1:E:734:THR:HG21	1:E:959:LEU:HD21	1.90	0.52
2:O:34:MET:HB3	2:O:51:ILE:HG23	1.90	0.52
1:B:1116:THR:OG1	1:B:1118:ASP:OD1	2.26	0.52
1:A:569:ILE:HG13	1:B:47:VAL:HG12	1.90	0.52
1:B:402:ILE:HD13	1:B:410:ILE:HD12	1.92	0.52
3:N:49:LEU:HG	3:N:58:PRO:HG2	1.92	0.52
1:A:327:VAL:HG11	1:A:528:LYS:HD2	1.92	0.52
1:B:543:PHE:HB3	1:B:576:VAL:HG11	1.91	0.52
1:B:1107:ARG:HH22	1:E:885:GLY:HA3	1.75	0.52
3:L:49:LEU:HG	3:L:58:PRO:HG2	1.91	0.52
2:O:35:SER:HB2	2:O:96:ALA:HB3	1.90	0.52
1:A:142:GLY:HA3	1:A:156:GLU:HB2	1.92	0.52
1:B:490:PHE:O	2:O:113:ARG:NH2	2.40	0.52
1:B:736:VAL:H	1:B:767:LEU:HD23	1.73	0.52
2:O:62:SER:O	2:O:86:ARG:NH2	2.43	0.52
1:A:37:TYR:CD2	1:A:204:TYR:HE2	2.28	0.52
1:A:382:VAL:HG12	1:B:983:ARG:HG3	1.92	0.52
1:E:130:VAL:HB	1:E:168:PHE:HB3	1.90	0.52
3:L:36:VAL:HG13	3:L:54:VAL:HG13	1.92	0.52
1:A:44:ARG:NH2	1:A:279:TYR:OH	2.32	0.51
1:A:435:ALA:HB1	1:A:508:TYR:HB3	1.92	0.51
1:B:303:LEU:HD21	1:B:313:TYR:CD1	2.44	0.51
1:E:924:ALA:O	1:E:928:ASN:ND2	2.43	0.51
2:O:51:ILE:HB	2:O:69:ILE:HD12	1.92	0.51
1:A:722:VAL:HG12	1:A:1065:VAL:HA	1.92	0.51
1:E:858:LEU:HD21	1:E:963:VAL:HG22	1.92	0.51
1:E:887:THR:HB	1:E:894:LEU:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:GLY:HA3	1:A:56:LEU:HB3	1.92	0.51
1:A:1036:GLN:NE2	1:A:1037:SER:O	2.43	0.51
1:B:661:GLU:O	1:B:695:TYR:OH	2.28	0.51
1:B:742:ILE:HG23	1:B:1000:ARG:HD2	1.93	0.51
1:B:987:PRO:HB3	1:E:413:GLY:HA2	1.92	0.51
1:B:1002:GLN:HG3	1:E:759:PHE:CZ	2.46	0.51
1:E:433:VAL:HG23	1:E:510:VAL:HG13	1.91	0.51
1:A:37:TYR:OH	1:A:54:LEU:O	2.19	0.51
1:E:494:SER:H	2:M:30:ARG:HB3	1.76	0.51
1:B:919:ASN:OD1	1:B:922:LEU:HB2	2.11	0.51
1:E:296:LEU:HD21	1:E:602:THR:HG22	1.92	0.51
1:E:349:SER:HA	1:E:451:TYR:HD2	1.76	0.51
2:H:115:ARG:NH2	2:H:117:TYR:OH	2.43	0.51
1:E:129:LYS:NZ	1:E:131:CYS:HB2	2.26	0.51
1:A:1011:GLN:O	1:A:1015:ALA:CB	2.59	0.50
1:B:33:THR:HG23	1:B:58:PHE:HE2	1.76	0.50
3:N:69:LYS:HA	3:N:74:ALA:HA	1.93	0.50
3:N:36:VAL:HG13	3:N:54:VAL:HG13	1.92	0.50
1:B:719:THR:HG23	1:B:1068:VAL:HG23	1.93	0.50
1:B:34:ARG:NH2	1:B:219:GLY:O	2.44	0.50
1:B:108:THR:HA	1:B:236:THR:HG22	1.94	0.50
1:B:371:SER:HA	2:H:110:GLY:HA3	1.93	0.50
1:B:756:TYR:OH	1:B:994:ASP:OD1	2.28	0.50
1:B:815:ARG:HH12	1:B:820:ASP:HA	1.77	0.50
1:E:367:VAL:O	1:E:371:SER:OG	2.24	0.50
1:E:766:ALA:O	1:E:770:ILE:HG12	2.11	0.50
3:P:69:LYS:HA	3:P:74:ALA:HA	1.94	0.50
1:B:50:SER:HA	1:B:276:LEU:HA	1.94	0.50
1:B:52:GLN:HB3	1:B:274:THR:HG22	1.92	0.50
1:E:445:VAL:HA	1:E:499:PRO:HG2	1.94	0.50
1:E:647:ALA:HB2	1:E:668:ALA:HB3	1.94	0.50
2:H:34:MET:O	2:H:51:ILE:N	2.35	0.50
1:B:731:MET:SD	1:B:1018:ILE:HD13	2.52	0.50
1:A:86:PHE:HB2	1:A:238:PHE:HD1	1.77	0.49
1:A:787:GLN:OE1	1:E:703:ASN:ND2	2.38	0.49
1:A:1115:ILE:HG22	1:A:1137:VAL:HG13	1.92	0.49
1:B:189:LEU:HD21	1:B:210:ILE:HD12	1.93	0.49
1:A:661:GLU:O	1:A:695:TYR:OH	2.28	0.49
1:A:881:THR:HG21	1:A:1033:VAL:HG12	1.94	0.49
1:A:997:ILE:O	1:A:1001:LEU:HB3	2.11	0.49
1:B:373:SER:HB3	2:H:107:LEU:HD23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:454:ARG:HG2	1:B:492:LEU:HD13	1.95	0.49
1:E:560:LEU:HD12	1:E:561:PRO:HD2	1.95	0.49
1:A:55:PHE:HD2	1:A:275:PHE:CG	2.31	0.49
1:A:864:LEU:HA	1:E:667:GLY:HA2	1.94	0.49
1:B:392:PHE:HB2	1:B:524:VAL:HG13	1.94	0.49
3:P:88:ASP:OD1	3:P:88:ASP:N	2.46	0.49
1:B:129:LYS:HZ1	1:B:131:CYS:HB2	1.77	0.49
1:B:731:MET:H	1:B:774:GLN:HG2	1.78	0.49
1:E:1054:GLN:HB2	1:E:1061:VAL:HB	1.93	0.49
1:A:452:LEU:HD13	1:A:494:SER:HB3	1.93	0.49
1:B:493:GLN:HG2	2:O:31:ASN:HA	1.94	0.49
1:E:948:LEU:HA	1:E:951:VAL:HG12	1.95	0.49
1:B:121:ASN:OD1	1:B:122:ASN:N	2.46	0.49
1:B:611:LEU:HD21	1:B:666:ILE:HG23	1.95	0.49
1:B:761:THR:O	1:B:765:ARG:HB2	2.12	0.49
1:E:97:LYS:HG2	1:E:186:PHE:CE1	2.48	0.49
1:E:140:PHE:HA	1:E:241:LEU:HD22	1.93	0.49
1:A:983:ARG:HG2	1:E:390:LEU:HD21	1.95	0.49
1:B:899:PRO:HB2	1:B:917:TYR:HE1	1.77	0.49
2:H:66:ARG:NH2	2:H:89:ASP:OD2	2.43	0.49
1:A:737:ASP:OD1	1:A:740:MET:HB3	2.13	0.49
1:B:993:ILE:O	1:B:997:ILE:HD12	2.13	0.49
1:B:997:ILE:O	1:B:1001:LEU:CB	2.61	0.49
1:A:129:LYS:NZ	1:A:131:CYS:HB2	2.28	0.48
1:A:391:CYS:HB2	1:A:545:GLY:HA3	1.94	0.48
1:A:725:GLU:HG2	1:A:1064:HIS:CD2	2.48	0.48
1:B:920:GLN:HA	1:B:923:ILE:HG22	1.95	0.48
1:E:55:PHE:HD2	1:E:275:PHE:CG	2.31	0.48
1:A:742:ILE:HG23	1:A:1000:ARG:HD2	1.95	0.48
1:B:647:ALA:HB2	1:B:668:ALA:HB3	1.95	0.48
3:L:40:GLN:HB2	3:L:50:LEU:HD11	1.95	0.48
2:M:19:ARG:HH21	2:M:79:PHE:HD2	1.61	0.48
1:A:84:LEU:O	1:A:237:ARG:NH2	2.47	0.48
1:B:822:LEU:HD13	1:B:1061:VAL:HG21	1.95	0.48
1:B:740:MET:HB3	1:B:857:GLY:HA3	1.94	0.48
1:E:15:CYS:HA	1:E:158:ARG:HH21	1.78	0.48
2:M:44:GLY:HA2	3:N:90:TYR:CZ	2.48	0.48
1:A:905:ARG:HH21	1:A:1050:MET:HA	1.78	0.48
1:B:35:GLY:HA3	1:B:56:LEU:HB3	1.94	0.48
1:B:885:GLY:HA3	1:B:896:ILE:HD11	1.95	0.48
2:H:90:THR:HG23	2:H:128:THR:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:PHE:HB2	1:B:238:PHE:HD1	1.78	0.48
1:B:781:VAL:HG23	1:B:1029:MET:HG3	1.96	0.48
3:L:88:ASP:OD1	3:L:88:ASP:N	2.45	0.48
2:O:47:TRP:HZ2	2:O:50:VAL:HG12	1.78	0.48
1:A:43:PHE:O	1:E:566:GLY:HA2	2.13	0.48
1:A:1100:THR:HG23	1:A:1101:HIS:ND1	2.29	0.48
1:E:38:TYR:O	1:E:204:TYR:OH	2.20	0.48
1:E:189:LEU:HD21	1:E:210:ILE:HB	1.95	0.48
1:B:289:VAL:HG11	1:B:300:LYS:HD3	1.95	0.48
1:E:985:ASP:O	1:E:989:ALA:CB	2.62	0.48
1:A:714:ILE:HD12	1:A:1096:VAL:HG12	1.96	0.48
2:M:106:ASP:OD2	2:M:115:ARG:NH2	2.46	0.48
1:E:86:PHE:HB2	1:E:238:PHE:HD1	1.78	0.47
3:N:62:SER:OG	3:N:64:ARG:NE	2.45	0.47
1:A:712:ILE:HG23	1:A:1075:PHE:HB2	1.97	0.47
1:A:883:THR:O	1:A:896:ILE:N	2.47	0.47
1:E:714:ILE:HD12	1:E:1096:VAL:HG12	1.95	0.47
1:A:493:GLN:HG2	2:H:31:ASN:HA	1.95	0.47
1:A:997:ILE:O	1:A:1001:LEU:CB	2.63	0.47
1:E:770:ILE:HD11	1:E:1012:LEU:HD23	1.96	0.47
1:A:993:ILE:O	1:A:997:ILE:HG12	2.15	0.47
1:B:707:TYR:CD1	1:E:883:THR:HG22	2.49	0.47
1:B:716:THR:OG1	1:B:717:ASN:N	2.45	0.47
1:B:985:ASP:O	1:B:989:ALA:HB3	2.14	0.47
1:E:97:LYS:HE3	1:E:186:PHE:CD1	2.50	0.47
1:E:122:ASN:OD1	1:E:177:MET:N	2.48	0.47
2:M:90:THR:HG23	2:M:128:THR:HA	1.96	0.47
1:B:357:ARG:HH22	1:E:200:TYR:HE1	1.62	0.47
1:B:715:PRO:O	1:B:1110:TYR:N	2.42	0.47
1:B:804:GLN:O	1:B:817:PRO:HD2	2.15	0.47
1:B:889:GLY:HA3	1:B:1034:LEU:HD23	1.96	0.47
2:O:60:ALA:HB3	2:O:63:VAL:HG22	1.96	0.47
1:E:642:VAL:HG22	1:E:651:ILE:HG22	1.96	0.47
1:E:1100:THR:HG23	1:E:1101:HIS:ND1	2.29	0.47
2:M:60:ALA:HB3	2:M:63:VAL:HG22	1.95	0.47
1:E:289:VAL:HG11	1:E:300:LYS:HD3	1.95	0.47
2:H:4:LEU:HD12	2:H:121:TRP:HA	1.97	0.47
2:M:38:ARG:HD2	2:M:48:VAL:HG22	1.96	0.47
3:N:29:ASP:OD1	3:N:30:VAL:N	2.48	0.47
1:B:957:GLN:O	1:B:961:THR:OG1	2.26	0.47
1:A:159:VAL:HG23	1:A:160:TYR:CD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:23:GLN:OE1	1:E:23:GLN:N	2.43	0.47
1:A:210:ILE:HG13	1:A:217:PRO:HG3	1.97	0.47
1:A:393:THR:HA	1:A:522:ALA:HA	1.96	0.47
1:A:393:THR:HG21	1:A:519:HIS:H	1.79	0.47
1:B:344:ALA:HB3	1:B:347:PHE:HE1	1.78	0.47
1:B:431:GLY:HA2	1:B:515:PHE:HD1	1.80	0.47
1:B:650:LEU:HD21	1:B:653:ALA:HB3	1.97	0.47
1:B:1019:ARG:O	1:B:1023:ASN:ND2	2.38	0.47
2:O:38:ARG:HB2	2:O:91:ALA:HB3	1.96	0.47
3:P:36:VAL:HA	3:P:93:SER:HA	1.97	0.47
1:A:34:ARG:HG3	1:A:216:LEU:HD12	1.96	0.46
1:B:455:LEU:HD11	1:B:493:GLN:OE1	2.14	0.46
1:E:909:ILE:HG12	1:E:1036:GLN:NE2	2.30	0.46
1:E:946:GLY:O	1:E:950:ASP:HB2	2.14	0.46
3:P:36:VAL:HG13	3:P:54:VAL:HG13	1.96	0.46
1:A:788:ILE:HG23	1:A:876:ALA:HB2	1.97	0.46
1:E:712:ILE:HG23	1:E:1075:PHE:HB2	1.97	0.46
2:M:28:GLY:HA2	2:M:76:ASN:HD21	1.81	0.46
1:E:666:ILE:HD13	1:E:670:ILE:HG22	1.97	0.46
1:E:996:LEU:HB3	1:E:1000:ARG:NH1	2.30	0.46
1:A:34:ARG:NH1	1:A:217:PRO:O	2.47	0.46
2:H:47:TRP:CZ3	3:L:99:THR:HA	2.50	0.46
3:L:96:SER:OG	3:L:99:THR:O	2.33	0.46
3:P:49:LEU:HG	3:P:58:PRO:HG2	1.98	0.46
1:B:106:PHE:HD2	1:B:117:LEU:HB2	1.81	0.46
2:O:44:GLY:HA2	3:P:90:TYR:HE2	1.81	0.46
1:B:57:PRO:HB2	1:B:60:SER:HB2	1.98	0.46
1:B:466:ARG:NH1	1:B:468:ILE:HD11	2.30	0.46
1:E:100:ILE:HG22	1:E:242:LEU:HD22	1.98	0.46
1:E:740:MET:HG3	1:E:857:GLY:HA3	1.98	0.46
1:E:1129:VAL:HB	1:E:1132:ILE:HD11	1.97	0.46
1:B:722:VAL:HG22	1:B:930:ALA:HB1	1.98	0.46
1:B:766:ALA:O	1:B:770:ILE:HG12	2.16	0.46
1:E:393:THR:HG21	1:E:519:HIS:H	1.81	0.46
1:E:455:LEU:HD13	1:E:456:PHE:CE1	2.51	0.46
1:E:920:GLN:HA	1:E:923:ILE:HG22	1.98	0.46
1:A:987:PRO:HB3	1:B:413:GLY:HA2	1.98	0.46
1:B:438:SER:HB2	1:B:509:ARG:HG3	1.98	0.46
1:B:775:ASP:HA	1:B:778:THR:HG22	1.97	0.46
2:H:115:ARG:HG2	2:H:115:ARG:HH11	1.81	0.46
3:N:88:ASP:OD1	3:N:88:ASP:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:36:TRP:NE1	2:O:80:LEU:HB2	2.31	0.46
1:B:714:ILE:HD12	1:B:1096:VAL:HG12	1.98	0.45
1:B:814:LYS:HA	1:B:814:LYS:HD3	1.43	0.45
1:B:1095:PHE:HB3	1:B:1102:TRP:HE3	1.81	0.45
1:B:1135:ASN:OD1	1:B:1136:THR:N	2.48	0.45
1:A:862:PRO:HB3	1:E:646:ARG:NH1	2.32	0.45
1:B:355:ARG:NE	1:B:398:ASP:OD1	2.36	0.45
1:B:646:ARG:NH1	1:E:862:PRO:HB3	2.31	0.45
1:E:143:VAL:HG21	1:E:179:LEU:HD13	1.98	0.45
1:E:391:CYS:HB2	1:E:545:GLY:HA3	1.98	0.45
1:E:466:ARG:NH1	1:E:468:ILE:HD11	2.32	0.45
1:A:225:PRO:HD2	1:E:562:PHE:CZ	2.52	0.45
1:A:380:TYR:O	1:A:382:VAL:N	2.44	0.45
1:B:815:ARG:HB3	1:B:819:GLU:OE1	2.17	0.45
1:E:380:TYR:O	1:E:382:VAL:N	2.48	0.45
1:E:908:GLY:HA3	1:E:1036:GLN:OE1	2.17	0.45
1:B:291:CYS:HB3	1:B:301:CYS:HB2	1.37	0.45
1:B:337:PRO:HD2	1:B:358:ILE:HD12	1.98	0.45
1:B:422:ASN:ND2	1:B:454:ARG:O	2.50	0.45
1:A:295:PRO:HD2	1:A:608:VAL:HG21	1.98	0.45
1:A:801:ASN:OD1	1:A:802:PHE:N	2.50	0.45
1:B:1096:VAL:O	1:B:1102:TRP:HA	2.17	0.45
2:H:118:PHE:N	3:L:39:TYR:OH	2.49	0.45
1:A:1123:SER:HB2	1:B:914:ASN:HD22	1.82	0.45
1:E:896:ILE:HD13	1:E:896:ILE:HG21	1.76	0.45
3:L:38:TRP:HE1	3:L:91:CYS:HG	1.63	0.45
1:A:902:MET:SD	1:A:1049:LEU:HD23	2.57	0.45
1:B:99:ASN:OD1	1:B:190:ARG:NH1	2.34	0.45
1:B:437:ASN:C	1:B:437:ASN:ND2	2.65	0.45
1:B:997:ILE:O	1:B:1001:LEU:HB2	2.17	0.45
1:E:960:ASN:O	1:E:964:LYS:HG2	2.16	0.45
1:A:1086:LYS:HA	1:A:1086:LYS:HD3	1.83	0.45
1:B:728:PRO:HG3	1:B:951:VAL:HG11	1.98	0.45
1:E:728:PRO:HB3	1:E:951:VAL:HG21	1.99	0.45
1:E:1082:CYS:HB3	1:E:1134:ASN:HB3	1.97	0.45
1:E:1115:ILE:HG22	1:E:1137:VAL:HG13	1.99	0.45
2:H:33:TYR:CE2	2:H:113:ARG:HG2	2.52	0.45
3:L:29:ASP:OD1	3:L:30:VAL:N	2.50	0.45
3:L:45:LYS:NZ	3:L:46:ALA:O	2.47	0.45
1:A:490:PHE:O	2:H:53:SER:OG	2.35	0.45
1:A:650:LEU:HD21	1:A:653:ALA:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:202:LYS:HE3	1:E:204:TYR:OH	2.17	0.45
1:E:457:ARG:HG3	1:E:458:LYS:H	1.81	0.45
3:P:14:SER:HA	3:P:15:PRO:HD2	1.88	0.45
1:A:609:ALA:HB2	1:A:692:ILE:HD12	1.99	0.44
1:A:1080:ALA:HB3	1:A:1132:ILE:HG12	1.99	0.44
1:E:984:LEU:HB3	1:E:989:ALA:HB2	1.99	0.44
3:N:38:TRP:HB2	3:N:51:ILE:HG13	2.00	0.44
3:N:107:LYS:HD2	3:N:107:LYS:HA	1.59	0.44
1:A:666:ILE:HD13	1:A:670:ILE:HG22	2.00	0.44
1:B:326:ILE:HD11	1:B:533:LEU:HA	1.98	0.44
1:E:365:TYR:HD1	1:E:368:LEU:HD22	1.82	0.44
2:M:81:GLN:HE22	2:M:83:ASN:HB3	1.82	0.44
1:B:878:LEU:HD11	1:B:1053:PRO:O	2.18	0.44
1:E:426:PRO:HB3	1:E:463:PRO:HB3	2.00	0.44
1:E:959:LEU:O	1:E:963:VAL:HG23	2.17	0.44
1:A:1014:ARG:O	1:A:1018:ILE:HG12	2.17	0.44
1:E:905:ARG:NH2	1:E:1035:GLY:O	2.48	0.44
1:E:1080:ALA:HB3	1:E:1132:ILE:HG12	1.98	0.44
2:M:85:LEU:HD22	2:M:129:VAL:HG22	1.99	0.44
2:O:45:LEU:HD23	2:O:45:LEU:H	1.82	0.44
3:P:29:ASP:OD1	3:P:30:VAL:N	2.49	0.44
1:B:210:ILE:HG13	1:B:217:PRO:HG3	2.00	0.44
1:B:905:ARG:NE	1:B:1050:MET:HB3	2.32	0.44
1:E:736:VAL:H	1:E:767:LEU:HD13	1.82	0.44
1:A:54:LEU:HB3	1:A:270:LEU:HD23	2.00	0.44
1:A:99:ASN:O	1:A:102:ARG:NH2	2.45	0.44
1:B:130:VAL:HB	1:B:168:PHE:HB3	2.00	0.44
2:H:47:TRP:CD1	3:L:100:ARG:HD2	2.51	0.44
2:M:38:ARG:HB2	2:M:91:ALA:HB3	1.99	0.44
1:A:378:LYS:NZ	1:A:380:TYR:OH	2.31	0.44
1:A:763:LEU:HD12	1:A:1008:VAL:HG21	1.99	0.44
1:B:86:PHE:CZ	1:B:89:GLY:HA2	2.52	0.44
1:B:121:ASN:HD22	1:B:179:LEU:HD21	1.82	0.44
1:B:1129:VAL:HB	1:B:1132:ILE:HD11	2.00	0.44
1:E:86:PHE:CZ	1:E:89:GLY:HA2	2.52	0.44
2:M:19:ARG:NH1	2:M:81:GLN:HB2	2.32	0.44
2:O:37:VAL:HG22	3:P:100:ARG:NH2	2.33	0.44
3:P:45:LYS:HE3	3:P:46:ALA:O	2.17	0.44
1:A:525:CYS:HB2	1:A:526:GLY:H	1.62	0.44
1:A:826:VAL:HG22	1:A:949:GLN:NE2	2.32	0.44
1:B:364:ASP:HA	1:B:527:PRO:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:882:ILE:HA	1:B:898:PHE:HE1	1.83	0.44
1:B:1030:SER:HA	1:B:1034:LEU:HB2	2.00	0.44
2:H:60:ALA:HB3	2:H:63:VAL:HG22	1.99	0.44
1:A:931:ILE:HD13	1:A:934:ILE:HD12	2.00	0.44
3:N:92:SER:HB2	3:N:102:PHE:CZ	2.53	0.44
1:A:906:PHE:HA	1:A:909:ILE:HG22	2.00	0.43
1:B:129:LYS:NZ	1:B:131:CYS:HB2	2.32	0.43
1:B:934:ILE:HG23	1:B:938:LEU:HD13	1.99	0.43
1:A:816:SER:HB3	1:A:819:GLU:HB3	1.99	0.43
1:B:540:ASN:HA	1:B:549:THR:HA	2.00	0.43
1:E:657:ASN:OD1	5:E:1305:NAG:N2	2.52	0.43
1:E:742:ILE:HD11	1:E:1004:LEU:HD23	1.99	0.43
1:E:814:LYS:HD3	1:E:814:LYS:HA	1.32	0.43
3:P:15:PRO:HA	3:P:81:LEU:HB2	2.00	0.43
1:A:699:LEU:HD12	1:B:873:TYR:OH	2.19	0.43
1:A:825:LYS:HE2	1:A:939:SER:HA	2.00	0.43
1:B:91:TYR:OH	1:B:191:GLU:OE1	2.23	0.43
1:B:117:LEU:HD13	1:B:130:VAL:HG22	1.99	0.43
1:E:282:ASN:OD1	5:E:1303:NAG:N2	2.51	0.43
3:N:64:ARG:NH1	3:N:80:GLY:O	2.51	0.43
1:A:194:PHE:HE1	1:A:203:ILE:HG23	1.82	0.43
1:A:826:VAL:HG21	1:A:948:LEU:HD23	2.00	0.43
1:A:1031:GLU:OE2	1:E:1039:ARG:NE	2.38	0.43
1:B:712:ILE:HG23	1:B:1075:PHE:HB2	2.00	0.43
1:E:777:ASN:HA	1:E:780:GLU:OE1	2.19	0.43
3:L:68:SER:N	3:L:75:SER:O	2.46	0.43
1:A:243:ALA:HA	1:A:258:TRP:HZ2	1.83	0.43
1:B:974:SER:O	1:B:980:ILE:HD11	2.18	0.43
1:E:525:CYS:HB2	1:E:526:GLY:H	1.72	0.43
1:E:722:VAL:HG12	1:E:1065:VAL:HA	2.01	0.43
3:L:86:GLU:HA	3:L:108:VAL:HG23	2.01	0.43
2:M:99:GLY:HA2	2:M:119:ASP:HB2	1.99	0.43
1:B:1076:THR:N	1:B:1097:SER:OG	2.38	0.43
2:M:33:TYR:CE1	2:M:113:ARG:HG2	2.46	0.43
1:B:78:ARG:HB3	1:B:79:PHE:H	1.49	0.43
1:B:815:ARG:HG2	1:B:871:ALA:HB2	2.00	0.43
1:B:906:PHE:HA	1:B:909:ILE:HG12	2.00	0.43
1:E:979:ASP:O	1:E:983:ARG:HB2	2.19	0.43
1:A:365:TYR:HD1	1:A:368:LEU:HD22	1.83	0.43
1:A:734:THR:HG21	1:A:959:LEU:HD21	2.00	0.43
1:B:501:ASN:HD22	1:B:502:GLY:H	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:589:PRO:HD2	1:E:855:PHE:CG	2.54	0.43
1:B:971:GLY:O	1:B:995:ARG:NH1	2.52	0.43
1:E:727:LEU:HD11	1:E:1028:LYS:HE3	2.00	0.43
3:L:6:GLN:HG3	3:L:103:GLY:HA3	2.01	0.43
1:B:543:PHE:HD2	1:B:587:ILE:HD11	1.83	0.43
1:E:725:GLU:HG2	1:E:1064:HIS:CD2	2.53	0.43
3:N:36:VAL:HA	3:N:93:SER:HA	2.01	0.43
2:O:29:VAL:HG23	2:O:76:ASN:OD1	2.19	0.43
1:A:886:TRP:CH2	1:A:904:TYR:HB3	2.54	0.43
1:A:1090:PRO:HD3	1:A:1095:PHE:HE1	1.84	0.43
1:B:758:SER:O	1:B:762:GLN:HG2	2.19	0.43
1:B:1015:ALA:O	1:B:1019:ARG:HG2	2.19	0.43
1:E:454:ARG:HD2	1:E:457:ARG:HB3	2.01	0.43
1:E:729:VAL:O	1:E:777:ASN:ND2	2.52	0.43
1:E:1056:ALA:HB2	1:E:1061:VAL:HG23	2.01	0.43
1:A:289:VAL:HG11	1:A:300:LYS:HD3	2.00	0.42
1:A:454:ARG:HH22	1:A:467:ASP:HB3	1.84	0.42
1:B:927:PHE:HZ	1:B:1052:PHE:HE2	1.65	0.42
1:E:37:TYR:HB2	1:E:204:TYR:CD2	2.54	0.42
2:H:51:ILE:HG12	2:H:69:ILE:HD12	2.01	0.42
2:M:12:ILE:HD11	2:M:85:LEU:HD11	2.01	0.42
1:A:404:GLY:H	1:A:505:TYR:HA	1.84	0.42
1:A:455:LEU:HD21	2:H:111:TYR:CD1	2.54	0.42
1:A:726:ILE:O	1:A:947:LYS:HE3	2.19	0.42
1:A:731:MET:HG2	1:A:955:ASN:HD21	1.84	0.42
1:E:378:LYS:NZ	1:E:380:TYR:OH	2.41	0.42
1:E:444:LYS:HB2	1:E:444:LYS:HE3	1.62	0.42
1:E:726:ILE:O	1:E:947:LYS:HD2	2.19	0.42
1:A:129:LYS:HZ1	1:A:131:CYS:HB2	1.84	0.42
1:E:87:ASN:OD1	1:E:88:ASP:N	2.49	0.42
1:E:609:ALA:HB2	1:E:692:ILE:HD12	2.00	0.42
3:L:36:VAL:HA	3:L:93:SER:HA	2.00	0.42
1:B:816:SER:O	1:B:820:ASP:HB2	2.19	0.42
1:E:1086:LYS:HA	1:E:1125:ASN:HA	2.02	0.42
2:M:34:MET:HB3	2:M:51:ILE:HG23	2.00	0.42
1:A:117:LEU:HD13	1:A:130:VAL:HG22	2.02	0.42
1:B:54:LEU:HB3	1:B:270:LEU:HD23	2.00	0.42
1:B:141:LEU:HA	1:B:159:VAL:HG22	2.01	0.42
1:B:825:LYS:NZ	1:B:939:SER:O	2.41	0.42
1:E:784:GLN:OE1	1:E:1034:LEU:HD21	2.20	0.42
2:H:18:LEU:HB2	2:H:82:MET:SD	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:51:ILE:HB	3:P:54:VAL:HA	2.01	0.42
1:A:291:CYS:HA	1:A:297:SER:OG	2.20	0.42
1:A:308:VAL:HG22	1:A:602:THR:HG23	2.02	0.42
1:B:335:LEU:HD13	1:B:335:LEU:HA	1.81	0.42
1:B:1051:SER:HB3	1:B:1064:HIS:ND1	2.35	0.42
1:E:38:TYR:CD1	1:E:285:ILE:HD12	2.55	0.42
2:O:20:LEU:HD12	2:O:80:LEU:HD23	2.02	0.42
1:A:105:ILE:O	1:A:238:PHE:HA	2.20	0.42
1:A:452:LEU:HA	1:A:494:SER:HA	2.02	0.42
1:A:743:CYS:HB3	1:A:749:CYS:HB3	1.81	0.42
1:B:418:ILE:HA	1:B:422:ASN:OD1	2.19	0.42
2:H:29:VAL:HG23	2:H:76:ASN:OD1	2.20	0.42
1:A:741:TYR:CZ	1:A:966:LEU:HD13	2.53	0.42
1:B:326:ILE:HD12	1:B:534:VAL:H	1.85	0.42
1:B:560:LEU:H	1:B:563:GLN:NE2	2.18	0.42
1:B:741:TYR:CE2	1:B:966:LEU:HD13	2.55	0.42
1:B:1132:ILE:HG22	1:B:1134:ASN:H	1.85	0.42
1:B:1134:ASN:OD1	5:B:1307:NAG:N2	2.52	0.42
1:E:930:ALA:O	1:E:934:ILE:HG12	2.20	0.42
1:A:452:LEU:HD11	2:H:30:ARG:HH11	1.84	0.42
1:A:906:PHE:CD2	1:A:916:LEU:HB2	2.55	0.42
1:B:767:LEU:HD12	1:B:767:LEU:HA	1.89	0.42
1:B:957:GLN:O	1:B:961:THR:CB	2.68	0.42
1:A:646:ARG:NH1	1:B:862:PRO:HB3	2.35	0.42
1:A:814:LYS:HD3	1:A:814:LYS:HA	1.36	0.42
1:B:33:THR:HG22	1:B:220:PHE:HD1	1.85	0.42
1:B:484:GLU:OE1	1:B:484:GLU:N	2.53	0.42
1:B:725:GLU:HG2	1:B:1064:HIS:CD2	2.55	0.42
1:B:905:ARG:HG2	1:B:1036:GLN:HB2	2.02	0.42
1:B:1030:SER:HA	1:B:1034:LEU:HD22	2.00	0.42
1:E:645:THR:HG21	1:E:670:ILE:HG13	2.02	0.42
1:E:712:ILE:HB	1:E:1077:THR:HB	2.02	0.42
3:N:95:THR:HG1	3:N:99:THR:N	2.18	0.42
1:A:136:CYS:SG	1:A:137:ASN:N	2.93	0.41
1:A:763:LEU:HD21	1:A:1005:GLN:NE2	2.35	0.41
1:B:437:ASN:HB2	1:B:506:GLN:HG3	2.02	0.41
1:B:743:CYS:HB3	1:B:749:CYS:HB3	1.74	0.41
1:B:1082:CYS:HB2	1:B:1126:CYS:HB2	1.99	0.41
1:E:34:ARG:NH2	1:E:191:GLU:OE2	2.53	0.41
1:E:435:ALA:HB1	1:E:508:TYR:HB3	2.02	0.41
1:E:454:ARG:HA	1:E:491:PRO:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:897:PRO:HG2	1:E:900:MET:SD	2.60	0.41
1:E:909:ILE:HG12	1:E:1036:GLN:HE21	1.83	0.41
2:M:51:ILE:HB	2:M:69:ILE:HD12	2.01	0.41
3:P:86:GLU:HA	3:P:108:VAL:HG23	2.02	0.41
1:B:380:TYR:O	1:B:382:VAL:N	2.50	0.41
1:B:699:LEU:HD22	1:E:873:TYR:CE2	2.56	0.41
1:E:355:ARG:NE	1:E:398:ASP:OD1	2.40	0.41
2:H:40:ALA:HB3	2:H:43:LYS:HB2	2.02	0.41
3:P:9:SER:HA	3:P:107:LYS:O	2.20	0.41
1:A:191:GLU:O	1:A:205:SER:HA	2.20	0.41
1:A:452:LEU:HD11	2:H:30:ARG:NH1	2.35	0.41
1:E:980:ILE:HG23	1:E:984:LEU:HD13	2.01	0.41
1:A:1076:THR:O	1:A:1097:SER:HB3	2.20	0.41
2:M:37:VAL:HG21	2:M:45:LEU:HD13	2.02	0.41
2:M:43:LYS:O	3:N:90:TYR:OH	2.38	0.41
3:P:68:SER:N	3:P:75:SER:O	2.51	0.41
1:B:462:LYS:HE3	1:B:462:LYS:HB3	1.93	0.41
1:B:979:ASP:HB3	1:B:983:ARG:HH21	1.85	0.41
1:E:129:LYS:HZ1	1:E:131:CYS:HB2	1.86	0.41
1:E:351:TYR:CD1	1:E:452:LEU:HB2	2.55	0.41
1:E:484:GLU:HA	1:E:488:CYS:HB2	2.03	0.41
1:A:289:VAL:HG13	1:A:306:PHE:CE1	2.56	0.41
1:A:818:ILE:HG22	1:A:935:GLN:NE2	2.35	0.41
1:B:726:ILE:HD12	1:B:1061:VAL:HG22	2.02	0.41
1:E:395:VAL:HG12	1:E:515:PHE:HD1	1.84	0.41
2:O:45:LEU:HD21	3:P:102:PHE:CE2	2.56	0.41
3:P:7:PRO:O	3:P:106:THR:HG22	2.20	0.41
1:A:1086:LYS:HA	1:A:1125:ASN:HA	2.03	0.41
1:B:774:GLN:HA	1:B:777:ASN:ND2	2.35	0.41
1:E:295:PRO:HG2	1:E:610:VAL:HG22	2.02	0.41
1:E:1076:THR:N	1:E:1097:SER:OG	2.35	0.41
2:M:92:VAL:HA	2:M:126:LEU:HA	2.02	0.41
1:A:927:PHE:HZ	1:A:1052:PHE:HE2	1.69	0.41
1:B:444:LYS:HG3	1:B:446:GLY:H	1.86	0.41
1:B:1011:GLN:O	1:B:1015:ALA:N	2.44	0.41
1:E:697:MET:HG2	1:E:698:SER:O	2.21	0.41
1:E:902:MET:HG3	1:E:916:LEU:HD11	2.02	0.41
2:M:35:SER:HA	2:M:50:VAL:HA	2.03	0.41
3:P:29:ASP:HB3	3:P:96:SER:HB3	2.03	0.41
1:A:467:ASP:OD2	1:A:469:SER:OG	2.36	0.41
1:A:667:GLY:HA2	1:B:864:LEU:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:895:GLN:HG3	1:E:705:VAL:HG22	2.02	0.41
1:B:48:LEU:HD23	1:B:276:LEU:HD13	2.03	0.41
1:B:122:ASN:OD1	1:B:177:MET:HG2	2.21	0.41
1:B:204:TYR:HB3	1:B:223:LEU:HB3	2.03	0.41
1:B:242:LEU:HD23	1:B:242:LEU:HA	1.89	0.41
1:B:467:ASP:OD2	1:B:469:SER:OG	2.36	0.41
1:B:716:THR:HA	1:B:1110:TYR:HB3	2.03	0.41
1:B:896:ILE:HD13	1:B:896:ILE:HG21	1.72	0.41
1:B:985:ASP:O	1:B:989:ALA:HB2	2.21	0.41
1:E:65:PHE:CZ	1:E:84:LEU:HD13	2.56	0.41
1:E:782:PHE:HB3	1:E:873:TYR:HB3	2.03	0.41
1:E:934:ILE:HG23	1:E:938:LEU:HD13	2.02	0.41
1:E:989:ALA:O	1:E:993:ILE:HB	2.21	0.41
2:H:38:ARG:CZ	2:H:46:GLU:HB3	2.51	0.41
3:P:4:LEU:O	3:P:103:GLY:HA2	2.20	0.41
3:P:38:TRP:CZ3	3:P:76:LEU:HB2	2.55	0.41
1:A:960:ASN:HA	1:A:963:VAL:HG22	2.03	0.41
1:B:223:LEU:HD23	1:B:223:LEU:HA	1.88	0.41
1:B:979:ASP:O	1:B:983:ARG:HB3	2.20	0.41
1:B:1098:ASN:OD1	5:B:1306:NAG:N2	2.54	0.41
1:E:291:CYS:HA	1:E:297:SER:OG	2.21	0.41
1:A:291:CYS:HB3	1:A:301:CYS:HB2	1.38	0.40
1:A:448:ASN:N	1:A:448:ASN:OD1	2.52	0.40
1:B:143:VAL:HA	1:B:154:GLU:HG3	2.02	0.40
1:B:777:ASN:OD1	1:B:778:THR:N	2.54	0.40
1:E:99:ASN:HD22	1:E:178:ASP:N	2.14	0.40
1:E:303:LEU:HD21	1:E:313:TYR:CD1	2.55	0.40
1:E:650:LEU:HD21	1:E:653:ALA:HB3	2.01	0.40
1:E:849:LEU:O	1:E:853:GLN:HG2	2.20	0.40
3:N:29:ASP:HB3	3:N:96:SER:HB3	2.02	0.40
1:A:731:MET:SD	1:A:1018:ILE:HG13	2.62	0.40
1:B:357:ARG:HD3	1:E:230:PRO:HB2	2.03	0.40
1:B:740:MET:HA	1:B:744:GLY:HA2	2.03	0.40
1:E:133:PHE:HB2	1:E:135:PHE:CE1	2.56	0.40
1:E:788:ILE:HG23	1:E:876:ALA:HB2	2.03	0.40
2:O:118:PHE:CD2	2:O:121:TRP:HZ2	2.39	0.40
1:A:129:LYS:HD2	1:A:129:LYS:HA	1.91	0.40
1:A:355:ARG:NE	1:A:398:ASP:OD1	2.41	0.40
1:A:470:THR:HB	1:A:490:PHE:CE1	2.57	0.40
1:A:980:ILE:HG23	1:A:984:LEU:HD12	2.02	0.40
1:B:387:LEU:HD23	1:B:387:LEU:HA	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:101:ILE:HA	1:E:242:LEU:HD23	2.03	0.40
1:E:328:ARG:HD2	1:E:328:ARG:HA	1.96	0.40
1:E:1073:LYS:HA	1:E:1073:LYS:HD2	1.86	0.40
3:L:49:LEU:HD21	3:L:52:TYR:CD2	2.56	0.40
1:A:44:ARG:HH12	1:A:49:HIS:CE1	2.38	0.40
2:H:35:SER:OG	3:L:100:ARG:NH1	2.51	0.40
2:H:99:GLY:HA3	2:H:117:TYR:CZ	2.57	0.40
1:A:131:CYS:HB3	1:A:133:PHE:CZ	2.57	0.40
1:A:444:LYS:HB2	1:A:448:ASN:N	2.37	0.40
1:B:355:ARG:HD2	1:B:396:TYR:CD1	2.57	0.40
1:B:877:LEU:HD23	1:B:877:LEU:HA	1.86	0.40
3:L:45:LYS:HZ1	3:L:48:LYS:HB3	1.87	0.40
3:N:7:PRO:O	3:N:106:THR:HG22	2.22	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	A	1018/1271 (80%)	959 (94%)	59 (6%)	0	100 100
1	B	1018/1271 (80%)	965 (95%)	53 (5%)	0	100 100
1	E	1018/1271 (80%)	966 (95%)	52 (5%)	0	100 100
2	H	127/237 (54%)	114 (90%)	13 (10%)	0	100 100
2	M	127/237 (54%)	114 (90%)	13 (10%)	0	100 100
2	O	127/237 (54%)	113 (89%)	14 (11%)	0	100 100
3	L	106/216 (49%)	101 (95%)	5 (5%)	0	100 100
3	N	106/216 (49%)	99 (93%)	7 (7%)	0	100 100
3	P	106/216 (49%)	100 (94%)	6 (6%)	0	100 100
All	All	3753/5172 (73%)	3531 (94%)	222 (6%)	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	A	866/1109 (78%)	856 (99%)	10 (1%)	71 87
1	B	866/1109 (78%)	852 (98%)	14 (2%)	62 83
1	E	866/1109 (78%)	845 (98%)	21 (2%)	49 76
2	H	103/198 (52%)	101 (98%)	2 (2%)	57 80
2	M	103/198 (52%)	102 (99%)	1 (1%)	76 89
2	O	103/198 (52%)	103 (100%)	0	100 100
3	L	91/184 (50%)	86 (94%)	5 (6%)	21 56
3	N	91/184 (50%)	89 (98%)	2 (2%)	52 78
3	P	91/184 (50%)	88 (97%)	3 (3%)	38 69
All	All	3180/4473 (71%)	3122 (98%)	58 (2%)	61 81

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	378	LYS
1	A	444	LYS
1	A	445	VAL
1	A	503	VAL
1	A	506	GLN
1	A	710	ASN
1	A	810	SER
1	A	811	LYS
1	A	814	LYS
1	A	815	ARG
1	B	78	ARG
1	B	335	LEU
1	B	378	LYS
1	B	386	LYS
1	B	437	ASN

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Mol	Chain	Res	Type
1	B	501	ASN
1	B	503	VAL
1	B	506	GLN
1	B	811	LYS
1	B	813	SER
1	B	814	LYS
1	B	1010	GLN
1	B	1014	ARG
1	B	1058	HIS
1	E	78	ARG
1	E	329	PHE
1	E	386	LYS
1	E	444	LYS
1	E	445	VAL
1	E	454	ARG
1	E	455	LEU
1	E	498	GLN
1	E	500	THR
1	E	503	VAL
1	E	506	GLN
1	E	738	CYS
1	E	758	SER
1	E	759	PHE
1	E	761	THR
1	E	810	SER
1	E	811	LYS
1	E	813	SER
1	E	814	LYS
1	E	1010	GLN
1	E	1058	HIS
2	H	38	ARG
2	H	81	GLN
3	L	9	SER
3	L	11	VAL
3	L	40	GLN
3	L	41	GLN
3	L	51	ILE
2	M	38	ARG
3	N	51	ILE
3	N	107	LYS
3	P	11	VAL
3	P	40	GLN

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Mol	Chain	Res	Type
3	P	51	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	437	ASN
1	B	487	ASN
1	B	501	ASN
1	B	563	GLN
1	B	774	GLN
1	B	965	GLN
1	B	1119	ASN
1	E	926	GLN
1	E	1048	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	C	1	4,1	14,14,15	0.34	0	17,19,21	0.75	1 (5%)
4	NAG	C	2	4	14,14,15	0.61	0	17,19,21	0.91	2 (11%)
4	NAG	D	1	4,1	14,14,15	0.22	0	17,19,21	0.90	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	D	2	4	14,14,15	0.29	0	17,19,21	0.49	0
4	NAG	F	1	4,1	14,14,15	0.21	0	17,19,21	0.69	0
4	NAG	F	2	4	14,14,15	0.71	0	17,19,21	0.89	1 (5%)
4	NAG	G	1	4,1	14,14,15	0.31	0	17,19,21	1.04	1 (5%)
4	NAG	G	2	4	14,14,15	0.28	0	17,19,21	0.50	0

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

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

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	1	NAG	C1-O5-C5	4.04	117.67	112.19
4	C	2	NAG	C2-N2-C7	2.52	126.49	122.90
4	D	1	NAG	C2-N2-C7	2.48	126.43	122.90
4	F	2	NAG	C2-N2-C7	2.45	126.39	122.90
4	C	2	NAG	C1-O5-C5	2.08	115.02	112.19
4	C	1	NAG	O4-C4-C3	-2.01	105.70	110.35

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	2	NAG	O5-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6

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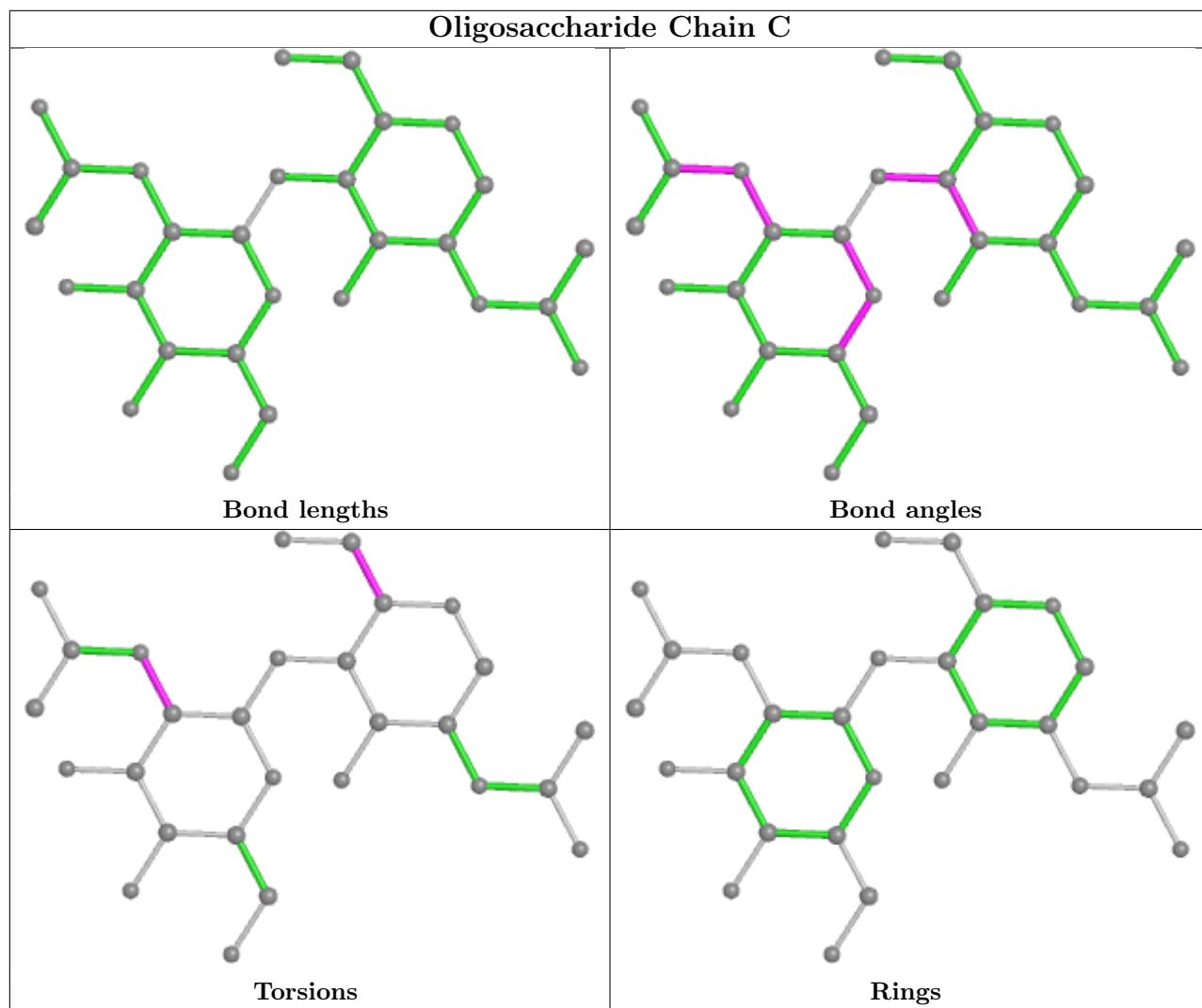
Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O5-C5-C6-O6
4	C	1	NAG	C4-C5-C6-O6
4	C	1	NAG	O5-C5-C6-O6
4	D	1	NAG	C4-C5-C6-O6
4	C	2	NAG	C3-C2-N2-C7
4	D	1	NAG	C3-C2-N2-C7
4	F	2	NAG	C3-C2-N2-C7

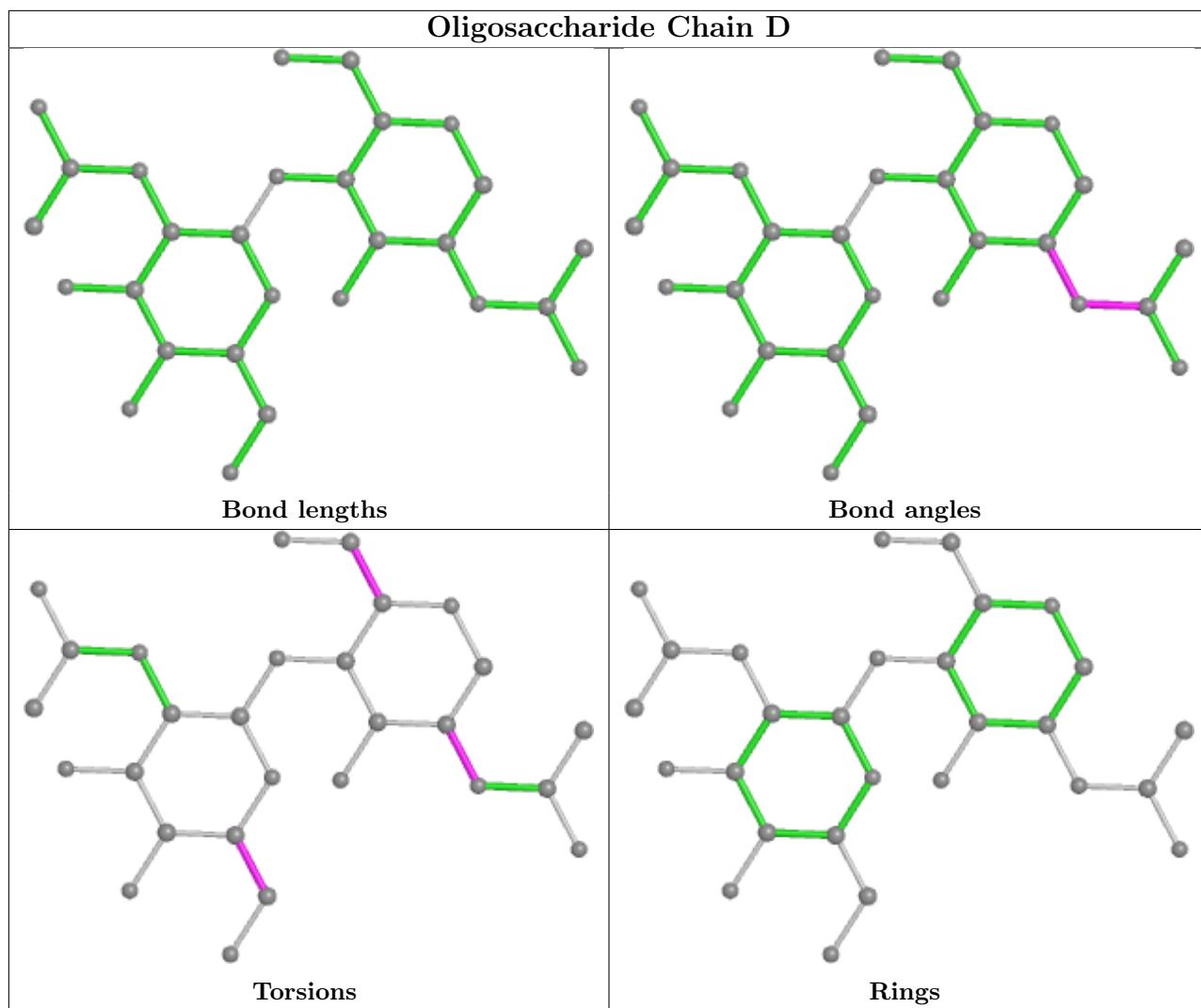
There are no ring outliers.

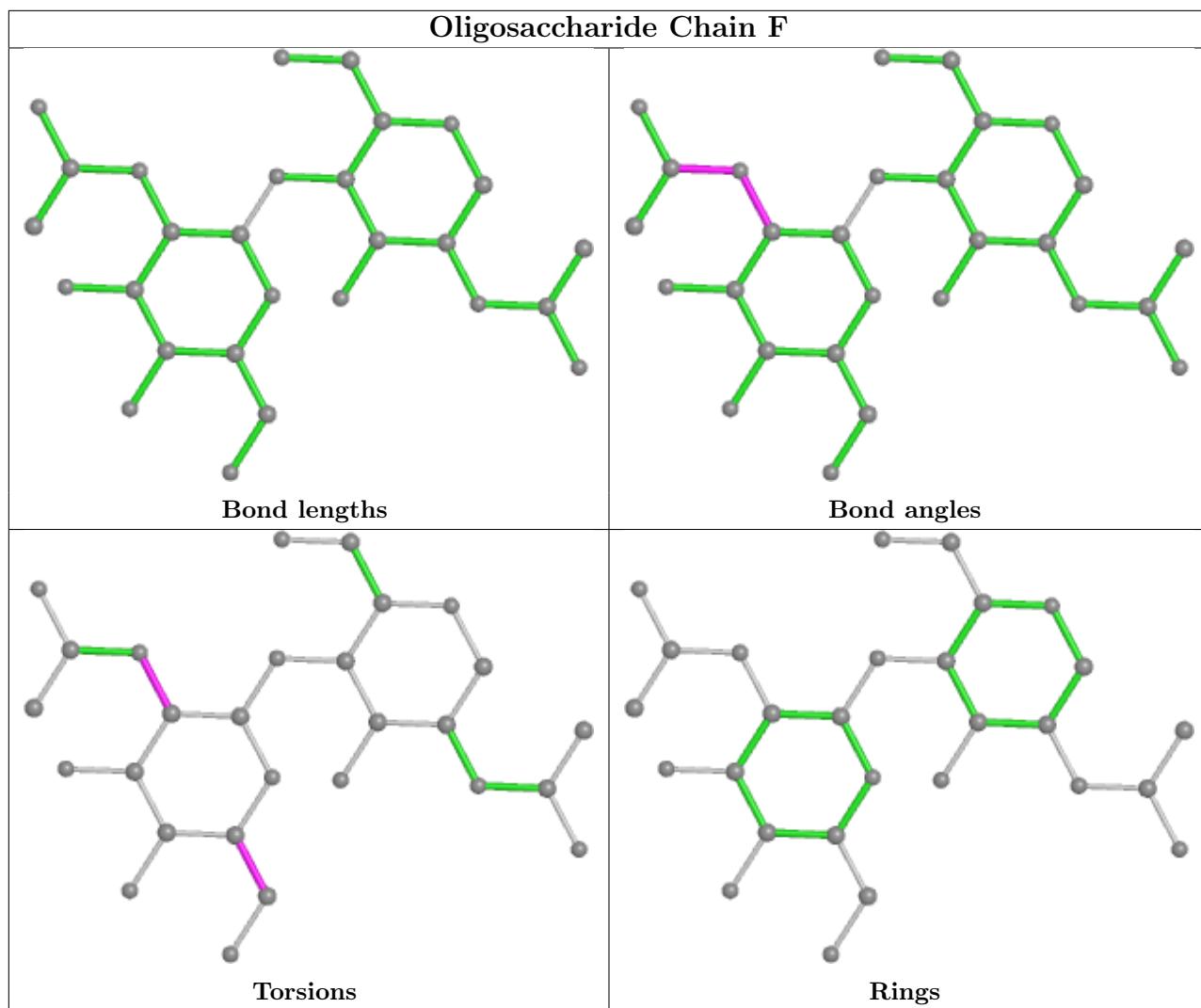
1 monomer is involved in 1 short contact:

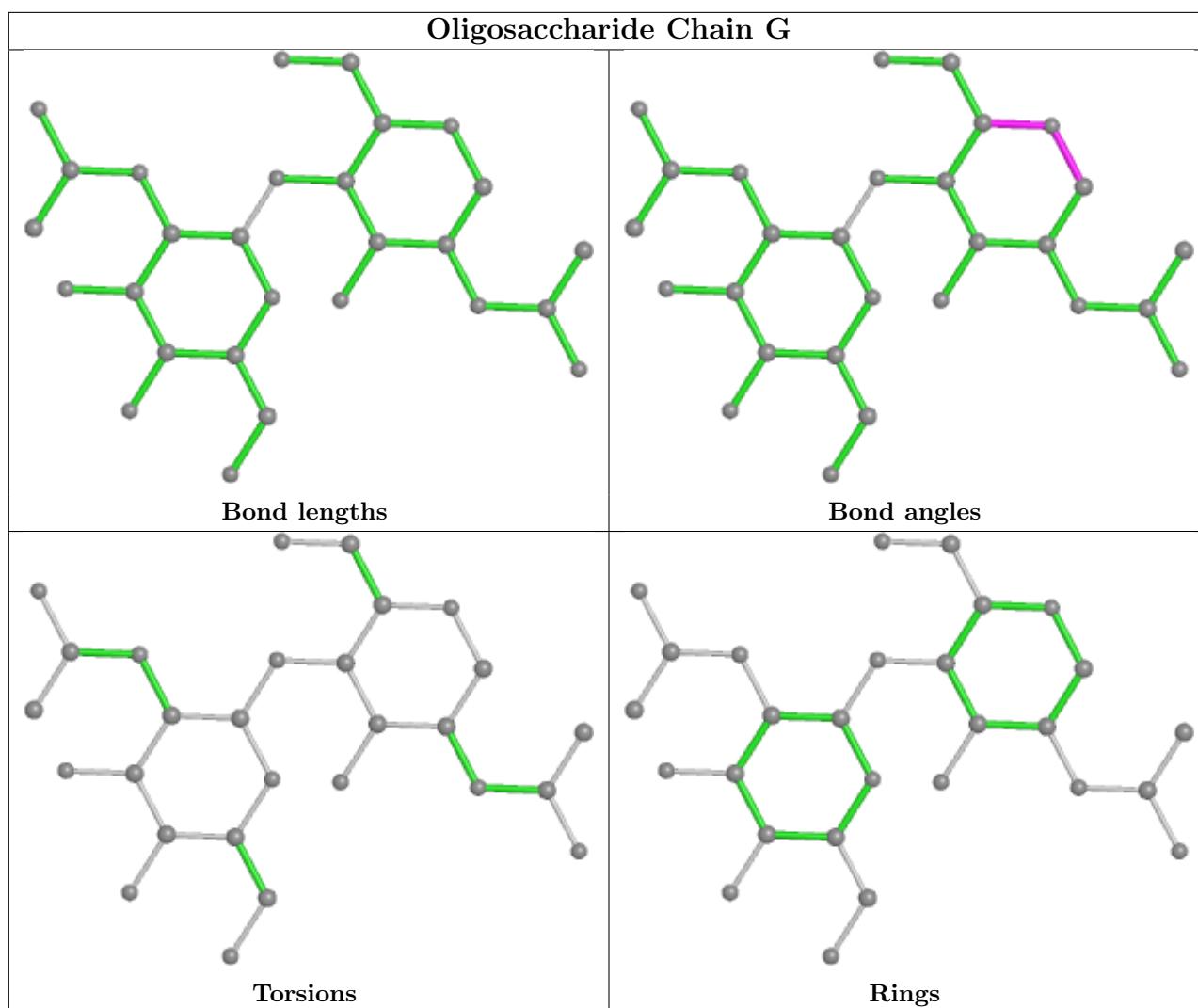
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1	NAG	1	0

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









## 5.6 Ligand geometry (i)

27 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
5	NAG	B	1303	1	14,14,15	0.37	0	17,19,21	0.95	1 (5%)
5	NAG	B	1306	1	14,14,15	0.82	1 (7%)	17,19,21	1.04	2 (11%)
5	NAG	A	1306	1	14,14,15	0.58	0	17,19,21	1.00	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	E	1306	1	14,14,15	0.24	0	17,19,21	0.54	0
5	NAG	E	1310	1	14,14,15	0.52	0	17,19,21	0.42	0
5	NAG	E	1303	1	14,14,15	0.59	0	17,19,21	1.31	2 (11%)
5	NAG	B	1302	1	14,14,15	0.38	0	17,19,21	0.45	0
5	NAG	B	1309	1	14,14,15	0.29	0	17,19,21	0.50	0
5	NAG	A	1307	1	14,14,15	0.30	0	17,19,21	0.53	0
5	NAG	B	1305	1	14,14,15	0.41	0	17,19,21	0.46	0
5	NAG	A	1305	1	14,14,15	0.53	0	17,19,21	0.55	0
5	NAG	E	1302	1	14,14,15	0.68	0	17,19,21	0.42	0
5	NAG	E	1307	1	14,14,15	0.47	0	17,19,21	1.01	2 (11%)
5	NAG	E	1309	1	14,14,15	0.40	0	17,19,21	0.35	0
5	NAG	A	1308	1	14,14,15	0.36	0	17,19,21	0.60	0
5	NAG	B	1304	1	14,14,15	0.18	0	17,19,21	0.78	1 (5%)
5	NAG	A	1302	1	14,14,15	0.44	0	17,19,21	0.93	2 (11%)
5	NAG	A	1303	1	14,14,15	0.41	0	17,19,21	1.12	2 (11%)
5	NAG	E	1304	1	14,14,15	0.39	0	17,19,21	0.56	0
5	NAG	B	1307	1	14,14,15	0.88	1 (7%)	17,19,21	0.77	0
5	NAG	B	1308	1	14,14,15	0.60	0	17,19,21	0.49	0
5	NAG	B	1301	1	14,14,15	0.31	0	17,19,21	0.56	0
5	NAG	A	1301	1	14,14,15	0.42	0	17,19,21	0.40	0
5	NAG	A	1304	1	14,14,15	0.24	0	17,19,21	0.62	0
5	NAG	E	1305	1	14,14,15	0.71	1 (7%)	17,19,21	1.37	3 (17%)
5	NAG	E	1301	1	14,14,15	0.43	0	17,19,21	0.46	0
5	NAG	E	1308	1	14,14,15	0.52	0	17,19,21	0.79	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	B	1303	1	-	3/6/23/26	0/1/1/1
5	NAG	B	1306	1	-	3/6/23/26	0/1/1/1
5	NAG	A	1306	1	-	3/6/23/26	0/1/1/1
5	NAG	E	1306	1	-	2/6/23/26	0/1/1/1
5	NAG	E	1310	1	-	1/6/23/26	0/1/1/1
5	NAG	E	1303	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1302	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1309	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1307	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1305	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1305	1	-	2/6/23/26	0/1/1/1
5	NAG	E	1302	1	-	2/6/23/26	0/1/1/1
5	NAG	E	1307	1	-	3/6/23/26	0/1/1/1
5	NAG	E	1309	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1302	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1303	1	-	3/6/23/26	0/1/1/1
5	NAG	E	1304	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1307	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1308	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
5	NAG	E	1305	1	-	1/6/23/26	0/1/1/1
5	NAG	E	1301	1	-	2/6/23/26	0/1/1/1
5	NAG	E	1308	1	-	3/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1307	NAG	C1-C2	3.03	1.56	1.52
5	B	1306	NAG	C1-C2	2.78	1.56	1.52
5	E	1305	NAG	C1-C2	2.48	1.56	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1303	NAG	C2-N2-C7	3.68	128.15	122.90
5	B	1303	NAG	C1-O5-C5	3.35	116.74	112.19
5	B	1306	NAG	C1-O5-C5	2.93	116.17	112.19
5	A	1303	NAG	C2-N2-C7	2.92	127.05	122.90
5	A	1306	NAG	C1-O5-C5	2.90	116.12	112.19
5	E	1305	NAG	C1-O5-C5	2.87	116.08	112.19
5	E	1307	NAG	C2-N2-C7	2.83	126.93	122.90
5	E	1305	NAG	C1-C2-N2	2.81	115.29	110.49
5	E	1305	NAG	C2-N2-C7	2.75	126.83	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1303	NAG	C1-O5-C5	2.66	115.80	112.19
5	A	1303	NAG	C1-O5-C5	2.52	115.61	112.19
5	E	1308	NAG	C2-N2-C7	2.46	126.40	122.90
5	B	1304	NAG	C1-O5-C5	2.45	115.51	112.19
5	A	1302	NAG	C1-O5-C5	2.37	115.41	112.19
5	A	1302	NAG	C2-N2-C7	2.37	126.28	122.90
5	A	1306	NAG	C2-N2-C7	2.29	126.16	122.90
5	B	1306	NAG	C2-N2-C7	2.28	126.15	122.90
5	E	1307	NAG	C1-O5-C5	2.10	115.03	112.19

There are no chirality outliers.

All (54) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	1304	NAG	O5-C5-C6-O6
5	A	1301	NAG	O5-C5-C6-O6
5	E	1307	NAG	C4-C5-C6-O6
5	A	1307	NAG	O5-C5-C6-O6
5	A	1308	NAG	O5-C5-C6-O6
5	B	1303	NAG	O5-C5-C6-O6
5	E	1302	NAG	C4-C5-C6-O6
5	A	1306	NAG	O5-C5-C6-O6
5	E	1304	NAG	C4-C5-C6-O6
5	A	1304	NAG	O5-C5-C6-O6
5	B	1302	NAG	O5-C5-C6-O6
5	A	1306	NAG	C4-C5-C6-O6
5	E	1302	NAG	O5-C5-C6-O6
5	E	1308	NAG	O5-C5-C6-O6
5	B	1309	NAG	O5-C5-C6-O6
5	E	1309	NAG	O5-C5-C6-O6
5	E	1306	NAG	C4-C5-C6-O6
5	A	1301	NAG	C4-C5-C6-O6
5	B	1306	NAG	O5-C5-C6-O6
5	E	1301	NAG	O5-C5-C6-O6
5	E	1306	NAG	O5-C5-C6-O6
5	E	1307	NAG	O5-C5-C6-O6
5	E	1308	NAG	C4-C5-C6-O6
5	A	1304	NAG	C4-C5-C6-O6
5	A	1305	NAG	C4-C5-C6-O6
5	B	1302	NAG	C4-C5-C6-O6
5	B	1306	NAG	C4-C5-C6-O6
5	A	1307	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	B	1303	NAG	C4-C5-C6-O6
5	B	1307	NAG	C8-C7-N2-C2
5	B	1307	NAG	O7-C7-N2-C2
5	B	1309	NAG	C4-C5-C6-O6
5	A	1308	NAG	C4-C5-C6-O6
5	E	1301	NAG	C4-C5-C6-O6
5	A	1303	NAG	C4-C5-C6-O6
5	E	1309	NAG	C4-C5-C6-O6
5	A	1303	NAG	O5-C5-C6-O6
5	A	1305	NAG	O5-C5-C6-O6
5	B	1301	NAG	C4-C5-C6-O6
5	E	1310	NAG	O5-C5-C6-O6
5	B	1308	NAG	O5-C5-C6-O6
5	B	1301	NAG	O5-C5-C6-O6
5	B	1303	NAG	C1-C2-N2-C7
5	B	1308	NAG	C1-C2-N2-C7
5	A	1302	NAG	C3-C2-N2-C7
5	B	1306	NAG	C3-C2-N2-C7
5	E	1303	NAG	C3-C2-N2-C7
5	E	1305	NAG	C3-C2-N2-C7
5	E	1307	NAG	C3-C2-N2-C7
5	E	1308	NAG	C3-C2-N2-C7
5	B	1307	NAG	C4-C5-C6-O6
5	A	1303	NAG	C3-C2-N2-C7
5	A	1306	NAG	C3-C2-N2-C7
5	B	1307	NAG	O5-C5-C6-O6

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1303	NAG	1	0
5	B	1306	NAG	1	0
5	E	1306	NAG	1	0
5	E	1303	NAG	1	0
5	B	1307	NAG	1	0
5	B	1308	NAG	1	0
5	E	1305	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.

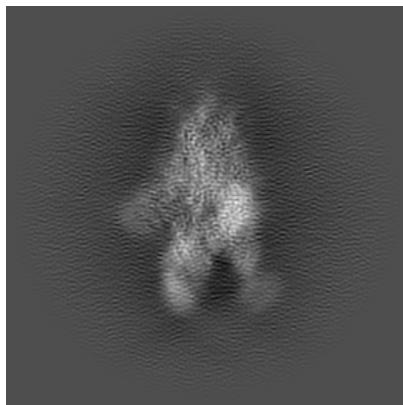
## 6 Map visualisation i

This section contains visualisations of the EMDB entry EMD-24319. These allow visual inspection of the internal detail of the map and identification of artifacts.

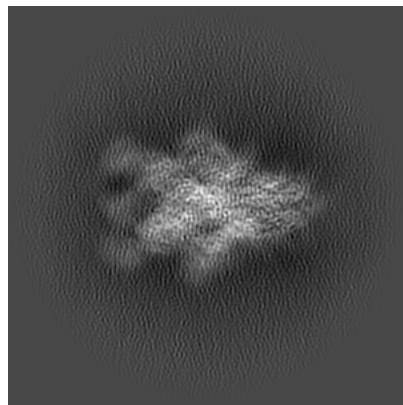
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections i

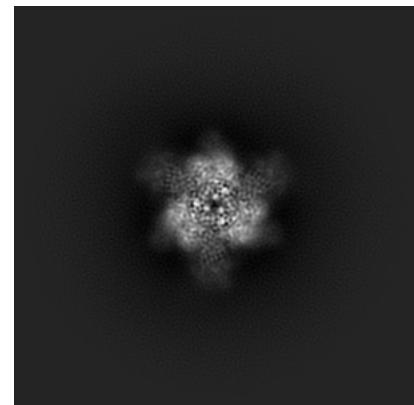
#### 6.1.1 Primary map



X



Y

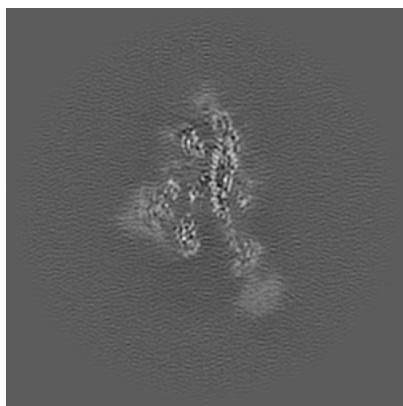


Z

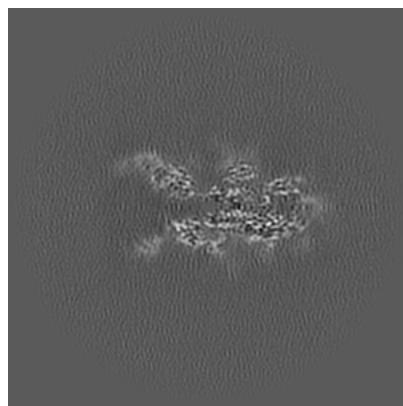
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices i

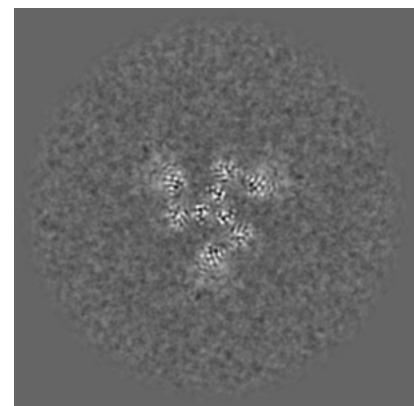
#### 6.2.1 Primary map



X Index: 216



Y Index: 216

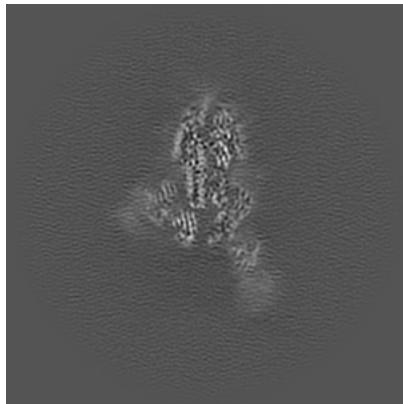


Z Index: 216

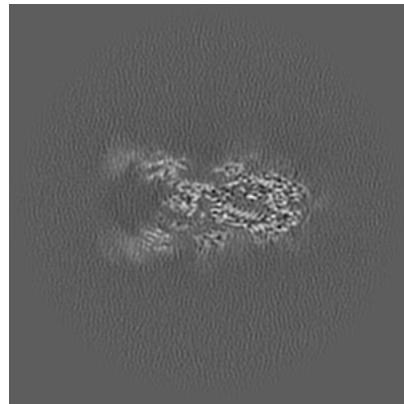
The images above show central slices of the map in three orthogonal directions.

### 6.3 Largest variance slices [\(i\)](#)

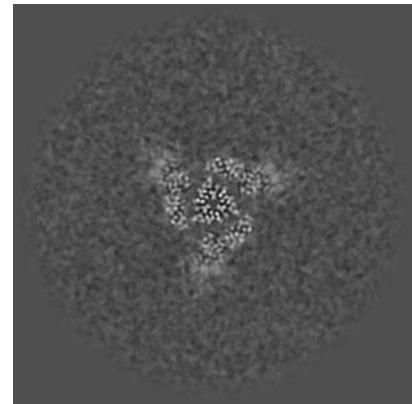
#### 6.3.1 Primary map



X Index: 224



Y Index: 202

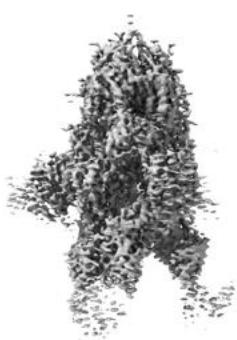


Z Index: 224

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 0.14. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

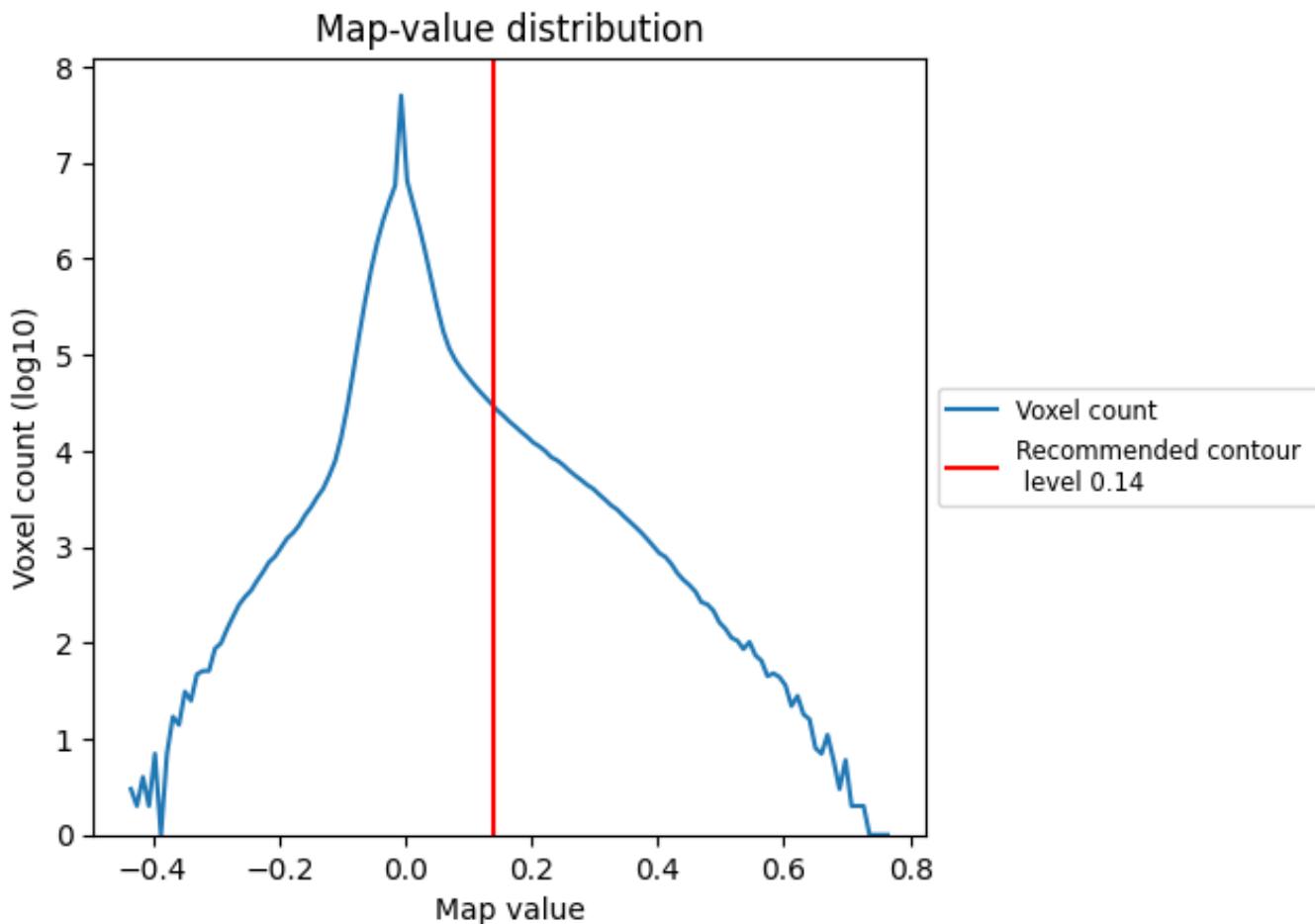
## 6.5 Mask visualisation

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

## 7 Map analysis (i)

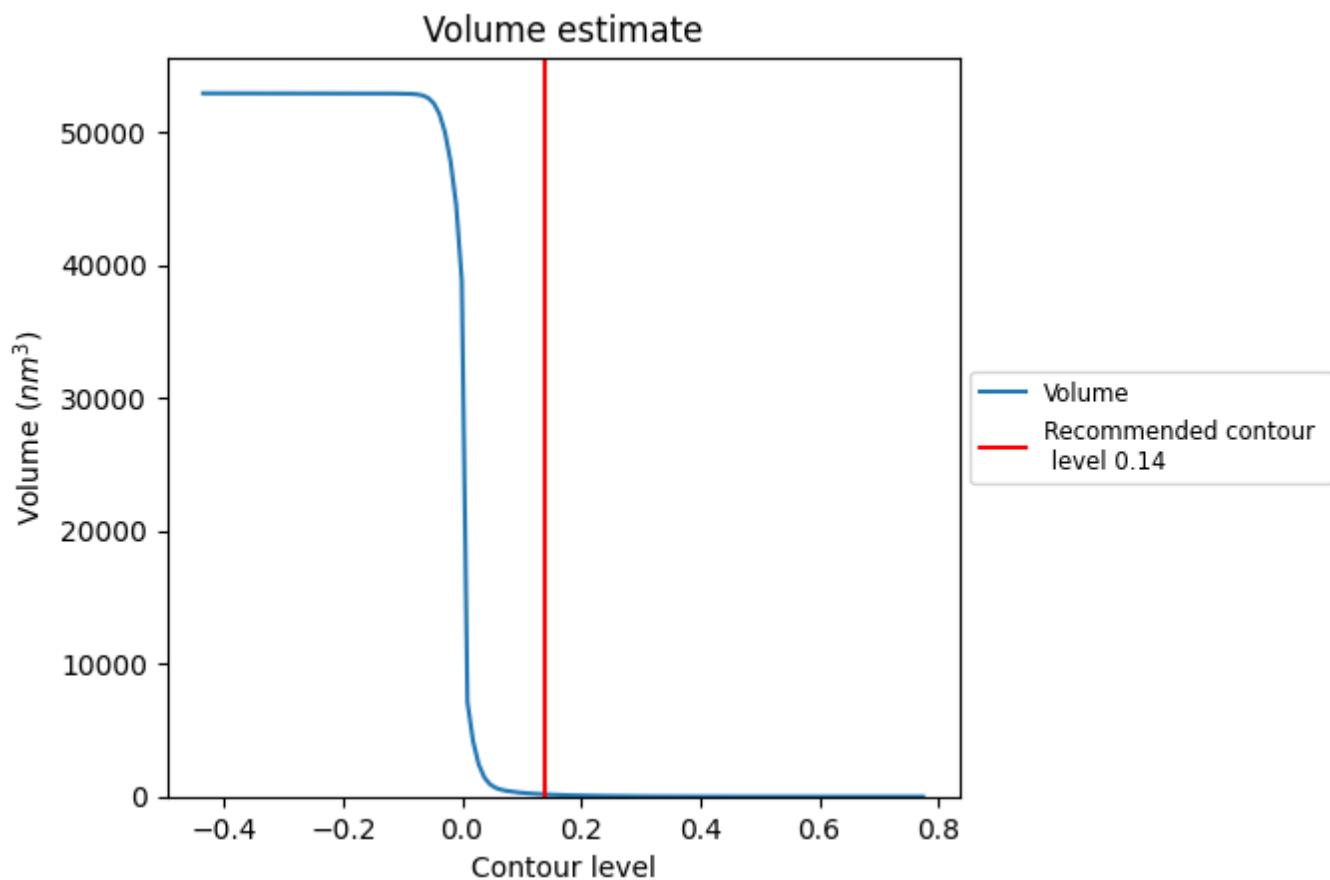
This section contains the results of statistical analysis of the map.

### 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.

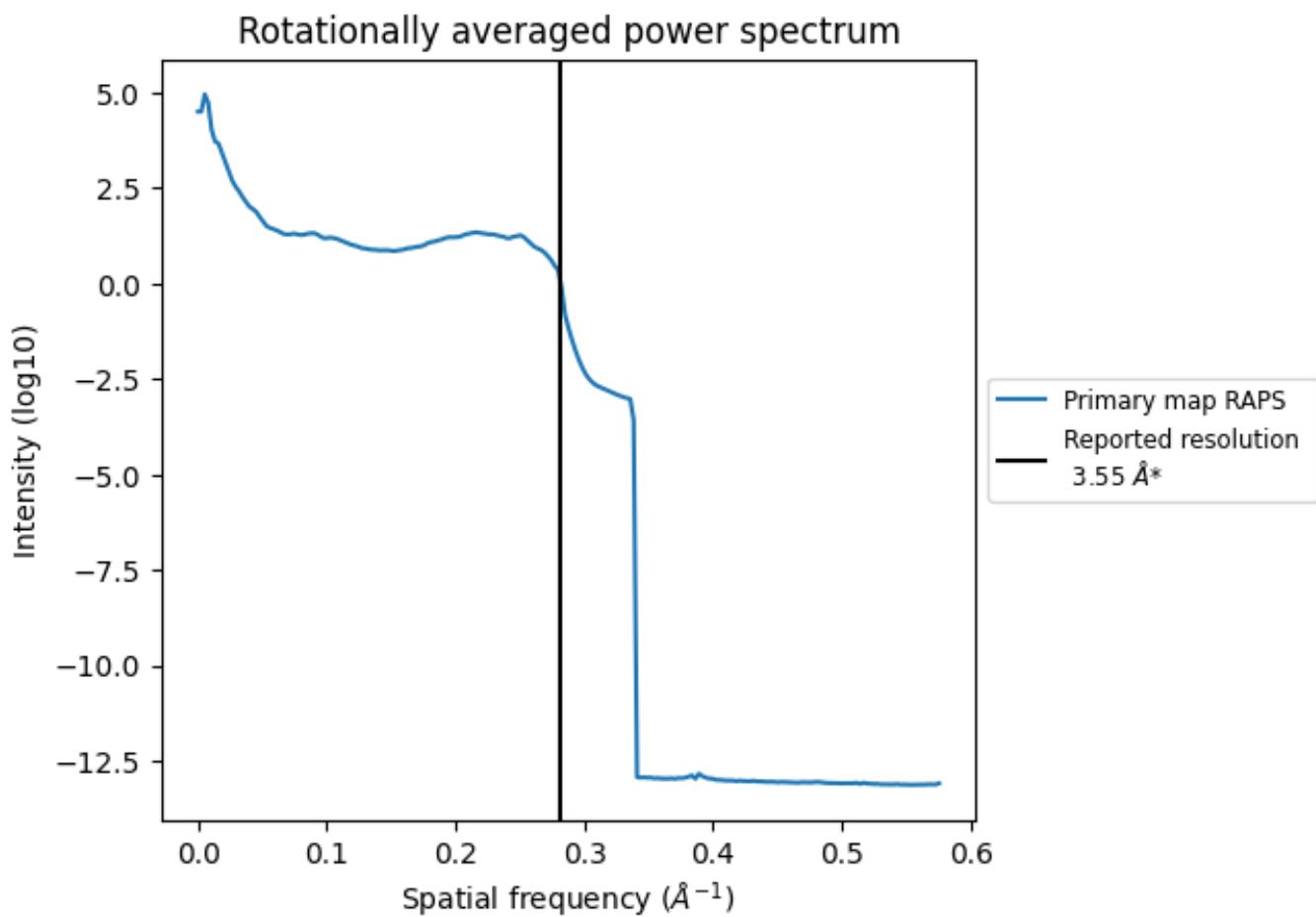
## 7.2 Volume estimate (i)



The volume at the recommended contour level is  $161 \text{ nm}^3$ ; this corresponds to an approximate mass of 145 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 [\(i\)](#)

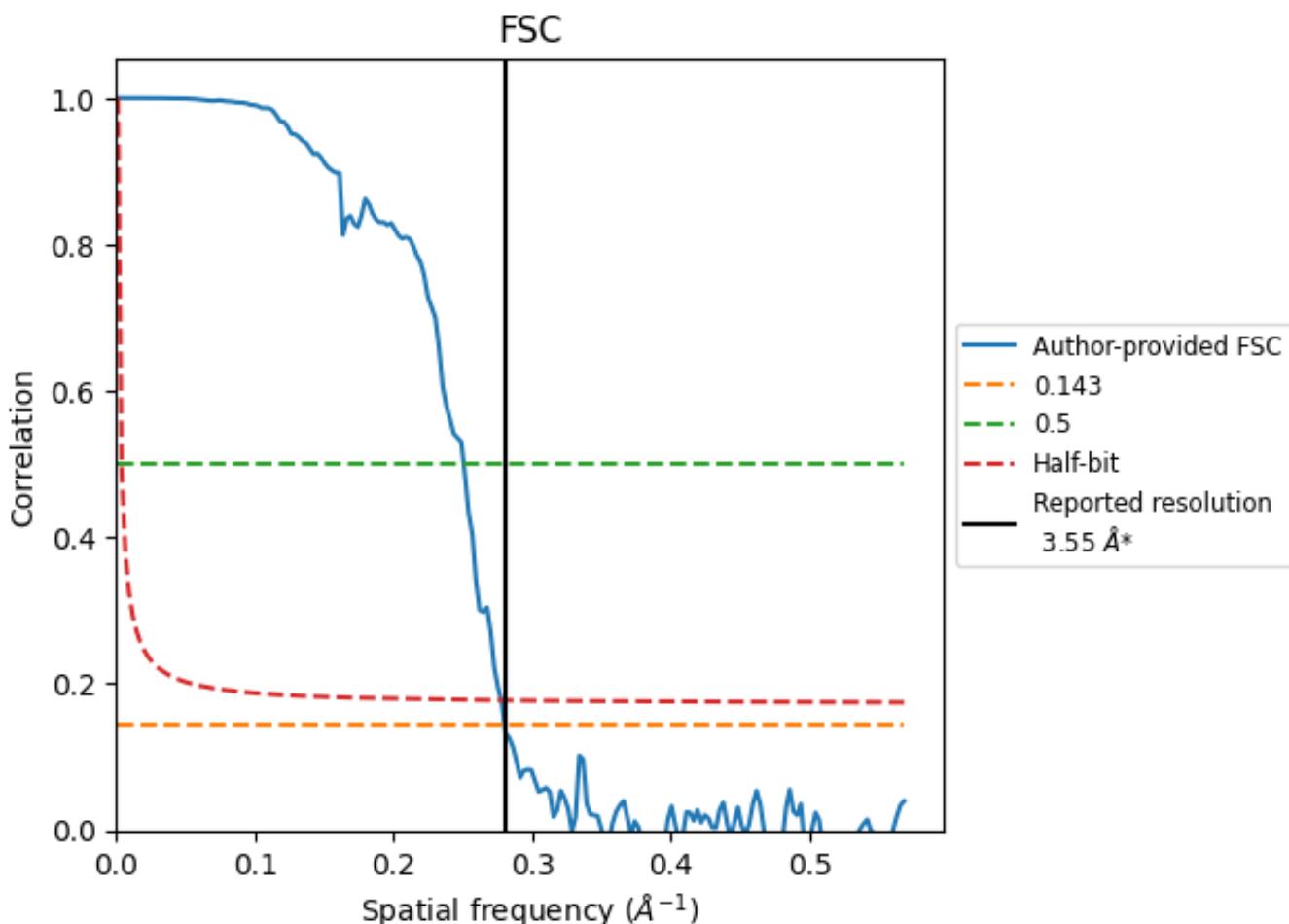


\*Reported resolution corresponds to spatial frequency of  $0.282 \text{ \AA}^{-1}$

## 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  $0.282 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [\(i\)](#)

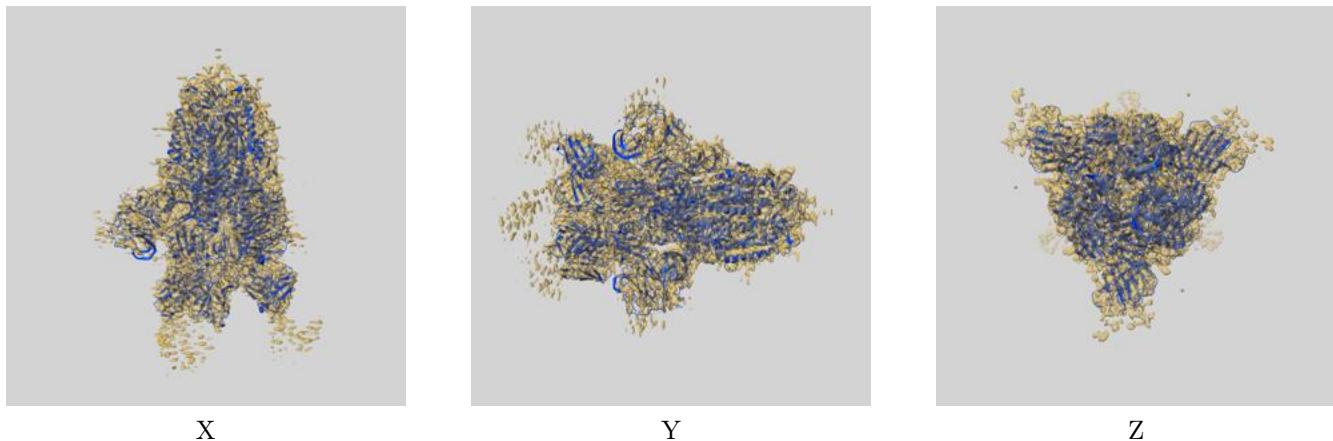
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.55	-	-
Author-provided FSC curve	3.57	3.99	3.60
Unmasked-calculated*	-	-	-

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

## 9 Map-model fit (i)

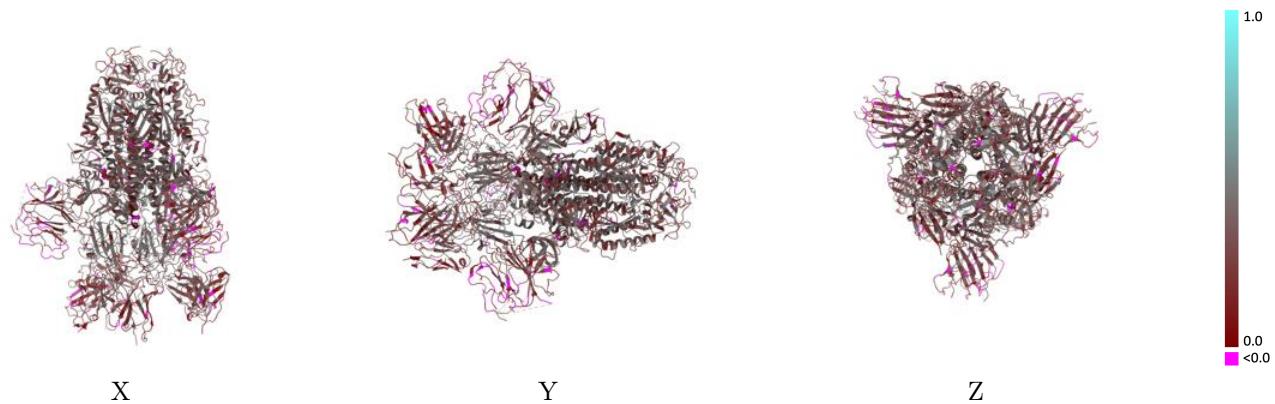
This section contains information regarding the fit between EMDB map EMD-24319 and PDB model 7R8N. Per-residue inclusion information can be found in section 3 on page 13.

### 9.1 Map-model overlay (i)



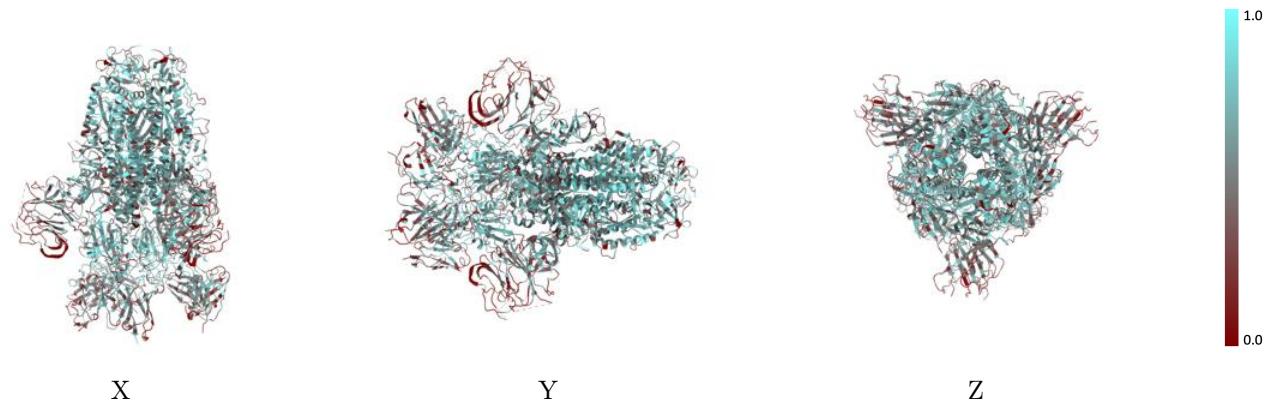
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



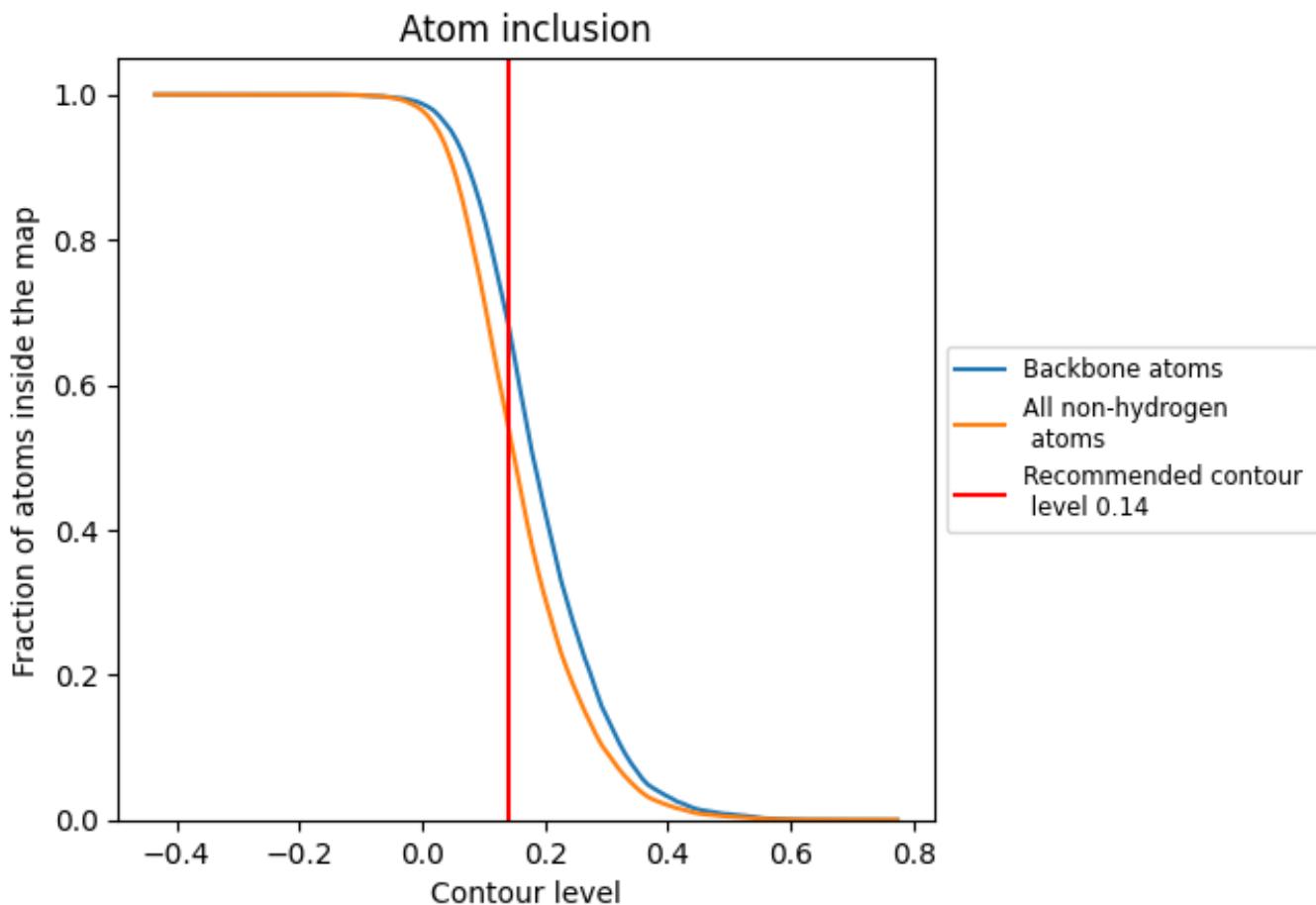
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.14).

## 9.4 Atom inclusion [\(i\)](#)



At the recommended contour level, 68% of all backbone atoms, 54% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5418	0.3040
A	0.5621	0.3160
B	0.5619	0.3130
C	0.0000	0.2530
D	0.3571	0.3560
E	0.5555	0.3090
F	0.0000	0.1350
G	0.4286	0.3230
H	0.5015	0.2750
L	0.4242	0.2520
M	0.4943	0.2720
N	0.4369	0.2570
O	0.5026	0.2790
P	0.4229	0.2420

