



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 01:56 PM UTC

PDB ID : 7WJY / pdb_00007wjy
EMDB ID : EMD-32552
Title : Omicron spike trimer with 6m6 antibody
Authors : Zhan, W.Q.; Zhang, X.; Chen, Z.G.; Sun, L.
Deposited on : 2022-01-08
Resolution : 3.24 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ 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:

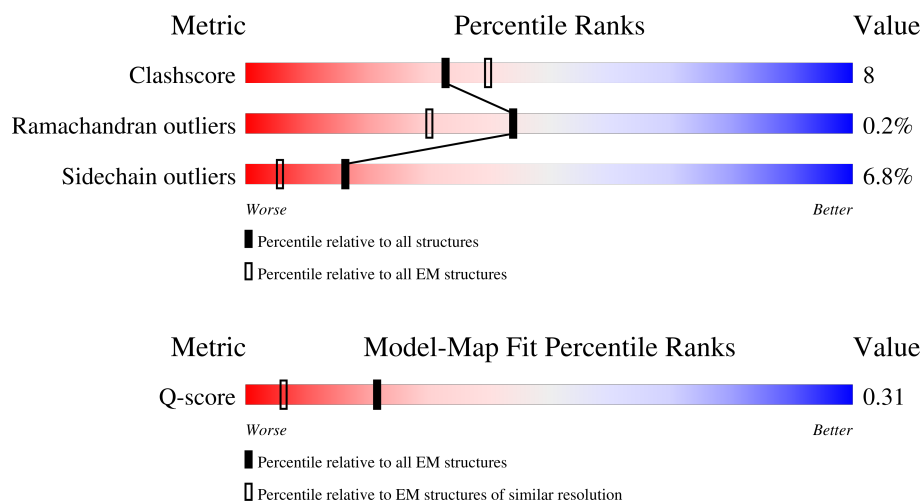
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.24 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	14594 (2.74 - 3.74)

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	1285	
1	D	1285	
1	G	1285	
2	B	227	

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Mol	Chain	Length	Quality of chain
2	E	227	55% 74% 25%
3	C	214	36% 40% 10% 50%
3	F	214	64% 78% 19% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 29429 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	1030	Total	C	N	O	S	0	0
			8014	5139	1331	1507	37		
1	D	1025	Total	C	N	O	S	0	0
			7978	5115	1325	1501	37		
1	G	1033	Total	C	N	O	S	0	0
			8050	5162	1341	1510	37		

There are 385 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	VAL	ALA	variant	UNP P0DTC2
A	?	-	HIS	deletion	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	95	ILE	THR	variant	UNP P0DTC2
A	145	ASP	GLY	variant	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	?	-	ASN	deletion	UNP P0DTC2
A	209	ILE	LEU	variant	UNP P0DTC2
A	212	GLU	-	insertion	UNP P0DTC2
A	213	PRO	-	insertion	UNP P0DTC2
A	214	GLU	-	insertion	UNP P0DTC2
A	339	ASP	GLY	variant	UNP P0DTC2
A	371	LEU	SER	variant	UNP P0DTC2
A	373	PRO	SER	variant	UNP P0DTC2
A	375	PHE	SER	variant	UNP P0DTC2
A	417	ASN	LYS	variant	UNP P0DTC2
A	440	LYS	ASN	variant	UNP P0DTC2
A	446	SER	GLY	variant	UNP P0DTC2
A	477	ASN	SER	variant	UNP P0DTC2
A	478	LYS	THR	variant	UNP P0DTC2
A	484	ALA	GLU	variant	UNP P0DTC2
A	493	ARG	GLN	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	496	SER	GLY	variant	UNP P0DTC2
A	498	ARG	GLN	variant	UNP P0DTC2
A	501	TYR	ASN	variant	UNP P0DTC2
A	505	HIS	TYR	variant	UNP P0DTC2
A	547	LYS	THR	variant	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2
A	655	TYR	HIS	variant	UNP P0DTC2
A	679	LYS	ASN	variant	UNP P0DTC2
A	681	HIS	PRO	variant	UNP P0DTC2
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	764	LYS	ASN	variant	UNP P0DTC2
A	796	TYR	ASP	variant	UNP P0DTC2
A	817	PRO	PHE	variant	UNP P0DTC2
A	856	LYS	ASN	variant	UNP P0DTC2
A	892	PRO	ALA	engineered mutation	UNP P0DTC2
A	899	PRO	ALA	engineered mutation	UNP P0DTC2
A	942	PRO	ALA	engineered mutation	UNP P0DTC2
A	954	HIS	GLN	variant	UNP P0DTC2
A	969	LYS	ASN	variant	UNP P0DTC2
A	981	PHE	LEU	variant	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
D	67	VAL	ALA	variant	UNP P0DTC2
D	?	-	HIS	deletion	UNP P0DTC2
D	?	-	VAL	deletion	UNP P0DTC2
D	95	ILE	THR	variant	UNP P0DTC2
D	145	ASP	GLY	variant	UNP P0DTC2
D	?	-	VAL	deletion	UNP P0DTC2
D	?	-	TYR	deletion	UNP P0DTC2
D	?	-	TYR	deletion	UNP P0DTC2
D	?	-	ASN	deletion	UNP P0DTC2
D	209	ILE	LEU	variant	UNP P0DTC2
D	212	GLU	-	insertion	UNP P0DTC2
D	213	PRO	-	insertion	UNP P0DTC2
D	214	GLU	-	insertion	UNP P0DTC2
D	339	ASP	GLY	variant	UNP P0DTC2
D	339	ASP	GLY	variant	UNP P0DTC2
D	371	LEU	SER	variant	UNP P0DTC2
D	373	PRO	SER	variant	UNP P0DTC2
D	375	PHE	SER	variant	UNP P0DTC2
D	417	ASN	LYS	variant	UNP P0DTC2
D	440	LYS	ASN	variant	UNP P0DTC2
D	446	SER	GLY	variant	UNP P0DTC2
D	477	ASN	SER	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	478	LYS	THR	variant	UNP P0DTC2
D	484	ALA	GLU	variant	UNP P0DTC2
D	493	ARG	GLN	variant	UNP P0DTC2
D	496	SER	GLY	variant	UNP P0DTC2
D	498	ARG	GLN	variant	UNP P0DTC2
D	501	TYR	ASN	variant	UNP P0DTC2
D	505	HIS	TYR	variant	UNP P0DTC2
D	547	LYS	THR	variant	UNP P0DTC2
D	614	GLY	ASP	variant	UNP P0DTC2
D	655	TYR	HIS	variant	UNP P0DTC2
D	679	LYS	ASN	variant	UNP P0DTC2
D	681	HIS	PRO	variant	UNP P0DTC2
D	682	GLY	ARG	engineered mutation	UNP P0DTC2
D	683	SER	ARG	engineered mutation	UNP P0DTC2
D	685	SER	ARG	engineered mutation	UNP P0DTC2
D	764	LYS	ASN	variant	UNP P0DTC2
D	796	TYR	ASP	variant	UNP P0DTC2
D	817	PRO	PHE	variant	UNP P0DTC2
D	856	LYS	ASN	variant	UNP P0DTC2
D	892	PRO	ALA	engineered mutation	UNP P0DTC2
D	899	PRO	ALA	engineered mutation	UNP P0DTC2
D	942	PRO	ALA	engineered mutation	UNP P0DTC2
D	954	HIS	GLN	variant	UNP P0DTC2
D	969	LYS	ASN	variant	UNP P0DTC2
D	981	PHE	LEU	variant	UNP P0DTC2
D	986	PRO	LYS	engineered mutation	UNP P0DTC2
D	987	PRO	VAL	engineered mutation	UNP P0DTC2
D	1209	GLY	-	expression tag	UNP P0DTC2
D	1210	SER	-	expression tag	UNP P0DTC2
D	1211	GLY	-	expression tag	UNP P0DTC2
D	1212	TYR	-	expression tag	UNP P0DTC2
D	1213	ILE	-	expression tag	UNP P0DTC2
D	1214	PRO	-	expression tag	UNP P0DTC2
D	1215	GLU	-	expression tag	UNP P0DTC2
D	1216	ALA	-	expression tag	UNP P0DTC2
D	1217	PRO	-	expression tag	UNP P0DTC2
D	1218	ARG	-	expression tag	UNP P0DTC2
D	1219	ASP	-	expression tag	UNP P0DTC2
D	1220	GLY	-	expression tag	UNP P0DTC2
D	1221	GLN	-	expression tag	UNP P0DTC2
D	1222	ALA	-	expression tag	UNP P0DTC2
D	1223	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1224	VAL	-	expression tag	UNP P0DTC2
D	1225	ARG	-	expression tag	UNP P0DTC2
D	1226	LYS	-	expression tag	UNP P0DTC2
D	1227	ASP	-	expression tag	UNP P0DTC2
D	1228	GLY	-	expression tag	UNP P0DTC2
D	1229	GLU	-	expression tag	UNP P0DTC2
D	1230	TRP	-	expression tag	UNP P0DTC2
D	1231	VAL	-	expression tag	UNP P0DTC2
D	1232	PHE	-	expression tag	UNP P0DTC2
D	1233	LEU	-	expression tag	UNP P0DTC2
D	1234	SER	-	expression tag	UNP P0DTC2
D	1235	THR	-	expression tag	UNP P0DTC2
D	1236	PHE	-	expression tag	UNP P0DTC2
D	1237	LEU	-	expression tag	UNP P0DTC2
D	1238	SER	-	expression tag	UNP P0DTC2
D	1239	GLY	-	expression tag	UNP P0DTC2
D	1240	LEU	-	expression tag	UNP P0DTC2
D	1241	GLU	-	expression tag	UNP P0DTC2
D	1242	VAL	-	expression tag	UNP P0DTC2
D	1243	LEU	-	expression tag	UNP P0DTC2
D	1244	PHE	-	expression tag	UNP P0DTC2
D	1245	GLN	-	expression tag	UNP P0DTC2
D	1246	GLY	-	expression tag	UNP P0DTC2
D	1247	PRO	-	expression tag	UNP P0DTC2
D	1248	GLY	-	expression tag	UNP P0DTC2
D	1249	GLY	-	expression tag	UNP P0DTC2
D	1250	TRP	-	expression tag	UNP P0DTC2
D	1251	SER	-	expression tag	UNP P0DTC2
D	1252	HIS	-	expression tag	UNP P0DTC2
D	1253	PRO	-	expression tag	UNP P0DTC2
D	1254	GLN	-	expression tag	UNP P0DTC2
D	1255	PHE	-	expression tag	UNP P0DTC2
D	1256	GLU	-	expression tag	UNP P0DTC2
D	1257	LYS	-	expression tag	UNP P0DTC2
D	1258	GLY	-	expression tag	UNP P0DTC2
D	1259	GLY	-	expression tag	UNP P0DTC2
D	1260	GLY	-	expression tag	UNP P0DTC2
D	1261	SER	-	expression tag	UNP P0DTC2
D	1262	GLY	-	expression tag	UNP P0DTC2
D	1263	GLY	-	expression tag	UNP P0DTC2
D	1264	GLY	-	expression tag	UNP P0DTC2
D	1265	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1266	GLY	-	expression tag	UNP P0DTC2
D	1267	GLY	-	expression tag	UNP P0DTC2
D	1268	SER	-	expression tag	UNP P0DTC2
D	1269	ALA	-	expression tag	UNP P0DTC2
D	1270	TRP	-	expression tag	UNP P0DTC2
D	1271	SER	-	expression tag	UNP P0DTC2
D	1272	HIS	-	expression tag	UNP P0DTC2
D	1273	PRO	-	expression tag	UNP P0DTC2
D	1274	GLN	-	expression tag	UNP P0DTC2
D	1275	PHE	-	expression tag	UNP P0DTC2
D	1276	GLU	-	expression tag	UNP P0DTC2
D	1277	LYS	-	expression tag	UNP P0DTC2
D	1278	GLY	-	expression tag	UNP P0DTC2
D	1279	GLY	-	expression tag	UNP P0DTC2
D	1280	SER	-	expression tag	UNP P0DTC2
D	1281	HIS	-	expression tag	UNP P0DTC2
D	1282	HIS	-	expression tag	UNP P0DTC2
D	1283	HIS	-	expression tag	UNP P0DTC2
D	1284	HIS	-	expression tag	UNP P0DTC2
D	1285	HIS	-	expression tag	UNP P0DTC2
D	1286	HIS	-	expression tag	UNP P0DTC2
D	1287	HIS	-	expression tag	UNP P0DTC2
D	1288	HIS	-	expression tag	UNP P0DTC2
G	67	VAL	ALA	variant	UNP P0DTC2
G	?	-	HIS	deletion	UNP P0DTC2
G	?	-	VAL	deletion	UNP P0DTC2
G	95	ILE	THR	variant	UNP P0DTC2
G	145	ASP	GLY	variant	UNP P0DTC2
G	?	-	VAL	deletion	UNP P0DTC2
G	?	-	TYR	deletion	UNP P0DTC2
G	?	-	TYR	deletion	UNP P0DTC2
G	?	-	ASN	deletion	UNP P0DTC2
G	209	ILE	LEU	variant	UNP P0DTC2
G	212	GLU	-	insertion	UNP P0DTC2
G	213	PRO	-	insertion	UNP P0DTC2
G	214	GLU	-	insertion	UNP P0DTC2
G	339	ASP	GLY	variant	UNP P0DTC2
G	371	LEU	SER	variant	UNP P0DTC2
G	373	PRO	SER	variant	UNP P0DTC2
G	375	PHE	SER	variant	UNP P0DTC2
G	417	ASN	LYS	variant	UNP P0DTC2
G	440	LYS	ASN	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	446	SER	GLY	variant	UNP P0DTC2
G	477	ASN	SER	variant	UNP P0DTC2
G	478	LYS	THR	variant	UNP P0DTC2
G	484	ALA	GLU	variant	UNP P0DTC2
G	493	ARG	GLN	variant	UNP P0DTC2
G	496	SER	GLY	variant	UNP P0DTC2
G	498	ARG	GLN	variant	UNP P0DTC2
G	501	TYR	ASN	variant	UNP P0DTC2
G	505	HIS	TYR	variant	UNP P0DTC2
G	547	LYS	THR	variant	UNP P0DTC2
G	614	GLY	ASP	variant	UNP P0DTC2
G	655	TYR	HIS	variant	UNP P0DTC2
G	679	LYS	ASN	variant	UNP P0DTC2
G	681	HIS	PRO	variant	UNP P0DTC2
G	682	GLY	ARG	engineered mutation	UNP P0DTC2
G	683	SER	ARG	engineered mutation	UNP P0DTC2
G	685	SER	ARG	engineered mutation	UNP P0DTC2
G	764	LYS	ASN	variant	UNP P0DTC2
G	796	TYR	ASP	variant	UNP P0DTC2
G	817	PRO	PHE	variant	UNP P0DTC2
G	856	LYS	ASN	variant	UNP P0DTC2
G	892	PRO	ALA	engineered mutation	UNP P0DTC2
G	899	PRO	ALA	engineered mutation	UNP P0DTC2
G	942	PRO	ALA	engineered mutation	UNP P0DTC2
G	954	HIS	GLN	variant	UNP P0DTC2
G	969	LYS	ASN	variant	UNP P0DTC2
G	981	PHE	LEU	variant	UNP P0DTC2
G	986	PRO	LYS	engineered mutation	UNP P0DTC2
G	987	PRO	VAL	engineered mutation	UNP P0DTC2
G	1209	GLY	-	expression tag	UNP P0DTC2
G	1210	SER	-	expression tag	UNP P0DTC2
G	1211	GLY	-	expression tag	UNP P0DTC2
G	1212	TYR	-	expression tag	UNP P0DTC2
G	1213	ILE	-	expression tag	UNP P0DTC2
G	1214	PRO	-	expression tag	UNP P0DTC2
G	1215	GLU	-	expression tag	UNP P0DTC2
G	1216	ALA	-	expression tag	UNP P0DTC2
G	1217	PRO	-	expression tag	UNP P0DTC2
G	1218	ARG	-	expression tag	UNP P0DTC2
G	1219	ASP	-	expression tag	UNP P0DTC2
G	1220	GLY	-	expression tag	UNP P0DTC2
G	1221	GLN	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1222	ALA	-	expression tag	UNP P0DTC2
G	1223	TYR	-	expression tag	UNP P0DTC2
G	1224	VAL	-	expression tag	UNP P0DTC2
G	1225	ARG	-	expression tag	UNP P0DTC2
G	1226	LYS	-	expression tag	UNP P0DTC2
G	1227	ASP	-	expression tag	UNP P0DTC2
G	1228	GLY	-	expression tag	UNP P0DTC2
G	1229	GLU	-	expression tag	UNP P0DTC2
G	1230	TRP	-	expression tag	UNP P0DTC2
G	1231	VAL	-	expression tag	UNP P0DTC2
G	1232	PHE	-	expression tag	UNP P0DTC2
G	1233	LEU	-	expression tag	UNP P0DTC2
G	1234	SER	-	expression tag	UNP P0DTC2
G	1235	THR	-	expression tag	UNP P0DTC2
G	1236	PHE	-	expression tag	UNP P0DTC2
G	1237	LEU	-	expression tag	UNP P0DTC2
G	1238	SER	-	expression tag	UNP P0DTC2
G	1239	GLY	-	expression tag	UNP P0DTC2
G	1240	LEU	-	expression tag	UNP P0DTC2
G	1241	GLU	-	expression tag	UNP P0DTC2
G	1242	VAL	-	expression tag	UNP P0DTC2
G	1243	LEU	-	expression tag	UNP P0DTC2
G	1244	PHE	-	expression tag	UNP P0DTC2
G	1245	GLN	-	expression tag	UNP P0DTC2
G	1246	GLY	-	expression tag	UNP P0DTC2
G	1247	PRO	-	expression tag	UNP P0DTC2
G	1248	GLY	-	expression tag	UNP P0DTC2
G	1249	GLY	-	expression tag	UNP P0DTC2
G	1250	TRP	-	expression tag	UNP P0DTC2
G	1251	SER	-	expression tag	UNP P0DTC2
G	1252	HIS	-	expression tag	UNP P0DTC2
G	1253	PRO	-	expression tag	UNP P0DTC2
G	1254	GLN	-	expression tag	UNP P0DTC2
G	1255	PHE	-	expression tag	UNP P0DTC2
G	1256	GLU	-	expression tag	UNP P0DTC2
G	1257	LYS	-	expression tag	UNP P0DTC2
G	1258	GLY	-	expression tag	UNP P0DTC2
G	1259	GLY	-	expression tag	UNP P0DTC2
G	1260	GLY	-	expression tag	UNP P0DTC2
G	1261	SER	-	expression tag	UNP P0DTC2
G	1262	GLY	-	expression tag	UNP P0DTC2
G	1263	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1264	GLY	-	expression tag	UNP P0DTC2
G	1265	SER	-	expression tag	UNP P0DTC2
G	1266	GLY	-	expression tag	UNP P0DTC2
G	1267	GLY	-	expression tag	UNP P0DTC2
G	1268	SER	-	expression tag	UNP P0DTC2
G	1269	ALA	-	expression tag	UNP P0DTC2
G	1270	TRP	-	expression tag	UNP P0DTC2
G	1271	SER	-	expression tag	UNP P0DTC2
G	1272	HIS	-	expression tag	UNP P0DTC2
G	1273	PRO	-	expression tag	UNP P0DTC2
G	1274	GLN	-	expression tag	UNP P0DTC2
G	1275	PHE	-	expression tag	UNP P0DTC2
G	1276	GLU	-	expression tag	UNP P0DTC2
G	1277	LYS	-	expression tag	UNP P0DTC2
G	1278	GLY	-	expression tag	UNP P0DTC2
G	1279	GLY	-	expression tag	UNP P0DTC2
G	1280	SER	-	expression tag	UNP P0DTC2
G	1281	HIS	-	expression tag	UNP P0DTC2
G	1282	HIS	-	expression tag	UNP P0DTC2
G	1283	HIS	-	expression tag	UNP P0DTC2
G	1284	HIS	-	expression tag	UNP P0DTC2
G	1285	HIS	-	expression tag	UNP P0DTC2
G	1286	HIS	-	expression tag	UNP P0DTC2
G	1287	HIS	-	expression tag	UNP P0DTC2
G	1288	HIS	-	expression tag	UNP P0DTC2

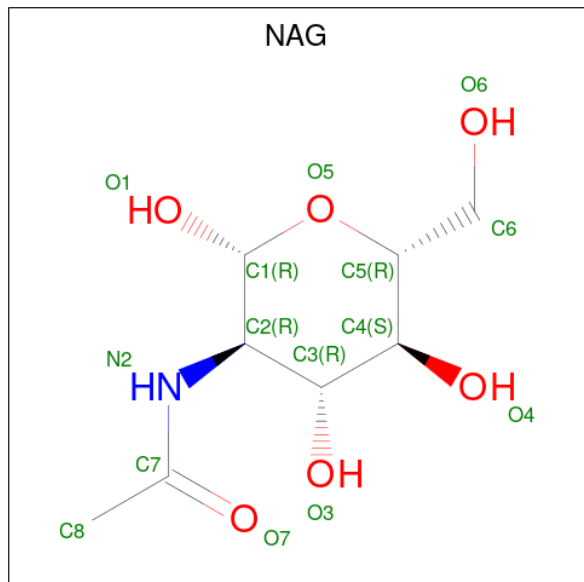
- Molecule 2 is a protein called 6m6 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	125	Total	C	N	O	S	0	0
			971	614	167	187	3		
2	E	226	Total	C	N	O	S	0	0
			1698	1073	286	334	5		

- Molecule 3 is a protein called 6m6 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	107	Total	C	N	O	S	0	0
			805	497	142	164	2		
3	F	210	Total	C	N	O	S	0	0
			1577	982	270	321	4		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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	D	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	

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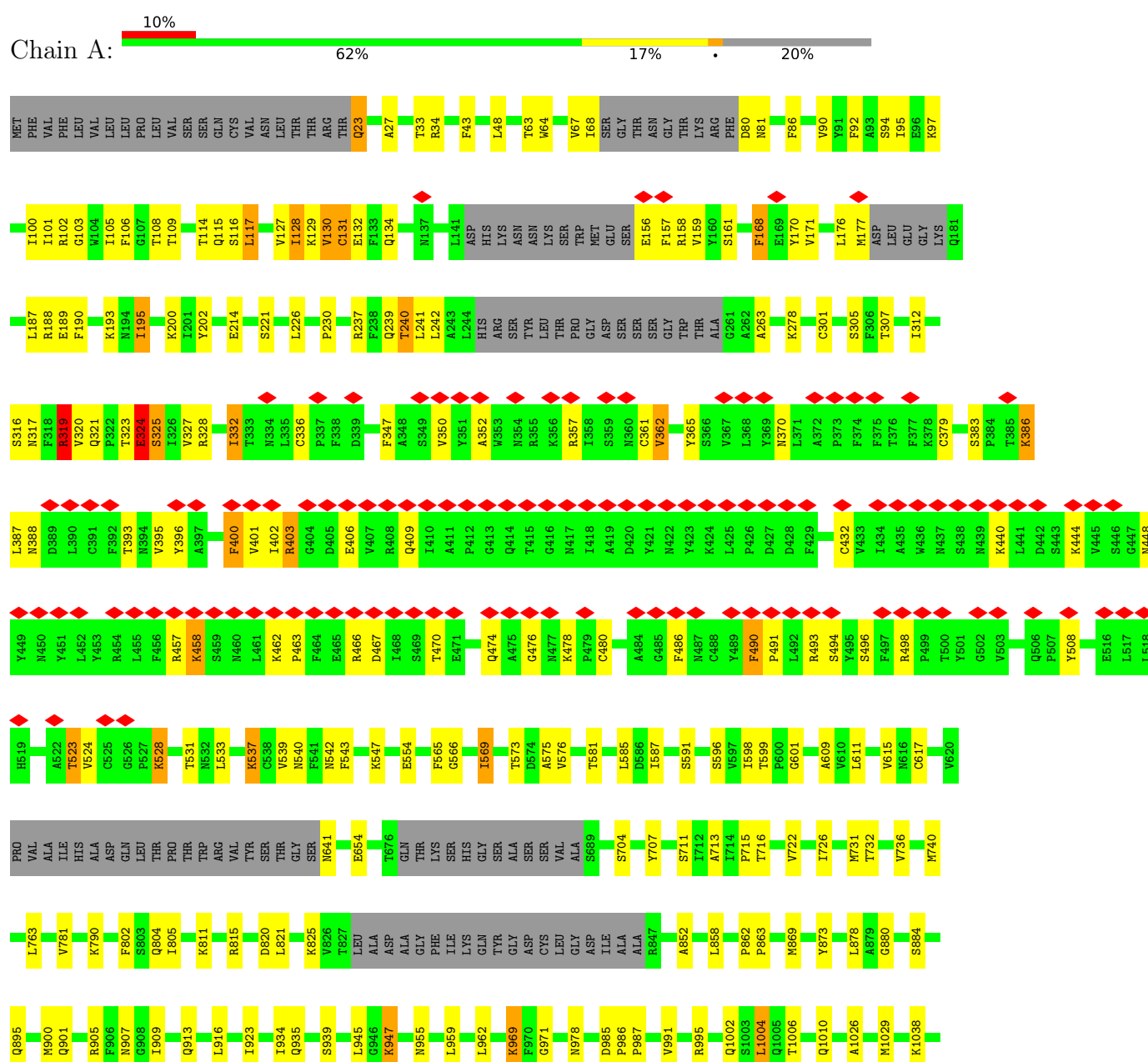
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Mol	Chain	Residues	Atoms				AltConf
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	G	1	Total	C	N	O	0
			14	8	1	5	
4	G	1	Total	C	N	O	0
			14	8	1	5	
4	G	1	Total	C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

3 Residue-property plots

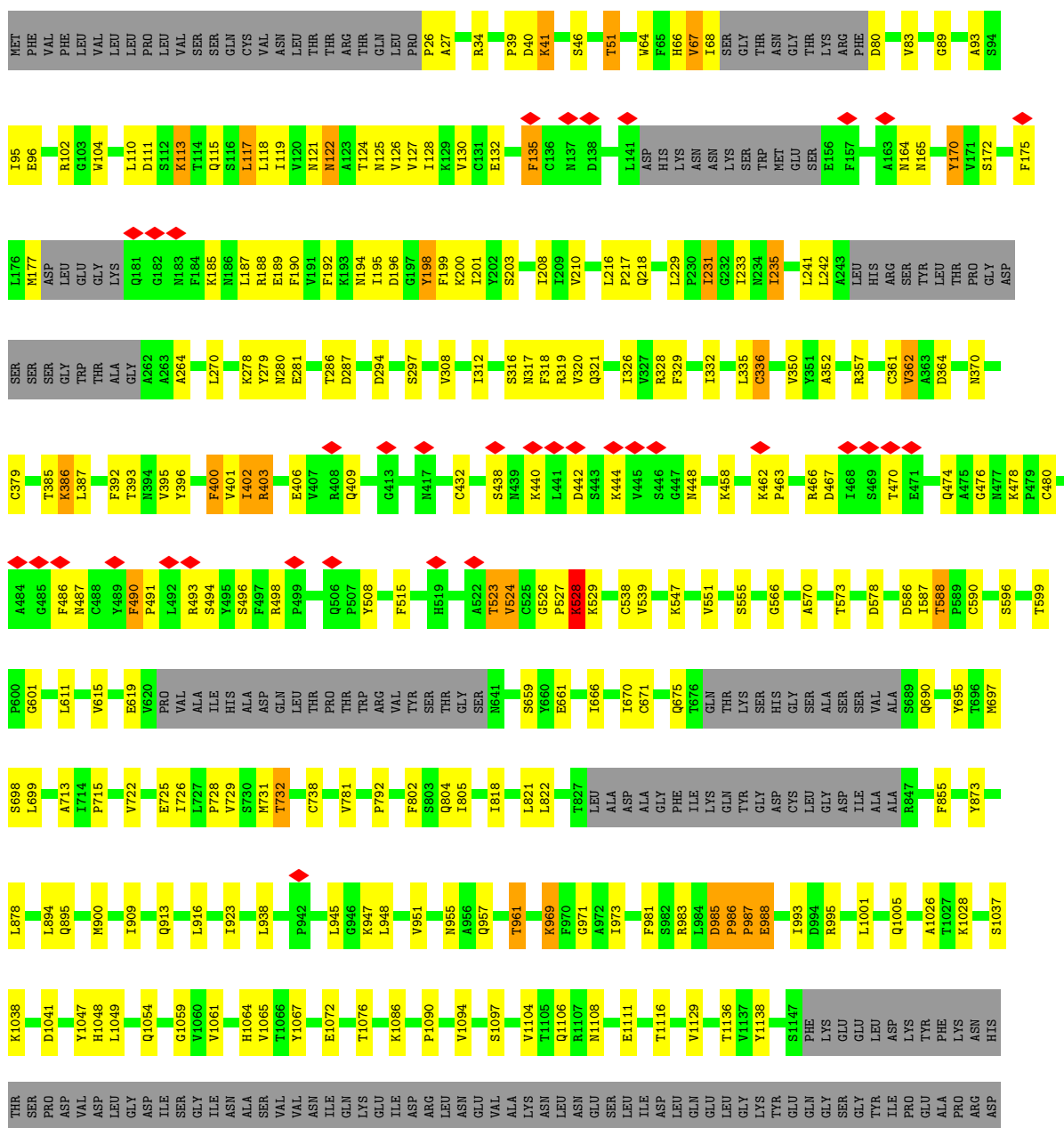
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

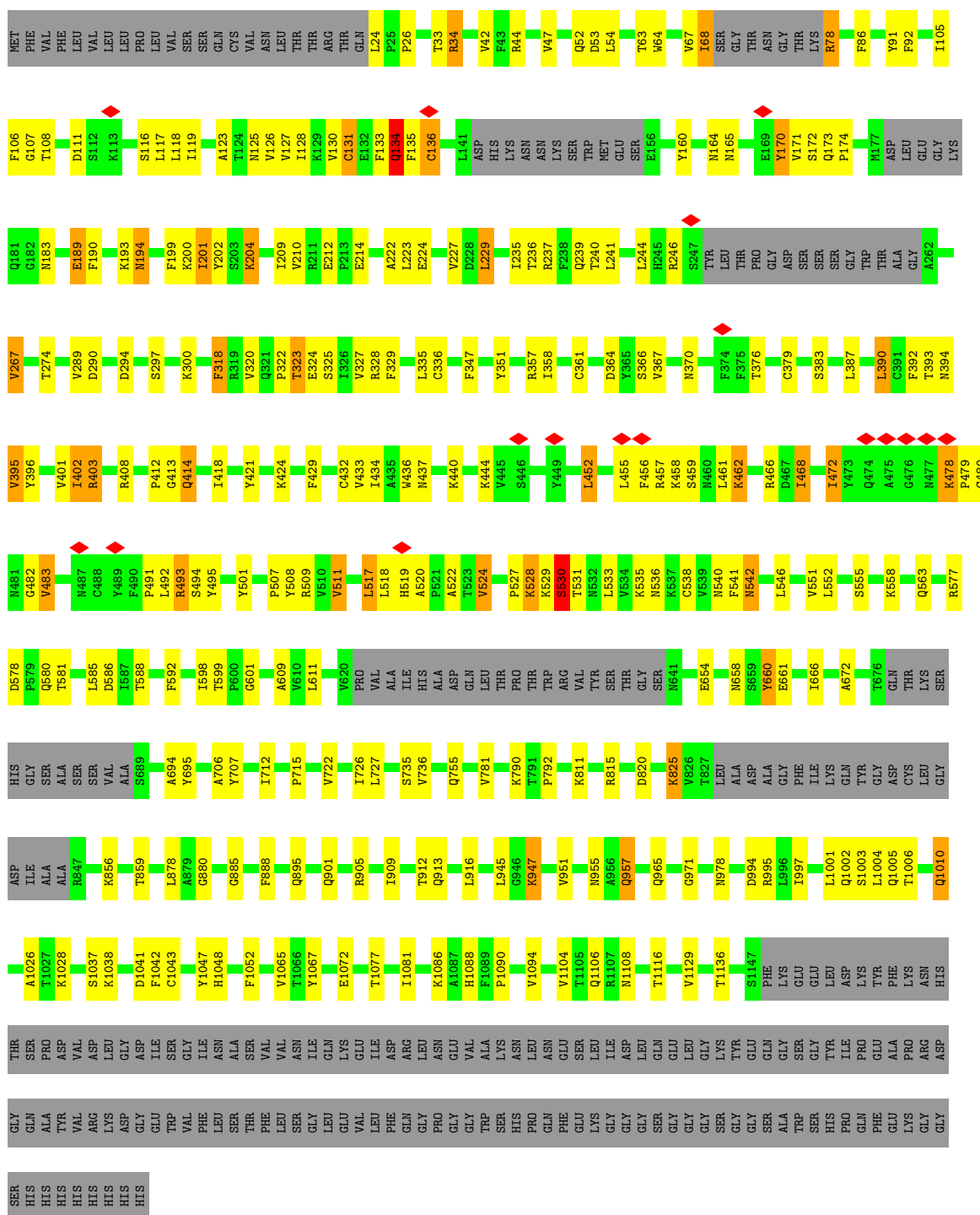
• Molecule 1: Spike glycoprotein



PHE LEU SER SER GLY LEU LEU VAL LEU PHE PHE GLN GLY GLY PRO PRO GLY GLY TRP SER HIS SER PRO PRO GLN PHE GLN GLY LYS GLY GLY GLY SER SER GLY GLY GLY GLY GLY GLY SER SER TRP TRP SER SER HIS HIS PRO PRO PHE PHE LYS GLY GLY GLY GLY HIS HIS HIS HIS HIS HIS HIS HIS

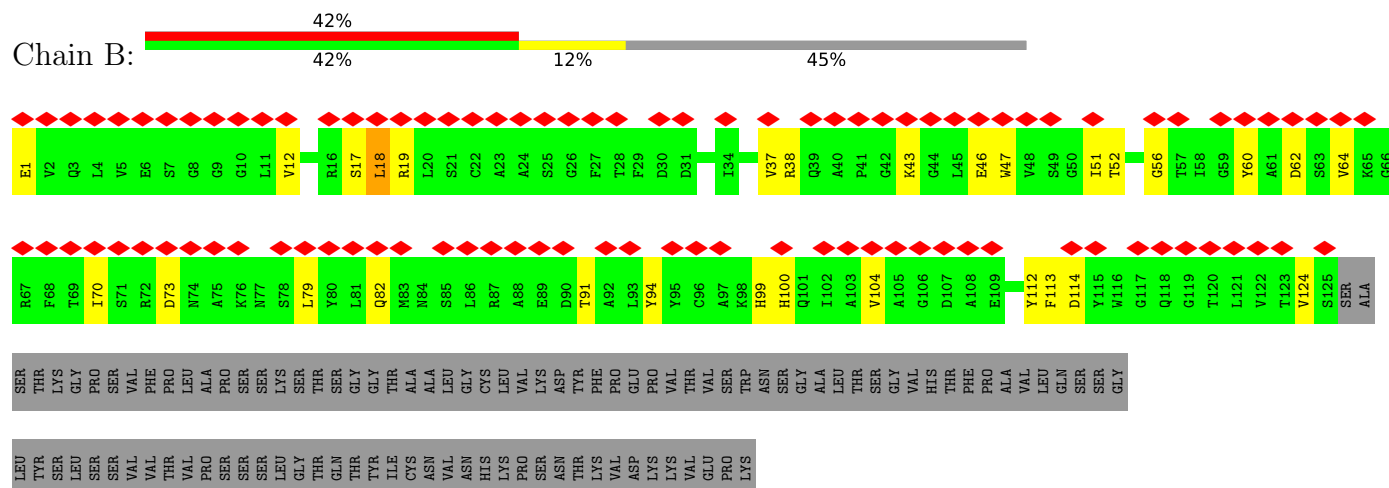
- Molecule 1: Spike glycoprotein





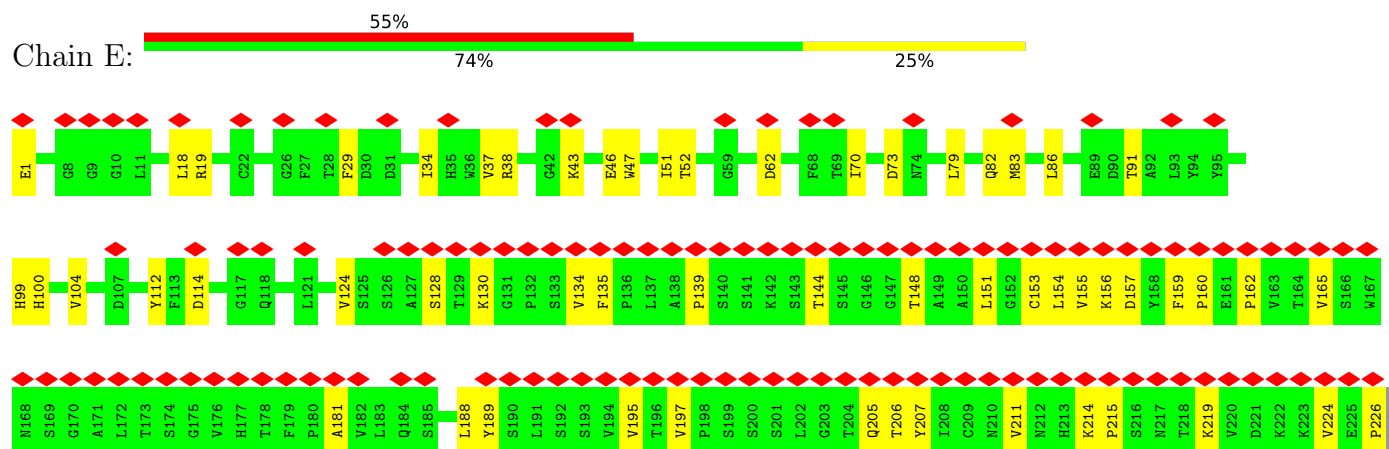
- Molecule 2: 6m6 heavy chain

Chain B:



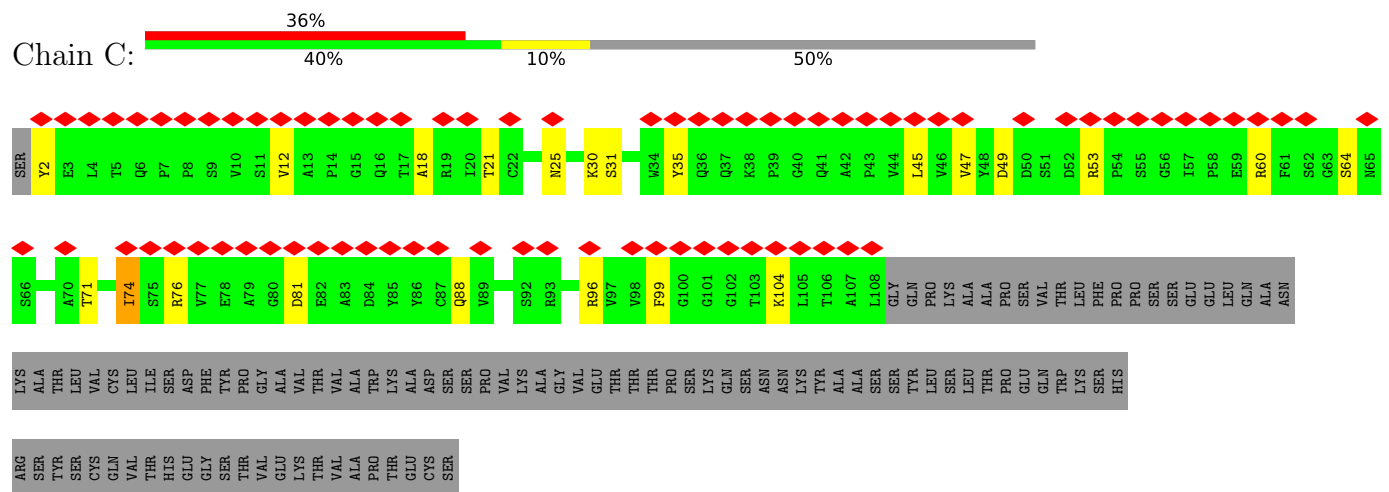
- Molecule 2: 6m6 heavy chain

Chain E:



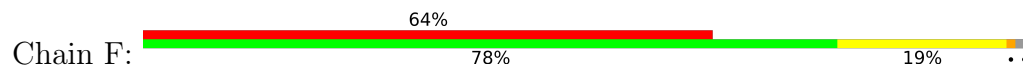
- Molecule 3: 6m6 light chain

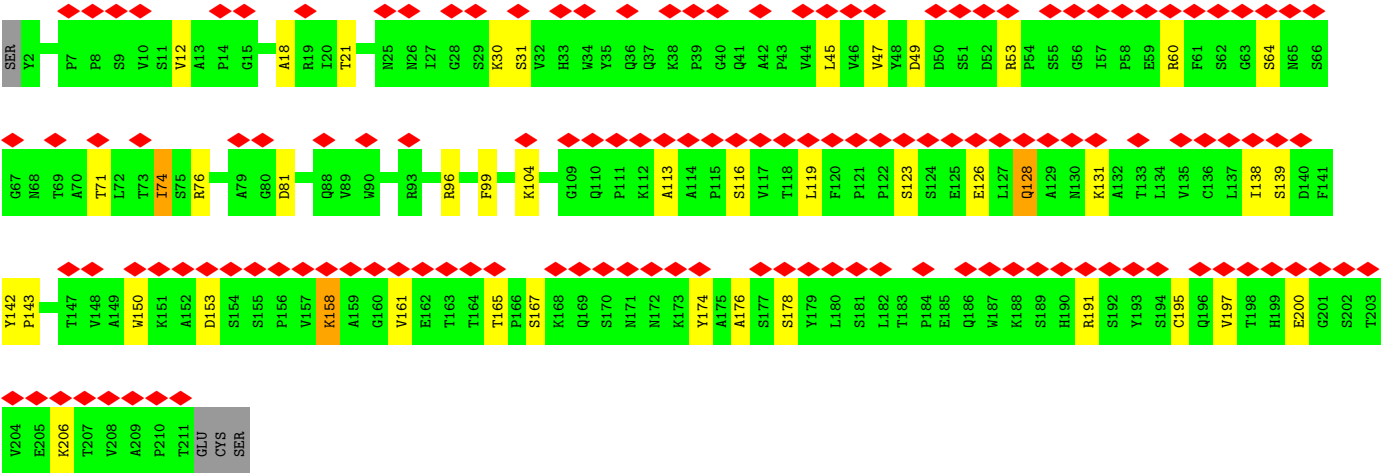
Chain C:



- Molecule 3: 6m6 light chain

Chain F:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	272354	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 ($e^-/\text{\AA}^2$)	58	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	1.698	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	340.48, 340.48, 340.48	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	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	0.18	0/8204	0.43	2/11173 (0.0%)
1	D	0.22	0/8167	0.49	5/11121 (0.0%)
1	G	0.24	0/8242	0.48	3/11223 (0.0%)
2	B	0.08	0/995	0.24	0/1351
2	E	0.10	0/1741	0.25	0/2374
3	C	0.09	0/823	0.25	0/1122
3	F	0.10	0/1616	0.26	0/2209
All	All	0.20	0/29788	0.44	10/40573 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	986	PRO	N-CA-C	10.89	123.99	110.70
1	G	134	GLN	N-CA-C	-7.23	101.77	113.19
1	A	991	VAL	N-CA-C	-7.07	106.99	113.71
1	D	985	ASP	CA-C-N	-6.81	113.36	120.38
1	D	985	ASP	C-N-CA	-6.81	113.36	120.38
1	D	988	GLU	N-CA-C	-6.20	105.88	113.50
1	G	136	CYS	N-CA-C	-6.16	97.68	110.80
1	D	529	LYS	N-CA-C	5.57	118.04	109.07
1	G	130	VAL	N-CA-C	-5.46	108.53	113.71
1	A	319	ARG	N-CA-C	5.36	116.31	107.20

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	8014	0	7801	138	0
1	D	7978	0	7760	150	0
1	G	8050	0	7836	167	0
2	B	971	0	918	17	0
2	E	1698	0	1644	27	0
3	C	805	0	763	13	0
3	F	1577	0	1518	26	0
4	A	98	0	91	0	0
4	D	126	0	117	0	0
4	G	112	0	104	0	0
All	All	29429	0	28552	488	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (488) 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:G:329:PHE:HE2	1:G:528:LYS:HB3	1.41	0.85
1:D:555:SER:HB3	1:D:586:ASP:HB2	1.62	0.80
1:D:361:CYS:SG	1:D:362:VAL:N	2.59	0.75
1:G:901:GLN:HE21	1:G:905:ARG:HE	1.35	0.75
1:D:102:ARG:HD2	1:D:121:ASN:HB2	1.68	0.75
1:A:105:ILE:HB	1:A:239:GLN:HB3	1.67	0.75
1:D:526:GLY:HA3	1:D:528:LYS:HE2	1.69	0.74
1:G:329:PHE:CE2	1:G:528:LYS:HB3	2.22	0.74
1:D:470:THR:HB	2:E:19:ARG:HH21	1.55	0.71
1:A:821:LEU:HD11	1:A:939:SER:HB2	1.74	0.70
1:A:361:CYS:SG	1:A:362:VAL:N	2.65	0.70
1:D:329:PHE:HD2	1:D:528:LYS:HB3	1.57	0.69
3:F:119:LEU:HD21	3:F:195:CYS:HB3	1.72	0.69
1:D:599:THR:HG22	1:D:601:GLY:H	1.58	0.69
1:G:472:ILE:HG21	1:G:482:GLY:H	1.57	0.69
1:D:122:ASN:HD21	1:D:124:THR:HG22	1.57	0.68
1:D:1047:TYR:HB2	1:D:1067:TYR:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:150:TRP:NE1	3:F:178:SER:OG	2.27	0.68
1:A:95:ILE:HG23	1:A:187:LEU:HD13	1.76	0.67
2:B:17:SER:HB3	2:B:82:GLN:HE22	1.58	0.67
1:G:402:ILE:HG13	1:G:418:ILE:HG21	1.76	0.67
1:G:123:ALA:O	1:G:125:ASN:ND2	2.29	0.66
1:G:563:GLN:O	1:G:577:ARG:NH1	2.29	0.66
1:G:412:PRO:O	1:G:414:GLN:NE2	2.29	0.65
3:C:21:THR:HG22	3:C:71:THR:HG22	1.79	0.65
1:D:895:GLN:NE2	1:G:706:ALA:O	2.29	0.65
1:A:67:VAL:HG22	1:A:80:ASP:HB3	1.78	0.65
1:G:329:PHE:HE2	1:G:528:LYS:CB	2.08	0.65
1:D:40:ASP:HB2	1:G:519:HIS:HE1	1.62	0.64
1:D:46:SER:HA	1:D:279:TYR:O	1.98	0.64
1:G:811:LYS:HD3	1:G:815:ARG:H	1.62	0.64
2:E:144:THR:H	2:E:148:THR:HG21	1.61	0.64
3:C:18:ALA:HB3	3:C:74:ILE:HD11	1.79	0.64
1:D:329:PHE:CD2	1:D:528:LYS:HB3	2.32	0.64
3:F:153:ASP:O	3:F:191:ARG:NH2	2.31	0.63
1:G:119:ILE:HA	1:G:128:ILE:HG22	1.81	0.63
1:A:478:LYS:NZ	1:A:486:PHE:O	2.29	0.63
1:A:474:GLN:HG3	1:A:476:GLY:H	1.64	0.63
1:D:1037:SER:H	1:D:1048:HIS:HD2	1.43	0.63
1:A:67:VAL:HB	1:A:263:ALA:HB3	1.81	0.63
1:G:327:VAL:HA	1:G:542:ASN:HB3	1.79	0.63
1:A:466:ARG:HH12	2:B:73:ASP:HA	1.62	0.63
3:F:21:THR:HG22	3:F:71:THR:HG22	1.79	0.62
3:F:167:SER:HB3	3:F:174:TYR:HB3	1.80	0.62
1:A:615:VAL:HG12	1:A:617:CYS:H	1.64	0.62
1:A:1090:PRO:O	1:G:913:GLN:NE2	2.33	0.62
1:D:474:GLN:HG3	1:D:476:GLY:H	1.63	0.62
1:D:478:LYS:NZ	1:D:486:PHE:O	2.31	0.62
1:D:596:SER:HB2	1:D:611:LEU:HB3	1.82	0.62
2:E:181:ALA:HB1	2:E:189:TYR:HB3	1.81	0.62
1:G:541:PHE:HB3	1:G:552:LEU:HD11	1.82	0.61
1:A:869:MET:HE1	1:D:697:MET:HG3	1.83	0.61
3:F:18:ALA:HB3	3:F:74:ILE:HD11	1.82	0.61
1:G:193:LYS:HB2	1:G:200:LYS:HB2	1.83	0.61
1:G:599:THR:HG22	1:G:601:GLY:H	1.65	0.60
1:A:109:THR:HG1	1:A:114:THR:HG1	1.48	0.60
1:A:1116:THR:HG22	1:A:1138:TYR:HB3	1.83	0.60
1:D:913:GLN:NE2	1:G:1090:PRO:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:852:ALA:HB1	1:D:570:ALA:HB2	1.83	0.60
1:G:811:LYS:NZ	1:G:820:ASP:OD1	2.34	0.60
1:A:566:GLY:HA3	1:A:575:ALA:HB3	1.83	0.60
1:D:350:VAL:HA	1:D:400:PHE:HB2	1.84	0.59
1:G:412:PRO:HG3	1:G:429:PHE:HB3	1.84	0.59
1:G:965:GLN:NE2	1:G:1003:SER:OG	2.35	0.59
1:G:86:PHE:HE2	1:G:194:ASN:HB2	1.68	0.59
1:A:448:ASN:HD21	1:A:498:ARG:HH22	1.51	0.59
1:G:1047:TYR:HB2	1:G:1067:TYR:HB3	1.85	0.59
1:G:323:THR:HG22	1:G:538:CYS:O	2.03	0.59
1:A:81:ASN:ND2	1:A:240:THR:O	2.36	0.59
1:A:599:THR:HG22	1:A:601:GLY:H	1.68	0.58
3:F:60:ARG:NH2	3:F:76:ARG:O	2.36	0.58
1:A:987:PRO:HD3	1:G:413:GLY:HA3	1.85	0.58
1:G:135:PHE:HA	1:G:160:TYR:HA	1.84	0.58
1:A:554:GLU:HA	1:A:585:LEU:HA	1.84	0.58
1:D:490:PHE:HD1	1:D:491:PRO:HD2	1.69	0.58
1:D:466:ARG:HH12	2:E:73:ASP:HA	1.67	0.58
1:G:878:LEU:HD21	1:G:1052:PHE:HB3	1.86	0.58
3:F:60:ARG:NH2	3:F:81:ASP:OD2	2.37	0.58
1:A:1047:TYR:HB2	1:A:1067:TYR:HB3	1.86	0.58
1:A:470:THR:OG1	2:B:82:GLN:OE1	2.22	0.57
1:D:95:ILE:HG12	1:D:187:LEU:HD13	1.86	0.57
1:G:736:VAL:HG21	1:G:1004:LEU:HD11	1.85	0.57
1:D:34:ARG:NH2	1:D:218:GLN:O	2.36	0.57
2:E:155:VAL:HG21	2:E:211:VAL:HG21	1.87	0.57
1:A:901:GLN:HE21	1:A:905:ARG:HE	1.52	0.57
1:A:934:ILE:HD13	1:A:1063:LEU:HD22	1.87	0.57
1:A:94:SER:HB2	1:A:188:ARG:HG3	1.86	0.57
1:A:913:GLN:NE2	1:D:1090:PRO:O	2.37	0.57
1:A:969:LYS:NZ	1:G:755:GLN:OE1	2.37	0.57
1:G:392:PHE:HB2	1:G:524:VAL:HG23	1.87	0.57
3:C:60:ARG:NH2	3:C:76:ARG:O	2.37	0.57
1:D:318:PHE:CZ	1:D:320:VAL:HG23	2.40	0.57
2:E:134:VAL:HG22	2:E:155:VAL:HG22	1.87	0.57
2:E:165:VAL:HG12	2:E:211:VAL:HG22	1.85	0.57
1:G:455:LEU:H	1:G:491:PRO:HB2	1.68	0.57
1:D:916:LEU:HD12	1:D:923:ILE:HD12	1.86	0.57
1:D:945:LEU:HD12	1:D:948:LEU:HD12	1.87	0.56
1:G:390:LEU:HD22	1:G:517:LEU:HD21	1.87	0.56
1:A:361:CYS:H	1:A:524:VAL:HG22	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:47:VAL:HG22	3:C:53:ARG:HB3	1.87	0.56
1:D:909:ILE:O	1:D:1108:ASN:ND2	2.38	0.56
1:G:229:LEU:HD13	1:G:229:LEU:H	1.69	0.56
1:D:115:GLN:NE2	1:D:130:VAL:O	2.38	0.56
3:F:47:VAL:HG22	3:F:53:ARG:HB3	1.87	0.56
1:A:1002:GLN:OE1	1:G:1002:GLN:NE2	2.39	0.56
1:A:802:PHE:HD1	1:A:805:ILE:HD11	1.70	0.56
2:E:62:ASP:OD2	3:F:96:ARG:NH2	2.38	0.56
1:A:713:ALA:HB2	1:G:895:GLN:HG2	1.88	0.56
1:A:23:GLN:O	1:A:23:GLN:NE2	2.39	0.56
1:A:736:VAL:HG21	1:A:1004:LEU:HD11	1.88	0.55
3:C:31:SER:OG	3:C:49:ASP:OD1	2.24	0.55
1:D:470:THR:OG1	2:E:82:GLN:OE1	2.22	0.55
1:D:726:ILE:HB	1:D:947:LYS:HD3	1.89	0.55
1:G:24:LEU:O	1:G:26:PRO:HD3	2.06	0.55
1:G:366:SER:O	1:G:370:ASN:ND2	2.40	0.55
1:A:493:ARG:NH1	1:A:494:SER:O	2.40	0.55
2:B:62:ASP:OD2	3:C:96:ARG:NH2	2.40	0.55
1:A:547:LYS:O	1:G:978:ASN:ND2	2.40	0.55
1:D:551:VAL:HB	1:D:588:THR:HG23	1.88	0.55
1:G:1006:THR:O	1:G:1010:GLN:NE2	2.37	0.55
3:C:60:ARG:NH2	3:C:81:ASP:OD2	2.39	0.55
1:A:811:LYS:NZ	1:A:820:ASP:OD1	2.30	0.55
1:A:406:GLU:HB3	1:A:409:GLN:HE21	1.72	0.54
1:G:401:VAL:HG12	1:G:509:ARG:HG2	1.89	0.54
1:A:711:SER:OG	1:G:895:GLN:NE2	2.41	0.54
2:E:159:PHE:HB3	2:E:160:PRO:HD3	1.89	0.54
1:D:722:VAL:HG22	1:D:1065:VAL:HG22	1.89	0.54
2:E:207:TYR:HB3	2:E:224:VAL:HB	1.89	0.54
1:D:493:ARG:NH1	1:D:494:SER:O	2.41	0.54
1:A:490:PHE:HD1	1:A:491:PRO:HD2	1.72	0.54
1:D:406:GLU:HB3	1:D:409:GLN:HE21	1.72	0.54
3:F:31:SER:OG	3:F:49:ASP:OD1	2.24	0.54
1:D:1038:LYS:HB2	1:D:1038:LYS:HZ2	1.72	0.53
1:G:436:TRP:HZ3	1:G:511:VAL:HG12	1.72	0.53
1:D:951:VAL:O	1:D:955:ASN:ND2	2.33	0.53
1:D:208:ILE:HD11	1:D:210:VAL:HG22	1.89	0.53
1:D:352:ALA:HA	1:D:466:ARG:HD2	1.90	0.53
1:D:802:PHE:HD1	1:D:805:ILE:HD11	1.73	0.53
1:A:81:ASN:OD1	1:A:239:GLN:NE2	2.40	0.53
2:E:151:LEU:H	2:E:197:VAL:HG21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:735:SER:OG	1:G:859:THR:OG1	2.26	0.53
1:A:48:LEU:HD13	1:A:305:SER:HA	1.90	0.53
1:D:118:LEU:H	1:D:118:LEU:HD12	1.74	0.53
1:A:1006:THR:OG1	1:G:1005:GLN:NE2	2.41	0.53
1:A:1038:LYS:HE3	1:G:1038:LYS:HZ1	1.72	0.53
1:G:189:GLU:HB2	1:G:223:LEU:HD21	1.91	0.53
1:D:781:VAL:HG22	1:D:1026:ALA:HB2	1.90	0.53
1:G:116:SER:OG	1:G:131:CYS:O	2.27	0.53
1:G:880:GLY:O	1:G:885:GLY:N	2.42	0.53
1:G:199:PHE:HD2	1:G:201:ILE:HG12	1.74	0.52
1:G:434:ILE:HB	1:G:511:VAL:HG13	1.90	0.52
1:D:110:LEU:HD23	1:D:110:LEU:H	1.73	0.52
1:D:659:SER:HB3	1:D:698:SER:HB2	1.91	0.52
1:D:195:ILE:HG13	1:D:200:LYS:HD3	1.92	0.52
1:A:916:LEU:HD12	1:A:923:ILE:HD12	1.92	0.52
1:G:204:LYS:NZ	1:G:222:ALA:O	2.41	0.52
1:A:128:ILE:HG23	1:A:170:TYR:HB3	1.92	0.52
1:G:329:PHE:O	1:G:580:GLN:NE2	2.41	0.52
1:A:115:GLN:NE2	1:A:132:GLU:OE2	2.42	0.52
1:A:462:LYS:HD2	1:A:463:PRO:HD2	1.92	0.52
1:D:326:ILE:HD12	1:D:539:VAL:HG21	1.90	0.52
2:E:70:ILE:HD11	2:E:79:LEU:HD21	1.92	0.52
1:D:328:ARG:NH1	1:D:578:ASP:OD2	2.43	0.52
1:D:448:ASN:ND2	1:D:496:SER:OG	2.43	0.52
3:C:64:SER:OG	3:C:71:THR:OG1	2.27	0.52
1:D:336:CYS:N	1:D:361:CYS:SG	2.82	0.52
1:G:52:GLN:OE1	1:G:274:THR:OG1	2.23	0.52
1:A:880:GLY:O	1:A:884:SER:OG	2.24	0.51
3:F:123:SER:N	3:F:126:GLU:OE2	2.42	0.51
1:G:201:ILE:HD12	1:G:227:VAL:HG23	1.92	0.51
1:D:969:LYS:H	1:D:969:LYS:HD2	1.76	0.51
2:E:135:PHE:HB2	2:E:154:LEU:HB3	1.92	0.51
1:D:403:ARG:HB2	1:D:508:TYR:HD2	1.75	0.51
1:D:821:LEU:HD23	1:D:821:LEU:H	1.76	0.51
1:G:107:GLY:H	1:G:235:ILE:HG23	1.74	0.51
1:G:909:ILE:O	1:G:1108:ASN:ND2	2.44	0.51
1:D:804:GLN:HB3	1:D:818:ILE:HG13	1.92	0.51
1:A:312:ILE:HG12	1:A:598:ILE:HG13	1.91	0.51
1:D:124:THR:HG23	1:D:125:ASN:HD22	1.76	0.51
1:G:164:ASN:OD1	1:G:165:ASN:ND2	2.44	0.51
1:G:555:SER:HB3	1:G:586:ASP:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:328:ARG:HH11	1:G:533:LEU:HD13	1.76	0.51
1:D:983:ARG:HH22	1:G:517:LEU:HD12	1.76	0.51
1:A:573:THR:HG22	1:A:587:ILE:HD11	1.92	0.51
1:G:552:LEU:HB3	1:G:585:LEU:HD23	1.93	0.51
1:A:403:ARG:HB2	1:A:508:TYR:HD2	1.76	0.50
1:A:804:GLN:OE1	1:A:935:GLN:NE2	2.39	0.50
2:E:100:HIS:HB2	2:E:114:ASP:HB2	1.94	0.50
1:D:46:SER:CA	1:D:279:TYR:O	2.58	0.50
1:G:105:ILE:HG13	1:G:241:LEU:HD11	1.93	0.50
1:A:34:ARG:NH1	1:A:189:GLU:OE2	2.40	0.50
1:D:462:LYS:HD2	1:D:463:PRO:HD2	1.92	0.50
1:A:565:PHE:HB2	1:G:42:VAL:HG22	1.93	0.50
3:F:150:TRP:HE1	3:F:178:SER:HG	1.57	0.50
2:B:38:ARG:NH1	2:B:46:GLU:OE1	2.45	0.50
1:D:573:THR:HG22	1:D:587:ILE:HD11	1.94	0.50
1:G:825:LYS:HG2	1:G:945:LEU:HD23	1.93	0.50
1:A:34:ARG:NH1	1:A:221:SER:OG	2.44	0.50
2:B:70:ILE:HD11	2:B:79:LEU:HD21	1.92	0.50
3:F:64:SER:OG	3:F:71:THR:OG1	2.30	0.50
1:G:551:VAL:HB	1:G:588:THR:HG23	1.94	0.50
1:A:470:THR:HB	2:B:19:ARG:HH21	1.76	0.50
1:A:320:VAL:HG21	1:A:591:SER:HB2	1.94	0.49
1:A:336:CYS:N	1:A:361:CYS:SG	2.85	0.49
1:A:985:ASP:OD1	1:A:985:ASP:N	2.41	0.49
1:D:971:GLY:HA3	1:D:995:ARG:HE	1.77	0.49
2:E:38:ARG:NH1	2:E:46:GLU:OE1	2.45	0.49
1:A:134:GLN:HB3	1:A:161:SER:HB2	1.94	0.49
1:A:858:LEU:HD23	1:A:959:LEU:HD22	1.93	0.49
1:D:448:ASN:HD21	1:D:498:ARG:HH22	1.59	0.49
2:E:157:ASP:HA	2:E:188:LEU:HD13	1.93	0.49
1:G:393:THR:HG21	1:G:520:ALA:HB3	1.93	0.49
1:D:40:ASP:HB2	1:G:519:HIS:CE1	2.45	0.49
1:D:104:TRP:HB2	1:D:119:ILE:HD12	1.94	0.49
1:D:216:LEU:HD12	1:D:217:PRO:HD2	1.94	0.49
1:G:452:LEU:HG	1:G:492:LEU:HB3	1.95	0.49
1:A:350:VAL:HA	1:A:400:PHE:HB2	1.93	0.49
1:D:164:ASN:OD1	1:D:165:ASN:ND2	2.34	0.49
1:G:478:LYS:HD2	1:G:479:PRO:HD2	1.95	0.49
3:F:138:ILE:HD11	3:F:176:ALA:HB3	1.95	0.49
1:G:244:LEU:HG	1:G:246:ARG:HG2	1.95	0.49
1:A:352:ALA:HA	1:A:466:ARG:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:183:ASN:ND2	1:G:209:ILE:O	2.46	0.49
1:G:1037:SER:H	1:G:1048:HIS:HD2	1.60	0.49
1:A:317:ASN:HB3	1:A:319:ARG:HH22	1.77	0.49
1:A:332:ILE:HD13	1:A:332:ILE:H	1.77	0.48
1:A:383:SER:OG	1:A:386:LYS:NZ	2.46	0.48
2:B:100:HIS:HB2	2:B:114:ASP:HB2	1.95	0.48
1:D:318:PHE:CE1	1:D:320:VAL:HG23	2.48	0.48
1:D:1106:GLN:NE2	1:D:1111:GLU:OE1	2.45	0.48
1:A:130:VAL:HG12	1:A:168:PHE:HB2	1.94	0.48
1:G:327:VAL:HG11	1:G:528:LYS:NZ	2.28	0.48
1:G:661:GLU:O	1:G:695:TYR:OH	2.29	0.48
1:A:86:PHE:HE1	1:A:90:VAL:HG22	1.77	0.48
2:B:91:THR:HG22	2:B:124:VAL:H	1.77	0.48
1:G:658:ASN:ND2	1:G:660:TYR:OH	2.46	0.48
1:G:323:THR:O	1:G:324:GLU:HB2	2.13	0.48
1:G:357:ARG:NH1	1:G:396:TYR:OH	2.47	0.48
1:A:92:PHE:HB3	1:A:190:PHE:HB2	1.96	0.48
1:D:67:VAL:HG22	1:D:80:ASP:HB3	1.94	0.48
1:G:658:ASN:OD1	1:G:658:ASN:N	2.43	0.48
1:D:194:ASN:HD22	1:D:235:ILE:HG22	1.79	0.48
1:G:393:THR:HA	1:G:522:ALA:HA	1.96	0.48
1:G:578:ASP:HB3	1:G:581:THR:HG22	1.96	0.48
1:A:127:VAL:HG12	1:A:171:VAL:HG12	1.96	0.48
1:A:716:THR:HG21	1:A:1073:LYS:HE2	1.96	0.48
1:D:729:VAL:HG23	1:D:1059:GLY:HA2	1.96	0.48
1:A:27:ALA:HB3	1:A:64:TRP:HE3	1.79	0.48
1:A:64:TRP:HE1	1:A:214:GLU:HG2	1.79	0.48
1:A:67:VAL:N	1:A:263:ALA:O	2.44	0.48
1:G:68:ILE:HG12	1:G:78:ARG:HA	1.95	0.48
1:A:103:GLY:HA3	1:A:241:LEU:HB3	1.96	0.47
1:A:106:PHE:HB2	1:A:117:LEU:HB3	1.95	0.47
1:D:64:TRP:HE1	1:D:264:ALA:HB1	1.79	0.47
1:G:666:ILE:HD11	1:G:672:ALA:HB2	1.95	0.47
2:E:83:MET:HB3	2:E:86:LEU:HD21	1.95	0.47
2:E:128:SER:OG	2:E:130:LYS:NZ	2.44	0.47
1:G:44:ARG:HD3	1:G:47:VAL:HG21	1.95	0.47
1:A:193:LYS:HE2	1:A:202:TYR:HE2	1.79	0.47
1:A:569:ILE:HG23	1:G:47:VAL:HG12	1.97	0.47
1:A:869:MET:HE2	1:D:699:LEU:HD21	1.97	0.47
2:E:47:TRP:HB2	3:F:99:PHE:HE2	1.79	0.47
1:D:725:GLU:OE1	1:D:1064:HIS:NE2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:981:PHE:HZ	1:D:993:ILE:HD12	1.79	0.47
1:G:357:ARG:NH2	1:G:394:ASN:OD1	2.47	0.47
1:A:726:ILE:O	1:A:947:LYS:NZ	2.38	0.47
1:G:108:THR:O	1:G:237:ARG:NH2	2.40	0.47
1:A:357:ARG:HG3	1:A:396:TYR:HE1	1.80	0.47
1:A:448:ASN:ND2	1:A:496:SER:OG	2.47	0.47
1:D:986:PRO:N	1:D:987:PRO:HD3	2.28	0.47
1:D:1005:GLN:NE2	1:G:1006:THR:OG1	2.47	0.47
3:F:206:LYS:HB2	3:F:206:LYS:HZ2	1.79	0.47
1:G:325:SER:HA	1:G:540:ASN:HB2	1.96	0.47
1:G:403:ARG:CZ	1:G:495:TYR:HB2	2.44	0.47
2:E:91:THR:HG22	2:E:124:VAL:H	1.79	0.47
2:B:47:TRP:HB2	3:C:99:PHE:HE2	1.79	0.47
1:D:229:LEU:HD23	1:D:229:LEU:H	1.80	0.47
1:A:1029:MET:HE1	1:A:1060:VAL:HG21	1.96	0.47
1:G:328:ARG:NH1	1:G:578:ASP:OD2	2.48	0.47
1:G:364:ASP:OD2	1:G:366:SER:OG	2.26	0.46
1:A:722:VAL:HG22	1:A:1065:VAL:HG22	1.97	0.46
1:A:825:LYS:HD2	1:A:945:LEU:HD23	1.97	0.46
1:D:287:ASP:OD1	1:D:287:ASP:N	2.48	0.46
1:D:1054:GLN:HB2	1:D:1061:VAL:HB	1.98	0.46
3:F:116:SER:H	3:F:139:SER:HB2	1.81	0.46
1:A:731:MET:HG3	1:A:955:ASN:HD21	1.80	0.46
1:G:126:VAL:HG12	1:G:128:ILE:HG12	1.98	0.46
1:G:403:ARG:HB2	1:G:507:PRO:HA	1.97	0.46
1:G:971:GLY:O	1:G:995:ARG:NE	2.49	0.46
1:D:725:GLU:OE2	1:D:1028:LYS:NZ	2.33	0.46
1:A:740:MET:SD	1:D:319:ARG:NH2	2.88	0.46
1:D:95:ILE:HG22	1:D:185:LYS:HE3	1.96	0.46
1:D:192:PHE:HE1	1:D:201:ILE:HG23	1.81	0.46
1:G:535:LYS:HG3	1:G:536:ASN:H	1.80	0.46
1:A:537:LYS:HG2	1:A:539:VAL:HG13	1.96	0.46
1:A:596:SER:HB2	1:A:611:LEU:HB3	1.97	0.46
1:D:551:VAL:N	1:D:588:THR:O	2.42	0.46
1:D:67:VAL:HG11	1:D:242:LEU:HD13	1.98	0.46
1:D:957:GLN:O	1:D:961:THR:OG1	2.30	0.46
1:G:290:ASP:O	1:G:297:SER:HB3	2.14	0.46
1:G:63:THR:HB	1:G:267:VAL:HG23	1.97	0.46
1:G:86:PHE:N	1:G:236:THR:O	2.48	0.46
2:B:51:ILE:HD12	2:B:79:LEU:HD11	1.98	0.46
1:G:379:CYS:HA	1:G:432:CYS:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:PRO:HA	1:A:1072:GLU:HA	1.98	0.45
1:A:909:ILE:HG21	1:A:1047:TYR:HB3	1.98	0.45
1:D:128:ILE:HB	1:D:170:TYR:HB3	1.98	0.45
1:D:715:PRO:HA	1:D:1072:GLU:HA	1.99	0.45
2:E:51:ILE:HD12	2:E:79:LEU:HD11	1.98	0.45
1:A:365:TYR:HD1	1:A:388:ASN:HD21	1.64	0.45
1:D:39:PRO:HG3	1:D:51:THR:HG21	1.97	0.45
1:D:122:ASN:OD1	1:D:125:ASN:ND2	2.49	0.45
1:G:358:ILE:HB	1:G:395:VAL:HG13	1.98	0.45
2:B:113:PHE:H	3:C:35:TYR:HH	1.63	0.45
1:D:317:ASN:HD21	1:D:319:ARG:NH2	2.13	0.45
1:A:102:ARG:HA	1:A:177:MET:HE1	1.97	0.45
1:G:92:PHE:HB3	1:G:190:PHE:HB2	1.97	0.45
1:G:726:ILE:O	1:G:947:LYS:NZ	2.36	0.45
1:G:598:ILE:HB	1:G:609:ALA:HB3	1.99	0.45
1:A:543:PHE:HD2	1:A:576:VAL:HG21	1.80	0.45
3:F:119:LEU:HD23	3:F:206:LYS:HB3	1.99	0.45
1:G:64:TRP:HZ2	1:G:214:GLU:HB2	1.80	0.45
1:G:327:VAL:O	1:G:530:SER:HA	2.17	0.45
1:G:611:LEU:HD22	1:G:666:ILE:HG23	1.99	0.45
1:A:858:LEU:HD21	1:A:962:LEU:HD23	1.99	0.45
1:D:386:LYS:HZ1	1:G:456:PHE:HB3	1.82	0.45
1:D:1116:THR:HG22	1:D:1138:TYR:HD2	1.82	0.45
1:G:437:ASN:HA	1:G:508:TYR:HD1	1.81	0.44
3:C:35:TYR:OH	3:C:88:GLN:NE2	2.50	0.44
1:G:200:LYS:HB3	1:G:202:TYR:CE2	2.52	0.44
1:G:1081:ILE:HG13	1:G:1088:HIS:HB2	1.98	0.44
3:F:113:ALA:HB3	3:F:142:TYR:H	1.82	0.44
1:G:327:VAL:HG11	1:G:528:LYS:HZ2	1.82	0.44
1:G:727:LEU:HD11	1:G:1028:LYS:HD2	1.99	0.44
1:A:478:LYS:HB2	1:A:478:LYS:HE3	1.80	0.44
1:D:280:ASN:HB2	1:D:286:THR:HG23	1.99	0.44
2:E:139:PRO:HD2	2:E:226:PRO:HA	2.00	0.44
1:G:92:PHE:O	1:G:190:PHE:N	2.48	0.44
1:G:722:VAL:HG22	1:G:1065:VAL:HG22	1.99	0.44
1:A:781:VAL:HG22	1:A:1026:ALA:HB2	1.99	0.44
1:G:318:PHE:HE1	1:G:320:VAL:HG23	1.83	0.44
1:G:367:VAL:HA	1:G:370:ASN:HD21	1.81	0.44
1:G:712:ILE:HD13	1:G:1094:VAL:HG21	1.99	0.44
1:A:986:PRO:N	1:A:987:PRO:HD2	2.33	0.44
1:D:177:MET:HG2	1:D:188:ARG:HD3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:385:THR:HG23	1:D:386:LYS:HD3	1.99	0.44
1:A:316:SER:OG	1:A:317:ASN:N	2.51	0.44
3:C:12:VAL:HG11	3:C:18:ALA:HB2	1.99	0.44
1:D:731:MET:HG2	1:D:732:THR:H	1.83	0.44
1:G:170:TYR:HD2	1:G:229:LEU:HB3	1.82	0.44
1:G:294:ASP:OD1	1:G:294:ASP:N	2.51	0.44
1:D:294:ASP:OD1	1:D:297:SER:OG	2.31	0.44
2:E:29:PHE:HE1	2:E:34:ILE:HD12	1.83	0.44
1:G:53:ASP:OD1	1:G:54:LEU:N	2.45	0.44
1:A:168:PHE:HZ	1:A:230:PRO:HD2	1.82	0.44
1:D:122:ASN:OD1	1:D:125:ASN:N	2.50	0.43
1:A:320:VAL:CG2	1:A:591:SER:HB2	2.48	0.43
1:D:312:ILE:HD11	1:D:596:SER:HB3	2.00	0.43
1:G:210:VAL:HG22	1:G:212:GLU:H	1.82	0.43
1:G:318:PHE:CD1	1:G:318:PHE:C	2.96	0.43
1:D:199:PHE:HB2	1:D:231:ILE:HG21	2.00	0.43
1:G:457:ARG:HG2	1:G:459:SER:H	1.83	0.43
2:E:214:LYS:HB2	2:E:215:PRO:HD3	1.99	0.43
1:G:387:LEU:HD22	1:G:392:PHE:HZ	1.84	0.43
1:A:985:ASP:HB2	1:A:987:PRO:HD2	2.00	0.43
1:D:316:SER:OG	1:D:317:ASN:N	2.52	0.43
1:D:438:SER:OG	1:D:442:ASP:OD2	2.36	0.43
1:G:105:ILE:HA	1:G:118:LEU:HA	2.00	0.43
1:G:111:ASP:HA	1:G:134:GLN:HG2	2.01	0.43
1:G:421:TYR:HA	1:G:461:LEU:HD13	2.01	0.43
1:G:462:LYS:HE3	1:G:462:LYS:HB2	1.94	0.43
1:A:347:PHE:C	2:B:56:GLY:HA2	2.44	0.43
1:D:189:GLU:O	1:D:203:SER:HA	2.18	0.43
1:D:364:ASP:HA	1:D:527:PRO:HG3	1.99	0.43
3:F:128:GLN:H	3:F:128:GLN:NE2	2.17	0.43
1:G:994:ASP:HA	1:G:997:ILE:HG22	1.99	0.43
1:D:93:ALA:HB1	1:D:187:LEU:HD11	2.00	0.43
3:F:12:VAL:HG11	3:F:18:ALA:HB2	2.00	0.43
1:G:912:THR:OG1	1:G:1106:GLN:NE2	2.50	0.43
1:D:379:CYS:HA	1:D:432:CYS:HA	2.01	0.43
1:D:728:PRO:HD3	1:D:947:LYS:HZ3	1.84	0.43
1:D:855:PHE:HA	1:G:592:PHE:HZ	1.83	0.43
1:A:328:ARG:NH1	1:A:533:LEU:HD22	2.34	0.43
1:D:661:GLU:O	1:D:695:TYR:OH	2.32	0.43
1:D:675:GLN:O	1:D:690:GLN:NE2	2.52	0.42
3:F:142:TYR:HB3	3:F:143:PRO:HD3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1028:LYS:NZ	1:G:1042:PHE:O	2.42	0.42
1:D:900:MET:HE1	1:G:1094:VAL:HG23	2.01	0.42
1:D:357:ARG:HG3	1:D:396:TYR:HE1	1.82	0.42
1:D:909:ILE:HD13	1:D:1049:LEU:HD21	2.01	0.42
1:G:105:ILE:HG12	1:G:118:LEU:HB3	2.01	0.42
1:G:1037:SER:OG	1:G:1043:CYS:SG	2.68	0.42
1:A:43:PHE:HB3	1:D:566:GLY:HA2	2.01	0.42
1:A:763:LEU:HD13	1:A:1004:LEU:HD12	2.01	0.42
2:B:12:VAL:HG11	2:B:18:LEU:HD23	2.02	0.42
1:D:41:LYS:HE2	1:D:41:LYS:HB3	1.90	0.42
1:D:170:TYR:CE1	1:D:172:SER:HB3	2.55	0.42
1:G:289:VAL:HG11	1:G:300:LYS:HE3	1.99	0.42
1:A:67:VAL:HG11	1:A:242:LEU:HD13	2.01	0.42
1:A:97:LYS:HA	1:A:97:LYS:HD2	1.83	0.42
1:D:110:LEU:HB2	1:D:135:PHE:HD2	1.84	0.42
1:D:198:TYR:OH	1:G:394:ASN:ND2	2.53	0.42
1:D:981:PHE:CZ	1:D:993:ILE:HD12	2.55	0.42
2:E:160:PRO:C	2:E:162:PRO:HD3	2.44	0.42
1:A:327:VAL:HA	1:A:542:ASN:HB3	2.01	0.42
1:A:707:TYR:HB3	1:G:792:PRO:HG3	2.02	0.42
1:A:971:GLY:HA3	1:A:995:ARG:HH21	1.85	0.42
1:D:615:VAL:HG13	1:D:619:GLU:HB3	2.01	0.42
1:A:907:ASN:HD21	1:A:913:GLN:HB3	1.83	0.42
1:A:116:SER:N	1:A:131:CYS:O	2.51	0.42
1:A:900:MET:HE1	1:D:1094:VAL:HG23	2.02	0.42
1:G:170:TYR:C	1:G:172:SER:H	2.26	0.42
1:A:641:ASN:ND2	1:A:654:GLU:OE1	2.53	0.42
1:D:126:VAL:HG23	1:D:175:PHE:HA	2.02	0.42
1:D:195:ILE:HG22	1:D:196:ASP:H	1.84	0.42
1:D:478:LYS:HD2	1:D:487:ASN:HB2	2.02	0.42
2:B:60:TYR:HB3	2:B:64:VAL:HG23	2.02	0.42
1:D:671:CYS:SG	1:D:697:MET:HB3	2.60	0.42
1:D:894:LEU:HD13	1:G:715:PRO:HD3	2.02	0.42
3:F:131:LYS:HA	3:F:131:LYS:HD2	1.91	0.42
1:A:109:THR:HA	1:A:237:ARG:NH2	2.35	0.41
1:D:111:ASP:OD1	1:D:113:LYS:NZ	2.53	0.41
1:G:106:PHE:HD2	1:G:235:ILE:HG21	1.85	0.41
1:G:781:VAL:HG22	1:G:1026:ALA:HB2	2.02	0.41
1:G:951:VAL:O	1:G:955:ASN:ND2	2.53	0.41
1:A:726:ILE:HB	1:A:947:LYS:HD3	2.01	0.41
1:A:325:SER:HA	1:A:540:ASN:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:790:LYS:HE2	1:A:790:LYS:HB2	1.93	0.41
1:D:900:MET:SD	1:G:1077:THR:OG1	2.64	0.41
1:D:1076:THR:HB	1:D:1097:SER:HB3	2.02	0.41
1:A:523:THR:HG22	1:A:524:VAL:H	1.85	0.41
1:A:598:ILE:HB	1:A:609:ALA:HB3	2.02	0.41
1:G:170:TYR:CD2	1:G:229:LEU:HB3	2.56	0.41
1:G:173:GLN:N	1:G:174:PRO:HD2	2.35	0.41
1:G:329:PHE:CE2	1:G:528:LYS:CB	2.93	0.41
1:A:713:ALA:HB3	1:G:895:GLN:H	1.86	0.41
1:G:118:LEU:HD21	1:G:133:PHE:HE2	1.84	0.41
1:G:414:GLN:HE21	1:G:414:GLN:HB2	1.62	0.41
1:A:100:ILE:HB	1:A:263:ALA:HB2	2.03	0.41
3:C:2:TYR:OH	3:C:25:ASN:N	2.48	0.41
1:G:493:ARG:NH2	1:G:494:SER:O	2.51	0.41
1:G:551:VAL:N	1:G:588:THR:O	2.42	0.41
1:A:895:GLN:HG2	1:D:713:ALA:HB2	2.01	0.41
1:D:117:LEU:HD23	1:D:233:ILE:HG21	2.02	0.41
1:D:523:THR:HB	1:D:524:VAL:H	1.48	0.41
1:D:822:LEU:HD21	1:D:938:LEU:HD13	2.01	0.41
1:G:466:ARG:HG3	1:G:468:ILE:HG13	2.02	0.41
1:A:467:ASP:OD1	1:A:467:ASP:N	2.54	0.41
1:A:862:PRO:HA	1:A:863:PRO:HD3	1.94	0.41
1:A:873:TYR:CZ	1:D:699:LEU:HD22	2.55	0.41
2:B:38:ARG:HA	2:B:94:TYR:HA	2.03	0.41
2:B:99:HIS:CE1	2:B:112:TYR:H	2.39	0.41
1:D:110:LEU:HB2	1:D:135:PHE:CD2	2.55	0.41
1:D:400:PHE:N	1:D:400:PHE:CD1	2.89	0.41
1:D:526:GLY:HA2	1:D:527:PRO:HD3	1.92	0.41
3:F:165:THR:HG23	3:F:176:ALA:HB1	2.02	0.41
1:G:888:PHE:HD1	1:G:888:PHE:H	1.67	0.41
1:G:957:GLN:HE21	1:G:957:GLN:HB3	1.61	0.41
1:A:156:GLU:HB3	1:A:157:PHE:H	1.69	0.41
1:A:379:CYS:HA	1:A:432:CYS:HA	2.04	0.41
1:A:962:LEU:HD11	1:A:1004:LEU:HD22	2.03	0.41
1:D:89:GLY:HA3	1:D:270:LEU:HD12	2.03	0.41
1:G:455:LEU:HD21	1:G:493:ARG:HG3	2.04	0.40
1:A:195:ILE:HD11	1:A:200:LYS:HD2	2.03	0.40
1:A:323:THR:O	1:A:324:GLU:HB2	2.19	0.40
1:D:241:LEU:HD23	1:D:241:LEU:H	1.85	0.40
3:F:158:LYS:H	3:F:158:LYS:HD3	1.86	0.40
1:G:239:GLN:HE21	1:G:240:THR:N	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:715:PRO:HA	1:G:1072:GLU:HA	2.02	0.40
1:A:704:SER:HB3	1:G:790:LYS:HZ3	1.86	0.40
1:A:811:LYS:HD3	1:A:815:ARG:H	1.85	0.40
1:D:26:PRO:HB2	1:D:27:ALA:H	1.76	0.40
1:D:190:PHE:HB3	1:D:192:PHE:CZ	2.55	0.40
1:D:467:ASP:OD1	1:D:467:ASP:N	2.55	0.40
1:D:666:ILE:HD12	1:D:670:ILE:HG22	2.03	0.40
1:D:983:ARG:O	1:G:383:SER:N	2.54	0.40
1:G:480:CYS:O	1:G:483:VAL:HG22	2.21	0.40
1:A:978:ASN:HB3	1:D:547:LYS:HE2	2.03	0.40
1:D:402:ILE:HD11	1:D:406:GLU:HB2	2.03	0.40
1:G:201:ILE:HD11	1:G:229:LEU:HD21	2.02	0.40
1:G:654:GLU:O	1:G:694:ALA:N	2.52	0.40
1:A:457:ARG:HG2	1:A:458:LYS:H	1.87	0.40
1:A:528:LYS:HA	1:A:528:LYS:HD3	1.56	0.40
1:D:392:PHE:CD1	1:D:515:PHE:HB3	2.56	0.40
1:D:792:PRO:HG3	1:G:707:TYR:HB3	2.03	0.40
2:E:99:HIS:CE1	2:E:112:TYR:H	2.39	0.40
1:G:34:ARG:NH1	1:G:91:TYR:OH	2.54	0.40
1:G:106:PHE:HB3	1:G:235:ILE:HD13	2.04	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	1014/1285 (79%)	932 (92%)	81 (8%)	1 (0%)	48 77
1	D	1009/1285 (78%)	916 (91%)	91 (9%)	2 (0%)	43 72
1	G	1017/1285 (79%)	940 (92%)	72 (7%)	5 (0%)	24 56
2	B	123/227 (54%)	114 (93%)	9 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	224/227 (99%)	202 (90%)	22 (10%)	0	100	100
3	C	105/214 (49%)	98 (93%)	7 (7%)	0	100	100
3	F	208/214 (97%)	189 (91%)	19 (9%)	0	100	100
All	All	3700/4737 (78%)	3391 (92%)	301 (8%)	8 (0%)	44	72

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	987	PRO
1	A	324	GLU
1	G	323	THR
1	D	528	LYS
1	G	529	LYS
1	G	322	PRO
1	G	530	SER
1	G	527	PRO

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	888/1115 (80%)	829 (93%)	59 (7%)	15	44
1	D	884/1115 (79%)	824 (93%)	60 (7%)	14	43
1	G	892/1115 (80%)	823 (92%)	69 (8%)	12	39
2	B	99/187 (53%)	93 (94%)	6 (6%)	17	47
2	E	186/187 (100%)	174 (94%)	12 (6%)	15	45
3	C	88/180 (49%)	84 (96%)	4 (4%)	24	55
3	F	176/180 (98%)	167 (95%)	9 (5%)	21	52
All	All	3213/4079 (79%)	2994 (93%)	219 (7%)	16	43

All (219) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	33	THR
1	A	63	THR
1	A	68	ILE
1	A	101	ILE
1	A	108	THR
1	A	117	LEU
1	A	128	ILE
1	A	129	LYS
1	A	130	VAL
1	A	131	CYS
1	A	158	ARG
1	A	159	VAL
1	A	168	PHE
1	A	176	LEU
1	A	195	ILE
1	A	226	LEU
1	A	240	THR
1	A	278	LYS
1	A	301	CYS
1	A	307	THR
1	A	319	ARG
1	A	321	GLN
1	A	324	GLU
1	A	325	SER
1	A	332	ILE
1	A	362	VAL
1	A	370	ASN
1	A	386	LYS
1	A	387	LEU
1	A	393	THR
1	A	395	VAL
1	A	400	PHE
1	A	401	VAL
1	A	402	ILE
1	A	403	ARG
1	A	440	LYS
1	A	444	LYS
1	A	458	LYS
1	A	480	CYS
1	A	490	PHE
1	A	523	THR
1	A	528	LYS

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Mol	Chain	Res	Type
1	A	531	THR
1	A	537	LYS
1	A	569	ILE
1	A	581	THR
1	A	732	THR
1	A	878	LEU
1	A	947	LYS
1	A	969	LYS
1	A	1004	LEU
1	A	1010	GLN
1	A	1041	ASP
1	A	1086	LYS
1	A	1094	VAL
1	A	1104	VAL
1	A	1129	VAL
1	A	1136	THR
2	B	1	GLU
2	B	18	LEU
2	B	37	VAL
2	B	43	LYS
2	B	52	THR
2	B	104	VAL
3	C	30	LYS
3	C	45	LEU
3	C	74	ILE
3	C	104	LYS
1	D	41	LYS
1	D	51	THR
1	D	66	HIS
1	D	67	VAL
1	D	68	ILE
1	D	83	VAL
1	D	96	GLU
1	D	113	LYS
1	D	117	LEU
1	D	122	ASN
1	D	127	VAL
1	D	132	GLU
1	D	135	PHE
1	D	170	TYR
1	D	198	TYR
1	D	231	ILE

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Mol	Chain	Res	Type
1	D	235	ILE
1	D	278	LYS
1	D	281	GLU
1	D	308	VAL
1	D	321	GLN
1	D	332	ILE
1	D	335	LEU
1	D	336	CYS
1	D	362	VAL
1	D	370	ASN
1	D	386	LYS
1	D	387	LEU
1	D	393	THR
1	D	395	VAL
1	D	400	PHE
1	D	401	VAL
1	D	402	ILE
1	D	403	ARG
1	D	440	LYS
1	D	444	LYS
1	D	458	LYS
1	D	480	CYS
1	D	490	PHE
1	D	523	THR
1	D	524	VAL
1	D	528	LYS
1	D	538	CYS
1	D	588	THR
1	D	590	CYS
1	D	732	THR
1	D	738	CYS
1	D	873	TYR
1	D	878	LEU
1	D	961	THR
1	D	969	LYS
1	D	973	ILE
1	D	985	ASP
1	D	988	GLU
1	D	1001	LEU
1	D	1041	ASP
1	D	1086	LYS
1	D	1104	VAL

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Mol	Chain	Res	Type
1	D	1129	VAL
1	D	1136	THR
2	E	1	GLU
2	E	18	LEU
2	E	37	VAL
2	E	43	LYS
2	E	52	THR
2	E	104	VAL
2	E	153	CYS
2	E	156	LYS
2	E	195	VAL
2	E	205	GLN
2	E	206	THR
2	E	219	LYS
3	F	30	LYS
3	F	45	LEU
3	F	74	ILE
3	F	104	LYS
3	F	128	GLN
3	F	158	LYS
3	F	161	VAL
3	F	197	VAL
3	F	200	GLU
1	G	33	THR
1	G	34	ARG
1	G	67	VAL
1	G	68	ILE
1	G	78	ARG
1	G	117	LEU
1	G	127	VAL
1	G	131	CYS
1	G	134	GLN
1	G	136	CYS
1	G	170	TYR
1	G	171	VAL
1	G	189	GLU
1	G	194	ASN
1	G	201	ILE
1	G	204	LYS
1	G	224	GLU
1	G	229	LEU
1	G	267	VAL

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Mol	Chain	Res	Type
1	G	318	PHE
1	G	335	LEU
1	G	336	CYS
1	G	347	PHE
1	G	351	TYR
1	G	361	CYS
1	G	376	THR
1	G	390	LEU
1	G	395	VAL
1	G	402	ILE
1	G	403	ARG
1	G	408	ARG
1	G	414	GLN
1	G	424	LYS
1	G	433	VAL
1	G	440	LYS
1	G	444	LYS
1	G	452	LEU
1	G	458	LYS
1	G	462	LYS
1	G	468	ILE
1	G	472	ILE
1	G	478	LYS
1	G	483	VAL
1	G	493	ARG
1	G	501	TYR
1	G	511	VAL
1	G	517	LEU
1	G	518	LEU
1	G	524	VAL
1	G	528	LYS
1	G	530	SER
1	G	531	THR
1	G	542	ASN
1	G	546	LEU
1	G	558	LYS
1	G	660	TYR
1	G	825	LYS
1	G	856	LYS
1	G	916	LEU
1	G	947	LYS
1	G	957	GLN

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Mol	Chain	Res	Type
1	G	1001	LEU
1	G	1010	GLN
1	G	1041	ASP
1	G	1086	LYS
1	G	1104	VAL
1	G	1116	THR
1	G	1129	VAL
1	G	1136	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (97) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	115	GLN
1	A	183	ASN
1	A	388	ASN
1	A	414	GLN
1	A	439	ASN
1	A	448	ASN
1	A	506	GLN
1	A	641	ASN
1	A	644	GLN
1	A	774	GLN
1	A	784	GLN
1	A	853	GLN
1	A	895	GLN
1	A	901	GLN
1	A	913	GLN
1	A	949	GLN
1	A	955	ASN
1	A	1005	GLN
1	A	1010	GLN
1	A	1011	GLN
1	A	1048	HIS
1	A	1119	ASN
2	B	39	GLN
2	B	82	GLN
2	B	118	GLN
3	C	6	GLN
3	C	37	GLN
3	C	88	GLN
1	D	52	GLN

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Mol	Chain	Res	Type
1	D	66	HIS
1	D	81	ASN
1	D	125	ASN
1	D	173	GLN
1	D	218	GLN
1	D	239	GLN
1	D	317	ASN
1	D	414	GLN
1	D	417	ASN
1	D	439	ASN
1	D	448	ASN
1	D	506	GLN
1	D	540	ASN
1	D	580	GLN
1	D	613	GLN
1	D	762	GLN
1	D	774	GLN
1	D	784	GLN
1	D	787	GLN
1	D	895	GLN
1	D	901	GLN
1	D	957	GLN
1	D	1011	GLN
1	D	1048	HIS
1	D	1083	HIS
1	D	1106	GLN
2	E	39	GLN
2	E	118	GLN
2	E	177	HIS
2	E	205	GLN
2	E	210	ASN
3	F	6	GLN
3	F	37	GLN
3	F	88	GLN
3	F	110	GLN
3	F	128	GLN
3	F	130	ASN
3	F	172	ASN
3	F	190	HIS
3	F	196	GLN
1	G	49	HIS
1	G	81	ASN

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Mol	Chain	Res	Type
1	G	165	ASN
1	G	239	GLN
1	G	317	ASN
1	G	370	ASN
1	G	394	ASN
1	G	414	GLN
1	G	519	HIS
1	G	540	ASN
1	G	563	GLN
1	G	564	GLN
1	G	613	GLN
1	G	703	ASN
1	G	762	GLN
1	G	784	GLN
1	G	804	GLN
1	G	853	GLN
1	G	895	GLN
1	G	901	GLN
1	G	913	GLN
1	G	965	GLN
1	G	1005	GLN
1	G	1011	GLN
1	G	1048	HIS
1	G	1054	GLN
1	G	1108	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

24 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	D	1304	1	14,14,15	0.28	0	17,19,21	0.61	0
4	NAG	G	1304	1	14,14,15	0.27	0	17,19,21	0.57	0
4	NAG	A	1301	1	14,14,15	0.29	0	17,19,21	0.58	0
4	NAG	D	1306	1	14,14,15	0.33	0	17,19,21	0.68	0
4	NAG	A	1302	1	14,14,15	0.28	0	17,19,21	0.71	0
4	NAG	G	1307	1	14,14,15	0.31	0	17,19,21	0.85	0
4	NAG	G	1302	1	14,14,15	0.29	0	17,19,21	0.87	1 (5%)
4	NAG	D	1305	1	14,14,15	0.29	0	17,19,21	0.72	0
4	NAG	A	1304	1	14,14,15	0.29	0	17,19,21	0.63	0
4	NAG	G	1303	1	14,14,15	0.27	0	17,19,21	0.59	0
4	NAG	G	1301	1	14,14,15	0.28	0	17,19,21	0.58	0
4	NAG	G	1305	1	14,14,15	0.33	0	17,19,21	0.68	0
4	NAG	D	1302	1	14,14,15	0.28	0	17,19,21	0.62	0
4	NAG	G	1308	1	14,14,15	0.41	0	17,19,21	0.75	0
4	NAG	A	1307	1	14,14,15	0.28	0	17,19,21	0.68	0
4	NAG	D	1309	1	14,14,15	0.31	0	17,19,21	0.72	0
4	NAG	D	1308	1	14,14,15	0.31	0	17,19,21	0.64	0
4	NAG	A	1303	1	14,14,15	0.29	0	17,19,21	0.66	0
4	NAG	D	1307	1	14,14,15	0.32	0	17,19,21	0.70	1 (5%)
4	NAG	G	1306	1	14,14,15	0.32	0	17,19,21	0.66	0
4	NAG	D	1301	1	14,14,15	0.26	0	17,19,21	0.69	0
4	NAG	A	1306	1	14,14,15	0.31	0	17,19,21	0.71	0
4	NAG	A	1305	1	14,14,15	0.32	0	17,19,21	0.66	0
4	NAG	D	1303	1	14,14,15	0.30	0	17,19,21	0.62	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	G	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1301	1	-	3/6/23/26	0/1/1/1
4	NAG	D	1306	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	G	1307	1	-	0/6/23/26	0/1/1/1
4	NAG	G	1302	1	-	1/6/23/26	0/1/1/1
4	NAG	D	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
4	NAG	G	1303	1	-	1/6/23/26	0/1/1/1
4	NAG	G	1301	1	-	2/6/23/26	0/1/1/1
4	NAG	G	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	D	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	G	1308	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1307	1	-	3/6/23/26	0/1/1/1
4	NAG	D	1309	1	-	0/6/23/26	0/1/1/1
4	NAG	D	1308	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1303	1	-	2/6/23/26	0/1/1/1
4	NAG	D	1307	1	-	0/6/23/26	0/1/1/1
4	NAG	G	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	D	1301	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	D	1303	1	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	1302	NAG	C4-C3-C2	-2.14	107.88	111.02
4	D	1307	NAG	C1-O5-C5	2.01	114.88	112.19

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1301	NAG	C8-C7-N2-C2
4	A	1301	NAG	O7-C7-N2-C2
4	D	1302	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	D	1302	NAG	O7-C7-N2-C2
4	D	1305	NAG	C8-C7-N2-C2
4	D	1305	NAG	O7-C7-N2-C2
4	G	1304	NAG	O7-C7-N2-C2
4	G	1304	NAG	C8-C7-N2-C2
4	A	1303	NAG	O7-C7-N2-C2
4	A	1302	NAG	C8-C7-N2-C2
4	A	1303	NAG	C8-C7-N2-C2
4	A	1302	NAG	O7-C7-N2-C2
4	A	1304	NAG	C8-C7-N2-C2
4	D	1306	NAG	C8-C7-N2-C2
4	G	1301	NAG	C8-C7-N2-C2
4	G	1301	NAG	O7-C7-N2-C2
4	A	1304	NAG	O7-C7-N2-C2
4	G	1305	NAG	C8-C7-N2-C2
4	D	1306	NAG	O7-C7-N2-C2
4	D	1304	NAG	C8-C7-N2-C2
4	G	1305	NAG	O7-C7-N2-C2
4	A	1305	NAG	C8-C7-N2-C2
4	G	1303	NAG	O5-C5-C6-O6
4	D	1304	NAG	O7-C7-N2-C2
4	A	1301	NAG	O5-C5-C6-O6
4	D	1303	NAG	C8-C7-N2-C2
4	A	1305	NAG	O7-C7-N2-C2
4	A	1307	NAG	C8-C7-N2-C2
4	D	1303	NAG	O7-C7-N2-C2
4	A	1307	NAG	O7-C7-N2-C2
4	A	1307	NAG	C1-C2-N2-C7
4	D	1303	NAG	C1-C2-N2-C7
4	D	1308	NAG	C1-C2-N2-C7
4	G	1308	NAG	C1-C2-N2-C7
4	G	1302	NAG	C8-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32552. These allow visual inspection of the internal detail of the map and identification of artifacts.

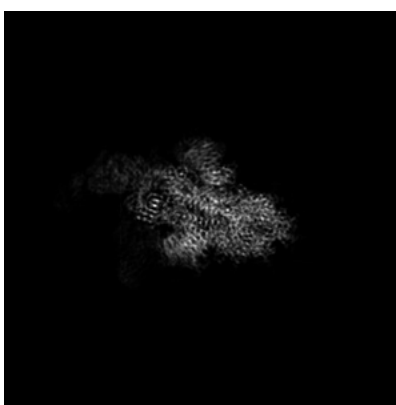
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

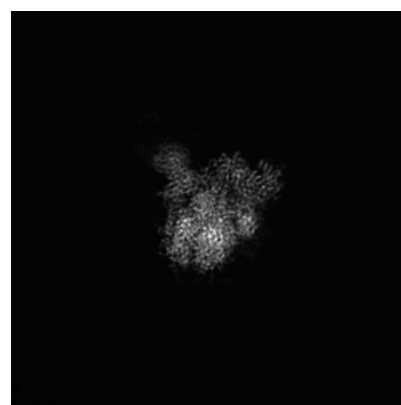
6.1.1 Primary map



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: 160



Y Index: 160



Z Index: 160

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

6.3 Largest variance slices [i](#)

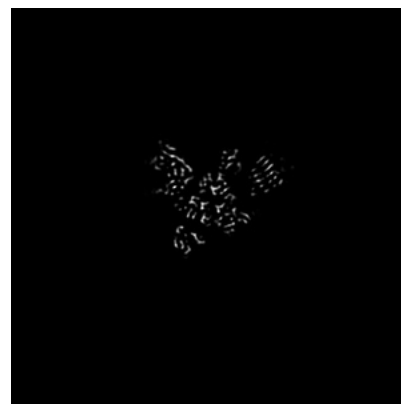
6.3.1 Primary map



X Index: 153



Y Index: 143

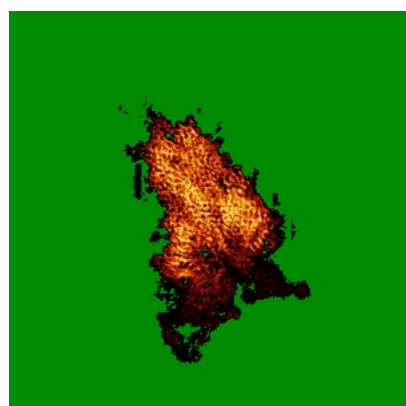


Z Index: 153

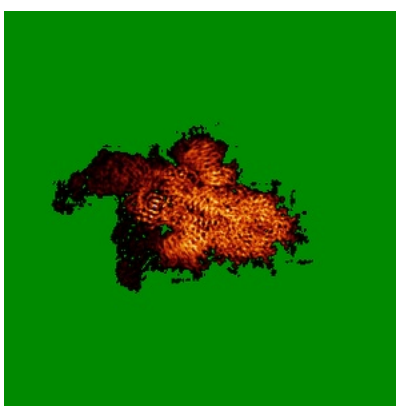
The images above show the largest variance slices of the map in three orthogonal directions.

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

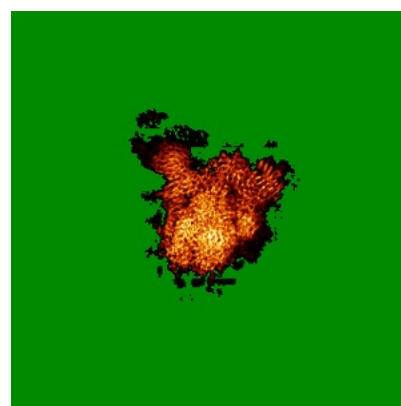
6.4.1 Primary map



X



Y

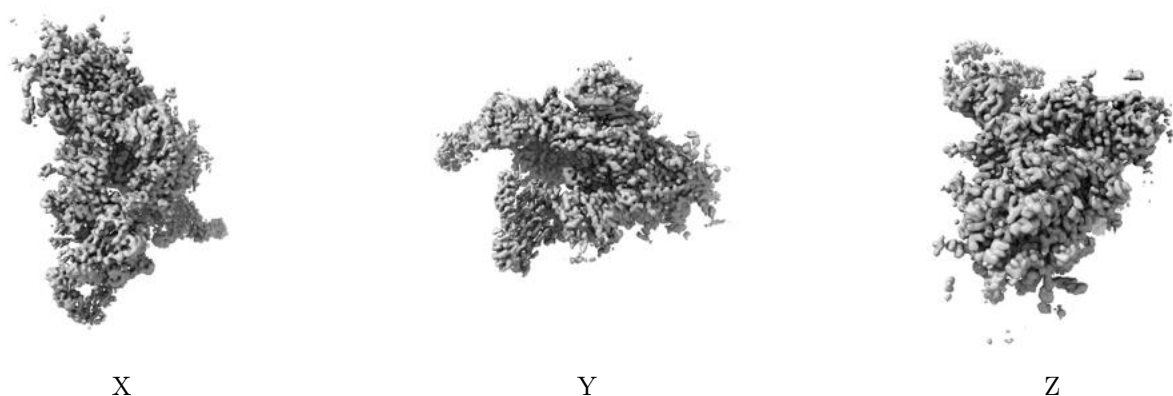


Z

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

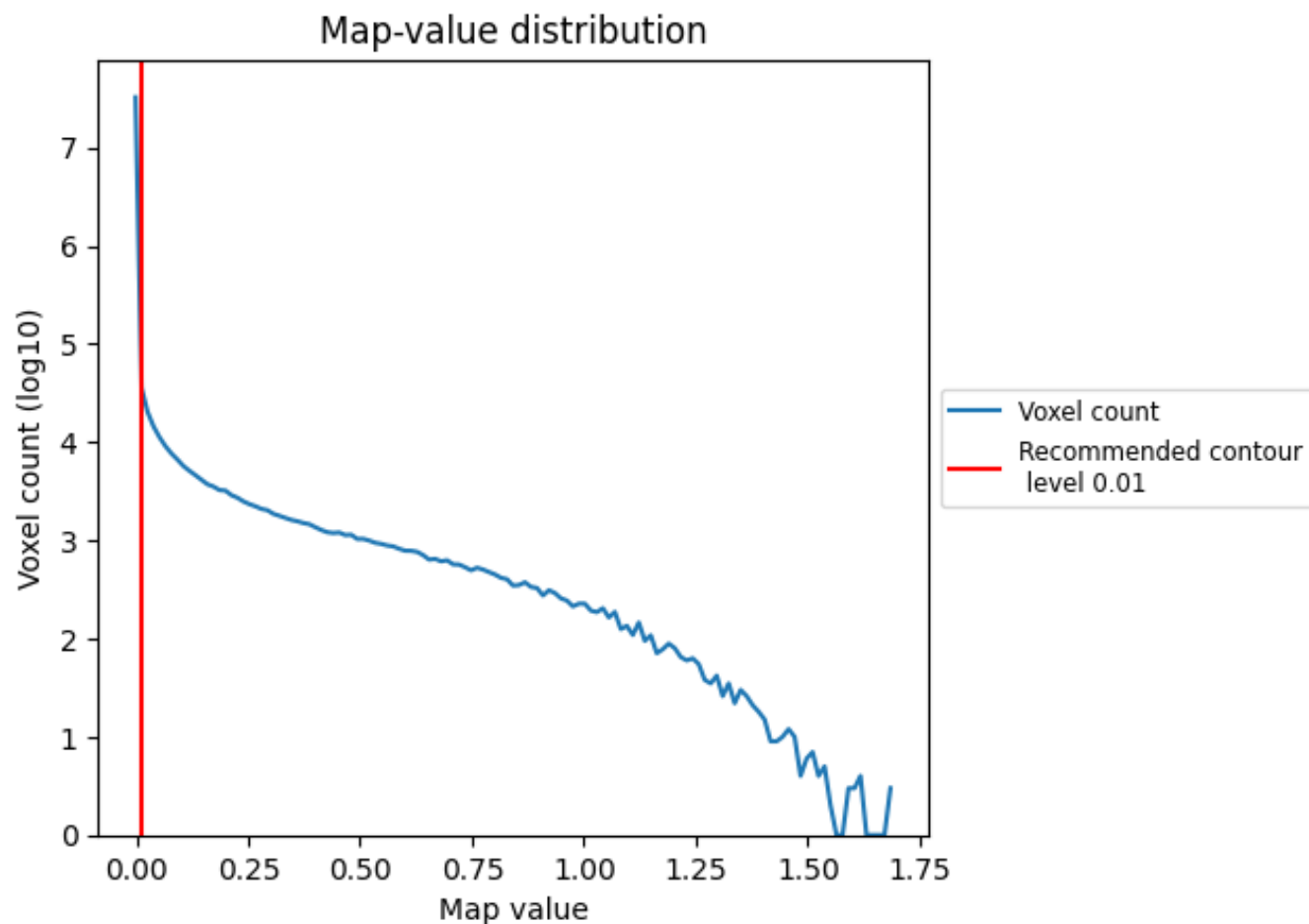
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

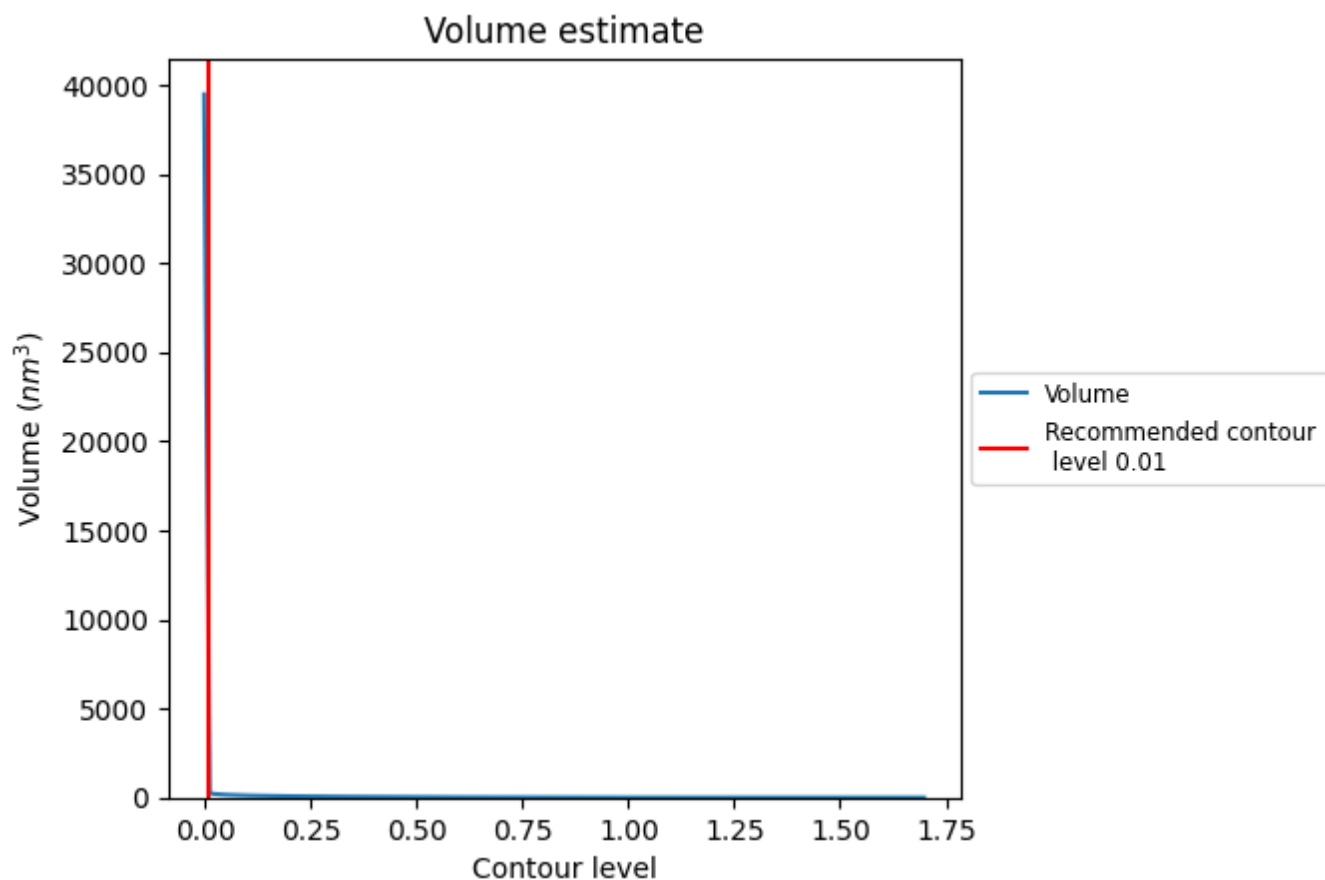
This section contains the results of statistical analysis of the map.

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.

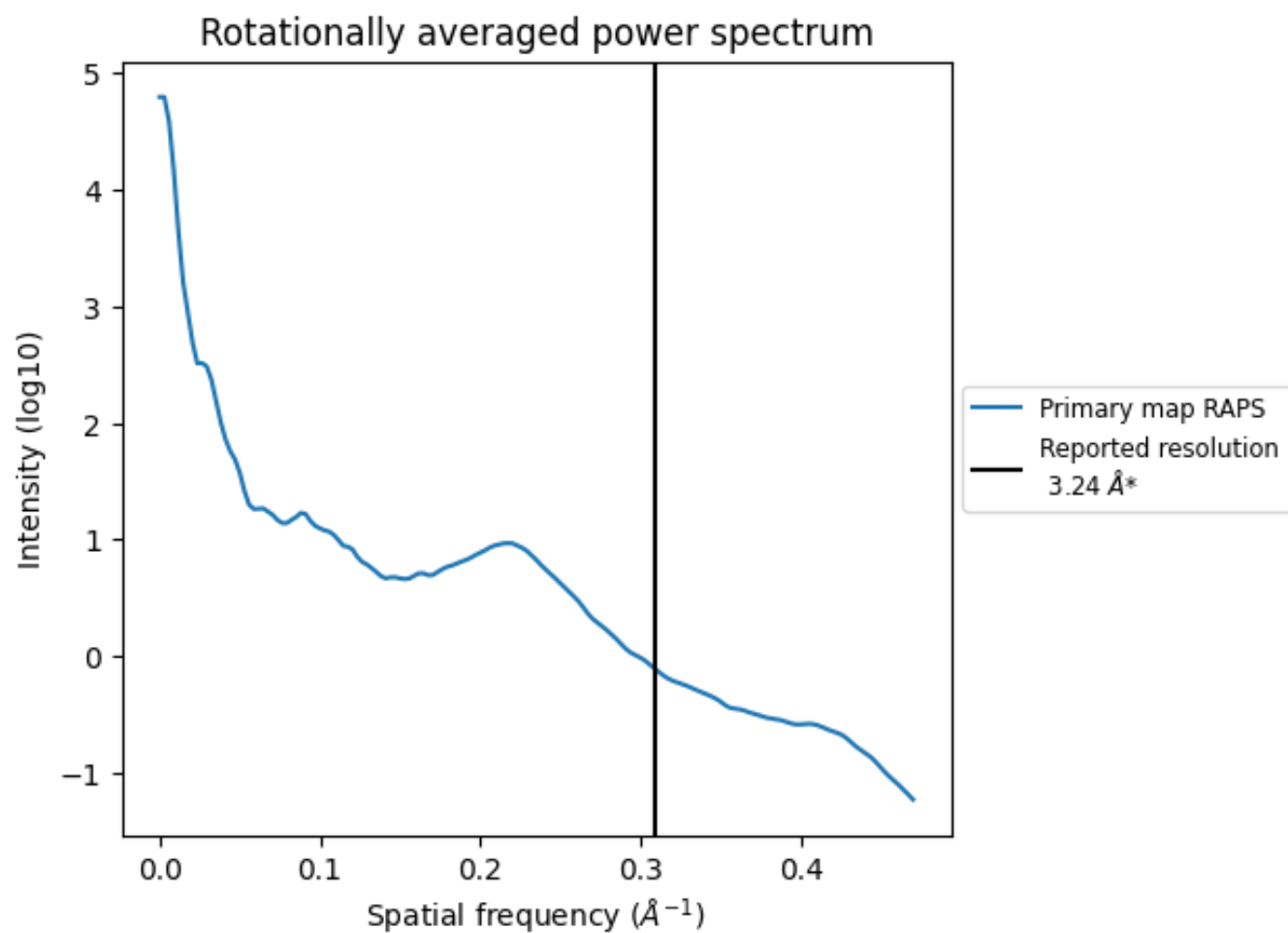
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4891 nm^3 ; this corresponds to an approximate mass of 4418 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 ⓘ

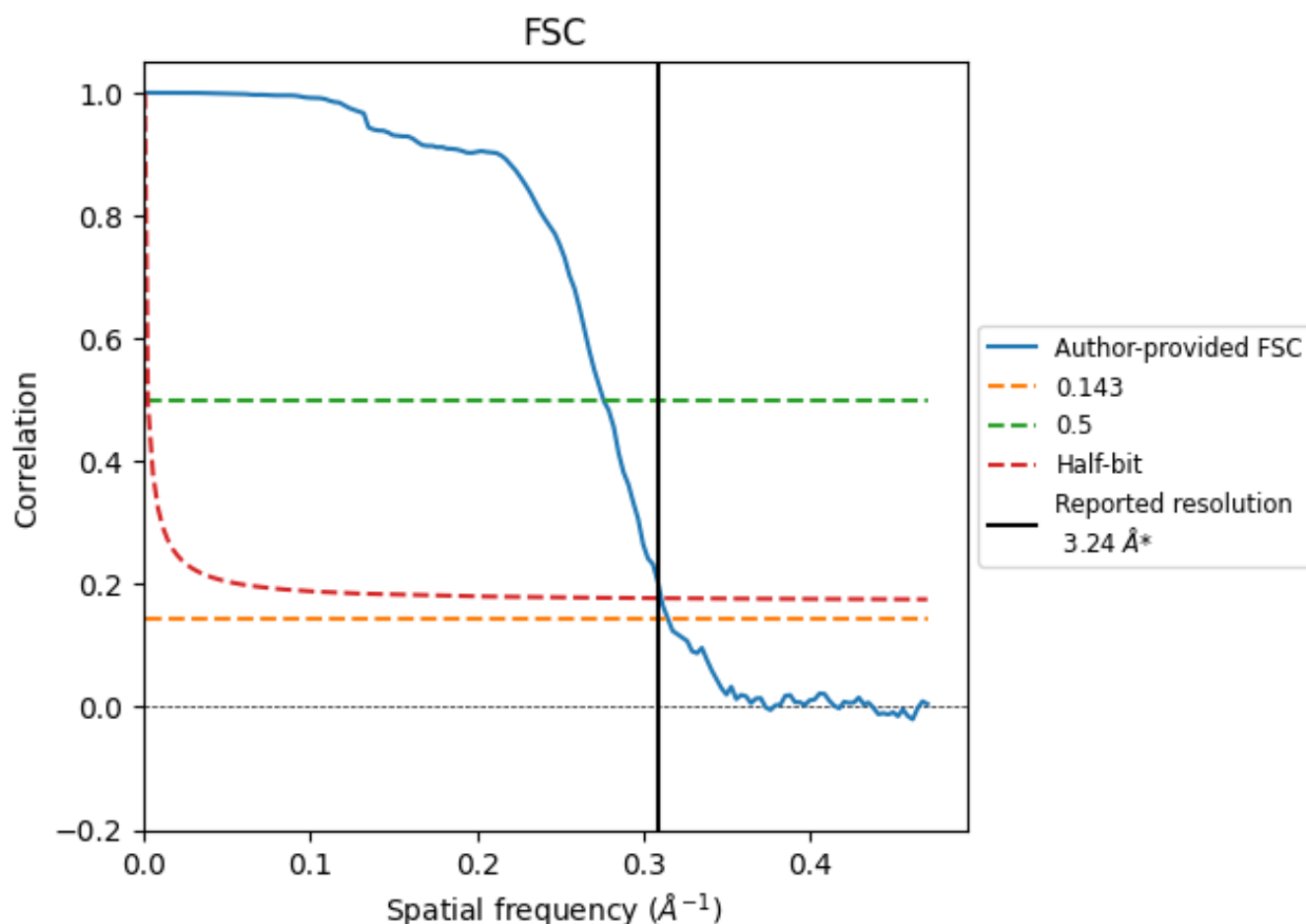


*Reported resolution corresponds to spatial frequency of 0.309 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.309 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.24	-	-
Author-provided FSC curve	3.18	3.63	3.22
Unmasked-calculated*	-	-	-

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

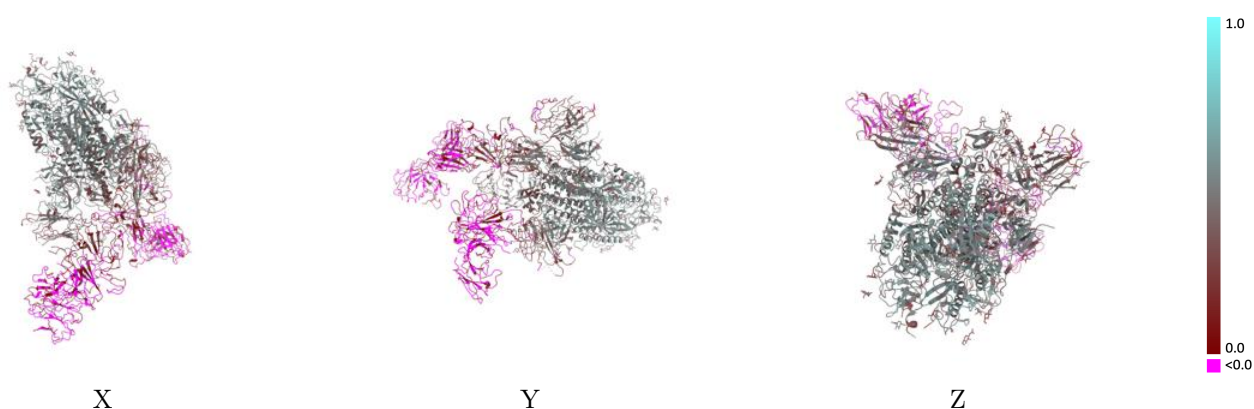
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32552 and PDB model 7WJY. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)

This section was not generated.

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

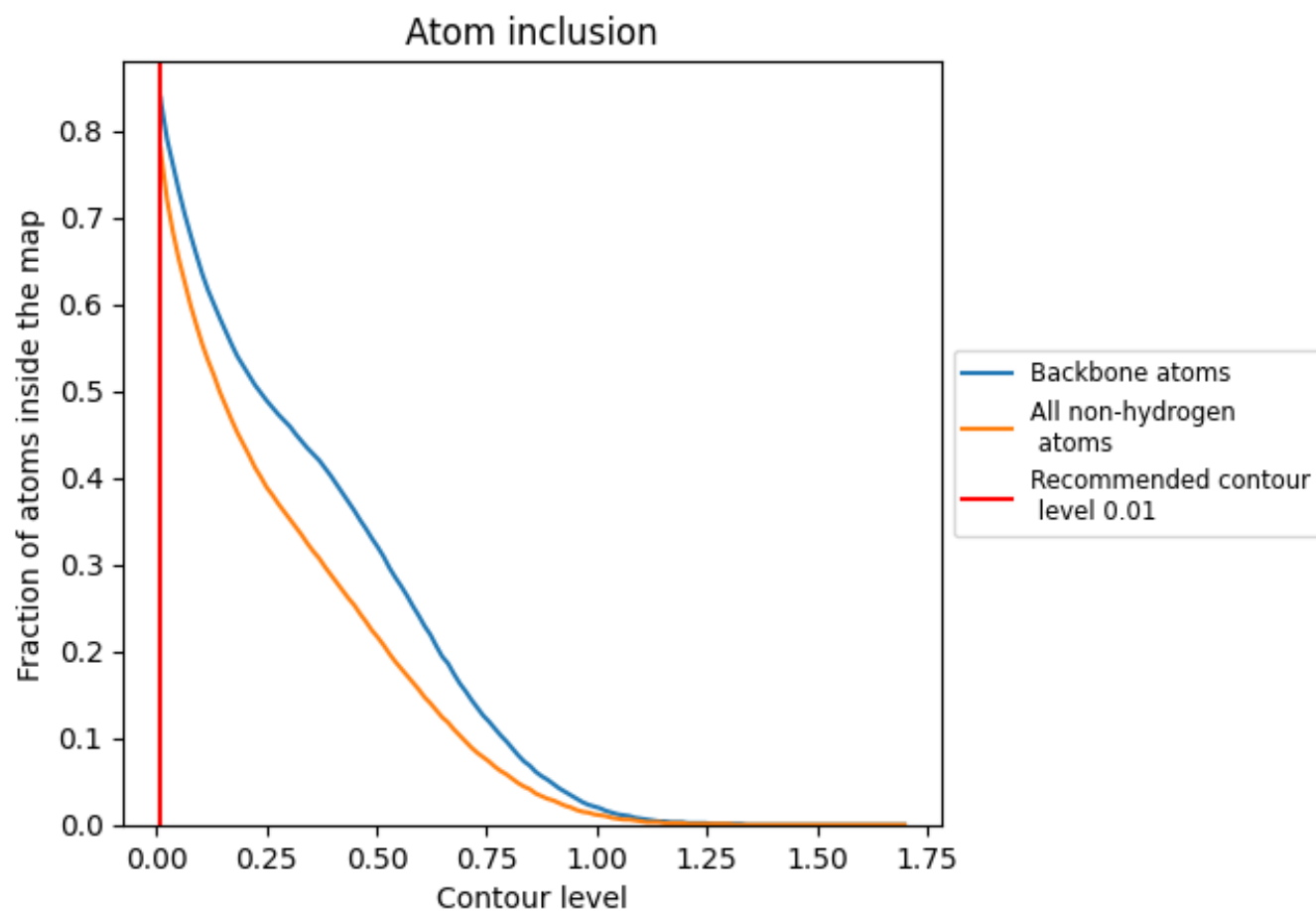


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 78% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7790	0.3100
A	0.8200	0.3630
B	0.2720	-0.0300
C	0.2480	-0.0420
D	0.8890	0.3730
E	0.3710	0.0030
F	0.3280	-0.0490
G	0.9100	0.4030

1.0

0.0

<0.0