



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:39 AM UTC

PDB ID : 7V26 / pdb_00007v26
EMDB ID : EMD-31637
Title : XG005-bound SARS-CoV-2 S
Authors : Zhan, W.Q.; Zhang, X.; Sun, L.; Chen, Z.G.
Deposited on : 2021-08-07
Resolution : 3.85 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

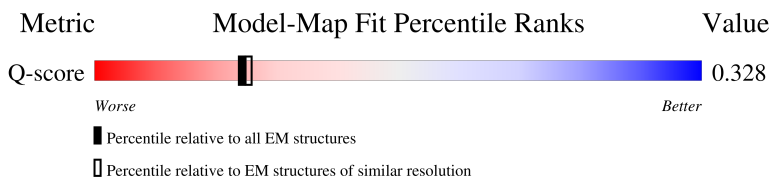
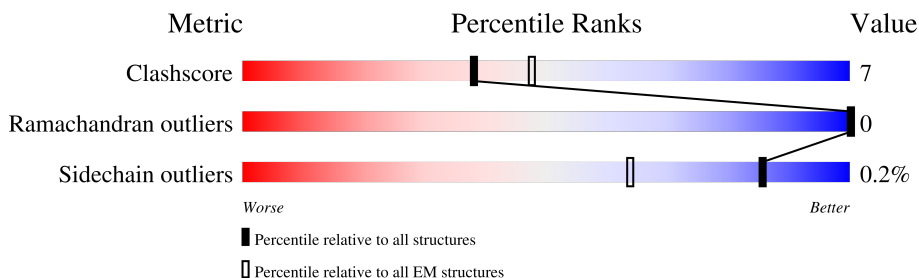
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.85 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	8989 (3.35 - 4.35)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1288	
1	C	1288	
1	E	1288	
2	a	232	

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Mol	Chain	Length	Quality of chain
2	c	232	29% 81% 16%
2	e	232	20% 78% 18%
3	b	215	6% 76% 19% 6%
3	d	215	35% 74% 20% 6%
3	f	215	22% 74% 20% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 35157 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1076	Total	C	N	O	S	0	0
			8342	5320	1396	1588	38		
1	C	1076	Total	C	N	O	S	0	0
			8342	5320	1396	1588	38		
1	E	1076	Total	C	N	O	S	0	0
			8342	5320	1396	1588	38		

There are 255 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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	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
A	1227	ASP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
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
A	1269	ALA	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
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
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
C	1224	VAL	-	expression tag	UNP P0DTC2
C	1225	ARG	-	expression tag	UNP P0DTC2
C	1226	LYS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1227	ASP	-	expression tag	UNP P0DTC2
C	1228	GLY	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2
C	1230	TRP	-	expression tag	UNP P0DTC2
C	1231	VAL	-	expression tag	UNP P0DTC2
C	1232	PHE	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	SER	-	expression tag	UNP P0DTC2
C	1235	THR	-	expression tag	UNP P0DTC2
C	1236	PHE	-	expression tag	UNP P0DTC2
C	1237	LEU	-	expression tag	UNP P0DTC2
C	1238	SER	-	expression tag	UNP P0DTC2
C	1239	GLY	-	expression tag	UNP P0DTC2
C	1240	LEU	-	expression tag	UNP P0DTC2
C	1241	GLU	-	expression tag	UNP P0DTC2
C	1242	VAL	-	expression tag	UNP P0DTC2
C	1243	LEU	-	expression tag	UNP P0DTC2
C	1244	PHE	-	expression tag	UNP P0DTC2
C	1245	GLN	-	expression tag	UNP P0DTC2
C	1246	GLY	-	expression tag	UNP P0DTC2
C	1247	PRO	-	expression tag	UNP P0DTC2
C	1248	GLY	-	expression tag	UNP P0DTC2
C	1249	GLY	-	expression tag	UNP P0DTC2
C	1250	TRP	-	expression tag	UNP P0DTC2
C	1251	SER	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	PRO	-	expression tag	UNP P0DTC2
C	1254	GLN	-	expression tag	UNP P0DTC2
C	1255	PHE	-	expression tag	UNP P0DTC2
C	1256	GLU	-	expression tag	UNP P0DTC2
C	1257	LYS	-	expression tag	UNP P0DTC2
C	1258	GLY	-	expression tag	UNP P0DTC2
C	1259	GLY	-	expression tag	UNP P0DTC2
C	1260	GLY	-	expression tag	UNP P0DTC2
C	1261	SER	-	expression tag	UNP P0DTC2
C	1262	GLY	-	expression tag	UNP P0DTC2
C	1263	GLY	-	expression tag	UNP P0DTC2
C	1264	GLY	-	expression tag	UNP P0DTC2
C	1265	SER	-	expression tag	UNP P0DTC2
C	1266	GLY	-	expression tag	UNP P0DTC2
C	1267	GLY	-	expression tag	UNP P0DTC2
C	1268	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1269	ALA	-	expression tag	UNP P0DTC2
C	1270	TRP	-	expression tag	UNP P0DTC2
C	1271	SER	-	expression tag	UNP P0DTC2
C	1272	HIS	-	expression tag	UNP P0DTC2
C	1273	PRO	-	expression tag	UNP P0DTC2
C	1274	GLN	-	expression tag	UNP P0DTC2
C	1275	PHE	-	expression tag	UNP P0DTC2
C	1276	GLU	-	expression tag	UNP P0DTC2
C	1277	LYS	-	expression tag	UNP P0DTC2
C	1278	GLY	-	expression tag	UNP P0DTC2
C	1279	GLY	-	expression tag	UNP P0DTC2
C	1280	SER	-	expression tag	UNP P0DTC2
C	1281	HIS	-	expression tag	UNP P0DTC2
C	1282	HIS	-	expression tag	UNP P0DTC2
C	1283	HIS	-	expression tag	UNP P0DTC2
C	1284	HIS	-	expression tag	UNP P0DTC2
C	1285	HIS	-	expression tag	UNP P0DTC2
C	1286	HIS	-	expression tag	UNP P0DTC2
C	1287	HIS	-	expression tag	UNP P0DTC2
C	1288	HIS	-	expression tag	UNP P0DTC2
E	682	GLY	ARG	engineered mutation	UNP P0DTC2
E	683	SER	ARG	engineered mutation	UNP P0DTC2
E	685	SER	ARG	engineered mutation	UNP P0DTC2
E	986	PRO	LYS	engineered mutation	UNP P0DTC2
E	987	PRO	VAL	engineered mutation	UNP P0DTC2
E	1209	GLY	-	expression tag	UNP P0DTC2
E	1210	SER	-	expression tag	UNP P0DTC2
E	1211	GLY	-	expression tag	UNP P0DTC2
E	1212	TYR	-	expression tag	UNP P0DTC2
E	1213	ILE	-	expression tag	UNP P0DTC2
E	1214	PRO	-	expression tag	UNP P0DTC2
E	1215	GLU	-	expression tag	UNP P0DTC2
E	1216	ALA	-	expression tag	UNP P0DTC2
E	1217	PRO	-	expression tag	UNP P0DTC2
E	1218	ARG	-	expression tag	UNP P0DTC2
E	1219	ASP	-	expression tag	UNP P0DTC2
E	1220	GLY	-	expression tag	UNP P0DTC2
E	1221	GLN	-	expression tag	UNP P0DTC2
E	1222	ALA	-	expression tag	UNP P0DTC2
E	1223	TYR	-	expression tag	UNP P0DTC2
E	1224	VAL	-	expression tag	UNP P0DTC2
E	1225	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1226	LYS	-	expression tag	UNP P0DTC2
E	1227	ASP	-	expression tag	UNP P0DTC2
E	1228	GLY	-	expression tag	UNP P0DTC2
E	1229	GLU	-	expression tag	UNP P0DTC2
E	1230	TRP	-	expression tag	UNP P0DTC2
E	1231	VAL	-	expression tag	UNP P0DTC2
E	1232	PHE	-	expression tag	UNP P0DTC2
E	1233	LEU	-	expression tag	UNP P0DTC2
E	1234	SER	-	expression tag	UNP P0DTC2
E	1235	THR	-	expression tag	UNP P0DTC2
E	1236	PHE	-	expression tag	UNP P0DTC2
E	1237	LEU	-	expression tag	UNP P0DTC2
E	1238	SER	-	expression tag	UNP P0DTC2
E	1239	GLY	-	expression tag	UNP P0DTC2
E	1240	LEU	-	expression tag	UNP P0DTC2
E	1241	GLU	-	expression tag	UNP P0DTC2
E	1242	VAL	-	expression tag	UNP P0DTC2
E	1243	LEU	-	expression tag	UNP P0DTC2
E	1244	PHE	-	expression tag	UNP P0DTC2
E	1245	GLN	-	expression tag	UNP P0DTC2
E	1246	GLY	-	expression tag	UNP P0DTC2
E	1247	PRO	-	expression tag	UNP P0DTC2
E	1248	GLY	-	expression tag	UNP P0DTC2
E	1249	GLY	-	expression tag	UNP P0DTC2
E	1250	TRP	-	expression tag	UNP P0DTC2
E	1251	SER	-	expression tag	UNP P0DTC2
E	1252	HIS	-	expression tag	UNP P0DTC2
E	1253	PRO	-	expression tag	UNP P0DTC2
E	1254	GLN	-	expression tag	UNP P0DTC2
E	1255	PHE	-	expression tag	UNP P0DTC2
E	1256	GLU	-	expression tag	UNP P0DTC2
E	1257	LYS	-	expression tag	UNP P0DTC2
E	1258	GLY	-	expression tag	UNP P0DTC2
E	1259	GLY	-	expression tag	UNP P0DTC2
E	1260	GLY	-	expression tag	UNP P0DTC2
E	1261	SER	-	expression tag	UNP P0DTC2
E	1262	GLY	-	expression tag	UNP P0DTC2
E	1263	GLY	-	expression tag	UNP P0DTC2
E	1264	GLY	-	expression tag	UNP P0DTC2
E	1265	SER	-	expression tag	UNP P0DTC2
E	1266	GLY	-	expression tag	UNP P0DTC2
E	1267	GLY	-	expression tag	UNP P0DTC2

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

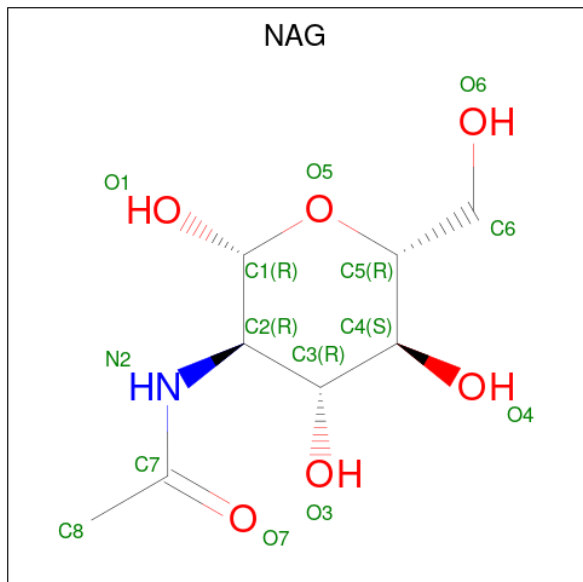
- Molecule 2 is a protein called XG005 Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	223	Total	C	N	O	S	0	0
			1664	1053	274	329	8		
2	c	223	Total	C	N	O	S	0	0
			1664	1053	274	329	8		
2	e	223	Total	C	N	O	S	0	0
			1664	1053	274	329	8		

- Molecule 3 is a protein called XG005 Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	203	Total	C	N	O	S	0	0
			1503	940	248	310	5		
3	d	203	Total	C	N	O	S	0	0
			1503	940	248	310	5		
3	f	203	Total	C	N	O	S	0	0
			1503	940	248	310	5		

- 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	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	

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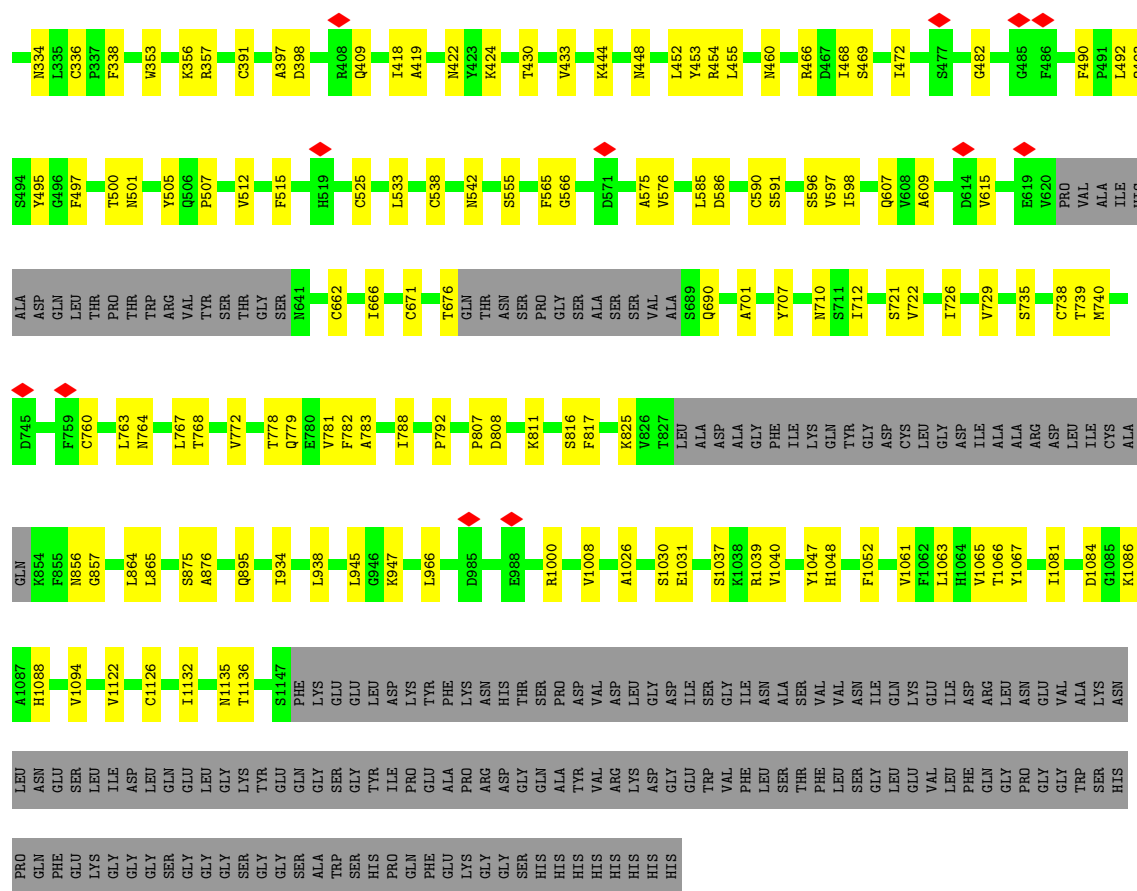
Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4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

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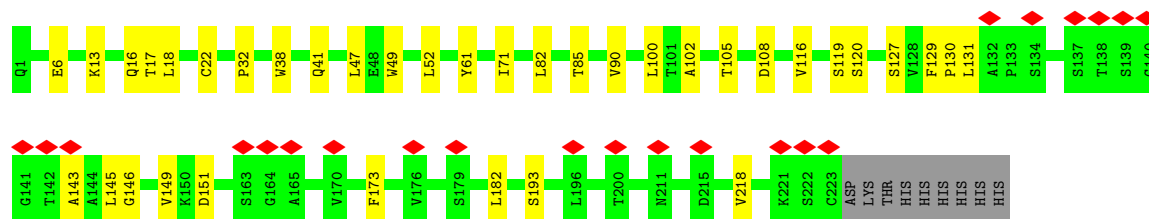
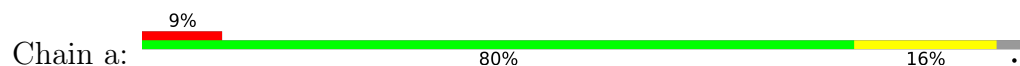
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Mol	Chain	Residues	Atoms				AltConf
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C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

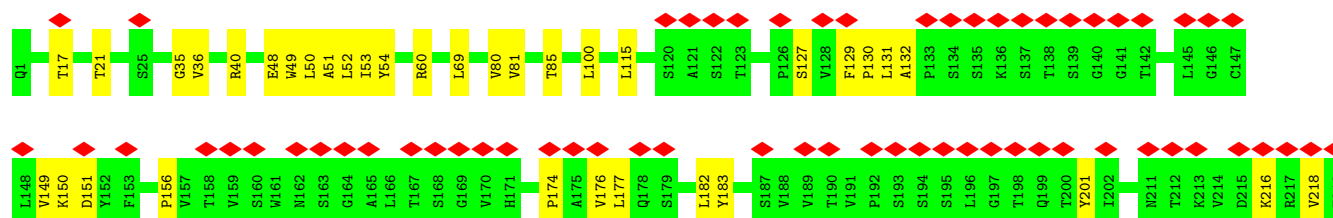
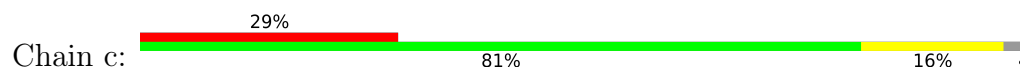




• Molecule 2: XG005 Heavy chain

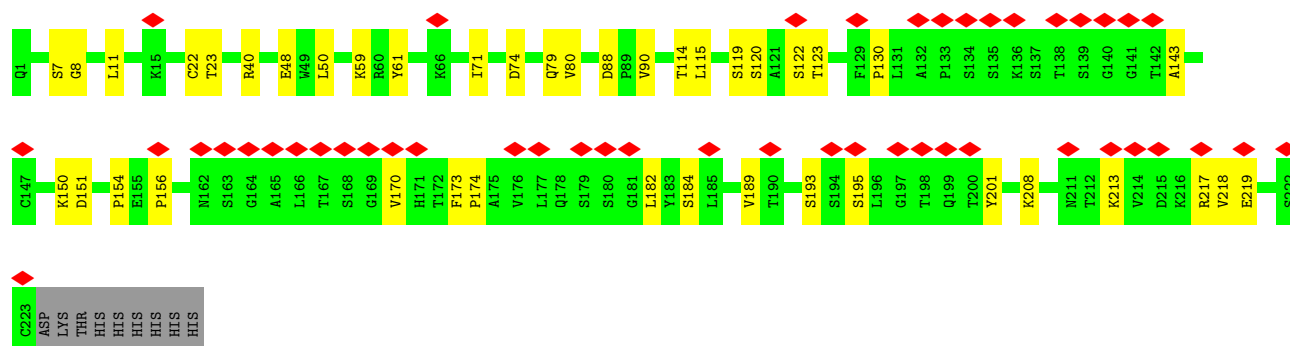
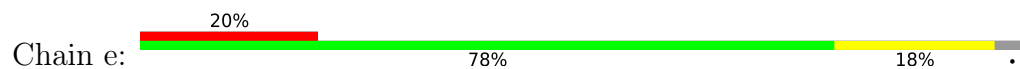


• Molecule 2: XG005 Heavy chain

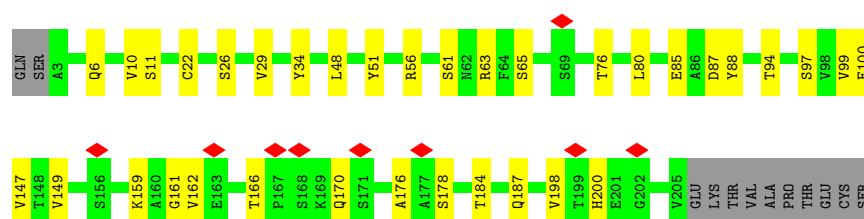
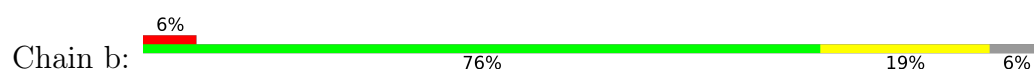




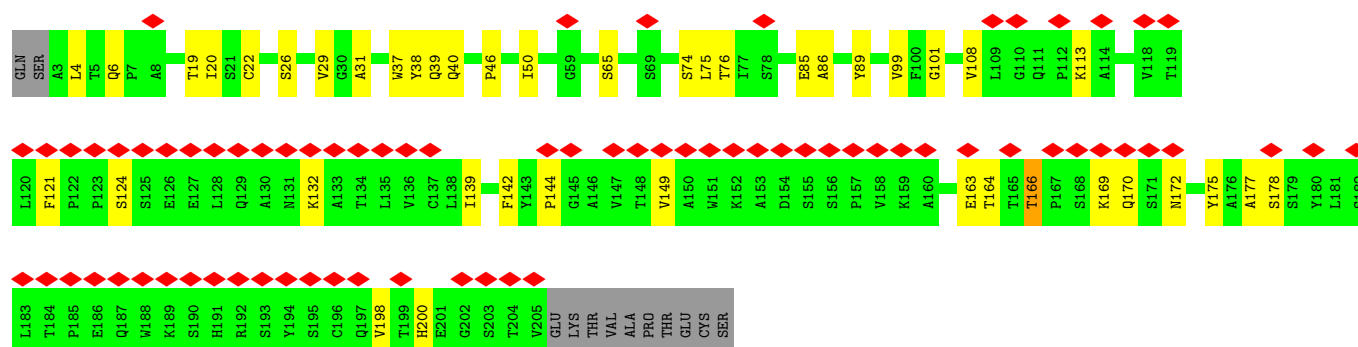
• Molecule 2: XG005 Heavy chain



• Molecule 3: XG005 Light Chain

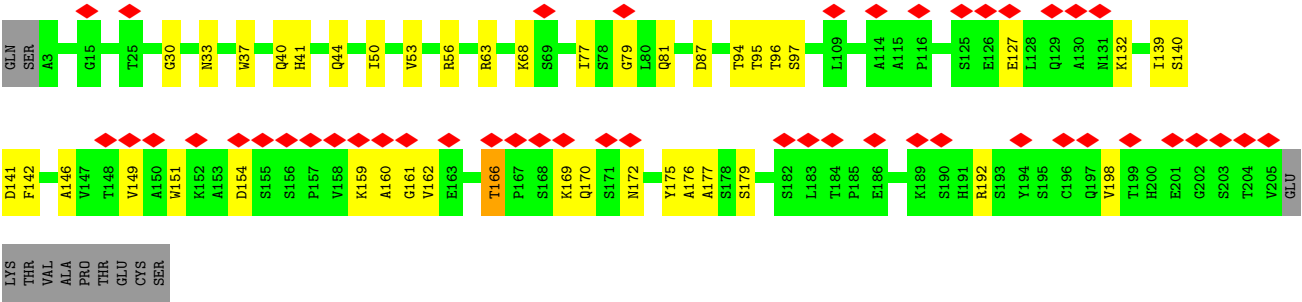


• Molecule 3: XG005 Light Chain



• Molecule 3: XG005 Light Chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109304	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.078	Depositor
Minimum map value	0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	410.032, 410.032, 410.032	wwPDB
Map dimensions	392, 392, 392	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.046, 1.046, 1.046	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	0.11	0/8538	0.30	0/11632
1	C	0.10	0/8538	0.28	0/11632
1	E	0.10	0/8538	0.29	0/11632
2	a	0.11	0/1704	0.31	1/2331 (0.0%)
2	c	0.11	0/1704	0.28	0/2331
2	e	0.12	0/1704	0.31	0/2331
3	b	0.12	0/1539	0.34	0/2103
3	d	0.12	0/1539	0.35	0/2103
3	f	0.12	0/1539	0.34	0/2103
All	All	0.11	0/35343	0.30	1/48198 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	a	90	VAL	N-CA-C	-6.15	107.86	113.71

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	8342	0	8066	127	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	8342	0	8066	132	0
1	E	8342	0	8066	125	0
2	a	1664	0	1665	26	0
2	c	1664	0	1665	25	0
2	e	1664	0	1665	27	0
3	b	1503	0	1454	29	0
3	d	1503	0	1454	29	0
3	f	1503	0	1454	32	0
4	A	210	0	195	5	0
4	C	210	0	195	0	0
4	E	210	0	195	3	0
All	All	35157	0	34140	512	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (512) 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:A:167:THR:HG22	1:A:168:PHE:H	1.01	1.12
1:A:167:THR:HG22	1:A:168:PHE:N	1.68	1.00
1:A:167:THR:CG2	1:A:168:PHE:H	1.75	1.00
1:C:391:CYS:HA	1:C:525:CYS:HB3	1.58	0.85
1:C:615:VAL:HG12	1:C:617:CYS:H	1.43	0.82
2:c:174:PRO:O	3:d:166:THR:HG22	1.80	0.81
3:f:139:ILE:HB	3:f:177:ALA:O	1.83	0.78
2:c:36:VAL:HG11	2:c:80:VAL:HG21	1.68	0.76
3:f:95:THR:HG23	3:f:96:THR:HG23	1.67	0.76
1:A:615:VAL:HG12	1:A:617:CYS:H	1.52	0.75
2:c:49:TRP:HE1	2:c:52:LEU:HB2	1.52	0.74
1:A:210:ILE:HG12	1:A:217:PRO:HG3	1.71	0.73
3:f:169:LYS:HE2	3:f:175:TYR:OH	1.88	0.73
3:d:139:ILE:HB	3:d:177:ALA:O	1.89	0.72
1:A:149:ASN:HB3	4:A:1315:NAG:HN2	1.54	0.71
3:b:159:LYS:HG3	3:b:162:VAL:HG12	1.73	0.71
3:d:169:LYS:HD2	3:d:175:TYR:OH	1.91	0.70
1:A:792:PRO:HG3	1:E:707:TYR:HB3	1.74	0.69
1:C:566:GLY:HA2	1:E:43:PHE:H	1.58	0.68
1:E:1126:CYS:HB2	1:E:1132:ILE:HG12	1.78	0.66
3:d:20:ILE:HD11	3:d:75:LEU:HB3	1.76	0.66
1:C:448:ASN:HB3	1:C:497:PHE:HB2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:GLN:HE22	1:A:274:THR:HG22	1.61	0.65
1:A:854:LYS:N	1:A:858:LEU:O	2.30	0.64
1:A:547:THR:O	1:C:978:ASN:ND2	2.31	0.64
1:C:130:VAL:HB	1:C:168:PHE:HB3	1.79	0.64
2:c:127:SER:H	2:c:149:VAL:HG23	1.62	0.64
2:a:52:LEU:HD21	2:a:100:LEU:HD22	1.80	0.64
2:e:174:PRO:O	3:f:166:THR:HG22	1.98	0.63
1:A:43:PHE:H	1:E:566:GLY:HA2	1.62	0.63
1:A:106:PHE:HB2	1:A:117:LEU:HB3	1.79	0.63
1:A:988:GLU:O	1:A:992:GLN:NE2	2.31	0.63
2:a:127:SER:H	2:a:149:VAL:HG13	1.63	0.63
1:E:293:LEU:HG	1:E:294:ASP:H	1.64	0.63
1:C:418:ILE:HG12	1:C:455:LEU:HD11	1.79	0.63
1:E:356:LYS:HB2	1:E:397:ALA:HB3	1.79	0.63
1:E:391:CYS:HA	1:E:525:CYS:HB3	1.81	0.62
1:A:167:THR:HG23	1:E:357:ARG:HE	1.64	0.62
3:b:63:ARG:HD2	3:b:80:LEU:H	1.64	0.62
1:C:454:ARG:HG3	1:C:491:PRO:HB2	1.81	0.62
1:A:701:ALA:HB3	1:C:787:GLN:HG3	1.82	0.62
1:E:246:ARG:HG2	1:E:258:TRP:HA	1.82	0.62
1:C:102:ARG:NH1	1:C:122:ASN:O	2.33	0.61
1:E:466:ARG:HE	1:E:468:ILE:HD11	1.66	0.61
1:E:108:THR:H	1:E:114:THR:HG21	1.65	0.61
1:C:822:LEU:HD22	1:C:945:LEU:HD21	1.83	0.60
1:C:201:PHE:HB3	1:C:229:LEU:HB2	1.81	0.60
1:E:433:VAL:HG12	1:E:512:VAL:HA	1.82	0.60
1:C:204:TYR:HB3	1:C:223:LEU:HB3	1.84	0.60
1:C:125:ASN:ND2	1:C:172:SER:O	2.35	0.60
1:E:54:LEU:HB3	1:E:270:LEU:HD13	1.83	0.60
1:E:1031:GLU:OE1	1:E:1039:ARG:NH1	2.35	0.60
1:A:452:LEU:HD13	1:A:492:LEU:HB3	1.83	0.59
2:e:40:ARG:HG2	2:e:50:LEU:HD21	1.84	0.59
1:E:726:ILE:HG22	1:E:1061:VAL:HG22	1.84	0.59
2:c:21:THR:HG22	2:c:81:VAL:HG22	1.84	0.59
1:E:424:LYS:HE2	1:E:460:ASN:HD21	1.67	0.59
1:A:350:VAL:HG12	1:A:400:PHE:HB2	1.85	0.59
1:A:472:ILE:HA	1:A:491:PRO:HD3	1.84	0.58
1:C:742:ILE:O	1:C:1000:ARG:NH1	2.35	0.58
2:a:143:ALA:HB3	2:a:193:SER:HB3	1.84	0.58
1:A:395:VAL:HG13	1:A:524:VAL:HG11	1.86	0.58
1:E:123:ALA:HA	1:E:177:MET:HE3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:e:23:THR:HG22	2:e:79:GLN:HG2	1.86	0.58
1:C:97:LYS:HE3	1:C:184:GLY:H	1.68	0.58
1:C:707:TYR:HB3	1:E:792:PRO:HG3	1.86	0.57
1:E:501:ASN:O	3:f:33:ASN:ND2	2.23	0.57
3:f:154:ASP:OD2	3:f:192:ARG:NH2	2.38	0.57
1:A:889:GLY:HA3	1:A:1034:LEU:HD23	1.87	0.57
1:E:229:LEU:HB3	1:E:231:ILE:HD12	1.87	0.57
1:A:973:ILE:HG22	1:A:992:GLN:HG2	1.86	0.57
1:A:1047:TYR:HB2	1:A:1067:TYR:HB3	1.87	0.57
3:f:41:HIS:HD2	3:f:44:GLN:HE21	1.51	0.57
1:E:778:THR:HG22	1:E:865:LEU:HD12	1.87	0.57
3:b:56:ARG:HD2	3:b:61:SER:HB3	1.87	0.57
1:E:353:TRP:O	1:E:466:ARG:NH2	2.38	0.56
3:f:37:TRP:HB2	3:f:50:ILE:HG12	1.87	0.56
1:C:804:GLN:NE2	1:C:935:GLN:OE1	2.36	0.56
1:C:1074:ASN:OD1	1:E:895:GLN:NE2	2.38	0.56
1:E:128:ILE:HB	1:E:170:TYR:HB3	1.87	0.56
1:A:596:SER:HB3	1:A:613:GLN:HE21	1.71	0.56
3:d:169:LYS:HB3	3:d:175:TYR:CE2	2.41	0.56
2:a:61:TYR:HE1	2:a:71:ILE:HG22	1.71	0.56
3:b:149:VAL:HG13	3:b:198:VAL:HG22	1.88	0.56
3:f:151:TRP:HE1	3:f:162:VAL:HG11	1.70	0.56
1:C:103:GLY:HA3	1:C:241:LEU:HB3	1.86	0.56
2:a:41:GLN:HB2	2:a:47:LEU:HG	1.87	0.56
1:E:201:PHE:HB3	1:E:229:LEU:HB2	1.88	0.56
3:f:40:GLN:HB3	3:f:87:ASP:HB3	1.88	0.56
2:e:22:CYS:HB3	2:e:80:VAL:HB	1.88	0.56
2:e:150:LYS:HG3	2:e:184:SER:HB2	1.87	0.56
1:E:312:ILE:HD11	1:E:596:SER:HB3	1.88	0.55
1:E:453:TYR:HB3	1:E:495:TYR:HE1	1.71	0.55
1:A:167:THR:CG2	1:A:168:PHE:N	2.41	0.55
1:C:127:VAL:HG12	1:C:129:LYS:HG2	1.89	0.55
1:E:99:ASN:O	1:E:102:ARG:NH2	2.37	0.55
2:e:74:ASP:HB2	2:e:79:GLN:H	1.72	0.55
1:A:715:PRO:HA	1:A:1072:GLU:HA	1.88	0.55
1:A:901:GLN:HE21	1:A:905:ARG:HE	1.53	0.55
1:C:448:ASN:ND2	1:C:450:ASN:OD1	2.39	0.55
1:E:452:LEU:HD13	1:E:492:LEU:HB3	1.88	0.55
2:c:17:THR:HG22	2:c:85:THR:HG22	1.88	0.55
1:A:15:CYS:HB3	1:A:158:ARG:HD2	1.88	0.55
1:A:394:ASN:ND2	1:C:200:TYR:OH	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1035:GLY:HA3	1:E:1040:VAL:HG21	1.87	0.55
3:b:149:VAL:HA	3:b:198:VAL:HG13	1.89	0.55
3:f:169:LYS:CE	3:f:175:TYR:OH	2.53	0.55
1:A:1077:THR:OG1	1:C:900:MET:SD	2.65	0.55
2:a:17:THR:HG23	2:a:85:THR:HG22	1.88	0.55
1:A:763:LEU:HD22	1:A:1008:VAL:HG21	1.89	0.55
1:C:597:VAL:HG22	1:C:610:VAL:HG12	1.87	0.54
4:E:1312:NAG:H83	4:E:1312:NAG:H3	1.88	0.54
1:C:19:THR:HG22	1:C:255:SER:HB3	1.88	0.54
1:C:1106:GLN:NE2	1:C:1111:GLU:OE1	2.39	0.54
1:E:825:LYS:NZ	1:E:938:LEU:O	2.37	0.54
1:E:409:GLN:HB3	1:E:419:ALA:HB2	1.89	0.54
2:a:6:GLU:HG3	2:a:22:CYS:HB3	1.90	0.54
3:b:144:PRO:HD2	3:b:200:HIS:HE1	1.73	0.54
3:f:169:LYS:HE2	3:f:175:TYR:CZ	2.43	0.54
2:e:151:ASP:HA	2:e:182:LEU:HD13	1.89	0.54
3:f:77:ILE:O	3:f:81:GLN:NE2	2.40	0.54
3:b:166:THR:HG21	3:b:178:SER:HB3	1.90	0.54
3:f:170:GLN:HG3	3:f:172:ASN:H	1.72	0.54
1:C:196:ASN:HD22	1:C:231:ILE:HD12	1.72	0.54
2:c:151:ASP:HA	2:c:182:LEU:HD13	1.90	0.54
3:d:38:TYR:HB2	3:d:89:TYR:HB2	1.89	0.54
1:C:825:LYS:NZ	1:C:938:LEU:O	2.36	0.53
1:C:1040:VAL:O	1:E:1030:SER:OG	2.25	0.53
2:c:127:SER:HB3	2:c:150:LYS:H	1.73	0.53
2:a:18:LEU:HD21	2:a:116:VAL:HG11	1.90	0.53
1:C:33:THR:OG1	1:C:219:GLY:O	2.27	0.53
1:C:645:THR:N	1:C:648:GLY:O	2.39	0.53
1:E:196:ASN:HB2	1:E:201:PHE:HD1	1.74	0.53
1:A:204:TYR:HB3	1:A:223:LEU:HB3	1.90	0.53
1:A:472:ILE:HD12	1:A:488:CYS:HB3	1.90	0.53
2:a:131:LEU:N	2:a:146:GLY:O	2.42	0.53
1:E:16:VAL:HA	4:E:1313:NAG:H82	1.90	0.53
3:d:39:GLN:HG3	3:d:86:ALA:HB3	1.90	0.53
1:A:731:MET:SD	1:A:1011:GLN:NE2	2.82	0.53
1:C:897:PRO:HG2	1:C:900:MET:HG3	1.91	0.53
3:f:127:GLU:HB2	3:f:132:LYS:HB3	1.91	0.52
1:A:426:PRO:HD3	1:A:463:PRO:HB3	1.92	0.52
1:C:816:SER:OG	1:C:817:PHE:N	2.42	0.52
2:a:130:PRO:HB3	2:a:218:VAL:HG13	1.90	0.52
2:a:49:TRP:HE1	2:a:52:LEU:HB2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:39:PRO:HG2	1:C:51:THR:HG21	1.91	0.52
1:C:122:ASN:OD1	1:C:123:ALA:N	2.41	0.52
2:e:11:LEU:HD21	2:e:154:PRO:HG3	1.91	0.52
1:C:433:VAL:HG22	1:C:512:VAL:HG22	1.91	0.52
2:c:35:GLY:O	2:c:100:LEU:N	2.39	0.52
3:f:159:LYS:HD3	3:f:161:GLY:H	1.74	0.52
1:A:787:GLN:HG3	1:E:701:ALA:HB3	1.90	0.52
1:C:453:TYR:HD2	1:C:455:LEU:HD13	1.74	0.52
1:A:644:GLN:NE2	1:A:645:THR:O	2.44	0.52
1:E:112:SER:HB3	1:E:134:GLN:HB2	1.91	0.52
1:E:276:LEU:HD22	1:E:301:CYS:HA	1.92	0.51
2:a:129:PHE:HE2	3:b:132:LYS:HD2	1.74	0.51
3:b:94:THR:HG1	3:b:97:SER:H	1.58	0.51
1:A:440:ASN:ND2	3:b:34:TYR:OH	2.43	0.51
1:E:326:ILE:O	1:E:542:ASN:N	2.35	0.51
3:d:149:VAL:HA	3:d:198:VAL:HG23	1.91	0.51
1:A:131:CYS:HB3	1:A:167:THR:H	1.76	0.51
1:A:115:GLN:HA	1:A:132:GLU:HB3	1.91	0.51
2:a:151:ASP:HA	2:a:182:LEU:HD13	1.92	0.51
3:b:99:VAL:HG22	3:b:101:GLY:H	1.74	0.51
2:c:129:PHE:HE2	3:d:132:LYS:HD2	1.74	0.51
1:C:119:ILE:HG23	1:C:128:ILE:HG23	1.93	0.51
1:E:710:ASN:HB2	4:E:1307:NAG:H83	1.91	0.51
1:E:712:ILE:HD13	1:E:1094:VAL:HG11	1.93	0.51
3:b:65:SER:HG	3:b:76:THR:HG1	1.55	0.51
3:d:4:LEU:HB2	3:d:101:GLY:HA3	1.92	0.51
1:A:1106:GLN:NE2	1:A:1111:GLU:OE1	2.44	0.51
3:f:142:PHE:HE2	3:f:146:ALA:HA	1.76	0.51
1:A:231:ILE:HD12	1:A:233:ILE:HG12	1.91	0.51
1:C:147:LYS:HE3	1:C:248:TYR:HB2	1.93	0.51
1:E:18:LEU:HD23	1:E:258:TRP:CD1	2.46	0.51
1:E:84:LEU:HB2	1:E:238:PHE:HB3	1.91	0.51
1:E:722:VAL:HG22	1:E:1065:VAL:HG22	1.93	0.51
2:c:51:ALA:HB2	2:c:69:LEU:HD21	1.94	0.50
1:A:1072:GLU:HG2	4:A:1308:NAG:H81	1.92	0.50
1:C:78:ARG:NE	1:C:80:ASP:OD1	2.41	0.50
1:C:420:ASP:HA	1:C:424:LYS:HD3	1.93	0.50
1:E:533:LEU:HD21	1:E:585:LEU:HD21	1.93	0.50
1:C:645:THR:HG23	1:C:647:ALA:H	1.77	0.50
3:b:26:SER:HA	3:b:29:VAL:HG12	1.94	0.50
1:A:39:PRO:HB3	1:A:51:THR:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:666:ILE:HG12	1:C:671:CYS:HA	1.93	0.50
1:E:172:SER:OG	1:E:173:GLN:N	2.45	0.50
2:e:115:LEU:HB3	2:e:156:PRO:HG3	1.94	0.50
1:A:350:VAL:HG21	1:A:418:ILE:HD11	1.93	0.50
2:a:108:ASP:OD1	2:a:108:ASP:N	2.43	0.50
2:c:50:LEU:HB3	2:c:69:LEU:HD11	1.93	0.50
2:e:7:SER:HA	2:e:114:THR:HG21	1.94	0.50
2:e:130:PRO:HB3	2:e:218:VAL:HG13	1.94	0.50
1:A:598:ILE:HD13	1:A:666:ILE:HD11	1.92	0.50
1:A:1105:THR:HB	1:A:1111:GLU:H	1.76	0.50
1:C:357:ARG:HH22	1:E:167:THR:HA	1.77	0.50
1:C:1091:ARG:HE	1:C:1121:PHE:HB3	1.76	0.50
3:b:147:VAL:HG11	3:b:200:HIS:HA	1.94	0.50
1:A:816:SER:OG	1:A:817:PHE:N	2.45	0.50
1:A:903:ALA:HB1	1:A:913:GLN:HB2	1.94	0.50
3:f:140:SER:OG	3:f:141:ASP:N	2.45	0.50
1:A:329:PHE:HE2	1:A:528:LYS:HB2	1.76	0.49
1:A:559:PHE:HB3	1:A:577:ARG:HH21	1.76	0.49
1:C:19:THR:HG23	1:C:20:THR:HG23	1.94	0.49
1:A:134:GLN:H	1:A:162:SER:HG	1.61	0.49
1:E:729:VAL:HG11	1:E:781:VAL:HG11	1.94	0.49
2:c:130:PRO:HB3	2:c:218:VAL:HG22	1.93	0.49
1:A:393:THR:HA	1:A:522:ALA:HA	1.95	0.49
1:C:498:GLN:HB3	1:C:501:ASN:HB2	1.93	0.49
1:C:902:MET:HB3	1:C:916:LEU:HD11	1.93	0.49
1:E:453:TYR:HB3	1:E:495:TYR:CE1	2.48	0.49
1:E:764:ASN:O	1:E:768:THR:HG23	2.13	0.49
1:E:1084:ASP:O	1:E:1086:LYS:NZ	2.44	0.49
3:f:162:VAL:HG12	3:f:179:SER:HB2	1.94	0.49
1:A:17:ASN:O	1:A:255:SER:OG	2.30	0.49
1:C:1047:TYR:HB2	1:C:1067:TYR:HB3	1.93	0.49
3:b:63:ARG:HH11	3:b:80:LEU:HB2	1.77	0.49
1:E:966:LEU:O	1:E:1000:ARG:NH1	2.46	0.49
3:d:85:GLU:HB3	3:d:108:VAL:HG23	1.94	0.49
2:e:119:SER:OG	2:e:120:SER:N	2.45	0.49
1:E:555:SER:HB3	1:E:586:ASP:HB2	1.94	0.49
1:A:290:ASP:HB2	1:A:293:LEU:HD13	1.95	0.49
1:E:195:LYS:HE3	1:E:202:LYS:HD2	1.94	0.49
3:b:159:LYS:HG2	3:b:161:GLY:H	1.78	0.49
1:C:402:ILE:HD12	1:C:410:ILE:HD11	1.95	0.48
3:d:169:LYS:HB3	3:d:175:TYR:CZ	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:b:6:GLN:NE2	3:b:102:GLY:O	2.46	0.48
1:C:294:ASP:O	1:C:297:SER:OG	2.30	0.48
1:E:454:ARG:HH12	1:E:469:SER:H	1.61	0.48
2:e:143:ALA:HB3	2:e:193:SER:HB2	1.95	0.48
1:A:68:ILE:HG22	1:A:262:ALA:HA	1.94	0.48
1:C:456:PHE:HB3	1:C:473:TYR:CD2	2.48	0.48
2:c:115:LEU:HB2	2:c:156:PRO:HG3	1.94	0.48
3:d:65:SER:O	3:d:76:THR:N	2.47	0.48
1:E:768:THR:O	1:E:772:VAL:HG23	2.14	0.48
3:d:6:GLN:HG2	3:d:22:CYS:HB3	1.94	0.48
1:C:1094:VAL:HG13	1:C:1096:VAL:HG13	1.95	0.48
1:E:1047:TYR:HB2	1:E:1067:TYR:HB3	1.94	0.48
3:f:142:PHE:HZ	3:f:177:ALA:HB2	1.78	0.48
1:A:431:GLY:HA2	1:A:515:PHE:H	1.78	0.48
1:E:808:ASP:HB3	1:E:811:LYS:HE2	1.96	0.48
2:e:59:LYS:NZ	2:e:71:ILE:O	2.43	0.48
1:C:605:SER:OG	1:C:606:ASN:N	2.46	0.48
1:C:726:ILE:HG12	1:C:1061:VAL:HG22	1.94	0.48
1:C:759:PHE:HD2	1:C:1001:LEU:HD21	1.78	0.48
1:A:91:TYR:N	1:A:268:GLY:O	2.42	0.48
1:A:802:PHE:HD1	1:A:805:ILE:HD11	1.78	0.48
1:C:1031:GLU:HB3	1:C:1037:SER:HB2	1.95	0.48
1:E:735:SER:HA	1:E:767:LEU:HD13	1.96	0.48
3:d:170:GLN:HG3	3:d:172:ASN:H	1.79	0.48
1:A:1094:VAL:HG23	1:C:900:MET:HE1	1.96	0.48
1:E:115:GLN:HA	1:E:132:GLU:HG3	1.95	0.48
1:E:142:GLY:HA2	1:E:244:LEU:H	1.79	0.48
1:E:328:ARG:HD2	1:E:533:LEU:HD13	1.95	0.48
1:A:722:VAL:HG22	1:A:1065:VAL:HG22	1.96	0.47
1:C:424:LYS:HG2	1:C:461:LEU:HD23	1.95	0.47
1:E:490:PHE:O	1:E:493:GLN:NE2	2.47	0.47
1:E:856:ASN:ND2	1:E:966:LEU:HD13	2.29	0.47
3:f:159:LYS:HD3	3:f:160:ALA:N	2.29	0.47
1:A:438:SER:O	1:A:438:SER:OG	2.32	0.47
1:E:1135:ASN:ND2	1:E:1136:THR:O	2.46	0.47
1:C:444:LYS:H	1:C:448:ASN:HB2	1.79	0.47
1:C:808:ASP:OD2	1:C:811:LYS:NZ	2.48	0.47
1:E:96:GLU:OE1	1:E:100:ILE:N	2.47	0.47
1:E:729:VAL:HG21	1:E:782:PHE:HE2	1.78	0.47
1:E:122:ASN:OD1	1:E:123:ALA:N	2.40	0.47
1:E:276:LEU:HB3	1:E:289:VAL:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:726:ILE:HD11	1:E:947:LYS:H	1.79	0.47
2:e:122:SER:OG	2:e:123:THR:N	2.46	0.47
3:b:11:SER:OG	3:b:107:THR:N	2.46	0.47
1:A:34:ARG:NH1	1:A:219:GLY:O	2.48	0.47
1:A:804:GLN:NE2	4:A:1307:NAG:O6	2.43	0.47
1:C:452:LEU:HD13	1:C:492:LEU:HD12	1.96	0.47
1:C:534:VAL:HG11	1:C:539:VAL:HG11	1.97	0.47
1:C:901:GLN:O	1:C:905:ARG:HG2	2.14	0.47
1:E:106:PHE:HB3	1:E:235:ILE:HG23	1.97	0.47
1:A:73:THR:HG23	1:A:75:GLY:H	1.79	0.47
1:A:221:SER:OG	1:A:222:ALA:N	2.45	0.47
1:C:453:TYR:CZ	1:C:493:GLN:HB2	2.50	0.47
1:E:565:PHE:HB2	1:E:576:VAL:HG12	1.96	0.47
1:C:14:GLN:HB2	1:C:158:ARG:HH21	1.80	0.47
1:C:34:ARG:NH1	1:C:219:GLY:O	2.48	0.47
1:C:445:VAL:HA	1:C:499:PRO:HG3	1.95	0.47
1:C:1126:CYS:HB2	1:C:1132:ILE:HG12	1.97	0.47
1:A:22:THR:HB	1:A:78:ARG:HG2	1.97	0.47
1:A:571:ASP:HB2	1:C:967:SER:HB2	1.95	0.47
1:A:974:SER:OG	1:A:975:SER:N	2.46	0.47
1:C:709:ASN:OD1	1:C:710:ASN:ND2	2.47	0.47
1:A:364:ASP:OD1	1:A:364:ASP:N	2.48	0.46
1:A:93:ALA:O	1:A:266:TYR:N	2.36	0.46
1:A:1030:SER:HA	1:A:1034:LEU:HD13	1.98	0.46
1:C:401:VAL:HG12	1:C:509:ARG:HA	1.98	0.46
1:E:79:PHE:CE1	1:E:242:LEU:HD23	2.51	0.46
1:E:472:ILE:HG12	1:E:482:GLY:HA2	1.97	0.46
1:E:175:PHE:HE1	1:E:177:MET:HE2	1.79	0.46
1:E:721:SER:OG	1:E:1066:THR:OG1	2.31	0.46
2:a:119:SER:OG	2:a:120:SER:N	2.46	0.46
3:d:142:PHE:HZ	3:d:177:ALA:HB2	1.79	0.46
1:A:81:ASN:ND2	1:A:138:ASP:OD1	2.49	0.46
2:a:105:THR:HA	3:b:51:TYR:HB2	1.97	0.46
1:C:444:LYS:HE3	2:c:60:ARG:HH11	1.80	0.46
1:C:802:PHE:HD1	1:C:805:ILE:HD11	1.79	0.46
1:E:591:SER:HB3	1:E:615:VAL:HG12	1.98	0.46
1:A:177:MET:HG2	1:A:179:LEU:HG	1.97	0.46
1:A:454:ARG:HH11	1:A:457:ARG:HG3	1.81	0.46
3:f:56:ARG:H	3:f:56:ARG:HD3	1.81	0.46
1:A:316:SER:OG	1:A:317:ASN:N	2.47	0.46
1:A:319:ARG:HH22	1:C:740:MET:HB2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:326:ILE:HD12	1:C:534:VAL:H	1.81	0.46
1:A:111:ASP:HA	1:A:134:GLN:HA	1.98	0.46
1:C:614:ASP:N	1:C:647:ALA:O	2.37	0.46
1:C:129:LYS:HB3	1:C:169:GLU:HG3	1.97	0.46
1:E:98:SER:HB2	1:E:100:ILE:HD11	1.98	0.46
1:E:215:ASP:OD1	1:E:215:ASP:N	2.47	0.46
1:E:430:THR:OG1	1:E:515:PHE:O	2.33	0.46
3:d:19:THR:OG1	3:d:74:SER:OG	2.25	0.46
3:d:144:PRO:HD2	3:d:200:HIS:HE1	1.81	0.46
1:A:1086:LYS:HD2	1:A:1122:VAL:HG21	1.96	0.45
3:d:113:LYS:HG2	3:d:200:HIS:HE2	1.79	0.45
2:e:150:LYS:HG2	2:e:151:ASP:H	1.80	0.45
1:A:101:ILE:HG22	1:A:242:LEU:HG	1.98	0.45
2:c:201:TYR:HB2	2:c:218:VAL:HB	1.98	0.45
3:d:40:GLN:HA	3:d:46:PRO:HA	1.98	0.45
1:A:987:PRO:O	1:A:990:GLU:HG2	2.16	0.45
1:C:245:HIS:O	1:C:259:THR:OG1	2.31	0.45
1:C:669:GLY:N	1:E:864:LEU:O	2.47	0.45
1:E:497:PHE:CE2	1:E:507:PRO:HB3	2.52	0.45
1:E:501:ASN:HD22	1:E:505:TYR:HD2	1.64	0.45
3:b:6:GLN:HB3	3:b:22:CYS:HB2	1.96	0.45
2:e:40:ARG:NE	2:e:48:GLU:OE2	2.42	0.45
1:C:98:SER:O	1:C:98:SER:OG	2.34	0.45
1:C:362:VAL:HA	1:C:525:CYS:O	2.17	0.45
1:C:392:PHE:O	1:C:523:THR:N	2.49	0.45
1:C:975:SER:O	1:C:1000:ARG:NH2	2.49	0.45
1:E:299:THR:OG1	1:E:597:VAL:HG11	2.17	0.45
3:d:142:PHE:HZ	3:d:177:ALA:CB	2.29	0.45
1:A:361:CYS:HB3	1:A:524:VAL:HG23	1.98	0.45
1:A:729:VAL:HG11	1:A:781:VAL:HG11	1.99	0.45
1:E:20:THR:HB	1:E:258:TRP:HZ2	1.82	0.45
1:E:538:CYS:HB2	1:E:590:CYS:HB3	1.51	0.45
1:A:53:ASP:OD1	1:A:54:LEU:N	2.50	0.45
1:C:599:THR:HB	1:C:608:VAL:HG12	1.98	0.45
1:A:1028:LYS:HB2	1:A:1028:LYS:HE3	1.76	0.45
1:E:565:PHE:HA	1:E:576:VAL:HA	1.99	0.45
1:E:816:SER:OG	1:E:817:PHE:N	2.49	0.45
3:b:87:ASP:OD1	3:b:88:TYR:N	2.48	0.45
1:C:500:THR:HG22	3:d:31:ALA:H	1.82	0.44
1:E:676:THR:HB	1:E:690:GLN:HG2	1.98	0.44
2:e:150:LYS:HB3	3:f:132:LYS:NZ	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:LEU:HB3	1:A:78:ARG:HH11	1.81	0.44
1:A:52:GLN:NE2	1:A:274:THR:HG22	2.30	0.44
1:C:277:LEU:HD13	1:C:285:ILE:HD13	2.00	0.44
1:E:97:LYS:HB3	1:E:186:PHE:HD1	1.82	0.44
1:A:167:THR:HG23	1:E:357:ARG:NE	2.32	0.44
1:E:662:CYS:HB2	1:E:671:CYS:HB3	1.58	0.44
1:C:411:ALA:HB3	1:C:414:GLN:HG3	1.99	0.44
1:E:20:THR:HB	1:E:258:TRP:CZ2	2.53	0.44
1:E:738:CYS:HB3	1:E:760:CYS:HB2	1.82	0.44
1:E:102:ARG:HD3	1:E:122:ASN:HA	2.00	0.44
1:A:1002:GLN:O	1:A:1006:THR:HG23	2.18	0.44
1:C:290:ASP:CG	1:C:293:LEU:HB2	2.42	0.44
1:C:472:ILE:HG22	1:C:490:PHE:HD1	1.83	0.44
3:f:142:PHE:HZ	3:f:177:ALA:CB	2.29	0.44
1:C:662:CYS:HB2	1:C:671:CYS:HB2	1.44	0.44
1:E:666:ILE:HG12	1:E:671:CYS:HA	1.99	0.44
1:E:788:ILE:HG23	1:E:876:ALA:HB2	2.00	0.44
2:e:170:VAL:HG13	2:e:189:VAL:HB	1.98	0.44
1:A:709:ASN:OD1	1:A:710:ASN:ND2	2.51	0.43
1:C:35:GLY:HA3	1:C:56:LEU:HB3	2.00	0.43
1:C:115:GLN:HB3	1:C:233:ILE:HG21	2.00	0.43
1:E:1037:SER:H	1:E:1048:HIS:HD2	1.66	0.43
2:a:108:ASP:HA	3:b:48:LEU:HD22	1.99	0.43
1:A:88:ASP:N	1:A:88:ASP:OD1	2.50	0.43
1:C:134:GLN:O	1:C:161:SER:OG	2.31	0.43
1:C:788:ILE:HG23	1:C:876:ALA:HB2	2.01	0.43
1:E:740:MET:HE3	1:E:857:GLY:HA2	1.99	0.43
1:E:763:LEU:HD22	1:E:1008:VAL:HG21	1.99	0.43
2:e:88:ASP:OD1	2:e:90:VAL:HG22	2.17	0.43
2:e:213:LYS:HA	2:e:213:LYS:HD3	1.82	0.43
1:A:149:ASN:HB3	4:A:1315:NAG:N2	2.29	0.43
1:A:336:CYS:HA	1:A:337:PRO:HD3	1.78	0.43
1:E:566:GLY:N	1:E:575:ALA:O	2.50	0.43
3:f:94:THR:HG1	3:f:97:SER:H	1.66	0.43
3:f:151:TRP:NE1	3:f:162:VAL:HG11	2.32	0.43
1:A:538:CYS:HB2	1:A:590:CYS:HB2	1.86	0.43
1:C:143:VAL:HG12	1:C:154:GLU:HA	2.00	0.43
2:c:176:VAL:HG22	3:d:164:THR:HA	2.00	0.43
1:A:1081:ILE:HG22	1:A:1133:VAL:HG23	1.99	0.43
1:E:19:THR:OG1	1:E:20:THR:N	2.52	0.43
2:c:127:SER:O	2:c:127:SER:OG	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:THR:HA	1:A:189:LEU:HA	2.00	0.43
2:a:13:LYS:HB2	2:a:16:GLN:HG3	2.00	0.43
1:A:404:GLY:HA3	1:A:504:GLY:HA2	2.00	0.43
1:A:778:THR:HG22	1:A:865:LEU:HD12	2.01	0.43
1:C:95:THR:HB	1:C:189:LEU:HD13	2.01	0.43
1:C:984:LEU:HB2	1:C:989:ALA:HB2	2.00	0.43
1:A:228:ASP:OD1	1:A:228:ASP:N	2.44	0.43
1:C:739:THR:O	1:C:744:GLY:N	2.52	0.43
1:E:231:ILE:HG22	1:E:233:ILE:HG23	2.00	0.43
2:a:145:LEU:HD23	2:a:145:LEU:H	1.84	0.43
1:A:327:VAL:HA	1:A:542:ASN:HB3	2.01	0.43
1:C:905:ARG:HH11	1:C:1036:GLN:HB2	1.83	0.43
1:E:500:THR:OG1	3:f:30:GLY:N	2.48	0.43
3:b:166:THR:OG1	3:b:176:ALA:O	2.28	0.43
2:c:130:PRO:HD3	2:c:216:LYS:HD3	2.00	0.43
1:C:880:GLY:O	1:C:884:SER:OG	2.31	0.42
1:E:726:ILE:HG21	1:E:945:LEU:HD13	2.01	0.42
1:E:781:VAL:HG22	1:E:1026:ALA:HB2	2.01	0.42
1:A:1135:ASN:ND2	1:A:1136:THR:O	2.52	0.42
3:d:26:SER:O	3:d:29:VAL:N	2.41	0.42
1:C:90:VAL:HG13	1:C:267:VAL:HG13	2.02	0.42
2:a:173:PHE:HZ	3:b:170:GLN:HB3	1.84	0.42
3:d:163:GLU:H	3:d:163:GLU:CD	2.27	0.42
2:e:217:ARG:HB3	2:e:219:GLU:OE2	2.19	0.42
1:C:140:PHE:HE2	1:C:246:ARG:HH12	1.68	0.42
1:E:934:ILE:HD13	1:E:934:ILE:HA	1.94	0.42
1:E:1081:ILE:O	1:E:1088:HIS:N	2.51	0.42
2:c:131:LEU:HD21	3:d:121:PHE:HB3	2.02	0.42
1:A:246:ARG:NH2	1:A:253:ASP:O	2.52	0.42
1:A:785:VAL:HG22	1:A:787:GLN:H	1.85	0.42
1:C:867:ASP:OD1	1:C:868:GLU:N	2.52	0.42
3:f:149:VAL:HA	3:f:198:VAL:HG23	2.02	0.42
1:A:788:ILE:HG23	1:A:876:ALA:HB2	2.01	0.42
1:A:1131:GLY:HA2	4:A:1305:NAG:H81	2.02	0.42
1:C:94:SER:HA	1:C:265:TYR:HA	2.02	0.42
1:E:448:ASN:HB3	1:E:497:PHE:HB2	2.01	0.42
2:a:49:TRP:HB2	3:b:100:PHE:HE1	1.84	0.42
2:a:145:LEU:HD12	2:a:218:VAL:HG11	2.02	0.42
2:c:40:ARG:HB3	2:c:48:GLU:HG2	2.01	0.42
3:d:37:TRP:HB2	3:d:50:ILE:HG22	2.02	0.42
1:A:599:THR:HB	1:A:608:VAL:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:569:ILE:HG13	1:C:570:ALA:H	1.84	0.42
1:E:398:ASP:HB2	1:E:512:VAL:HB	2.02	0.42
1:E:1086:LYS:HD3	1:E:1122:VAL:HG11	2.01	0.42
3:f:53:VAL:HG11	3:f:68:LYS:HE3	2.02	0.42
1:C:438:SER:HB2	1:C:509:ARG:HG3	2.01	0.42
1:C:444:LYS:HB2	2:c:54:TYR:CE2	2.55	0.42
1:E:336:CYS:O	1:E:338:PHE:N	2.52	0.42
1:A:431:GLY:HA3	1:A:514:SER:HA	2.02	0.41
1:A:441:LEU:HD12	2:a:32:PRO:HB2	2.02	0.41
1:C:97:LYS:HA	1:C:188:ASN:HD22	1.85	0.41
1:E:598:ILE:HB	1:E:609:ALA:HB3	2.02	0.41
3:b:85:GLU:HB2	3:b:107:THR:HA	2.02	0.41
3:d:99:VAL:HG22	3:d:101:GLY:H	1.85	0.41
2:e:170:VAL:HA	2:e:189:VAL:HA	2.01	0.41
1:C:27:ALA:HB3	1:C:64:TRP:HB3	2.01	0.41
1:C:713:ALA:HB2	1:E:895:GLN:HG2	2.01	0.41
1:C:978:ASN:N	1:C:978:ASN:OD1	2.52	0.41
2:a:6:GLU:HA	2:a:22:CYS:HA	2.01	0.41
3:b:10:VAL:HG12	3:b:10:VAL:O	2.20	0.41
2:e:59:LYS:HB3	2:e:61:TYR:CZ	2.54	0.41
1:A:202:LYS:HE2	1:A:202:LYS:HB2	1.89	0.41
1:C:129:LYS:HA	1:C:169:GLU:HA	2.02	0.41
1:C:912:THR:OG1	1:C:1106:GLN:NE2	2.52	0.41
3:b:48:LEU:HD21	3:b:51:TYR:HB3	2.02	0.41
1:A:15:CYS:CB	1:A:158:ARG:HD2	2.50	0.41
1:C:70:VAL:HG12	1:C:71:SER:H	1.85	0.41
1:C:778:THR:HG22	1:C:865:LEU:HD12	2.02	0.41
1:E:1052:PHE:HB2	1:E:1063:LEU:HB2	2.03	0.41
3:f:63:ARG:HB2	3:f:79:GLY:HA3	2.01	0.41
1:A:102:ARG:HG3	1:A:141:LEU:HD12	2.01	0.41
1:A:501:ASN:HD22	1:A:501:ASN:HA	1.71	0.41
1:A:112:SER:OG	1:A:134:GLN:N	2.52	0.41
1:E:779:GLN:O	1:E:783:ALA:HB3	2.21	0.41
2:a:38:TRP:CG	2:a:82:LEU:HD22	2.55	0.41
1:A:276:LEU:HB3	1:A:289:VAL:HG22	2.01	0.41
1:A:736:VAL:HG21	1:A:1004:LEU:HD11	2.03	0.41
1:C:417:LYS:HG3	1:C:455:LEU:HG	2.02	0.41
1:C:560:LEU:HB2	1:C:563:GLN:HB2	2.03	0.41
2:c:177:LEU:HD13	2:c:183:TYR:CE2	2.55	0.41
1:C:126:VAL:HG23	1:C:126:VAL:O	2.21	0.41
1:C:453:TYR:CD2	1:C:455:LEU:HD13	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:418:ILE:HG23	1:E:422:ASN:HD21	1.86	0.41
1:E:444:LYS:HE3	1:E:444:LYS:HB2	1.81	0.41
2:c:132:ALA:HB3	3:d:124:SER:HB3	2.02	0.41
1:A:367:VAL:O	1:A:371:SER:OG	2.39	0.41
1:A:402:ILE:HD11	1:A:510:VAL:HG21	2.03	0.41
1:A:713:ALA:HB3	1:C:894:LEU:HB3	2.02	0.41
1:A:741:TYR:OH	1:A:962:LEU:O	2.34	0.41
1:C:497:PHE:CZ	1:C:507:PRO:HB3	2.56	0.41
1:C:557:LYS:HE2	1:C:559:PHE:HE1	1.86	0.41
1:E:241:LEU:HD23	1:E:241:LEU:HA	1.95	0.41
1:E:334:ASN:OD1	1:E:334:ASN:N	2.53	0.41
1:E:453:TYR:CE2	1:E:455:LEU:HB2	2.56	0.41
2:a:102:ALA:HB3	2:a:105:THR:HG22	2.02	0.41
2:e:195:SER:O	2:e:201:TYR:OH	2.37	0.41
1:A:868:GLU:OE2	1:A:872:GLN:NE2	2.54	0.41
1:C:216:LEU:HA	1:C:217:PRO:HD3	1.90	0.41
1:E:738:CYS:SG	1:E:739:THR:N	2.93	0.41
1:E:807:PRO:HG3	1:E:875:SER:HB2	2.03	0.41
1:C:201:PHE:HB2	1:C:231:ILE:HD13	2.02	0.40
1:C:275:PHE:CE1	1:C:290:ASP:HA	2.56	0.40
1:E:95:THR:OG1	1:E:212:LEU:HD11	2.21	0.40
3:f:140:SER:HB2	3:f:176:ALA:HB1	2.04	0.40
1:A:742:ILE:O	1:A:1000:ARG:NH1	2.45	0.40
1:A:1090:PRO:HA	1:A:1120:THR:HG22	2.02	0.40
1:C:70:VAL:HG12	1:C:71:SER:N	2.36	0.40
2:c:36:VAL:O	2:c:53:ILE:N	2.50	0.40
2:e:8:GLY:O	2:e:208:LYS:NZ	2.42	0.40
2:e:173:PHE:HZ	3:f:170:GLN:HB3	1.86	0.40
1:A:91:TYR:CZ	1:A:93:ALA:HB2	2.56	0.40
1:A:808:ASP:OD1	1:A:808:ASP:N	2.53	0.40
1:C:92:PHE:O	1:C:192:PHE:N	2.45	0.40
1:C:534:VAL:HG13	1:C:537:LYS:HE2	2.02	0.40
1:E:97:LYS:HB3	1:E:186:PHE:HA	2.03	0.40
3:b:184:THR:OG1	3:b:187:GLN:HB2	2.22	0.40
1:A:84:LEU:HD13	1:A:267:VAL:HG11	2.04	0.40
1:A:442:ASP:OD1	1:A:509:ARG:NH2	2.55	0.40
1:C:559:PHE:HB2	1:C:577:ARG:HH21	1.87	0.40
1:A:858:LEU:H	1:A:858:LEU:HD23	1.87	0.40
1:C:24:LEU:HD13	1:C:78:ARG:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1068/1288 (83%)	1020 (96%)	48 (4%)	0	100	100
1	C	1068/1288 (83%)	1024 (96%)	44 (4%)	0	100	100
1	E	1068/1288 (83%)	1011 (95%)	57 (5%)	0	100	100
2	a	221/232 (95%)	210 (95%)	11 (5%)	0	100	100
2	c	221/232 (95%)	213 (96%)	8 (4%)	0	100	100
2	e	221/232 (95%)	211 (96%)	10 (4%)	0	100	100
3	b	201/215 (94%)	184 (92%)	17 (8%)	0	100	100
3	d	201/215 (94%)	177 (88%)	24 (12%)	0	100	100
3	f	201/215 (94%)	181 (90%)	20 (10%)	0	100	100
All	All	4470/5205 (86%)	4231 (95%)	239 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	923/1112 (83%)	921 (100%)	2 (0%)	87	87
1	C	923/1112 (83%)	923 (100%)	0	100	100
1	E	923/1112 (83%)	922 (100%)	1 (0%)	88	89
2	a	194/203 (96%)	194 (100%)	0	100	100
2	c	194/203 (96%)	194 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	e	194/203 (96%)	194 (100%)	0	100	100
3	b	170/181 (94%)	170 (100%)	0	100	100
3	d	170/181 (94%)	168 (99%)	2 (1%)	63	72
3	f	170/181 (94%)	169 (99%)	1 (1%)	78	80
All	All	3861/4488 (86%)	3855 (100%)	6 (0%)	85	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	274	THR
1	A	671	CYS
1	E	607	GLN
3	d	166	THR
3	d	178	SER
3	f	166	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (105) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	87	ASN
1	A	121	ASN
1	A	125	ASN
1	A	134	GLN
1	A	137	ASN
1	A	173	GLN
1	A	239	GLN
1	A	317	ASN
1	A	422	ASN
1	A	440	ASN
1	A	450	ASN
1	A	498	GLN
1	A	501	ASN
1	A	540	ASN
1	A	556	ASN
1	A	564	GLN
1	A	607	GLN
1	A	613	GLN
1	A	644	GLN
1	A	675	GLN

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Mol	Chain	Res	Type
1	A	710	ASN
1	A	762	GLN
1	A	774	GLN
1	A	784	GLN
1	A	901	GLN
1	A	926	GLN
1	A	935	GLN
1	A	949	GLN
1	A	954	GLN
1	A	957	GLN
1	A	992	GLN
1	A	1005	GLN
1	C	23	GLN
1	C	69	HIS
1	C	99	ASN
1	C	134	GLN
1	C	164	ASN
1	C	188	ASN
1	C	196	ASN
1	C	218	GLN
1	C	334	ASN
1	C	394	ASN
1	C	414	GLN
1	C	448	ASN
1	C	498	GLN
1	C	542	ASN
1	C	563	GLN
1	C	580	GLN
1	C	658	ASN
1	C	710	ASN
1	C	762	GLN
1	C	777	ASN
1	C	804	GLN
1	C	856	ASN
1	C	901	GLN
1	C	913	GLN
1	C	935	GLN
1	C	954	GLN
1	C	969	ASN
1	C	1010	GLN
1	C	1054	GLN
1	C	1064	HIS

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Mol	Chain	Res	Type
1	C	1106	GLN
1	C	1108	ASN
1	E	137	ASN
1	E	218	GLN
1	E	354	ASN
1	E	388	ASN
1	E	460	ASN
1	E	481	ASN
1	E	564	GLN
1	E	580	GLN
1	E	606	ASN
1	E	690	GLN
1	E	784	GLN
1	E	954	GLN
1	E	969	ASN
1	E	1005	GLN
1	E	1011	GLN
1	E	1048	HIS
2	a	162	ASN
2	a	178	GLN
2	a	204	ASN
3	b	33	ASN
3	b	40	GLN
3	b	81	GLN
3	b	170	GLN
3	b	200	HIS
2	c	41	GLN
2	c	78	ASN
2	c	162	ASN
2	c	178	GLN
2	c	204	ASN
2	c	211	ASN
3	d	40	GLN
3	d	71	ASN
3	d	81	GLN
3	d	111	GLN
2	e	162	ASN
2	e	171	HIS
2	e	178	GLN
2	e	211	ASN
3	f	44	GLN
3	f	170	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

45 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	E	1311	1	14,14,15	0.28	0	17,19,21	0.55	0
4	NAG	A	1314	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	A	1308	1	14,14,15	0.27	0	17,19,21	0.57	0
4	NAG	A	1302	1	14,14,15	0.26	0	17,19,21	0.43	0
4	NAG	C	1304	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	C	1309	1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	C	1314	1	14,14,15	0.25	0	17,19,21	0.44	0
4	NAG	C	1302	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	E	1306	1	14,14,15	0.29	0	17,19,21	0.57	0
4	NAG	E	1303	1	14,14,15	0.21	0	17,19,21	0.43	0
4	NAG	A	1312	1	14,14,15	0.25	0	17,19,21	0.45	0
4	NAG	E	1315	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	C	1313	1	14,14,15	0.25	0	17,19,21	0.42	0
4	NAG	E	1307	1	14,14,15	0.30	0	17,19,21	0.55	0
4	NAG	E	1314	1	14,14,15	0.27	0	17,19,21	0.55	0
4	NAG	E	1308	1	14,14,15	0.26	0	17,19,21	0.46	0
4	NAG	E	1313	1	14,14,15	0.24	0	17,19,21	0.42	0
4	NAG	A	1304	1	14,14,15	0.24	0	17,19,21	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1310	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	A	1315	1	14,14,15	0.58	0	17,19,21	0.70	1 (5%)
4	NAG	C	1312	1	14,14,15	0.25	0	17,19,21	0.45	0
4	NAG	C	1311	1	14,14,15	0.26	0	17,19,21	0.44	0
4	NAG	E	1305	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	C	1315	1	14,14,15	0.23	0	17,19,21	0.42	0
4	NAG	A	1309	1	14,14,15	0.21	0	17,19,21	0.46	0
4	NAG	E	1301	1	14,14,15	0.26	0	17,19,21	0.44	0
4	NAG	A	1313	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	C	1310	1	14,14,15	0.20	0	17,19,21	0.44	0
4	NAG	E	1310	1	14,14,15	0.28	0	17,19,21	0.56	0
4	NAG	E	1304	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	A	1311	1	14,14,15	0.28	0	17,19,21	0.43	0
4	NAG	A	1307	1	14,14,15	0.28	0	17,19,21	0.55	0
4	NAG	A	1301	1	14,14,15	0.45	0	17,19,21	0.45	0
4	NAG	C	1301	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	C	1303	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	C	1305	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	C	1307	1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	C	1308	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	A	1303	1	14,14,15	0.23	0	17,19,21	0.46	0
4	NAG	A	1306	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	E	1309	1	14,14,15	0.25	0	17,19,21	0.44	0
4	NAG	E	1302	1	14,14,15	0.24	0	17,19,21	0.45	0
4	NAG	A	1305	1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	C	1306	1	14,14,15	0.28	0	17,19,21	0.47	0
4	NAG	E	1312	1	14,14,15	0.47	0	17,19,21	1.34	2 (11%)

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	E	1311	1	-	4/6/23/26	0/1/1/1
4	NAG	A	1314	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1308	1	-	4/6/23/26	0/1/1/1
4	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1304	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1309	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1314	1	-	2/6/23/26	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
4	NAG	E	1312	1	-	6/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1312	NAG	C2-N2-C7	4.57	129.02	122.90
4	A	1315	NAG	C1-O5-C5	2.43	115.44	112.19
4	E	1312	NAG	C1-C2-N2	2.19	113.88	110.43

There are no chirality outliers.

All (101) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1301	NAG	O5-C5-C6-O6
4	C	1302	NAG	C4-C5-C6-O6
4	C	1307	NAG	O5-C5-C6-O6
4	C	1311	NAG	C4-C5-C6-O6
4	A	1307	NAG	O5-C5-C6-O6
4	E	1310	NAG	C4-C5-C6-O6
4	A	1308	NAG	O5-C5-C6-O6
4	A	1304	NAG	C4-C5-C6-O6
4	A	1303	NAG	O5-C5-C6-O6
4	A	1315	NAG	O5-C5-C6-O6
4	E	1313	NAG	O5-C5-C6-O6
4	C	1306	NAG	C4-C5-C6-O6
4	E	1302	NAG	C4-C5-C6-O6
4	A	1310	NAG	O5-C5-C6-O6
4	A	1313	NAG	O5-C5-C6-O6
4	A	1307	NAG	C4-C5-C6-O6
4	A	1314	NAG	O5-C5-C6-O6
4	C	1303	NAG	O5-C5-C6-O6
4	C	1307	NAG	C4-C5-C6-O6
4	E	1311	NAG	C4-C5-C6-O6
4	C	1301	NAG	O5-C5-C6-O6
4	C	1302	NAG	O5-C5-C6-O6
4	C	1308	NAG	O5-C5-C6-O6
4	E	1311	NAG	O5-C5-C6-O6
4	A	1301	NAG	C4-C5-C6-O6
4	A	1315	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	C	1313	NAG	O5-C5-C6-O6
4	A	1310	NAG	C4-C5-C6-O6
4	C	1311	NAG	O5-C5-C6-O6
4	E	1310	NAG	O5-C5-C6-O6
4	E	1312	NAG	C4-C5-C6-O6
4	A	1304	NAG	O5-C5-C6-O6
4	C	1306	NAG	O5-C5-C6-O6
4	A	1305	NAG	C4-C5-C6-O6
4	A	1314	NAG	C4-C5-C6-O6
4	E	1306	NAG	C4-C5-C6-O6
4	A	1308	NAG	C4-C5-C6-O6
4	A	1303	NAG	C4-C5-C6-O6
4	C	1313	NAG	C4-C5-C6-O6
4	E	1313	NAG	C4-C5-C6-O6
4	A	1305	NAG	O5-C5-C6-O6
4	C	1301	NAG	C4-C5-C6-O6
4	C	1308	NAG	C4-C5-C6-O6
4	A	1311	NAG	C8-C7-N2-C2
4	A	1311	NAG	O7-C7-N2-C2
4	A	1312	NAG	C8-C7-N2-C2
4	A	1312	NAG	O7-C7-N2-C2
4	C	1301	NAG	C8-C7-N2-C2
4	C	1301	NAG	O7-C7-N2-C2
4	C	1304	NAG	C8-C7-N2-C2
4	C	1304	NAG	O7-C7-N2-C2
4	C	1313	NAG	C8-C7-N2-C2
4	C	1313	NAG	O7-C7-N2-C2
4	E	1304	NAG	C8-C7-N2-C2
4	E	1304	NAG	O7-C7-N2-C2
4	E	1312	NAG	C8-C7-N2-C2
4	E	1312	NAG	O7-C7-N2-C2
4	E	1302	NAG	O5-C5-C6-O6
4	C	1305	NAG	O5-C5-C6-O6
4	C	1305	NAG	C4-C5-C6-O6
4	C	1304	NAG	C4-C5-C6-O6
4	E	1312	NAG	O5-C5-C6-O6
4	A	1302	NAG	C4-C5-C6-O6
4	A	1313	NAG	C4-C5-C6-O6
4	E	1306	NAG	O5-C5-C6-O6
4	E	1305	NAG	C4-C5-C6-O6
4	C	1310	NAG	O5-C5-C6-O6
4	C	1310	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	C	1314	NAG	C4-C5-C6-O6
4	E	1307	NAG	O5-C5-C6-O6
4	C	1304	NAG	O5-C5-C6-O6
4	A	1302	NAG	O5-C5-C6-O6
4	E	1304	NAG	O5-C5-C6-O6
4	A	1309	NAG	C4-C5-C6-O6
4	E	1305	NAG	O5-C5-C6-O6
4	C	1303	NAG	C4-C5-C6-O6
4	E	1314	NAG	C4-C5-C6-O6
4	C	1314	NAG	O5-C5-C6-O6
4	A	1307	NAG	C1-C2-N2-C7
4	A	1308	NAG	C1-C2-N2-C7
4	E	1310	NAG	C1-C2-N2-C7
4	E	1311	NAG	C1-C2-N2-C7
4	E	1314	NAG	C1-C2-N2-C7
4	A	1309	NAG	O5-C5-C6-O6
4	A	1307	NAG	C3-C2-N2-C7
4	A	1308	NAG	C3-C2-N2-C7
4	E	1306	NAG	C3-C2-N2-C7
4	E	1307	NAG	C3-C2-N2-C7
4	E	1310	NAG	C3-C2-N2-C7
4	E	1311	NAG	C3-C2-N2-C7
4	E	1314	NAG	C3-C2-N2-C7
4	A	1306	NAG	C4-C5-C6-O6
4	E	1314	NAG	O5-C5-C6-O6
4	C	1307	NAG	C1-C2-N2-C7
4	E	1306	NAG	C1-C2-N2-C7
4	E	1307	NAG	C1-C2-N2-C7
4	E	1312	NAG	C1-C2-N2-C7
4	A	1315	NAG	C3-C2-N2-C7
4	E	1312	NAG	C3-C2-N2-C7
4	C	1315	NAG	C4-C5-C6-O6
4	E	1308	NAG	C4-C5-C6-O6

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1308	NAG	1	0
4	E	1307	NAG	1	0
4	E	1313	NAG	1	0
4	A	1315	NAG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1307	NAG	1	0
4	A	1305	NAG	1	0
4	E	1312	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.

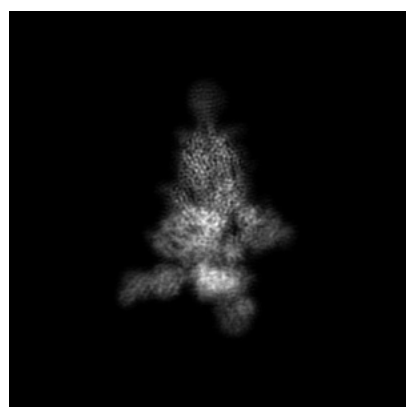
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31637. These allow visual inspection of the internal detail of the map and identification of artifacts.

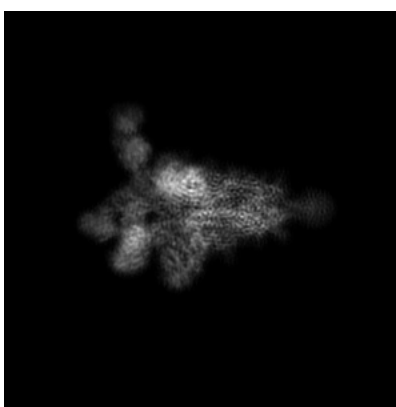
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

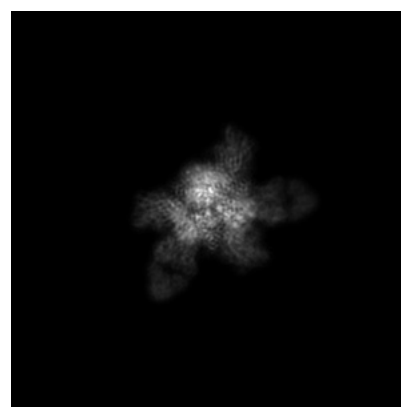
6.1.1 Primary map



X



Y

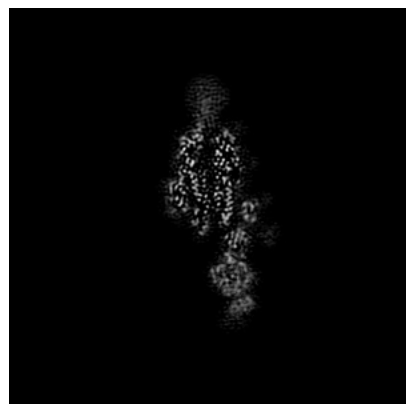


Z

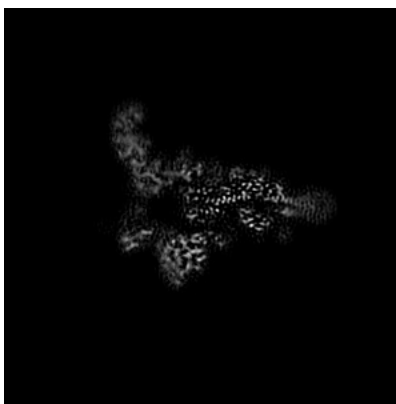
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

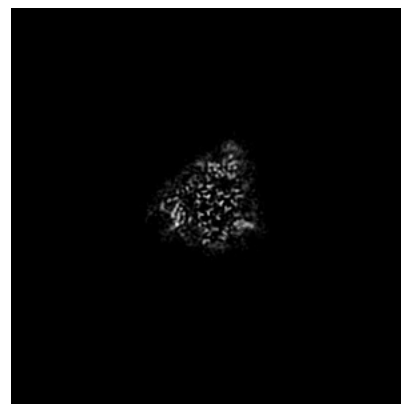
6.2.1 Primary map



X Index: 196



Y Index: 196

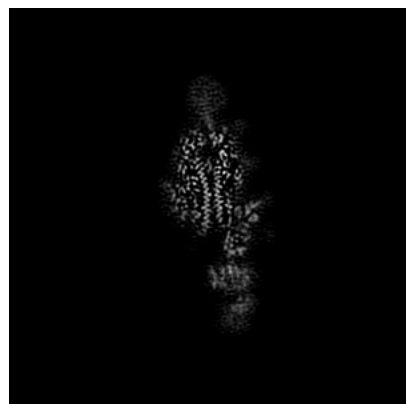


Z Index: 196

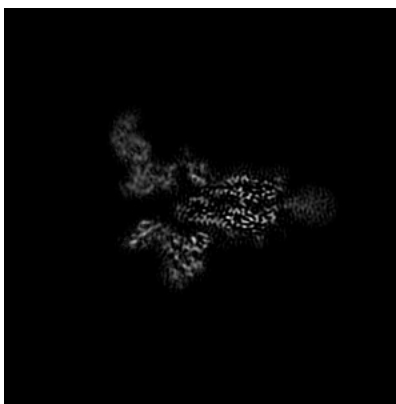
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

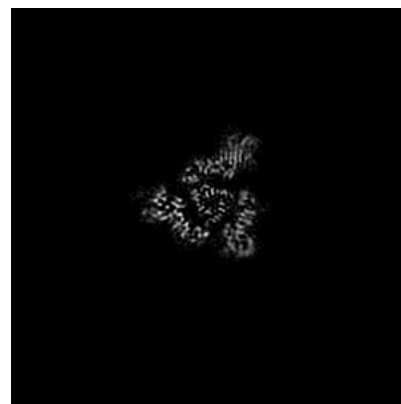
6.3.1 Primary map



X Index: 193



Y Index: 189

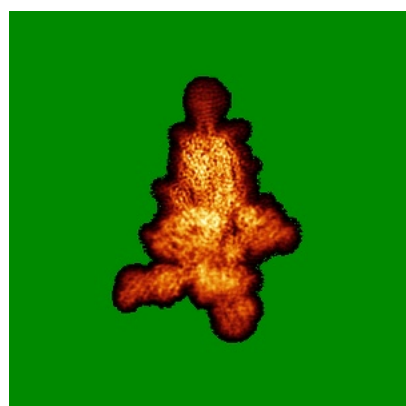


Z Index: 185

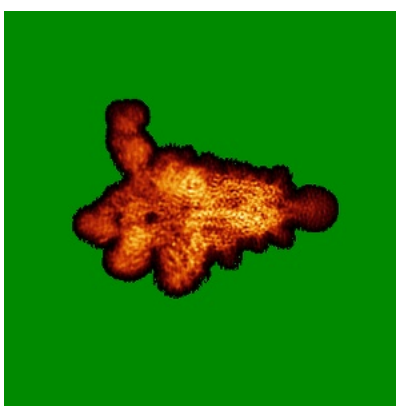
The images above show the largest variance slices of the map in three orthogonal directions.

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

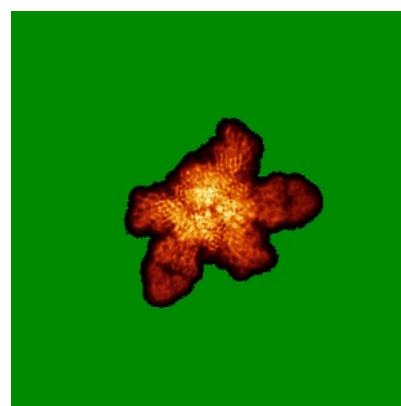
6.4.1 Primary map



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.

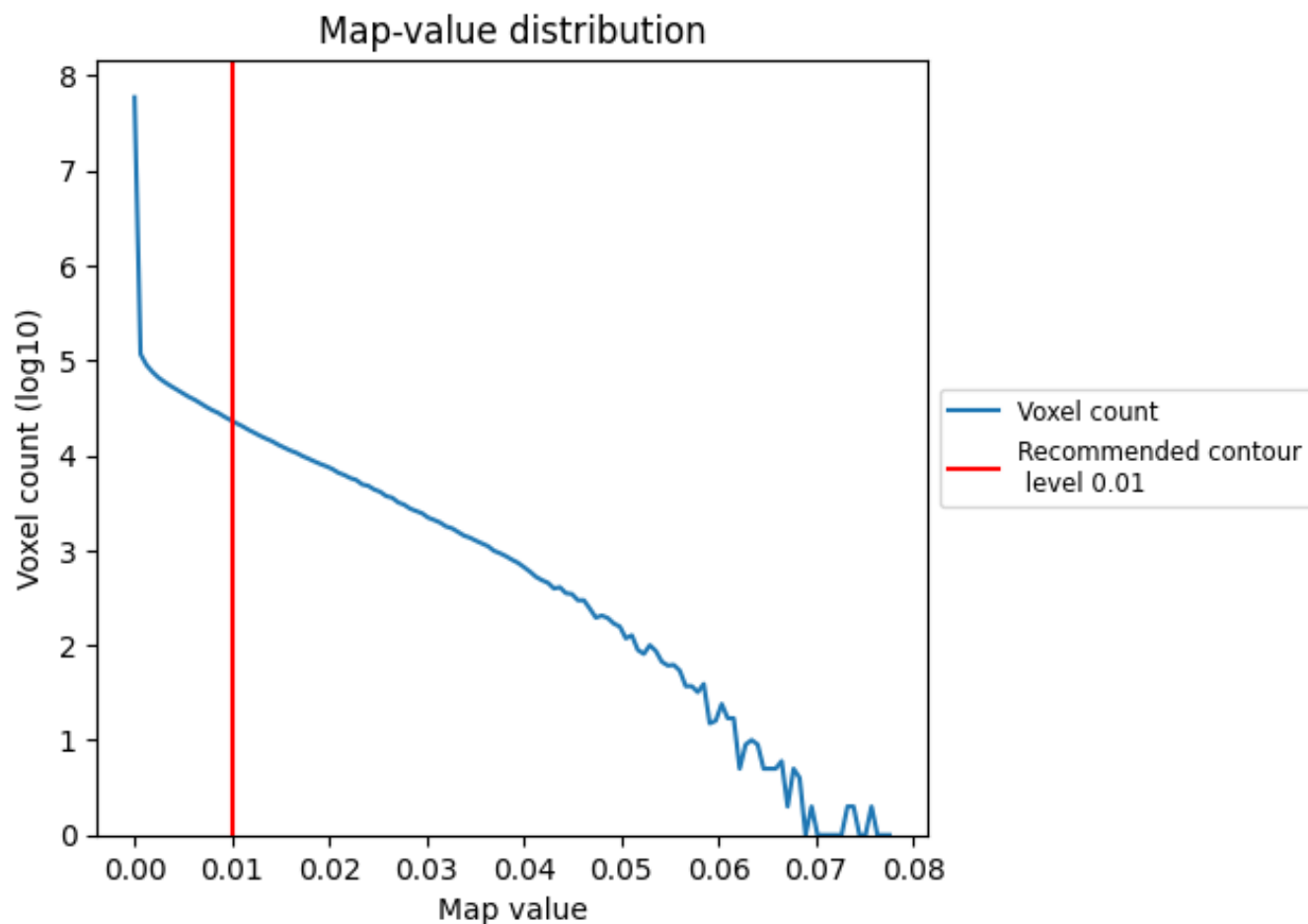
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

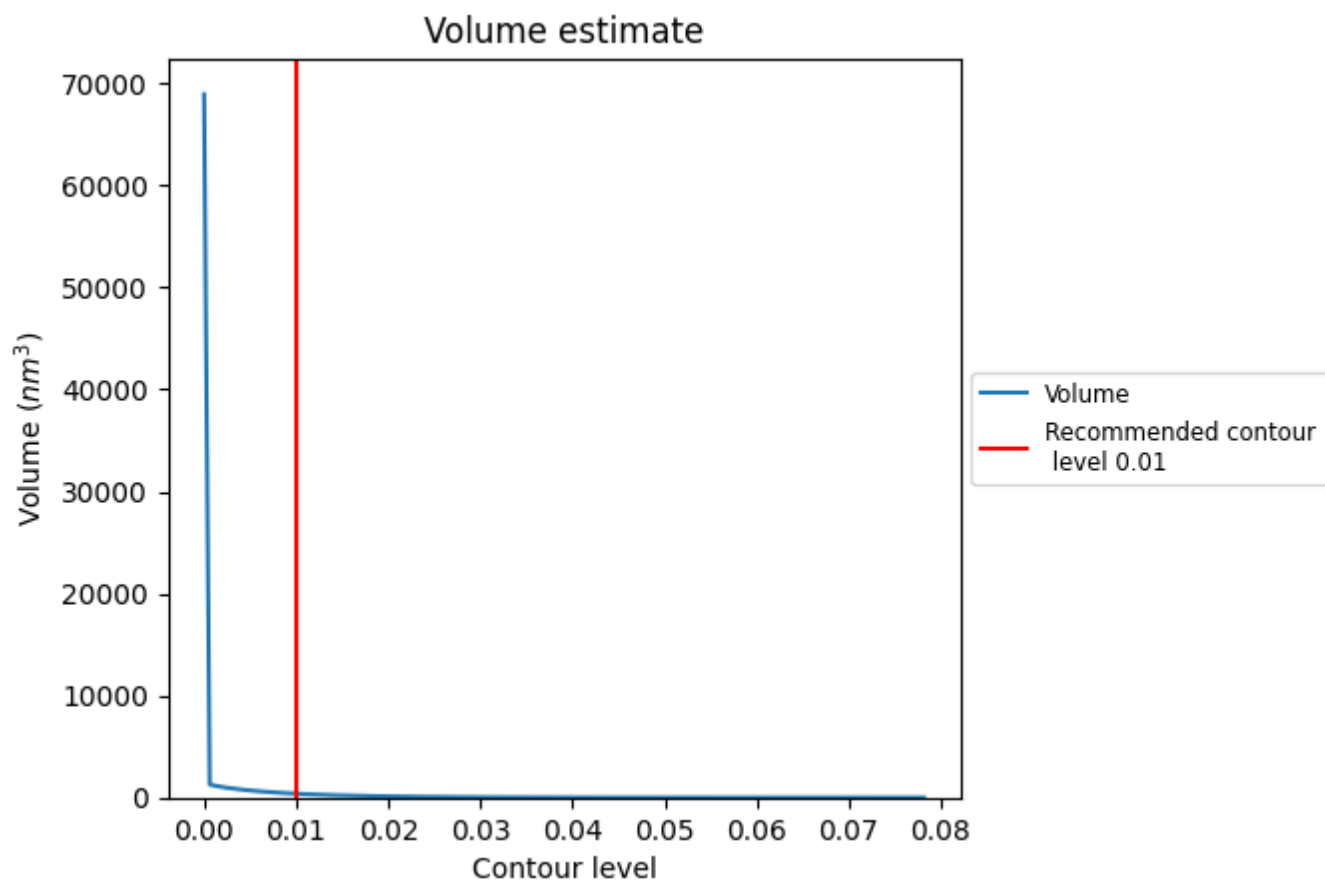
This section contains the results of statistical analysis of the map.

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.

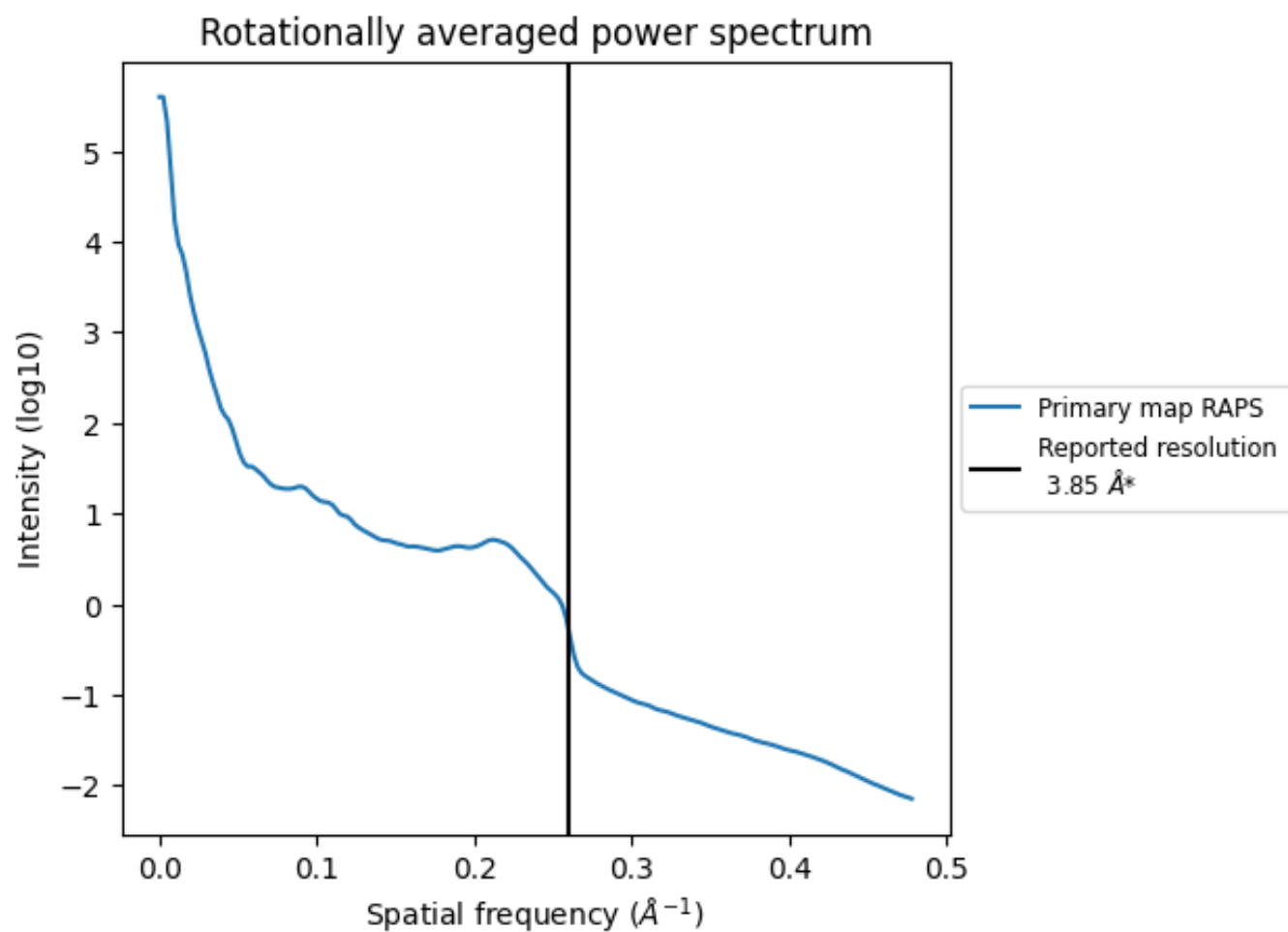
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 379 nm^3 ; this corresponds to an approximate mass of 342 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 0.260 Å⁻¹

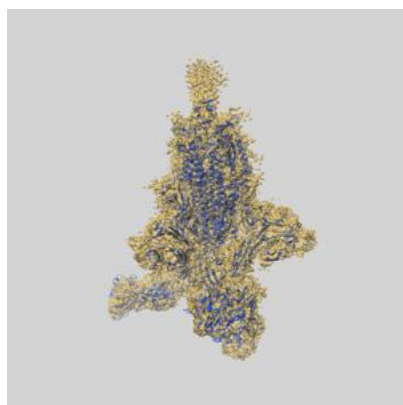
8 Fourier-Shell correlation ⓘ

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

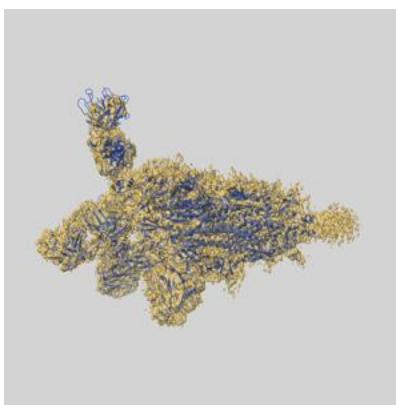
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31637 and PDB model 7V26. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

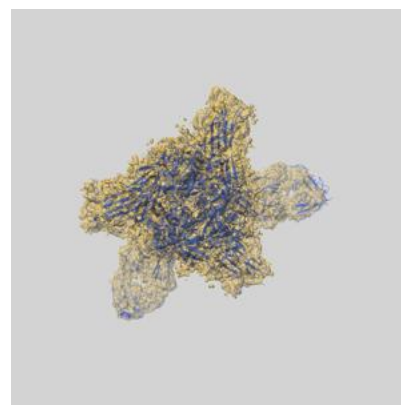
9.1 Map-model overlay [i](#)



X



Y



Z

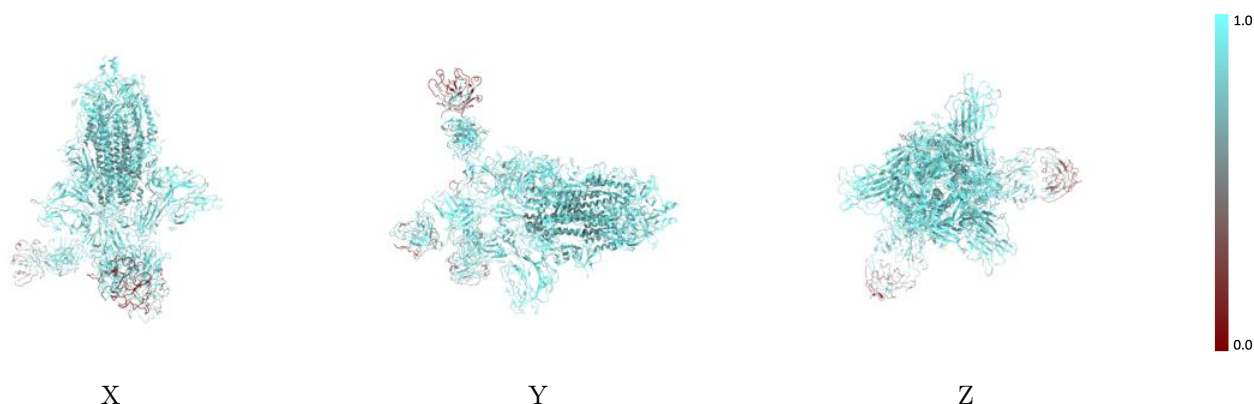
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



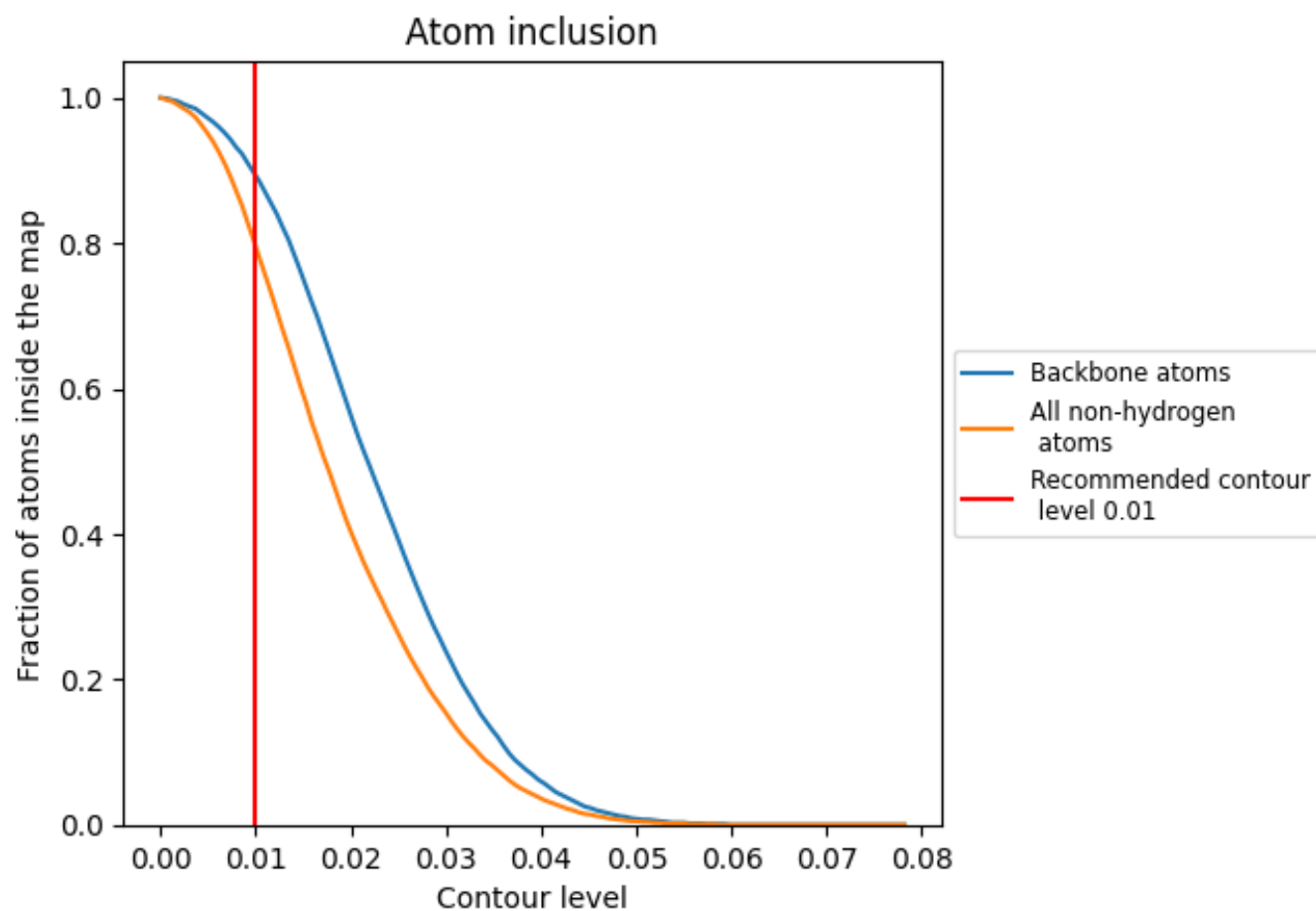
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 80% 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	0.7960	0.3280
A	0.8580	0.3910
C	0.8410	0.3690
E	0.8460	0.3670
a	0.7610	0.2490
b	0.7780	0.2340
c	0.5980	0.1790
d	0.5080	0.1450
e	0.6560	0.2190
f	0.6360	0.1690

1.0

0.0

<0.0