



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:11 PM UTC

PDB ID : 6QYD / pdb_00006qyd
EMDB ID : EMD-4677
Title : Cryo-EM structure of the head in mature bacteriophage phi29
Authors : Xu, J.W.; Wang, D.H.; Gui, M.; Xiang, Y.
Deposited on : 2019-03-08
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

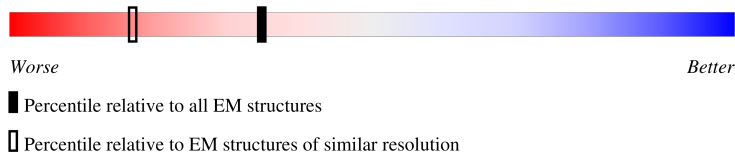
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : **FAILED**
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

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ELECTRON MICROSCOPY

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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	15020 (2.70 - 3.70)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1161205 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	433	Total	C	N	O	S	0	0
			3393	2144	578	663	8		
1	1B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1C	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	1D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1E	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	1F	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2A	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		
1	2B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3A	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	3B	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3C	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3E	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	4A	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4B	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4C	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4D	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4E	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	4F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5A	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5B	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5C	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5D	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5E	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	5F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6A	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6C	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	6D	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6E	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7A	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	7D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8A	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8B	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8D	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8F	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	9A	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1G	433	Total	C	N	O	S	0	0
			3393	2144	578	663	8		
1	1H	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1I	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	1J	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1K	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	1L	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2F	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		
1	2G	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2H	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2I	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2J	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3G	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	3H	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3I	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3J	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3K	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4G	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4H	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4I	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4J	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4K	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	4L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5G	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5H	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5I	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5J	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5K	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	5L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6G	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6H	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6I	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	6J	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	6K	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7G	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7H	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7I	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7J	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8G	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8H	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8I	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8J	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8L	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	9B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1M	433	Total	C	N	O	S	0	0
			3393	2144	578	663	8		
1	1N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1O	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	1P	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1Q	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	1R	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2K	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	2L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2M	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2O	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3M	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	3N	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3O	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3P	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3Q	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4M	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4N	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4O	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4P	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4Q	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	4R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5M	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5N	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5O	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5P	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5Q	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	5R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6M	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6O	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	6P	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6Q	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7M	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7O	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8M	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8N	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8O	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8P	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8Q	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8R	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	9C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1S	433	Total	C	N	O	S	0	0
			3393	2144	578	663	8		
1	1T	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	1U	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	1V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1W	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	1X	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2P	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		
1	2Q	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2S	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2T	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3S	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	3T	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3U	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3W	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4S	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4T	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4U	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4V	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4W	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	4X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	5S	435	Total 3422	C 2167	N 579	O 668	S 8	0	0
1	5T	435	Total 3422	C 2167	N 579	O 668	S 8	0	0
1	5U	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5V	435	Total 3422	C 2167	N 579	O 668	S 8	0	0
1	5W	445	Total 3483	C 2201	N 592	O 682	S 8	0	0
1	5X	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	6S	445	Total 3483	C 2201	N 592	O 682	S 8	0	0
1	6T	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	6U	435	Total 3422	C 2167	N 579	O 668	S 8	0	0
1	6V	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	6W	445	Total 3483	C 2201	N 592	O 682	S 8	0	0
1	6X	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7P	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7Q	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7R	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7S	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7T	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8S	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8T	445	Total 3483	C 2201	N 592	O 682	S 8	0	0
1	8U	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8V	445	Total 3483	C 2201	N 592	O 682	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8X	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	9D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1Y	433	Total	C	N	O	S	0	0
			3393	2144	578	663	8		
1	1Z	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1a	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	1b	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1c	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	1d	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2U	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		
1	2V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2Y	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3Y	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	3Z	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3a	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3b	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3c	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	3d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4Y	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	4Z	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4a	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4b	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	4c	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	4d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5Y	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5Z	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5a	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5b	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	5c	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	5d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6Y	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6Z	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6a	435	Total	C	N	O	S	0	0
			3422	2167	579	668	8		
1	6b	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6c	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	6d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7U	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	7Y	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8Y	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8Z	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8a	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8b	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	8c	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8d	445	Total	C	N	O	S	0	0
			3483	2201	592	682	8		
1	9E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

- Molecule 2 is a protein called Capsid fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1f	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1h	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2Z	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2a	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2b	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2c	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2d	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3e	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	3g	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3h	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4f	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5f	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6e	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6g	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6h	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7Z	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7a	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7b	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7c	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7d	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8e	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8h	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8j	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	9F	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1j	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1l	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2h	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3i	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3k	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4h	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5h	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6i	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6k	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	6l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7h	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8k	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8o	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8p	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9G	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1o	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1p	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	2n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3m	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3o	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3p	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4j	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5j	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6m	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6o	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6p	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8q	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8s	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	8t	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8u	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8v	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9H	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1q	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1r	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1s	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1t	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2o	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2p	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2q	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2s	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3q	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3s	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3t	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4l	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5l	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	6q	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	6r	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	6s	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	6t	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7o	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7p	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7q	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7r	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7s	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	8w	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	8x	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	8y	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	8z	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	9K	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	9L	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	9I	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	1u	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	1v	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	1w	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	1x	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	2t	280	Total 2106	C 1317	N 349	O 436	S 4	8	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	2u	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2w	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3u	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3w	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6u	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6w	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7t	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7u	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7w	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	9M	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9N	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	9O	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	9P	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9Q	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	9R	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9J	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

There are 330 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1e	123	GLU	ASP	conflict	UNP B3VMP4
1e	281	LEU	-	insertion	UNP B3VMP4
1f	123	GLU	ASP	conflict	UNP B3VMP4
1f	281	LEU	-	insertion	UNP B3VMP4
1g	123	GLU	ASP	conflict	UNP B3VMP4
1g	281	LEU	-	insertion	UNP B3VMP4
1h	123	GLU	ASP	conflict	UNP B3VMP4
1h	281	LEU	-	insertion	UNP B3VMP4
2Z	123	GLU	ASP	conflict	UNP B3VMP4
2Z	281	LEU	-	insertion	UNP B3VMP4
2a	123	GLU	ASP	conflict	UNP B3VMP4
2a	281	LEU	-	insertion	UNP B3VMP4
2b	123	GLU	ASP	conflict	UNP B3VMP4
2b	281	LEU	-	insertion	UNP B3VMP4
2c	123	GLU	ASP	conflict	UNP B3VMP4
2c	281	LEU	-	insertion	UNP B3VMP4
2d	123	GLU	ASP	conflict	UNP B3VMP4
2d	281	LEU	-	insertion	UNP B3VMP4
3e	123	GLU	ASP	conflict	UNP B3VMP4
3e	281	LEU	-	insertion	UNP B3VMP4
3f	123	GLU	ASP	conflict	UNP B3VMP4
3f	281	LEU	-	insertion	UNP B3VMP4
3g	123	GLU	ASP	conflict	UNP B3VMP4
3g	281	LEU	-	insertion	UNP B3VMP4
3h	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
3h	281	LEU	-	insertion	UNP B3VMP4
4e	123	GLU	ASP	conflict	UNP B3VMP4
4e	281	LEU	-	insertion	UNP B3VMP4
4f	123	GLU	ASP	conflict	UNP B3VMP4
4f	281	LEU	-	insertion	UNP B3VMP4
5e	123	GLU	ASP	conflict	UNP B3VMP4
5e	281	LEU	-	insertion	UNP B3VMP4
5f	123	GLU	ASP	conflict	UNP B3VMP4
5f	281	LEU	-	insertion	UNP B3VMP4
6e	123	GLU	ASP	conflict	UNP B3VMP4
6e	281	LEU	-	insertion	UNP B3VMP4
6f	123	GLU	ASP	conflict	UNP B3VMP4
6f	281	LEU	-	insertion	UNP B3VMP4
6g	123	GLU	ASP	conflict	UNP B3VMP4
6g	281	LEU	-	insertion	UNP B3VMP4
6h	123	GLU	ASP	conflict	UNP B3VMP4
6h	281	LEU	-	insertion	UNP B3VMP4
7Z	123	GLU	ASP	conflict	UNP B3VMP4
7Z	281	LEU	-	insertion	UNP B3VMP4
7a	123	GLU	ASP	conflict	UNP B3VMP4
7a	281	LEU	-	insertion	UNP B3VMP4
7b	123	GLU	ASP	conflict	UNP B3VMP4
7b	281	LEU	-	insertion	UNP B3VMP4
7c	123	GLU	ASP	conflict	UNP B3VMP4
7c	281	LEU	-	insertion	UNP B3VMP4
7d	123	GLU	ASP	conflict	UNP B3VMP4
7d	281	LEU	-	insertion	UNP B3VMP4
8e	123	GLU	ASP	conflict	UNP B3VMP4
8e	281	LEU	-	insertion	UNP B3VMP4
8f	123	GLU	ASP	conflict	UNP B3VMP4
8f	281	LEU	-	insertion	UNP B3VMP4
8g	123	GLU	ASP	conflict	UNP B3VMP4
8g	281	LEU	-	insertion	UNP B3VMP4
8h	123	GLU	ASP	conflict	UNP B3VMP4
8h	281	LEU	-	insertion	UNP B3VMP4
8i	123	GLU	ASP	conflict	UNP B3VMP4
8i	281	LEU	-	insertion	UNP B3VMP4
8j	123	GLU	ASP	conflict	UNP B3VMP4
8j	281	LEU	-	insertion	UNP B3VMP4
9F	123	GLU	ASP	conflict	UNP B3VMP4
9F	281	LEU	-	insertion	UNP B3VMP4
1i	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
1i	281	LEU	-	insertion	UNP B3VMP4
1j	123	GLU	ASP	conflict	UNP B3VMP4
1j	281	LEU	-	insertion	UNP B3VMP4
1k	123	GLU	ASP	conflict	UNP B3VMP4
1k	281	LEU	-	insertion	UNP B3VMP4
1l	123	GLU	ASP	conflict	UNP B3VMP4
1l	281	LEU	-	insertion	UNP B3VMP4
2e	123	GLU	ASP	conflict	UNP B3VMP4
2e	281	LEU	-	insertion	UNP B3VMP4
2f	123	GLU	ASP	conflict	UNP B3VMP4
2f	281	LEU	-	insertion	UNP B3VMP4
2g	123	GLU	ASP	conflict	UNP B3VMP4
2g	281	LEU	-	insertion	UNP B3VMP4
2h	123	GLU	ASP	conflict	UNP B3VMP4
2h	281	LEU	-	insertion	UNP B3VMP4
2i	123	GLU	ASP	conflict	UNP B3VMP4
2i	281	LEU	-	insertion	UNP B3VMP4
3i	123	GLU	ASP	conflict	UNP B3VMP4
3i	281	LEU	-	insertion	UNP B3VMP4
3j	123	GLU	ASP	conflict	UNP B3VMP4
3j	281	LEU	-	insertion	UNP B3VMP4
3k	123	GLU	ASP	conflict	UNP B3VMP4
3k	281	LEU	-	insertion	UNP B3VMP4
3l	123	GLU	ASP	conflict	UNP B3VMP4
3l	281	LEU	-	insertion	UNP B3VMP4
4g	123	GLU	ASP	conflict	UNP B3VMP4
4g	281	LEU	-	insertion	UNP B3VMP4
4h	123	GLU	ASP	conflict	UNP B3VMP4
4h	281	LEU	-	insertion	UNP B3VMP4
5g	123	GLU	ASP	conflict	UNP B3VMP4
5g	281	LEU	-	insertion	UNP B3VMP4
5h	123	GLU	ASP	conflict	UNP B3VMP4
5h	281	LEU	-	insertion	UNP B3VMP4
6i	123	GLU	ASP	conflict	UNP B3VMP4
6i	281	LEU	-	insertion	UNP B3VMP4
6j	123	GLU	ASP	conflict	UNP B3VMP4
6j	281	LEU	-	insertion	UNP B3VMP4
6k	123	GLU	ASP	conflict	UNP B3VMP4
6k	281	LEU	-	insertion	UNP B3VMP4
6l	123	GLU	ASP	conflict	UNP B3VMP4
6l	281	LEU	-	insertion	UNP B3VMP4
7e	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
7e	281	LEU	-	insertion	UNP B3VMP4
7f	123	GLU	ASP	conflict	UNP B3VMP4
7f	281	LEU	-	insertion	UNP B3VMP4
7g	123	GLU	ASP	conflict	UNP B3VMP4
7g	281	LEU	-	insertion	UNP B3VMP4
7h	123	GLU	ASP	conflict	UNP B3VMP4
7h	281	LEU	-	insertion	UNP B3VMP4
7i	123	GLU	ASP	conflict	UNP B3VMP4
7i	281	LEU	-	insertion	UNP B3VMP4
8k	123	GLU	ASP	conflict	UNP B3VMP4
8k	281	LEU	-	insertion	UNP B3VMP4
8l	123	GLU	ASP	conflict	UNP B3VMP4
8l	281	LEU	-	insertion	UNP B3VMP4
8m	123	GLU	ASP	conflict	UNP B3VMP4
8m	281	LEU	-	insertion	UNP B3VMP4
8n	123	GLU	ASP	conflict	UNP B3VMP4
8n	281	LEU	-	insertion	UNP B3VMP4
8o	123	GLU	ASP	conflict	UNP B3VMP4
8o	281	LEU	-	insertion	UNP B3VMP4
8p	123	GLU	ASP	conflict	UNP B3VMP4
8p	281	LEU	-	insertion	UNP B3VMP4
9G	123	GLU	ASP	conflict	UNP B3VMP4
9G	281	LEU	-	insertion	UNP B3VMP4
1m	123	GLU	ASP	conflict	UNP B3VMP4
1m	281	LEU	-	insertion	UNP B3VMP4
1n	123	GLU	ASP	conflict	UNP B3VMP4
1n	281	LEU	-	insertion	UNP B3VMP4
1o	123	GLU	ASP	conflict	UNP B3VMP4
1o	281	LEU	-	insertion	UNP B3VMP4
1p	123	GLU	ASP	conflict	UNP B3VMP4
1p	281	LEU	-	insertion	UNP B3VMP4
2j	123	GLU	ASP	conflict	UNP B3VMP4
2j	281	LEU	-	insertion	UNP B3VMP4
2k	123	GLU	ASP	conflict	UNP B3VMP4
2k	281	LEU	-	insertion	UNP B3VMP4
2l	123	GLU	ASP	conflict	UNP B3VMP4
2l	281	LEU	-	insertion	UNP B3VMP4
2m	123	GLU	ASP	conflict	UNP B3VMP4
2m	281	LEU	-	insertion	UNP B3VMP4
2n	123	GLU	ASP	conflict	UNP B3VMP4
2n	281	LEU	-	insertion	UNP B3VMP4
3m	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
3m	281	LEU	-	insertion	UNP B3VMP4
3n	123	GLU	ASP	conflict	UNP B3VMP4
3n	281	LEU	-	insertion	UNP B3VMP4
3o	123	GLU	ASP	conflict	UNP B3VMP4
3o	281	LEU	-	insertion	UNP B3VMP4
3p	123	GLU	ASP	conflict	UNP B3VMP4
3p	281	LEU	-	insertion	UNP B3VMP4
4i	123	GLU	ASP	conflict	UNP B3VMP4
4i	281	LEU	-	insertion	UNP B3VMP4
4j	123	GLU	ASP	conflict	UNP B3VMP4
4j	281	LEU	-	insertion	UNP B3VMP4
5i	123	GLU	ASP	conflict	UNP B3VMP4
5i	281	LEU	-	insertion	UNP B3VMP4
5j	123	GLU	ASP	conflict	UNP B3VMP4
5j	281	LEU	-	insertion	UNP B3VMP4
6m	123	GLU	ASP	conflict	UNP B3VMP4
6m	281	LEU	-	insertion	UNP B3VMP4
6n	123	GLU	ASP	conflict	UNP B3VMP4
6n	281	LEU	-	insertion	UNP B3VMP4
6o	123	GLU	ASP	conflict	UNP B3VMP4
6o	281	LEU	-	insertion	UNP B3VMP4
6p	123	GLU	ASP	conflict	UNP B3VMP4
6p	281	LEU	-	insertion	UNP B3VMP4
7j	123	GLU	ASP	conflict	UNP B3VMP4
7j	281	LEU	-	insertion	UNP B3VMP4
7k	123	GLU	ASP	conflict	UNP B3VMP4
7k	281	LEU	-	insertion	UNP B3VMP4
7l	123	GLU	ASP	conflict	UNP B3VMP4
7l	281	LEU	-	insertion	UNP B3VMP4
7m	123	GLU	ASP	conflict	UNP B3VMP4
7m	281	LEU	-	insertion	UNP B3VMP4
7n	123	GLU	ASP	conflict	UNP B3VMP4
7n	281	LEU	-	insertion	UNP B3VMP4
8q	123	GLU	ASP	conflict	UNP B3VMP4
8q	281	LEU	-	insertion	UNP B3VMP4
8r	123	GLU	ASP	conflict	UNP B3VMP4
8r	281	LEU	-	insertion	UNP B3VMP4
8s	123	GLU	ASP	conflict	UNP B3VMP4
8s	281	LEU	-	insertion	UNP B3VMP4
8t	123	GLU	ASP	conflict	UNP B3VMP4
8t	281	LEU	-	insertion	UNP B3VMP4
8u	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
8u	281	LEU	-	insertion	UNP B3VMP4
8v	123	GLU	ASP	conflict	UNP B3VMP4
8v	281	LEU	-	insertion	UNP B3VMP4
9H	123	GLU	ASP	conflict	UNP B3VMP4
9H	281	LEU	-	insertion	UNP B3VMP4
1q	123	GLU	ASP	conflict	UNP B3VMP4
1q	281	LEU	-	insertion	UNP B3VMP4
1r	123	GLU	ASP	conflict	UNP B3VMP4
1r	281	LEU	-	insertion	UNP B3VMP4
1s	123	GLU	ASP	conflict	UNP B3VMP4
1s	281	LEU	-	insertion	UNP B3VMP4
1t	123	GLU	ASP	conflict	UNP B3VMP4
1t	281	LEU	-	insertion	UNP B3VMP4
2o	123	GLU	ASP	conflict	UNP B3VMP4
2o	281	LEU	-	insertion	UNP B3VMP4
2p	123	GLU	ASP	conflict	UNP B3VMP4
2p	281	LEU	-	insertion	UNP B3VMP4
2q	123	GLU	ASP	conflict	UNP B3VMP4
2q	281	LEU	-	insertion	UNP B3VMP4
2r	123	GLU	ASP	conflict	UNP B3VMP4
2r	281	LEU	-	insertion	UNP B3VMP4
2s	123	GLU	ASP	conflict	UNP B3VMP4
2s	281	LEU	-	insertion	UNP B3VMP4
3q	123	GLU	ASP	conflict	UNP B3VMP4
3q	281	LEU	-	insertion	UNP B3VMP4
3r	123	GLU	ASP	conflict	UNP B3VMP4
3r	281	LEU	-	insertion	UNP B3VMP4
3s	123	GLU	ASP	conflict	UNP B3VMP4
3s	281	LEU	-	insertion	UNP B3VMP4
3t	123	GLU	ASP	conflict	UNP B3VMP4
3t	281	LEU	-	insertion	UNP B3VMP4
4k	123	GLU	ASP	conflict	UNP B3VMP4
4k	281	LEU	-	insertion	UNP B3VMP4
4l	123	GLU	ASP	conflict	UNP B3VMP4
4l	281	LEU	-	insertion	UNP B3VMP4
5k	123	GLU	ASP	conflict	UNP B3VMP4
5k	281	LEU	-	insertion	UNP B3VMP4
5l	123	GLU	ASP	conflict	UNP B3VMP4
5l	281	LEU	-	insertion	UNP B3VMP4
6q	123	GLU	ASP	conflict	UNP B3VMP4
6q	281	LEU	-	insertion	UNP B3VMP4
6r	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
6r	281	LEU	-	insertion	UNP B3VMP4
6s	123	GLU	ASP	conflict	UNP B3VMP4
6s	281	LEU	-	insertion	UNP B3VMP4
6t	123	GLU	ASP	conflict	UNP B3VMP4
6t	281	LEU	-	insertion	UNP B3VMP4
7o	123	GLU	ASP	conflict	UNP B3VMP4
7o	281	LEU	-	insertion	UNP B3VMP4
7p	123	GLU	ASP	conflict	UNP B3VMP4
7p	281	LEU	-	insertion	UNP B3VMP4
7q	123	GLU	ASP	conflict	UNP B3VMP4
7q	281	LEU	-	insertion	UNP B3VMP4
7r	123	GLU	ASP	conflict	UNP B3VMP4
7r	281	LEU	-	insertion	UNP B3VMP4
7s	123	GLU	ASP	conflict	UNP B3VMP4
7s	281	LEU	-	insertion	UNP B3VMP4
8w	123	GLU	ASP	conflict	UNP B3VMP4
8w	281	LEU	-	insertion	UNP B3VMP4
8x	123	GLU	ASP	conflict	UNP B3VMP4
8x	281	LEU	-	insertion	UNP B3VMP4
8y	123	GLU	ASP	conflict	UNP B3VMP4
8y	281	LEU	-	insertion	UNP B3VMP4
8z	123	GLU	ASP	conflict	UNP B3VMP4
8z	281	LEU	-	insertion	UNP B3VMP4
9K	123	GLU	ASP	conflict	UNP B3VMP4
9K	281	LEU	-	insertion	UNP B3VMP4
9L	123	GLU	ASP	conflict	UNP B3VMP4
9L	281	LEU	-	insertion	UNP B3VMP4
9I	123	GLU	ASP	conflict	UNP B3VMP4
9I	281	LEU	-	insertion	UNP B3VMP4
1u	123	GLU	ASP	conflict	UNP B3VMP4
1u	281	LEU	-	insertion	UNP B3VMP4
1v	123	GLU	ASP	conflict	UNP B3VMP4
1v	281	LEU	-	insertion	UNP B3VMP4
1w	123	GLU	ASP	conflict	UNP B3VMP4
1w	281	LEU	-	insertion	UNP B3VMP4
1x	123	GLU	ASP	conflict	UNP B3VMP4
1x	281	LEU	-	insertion	UNP B3VMP4
2t	123	GLU	ASP	conflict	UNP B3VMP4
2t	281	LEU	-	insertion	UNP B3VMP4
2u	123	GLU	ASP	conflict	UNP B3VMP4
2u	281	LEU	-	insertion	UNP B3VMP4
2v	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
2v	281	LEU	-	insertion	UNP B3VMP4
2w	123	GLU	ASP	conflict	UNP B3VMP4
2w	281	LEU	-	insertion	UNP B3VMP4
2x	123	GLU	ASP	conflict	UNP B3VMP4
2x	281	LEU	-	insertion	UNP B3VMP4
3u	123	GLU	ASP	conflict	UNP B3VMP4
3u	281	LEU	-	insertion	UNP B3VMP4
3v	123	GLU	ASP	conflict	UNP B3VMP4
3v	281	LEU	-	insertion	UNP B3VMP4
3w	123	GLU	ASP	conflict	UNP B3VMP4
3w	281	LEU	-	insertion	UNP B3VMP4
3x	123	GLU	ASP	conflict	UNP B3VMP4
3x	281	LEU	-	insertion	UNP B3VMP4
4m	123	GLU	ASP	conflict	UNP B3VMP4
4m	281	LEU	-	insertion	UNP B3VMP4
4n	123	GLU	ASP	conflict	UNP B3VMP4
4n	281	LEU	-	insertion	UNP B3VMP4
5m	123	GLU	ASP	conflict	UNP B3VMP4
5m	281	LEU	-	insertion	UNP B3VMP4
5n	123	GLU	ASP	conflict	UNP B3VMP4
5n	281	LEU	-	insertion	UNP B3VMP4
6u	123	GLU	ASP	conflict	UNP B3VMP4
6u	281	LEU	-	insertion	UNP B3VMP4
6v	123	GLU	ASP	conflict	UNP B3VMP4
6v	281	LEU	-	insertion	UNP B3VMP4
6w	123	GLU	ASP	conflict	UNP B3VMP4
6w	281	LEU	-	insertion	UNP B3VMP4
6x	123	GLU	ASP	conflict	UNP B3VMP4
6x	281	LEU	-	insertion	UNP B3VMP4
7t	123	GLU	ASP	conflict	UNP B3VMP4
7t	281	LEU	-	insertion	UNP B3VMP4
7u	123	GLU	ASP	conflict	UNP B3VMP4
7u	281	LEU	-	insertion	UNP B3VMP4
7v	123	GLU	ASP	conflict	UNP B3VMP4
7v	281	LEU	-	insertion	UNP B3VMP4
7w	123	GLU	ASP	conflict	UNP B3VMP4
7w	281	LEU	-	insertion	UNP B3VMP4
7x	123	GLU	ASP	conflict	UNP B3VMP4
7x	281	LEU	-	insertion	UNP B3VMP4
9M	123	GLU	ASP	conflict	UNP B3VMP4
9M	281	LEU	-	insertion	UNP B3VMP4
9N	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
9N	281	LEU	-	insertion	UNP B3VMP4
9O	123	GLU	ASP	conflict	UNP B3VMP4
9O	281	LEU	-	insertion	UNP B3VMP4
9P	123	GLU	ASP	conflict	UNP B3VMP4
9P	281	LEU	-	insertion	UNP B3VMP4
9Q	123	GLU	ASP	conflict	UNP B3VMP4
9Q	281	LEU	-	insertion	UNP B3VMP4
9R	123	GLU	ASP	conflict	UNP B3VMP4
9R	281	LEU	-	insertion	UNP B3VMP4
9J	123	GLU	ASP	conflict	UNP B3VMP4
9J	281	LEU	-	insertion	UNP B3VMP4

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36730	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	22.084	Depositor
Minimum map value	-0.418	Depositor
Average map value	0.103	Depositor
Map value standard deviation	0.764	Depositor
Recommended contour level	3	Depositor
Map size ($\text{\AA}$)	740.8544, 740.8544, 740.8544	wwPDB
Map dimensions	572, 572, 572	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2952, 1.2952, 1.2952	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

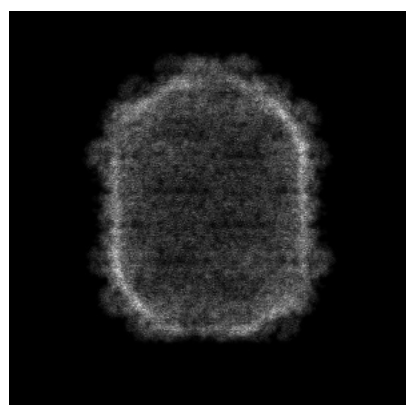
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4677. These allow visual inspection of the internal detail of the map and identification of artifacts.

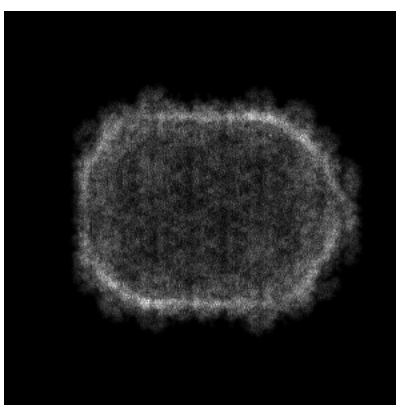
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

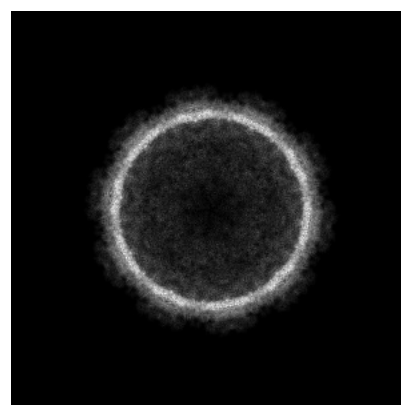
5.1.1 Primary map



X



Y

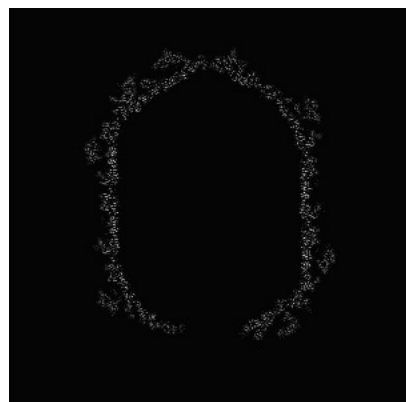


Z

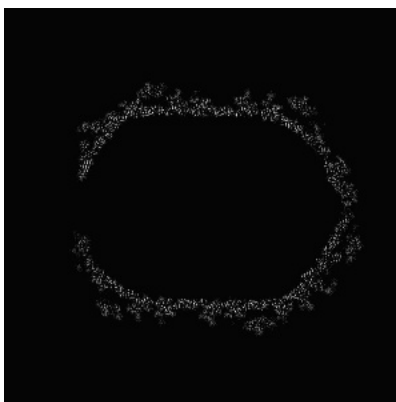
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

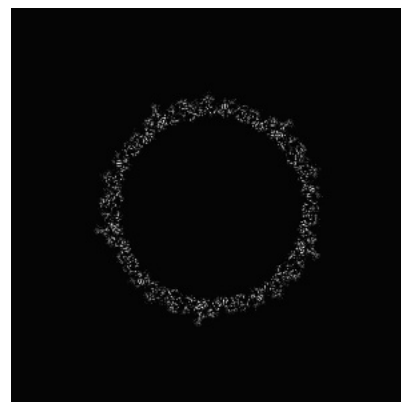
5.2.1 Primary map



X Index: 286



Y Index: 286

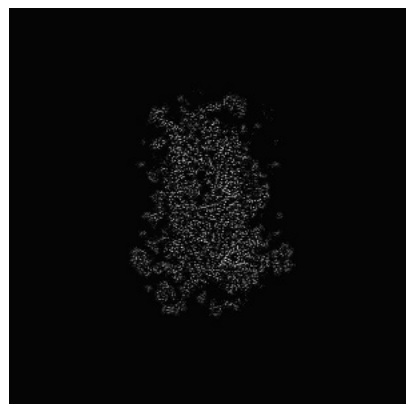


Z Index: 286

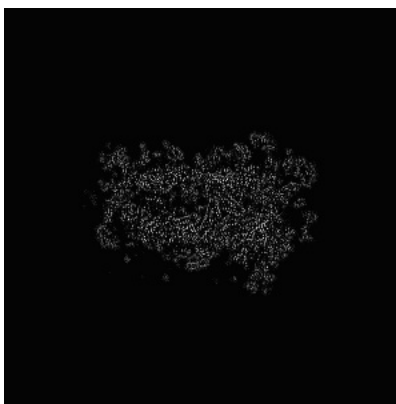
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

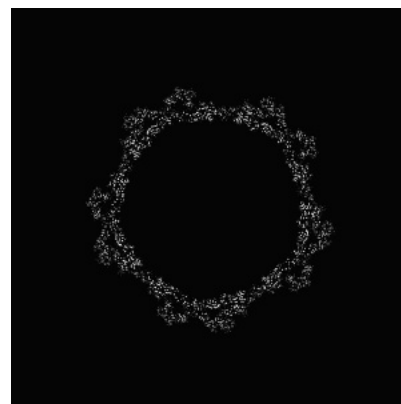
5.3.1 Primary map



X Index: 153



Y Index: 418

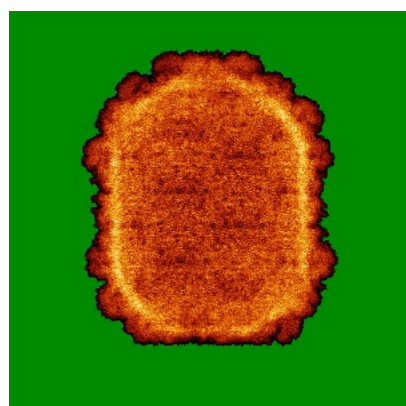


Z Index: 377

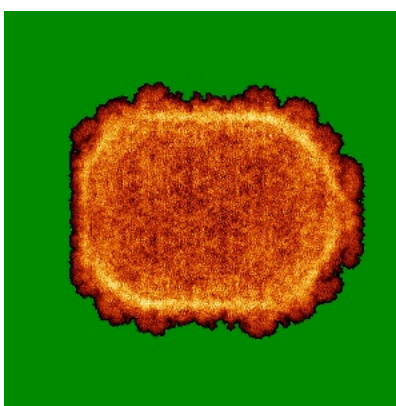
The images above show the largest variance slices of the map in three orthogonal directions.

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

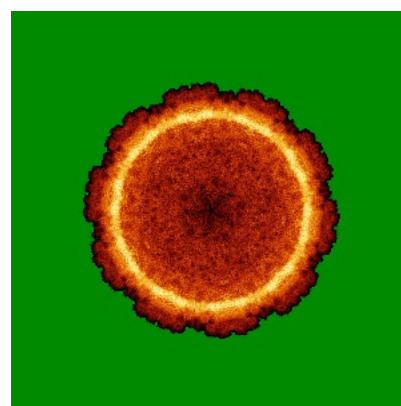
5.4.1 Primary map



X



Y

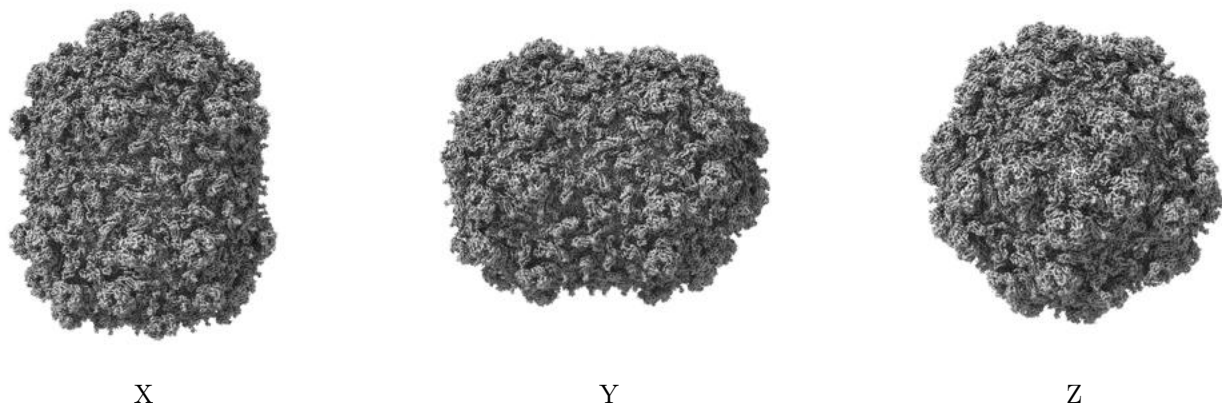


Z

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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

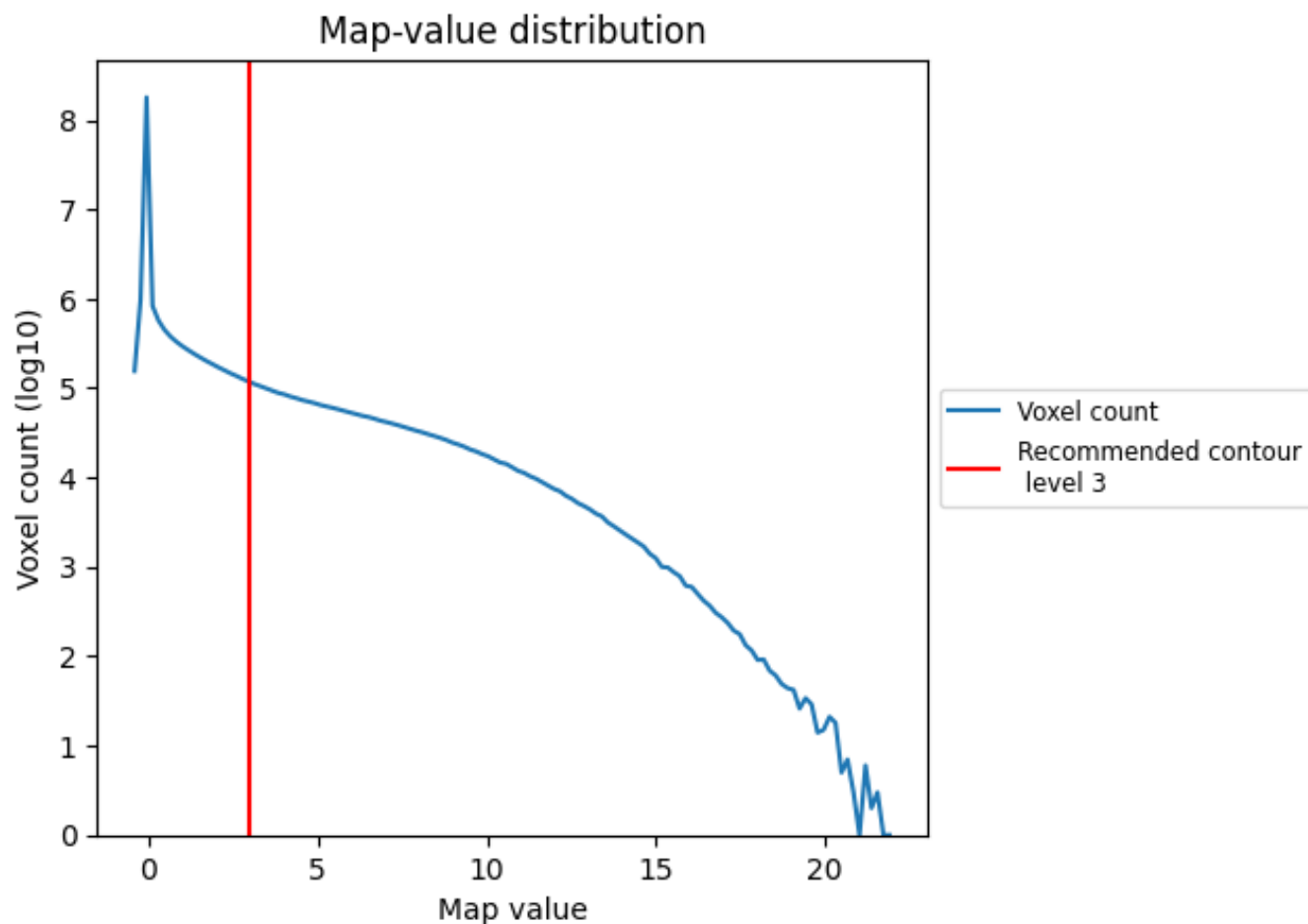
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

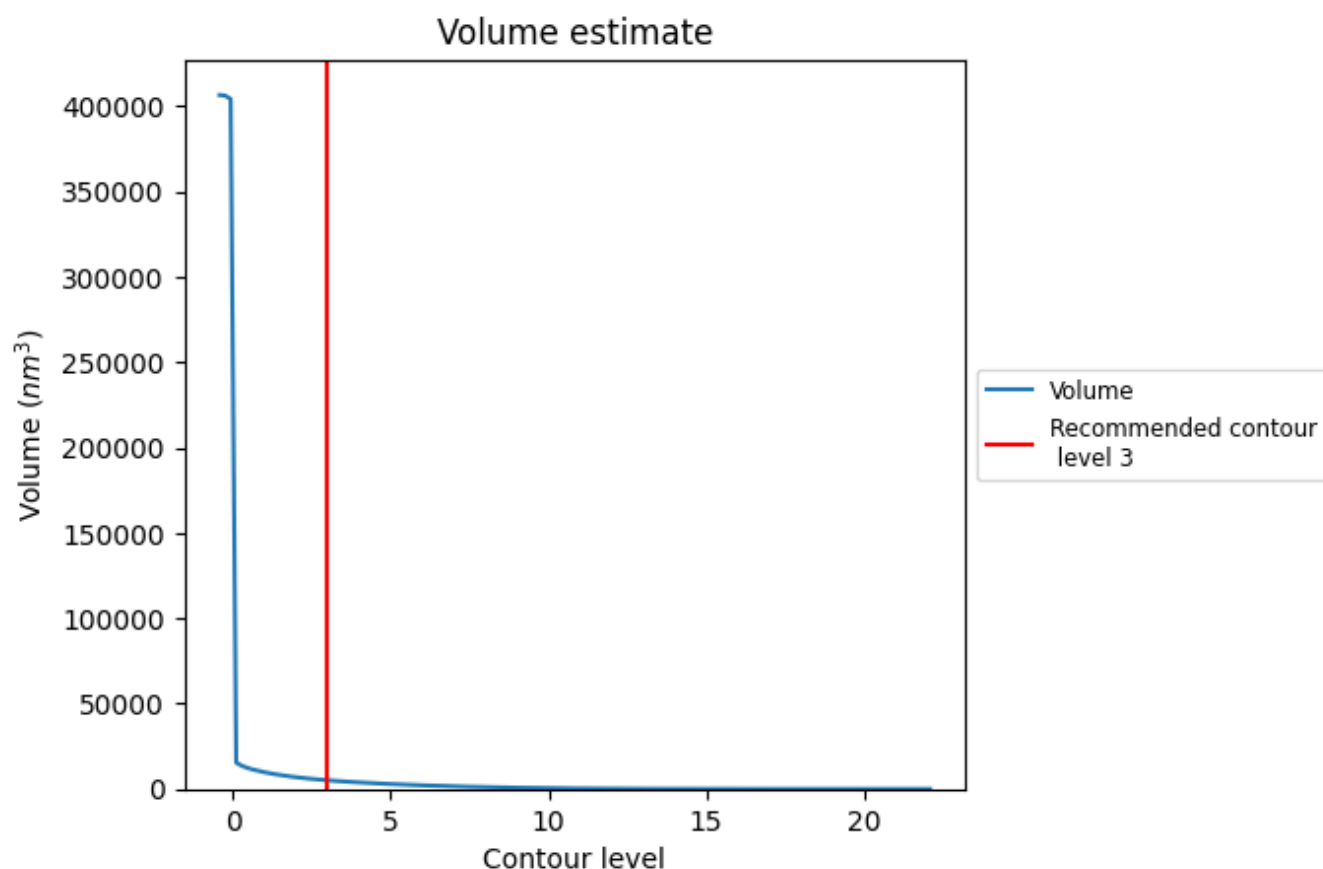
This section contains the results of statistical analysis of the map.

6.1 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.

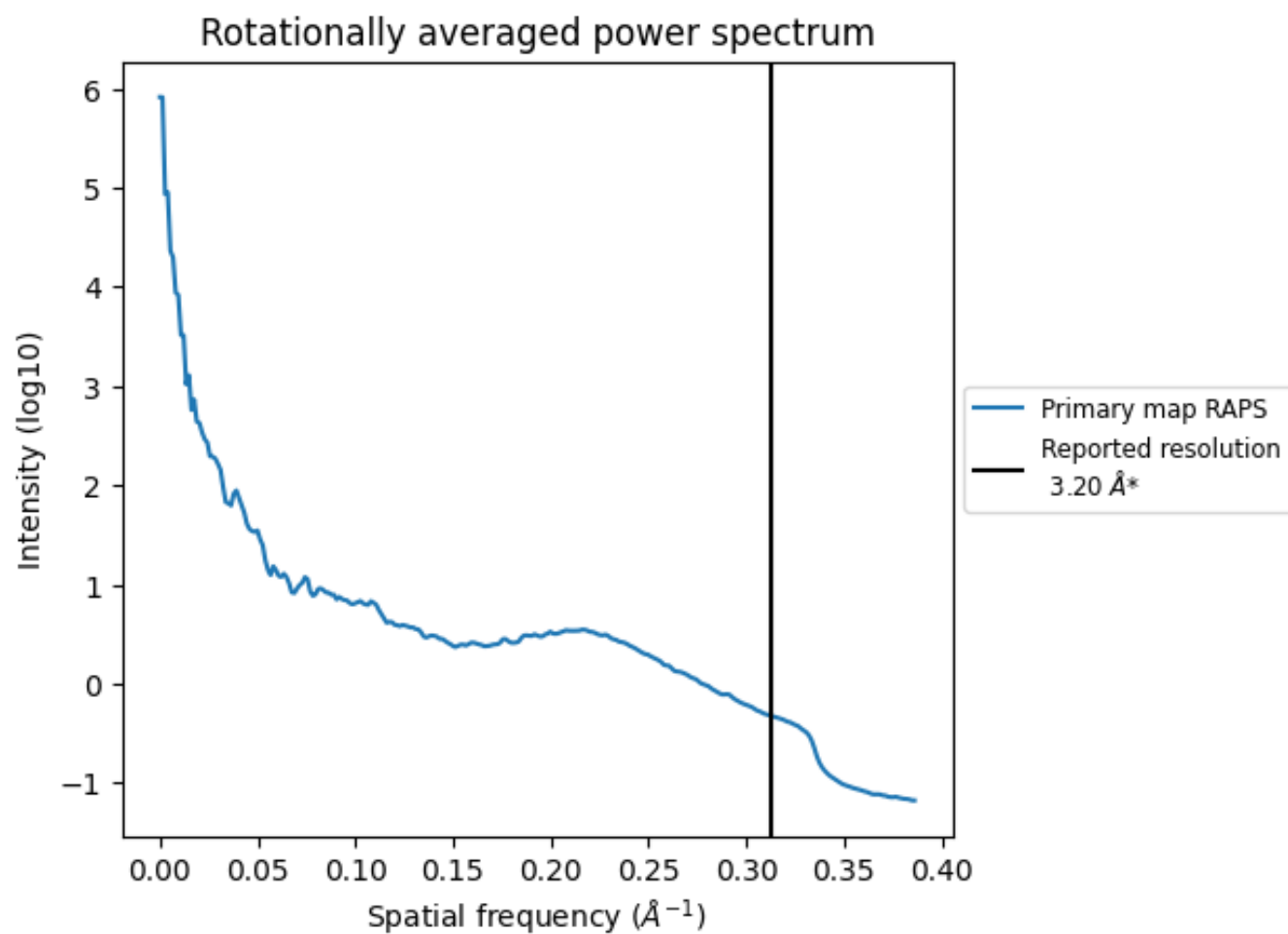
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 5075 nm^3 ; this corresponds to an approximate mass of 4584 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

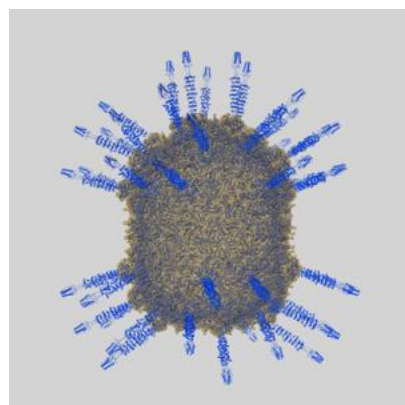
7 Fourier-Shell correlation

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

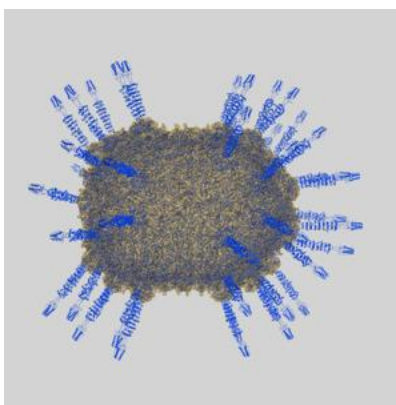
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4677 and PDB model 6QYD. Per-residue inclusion information can be found in section ?? on page ??.

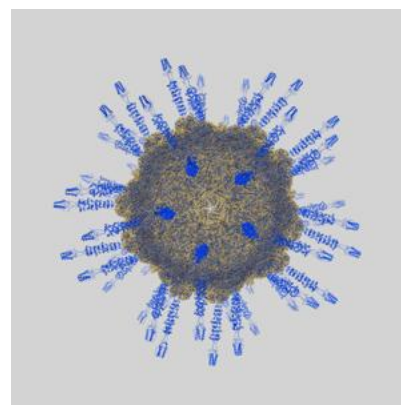
8.1 Map-model overlay [i](#)



X



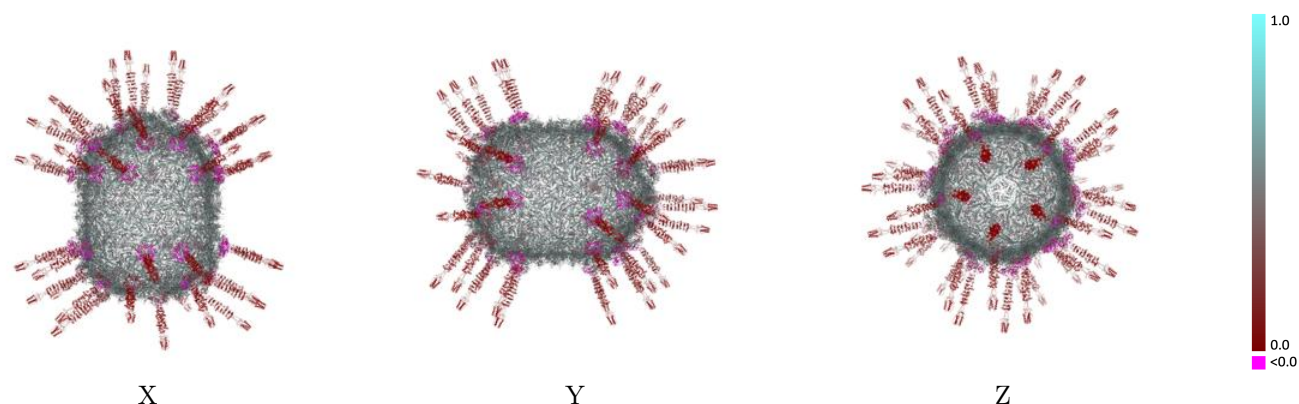
Y



Z

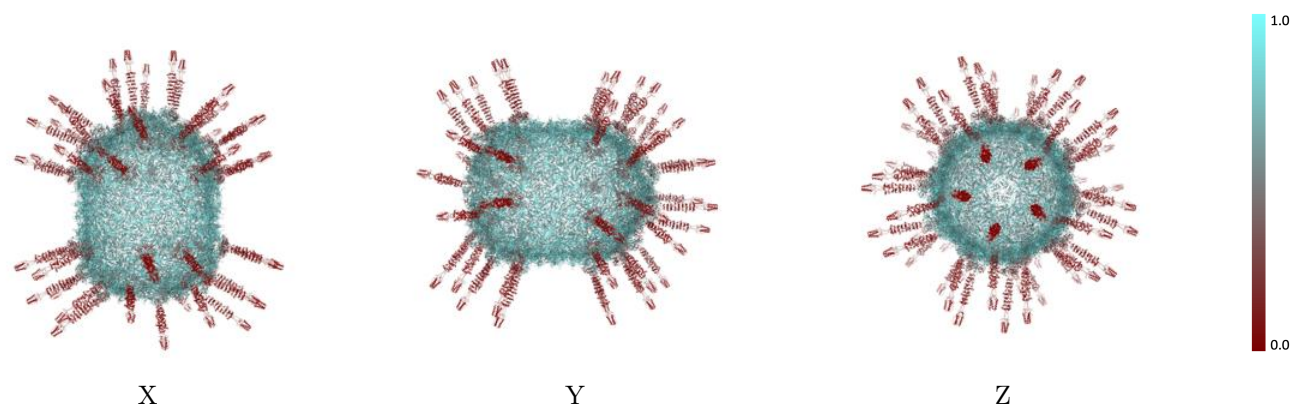
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



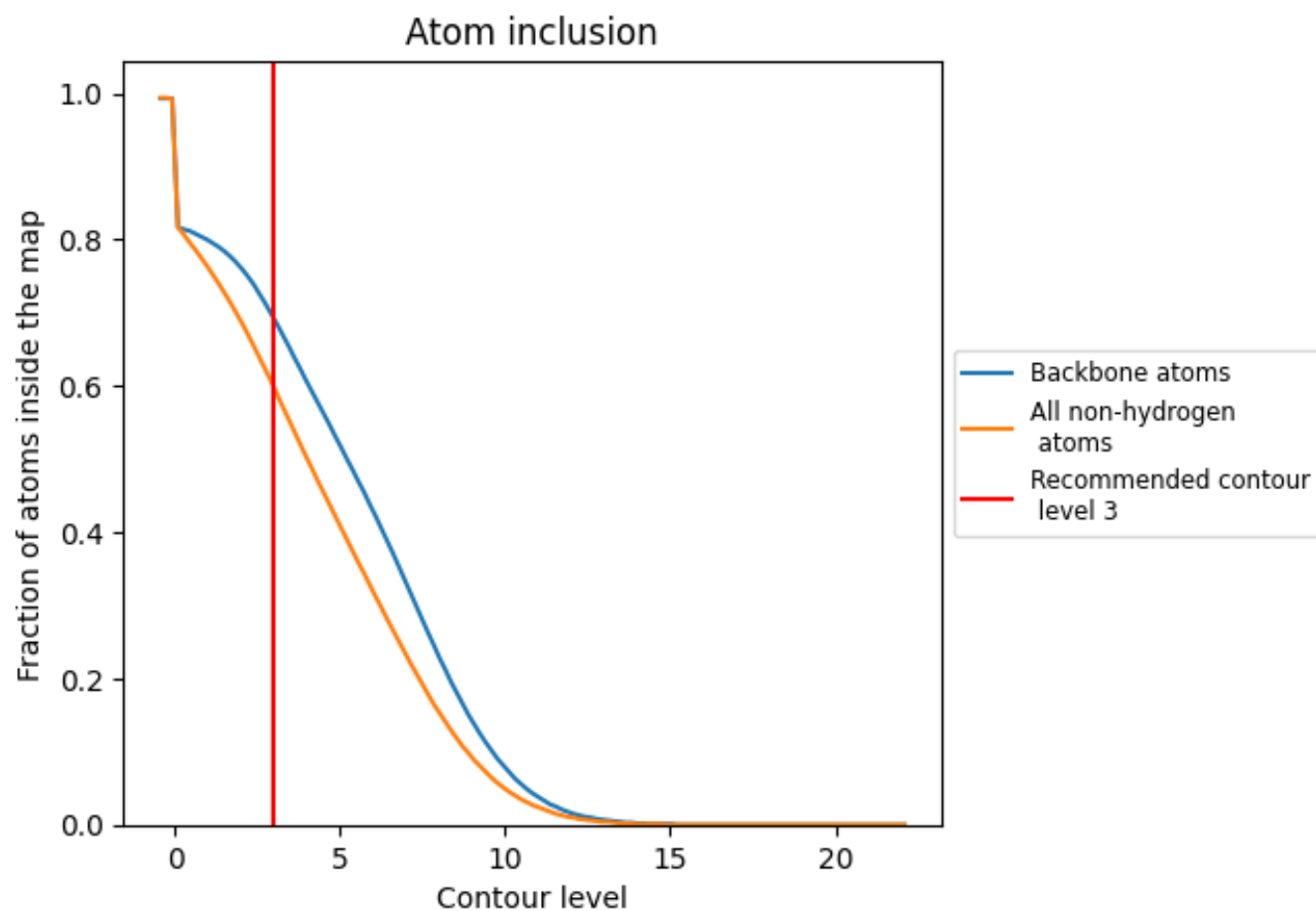
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

8.3 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 (3).

8.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5990	 0.3850
1A	 0.6600	 0.4900
1B	 0.7650	 0.5290
1C	 0.7690	 0.5280
1D	 0.7630	 0.5220
1E	 0.7420	 0.5230
1F	 0.7120	 0.5030
1G	 0.6460	 0.4800
1H	 0.7640	 0.5230
1I	 0.7670	 0.5200
1J	 0.7580	 0.5120
1K	 0.7360	 0.5140
1L	 0.7070	 0.4960
1M	 0.6480	 0.4790
1N	 0.7590	 0.5220
1O	 0.7670	 0.5190
1P	 0.7600	 0.5150
1Q	 0.7340	 0.5150
1R	 0.7120	 0.4980
1S	 0.6500	 0.4800
1T	 0.7620	 0.5220
1U	 0.7640	 0.5200
1V	 0.7580	 0.5140
1W	 0.7380	 0.5140
1X	 0.7120	 0.4960
1Y	 0.6540	 0.4800
1Z	 0.7600	 0.5220
1a	 0.7640	 0.5200
1b	 0.7540	 0.5150
1c	 0.7350	 0.5150
1d	 0.7090	 0.4980
1e	 0.2640	 0.1710
1f	 0.2900	 0.1880
1g	 0.2660	 0.1670
1h	 0.2740	 0.1730



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Chain	Atom inclusion	Q-score
1i	0.1970	0.0850
1j	0.2150	0.0910
1k	0.2190	0.1000
1l	0.2160	0.0970
1m	0.2000	0.0870
1n	0.2120	0.0890
1o	0.2180	0.0990
1p	0.2150	0.0930
1q	0.1960	0.0840
1r	0.2100	0.0860
1s	0.2130	0.0930
1t	0.2030	0.0850
1u	0.1980	0.0850
1v	0.2170	0.0920
1w	0.2170	0.0990
1x	0.2110	0.0920
2A	0.7870	0.5360
2B	0.7960	0.5340
2C	0.8050	0.5380
2D	0.7730	0.5340
2E	0.7790	0.5310
2F	0.7810	0.5270
2G	0.7860	0.5250
2H	0.7940	0.5300
2I	0.7720	0.5260
2J	0.7730	0.5230
2K	0.7830	0.5260
2L	0.7850	0.5250
2M	0.7960	0.5280
2N	0.7710	0.5270
2O	0.7710	0.5200
2P	0.7790	0.5270
2Q	0.7850	0.5250
2R	0.7980	0.5280
2S	0.7710	0.5270
2T	0.7720	0.5210
2U	0.7780	0.5240
2V	0.7850	0.5210
2W	0.7940	0.5270
2X	0.7670	0.5270
2Y	0.7720	0.5200
2Z	0.2920	0.1950

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Chain	Atom inclusion	Q-score
2a	 0.2900	 0.1830
2b	 0.2890	 0.1730
2c	 0.2720	 0.1730
2d	 0.2760	 0.1750
2e	 0.1900	 0.0700
2f	 0.1180	 -0.0060
2g	 0.0980	 -0.0180
2h	 0.1040	 -0.0180
2i	 0.2290	 0.1100
2j	 0.1910	 0.0680
2k	 0.1180	 -0.0050
2l	 0.0990	 -0.0180
2m	 0.1020	 -0.0190
2n	 0.2300	 0.1120
2o	 0.1800	 0.0640
2p	 0.1080	 -0.0090
2q	 0.0960	 -0.0190
2r	 0.1010	 -0.0210
2s	 0.2250	 0.1070
2t	 0.1910	 0.0730
2u	 0.1170	 -0.0010
2v	 0.1000	 -0.0190
2w	 0.1070	 -0.0180
2x	 0.2270	 0.1090
3A	 0.7960	 0.5220
3B	 0.7840	 0.5160
3C	 0.8010	 0.5290
3D	 0.7930	 0.5260
3E	 0.7830	 0.5260
3F	 0.7920	 0.5310
3G	 0.7870	 0.5110
3H	 0.7820	 0.5070
3I	 0.7890	 0.5190
3J	 0.7860	 0.5160
3K	 0.7780	 0.5180
3L	 0.7890	 0.5210
3M	 0.7850	 0.5090
3N	 0.7800	 0.5080
3O	 0.7920	 0.5200
3P	 0.7870	 0.5160
3Q	 0.7790	 0.5200
3R	 0.7870	 0.5210

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Chain	Atom inclusion	Q-score
3S	 0.7880	 0.5120
3T	 0.7830	 0.5100
3U	 0.7950	 0.5220
3V	 0.7930	 0.5190
3W	 0.7820	 0.5190
3X	 0.7850	 0.5200
3Y	 0.7930	 0.5080
3Z	 0.7760	 0.5050
3a	 0.7900	 0.5170
3b	 0.7870	 0.5170
3c	 0.7770	 0.5180
3d	 0.7840	 0.5160
3e	 0.2780	 0.1720
3f	 0.2770	 0.1790
3g	 0.2570	 0.1360
3h	 0.2640	 0.1470
3i	 0.1240	 0.0080
3j	 0.2050	 0.0940
3k	 0.1820	 0.0530
3l	 0.1390	 0.0240
3m	 0.1250	 0.0060
3n	 0.2010	 0.0910
3o	 0.1730	 0.0480
3p	 0.1350	 0.0220
3q	 0.1220	 0.0040
3r	 0.1970	 0.0870
3s	 0.1640	 0.0390
3t	 0.1290	 0.0180
3u	 0.1270	 0.0110
3v	 0.2060	 0.0940
3w	 0.1680	 0.0400
3x	 0.1290	 0.0160
4A	 0.8050	 0.5330
4B	 0.7960	 0.5160
4C	 0.7950	 0.5200
4D	 0.8080	 0.5270
4E	 0.7880	 0.5240
4F	 0.7930	 0.5300
4G	 0.8020	 0.5240
4H	 0.7880	 0.5070
4I	 0.7900	 0.5110
4J	 0.8030	 0.5190

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Chain	Atom inclusion	Q-score
4K	 0.7890	 0.5150
4L	 0.7880	 0.5220
4M	 0.8060	 0.5250
4N	 0.7880	 0.5080
4O	 0.7850	 0.5120
4P	 0.8000	 0.5190
4Q	 0.7900	 0.5150
4R	 0.7870	 0.5190
4S	 0.8030	 0.5240
4T	 0.7930	 0.5080
4U	 0.7900	 0.5130
4V	 0.8050	 0.5190
4W	 0.7850	 0.5160
4X	 0.7870	 0.5200
4Y	 0.7990	 0.5210
4Z	 0.7880	 0.5010
4a	 0.7850	 0.5090
4b	 0.7980	 0.5110
4c	 0.7840	 0.5120
4d	 0.7890	 0.5180
4e	 0.2750	 0.1520
4f	 0.2710	 0.1580
4g	 0.1300	 0.0090
4h	 0.1090	 -0.0200
4i	 0.1320	 0.0100
4j	 0.1120	 -0.0210
4k	 0.1230	 0.0070
4l	 0.1110	 -0.0240
4m	 0.1320	 0.0140
4n	 0.1140	 -0.0190
5A	 0.8040	 0.5280
5B	 0.7980	 0.5150
5C	 0.7950	 0.5220
5D	 0.8050	 0.5270
5E	 0.7880	 0.5160
5F	 0.7990	 0.5280
5G	 0.8020	 0.5170
5H	 0.7900	 0.5060
5I	 0.7910	 0.5100
5J	 0.7960	 0.5180
5K	 0.7790	 0.5060
5L	 0.7890	 0.5170

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Chain	Atom inclusion	Q-score
5M	 0.8000	 0.5180
5N	 0.7940	 0.5060
5O	 0.7940	 0.5080
5P	 0.7940	 0.5170
5Q	 0.7770	 0.5050
5R	 0.7920	 0.5190
5S	 0.8030	 0.5210
5T	 0.7900	 0.5080
5U	 0.7920	 0.5110
5V	 0.7970	 0.5160
5W	 0.7790	 0.5060
5X	 0.7930	 0.5190
5Y	 0.7930	 0.5140
5Z	 0.7930	 0.5070
5a	 0.7900	 0.5090
5b	 0.8000	 0.5120
5c	 0.7750	 0.5010
5d	 0.7860	 0.5130
5e	 0.2640	 0.1560
5f	 0.2780	 0.1690
5g	 0.1310	 0.0140
5h	 0.1270	 0.0100
5i	 0.1340	 0.0150
5j	 0.1360	 0.0140
5k	 0.1340	 0.0150
5l	 0.1270	 0.0110
5m	 0.1430	 0.0250
5n	 0.1290	 0.0130
6A	 0.7960	 0.5320
6B	 0.7930	 0.5330
6C	 0.7920	 0.5210
6D	 0.7950	 0.5200
6E	 0.8020	 0.5250
6F	 0.7960	 0.5310
6G	 0.7910	 0.5240
6H	 0.7900	 0.5230
6I	 0.7860	 0.5100
6J	 0.7900	 0.5120
6K	 0.7970	 0.5160
6L	 0.7930	 0.5210
6M	 0.7850	 0.5250
6N	 0.7820	 0.5230

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Chain	Atom inclusion	Q-score
6O	 0.7870	 0.5110
6P	 0.7890	 0.5130
6Q	 0.7980	 0.5180
6R	 0.7910	 0.5220
6S	 0.7850	 0.5260
6T	 0.7890	 0.5250
6U	 0.7900	 0.5120
6V	 0.7880	 0.5140
6W	 0.7920	 0.5190
6X	 0.7930	 0.5220
6Y	 0.7770	 0.5130
6Z	 0.7770	 0.5130
6a	 0.7820	 0.5050
6b	 0.7930	 0.5060
6c	 0.7910	 0.5090
6d	 0.7850	 0.5100
6e	 0.2480	 0.1420
6f	 0.2730	 0.1550
6g	 0.2640	 0.1600
6h	 0.2740	 0.1640
6i	 0.0900	 -0.0180
6j	 0.0910	 -0.0200
6k	 0.1280	 0.0090
6l	 0.1420	 0.0360
6m	 0.0960	 -0.0210
6n	 0.0930	 -0.0240
6o	 0.1390	 0.0170
6p	 0.1530	 0.0400
6q	 0.0920	 -0.0210
6r	 0.0920	 -0.0240
6s	 0.1280	 0.0120
6t	 0.1510	 0.0420
6u	 0.1040	 -0.0100
6v	 0.0960	 -0.0190
6w	 0.1350	 0.0200
6x	 0.1720	 0.0580
7A	 0.7940	 0.5430
7B	 0.7780	 0.5380
7C	 0.7900	 0.5390
7D	 0.7900	 0.5390
7E	 0.7960	 0.5350
7F	 0.7830	 0.5340

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Chain	Atom inclusion	Q-score
7G	 0.7740	 0.5260
7H	 0.7850	 0.5240
7I	 0.7850	 0.5260
7J	 0.7860	 0.5250
7K	 0.7810	 0.5330
7L	 0.7680	 0.5270
7M	 0.7850	 0.5260
7N	 0.7800	 0.5260
7O	 0.7920	 0.5250
7P	 0.7840	 0.5360
7Q	 0.7690	 0.5300
7R	 0.7900	 0.5310
7S	 0.7830	 0.5280
7T	 0.7940	 0.5270
7U	 0.7810	 0.5250
7V	 0.7690	 0.5200
7W	 0.7790	 0.5250
7X	 0.7730	 0.5200
7Y	 0.7790	 0.5190
7Z	 0.2870	 0.1750
7a	 0.2650	 0.1630
7b	 0.2690	 0.1560
7c	 0.2760	 0.1740
7d	 0.2840	 0.1700
7e	 0.1210	 -0.0060
7f	 0.1460	 0.0350
7g	 0.1170	 0.0010
7h	 0.1860	 0.0710
7i	 0.1250	 0.0080
7j	 0.1270	 0.0050
7k	 0.1620	 0.0460
7l	 0.1310	 0.0130
7m	 0.2060	 0.0850
7n	 0.1280	 0.0100
7o	 0.1220	 -0.0050
7p	 0.1470	 0.0350
7q	 0.1270	 0.0070
7r	 0.2060	 0.0830
7s	 0.1260	 0.0080
7t	 0.1210	 -0.0050
7u	 0.1290	 0.0220
7v	 0.1350	 0.0170

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Chain	Atom inclusion	Q-score
7w	 0.2010	 0.0880
7x	 0.1360	 0.0190
8A	 0.7530	 0.5280
8B	 0.7580	 0.5340
8C	 0.7750	 0.5280
8D	 0.7730	 0.5330
8E	 0.7770	 0.5360
8F	 0.7590	 0.5290
8G	 0.7440	 0.5100
8H	 0.7580	 0.5170
8I	 0.7680	 0.5170
8J	 0.7610	 0.5210
8K	 0.7630	 0.5200
8L	 0.7510	 0.5130
8M	 0.7490	 0.5180
8N	 0.7570	 0.5220
8O	 0.7710	 0.5180
8P	 0.7670	 0.5230
8Q	 0.7650	 0.5260
8R	 0.7510	 0.5200
8S	 0.7480	 0.5200
8T	 0.7590	 0.5230
8U	 0.7690	 0.5200
8V	 0.7690	 0.5240
8W	 0.7670	 0.5240
8X	 0.7500	 0.5200
8Y	 0.7350	 0.5080
8Z	 0.7420	 0.5140
8a	 0.7570	 0.5100
8b	 0.7590	 0.5100
8c	 0.7620	 0.5130
8d	 0.7440	 0.5060
8e	 0.2540	 0.1630
8f	 0.2440	 0.1410
8g	 0.2530	 0.1610
8h	 0.2550	 0.1470
8i	 0.2410	 0.1380
8j	 0.2620	 0.1550
8k	 0.2510	 0.1600
8l	 0.2160	 0.1160
8m	 0.1390	 0.0430
8n	 0.0960	 -0.0200

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Chain	Atom inclusion	Q-score
8o	 0.1100	 -0.0000
8p	 0.1370	 0.0300
8q	 0.2520	 0.1600
8r	 0.2300	 0.1280
8s	 0.1290	 0.0310
8t	 0.0980	 -0.0210
8u	 0.1100	 0.0010
8v	 0.1570	 0.0420
8w	 0.2500	 0.1640
8x	 0.2250	 0.1250
8y	 0.1330	 0.0330
8z	 0.0980	 -0.0190
9A	 0.7470	 0.5330
9B	 0.7300	 0.5090
9C	 0.7390	 0.5170
9D	 0.7430	 0.5220
9E	 0.7290	 0.5140
9F	 0.2470	 0.1510
9G	 0.2570	 0.1640
9H	 0.2610	 0.1670
9I	 0.2590	 0.1720
9J	 0.2570	 0.1760
9K	 0.1090	 0.0020
9L	 0.1510	 0.0370
9M	 0.2520	 0.1630
9N	 0.2140	 0.1100
9O	 0.1540	 0.0640
9P	 0.1210	 0.0080
9Q	 0.1290	 0.0220
9R	 0.1680	 0.0500