WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB EM Validation Report ⓘ

Jan 29, 2024 – 12:45 PM EST

PDB ID	:	8VGR
EMDB ID	:	EMD-43222
Title	:	Cryo-EM structure of Tulane virus 9-6-17 variant capsid protein VP1 5-12-18
Authors	:	Sun, C.; Jiang, W.
Deposited on	:	2023-12-27
Resolution	:	3.20 Å(reported)
Based on initial model	:	8VG6

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

|		
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.20 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	Percentile Ranks	Value
Clashscore		14
Ramachandran outliers		0.2%
Sidechain outliers		9.0%

Worse   *Better*

■ Percentile relative to all structures

▯ Percentile relative to all EM structures
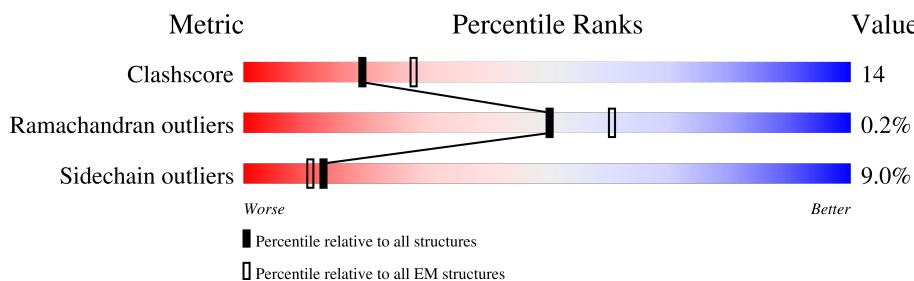
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	A	534	23% 62% 30% • 5%
1	B	534	21% 67% 26% • 5%
1	C	534	33% 72% 22% • •
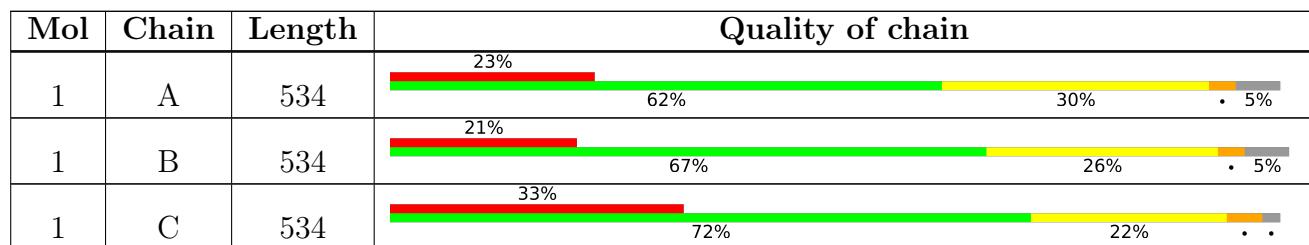
2 Entry composition ⓘ

There is only 1 type of molecule in this entry. The entry contains 23289 atoms, of which 11493 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 Capsid protein.

| Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	508	Total	C	H	N	O	S	0	0
			7685	2510	3792	626	740	17		
1	B	508	Total	C	H	N	O	S	0	0
			7685	2510	3792	626	740	17		
1	C	525	Total	C	H	N	O	S	0	0
			7919	2578	3909	646	769	17		

There are 24 discrepancies between the modelled and reference sequences:

| Chain	Residue	Modelled	Actual	Comment	Reference
A	3	SER	ASN	conflict	UNP B2Y6D0
A	284	HIS	ASN	conflict	UNP B2Y6D0
A	334	VAL	PHE	conflict	UNP B2Y6D0
A	335	GLU	ALA	conflict	UNP B2Y6D0
A	343	THR	ALA	conflict	UNP B2Y6D0
A	367	LYS	SER	conflict	UNP B2Y6D0
A	451	MET	ILE	conflict	UNP B2Y6D0
A	452	CYS	ARG	conflict	UNP B2Y6D0
B	3	SER	ASN	conflict	UNP B2Y6D0
B	284	HIS	ASN	conflict	UNP B2Y6D0
B	334	VAL	PHE	conflict	UNP B2Y6D0
B	335	GLU	ALA	conflict	UNP B2Y6D0
B	343	THR	ALA	conflict	UNP B2Y6D0
B	367	LYS	SER	conflict	UNP B2Y6D0
B	451	MET	ILE	conflict	UNP B2Y6D0
B	452	CYS	ARG	conflict	UNP B2Y6D0
C	3	SER	ASN	conflict	UNP B2Y6D0
C	284	HIS	ASN	conflict	UNP B2Y6D0
C	334	VAL	PHE	conflict	UNP B2Y6D0
C	335	GLU	ALA	conflict	UNP B2Y6D0
C	343	THR	ALA	conflict	UNP B2Y6D0
C	367	LYS	SER	conflict	UNP B2Y6D0
C	451	MET	ILE	conflict	UNP B2Y6D0
C	452	CYS	ARG	conflict	UNP B2Y6D0

3   Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Capsid protein

Chain A:

- Molecule 1: Capsid protein

Chain B:

● Molecule 1: Capsid protein

Chain C:
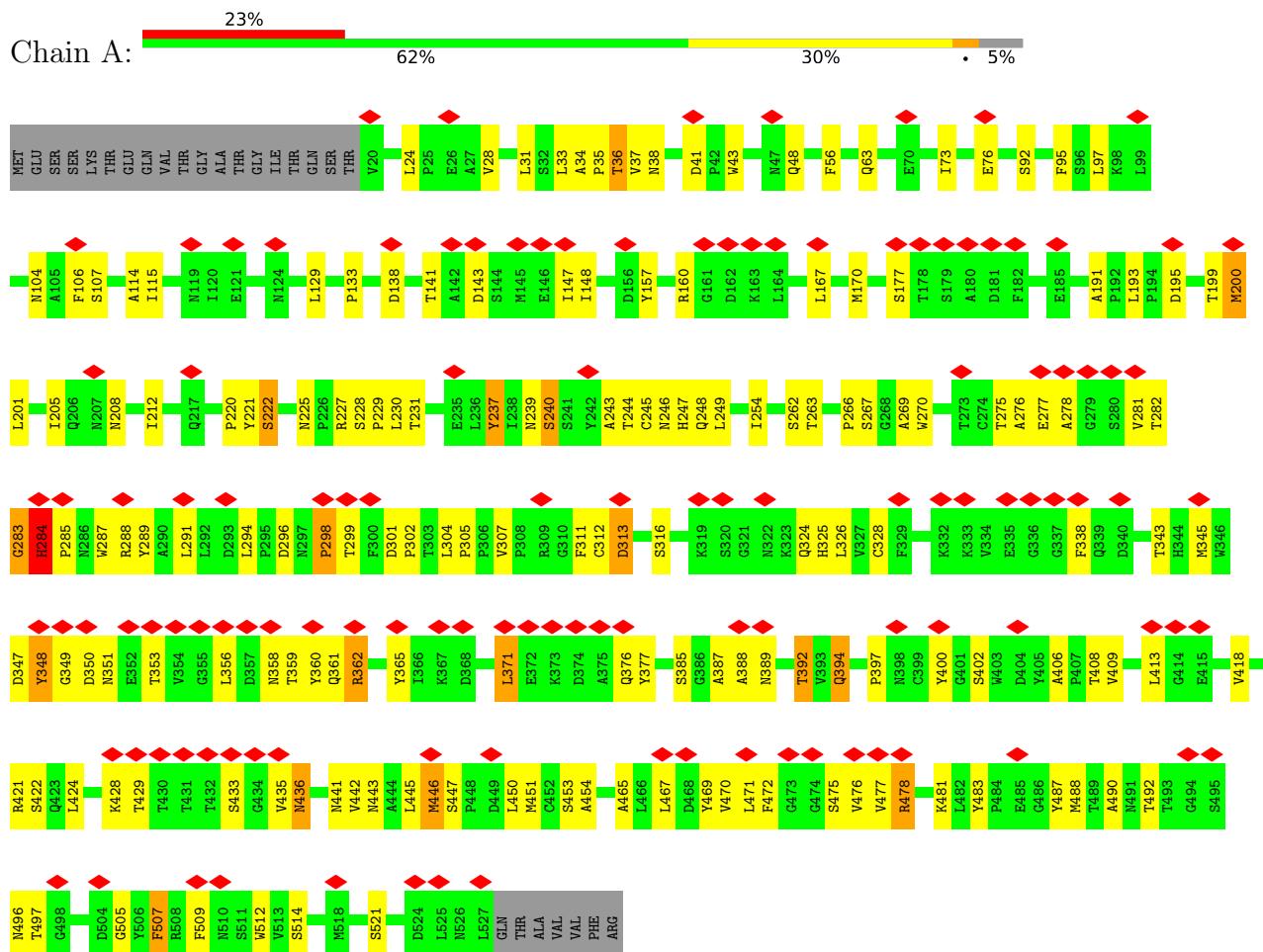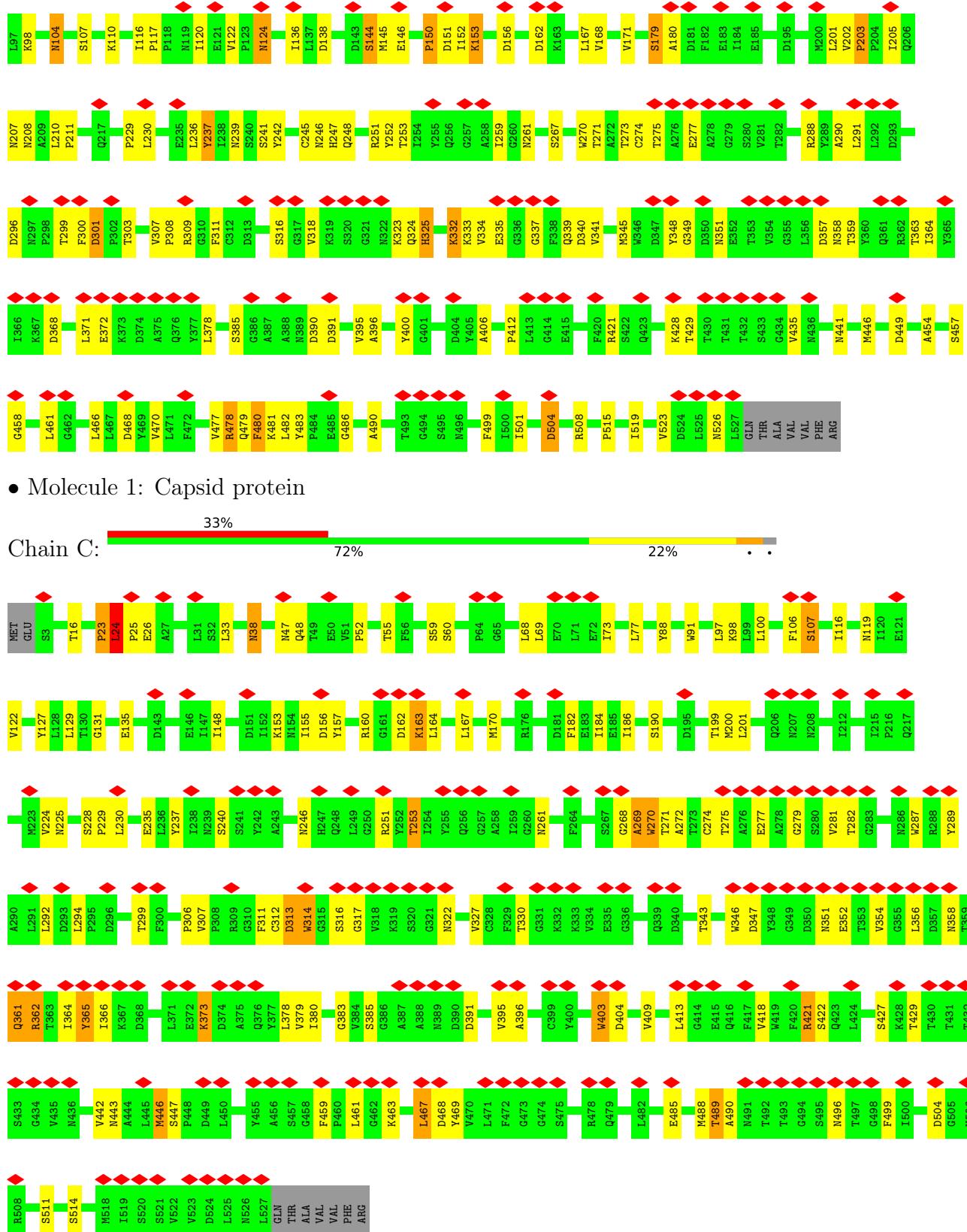
4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	11645	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	23	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	30.846	Depositor
Minimum map value	-20.036	Depositor
Average map value	-0.115	Depositor
Map value standard deviation	2.063	Depositor
Recommended contour level	8.0	Depositor
Map size (Å)	622.8, 622.8, 622.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2975, 1.2975, 1.2975	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.30	0/4011	0.54	3/5502 (0.1%)
1	B	0.31	0/4011	0.53	2/5502 (0.0%)
1	C	0.30	0/4128	0.54	2/5661 (0.0%)
All	All	0.30	0/12150	0.54	7/16665 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	4
All	All	0	5

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	76	GLU	C-N-CA	8.03	141.76	121.70
1	B	150	PRO	CA-N-CD	-7.09	101.57	111.50
1	B	124	ASN	C-N-CA	6.70	138.45	121.70
1	C	274	CYS	C-N-CA	5.87	136.37	121.70
1	A	298	PRO	C-N-CA	5.80	136.19	121.70
1	A	360	TYR	C-N-CA	5.79	136.18	121.70
1	C	361	GLN	C-N-CA	5.46	135.36	121.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	284	HIS	Peptide

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Mol	Chain	Res	Type	Group
1	C	23	PRO	Peptide
1	C	24	LEU	Peptide
1	C	269	ALA	Peptide
1	C	313	ASP	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3893	3792	3791	142	0
1	B	3893	3792	3791	99	0
1	C	4010	3909	3908	100	0
All	All	11796	11493	11490	326	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 14.

All (326) 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:C:312:CYS:SG	1:C:360:TYR:OH	2.24	0.94
1:C:282:THR:OG1	1:C:352:GLU:OE1	1.91	0.86
1:C:162:ASP:OD1	1:C:163:LYS:N	2.12	0.83
1:A:299:THR:OG1	1:A:305:PRO:O	1.97	0.81
1:A:160:ARG:O	1:C:119:ASN:ND2	2.15	0.79
1:C:312:CYS:HG	1:C:360:TYR:HH	1.20	0.75
1:A:282:THR:HG22	1:A:284:HIS:H	1.54	0.73
1:C:116:ILE:HD13	1:C:122:VAL:HG22	1.71	0.73
1:B:104:ASN:OD1	1:B:107:SER:OG	2.07	0.72
1:B:211:PRO:O	1:C:127:TYR:OH	2.06	0.72
1:A:446:MET:O	1:A:447:SER:OG	2.07	0.72
1:A:239:ASN:ND2	1:A:497:THR:O	2.22	0.71
1:B:340:ASP:OD1	1:B:341:VAL:N	2.23	0.71
1:A:467:LEU:HD13	1:A:509:PHE:CE1	2.26	0.71
1:C:261:ASN:ND2	1:C:307:VAL:HG23	2.06	0.69
1:B:390:ASP:OD1	1:B:441:ASN:N	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ASP:O	1:A:299:THR:N	2.25	0.69
1:A:245:CYS:SG	1:A:445:LEU:HD22	2.33	0.68
1:C:314:TRP:CH2	1:C:442:VAL:HG21	2.29	0.67
1:B:98:LYS:NZ	1:B:146:GLU:OE2	2.22	0.67
1:A:450:LEU:HD22	1:A:507:PHE:CZ	2.29	0.67
1:A:291:LEU:HD13	1:A:362:ARG:NH1	2.09	0.66
1:B:345:MET:CG	1:B:435:VAL:HG21	2.26	0.66
1:A:73:ILE:O	1:A:73:ILE:HG22	1.96	0.65
1:A:231:THR:HG21	1:A:424:LEU:HD12	1.79	0.64
1:B:345:MET:HG3	1:B:435:VAL:HG21	1.79	0.64
1:C:261:ASN:HD22	1:C:307:VAL:HG23	1.59	0.64
1:B:116:ILE:HD12	1:B:116:ILE:O	1.97	0.64
1:A:467:LEU:HD11	1:A:507:PHE:HB2	1.79	0.63
1:A:475:SER:O	1:A:477:VAL:HG13	1.98	0.63
1:C:157:TYR:CD1	1:C:199:THR:HG21	2.34	0.63
1:A:35:PRO:HB3	1:C:25:PRO:HB3	1.80	0.62
1:C:311:PHE:HE2	1:C:379:VAL:HG11	1.63	0.62
1:C:307:VAL:HG21	1:C:360:TYR:HD2	1.64	0.62
1:B:80:TYR:OH	1:C:131:GLY:O	2.17	0.62
1:A:481:LYS:NZ	1:A:483:TYR:OH	2.34	0.61
1:C:73:ILE:HA	1:C:77:LEU:HD11	1.82	0.61
1:B:208:ASN:ND2	1:B:208:ASN:O	2.33	0.61
1:B:239:ASN:OD1	1:B:241:SER:OG	2.13	0.61
1:C:251:ARG:HH22	1:C:409:VAL:HG23	1.65	0.61
1:A:245:CYS:SG	1:A:247:HIS:NE2	2.73	0.61
1:C:322:ASN:ND2	1:C:351:ASN:OD1	2.33	0.60
1:A:129:LEU:HD12	1:A:170:MET:HE2	1.82	0.60
1:C:307:VAL:HG21	1:C:360:TYR:CD2	2.36	0.60
1:B:46:LEU:O	1:B:46:LEU:HD12	2.01	0.60
1:A:254:ILE:HD11	1:A:454:ALA:HB1	1.84	0.60
1:B:150:PRO:HD2	1:B:150:PRO:O	2.01	0.60
1:B:325:HIS:NE2	1:B:345:MET:SD	2.75	0.60
1:C:330:THR:HG1	1:C:346:TRP:HZ2	1.49	0.60
1:A:97:LEU:HD13	1:A:167:LEU:HD22	1.84	0.59
1:B:41:ASP:HB3	1:B:44:VAL:HG23	1.84	0.59
1:A:296:ASP:O	1:A:299:THR:HG22	2.03	0.59
1:C:373:LYS:O	1:C:373:LYS:NZ	2.26	0.59
1:A:281:VAL:HG13	1:A:287:TRP:O	2.02	0.59
1:B:323:LYS:NZ	1:B:324:GLN:O	2.36	0.58
1:C:292:LEU:CD2	1:C:364:ILE:HD11	2.33	0.58
1:A:177:SER:OG	1:A:177:SER:O	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:PRO:O	1:A:402:SER:OG	2.21	0.58
1:A:435:VAL:HG13	1:A:435:VAL:O	2.04	0.58
1:A:418:VAL:O	1:A:418:VAL:HG13	2.04	0.58
1:B:301:ASP:OD1	1:B:301:ASP:N	2.37	0.57
1:A:28:VAL:HG13	1:A:195:ASP:OD1	2.04	0.57
1:B:271:THR:HG23	1:B:378:LEU:HD11	1.86	0.57
1:B:69:LEU:HD21	1:B:71:LEU:HD11	1.87	0.57
1:A:212:ILE:CG2	1:B:205:ILE:HD12	2.35	0.57
1:A:450:LEU:HD13	1:A:507:PHE:CE1	2.39	0.56
1:C:292:LEU:HD21	1:C:364:ILE:HD11	1.87	0.56
1:A:106:PHE:O	1:A:177:SER:OG	2.23	0.56
1:A:421:ARG:NH1	1:A:441:ASN:OD1	2.39	0.56
1:A:294:LEU:CB	1:A:299:THR:HG21	2.36	0.56
1:B:47:ASN:OD1	1:B:96:SER:OG	2.07	0.56
1:A:212:ILE:HG21	1:B:205:ILE:HD12	1.87	0.56
1:C:271:THR:HG22	1:C:380:ILE:HG12	1.87	0.56
1:C:59:SER:OG	1:C:60:SER:N	2.37	0.55
1:A:104:ASN:OD1	1:A:107:SER:OG	2.24	0.55
1:A:350:ASP:O	1:A:358:ASN:O	2.24	0.55
1:B:332:LYS:NZ	1:B:372:GLU:OE2	2.39	0.55
1:C:354:VAL:HB	1:C:356:LEU:HD12	1.89	0.55
1:C:446:MET:SD	1:C:446:MET:N	2.78	0.55
1:A:301:ASP:N	1:A:301:ASP:OD1	2.39	0.55
1:A:148:ILE:HG23	1:A:193:LEU:HD11	1.88	0.54
1:A:228:SER:HB2	1:A:442:VAL:HG11	1.89	0.54
1:C:292:LEU:HG	1:C:364:ILE:HD11	1.89	0.54
1:A:281:VAL:HG22	1:A:289:TYR:HD1	1.73	0.54
1:C:346:TRP:HE3	1:C:364:ILE:HG21	1.71	0.54
1:C:443:ASN:OD1	1:C:443:ASN:N	2.41	0.54
1:B:251:ARG:O	1:B:259:ILE:HG21	2.08	0.54
1:C:25:PRO:C	1:C:26:GLU:OE2	2.46	0.54
1:C:391:ASP:OD1	1:C:391:ASP:N	2.40	0.54
1:A:201:LEU:HD22	1:B:80:TYR:CE1	2.42	0.54
1:A:254:ILE:HD11	1:A:454:ALA:CB	2.37	0.54
1:A:239:ASN:OD1	1:A:240:SER:N	2.41	0.54
1:A:263:THR:HG21	1:A:269:ALA:CB	2.38	0.54
1:A:230:LEU:HD21	1:B:230:LEU:HD11	1.90	0.53
1:B:395:VAL:O	1:B:395:VAL:HG13	2.09	0.53
1:C:294:LEU:HD21	1:C:306:PRO:HA	1.89	0.53
1:B:117:PRO:HB2	1:B:120:ILE:HD13	1.90	0.53
1:A:467:LEU:HD13	1:A:509:PHE:CD1	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:TYR:CD2	1:A:471:LEU:HD21	2.44	0.52
1:C:88:TYR:O	1:C:160:ARG:NH2	2.42	0.52
1:A:38:ASN:ND2	1:A:199:THR:O	2.43	0.52
1:A:276:ALA:HB2	1:A:371:LEU:HD22	1.90	0.52
1:C:281:VAL:HG22	1:C:289:TYR:HE1	1.72	0.52
1:A:351:ASN:O	1:A:353:THR:N	2.42	0.52
1:C:33:LEU:HD12	1:C:156:ASP:OD2	2.09	0.52
1:C:292:LEU:CG	1:C:364:ILE:HD11	2.39	0.52
1:A:388:ALA:HA	1:A:389:ASN:CB	2.40	0.52
1:A:283:GLY:O	1:A:284:HIS:ND1	2.43	0.51
1:A:325:HIS:ND1	1:A:345:MET:SD	2.76	0.51
1:C:148:ILE:HG22	1:C:148:ILE:O	2.10	0.51
1:A:33:LEU:HD11	1:C:156:ASP:HA	1.93	0.51
1:A:294:LEU:HD12	1:A:362:ARG:HH21	1.76	0.51
1:B:290:ALA:HB3	1:B:364:ILE:HG13	1.93	0.51
1:A:35:PRO:CB	1:C:25:PRO:HB3	2.41	0.51
1:A:267:SER:OG	1:B:229:PRO:O	2.27	0.51
1:A:288:ARG:CB	1:A:371:LEU:HD12	2.41	0.50
1:A:31:LEU:HB3	1:A:34:ALA:HB3	1.92	0.50
1:B:248:GLN:OE1	1:B:406:ALA:N	2.40	0.50
1:A:446:MET:O	1:A:446:MET:SD	2.70	0.50
1:B:270:TRP:O	1:B:271:THR:OG1	2.23	0.50
1:C:91:TRP:HZ2	1:C:164:LEU:HD21	1.75	0.50
1:A:282:THR:C	1:A:284:HIS:N	2.65	0.50
1:A:467:LEU:HD13	1:A:509:PHE:CZ	2.46	0.50
1:A:496:ASN:C	1:A:496:ASN:OD1	2.50	0.50
1:A:291:LEU:HD13	1:A:362:ARG:HH12	1.74	0.50
1:C:235:GLU:OE1	1:C:421:ARG:NH1	2.45	0.50
1:B:454:ALA:O	1:B:458:GLY:N	2.40	0.50
1:C:24:LEU:O	1:C:26:GLU:OE2	2.29	0.50
1:A:48:GLN:HG2	1:A:191:ALA:HB2	1.94	0.49
1:C:314:TRP:CZ3	1:C:442:VAL:HG11	2.47	0.49
1:C:135:GLU:OE1	1:C:135:GLU:HA	2.12	0.49
1:C:446:MET:N	1:C:446:MET:HE3	2.27	0.49
1:A:104:ASN:OD1	1:A:104:ASN:N	2.45	0.49
1:B:334:VAL:O	1:B:337:GLY:N	2.39	0.49
1:A:281:VAL:HG22	1:A:289:TYR:CD1	2.48	0.49
1:A:288:ARG:HB2	1:A:371:LEU:HD12	1.93	0.49
1:A:470:VAL:HG13	1:A:476:VAL:HG22	1.93	0.49
1:B:446:MET:HE1	1:B:482:LEU:HD13	1.95	0.49
1:B:477:VAL:O	1:B:477:VAL:HG13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:224:VAL:HG23	1:C:225:ASN:CB	2.43	0.49
1:C:313:ASP:OD1	1:C:313:ASP:N	2.45	0.48
1:C:346:TRP:CH2	1:C:379:VAL:HG22	2.48	0.48
1:A:129:LEU:HD12	1:A:170:MET:CE	2.42	0.48
1:A:477:VAL:HG23	1:A:478:ARG:HD2	1.95	0.48
1:B:412:PRO:HG2	1:B:483:TYR:OH	2.13	0.48
1:B:86:ARG:NH1	1:B:208:ASN:O	2.47	0.48
1:C:489:THR:OG1	1:C:490:ALA:N	2.47	0.47
1:A:465:ALA:HB1	1:A:509:PHE:CD2	2.49	0.47
1:B:325:HIS:NE2	1:B:345:MET:CE	2.77	0.47
1:B:351:ASN:OD1	1:B:358:ASN:ND2	2.48	0.47
1:B:72:GLU:OE1	1:B:461:LEU:HD13	2.13	0.47
1:B:481:LYS:CG	1:B:519:ILE:HD11	2.44	0.47
1:B:120:ILE:HD12	1:B:120:ILE:N	2.28	0.47
1:C:23:PRO:O	1:C:25:PRO:CD	2.62	0.47
1:C:281:VAL:HG21	1:C:287:TRP:O	2.14	0.47
1:A:249:LEU:HD13	1:A:311:PHE:O	2.14	0.47
1:A:313:ASP:OD1	1:A:313:ASP:C	2.53	0.47
1:A:409:VAL:HG21	1:A:487:TYR:CE2	2.50	0.47
1:B:470:VAL:O	1:B:470:VAL:HG12	2.15	0.47
1:B:237:TYR:HH	1:B:242:TYR:HE1	1.59	0.47
1:C:314:TRP:CH2	1:C:442:VAL:HG11	2.50	0.47
1:A:349:GLY:O	1:A:365:TYR:CZ	2.68	0.47
1:A:277:GLU:O	1:A:278:ALA:HB3	2.14	0.47
1:B:104:ASN:HA	1:C:107:SER:O	2.15	0.47
1:B:124:ASN:OD1	1:B:124:ASN:N	2.48	0.47
1:B:245:CYS:HG	1:B:247:HIS:CE1	2.33	0.47
1:A:326:LEU:HD12	1:A:326:LEU:H	1.79	0.47
1:A:35:PRO:O	1:A:36:THR:C	2.53	0.47
1:C:26:GLU:O	1:C:26:GLU:HG2	2.15	0.47
1:A:472:PHE:N	1:A:472:PHE:CD1	2.83	0.46
1:C:316:SER:OG	1:C:317:GLY:N	2.47	0.46
1:C:467:LEU:HD12	1:C:467:LEU:O	2.15	0.46
1:A:294:LEU:HB3	1:A:299:THR:HG21	1.97	0.46
1:B:146:GLU:HA	1:B:146:GLU:OE1	2.13	0.46
1:B:368:ASP:O	1:B:371:LEU:HD13	2.16	0.46
1:B:429:THR:HG21	1:B:435:VAL:N	2.31	0.46
1:C:88:TYR:HA	1:C:200:MET:O	2.15	0.46
1:C:327:VAL:N	1:C:383:GLY:O	2.46	0.46
1:C:395:VAL:HG12	1:C:396:ALA:H	1.80	0.46
1:A:343:THR:O	1:A:435:VAL:HG11	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:468:ASP:OD2	1:B:508:ARG:NH2	2.49	0.46
1:B:261:ASN:OD1	1:B:307:VAL:HG23	2.16	0.46
1:B:299:THR:HG22	1:B:300:PHE:N	2.31	0.46
1:A:394:GLN:O	1:A:394:GLN:OE1	2.34	0.46
1:C:299:THR:OG1	1:C:362:ARG:NH1	2.45	0.46
1:A:73:ILE:O	1:A:73:ILE:CG2	2.64	0.46
1:A:222:SER:O	1:A:222:SER:OG	2.30	0.46
1:B:504:ASP:OD1	1:B:504:ASP:N	2.48	0.46
1:C:421:ARG:O	1:C:422:SER:OG	2.32	0.45
1:A:307:VAL:HB	1:A:361:GLN:HB3	1.99	0.45
1:A:433:SER:HB2	1:A:435:VAL:HG12	1.97	0.45
1:B:371:LEU:HD12	1:B:371:LEU:N	2.30	0.45
1:A:450:LEU:HD13	1:A:507:PHE:HE1	1.79	0.45
1:A:467:LEU:CD1	1:A:507:PHE:HB2	2.47	0.45
1:A:114:ALA:CB	1:A:129:LEU:HD22	2.46	0.45
1:A:208:ASN:C	1:A:208:ASN:OD1	2.53	0.45
1:A:263:THR:HG21	1:A:269:ALA:HB3	1.98	0.45
1:A:358:ASN:O	1:A:359:THR:HB	2.17	0.45
1:A:477:VAL:C	1:A:478:ARG:HD2	2.38	0.45
1:A:481:LYS:O	1:A:488:MET:HA	2.17	0.45
1:B:151:ASP:OD2	1:B:153:LYS:HE2	2.17	0.45
1:B:207:ASN:O	1:B:208:ASN:HB3	2.16	0.45
1:B:237:TYR:HA	1:B:499:PHE:O	2.17	0.45
1:C:68:LEU:O	1:C:69:LEU:HD12	2.16	0.45
1:A:283:GLY:HA3	1:A:287:TRP:H	1.82	0.44
1:B:171:VAL:HG23	1:B:171:VAL:O	2.17	0.44
1:A:243:ALA:O	1:A:244:THR:HG23	2.17	0.44
1:A:445:LEU:HD21	1:A:487:TYR:HB3	1.99	0.44
1:A:470:VAL:HG22	1:A:476:VAL:HG22	1.98	0.44
1:B:179:SER:OG	1:B:180:ALA:N	2.49	0.44
1:B:251:ARG:CZ	1:B:406:ALA:HB1	2.46	0.44
1:C:272:ALA:O	1:C:379:VAL:N	2.49	0.44
1:C:378:LEU:HD13	1:C:379:VAL:N	2.32	0.44
1:B:116:ILE:HD12	1:B:116:ILE:C	2.37	0.44
1:B:357:ASP:O	1:B:359:THR:HG23	2.17	0.44
1:A:41:ASP:OD1	1:A:43:TRP:N	2.46	0.44
1:A:316:SER:HA	1:A:392:THR:HG22	1.98	0.44
1:A:313:ASP:OD1	1:A:313:ASP:O	2.35	0.44
1:B:333:LYS:NZ	1:B:339:GLN:OE1	2.50	0.44
1:A:228:SER:CB	1:A:442:VAL:HG11	2.47	0.44
1:A:294:LEU:HB2	1:A:299:THR:HG21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:LEU:HD12	1:B:211:PRO:HB2	2.00	0.44
1:C:269:ALA:O	1:C:270:TRP:C	2.56	0.44
1:A:298:PRO:O	1:A:301:ASP:OD1	2.36	0.43
1:B:64:PRO:HA	1:B:171:VAL:HG23	1.99	0.43
1:B:466:LEU:HD11	1:B:479:GLN:HB3	2.00	0.43
1:B:480:PHE:CD2	1:B:490:ALA:HB2	2.53	0.43
1:A:296:ASP:O	1:A:299:THR:CB	2.67	0.43
1:C:224:VAL:HG23	1:C:225:ASN:HB2	2.00	0.43
1:C:275:THR:O	1:C:277:GLU:N	2.46	0.43
1:C:287:TRP:HA	1:C:366:ILE:O	2.18	0.43
1:C:184:ILE:HG22	1:C:186:ILE:HG12	2.00	0.43
1:C:347:ASP:HB3	1:C:365:TYR:CD2	2.54	0.43
1:A:138:ASP:HB3	1:A:141:THR:HG23	2.01	0.43
1:A:225:ASN:OD1	1:A:227:ARG:N	2.50	0.43
1:B:345:MET:HG2	1:B:435:VAL:HG21	2.00	0.43
1:A:465:ALA:HB2	1:A:512:TRP:CZ3	2.54	0.43
1:B:291:LEU:HD13	1:B:363:THR:HG22	1.99	0.43
1:B:316:SER:O	1:B:318:VAL:HG23	2.19	0.43
1:C:313:ASP:HA	1:C:314:TRP:O	2.18	0.43
1:A:24:LEU:HD13	1:A:133:PRO:CG	2.49	0.43
1:A:471:LEU:HB3	1:A:472:PHE:CD1	2.54	0.43
1:C:38:ASN:OD1	1:C:38:ASN:N	2.51	0.43
1:C:52:PRO:O	1:C:463:LYS:NZ	2.48	0.43
1:A:114:ALA:HB3	1:A:129:LEU:HD22	2.01	0.43
1:A:248:GLN:HB3	1:A:406:ALA:HB3	2.00	0.43
1:C:91:TRP:CZ2	1:C:164:LEU:HD21	2.53	0.43
1:C:129:LEU:HD13	1:C:170:MET:HE3	2.01	0.43
1:A:229:PRO:HB3	1:A:266:PRO:O	2.19	0.42
1:A:115:ILE:HD11	1:A:147:ILE:HD11	2.01	0.42
1:C:279:GLY:O	1:C:281:VAL:HG23	2.19	0.42
1:A:388:ALA:HA	1:A:389:ASN:HB3	2.01	0.42
1:B:37:VAL:HG13	1:B:37:VAL:O	2.20	0.42
1:B:122:VAL:CG2	1:B:168:VAL:HG21	2.49	0.42
1:B:246:ASN:ND2	1:B:396:ALA:O	2.52	0.42
1:B:122:VAL:HG13	1:B:122:VAL:O	2.20	0.42
1:B:152:ILE:N	1:B:152:ILE:HD12	2.35	0.42
1:B:156:ASP:N	1:B:156:ASP:OD1	2.53	0.42
1:B:205:ILE:O	1:B:205:ILE:CG1	2.67	0.42
1:B:80:TYR:O	1:B:84:LEU:HD22	2.20	0.42
1:B:86:ARG:HD2	1:B:210:LEU:CD1	2.50	0.42
1:C:224:VAL:HA	1:C:225:ASN:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:PRO:HG2	1:A:200:MET:HG3	2.01	0.42
1:C:230:LEU:HG	1:C:268:GLY:HA2	2.01	0.42
1:B:277:GLU:O	1:B:288:ARG:NH1	2.44	0.42
1:C:316:SER:O	1:C:358:ASN:ND2	2.53	0.42
1:B:478:ARG:NH2	1:B:523:VAL:HG23	2.35	0.42
1:B:481:LYS:NZ	1:B:515:PRO:O	2.52	0.42
1:C:361:GLN:HA	1:C:362:ARG:CB	2.49	0.42
1:C:395:VAL:HG12	1:C:396:ALA:N	2.35	0.42
1:A:220:PRO:HD2	1:A:505:GLY:O	2.20	0.42
1:B:202:VAL:HB	1:B:203:PRO:HD2	2.02	0.42
1:C:306:PRO:HG3	1:C:403:TRP:CE2	2.54	0.42
1:A:446:MET:SD	1:A:446:MET:C	2.98	0.41
1:B:144:SER:O	1:B:144:SER:OG	2.27	0.41
1:B:236:LEU:O	1:B:501:ILE:N	2.45	0.41
1:B:307:VAL:HB	1:B:308:PRO:HD2	2.01	0.41
1:C:446:MET:N	1:C:446:MET:CE	2.84	0.41
1:A:490:ALA:O	1:A:492:THR:HG23	2.20	0.41
1:A:296:ASP:O	1:A:299:THR:CG2	2.67	0.41
1:B:252:TYR:O	1:B:486:GLY:HA3	2.20	0.41
1:A:41:ASP:OD2	1:B:201:LEU:HD11	2.20	0.41
1:A:199:THR:HG22	1:A:200:MET:H	1.85	0.41
1:A:324:GLN:CG	1:A:387:ALA:HB3	2.51	0.41
1:C:289:TYR:OH	1:C:352:GLU:OE2	2.38	0.41
1:C:311:PHE:C	1:C:311:PHE:CD1	2.94	0.41
1:A:37:VAL:O	1:A:37:VAL:HG13	2.21	0.41
1:B:349:GLY:HA2	1:B:363:THR:O	2.21	0.41
1:C:97:LEU:HD22	1:C:167:LEU:HD13	2.02	0.41
1:C:224:VAL:HG23	1:C:225:ASN:HB3	2.02	0.41
1:C:306:PRO:O	1:C:307:VAL:HG13	2.20	0.41
1:A:225:ASN:ND2	1:A:422:SER:OG	2.54	0.41
1:A:237:TYR:CD1	1:A:421:ARG:HG2	2.56	0.41
1:A:282:THR:O	1:A:284:HIS:N	2.54	0.41
1:A:451:MET:O	1:A:454:ALA:N	2.54	0.41
1:C:153:LYS:HG3	1:C:155:ILE:O	2.21	0.41
1:C:229:PRO:C	1:C:268:GLY:O	2.59	0.41
1:C:418:VAL:O	1:C:418:VAL:HG23	2.20	0.41
1:A:34:ALA:HA	1:A:157:TYR:CE1	2.56	0.41
1:A:225:ASN:OD1	1:A:225:ASN:C	2.58	0.41
1:A:348:TYR:HE2	1:A:361:GLN:HA	1.86	0.41
1:A:359:THR:HG22	1:A:397:PRO:HB3	2.02	0.41
1:A:429:THR:HG22	1:A:436:ASN:OD1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:ASN:OD1	1:A:443:ASN:N	2.54	0.41
1:C:361:GLN:HB3	1:C:362:ARG:C	2.40	0.41
1:C:314:TRP:CE3	1:C:314:TRP:N	2.89	0.41
1:A:275:THR:HG22	1:A:376:GLN:OE1	2.20	0.40
1:B:519:ILE:N	1:B:519:ILE:HD13	2.36	0.40
1:C:240:SER:OG	1:C:496:ASN:OD1	2.36	0.40
1:A:469:TYR:HA	1:A:507:PHE:HB3	2.03	0.40
1:B:151:ASP:O	1:B:151:ASP:OD1	2.39	0.40
1:B:207:ASN:N	1:B:207:ASN:OD1	2.54	0.40
1:C:413:LEU:HD23	1:C:413:LEU:HA	1.97	0.40
1:A:298:PRO:O	1:A:304:LEU:HD12	2.22	0.40
1:A:338:PHE:O	1:B:428:LYS:HB2	2.21	0.40
1:B:477:VAL:O	1:B:477:VAL:CG1	2.70	0.40
1:A:41:ASP:OD1	1:A:41:ASP:C	2.60	0.40
1:A:371:LEU:HD23	1:A:377:TYR:CE1	2.56	0.40
1:B:110:LYS:HD2	1:B:136:ILE:CG2	2.52	0.40
1:A:56:PHE:CD1	1:A:56:PHE:N	2.90	0.40
1:A:201:LEU:CD2	1:B:80:TYR:CZ	3.04	0.40
1:B:122:VAL:HG21	1:B:168:VAL:HG21	2.04	0.40
1:C:48:GLN:OE1	1:C:98:LYS:HG3	2.22	0.40
1:C:253:THR:HG22	1:C:485:GLU:O	2.21	0.40
1:C:294:LEU:HD11	1:C:362:ARG:HD3	2.04	0.40
1:C:421:ARG:HA	1:C:442:VAL:O	2.22	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	506/534 (95%)	441 (87%)	62 (12%)	3 (1%)	25	64
1	B	506/534 (95%)	452 (89%)	54 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	523/534 (98%)	465 (89%)	58 (11%)	0	100	100
All	All	1535/1602 (96%)	1358 (88%)	174 (11%)	3 (0%)	50	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	HIS
1	A	285	PRO
1	A	283	GLY

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	431/453 (95%)	395 (92%)	36 (8%)	11	39
1	B	431/453 (95%)	391 (91%)	40 (9%)	9	33
1	C	445/453 (98%)	403 (91%)	42 (9%)	8	33
All	All	1307/1359 (96%)	1189 (91%)	118 (9%)	13	34

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	THR
1	A	63	GLN
1	A	92	SER
1	A	95	PHE
1	A	143	ASP
1	A	200	MET
1	A	205	ILE
1	A	221	TYR
1	A	222	SER
1	A	237	TYR
1	A	240	SER
1	A	246	ASN

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Mol	Chain	Res	Type
1	A	262	SER
1	A	270	TRP
1	A	312	CYS
1	A	313	ASP
1	A	328	CYS
1	A	347	ASP
1	A	348	TYR
1	A	356	LEU
1	A	362	ARG
1	A	371	LEU
1	A	385	SER
1	A	392	THR
1	A	394	GLN
1	A	400	TYR
1	A	408	THR
1	A	413	LEU
1	A	428	LYS
1	A	436	ASN
1	A	446	MET
1	A	453	SER
1	A	478	ARG
1	A	507	PHE
1	A	514	SER
1	A	521	SER
1	B	38	ASN
1	B	47	ASN
1	B	50	GLU
1	B	66	SER
1	B	91	TRP
1	B	92	SER
1	B	104	ASN
1	B	138	ASP
1	B	144	SER
1	B	145	MET
1	B	153	LYS
1	B	162	ASP
1	B	167	LEU
1	B	179	SER
1	B	203	PRO
1	B	237	TYR
1	B	253	THR
1	B	267	SER

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Mol	Chain	Res	Type
1	B	273	THR
1	B	274	CYS
1	B	275	THR
1	B	296	ASP
1	B	301	ASP
1	B	303	THR
1	B	309	ARG
1	B	311	PHE
1	B	325	HIS
1	B	332	LYS
1	B	335	GLU
1	B	348	TYR
1	B	385	SER
1	B	391	ASP
1	B	400	TYR
1	B	421	ARG
1	B	449	ASP
1	B	457	SER
1	B	478	ARG
1	B	480	PHE
1	B	504	ASP
1	B	526	ASN
1	C	16	THR
1	C	24	LEU
1	C	38	ASN
1	C	47	ASN
1	C	55	THR
1	C	100	LEU
1	C	106	PHE
1	C	107	SER
1	C	163	LYS
1	C	182	PHE
1	C	190	SER
1	C	201	LEU
1	C	228	SER
1	C	237	TYR
1	C	246	ASN
1	C	253	THR
1	C	270	TRP
1	C	314	TRP
1	C	343	THR
1	C	360	TYR

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Mol	Chain	Res	Type
1	C	362	ARG
1	C	365	TYR
1	C	373	LYS
1	C	385	SER
1	C	403	TRP
1	C	404	ASP
1	C	421	ARG
1	C	427	SER
1	C	429	THR
1	C	446	MET
1	C	447	SER
1	C	459	PHE
1	C	461	LEU
1	C	467	LEU
1	C	468	ASP
1	C	469	TYR
1	C	488	MET
1	C	489	THR
1	C	499	PHE
1	C	504	ASP
1	C	511	SER
1	C	514	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	443	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-43222. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections ⓘ
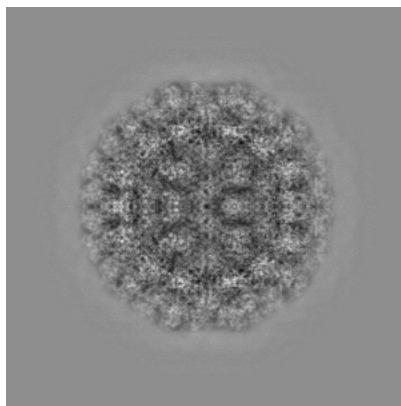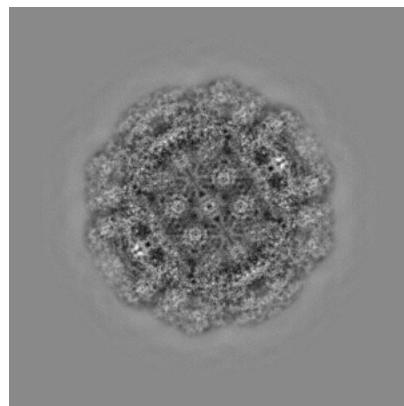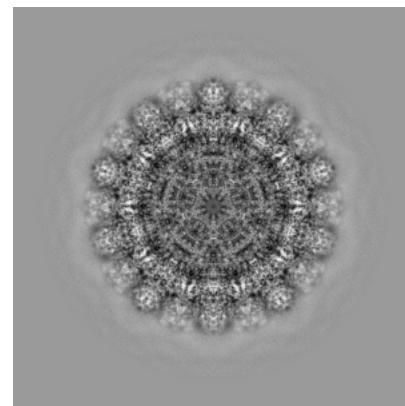
6.1.1 Primary map

| X | Y | Z |

6.1.2 Raw map

| X | Y | Z |
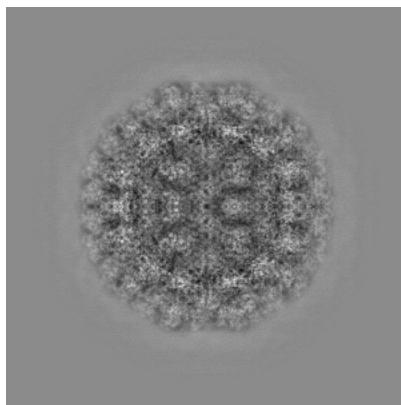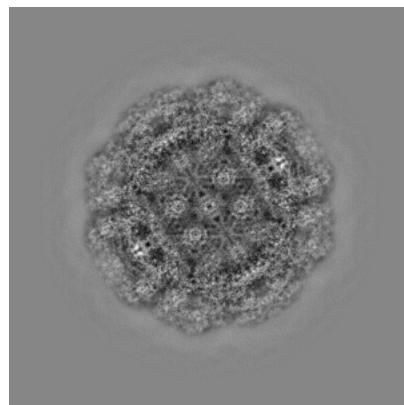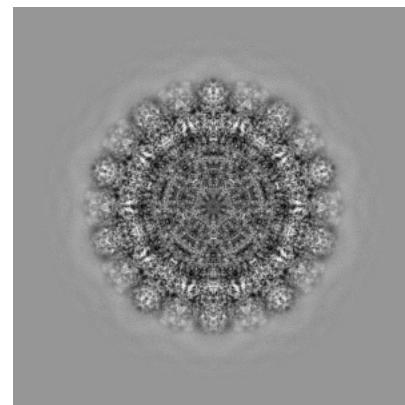
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)
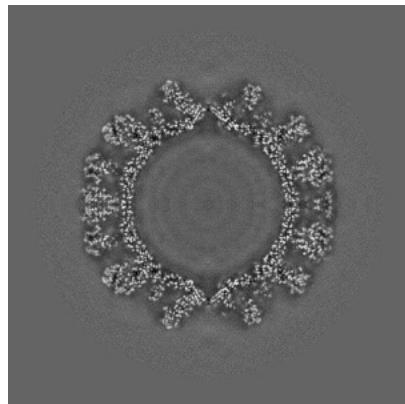
6.2.1 Primary map
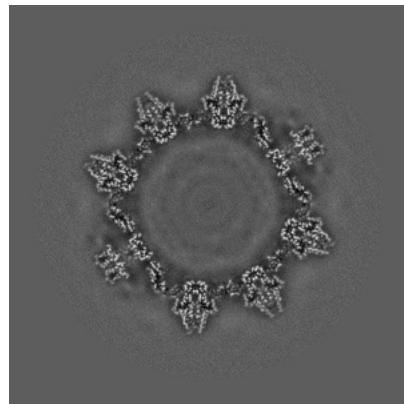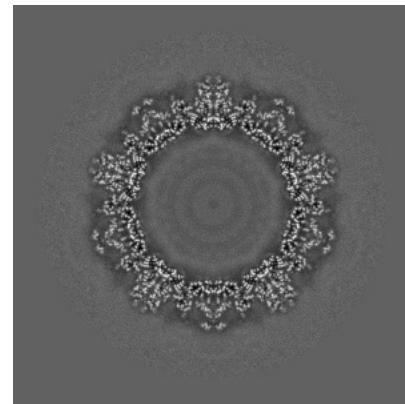
| X Index: 240 | Y Index: 240 | Z Index: 240 |

6.2.2 Raw map
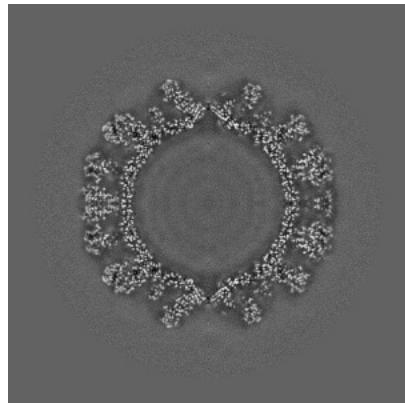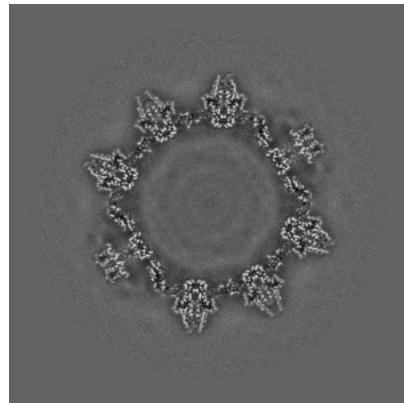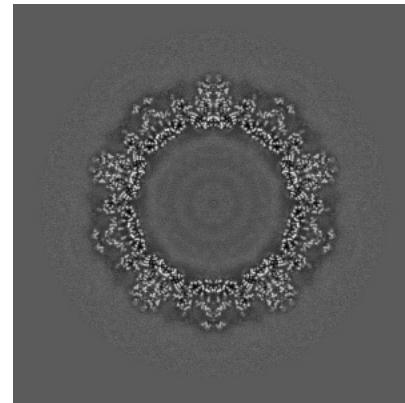
| X Index: 240 | Y Index: 240 | Z Index: 240 |

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

6.3 Largest variance slices (i)

6.3.1 Primary map
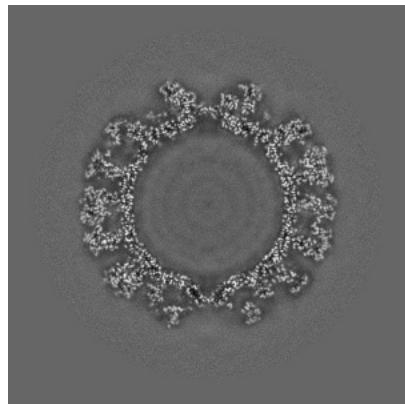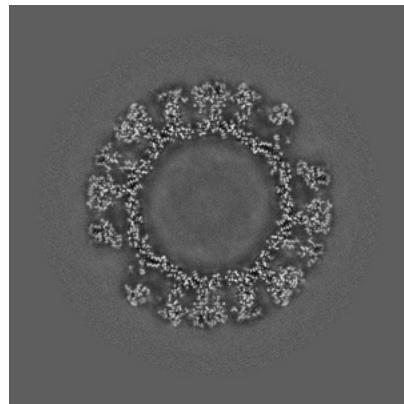
X Index: 236	Y Index: 201	Z Index: 200
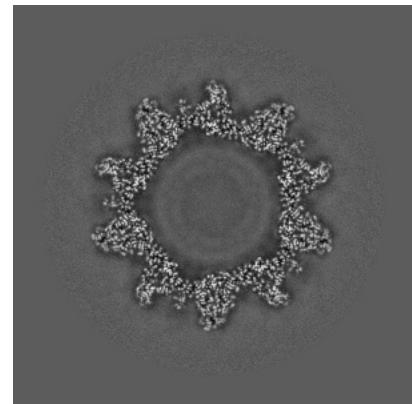
6.3.2 Raw map
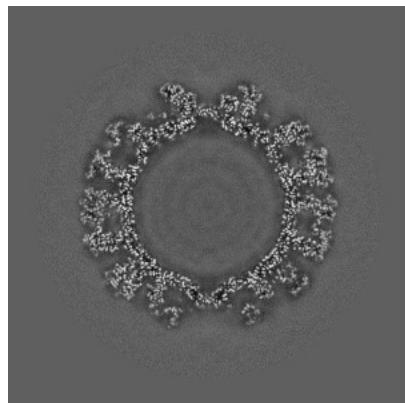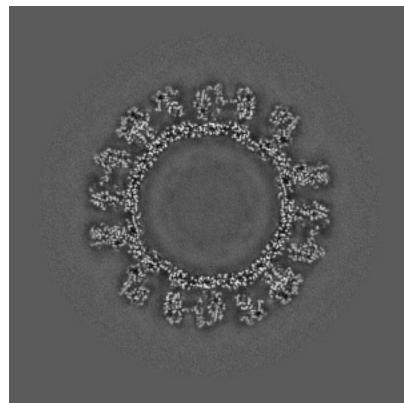
X Index: 235	Y Index: 207	Z Index: 280
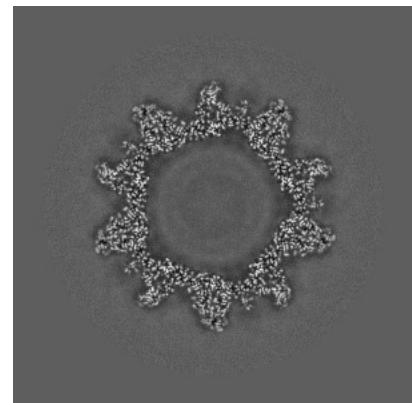
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

6.4.1 Primary map
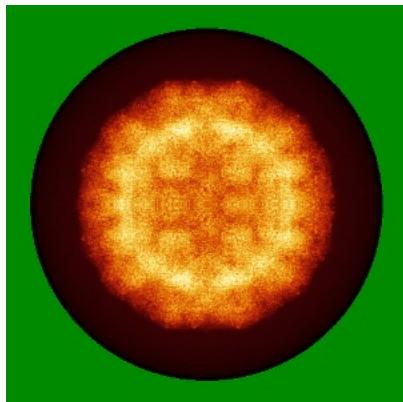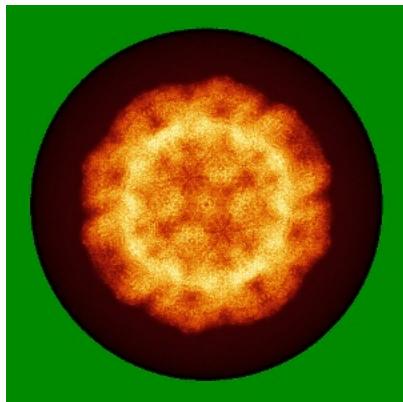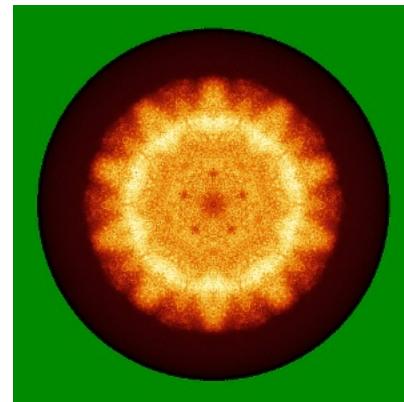
| X | Y | Z |

6.4.2 Raw map

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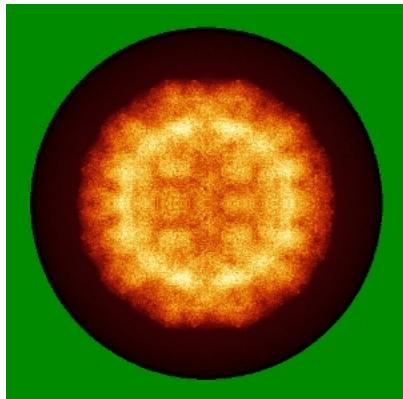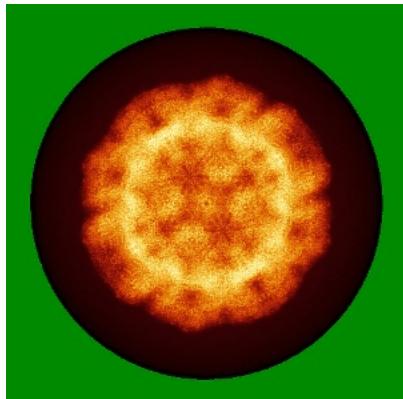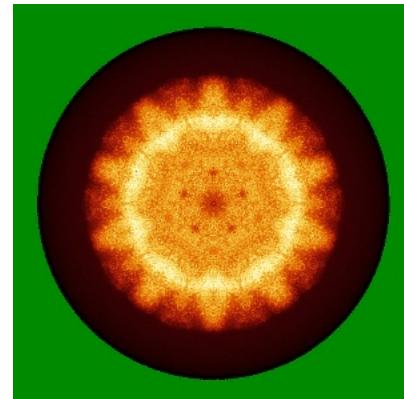
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5　Orthogonal surface views　ⓘ

6.5.1　Primary map

X	Y	Z
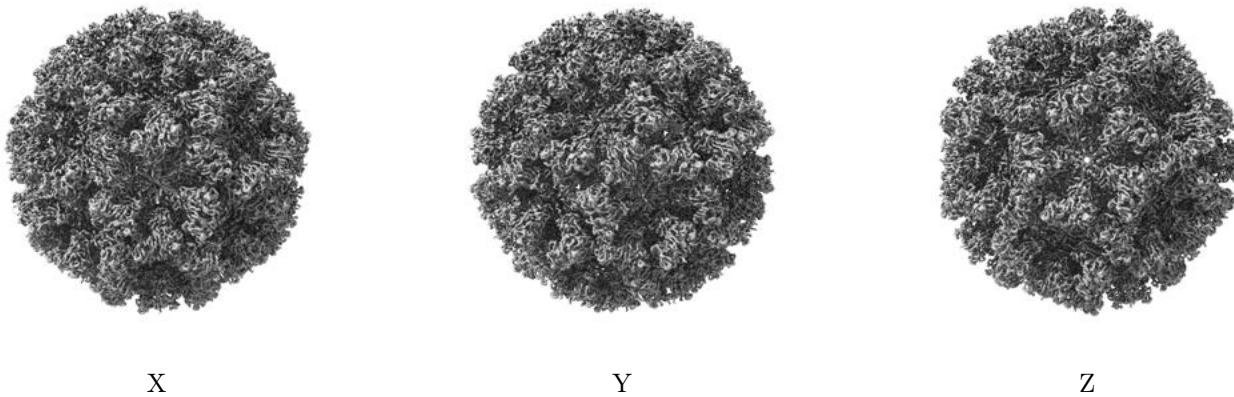
The images above show the 3D surface view of the map at the recommended contour level 8.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2　Raw map

X	Y	Z
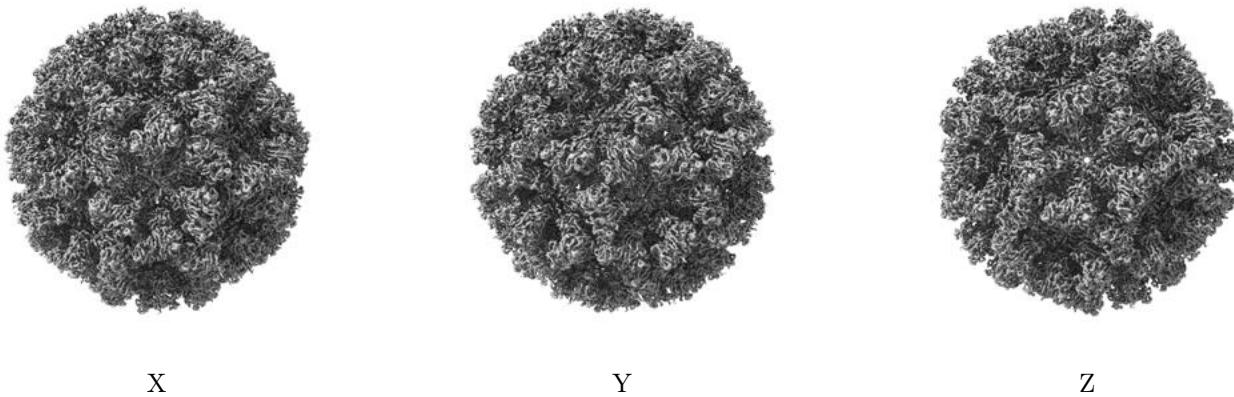
These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

A mask typically either:

- Encompasses the whole structure

- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

6.6.1 emd_43222_msk_1.map (i)

| X | Y | Z |
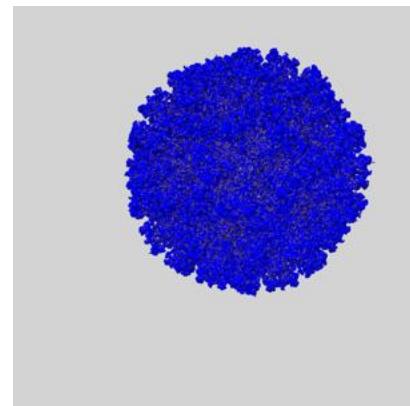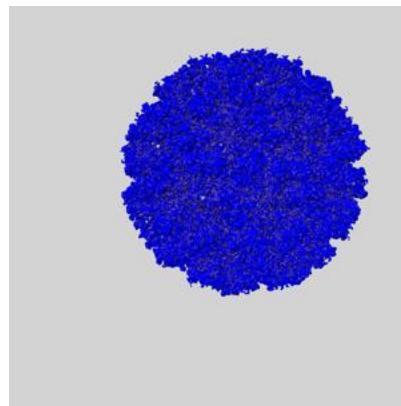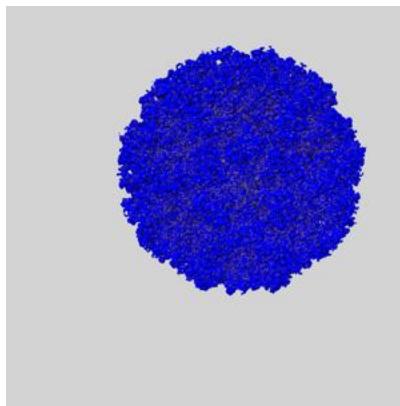
6.6.2 emd_43222_msk_2.map (i)

| X | Y | Z |
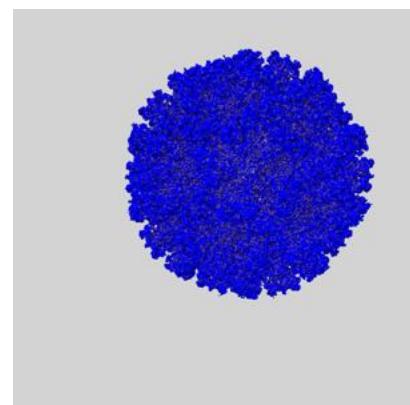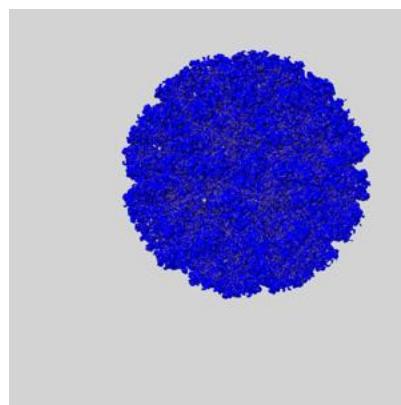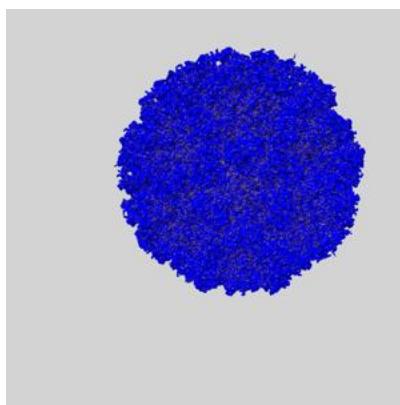
7 Map analysis ⓘ

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

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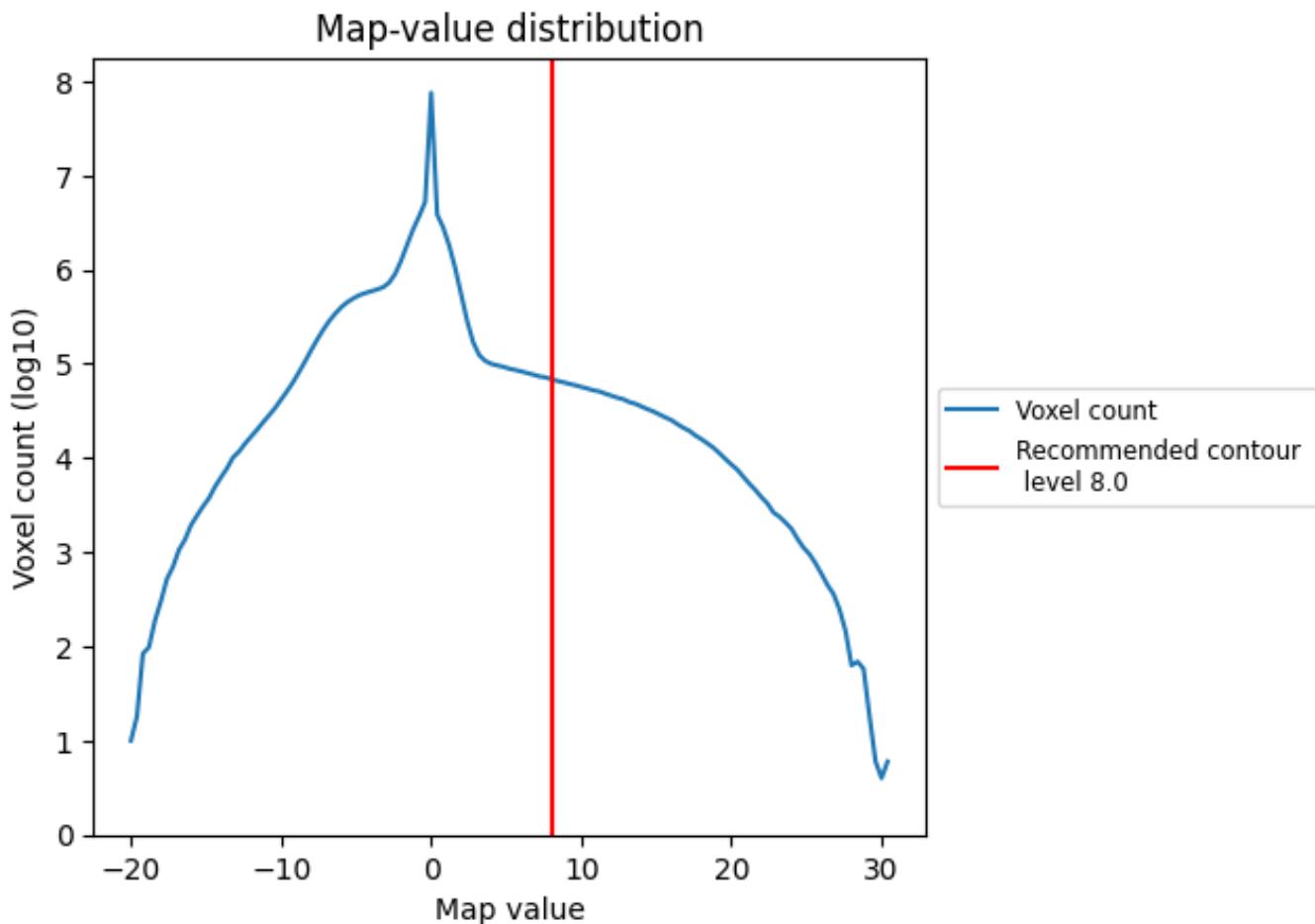
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate ⓘ
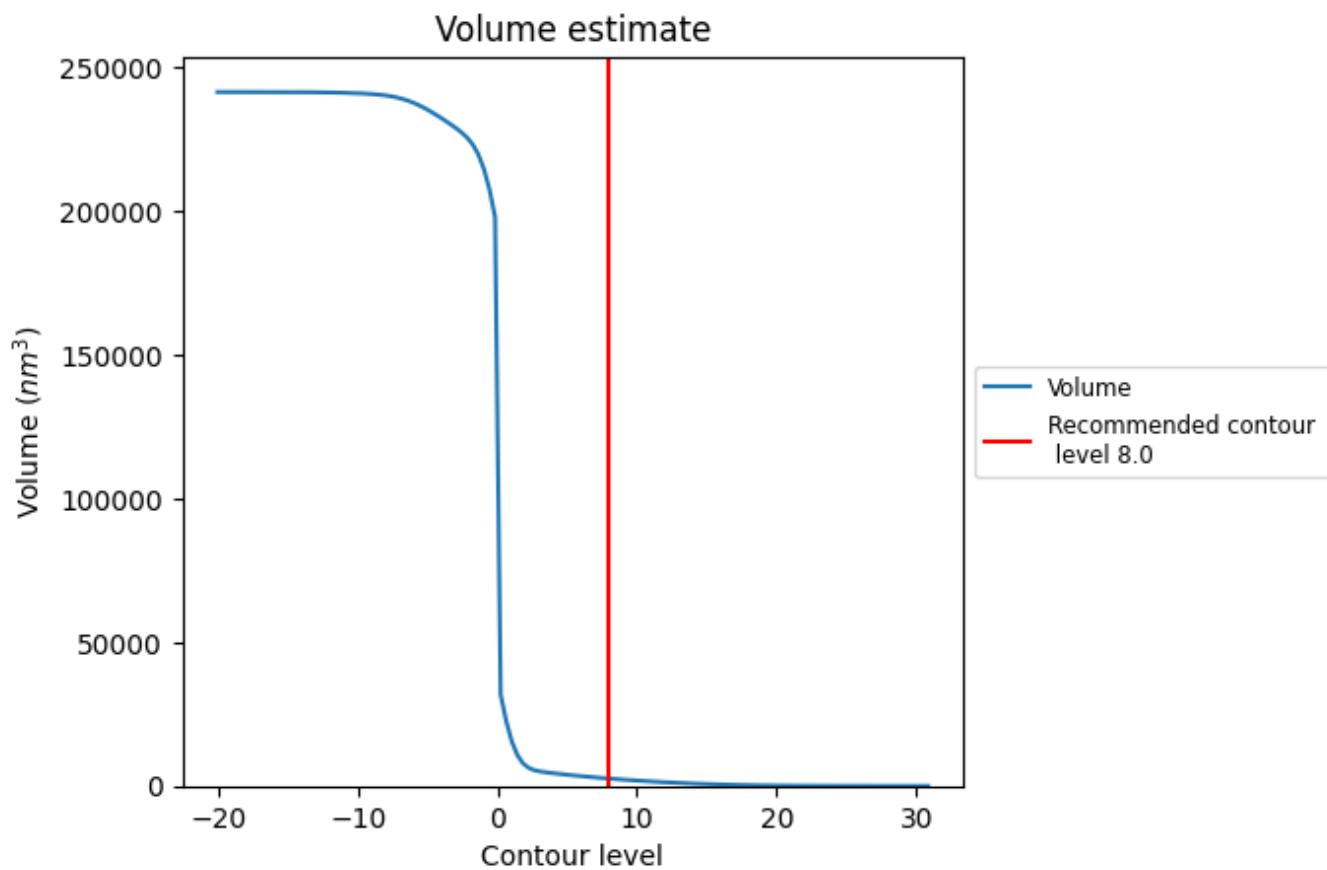
The volume at the recommended contour level is 2565 nm^3; this corresponds to an approximate mass of 2317 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)
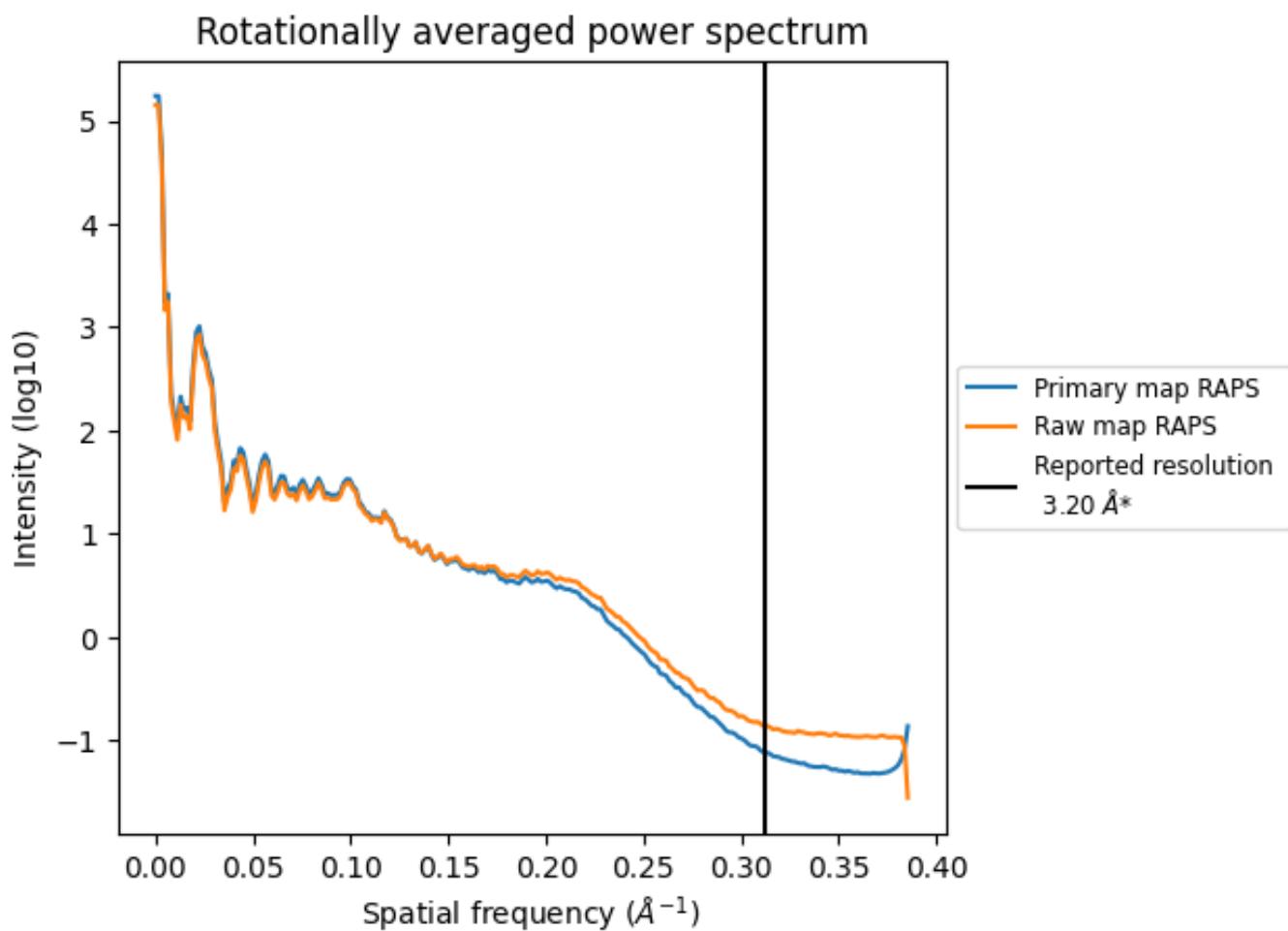
*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)
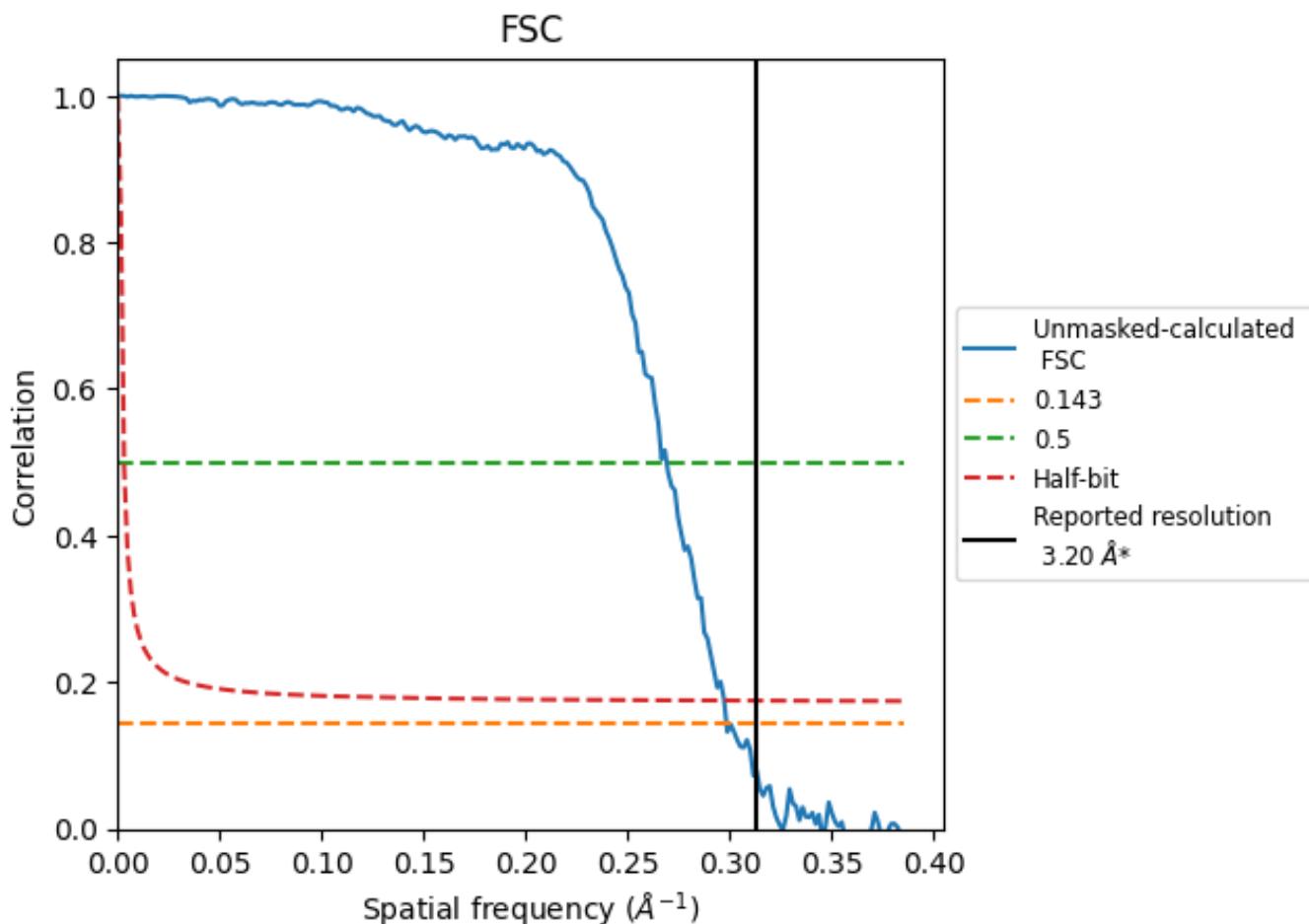
*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8.2   Resolution estimates (i)

| Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.35	3.72	3.36

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

9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-43222 and PDB model 8VGR. Per-residue inclusion information can be found in section 3 on page 4.

## 9.1 Map-model overlays

9.1.1 Map-model overlay ⓘ
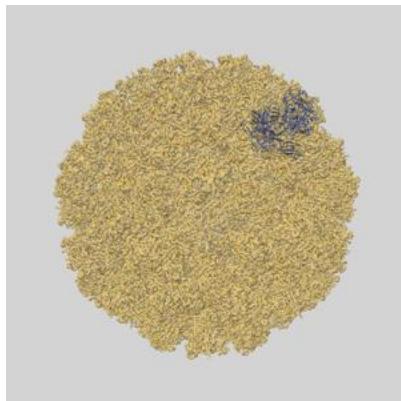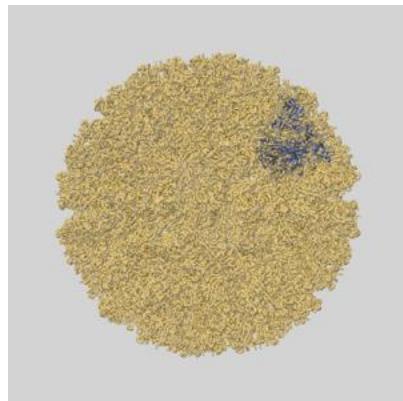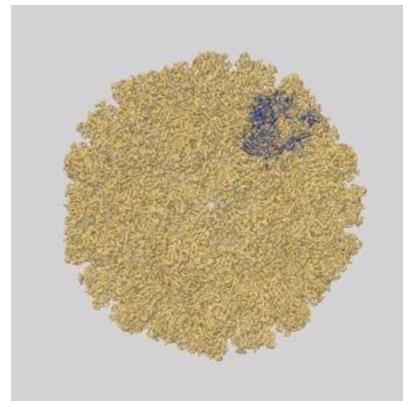
| X | Y | Z |

9.1.2 Map-model assembly overlay ⓘ
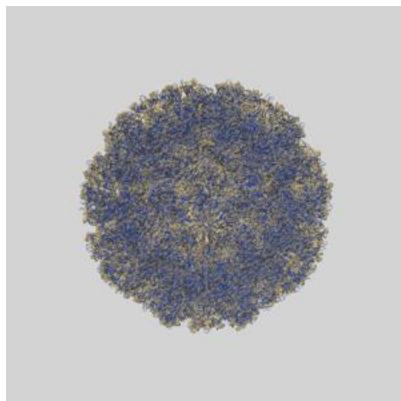

| X | Y | Z |
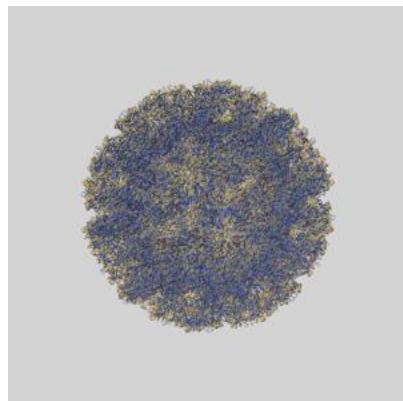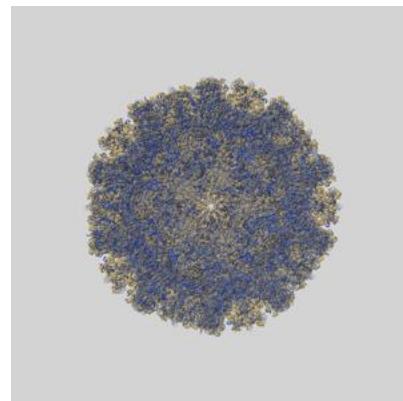
The images above show the 3D surface view of the map at the recommended contour level 8.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model ⓘ

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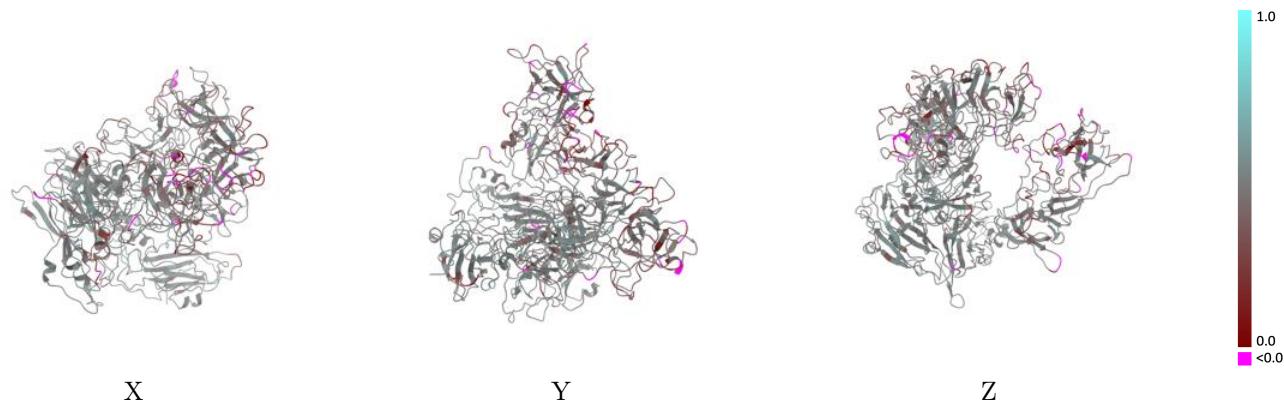
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

X   Y   Z
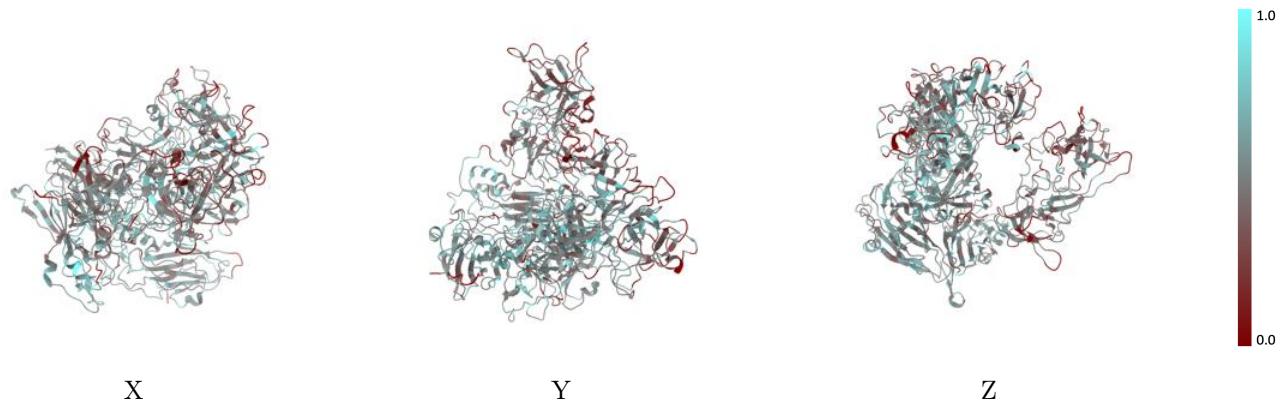
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (8.0).

9.4　Atom inclusion ⓘ
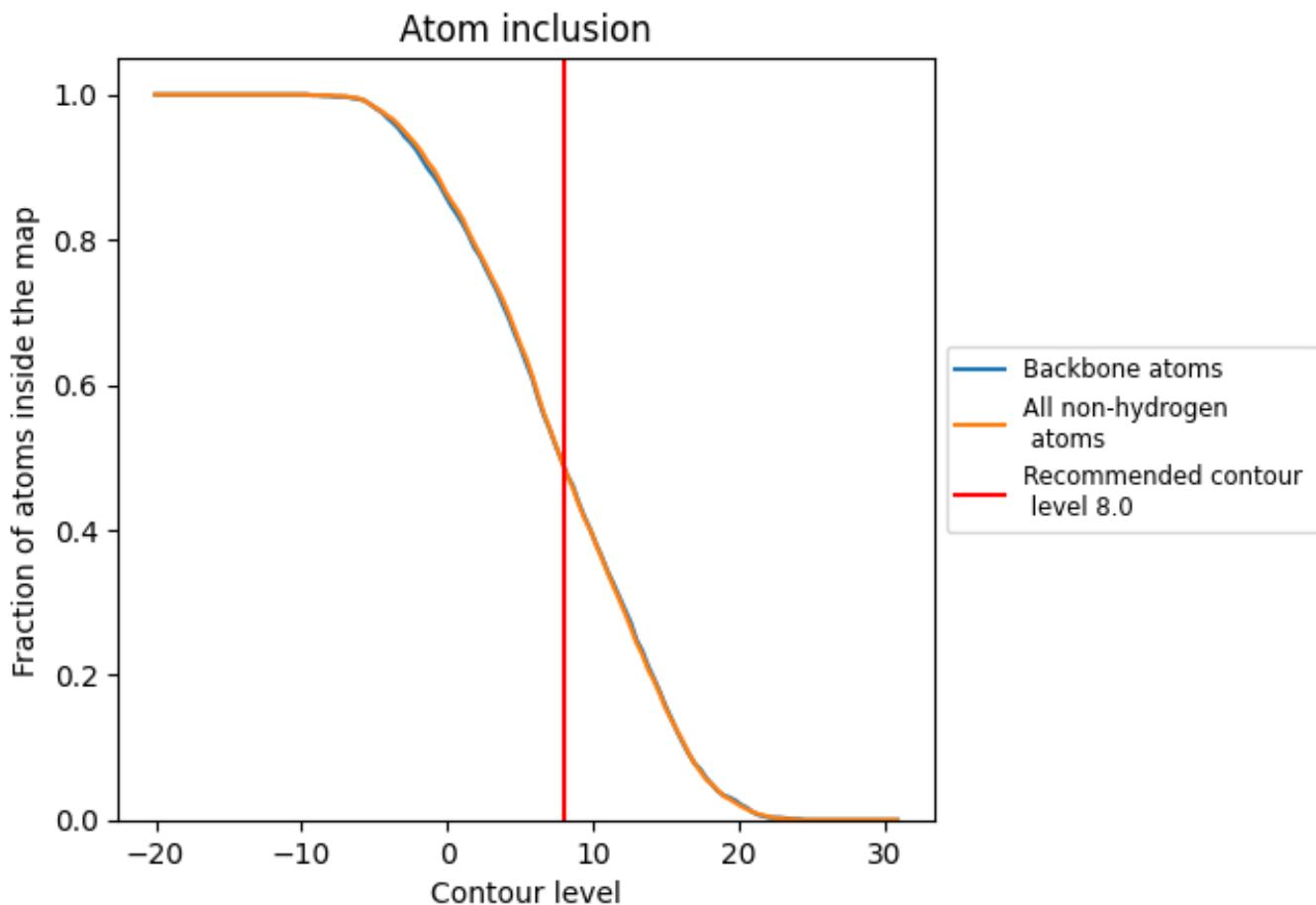
At the recommended contour level, 49% of all backbone atoms, 48% of all non-hydrogen atoms, are inside the map.

9.5   Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (8.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4850	0.4450
A	0.5160	0.4510
B	0.5100	0.4530
C	0.4640	0.4310

1.0

0.0
<0.0