Full wwPDB EM Validation Report (i)

Nov 9, 2022 – 06:26 AM EST

PDB ID	:	6ORV
EMDB ID	:	EMD-20179
Title	:	Non-peptide agonist (TT-OAD2) bound to the Glucagon-Like peptide-1 (GLP-1) Receptor
Authors	:	Belousoff, M.J.; Liang, Y.L.; Danev, R.
Deposited on	:	2019-05-01
Resolution	:	3.00 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

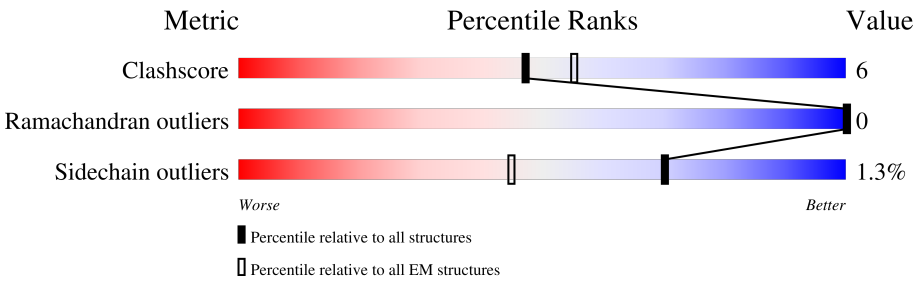
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	AP	394	• 43% 6% 51%
2	BP	350	• 80% 17% •
3	GP	71	10% 76% • 20%
4	NP	138	78% 13% 9%
5	RP	491	6% 46% 10% • 43%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8041 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 Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	AP	195	1654	1049	303	297	5	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	54	ASN	SER	conflict	UNP P63092
AP	226	ALA	GLY	conflict	UNP P63092
AP	268	ALA	GLU	conflict	UNP P63092
AP	271	LYS	ASN	conflict	UNP P63092
AP	274	ASP	LYS	conflict	UNP P63092
AP	280	LYS	ARG	conflict	UNP P63092
AP	284	ASP	THR	conflict	UNP P63092
AP	285	THR	ILE	conflict	UNP P63092

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	BP	338	2600	1604	467	508	21	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BP	-9	MET	-	expression tag	UNP P62873
BP	-8	HIS	-	expression tag	UNP P62873
BP	-7	HIS	-	expression tag	UNP P62873
BP	-6	HIS	-	expression tag	UNP P62873
BP	-5	HIS	-	expression tag	UNP P62873
BP	-4	HIS	-	expression tag	UNP P62873
BP	-3	HIS	-	expression tag	UNP P62873

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Chain	Residue	Modelled	Actual	Comment	Reference
BP	-2	GLY	-	expression tag	UNP P62873
BP	-1	SER	-	expression tag	UNP P62873
BP	0	SER	-	expression tag	UNP P62873
BP	1	GLY	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	GP	57	436	273	77	83	3	0	0

- Molecule 4 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	NP	126	961	599	168	188	6	0	0

- Molecule 5 is a protein called Glucagon-like peptide 1 receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	RP	281	2329	1563	372	382	12	0	0

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
RP	-8	MET	-	initiating methionine	UNP P43220
RP	-7	LYS	-	expression tag	UNP P43220
RP	-6	THR	-	expression tag	UNP P43220
RP	-5	ILE	-	expression tag	UNP P43220
RP	-4	ILE	-	expression tag	UNP P43220
RP	-3	ALA	-	expression tag	UNP P43220
RP	-2	LEU	-	expression tag	UNP P43220
RP	-1	SER	-	expression tag	UNP P43220
RP	0	TYR	-	expression tag	UNP P43220
RP	1	ILE	-	expression tag	UNP P43220
RP	2	PHE	-	expression tag	UNP P43220
RP	3	CYS	-	expression tag	UNP P43220
RP	4	LEU	-	expression tag	UNP P43220
RP	5	VAL	-	expression tag	UNP P43220
RP	6	PHE	-	expression tag	UNP P43220

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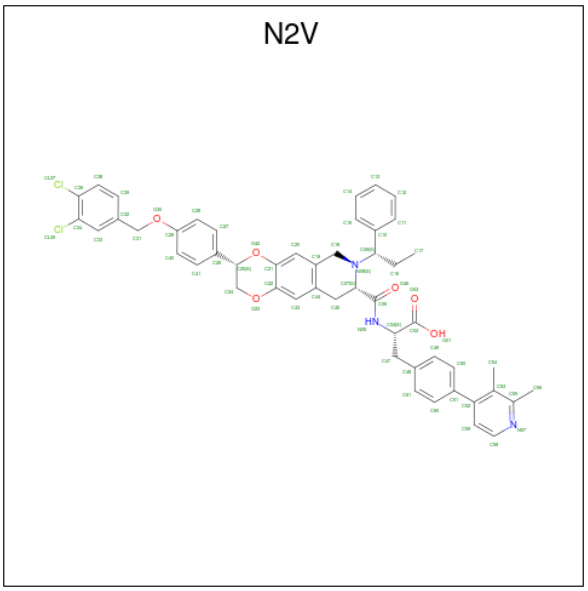
Chain	Residue	Modelled	Actual	Comment	Reference
RP	7	ALA	-	expression tag	UNP P43220
RP	8	ASP	-	expression tag	UNP P43220
RP	9	TYR	-	expression tag	UNP P43220
RP	10	LYS	-	expression tag	UNP P43220
RP	11	ASP	-	expression tag	UNP P43220
RP	12	ASP	-	expression tag	UNP P43220
RP	13	ASP	-	expression tag	UNP P43220
RP	14	ASP	-	expression tag	UNP P43220
RP	15	LEU	-	expression tag	UNP P43220
RP	16	GLU	-	expression tag	UNP P43220
RP	17	VAL	-	expression tag	UNP P43220
RP	18	LEU	-	expression tag	UNP P43220
RP	19	PHE	-	expression tag	UNP P43220
RP	20	GLN	-	expression tag	UNP P43220
RP	21	GLY	-	expression tag	UNP P43220
RP	22	PRO	-	expression tag	UNP P43220
RP	23	ALA	-	expression tag	UNP P43220
RP	260	PHE	LEU	conflict	UNP P43220
RP	464	PRO	-	expression tag	UNP P43220
RP	465	ALA	-	expression tag	UNP P43220
RP	466	GLY	-	expression tag	UNP P43220
RP	467	LEU	-	expression tag	UNP P43220
RP	468	GLU	-	expression tag	UNP P43220
RP	469	VAL	-	expression tag	UNP P43220
RP	470	LEU	-	expression tag	UNP P43220
RP	471	PHE	-	expression tag	UNP P43220
RP	472	GLN	-	expression tag	UNP P43220
RP	473	GLY	-	expression tag	UNP P43220
RP	474	PRO	-	expression tag	UNP P43220
RP	475	HIS	-	expression tag	UNP P43220
RP	476	HIS	-	expression tag	UNP P43220
RP	477	HIS	-	expression tag	UNP P43220
RP	478	HIS	-	expression tag	UNP P43220
RP	479	HIS	-	expression tag	UNP P43220
RP	480	HIS	-	expression tag	UNP P43220
RP	481	HIS	-	expression tag	UNP P43220
RP	482	HIS	-	expression tag	UNP P43220

- Molecule 6 is N-{(3S,8S)-3-{4-[(3,4-dichlorophenyl)methoxy]phenyl}-7-[(1S)-1-phenylpropyl]-2,3,6,7,8,9-hexahydro[1,4]dioxino[2,3-g]isoquinoline-8-carbonyl}-4-(2,3-dimethylpyridin-4-yl)-L-phenylalanine (three-letter code: N2V) (formula: $C_{50}H_{47}Cl_2N_3O_6$) (labeled as "Ligand of Interest" by depositor).



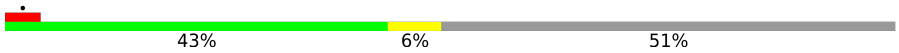
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Cl	N	O	
6	RP	1	61	50	2	3	6	0

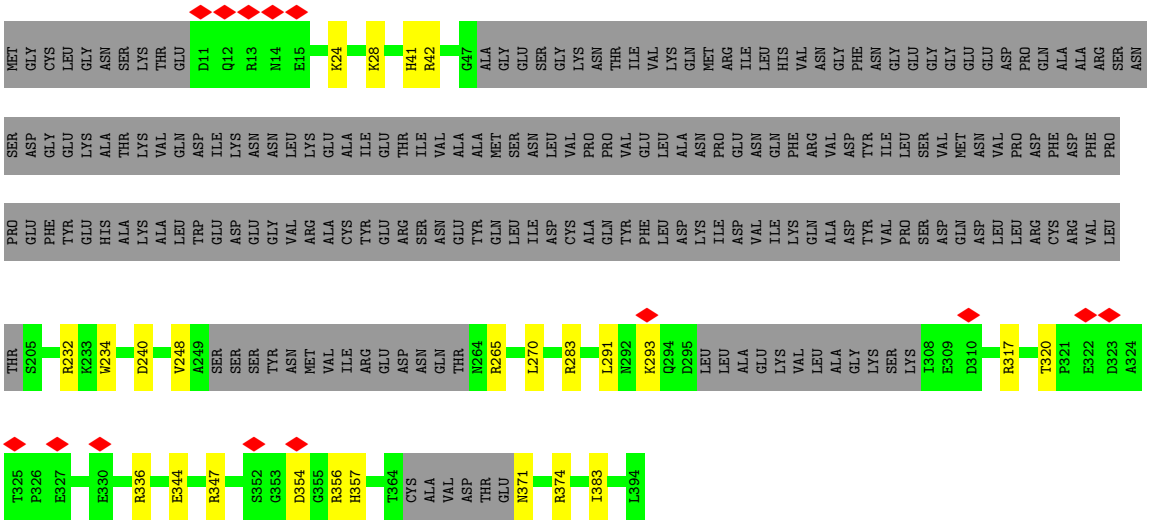
3 Residue-property plots (i)

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: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

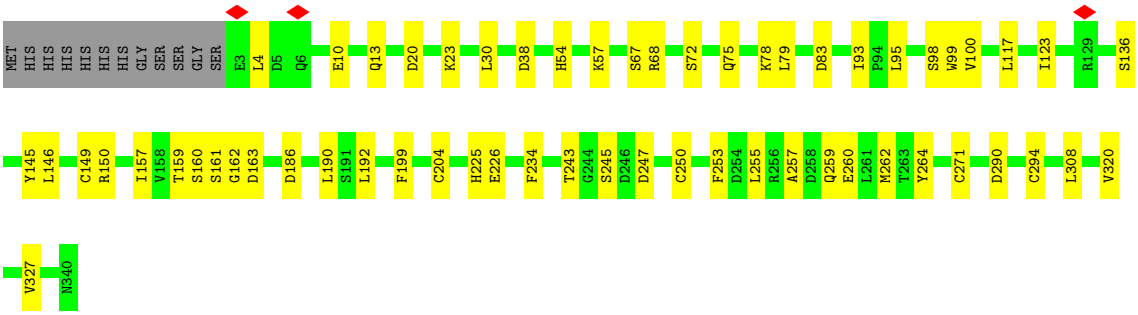
Chain AP:





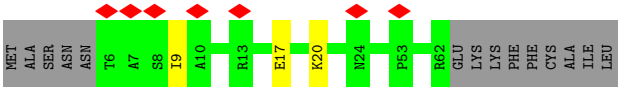
• Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain BP:



• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

Chain GP:

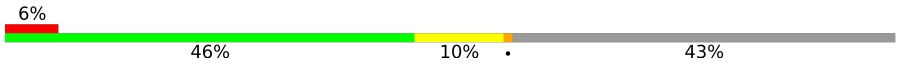


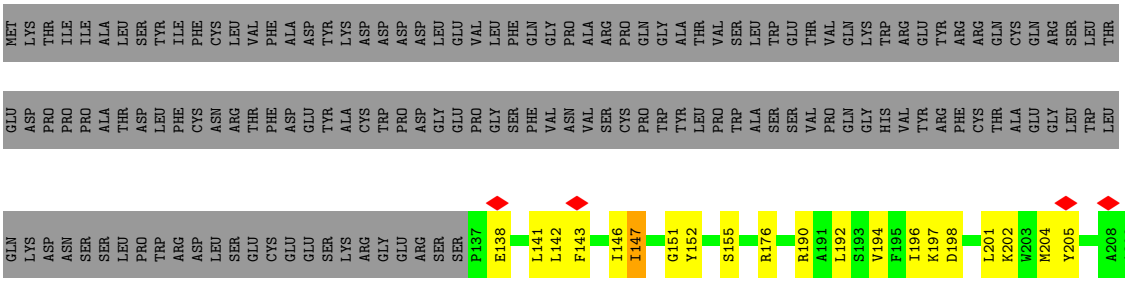
- Molecule 4: Nanobody 35

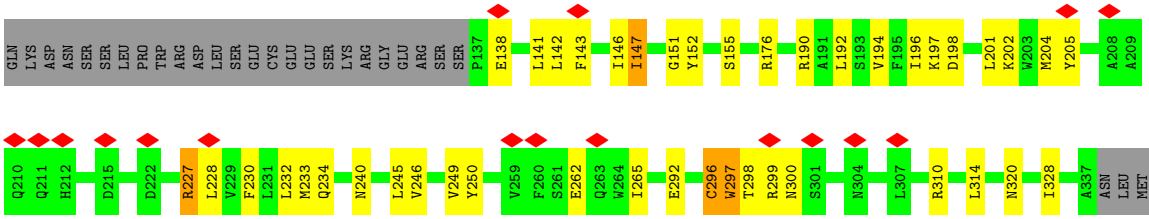
Chain NP:

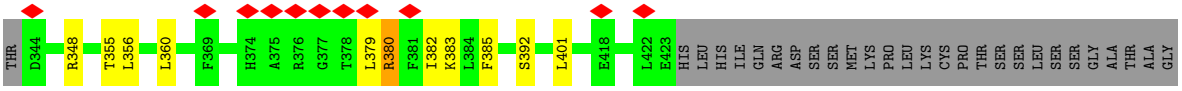
- Molecule 5: Glucagon-like peptide 1 receptor

Chain RP:









4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	85978	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	66.65	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.161	Depositor
Minimum map value	-0.113	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.019	Depositor
Map size (Å)	237.888, 237.888, 237.888	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: N2V

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	AP	0.39	0/1687	0.50	0/2266
2	BP	0.45	0/2647	0.58	0/3589
3	GP	0.30	0/442	0.49	0/597
4	NP	0.47	0/981	0.57	0/1329
5	RP	0.40	0/2396	0.56	0/3257
All	All	0.42	0/8153	0.55	0/11038

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AP	1654	0	1622	13	0
2	BP	2600	0	2505	37	0
3	GP	436	0	448	2	0
4	NP	961	0	928	11	0
5	RP	2329	0	2365	42	0
6	RP	61	0	0	1	0
All	All	8041	0	7868	100	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 6.

All (100) 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)
5:RP:202:LYS:HA	5:RP:202:LYS:HE2	1.69	0.74
2:BP:54:HIS:HE2	2:BP:72:SER:HG	1.35	0.73
5:RP:190:ARG:HH11	5:RP:240:ASN:HD22	1.41	0.68
5:RP:202:LYS:HE2	5:RP:202:LYS:CA	2.24	0.67
4:NP:88:PRO:HA	4:NP:126:VAL:HG21	1.78	0.66
5:RP:380:ARG:HG3	5:RP:383:LYS:HB3	1.79	0.65
5:RP:228:LEU:C	5:RP:228:LEU:HD23	2.18	0.64
5:RP:246:VAL:HA	5:RP:249:VAL:HG22	1.82	0.62
5:RP:227:ARG:H	5:RP:227:ARG:HD3	1.64	0.62
2:BP:160:SER:HB3	2:BP:190:LEU:HD23	1.83	0.61
2:BP:226:GLU:O	4:NP:98:ARG:NH2	2.35	0.60
1:AP:240:ASP:OD2	2:BP:57:LYS:NZ	2.35	0.59
2:BP:245:SER:OG	2:BP:247:ASP:OD1	2.21	0.58
2:BP:149:CYS:HB2	2:BP:157:ILE:HD11	1.86	0.58
5:RP:232:LEU:C	5:RP:232:LEU:HD23	2.24	0.57
5:RP:382:ILE:HA	5:RP:385:PHE:HB3	1.86	0.57
2:BP:225:HIS:NE2	2:BP:243:THR:OG1	2.31	0.57
5:RP:197:LYS:HE3	5:RP:233:MET:SD	2.45	0.57
4:NP:28:THR:OG1	4:NP:31:ASN:ND2	2.38	0.56
5:RP:262:GLU:HA	5:RP:265:ILE:HG22	1.87	0.56
2:BP:271:CYS:HB2	2:BP:290:ASP:HB2	1.88	0.56
2:BP:161:SER:OG	2:BP:163:ASP:OD1	2.21	0.55
2:BP:79:LEU:HB3	2:BP:93:ILE:HB	1.88	0.54
2:BP:149:CYS:O	2:BP:150:ARG:NH1	2.39	0.54
5:RP:201:LEU:HD12	5:RP:204:MET:HE3	1.88	0.54
2:BP:146:LEU:HD11	2:BP:159:THR:HB	1.89	0.54
5:RP:198:ASP:O	5:RP:202:LYS:HG2	2.08	0.54
1:AP:354:ASP:OD1	1:AP:356:ARG:NH1	2.41	0.53
5:RP:227:ARG:HH11	5:RP:296:CYS:HB3	1.73	0.53
1:AP:232:ARG:HH21	2:BP:204:CYS:HB3	1.74	0.53
1:AP:344:GLU:OE2	1:AP:347:ARG:NH2	2.43	0.52
2:BP:10:GLU:OE1	2:BP:13:GLN:NE2	2.42	0.52
5:RP:146:ILE:HG13	5:RP:147:ILE:HD13	1.91	0.52
5:RP:292:GLU:OE2	5:RP:300:ASN:N	2.40	0.51
2:BP:192:LEU:HD23	2:BP:199:PHE:HB3	1.91	0.50
1:AP:265:ARG:HH21	1:AP:293:LYS:HG3	1.76	0.50
5:RP:192:LEU:O	5:RP:196:ILE:HG12	2.12	0.50
5:RP:201:LEU:HG	5:RP:205:TYR:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:RP:232:LEU:HD23	5:RP:232:LEU:O	2.12	0.50
2:BP:145:TYR:OH	2:BP:186:ASP:OD2	2.25	0.50
5:RP:152:TYR:CD2	5:RP:194:VAL:HG21	2.47	0.50
1:AP:371:ASN:OD1	1:AP:374:ARG:NH1	2.45	0.49
2:BP:57:LYS:HG3	2:BP:75:GLN:HG3	1.95	0.49
2:BP:79:LEU:HB2	2:BP:95:LEU:HD21	1.94	0.49
5:RP:245:LEU:HA	5:RP:320:ASN:HD21	1.77	0.48
1:AP:270:LEU:HD21	1:AP:344:GLU:HB3	1.95	0.48
4:NP:69:THR:HG22	4:NP:82:GLN:HB3	1.94	0.48
4:NP:29:PHE:O	4:NP:72:ARG:NH2	2.46	0.48
2:BP:250:CYS:HB2	2:BP:264:TYR:HB2	1.95	0.48
2:BP:320:VAL:HG22	2:BP:327:VAL:HG22	1.96	0.48
1:AP:234:TRP:HB2	2:BP:117:LEU:HD21	1.96	0.48
5:RP:147:ILE:O	5:RP:151:GLY:N	2.44	0.48
1:AP:41:HIS:HE1	1:AP:383:ILE:HG13	1.79	0.47
5:RP:227:ARG:CD	5:RP:227:ARG:N	2.78	0.47
2:BP:123:ILE:O	2:BP:136:SER:N	2.44	0.47
2:BP:4:LEU:HB3	3:GP:9:ILE:HG22	1.95	0.47
2:BP:68:ARG:NE	2:BP:83:ASP:OD1	2.44	0.47
2:BP:67:SER:O	2:BP:67:SER:OG	2.29	0.47
4:NP:29:PHE:HZ	4:NP:79:LEU:HB2	1.80	0.47
1:AP:248:VAL:HB	1:AP:291:LEU:HD23	1.96	0.46
2:BP:234:PHE:HE1	2:BP:255:LEU:HD11	1.81	0.46
3:GP:17:GLU:HA	3:GP:20:LYS:HE2	1.98	0.46
2:BP:294:CYS:HB2	2:BP:308:LEU:HB2	1.96	0.46
2:BP:257:ALA:O	2:BP:259:GLN:NE2	2.45	0.46
5:RP:355:THR:HA	5:RP:401:LEU:HD13	1.97	0.45
1:AP:283:ARG:HH12	4:NP:105:ARG:HH21	1.65	0.45
2:BP:95:LEU:HD13	2:BP:100:VAL:HG21	1.97	0.45
5:RP:298:THR:OG1	5:RP:299:ARG:N	2.50	0.45
5:RP:202:LYS:HE2	5:RP:202:LYS:N	2.32	0.44
4:NP:52:SER:OG	4:NP:53:GLN:N	2.50	0.44
2:BP:30:LEU:HD23	2:BP:262:MET:HB2	2.00	0.44
5:RP:230:PHE:CE1	5:RP:297:TRP:HA	2.53	0.44
2:BP:162:GLY:HA2	2:BP:186:ASP:HB2	1.99	0.44
5:RP:230:PHE:O	5:RP:234:GLN:HG2	2.17	0.43
2:BP:38:ASP:N	2:BP:38:ASP:OD1	2.50	0.43
2:BP:99:TRP:HB3	2:BP:117:LEU:HD12	2.01	0.43
5:RP:151:GLY:O	5:RP:155:SER:OG	2.32	0.43
5:RP:155:SER:OG	5:RP:392:SER:O	2.37	0.43
5:RP:310:ARG:HG2	5:RP:314:LEU:HD23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:RP:201:LEU:HA	5:RP:204:MET:CE	2.48	0.43
4:NP:39:GLN:HB2	4:NP:45:LEU:HG	2.01	0.43
5:RP:202:LYS:CA	5:RP:202:LYS:CE	2.94	0.43
2:BP:253:PHE:HA	2:BP:260:GLU:HA	2.01	0.43
4:NP:82:GLN:NE2	4:NP:84:ASN:OD1	2.52	0.43
6:RP:501:N2V:C15	6:RP:501:N2V:C17	2.93	0.42
4:NP:6:GLU:HA	4:NP:22:CYS:HA	2.01	0.42
5:RP:152:TYR:CE2	5:RP:194:VAL:HG21	2.53	0.42
1:AP:320:THR:HB	1:AP:336:ARG:HA	2.02	0.41
2:BP:20:ASP:HA	2:BP:23:LYS:HB2	2.01	0.41
2:BP:75:GLN:O	2:BP:98:SER:OG	2.37	0.41
2:BP:78:LYS:HD3	2:BP:78:LYS:HA	1.78	0.41
5:RP:176:ARG:HB3	5:RP:250:TYR:HE2	1.85	0.41
5:RP:328:ILE:HD13	5:RP:328:ILE:HA	1.91	0.41
5:RP:143:PHE:HA	5:RP:146:ILE:HG12	2.03	0.41
5:RP:201:LEU:HD12	5:RP:204:MET:CE	2.50	0.41
5:RP:227:ARG:HD3	5:RP:227:ARG:N	2.33	0.41
5:RP:356:LEU:HG	5:RP:360:LEU:HD13	2.03	0.41
1:AP:283:ARG:O	1:AP:357:HIS:ND1	2.53	0.40
5:RP:138:GLU:HA	5:RP:141:LEU:HG	2.04	0.40
5:RP:142:LEU:O	5:RP:146:ILE:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AP	185/394 (47%)	174 (94%)	11 (6%)	0	100	100
2	BP	336/350 (96%)	322 (96%)	14 (4%)	0	100	100
3	GP	55/71 (78%)	54 (98%)	1 (2%)	0	100	100
4	NP	124/138 (90%)	116 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	RP	277/491 (56%)	268 (97%)	9 (3%)	0	100	100
All	All	977/1444 (68%)	934 (96%)	43 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AP	177/349 (51%)	173 (98%)	4 (2%)	50	80
2	BP	281/291 (97%)	281 (100%)	0	100	100
3	GP	46/58 (79%)	46 (100%)	0	100	100
4	NP	104/115 (90%)	104 (100%)	0	100	100
5	RP	250/436 (57%)	243 (97%)	7 (3%)	43	77
All	All	858/1249 (69%)	847 (99%)	11 (1%)	70	89

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AP	24	LYS
1	AP	28	LYS
1	AP	42	ARG
1	AP	317	ARG
5	RP	147	ILE
5	RP	227	ARG
5	RP	296	CYS
5	RP	297	TRP
5	RP	348	ARG
5	RP	379	LEU
5	RP	380	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	AP	23	ASN
1	AP	31	GLN
1	AP	41	HIS
1	AP	227	GLN
1	AP	267	GLN
1	AP	278	ASN
1	AP	292	ASN
2	BP	17	GLN
2	BP	32	GLN
2	BP	88	ASN
2	BP	132	ASN
2	BP	340	ASN
3	GP	59	ASN
4	NP	31	ASN
5	RP	234	GLN
5	RP	240	ASN
5	RP	320	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	N2V	RP	501	-	68,68,68	1.49	11 (16%)	93,97,97	1.19	10 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	N2V	RP	501	-	-	16/39/60/60	0/8/8/8

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	RP	501	N2V	C06-N05	5.15	1.45	1.34
6	RP	501	N2V	O23-C22	5.07	1.43	1.37
6	RP	501	N2V	O42-C21	4.44	1.44	1.38
6	RP	501	N2V	C07-N08	2.73	1.52	1.48
6	RP	501	N2V	C18-N08	2.67	1.48	1.47
6	RP	501	N2V	C44-C19	-2.65	1.35	1.40
6	RP	501	N2V	O46-C06	-2.32	1.18	1.23
6	RP	501	N2V	C34-CL35	2.26	1.79	1.73
6	RP	501	N2V	C36-CL37	2.21	1.78	1.73
6	RP	501	N2V	C26-C25	2.20	1.55	1.51
6	RP	501	N2V	O23-C24	-2.09	1.38	1.44

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	RP	501	N2V	C18-N08-C07	4.34	115.26	108.80
6	RP	501	N2V	C06-C07-N08	-2.71	107.50	111.84
6	RP	501	N2V	C58-N57-C55	2.65	121.58	118.33
6	RP	501	N2V	C56-C55-C53	-2.52	119.38	121.80
6	RP	501	N2V	C59-C58-N57	-2.40	120.98	123.96
6	RP	501	N2V	C21-O42-C25	-2.16	111.88	115.50
6	RP	501	N2V	C31-O30-C29	-2.16	112.33	117.65
6	RP	501	N2V	O01-C02-C04	2.10	120.38	113.40
6	RP	501	N2V	C45-C07-N08	2.09	116.61	111.47
6	RP	501	N2V	O23-C22-C43	2.02	120.16	117.05

There are no chirality outliers.

All (16) torsion outliers are listed below:

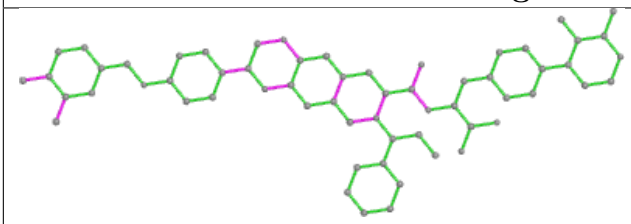
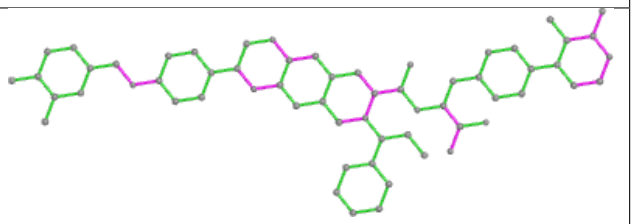
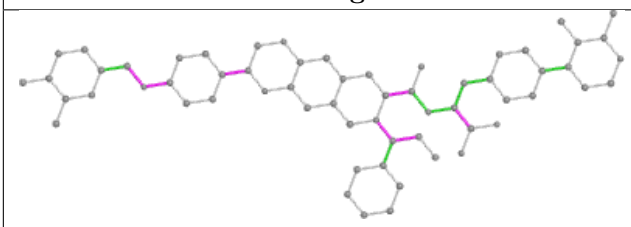
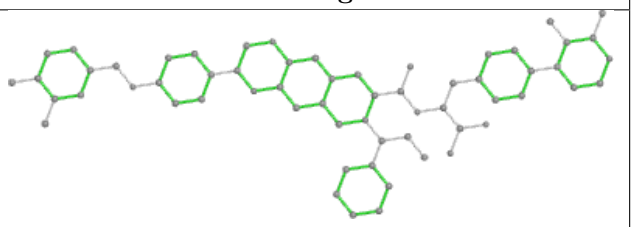
Mol	Chain	Res	Type	Atoms
6	RP	501	N2V	C10-C09-C16-C17
6	RP	501	N2V	N05-C06-C07-C45
6	RP	501	N2V	O46-C06-C07-C45
6	RP	501	N2V	C10-C09-N08-C07
6	RP	501	N2V	C16-C09-N08-C07
6	RP	501	N2V	C40-C29-O30-C31
6	RP	501	N2V	C28-C29-O30-C31
6	RP	501	N2V	N08-C09-C16-C17
6	RP	501	N2V	C32-C31-O30-C29
6	RP	501	N2V	O01-C02-C04-C47
6	RP	501	N2V	N05-C06-C07-N08
6	RP	501	N2V	C16-C09-N08-C18
6	RP	501	N2V	O03-C02-C04-C47
6	RP	501	N2V	O46-C06-C07-N08
6	RP	501	N2V	O42-C25-C26-C41
6	RP	501	N2V	O42-C25-C26-C27

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	RP	501	N2V	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand N2V RP 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

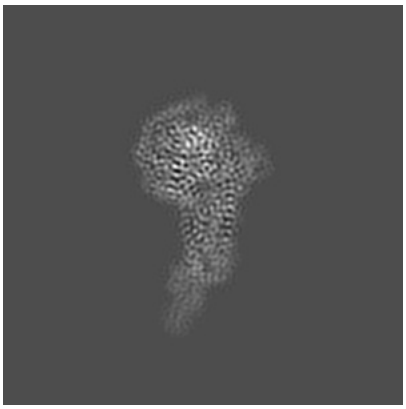
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-20179. These allow visual inspection of the internal detail of the map and identification of artifacts.

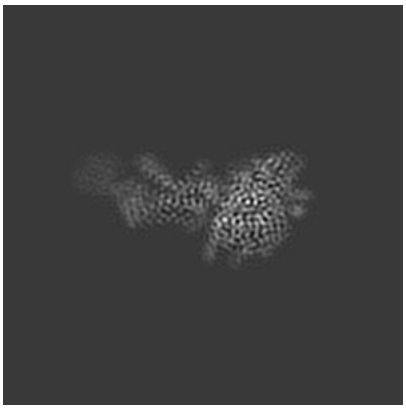
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

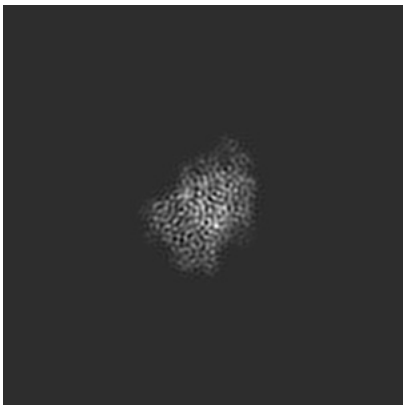
6.1.1 Primary map



X

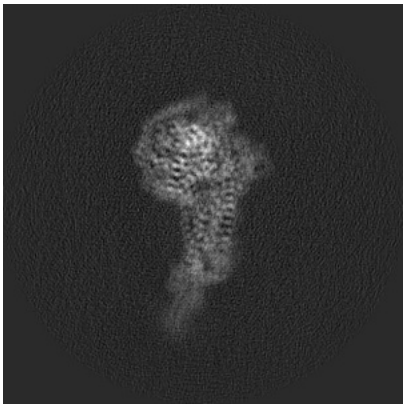


Y

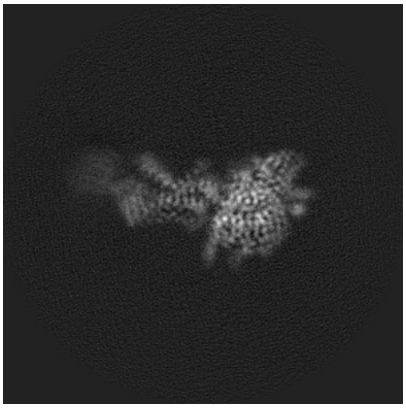


Z

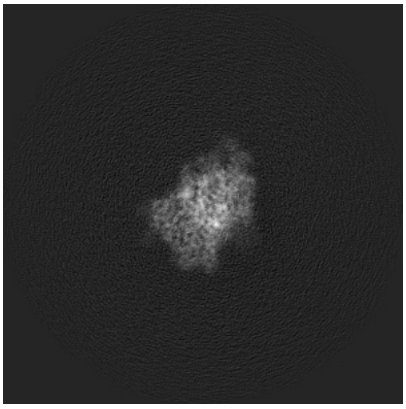
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices (i)

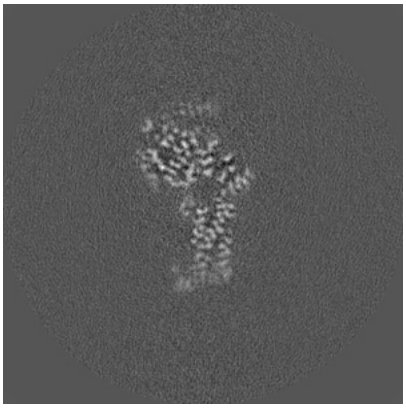
6.2.1 Primary map

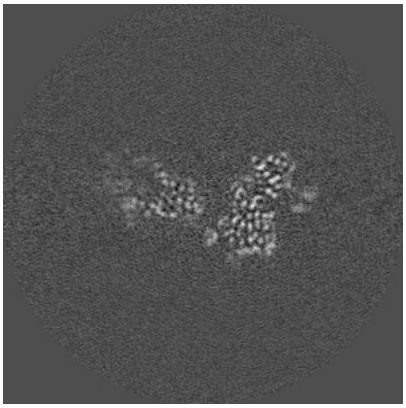
X Index: 144

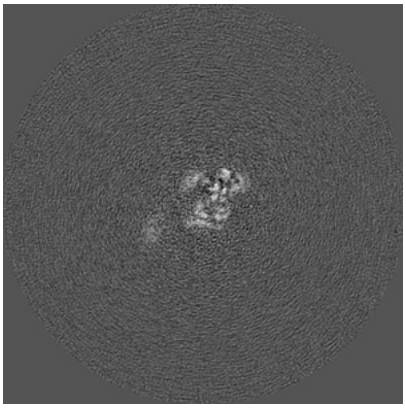
Y Index: 144

Z Index: 144

6.2.2 Raw map


X Index: 144


Y Index: 144


Z Index: 144

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

6.3 Largest variance slices (i)

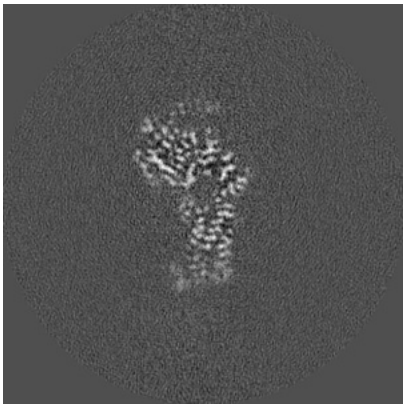
6.3.1 Primary map

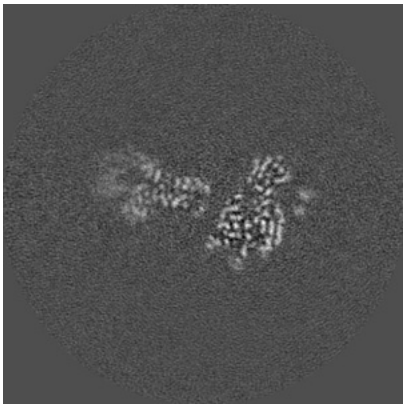
X Index: 146

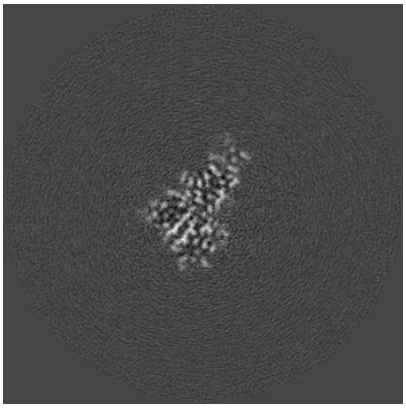
Y Index: 138

Z Index: 171

6.3.2 Raw map


X Index: 145


Y Index: 138


Z Index: 171

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.019. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

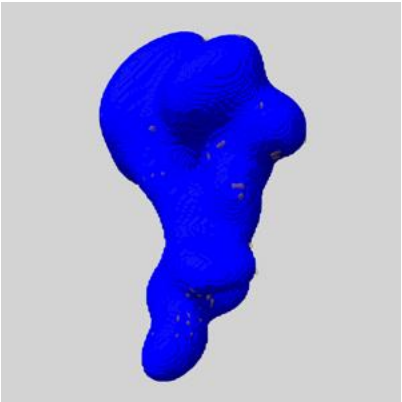
6.5 Mask visualisation (i)

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

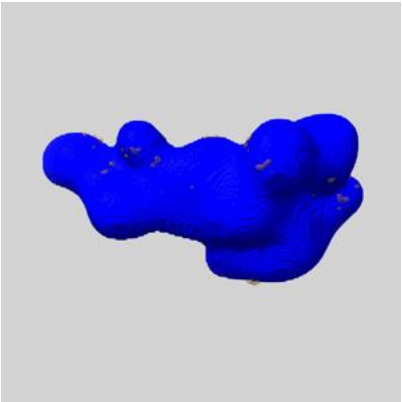
A mask typically either:

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

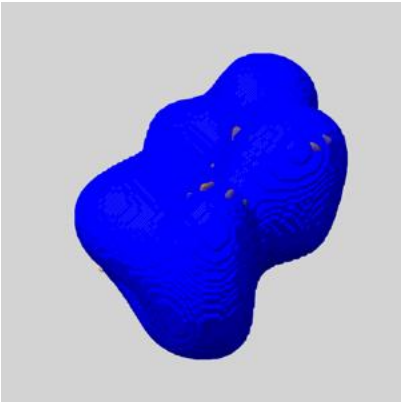
6.5.1 emd_20179_msk_1.map (i)



X



Y

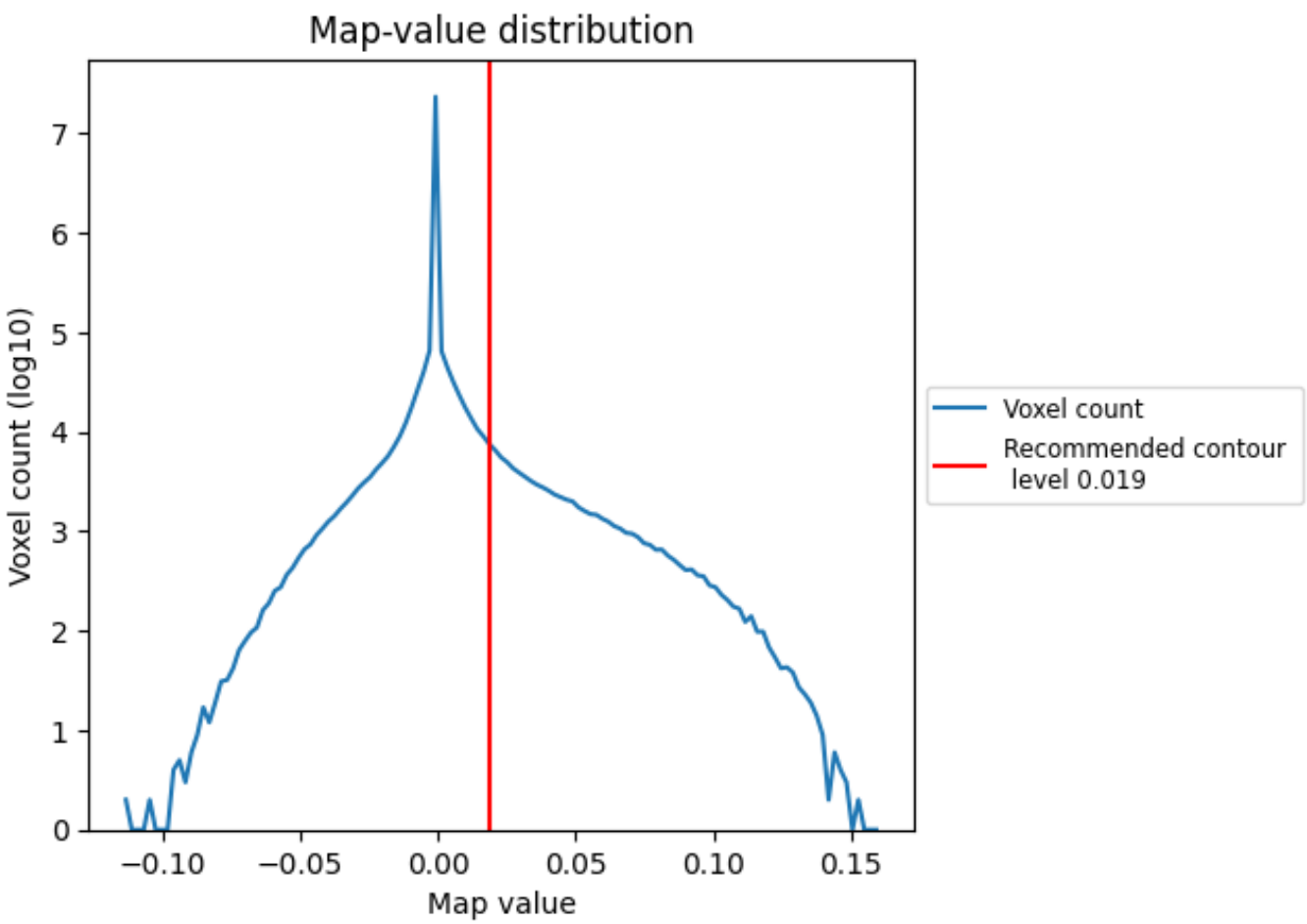


Z

7 Map analysis (i)

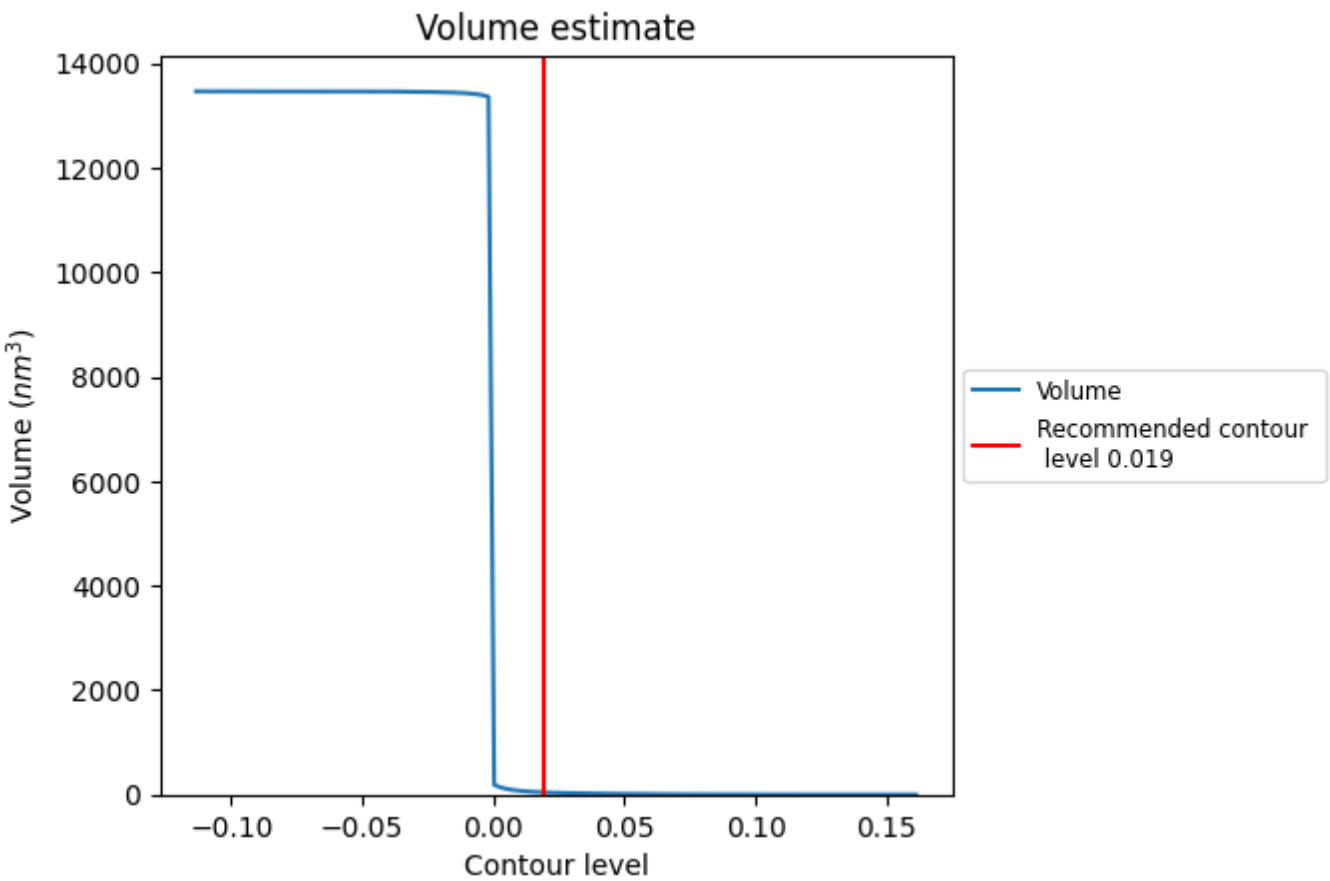
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

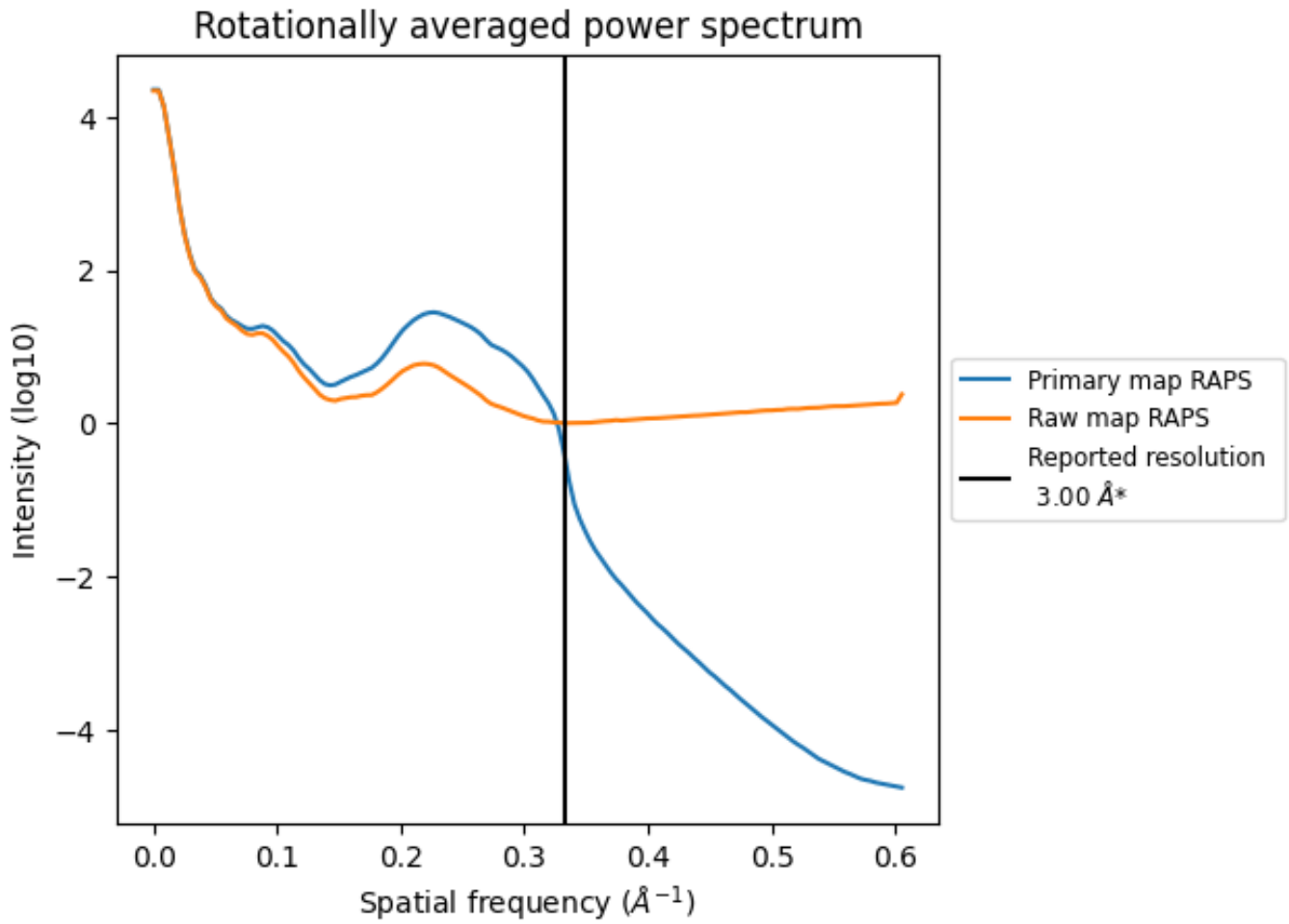
7.2 Volume estimate (i)



The volume at the recommended contour level is 43 nm^3; this corresponds to an approximate mass of 39 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)

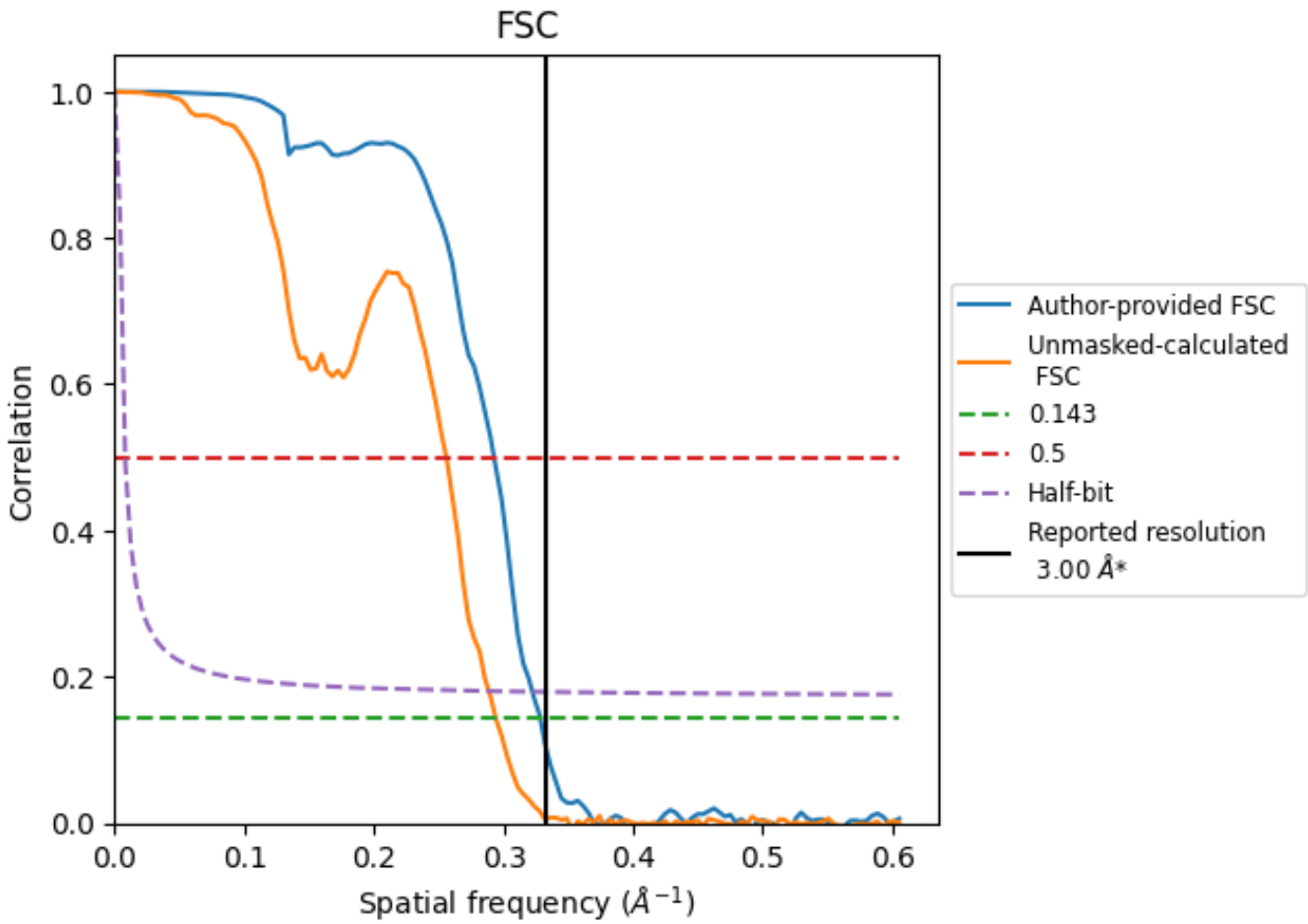


*Reported resolution corresponds to spatial frequency of 0.333 Å^{-1}

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 0.333 Å^{-1}

8.2 Resolution estimates (i)

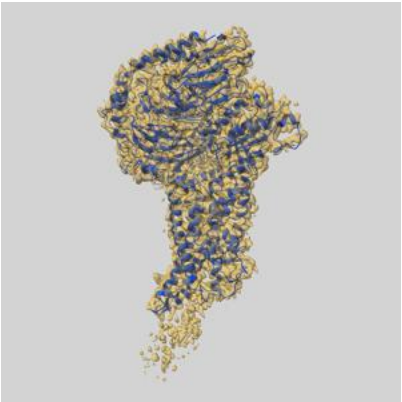
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.05	3.42	3.10
Unmasked-calculated*	3.40	3.91	3.46

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.40 differs from the reported value 3.0 by more than 10 %

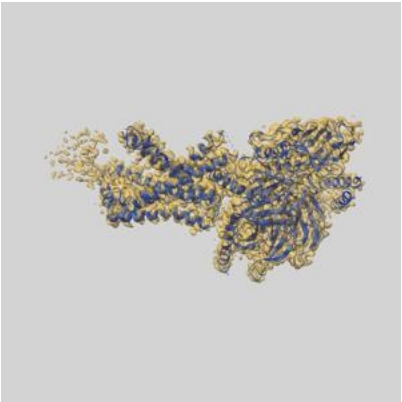
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-20179 and PDB model 6ORV. Per-residue inclusion information can be found in section 3 on page 7.

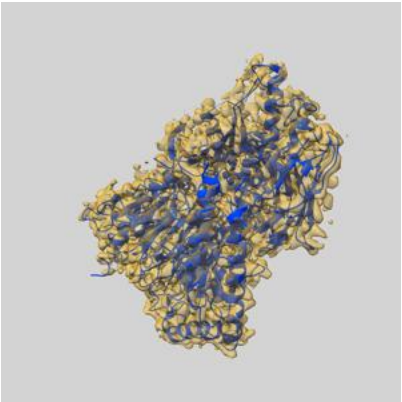
9.1 Map-model overlay (i)



X



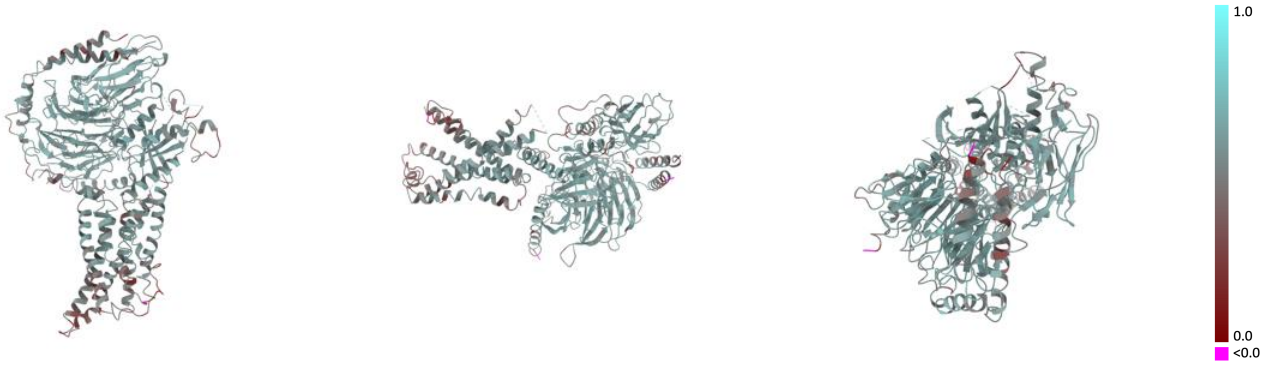
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

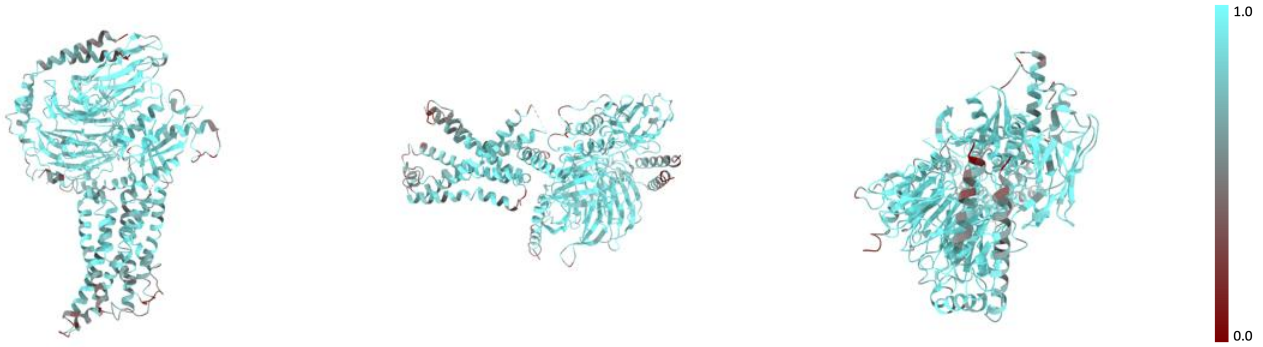
9.2 Q-score mapped to coordinate model (i)



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.

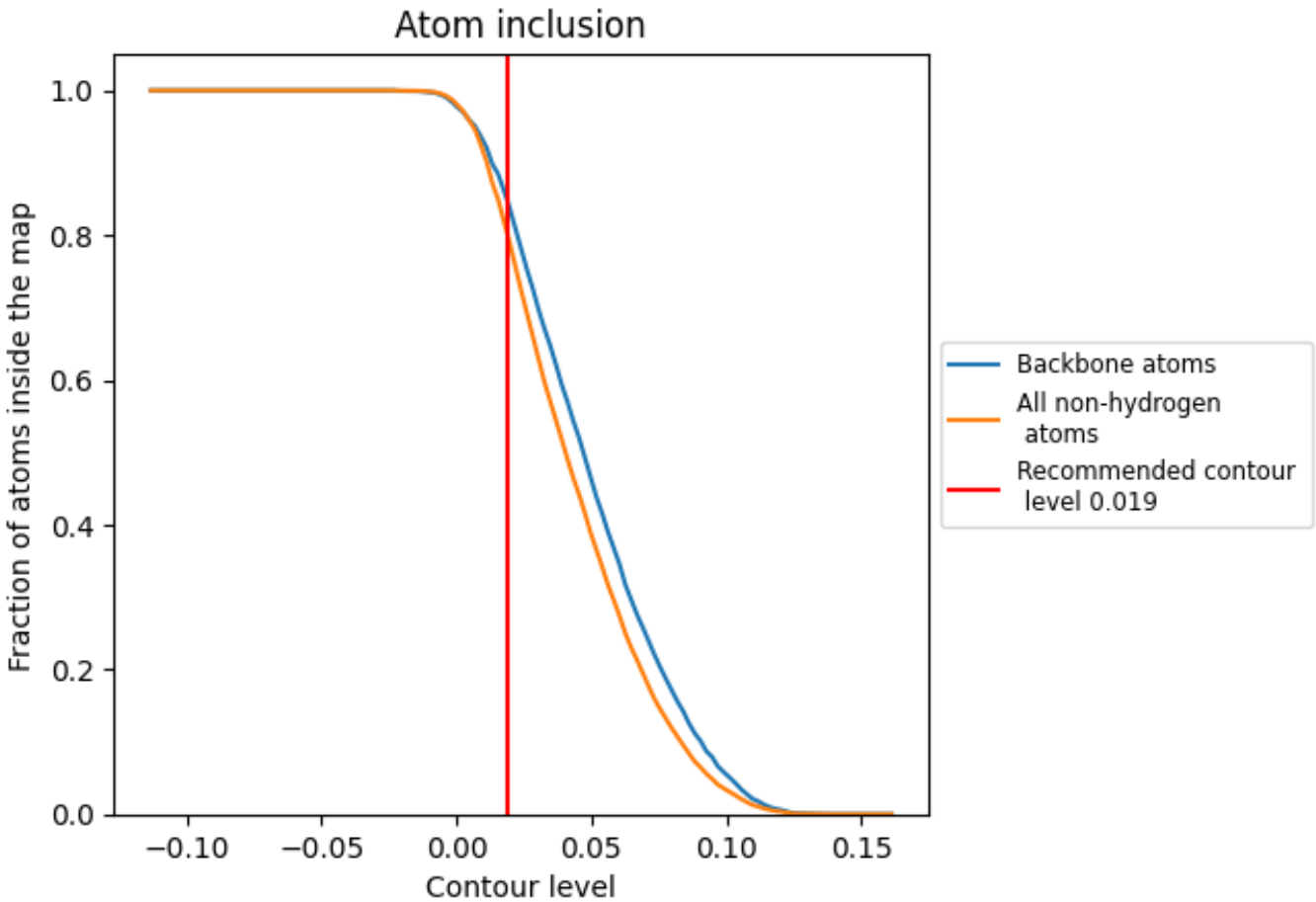
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.019).

9.4 Atom inclusion (i)



At the recommended contour level, 85% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7997	0.5380
AP	0.8136	0.5480
BP	0.8752	0.5780
GP	0.6970	0.5040
NP	0.8550	0.5730
RP	0.7046	0.4780