



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:55 PM UTC

PDB ID : 6AVR / pdb_00006avr
EMDB ID : EMD-7012
Title : Human alpha-V beta-3 Integrin (intermediate conformation) in complex with the therapeutic antibody LM609
Authors : Borst, A.J.; James, Z.N.; Zagotta, W.N.; Ginsberg, M.; Rey, F.A.; DiMaio, F.; Backovic, M.; Veesler, D.
Deposited on : 2017-09-04
Resolution : 35.00 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 ⓘ 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:

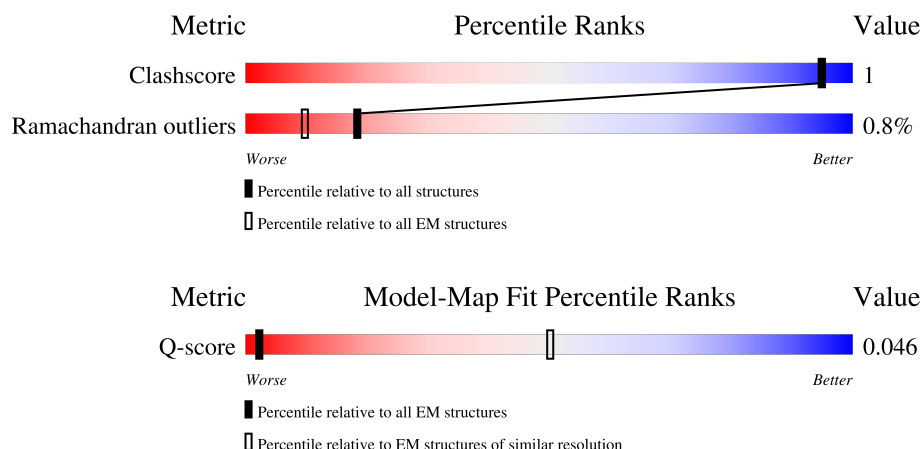
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 35.00 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	12 (35.00 - 35.00)

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

Mol	Chain	Length	Quality of chain
1	A	957	18% 89% 7% .
2	B	692	34% 90% 8% ..
3	H	257	6% 78% 5% 17%
4	L	214	92% 6% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10016 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 Integrin alpha-V.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	924	Total	C	N	O	0	0
			4547	2699	924	924		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	753	ILE	VAL	conflict	UNP P06756

- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	685	Total	C	N	O	0	0
			3375	2005	685	685		

- Molecule 3 is a protein called Fab LM609 heavy chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	H	214	Total	C	N	O	0	0
			1052	624	214	214		

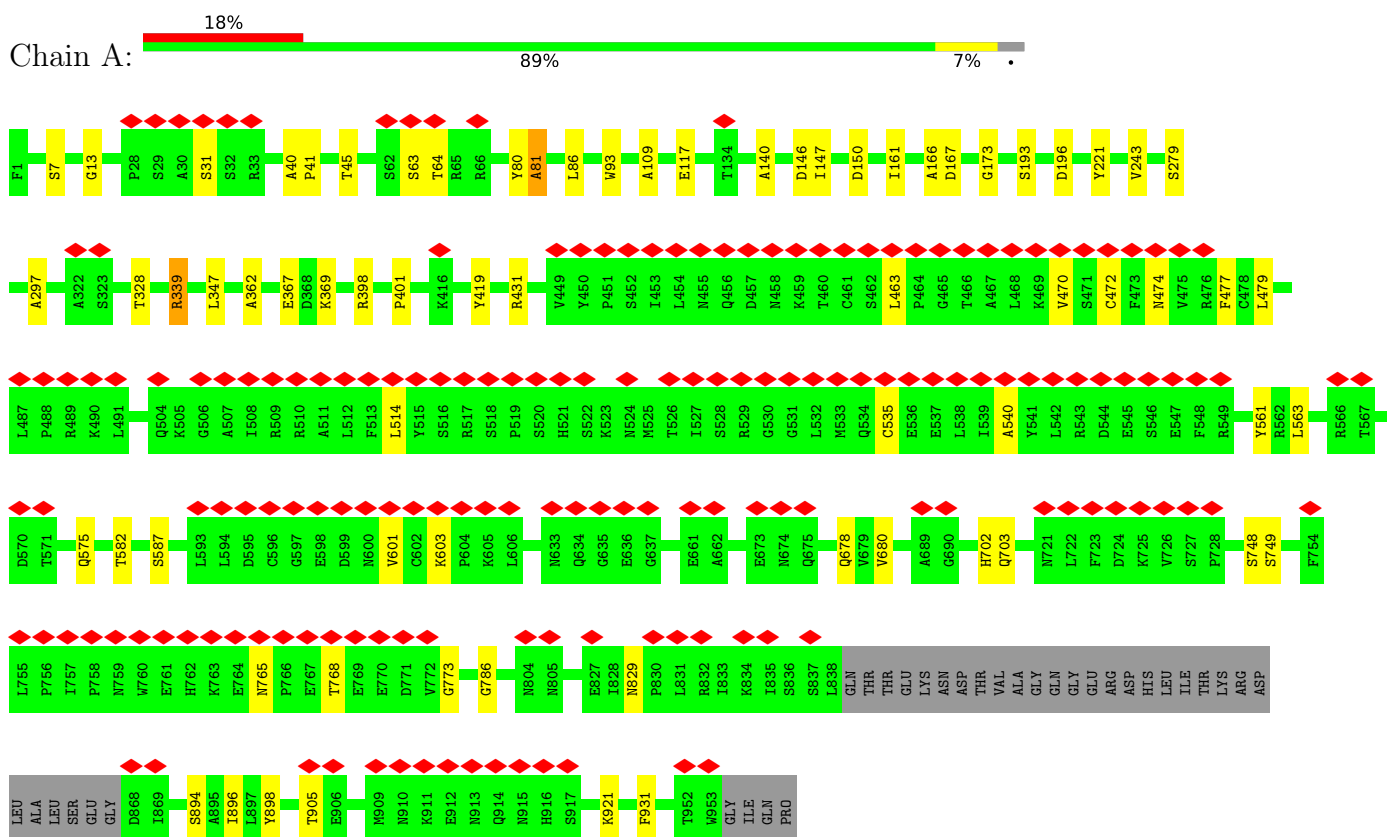
- Molecule 4 is a protein called Fab LM609 light chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	L	211	Total	C	N	O	0	0
			1042	620	211	211		

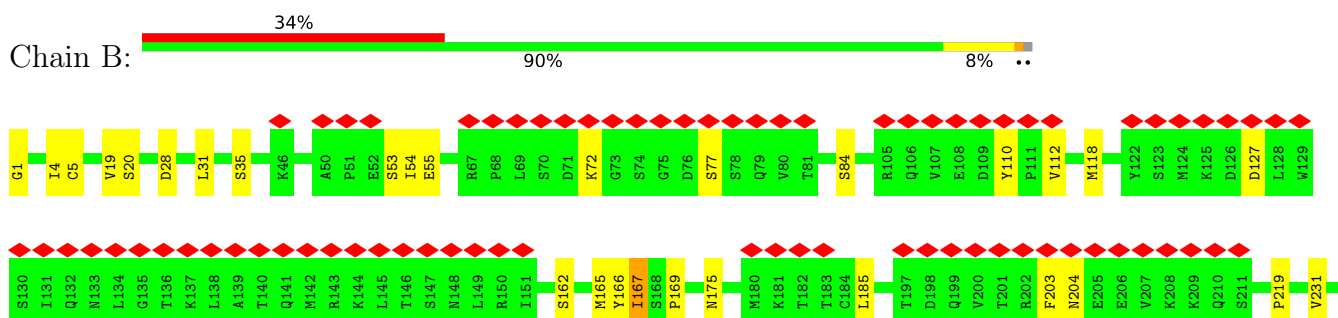
3 Residue-property plots

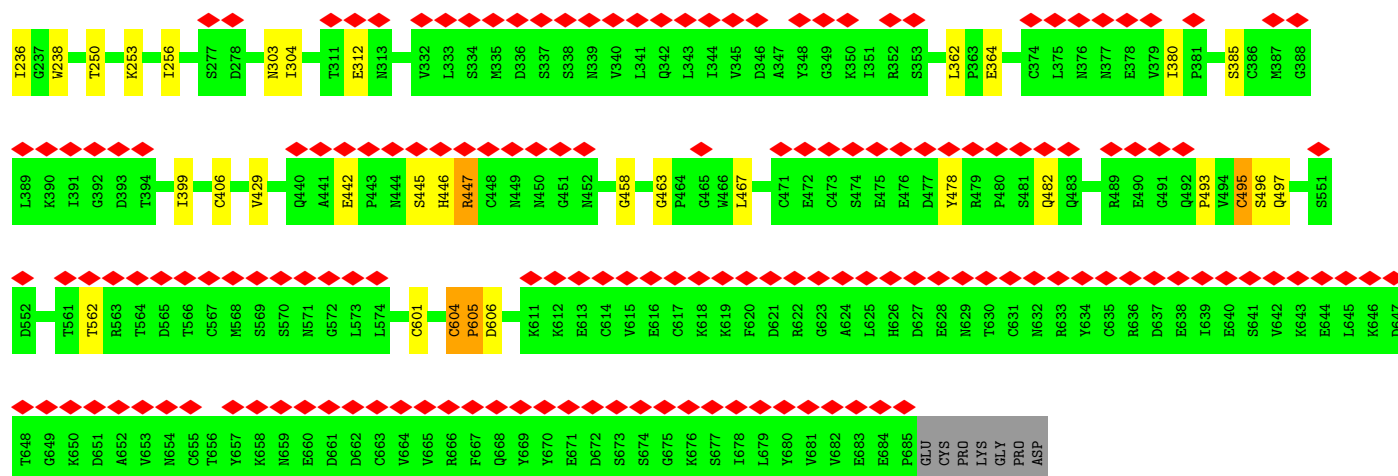
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Integrin alpha-V

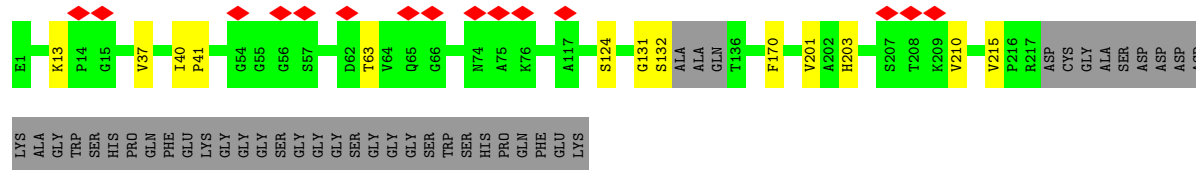
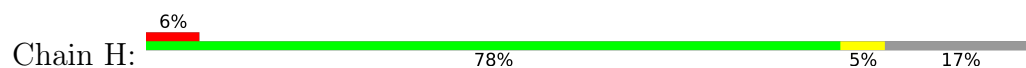


• Molecule 2: Integrin beta-3

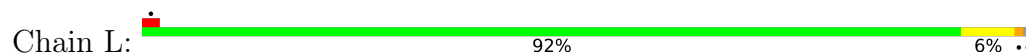




• Molecule 3: Fab LM609 heavy chain



• Molecule 4: Fab LM609 light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	650	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI 12	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	32.642	Depositor
Minimum map value	-14.180	Depositor
Average map value	0.068	Depositor
Map value standard deviation	0.963	Depositor
Recommended contour level	3.8	Depositor
Map size ($\text{\AA}$)	461.5776, 461.5776, 461.5776	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.2054, 3.2054, 3.2054	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.85	3/4545 (0.1%)	1.66	93/6316 (1.5%)
2	B	0.86	2/3374 (0.1%)	1.59	56/4692 (1.2%)
3	H	0.80	0/1050	1.46	17/1456 (1.2%)
4	L	0.76	0/1040	1.53	17/1445 (1.2%)
All	All	0.84	5/10009 (0.0%)	1.60	183/13909 (1.3%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	604	CYS	CA-C	-6.75	1.45	1.53
1	A	81	ALA	CA-C	-6.28	1.44	1.53
2	B	605	PRO	N-CA	-6.01	1.40	1.47
1	A	894	SER	CA-CB	-5.25	1.46	1.53
1	A	109	ALA	CA-CB	-5.00	1.46	1.53

All (183) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	362	ALA	CA-C-N	9.65	129.40	119.56
1	A	362	ALA	C-N-CA	9.65	129.40	119.56
2	B	175	ASN	CA-C-N	8.76	130.79	119.84
2	B	175	ASN	C-N-CA	8.76	130.79	119.84
1	A	40	ALA	CA-C-N	8.63	129.49	119.47
1	A	40	ALA	C-N-CA	8.63	129.49	119.47
4	L	32	HIS	CB-CA-C	-8.60	98.83	111.91
1	A	173	GLY	CA-C-N	8.55	128.28	119.56
1	A	173	GLY	C-N-CA	8.55	128.28	119.56
2	B	53	SER	N-CA-C	-8.33	102.31	114.39
1	A	297	ALA	CA-C-N	8.12	127.84	119.56
1	A	297	ALA	C-N-CA	8.12	127.84	119.56
1	A	347	LEU	N-CA-C	-8.11	103.98	114.04
2	B	493	PRO	N-CA-C	-8.07	99.10	111.13
1	A	894	SER	N-CA-CB	-7.79	98.31	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	362	LEU	CA-C-N	7.53	127.45	119.85
2	B	362	LEU	C-N-CA	7.53	127.45	119.85
4	L	199	LYS	N-CA-C	-7.50	100.66	110.33
1	A	243	VAL	CA-C-N	7.43	127.14	119.56
1	A	243	VAL	C-N-CA	7.43	127.14	119.56
1	A	339	ARG	CA-C-N	7.42	131.21	120.38
1	A	339	ARG	C-N-CA	7.42	131.21	120.38
2	B	165	MET	CA-C-N	-7.34	110.67	121.24
2	B	165	MET	C-N-CA	-7.34	110.67	121.24
1	A	773	GLY	CA-C-N	7.32	127.37	119.90
1	A	773	GLY	C-N-CA	7.32	127.37	119.90
1	A	470	VAL	N-CA-C	7.26	118.28	108.11
2	B	20	SER	CA-C-N	7.25	126.95	119.56
2	B	20	SER	C-N-CA	7.25	126.95	119.56
1	A	196	ASP	CA-C-N	7.17	126.88	119.56
1	A	196	ASP	C-N-CA	7.17	126.88	119.56
2	B	166	TYR	N-CA-C	-7.16	99.06	109.59
1	A	603	LYS	CA-C-N	7.09	127.51	119.92
1	A	603	LYS	C-N-CA	7.09	127.51	119.92
3	H	203	HIS	CA-C-N	6.93	127.22	119.32
3	H	203	HIS	C-N-CA	6.93	127.22	119.32
1	A	829	ASN	CA-C-N	6.93	126.56	119.56
1	A	829	ASN	C-N-CA	6.93	126.56	119.56
1	A	31	SER	N-CA-C	6.91	117.71	108.38
1	A	479	LEU	N-CA-C	6.91	120.92	108.69
2	B	250	THR	N-CA-C	6.85	119.28	108.79
1	A	161	ILE	N-CA-C	6.83	118.18	108.42
1	A	575	GLN	CA-C-N	6.72	126.90	120.31
1	A	575	GLN	C-N-CA	6.72	126.90	120.31
2	B	185	LEU	CA-C-N	6.72	126.67	120.21
2	B	185	LEU	C-N-CA	6.72	126.67	120.21
1	A	13	GLY	CA-C-N	6.71	126.75	119.90
1	A	13	GLY	C-N-CA	6.71	126.75	119.90
1	A	896	ILE	N-CA-C	6.66	118.19	108.53
2	B	406	CYS	CA-C-N	6.56	126.54	119.78
2	B	406	CYS	C-N-CA	6.56	126.54	119.78
1	A	147	ILE	N-CA-C	6.52	121.28	111.89
1	A	463	LEU	N-CA-C	-6.40	101.59	109.65
1	A	601	VAL	CA-C-N	-6.37	112.03	120.95
1	A	601	VAL	C-N-CA	-6.37	112.03	120.95
4	L	96	HIS	CB-CA-C	6.30	120.43	109.65
1	A	401	PRO	CA-C-N	6.29	126.20	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	401	PRO	C-N-CA	6.29	126.20	119.28
1	A	561	TYR	N-CA-C	6.23	119.55	109.40
4	L	203	SER	CA-C-N	6.22	126.19	119.78
4	L	203	SER	C-N-CA	6.22	126.19	119.78
1	A	328	THR	N-CA-C	6.21	118.74	108.99
1	A	786	GLY	CA-C-N	6.20	125.83	119.56
1	A	786	GLY	C-N-CA	6.20	125.83	119.56
3	H	63	THR	CA-C-N	6.20	128.68	122.66
3	H	63	THR	C-N-CA	6.20	128.68	122.66
2	B	110	TYR	CA-C-N	6.19	126.15	119.78
2	B	110	TYR	C-N-CA	6.19	126.15	119.78
1	A	109	ALA	CA-C-N	6.16	125.84	119.56
1	A	109	ALA	C-N-CA	6.16	125.84	119.56
1	A	931	PHE	CA-C-N	6.08	125.70	119.56
1	A	931	PHE	C-N-CA	6.08	125.70	119.56
1	A	898	TYR	CB-CA-C	-6.03	99.29	109.72
2	B	256	ILE	N-CA-C	6.02	116.16	108.82
2	B	312	GLU	N-CA-C	6.00	117.83	111.28
3	H	124	SER	CA-C-N	-5.99	115.76	123.19
3	H	124	SER	C-N-CA	-5.99	115.76	123.19
2	B	167	ILE	N-CA-C	5.98	121.78	109.34
2	B	380	ILE	CA-C-N	5.98	125.89	119.85
2	B	380	ILE	C-N-CA	5.98	125.89	119.85
1	A	86	LEU	N-CA-C	-5.97	105.99	113.28
1	A	146	ASP	CA-C-N	5.96	130.82	120.86
1	A	146	ASP	C-N-CA	5.96	130.82	120.86
1	A	140	ALA	CA-C-N	5.92	125.60	119.56
1	A	140	ALA	C-N-CA	5.92	125.60	119.56
1	A	81	ALA	CA-C-N	-5.88	113.09	121.50
1	A	81	ALA	C-N-CA	-5.88	113.09	121.50
2	B	385	SER	N-CA-C	5.88	118.00	109.07
3	H	215	VAL	CA-C-N	5.80	125.75	119.78
3	H	215	VAL	C-N-CA	5.80	125.75	119.78
4	L	50	TYR	N-CA-CB	-5.79	103.14	111.70
3	H	201	VAL	N-CA-C	5.77	116.17	107.80
1	A	472	CYS	N-CA-C	5.76	117.54	108.96
1	A	45	THR	CA-C-N	5.76	127.99	120.28
1	A	45	THR	C-N-CA	5.76	127.99	120.28
1	A	167	ASP	N-CA-C	5.74	121.20	112.54
2	B	478	TYR	N-CA-C	-5.74	104.85	112.94
1	A	514	LEU	N-CA-C	5.71	117.50	111.28
1	A	921	LYS	N-CA-C	5.70	117.70	108.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	477	PHE	N-CA-C	5.70	118.08	107.99
2	B	169	PRO	CA-C-N	5.68	126.94	119.84
2	B	169	PRO	C-N-CA	5.68	126.94	119.84
2	B	1	GLY	CA-C-N	5.68	126.94	119.84
2	B	1	GLY	C-N-CA	5.68	126.94	119.84
4	L	55	ILE	N-CA-C	5.64	121.07	109.34
1	A	540	ALA	CA-C-N	5.63	130.26	122.77
1	A	540	ALA	C-N-CA	5.63	130.26	122.77
2	B	463	GLY	CA-C-N	5.63	125.64	119.90
2	B	463	GLY	C-N-CA	5.63	125.64	119.90
4	L	118	PHE	CA-C-N	5.62	126.17	120.38
4	L	118	PHE	C-N-CA	5.62	126.17	120.38
2	B	562	THR	N-CA-C	-5.61	105.78	113.30
2	B	304	ILE	CB-CA-C	-5.61	103.29	110.98
4	L	58	ILE	CA-C-N	5.60	125.55	119.78
4	L	58	ILE	C-N-CA	5.60	125.55	119.78
3	H	170	PHE	CA-C-N	5.59	125.52	119.76
3	H	170	PHE	C-N-CA	5.59	125.52	119.76
2	B	399	ILE	N-CA-C	5.51	115.83	108.11
3	H	40	ILE	CA-C-N	5.50	126.71	119.84
3	H	40	ILE	C-N-CA	5.50	126.71	119.84
1	A	431	ARG	N-CA-C	5.49	117.53	109.24
2	B	31	LEU	CA-C-N	5.49	126.70	119.84
2	B	31	LEU	C-N-CA	5.49	126.70	119.84
2	B	5	CYS	CA-C-N	5.48	127.63	120.28
2	B	5	CYS	C-N-CA	5.48	127.63	120.28
1	A	419	TYR	CA-C-N	5.48	125.38	119.85
1	A	419	TYR	C-N-CA	5.48	125.38	119.85
2	B	601	CYS	CA-C-N	5.48	125.56	119.32
2	B	601	CYS	C-N-CA	5.48	125.56	119.32
4	L	206	VAL	N-CA-C	5.45	115.74	108.11
1	A	221	TYR	N-CA-C	5.45	119.14	111.52
1	A	587	SER	N-CA-C	5.44	117.34	109.07
2	B	19	VAL	N-CA-C	5.42	116.08	110.82
2	B	118	MET	N-CA-C	5.40	118.61	109.76
2	B	112	VAL	N-CA-C	5.38	115.65	108.11
1	A	193	SER	N-CA-C	5.37	117.22	111.36
2	B	303	ASN	N-CA-C	5.37	118.99	111.74
4	L	98	PHE	N-CA-CB	-5.37	101.91	111.08
1	A	150	ASP	N-CA-C	-5.36	105.52	111.36
1	A	680	VAL	N-CA-C	5.36	115.70	107.77
1	A	81	ALA	N-CA-CB	5.36	118.59	110.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	367	GLU	N-CA-C	-5.35	101.94	109.96
3	H	210	VAL	N-CA-C	5.35	115.59	108.11
1	A	474	ASN	N-CA-C	5.34	117.01	108.41
4	L	50	TYR	CA-C-N	5.33	131.72	121.54
4	L	50	TYR	C-N-CA	5.33	131.72	121.54
2	B	238	TRP	CB-CA-C	-5.33	101.16	109.84
4	L	119	PRO	CA-C-N	5.32	125.24	119.76
4	L	119	PRO	C-N-CA	5.32	125.24	119.76
1	A	279	SER	CA-C-N	-5.32	116.59	123.19
1	A	279	SER	C-N-CA	-5.32	116.59	123.19
2	B	429	VAL	N-CA-C	5.32	115.55	108.11
1	A	582	THR	CA-C-N	5.30	125.20	119.85
1	A	582	THR	C-N-CA	5.30	125.20	119.85
1	A	678	GLN	N-CA-C	5.30	117.31	108.99
1	A	7	SER	CA-C-N	5.29	125.27	120.03
1	A	7	SER	C-N-CA	5.29	125.27	120.03
1	A	80	TYR	N-CA-C	-5.29	99.53	110.80
2	B	605	PRO	N-CA-C	-5.24	102.86	111.15
2	B	72	LYS	CA-C-N	5.23	126.67	120.14
2	B	72	LYS	C-N-CA	5.23	126.67	120.14
2	B	231	VAL	N-CA-C	5.23	116.70	111.00
1	A	563	LEU	N-CA-C	-5.21	100.82	109.46
2	B	236	ILE	CB-CA-C	5.20	120.69	112.26
2	B	442	GLU	CA-C-N	5.20	126.34	119.84
2	B	442	GLU	C-N-CA	5.20	126.34	119.84
1	A	398	ARG	N-CA-C	-5.17	105.33	111.69
2	B	127	ASP	N-CA-C	-5.14	105.36	111.69
3	H	13	LYS	CA-C-N	5.12	125.12	119.90
3	H	13	LYS	C-N-CA	5.12	125.12	119.90
1	A	369	LYS	CA-C-N	5.11	129.37	120.68
1	A	369	LYS	C-N-CA	5.11	129.37	120.68
1	A	41	PRO	N-CA-C	5.10	121.20	113.81
3	H	37	VAL	CB-CA-C	5.07	117.73	110.33
1	A	117	GLU	CA-C-N	5.07	127.07	120.28
1	A	117	GLU	C-N-CA	5.07	127.07	120.28
1	A	93	TRP	N-CA-C	5.06	118.58	111.74
2	B	169	PRO	N-CA-C	-5.06	104.53	110.70
2	B	364	GLU	N-CA-C	5.05	117.52	111.71
1	A	765	ASN	CA-C-N	5.05	124.95	119.85
1	A	765	ASN	C-N-CA	5.05	124.95	119.85
1	A	905	THR	N-CA-C	5.05	117.44	111.33
1	A	535	CYS	N-CA-C	5.02	116.44	108.96

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4547	0	2076	5	0
2	B	3375	0	1470	8	0
3	H	1052	0	476	1	0
4	L	1042	0	447	4	0
All	All	10016	0	4469	16	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 1.

All (16) 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)
4:L:198:HIS:C	4:L:199:LYS:O	2.46	0.53
1:A:81:ALA:HB2	4:L:56:SER:N	2.28	0.48
1:A:63:SER:O	1:A:64:THR:C	2.58	0.47
2:B:604:CYS:O	2:B:605:PRO:C	2.55	0.47
1:A:702:HIS:O	1:A:703:GLN:C	2.62	0.43
2:B:605:PRO:O	2:B:606:ASP:C	2.61	0.43
4:L:29:ILE:O	4:L:30:SER:C	2.62	0.43
2:B:495:CYS:O	2:B:496:SER:C	2.61	0.42
1:A:81:ALA:HB2	4:L:55:ILE:C	2.44	0.42
2:B:54:ILE:O	2:B:55:GLU:C	2.61	0.42
2:B:446:HIS:O	2:B:447:ARG:CB	2.67	0.42
2:B:28:ASP:H	2:B:458:GLY:HA3	1.84	0.42
3:H:131:GLY:O	3:H:132:SER:C	2.61	0.42
1:A:748:SER:O	1:A:749:SER:C	2.64	0.41
2:B:219:PRO:HA	2:B:253:LYS:O	2.21	0.41
2:B:203:PHE:O	2:B:204:ASN:C	2.63	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	920/957 (96%)	883 (96%)	34 (4%)	3 (0%)	36	72
2	B	683/692 (99%)	637 (93%)	34 (5%)	12 (2%)	6	34
3	H	210/257 (82%)	209 (100%)	0	1 (0%)	24	63
4	L	207/214 (97%)	195 (94%)	11 (5%)	1 (0%)	24	63
All	All	2020/2120 (95%)	1924 (95%)	79 (4%)	17 (1%)	18	54

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	35	SER
2	B	167	ILE
2	B	467	LEU
1	A	339	ARG
1	A	166	ALA
1	A	768	THR
2	B	77	SER
2	B	445	SER
2	B	495	CYS
2	B	497	GLN
4	L	56	SER
2	B	84	SER
2	B	162	SER
2	B	447	ARG
2	B	482	GLN
2	B	4	ILE
3	H	41	PRO

5.3.2 Protein sidechains

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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-7012. These allow visual inspection of the internal detail of the map and identification of artifacts.

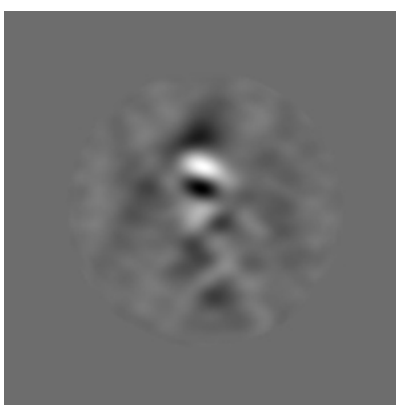
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

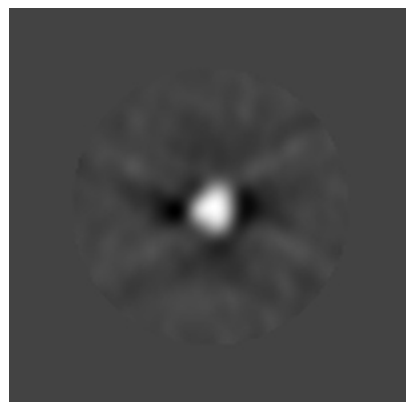


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 72



Y Index: 72

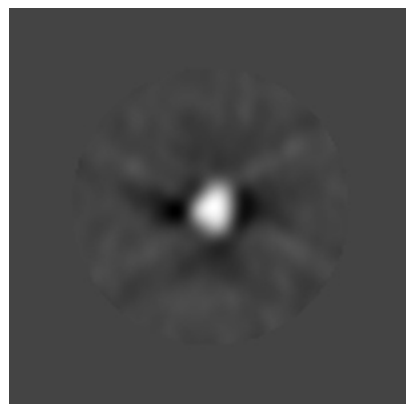


Z Index: 72

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: 73



Y Index: 74

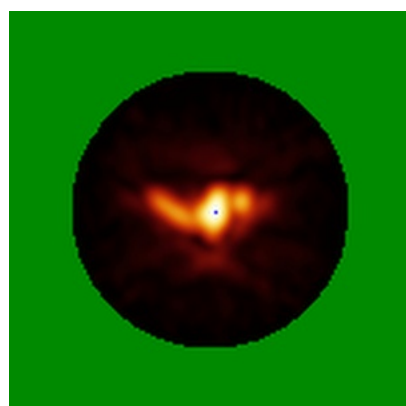


Z Index: 72

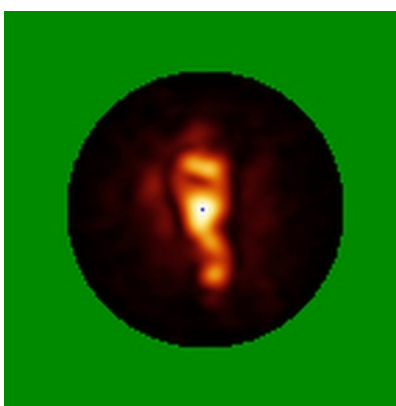
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

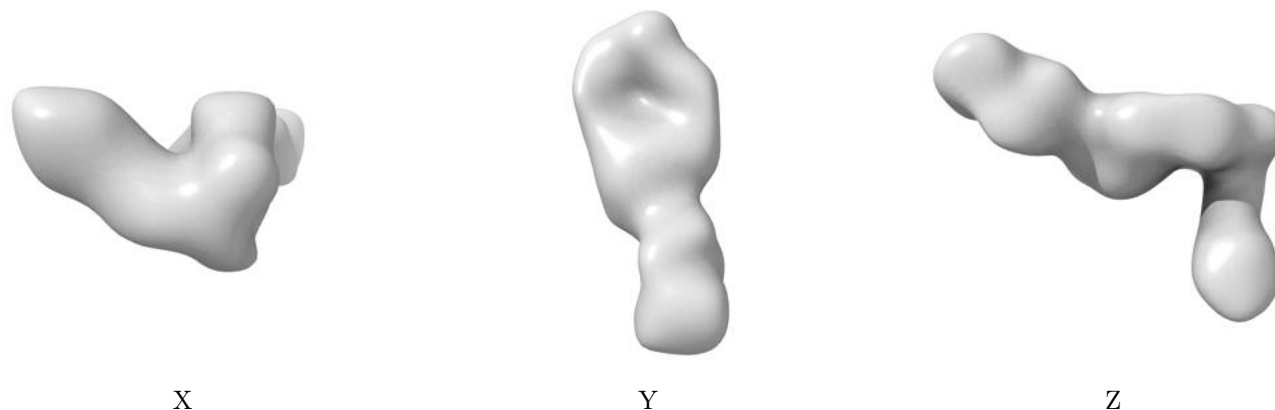


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

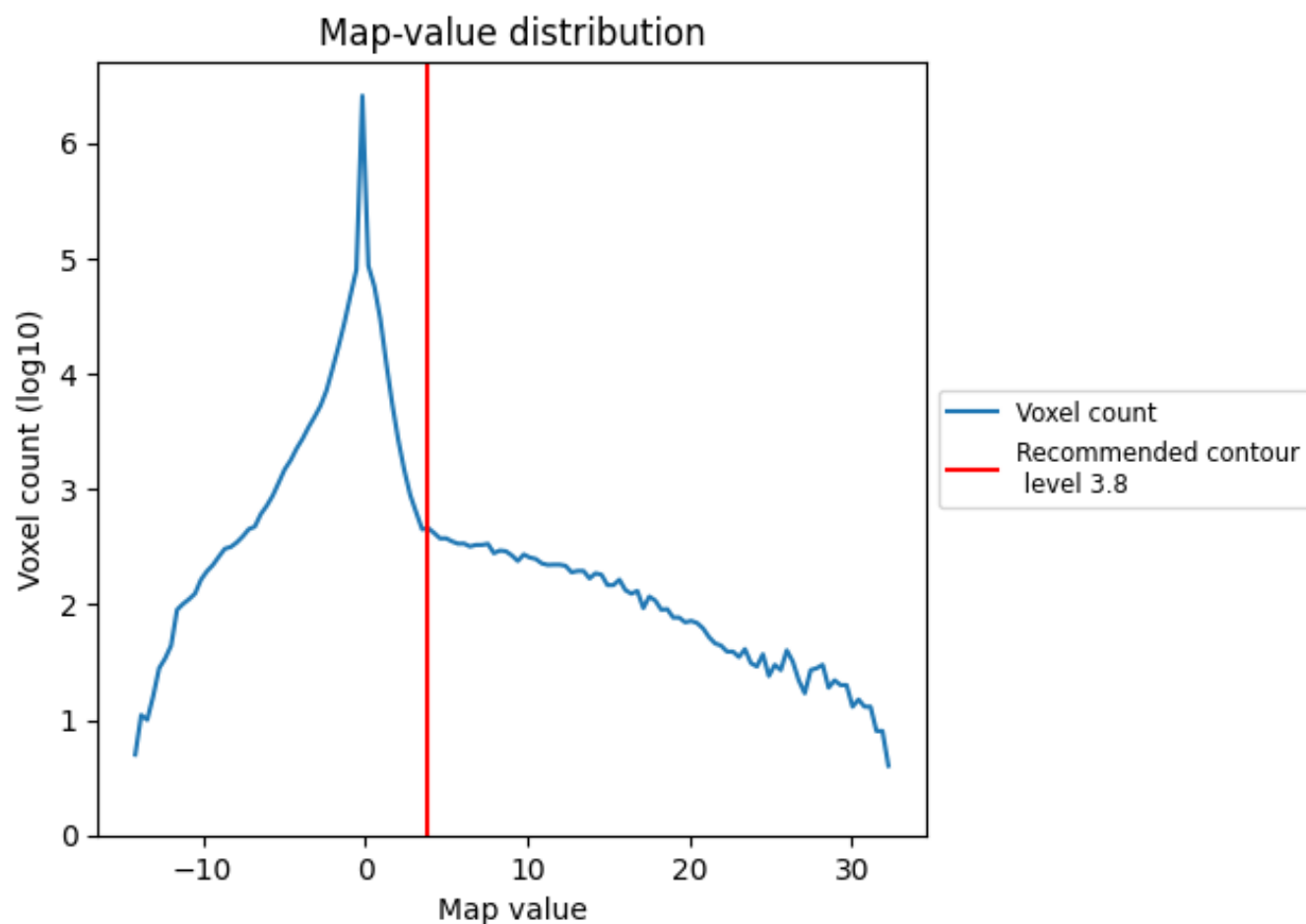
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

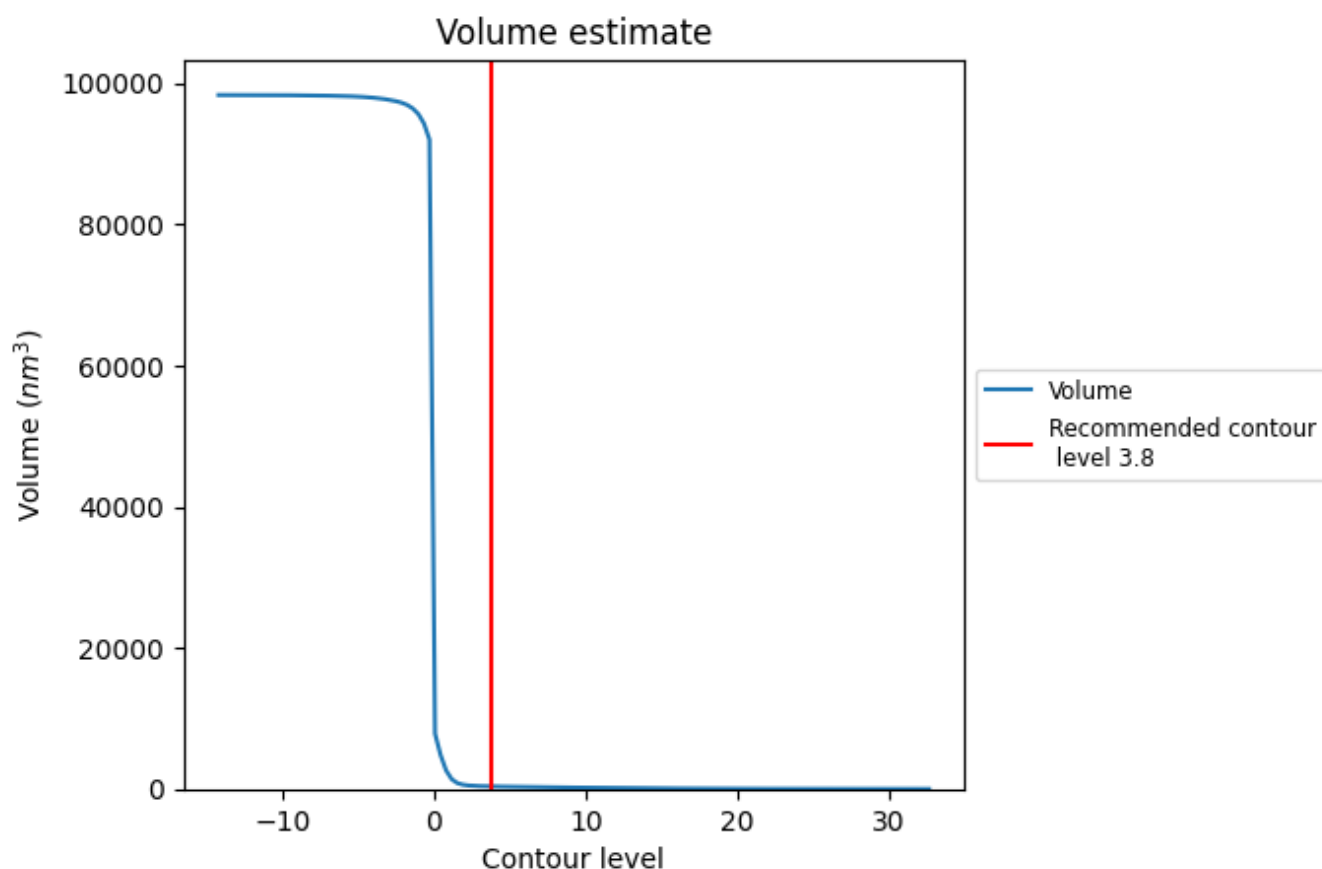
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

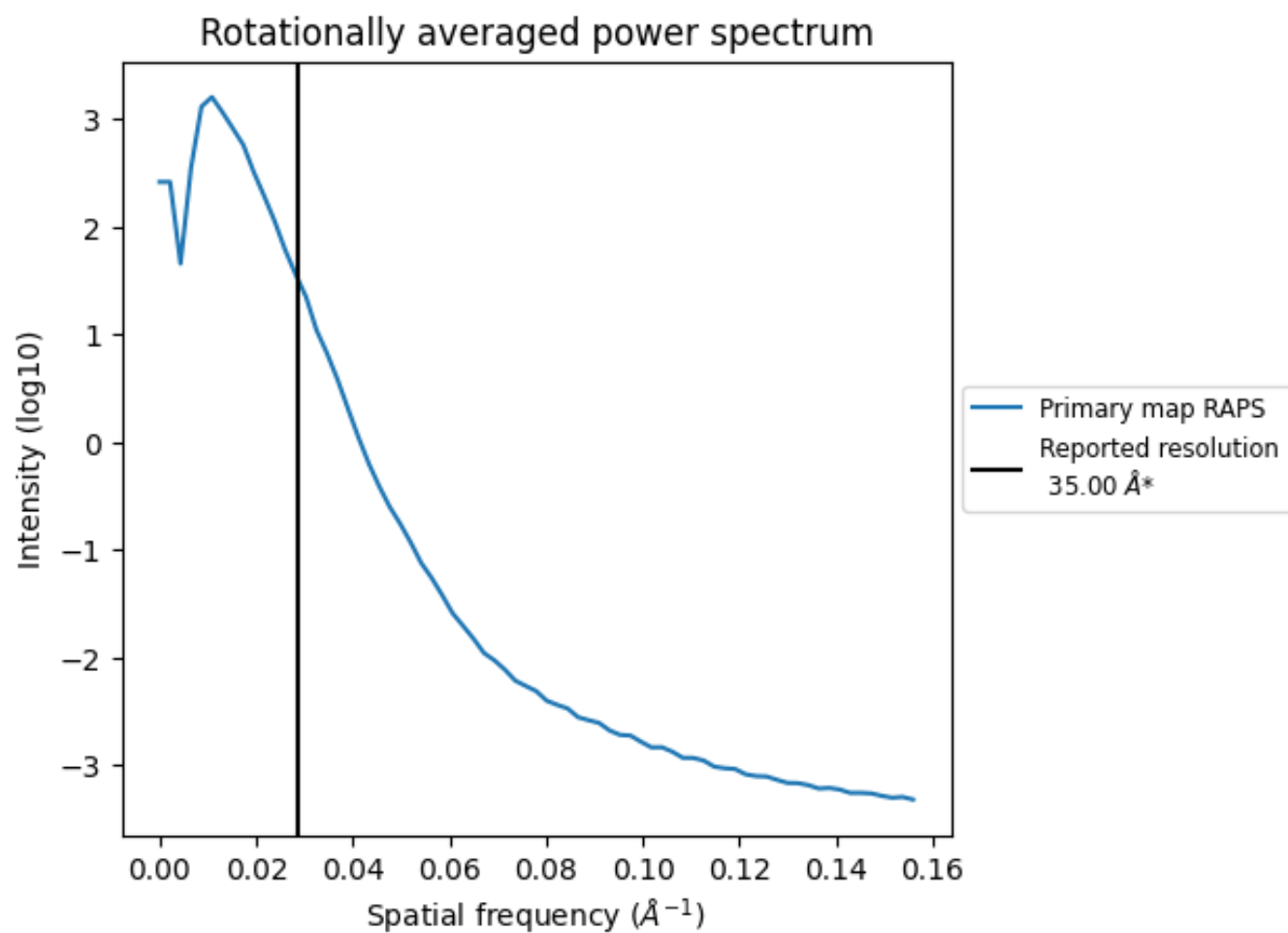
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 363 nm³; this corresponds to an approximate mass of 328 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.029 Å⁻¹

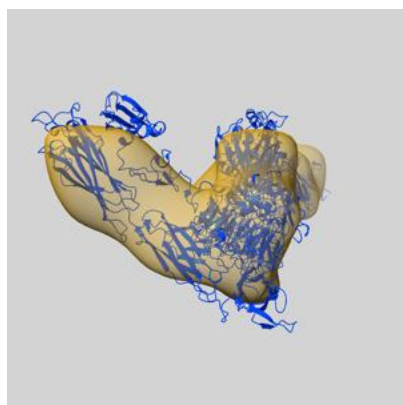
8 Fourier-Shell correlation

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

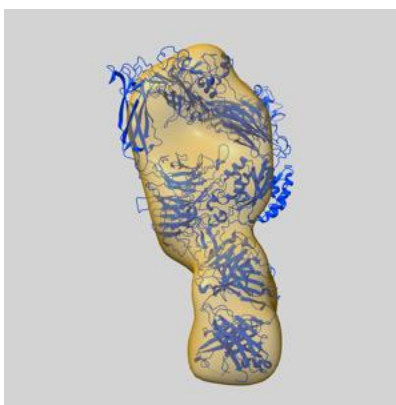
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7012 and PDB model 6AVR. Per-residue inclusion information can be found in section [3](#) on page [4](#).

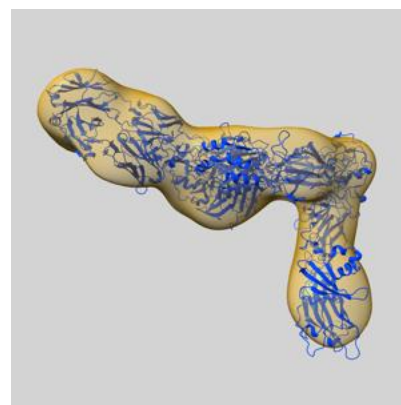
9.1 Map-model overlay [i](#)



X



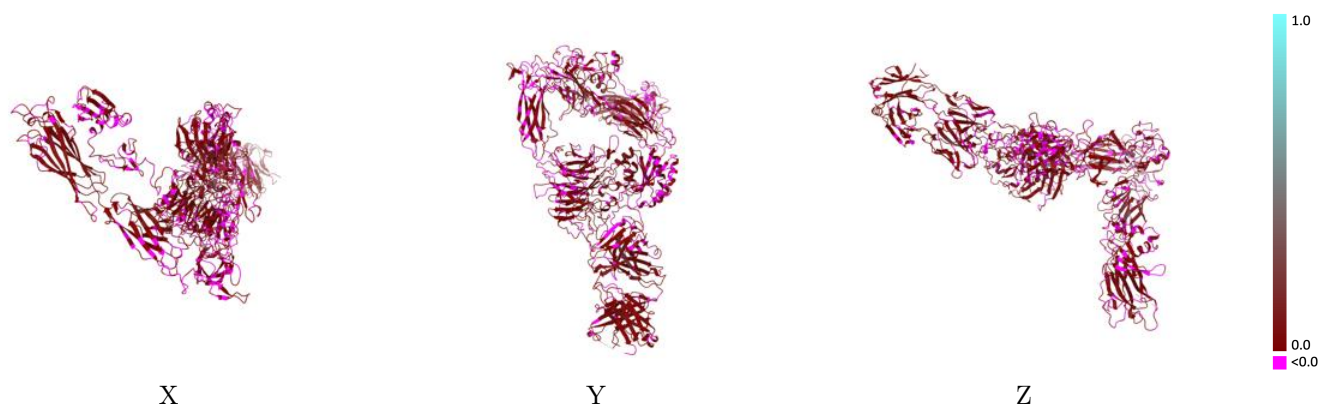
Y



Z

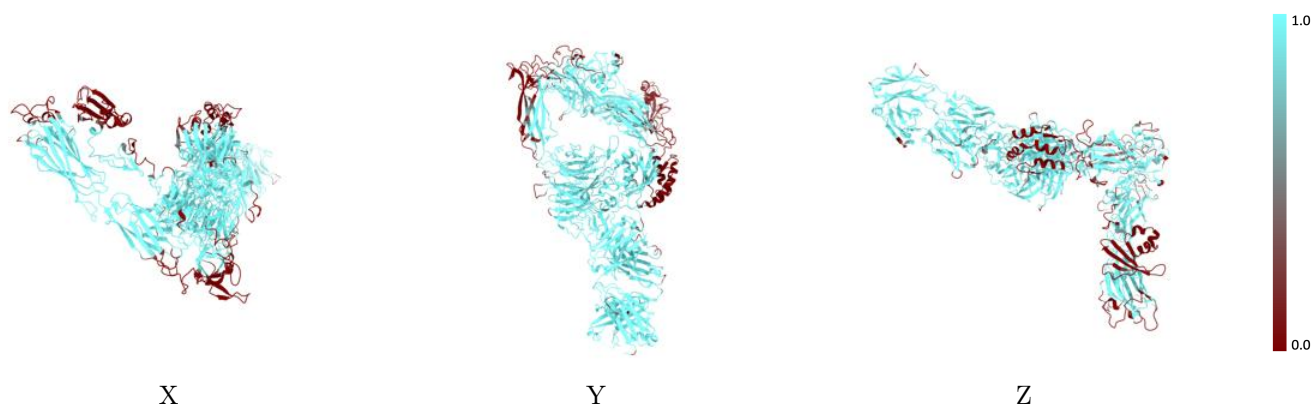
The images above show the 3D surface view of the map at the recommended contour level 3.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



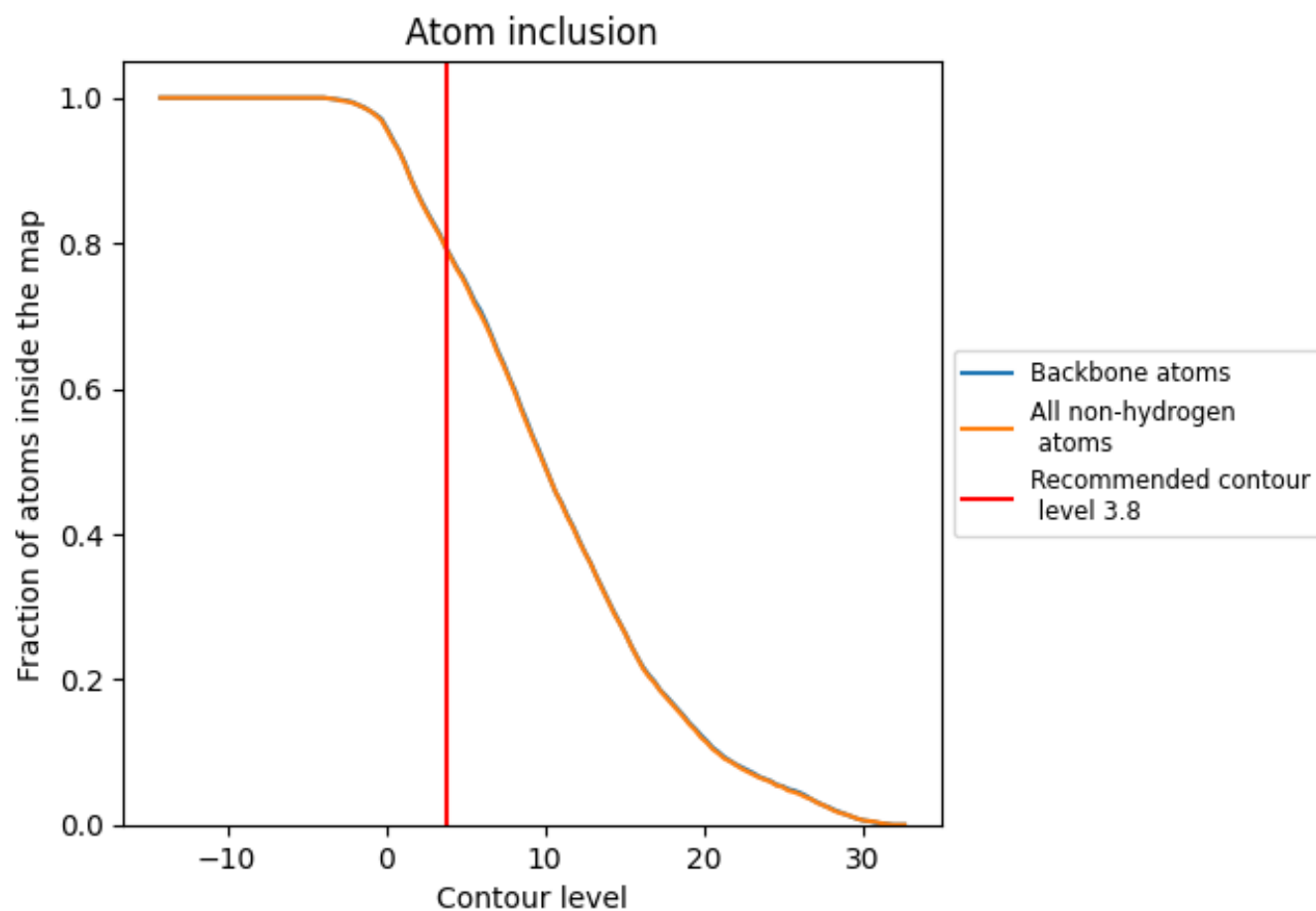
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



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).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% 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 (3.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7920	0.0460
A	0.8150	0.0470
B	0.6610	0.0390
H	0.9320	0.0650
L	0.9720	0.0470

