



Full wwPDB EM Validation Report ⓘ

May 6, 2025 – 06:30 AM EDT

PDB ID : 7N9S / pdb_00007n9s
EMDB ID : EMD-24261
Title : TcdB and frizzled-2 CRD complex
Authors : Jiang, M.; Zhang, J.
Deposited on : 2021-06-18
Resolution : 5.10 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

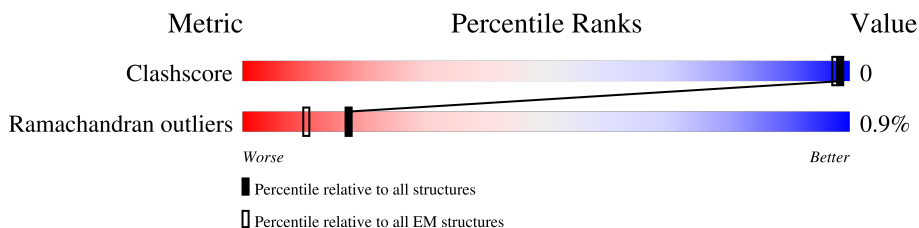
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.10 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	210492	15764
Ramachandran outliers	207382	16835

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	B	121	<div> <div>21%</div> <div>91%</div> <div>9%</div> </div>
2	A	2365	<div> <div>18%</div> <div>96%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7458 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 Frizzled-2.

Mol	Chain	Residues	Atoms			AltConf	Trace
1	B	121	Total 363	C 242	N 121	0	0

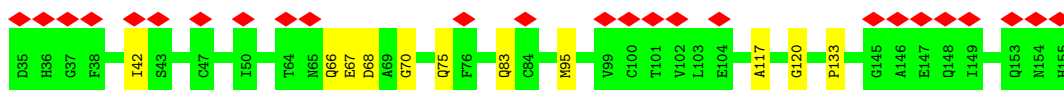
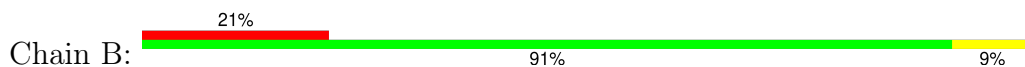
- Molecule 2 is a protein called Toxin B.

Mol	Chain	Residues	Atoms			AltConf	Trace
2	A	2365	Total 7095	C 4730	N 2365	0	0

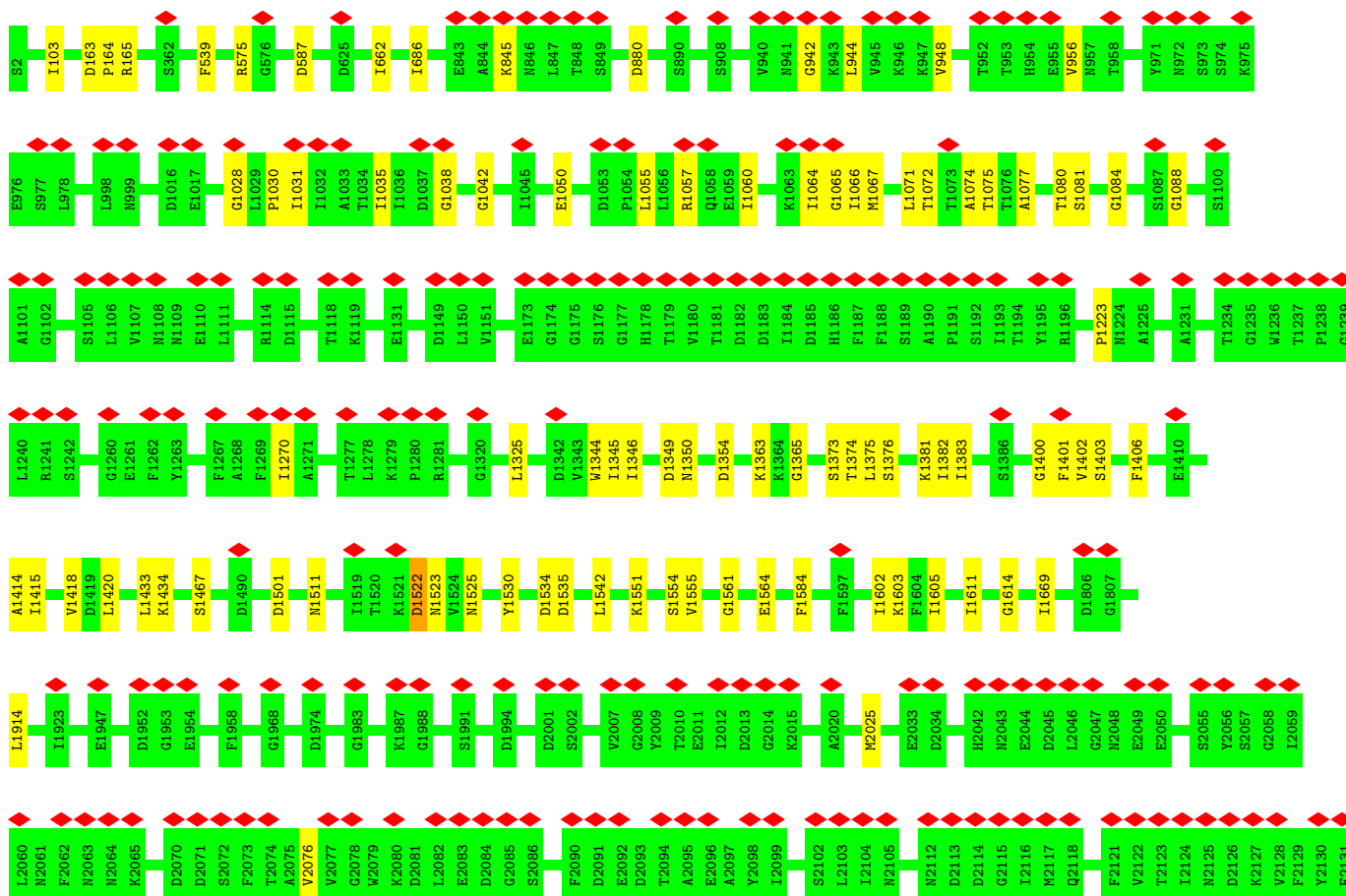
3 Residue-property plots [i](#)

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: Frizzled-2



• Molecule 2: Toxin B



W2314	F2315	E2316	G2317	E2318	S2319	I2320	N2321	Y2322	T2323	G2324	N2325	L2326	D2327	L2328	D2329	E2330	K2331	R2332	Y2333	Y2334	F2335	T2336	D2337	E2338	Y2339	I2340	A2341	A2342	T2343	G2344	S2345	V2346	I2347	I2348	D2349	G2350	E2351	E2352	Y2353	Y2354	F2355	D2356	P2357	D2358	T2359	A2360	Q2361	L2362	V2363	I2364	S2365	E2366	G2254	L2255	I2256	S2257	F2258	E2259	N2260	N2261	N2262	Y2263	Y2264	F2265	N2266	E2267	N2268	Q2269	E2270	M2271	Q2272	F2273	G2274	Y2275	I2276	N2277	I2278	E2279	D2280	K2281	M2282	F2283	Y2284	F2285	G2286	E2287	D2288	G2289	V2290	M2291	Q2292	I2293	G2294	V2295	F2296	N2297	T2298	P2299	D2300	G2301	F2302	K2303	Y2304	F2305	A2306	H2307	Q2308	N2309	T2310	L2311	D2312	E2313																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81240	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	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	0.097	Depositor
Minimum map value	-0.035	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	453.9582, 453.9582, 453.9582	wwPDB
Map dimensions	428, 428, 428	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06065, 1.06065, 1.06065	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	B	1.66	2/362 (0.6%)	2.23	17/361 (4.7%)
2	A	0.81	8/7094 (0.1%)	1.23	125/7093 (1.8%)
All	All	0.88	10/7456 (0.1%)	1.30	142/7454 (1.9%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1561	GLY	N-CA	-6.43	1.37	1.45
2	A	1084	GLY	N-CA	-6.40	1.38	1.45
1	B	120	GLY	N-CA	-6.19	1.38	1.45
1	B	70	GLY	N-CA	-6.17	1.38	1.45
2	A	1042	GLY	N-CA	-6.02	1.38	1.45
2	A	942	GLY	N-CA	-5.73	1.37	1.45
2	A	1365	GLY	N-CA	-5.56	1.37	1.45
2	A	1400	GLY	N-CA	-5.38	1.37	1.45
2	A	1088	GLY	N-CA	-5.28	1.37	1.45
2	A	1028	GLY	N-CA	-5.26	1.37	1.44

All (142) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1066	ILE	CA-C-N	10.62	141.83	121.54
2	A	1066	ILE	C-N-CA	10.62	141.83	121.54
2	A	1525	ASN	CA-C-N	8.66	130.63	121.97
2	A	1525	ASN	C-N-CA	8.66	130.63	121.97
2	A	1065	GLY	N-CA-C	8.09	128.53	115.67
1	B	75	GLN	N-CA-C	-7.79	102.11	111.69
2	A	1535	ASP	CA-C-N	7.36	130.68	122.22
2	A	1535	ASP	C-N-CA	7.36	130.68	122.22
2	A	1522	ASP	N-CA-C	7.29	126.32	110.80
2	A	1064	ILE	CA-C-N	6.78	131.34	122.26
2	A	1064	ILE	C-N-CA	6.78	131.34	122.26
2	A	1611	ILE	CA-C-N	6.74	130.79	122.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1611	ILE	C-N-CA	6.74	130.79	122.37
2	A	1354	ASP	CA-C-N	6.71	130.75	122.37
2	A	1354	ASP	C-N-CA	6.71	130.75	122.37
2	A	1030	PRO	CA-C-N	6.53	131.16	122.93
2	A	1030	PRO	C-N-CA	6.53	131.16	122.93
2	A	944	LEU	CA-C-N	6.36	131.47	123.14
2	A	944	LEU	C-N-CA	6.36	131.47	123.14
2	A	1031	ILE	CA-C-N	6.34	131.81	122.99
2	A	1031	ILE	C-N-CA	6.34	131.81	122.99
2	A	1381	LYS	CA-C-N	6.19	131.33	123.10
2	A	1381	LYS	C-N-CA	6.19	131.33	123.10
2	A	1077	ALA	CA-C-N	6.17	128.34	120.56
2	A	1077	ALA	C-N-CA	6.17	128.34	120.56
2	A	1383	ILE	CA-C-N	6.12	131.31	122.44
2	A	1383	ILE	C-N-CA	6.12	131.31	122.44
2	A	1035	ILE	CA-C-N	6.08	130.89	122.93
2	A	1035	ILE	C-N-CA	6.08	130.89	122.93
1	B	95	MET	CA-C-N	6.04	128.37	120.28
1	B	95	MET	C-N-CA	6.04	128.37	120.28
2	A	1084	GLY	CA-C-N	5.98	128.61	120.77
2	A	1084	GLY	C-N-CA	5.98	128.61	120.77
2	A	1349	ASP	CA-C-N	5.97	128.21	120.44
2	A	1349	ASP	C-N-CA	5.97	128.21	120.44
1	B	83	GLN	CA-C-N	5.96	128.54	120.38
1	B	83	GLN	C-N-CA	5.96	128.54	120.38
2	A	1401	PHE	CA-C-N	5.95	130.57	123.19
2	A	1401	PHE	C-N-CA	5.95	130.57	123.19
2	A	1080	THR	CA-C-N	5.86	128.06	120.44
2	A	1080	THR	C-N-CA	5.86	128.06	120.44
2	A	1418	VAL	CA-C-N	5.84	130.78	122.72
2	A	1418	VAL	C-N-CA	5.84	130.78	122.72
2	A	1534	ASP	CA-C-N	5.83	130.90	121.98
2	A	1534	ASP	C-N-CA	5.83	130.90	121.98
2	A	1270	ILE	N-CA-C	-5.82	107.03	111.62
2	A	1344	TRP	CA-C-N	5.81	130.68	123.12
2	A	1344	TRP	C-N-CA	5.81	130.68	123.12
2	A	1402	VAL	CA-C-N	5.78	130.45	122.77
2	A	1402	VAL	C-N-CA	5.78	130.45	122.77
2	A	1403	SER	CA-C-N	5.70	131.20	122.77
2	A	1403	SER	C-N-CA	5.70	131.20	122.77
2	A	1038	GLY	CA-C-N	5.67	130.89	123.06
2	A	1038	GLY	C-N-CA	5.67	130.89	123.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1050	GLU	CA-C-N	5.67	131.16	122.93
2	A	1050	GLU	C-N-CA	5.67	131.16	122.93
2	A	1554	SER	CA-C-N	5.67	130.82	122.94
2	A	1554	SER	C-N-CA	5.67	130.82	122.94
2	A	1374	THR	CA-C-N	5.65	129.94	122.42
2	A	1374	THR	C-N-CA	5.65	129.94	122.42
2	A	1325	LEU	CA-C-N	5.64	130.95	123.00
2	A	1325	LEU	C-N-CA	5.64	130.95	123.00
2	A	1350	ASN	CA-C-N	5.63	129.55	120.82
2	A	1350	ASN	C-N-CA	5.63	129.55	120.82
2	A	1376	SER	CA-C-N	5.60	130.55	123.10
2	A	1376	SER	C-N-CA	5.60	130.55	123.10
2	A	1525	ASN	N-CA-C	5.59	118.75	110.48
2	A	1363	LYS	CA-C-N	5.58	130.61	122.85
2	A	1363	LYS	C-N-CA	5.58	130.61	122.85
2	A	1375	LEU	CA-C-N	5.56	130.83	122.99
2	A	1375	LEU	C-N-CA	5.56	130.83	122.99
2	A	1414	ALA	CA-C-N	5.55	130.86	122.98
2	A	1414	ALA	C-N-CA	5.55	130.86	122.98
2	A	1382	ILE	CA-C-N	5.51	130.36	123.14
2	A	1382	ILE	C-N-CA	5.51	130.36	123.14
2	A	1057	ARG	CA-C-N	5.51	128.22	120.28
2	A	1057	ARG	C-N-CA	5.51	128.22	120.28
2	A	1072	THR	CA-C-N	5.50	127.65	120.28
2	A	1072	THR	C-N-CA	5.50	127.65	120.28
2	A	1415	ILE	CA-C-N	5.49	130.57	123.10
2	A	1415	ILE	C-N-CA	5.49	130.57	123.10
2	A	1605	ILE	CA-C-N	5.47	130.80	122.65
2	A	1605	ILE	C-N-CA	5.47	130.80	122.65
2	A	1555	VAL	CA-C-N	5.46	130.69	122.99
2	A	1555	VAL	C-N-CA	5.46	130.69	122.99
2	A	1055	LEU	CA-C-N	5.45	127.58	120.28
2	A	1055	LEU	C-N-CA	5.45	127.58	120.28
2	A	1081	SER	CA-C-N	5.44	127.51	120.44
2	A	1081	SER	C-N-CA	5.44	127.51	120.44
2	A	1345	ILE	CA-C-N	5.42	130.31	123.10
2	A	1345	ILE	C-N-CA	5.42	130.31	123.10
1	B	117	ALA	CA-C-N	5.41	127.48	120.44
1	B	117	ALA	C-N-CA	5.41	127.48	120.44
2	A	1028	GLY	N-CA-C	5.41	117.73	110.43
2	A	1603	LYS	CA-C-N	5.37	130.41	123.00
2	A	1603	LYS	C-N-CA	5.37	130.41	123.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1060	ILE	CA-C-N	5.32	129.12	120.60
2	A	1060	ILE	C-N-CA	5.32	129.12	120.60
2	A	1074	ALA	CA-C-N	5.29	127.32	120.44
2	A	1074	ALA	C-N-CA	5.29	127.32	120.44
1	B	42	ILE	CA-C-N	5.29	130.17	122.08
1	B	42	ILE	C-N-CA	5.29	130.17	122.08
2	A	1501	ASP	CA-C-N	5.28	128.31	120.17
2	A	1501	ASP	C-N-CA	5.28	128.31	120.17
2	A	1346	ILE	CA-C-N	5.27	129.37	121.72
2	A	1346	ILE	C-N-CA	5.27	129.37	121.72
2	A	1614	GLY	CA-C-N	5.24	130.38	123.05
2	A	1614	GLY	C-N-CA	5.24	130.38	123.05
2	A	1406	PHE	CA-C-N	5.23	130.37	123.05
2	A	1406	PHE	C-N-CA	5.23	130.37	123.05
2	A	1542	LEU	CA-C-N	5.21	130.75	122.94
2	A	1542	LEU	C-N-CA	5.21	130.75	122.94
2	A	1434	LYS	CA-C-N	5.20	127.20	120.70
2	A	1434	LYS	C-N-CA	5.20	127.20	120.70
1	B	67	GLU	CA-C-N	5.18	127.17	120.44
1	B	67	GLU	C-N-CA	5.18	127.17	120.44
2	A	1075	THR	CA-C-N	5.18	127.17	120.44
2	A	1075	THR	C-N-CA	5.18	127.17	120.44
2	A	1523	ASN	CA-C-N	5.17	127.80	122.27
2	A	1523	ASN	C-N-CA	5.17	127.80	122.27
2	A	1530	TYR	CA-C-N	5.15	130.30	122.11
2	A	1530	TYR	C-N-CA	5.15	130.30	122.11
2	A	1420	LEU	CA-C-N	5.14	127.44	120.65
2	A	1420	LEU	C-N-CA	5.14	127.44	120.65
2	A	1433	LEU	CA-C-N	5.12	127.45	120.54
2	A	1433	LEU	C-N-CA	5.12	127.45	120.54
1	B	66	GLN	CA-C-N	5.08	127.05	120.44
1	B	66	GLN	C-N-CA	5.08	127.05	120.44
1	B	68	ASP	CA-C-N	5.08	127.05	120.44
1	B	68	ASP	C-N-CA	5.08	127.05	120.44
2	A	1564	GLU	CA-C-N	5.08	127.15	120.60
2	A	1564	GLU	C-N-CA	5.08	127.15	120.60
2	A	1584	PHE	CA-C-N	5.07	127.08	120.28
2	A	1584	PHE	C-N-CA	5.07	127.08	120.28
2	A	1373	SER	CA-C-N	5.05	131.17	121.18
2	A	1373	SER	C-N-CA	5.05	131.17	121.18
1	B	133	PRO	CA-C-N	5.05	127.35	120.54
1	B	133	PRO	C-N-CA	5.05	127.35	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1561	GLY	CA-C-N	5.04	127.36	120.46
2	A	1561	GLY	C-N-CA	5.04	127.36	120.46
2	A	1551	LYS	CA-C-N	5.01	128.66	121.50
2	A	1551	LYS	C-N-CA	5.01	128.66	121.50

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	B	363	0	124	0	0
2	A	7095	0	2586	2	0
All	All	7458	0	2710	2	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 0.

All (2) 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)
2:A:163:ASP:C	2:A:165:ARG:H	2.25	0.45
2:A:163:ASP:C	2:A:165:ARG:N	2.78	0.41

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	B	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
2	A	2363/2365 (100%)	2141 (91%)	199 (8%)	23 (1%)	13	48
All	All	2482/2486 (100%)	2257 (91%)	202 (8%)	23 (1%)	17	50

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	103	ILE
2	A	164	PRO
2	A	686	ILE
2	A	880	ASP
2	A	1067	MET
2	A	1223	PRO
2	A	1522	ASP
2	A	1669	ILE
2	A	2076	VAL
2	A	539	PHE
2	A	575	ARG
2	A	587	ASP
2	A	662	ILE
2	A	1602	ILE
2	A	956	VAL
2	A	1511	ASN
2	A	1914	LEU
2	A	2025	MET
2	A	948	VAL
2	A	845	LYS
2	A	1071	LEU
2	A	1467	SER
2	A	2314	ASN

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

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.

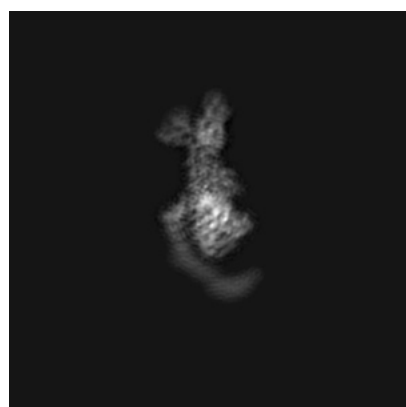
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24261. These allow visual inspection of the internal detail of the map and identification of artifacts.

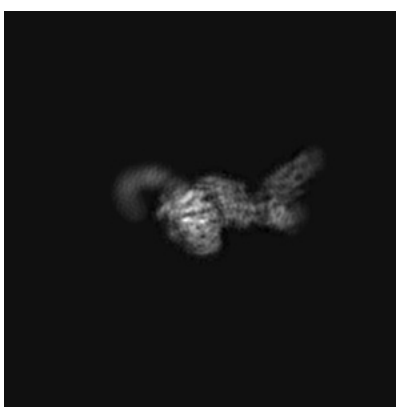
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

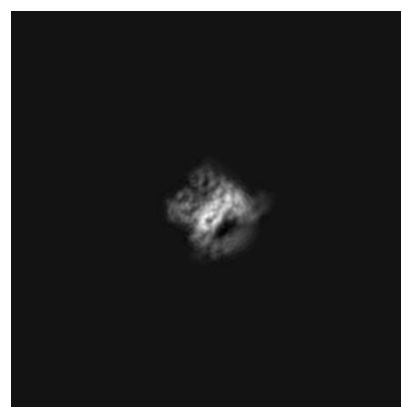
6.1.1 Primary map



X



Y

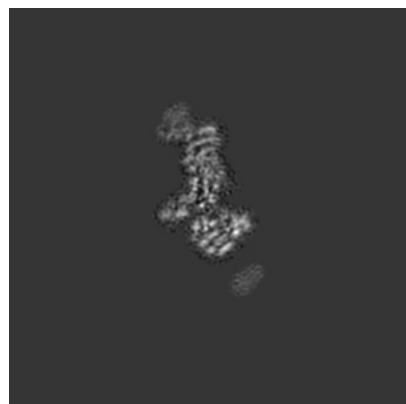


Z

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

6.2 Central slices [i](#)

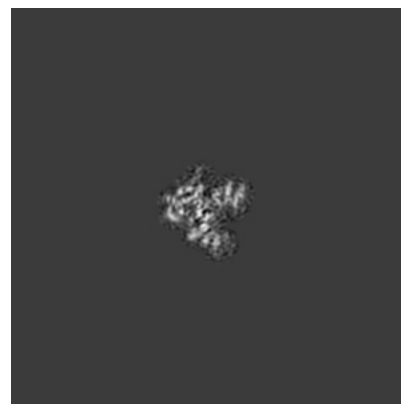
6.2.1 Primary map



X Index: 214



Y Index: 214

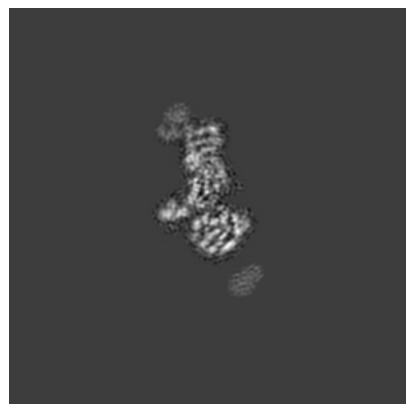


Z Index: 214

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

6.3 Largest variance slices [i](#)

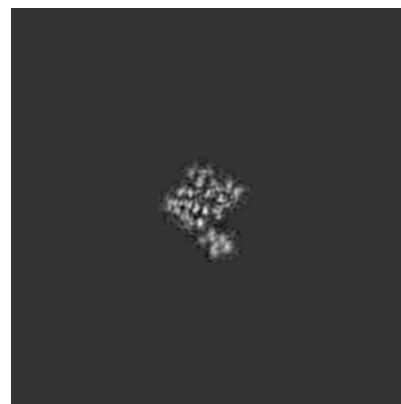
6.3.1 Primary map



X Index: 216



Y Index: 210

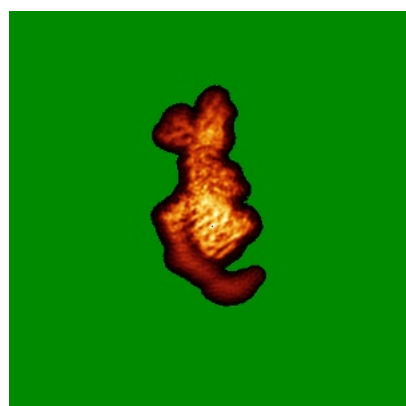


Z Index: 206

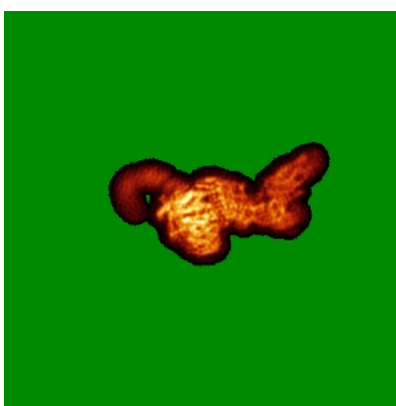
The images above show the largest variance slices of the map in three orthogonal directions.

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

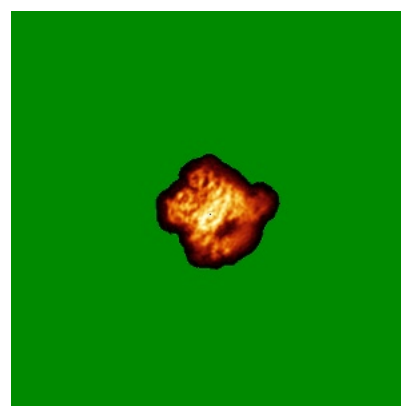
6.4.1 Primary map



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](#)

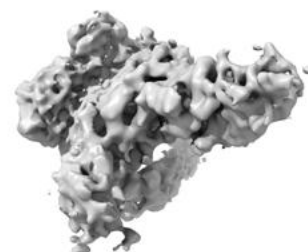
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

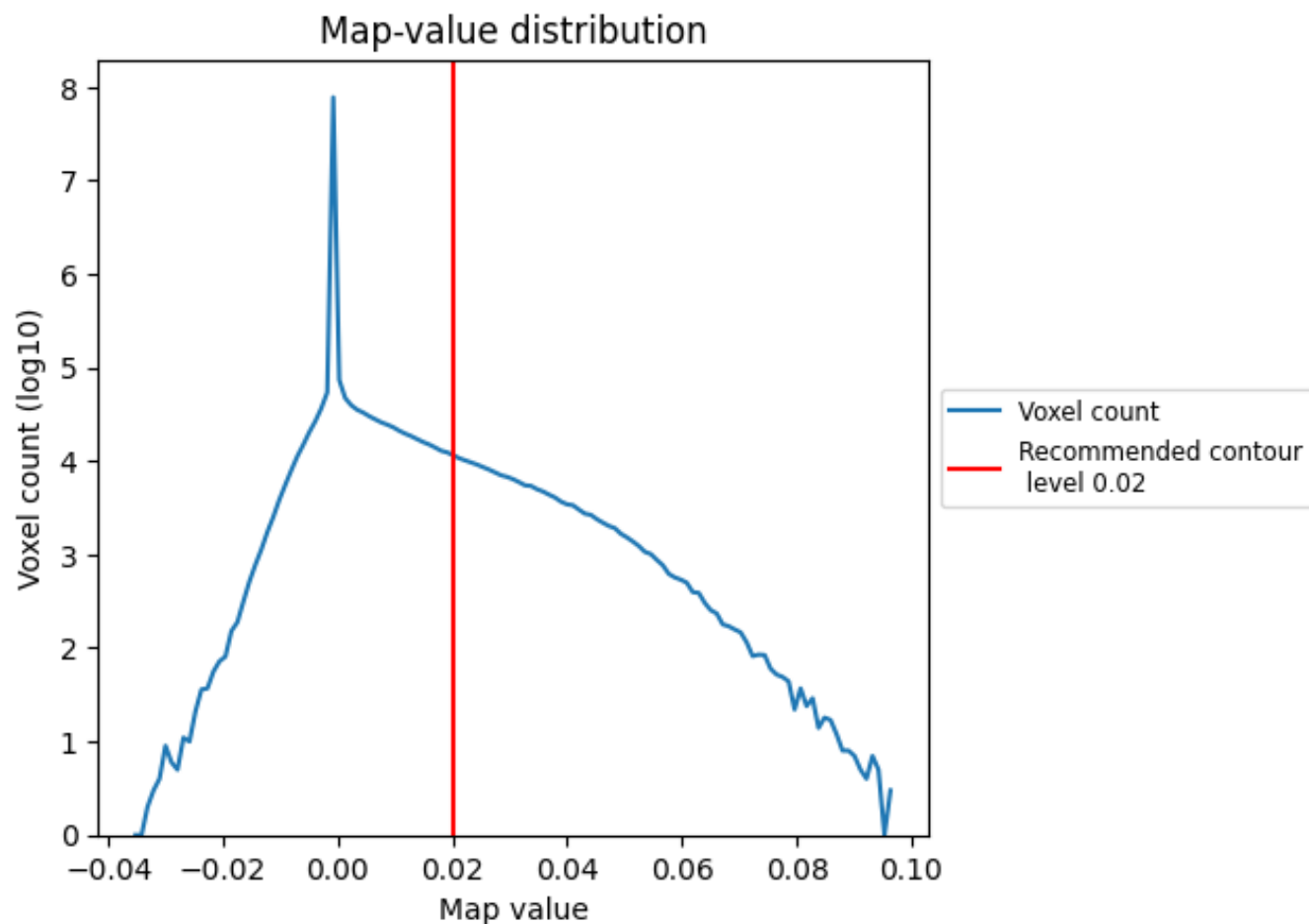
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

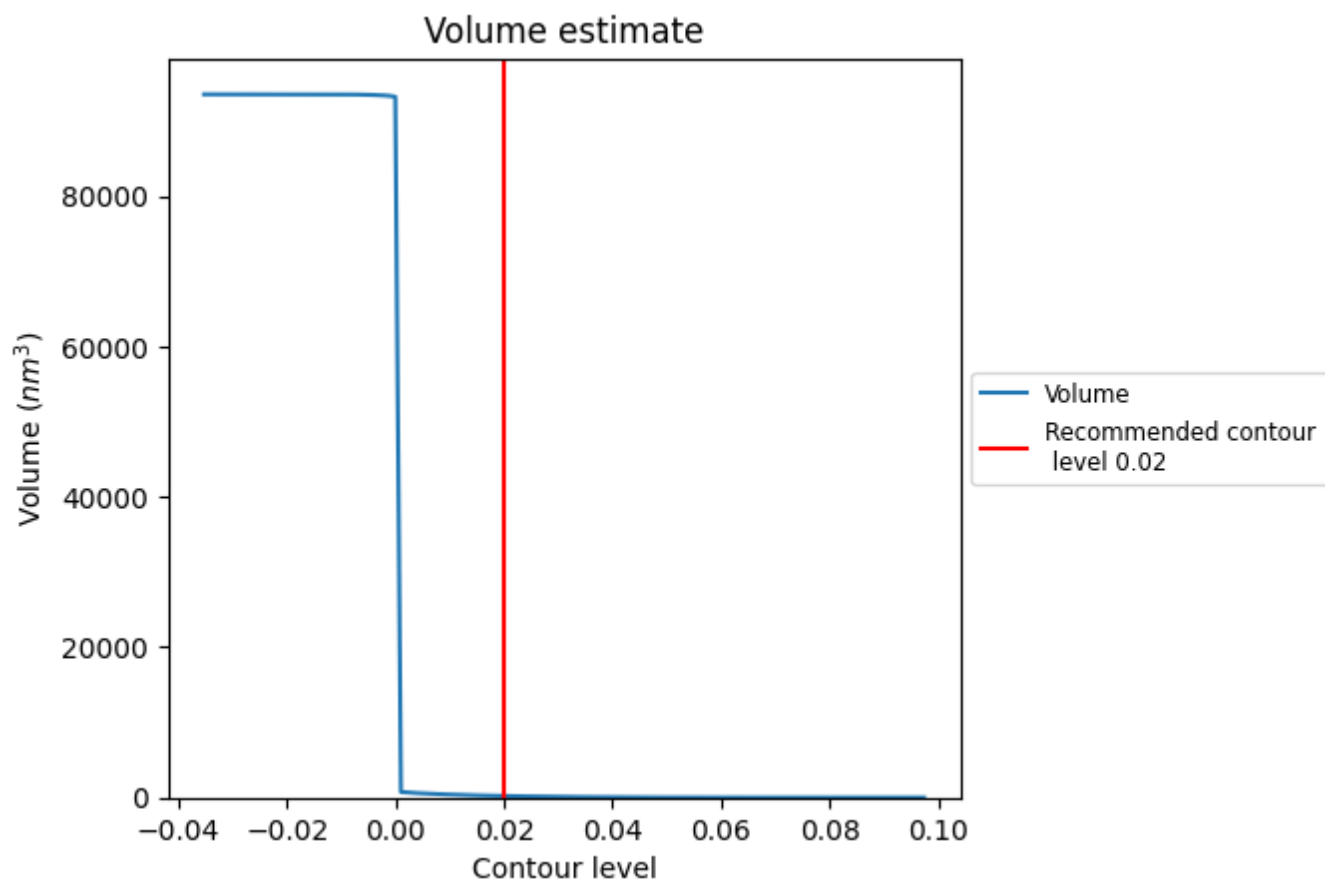
This section contains the results of statistical analysis of the map.

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.

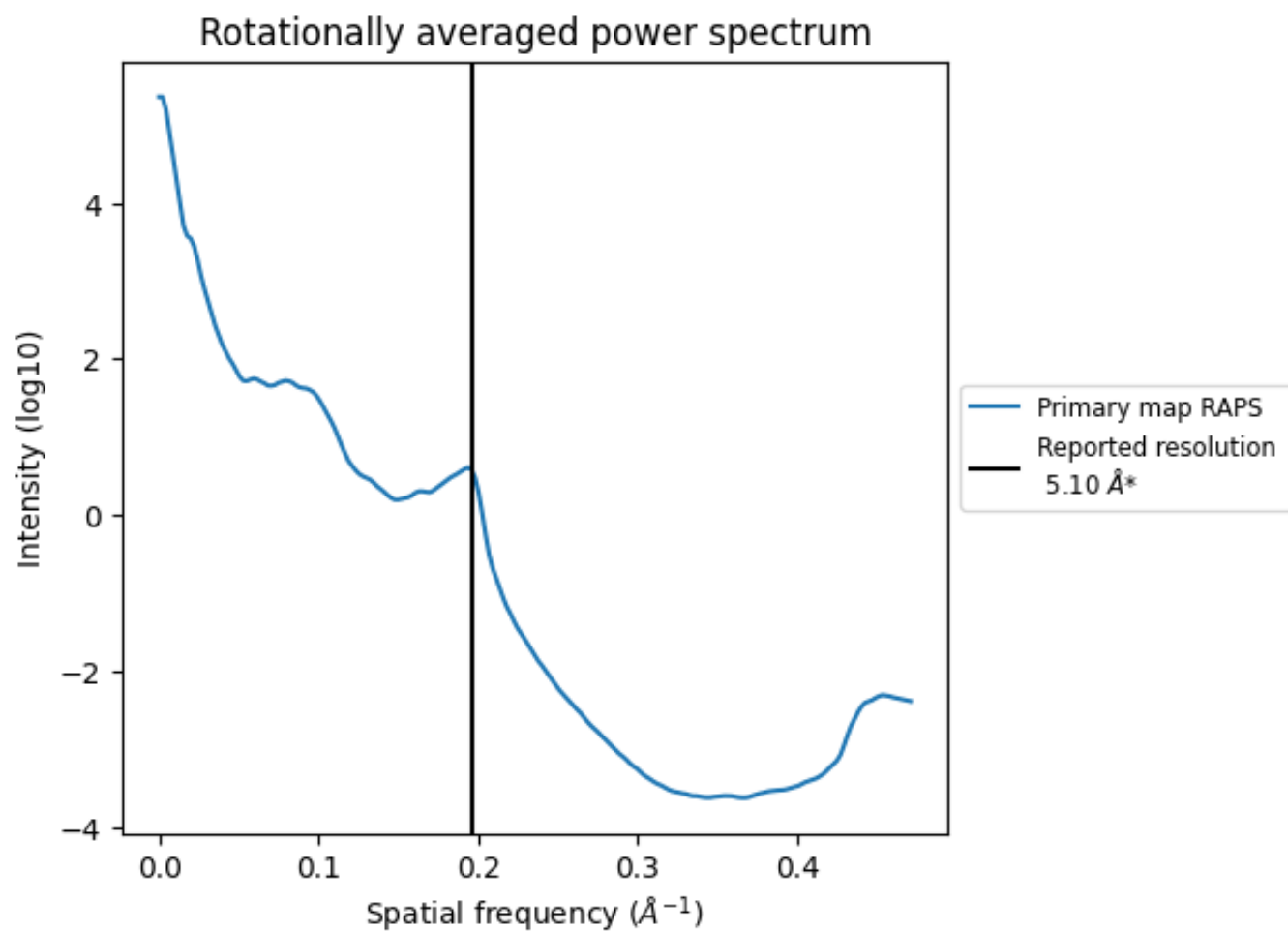
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 207 nm³; this corresponds to an approximate mass of 187 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 0.196 Å⁻¹

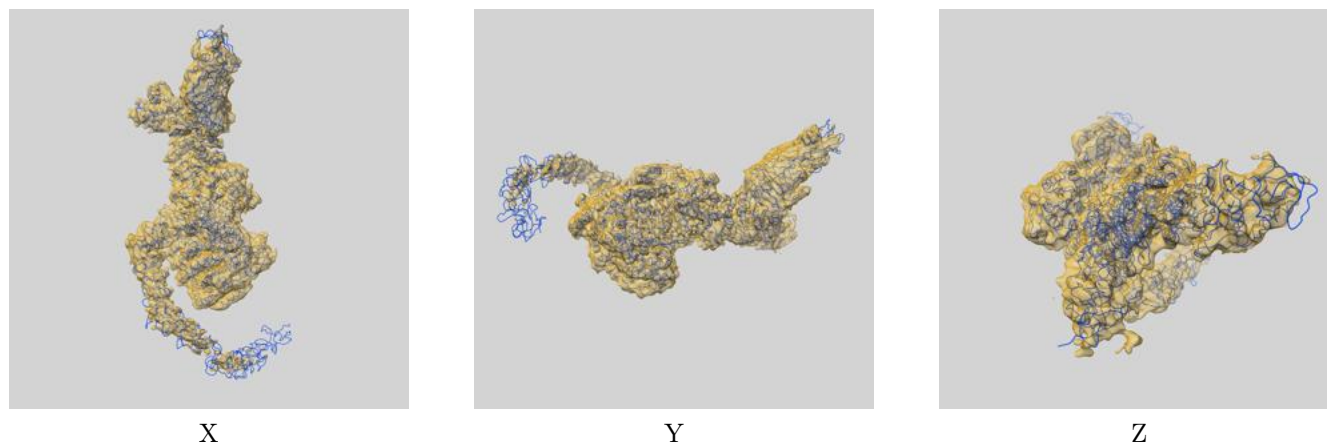
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

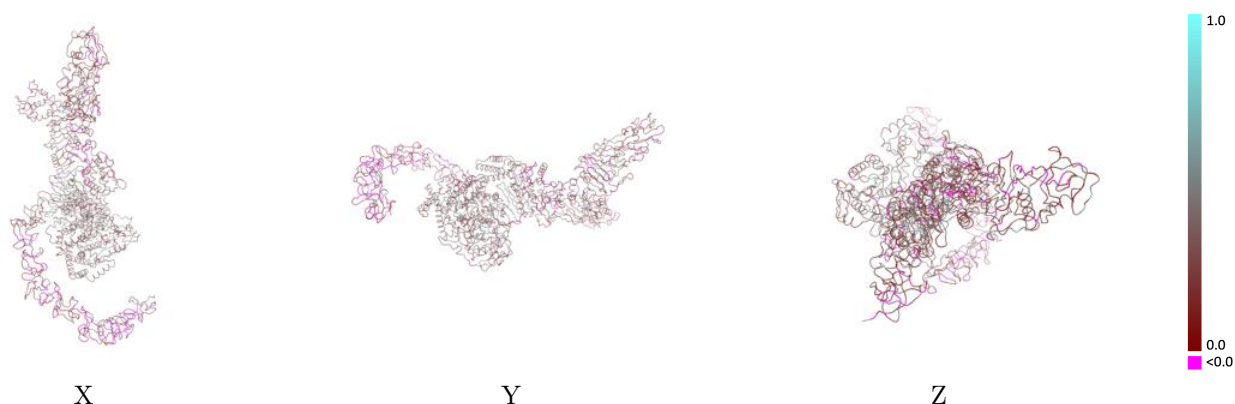
This section contains information regarding the fit between EMDB map EMD-24261 and PDB model 7N9S. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



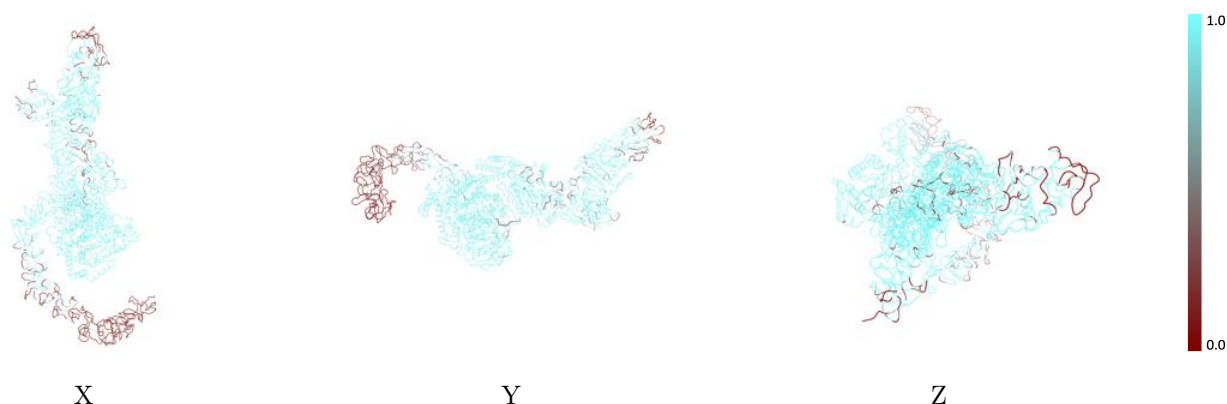
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



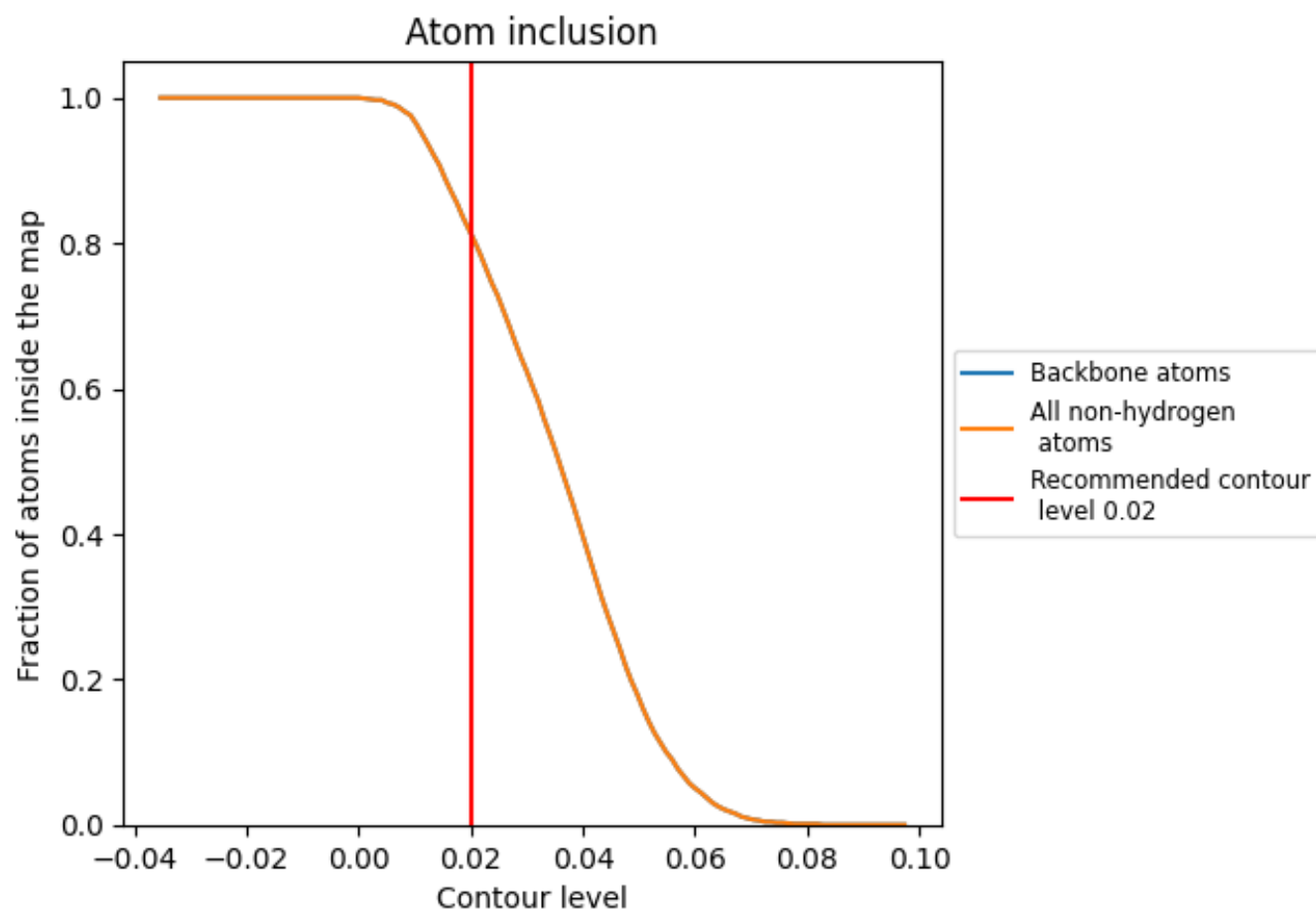
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8140	<div></div> 0.2760
A	<div></div> 0.8160	<div></div> 0.2780
B	<div></div> 0.7880	<div></div> 0.2250

