wwPDB EM Validation Summary Report

Dec 14, 2024 – 09:52 PM EST

PDB ID	:	1Q5A
EMDB ID	:	EMD-1052
Title	:	S-shaped trans interactions of cadherins model based on fitting C-cadherin (1L3W) to 3D map of desmosomes obtained by electron tomography
Authors	:	He, W.; Cowin, P.; Stokes, D.L.
Deposited on	:	2003-08-06
Resolution	:	30.00 Å(reported)
Based on initial model	:	1L3W

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

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

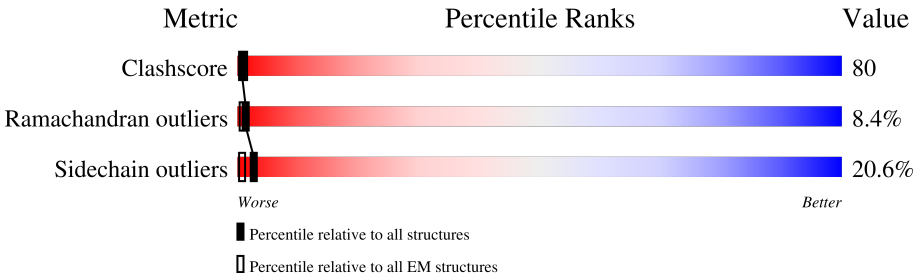
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 30.00 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	880	61% 17% 30% 10% • 39%
1	B	880	61% 16% 30% 11% • 39%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	801	-	-	X	-
2	NAG	A	805	X	-	X	-
2	NAG	A	806	X	-	X	-
2	NAG	A	807	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	809	-	-	X	-
2	NAG	A	810	-	-	X	-
2	NAG	A	902	X	-	X	-
2	NAG	A	903	X	-	-	-
2	NAG	A	904	-	-	X	-
2	NAG	B	801	-	-	X	-
2	NAG	B	805	X	-	X	-
2	NAG	B	806	X	-	X	-
2	NAG	B	807	-	-	X	-
2	NAG	B	809	-	-	X	-
2	NAG	B	810	-	-	X	-
2	NAG	B	902	X	-	X	-
2	NAG	B	903	X	-	-	-
2	NAG	B	904	-	-	X	-
3	NDG	A	811	-	-	X	-
3	NDG	B	811	-	-	X	-

2 Entry composition (i)

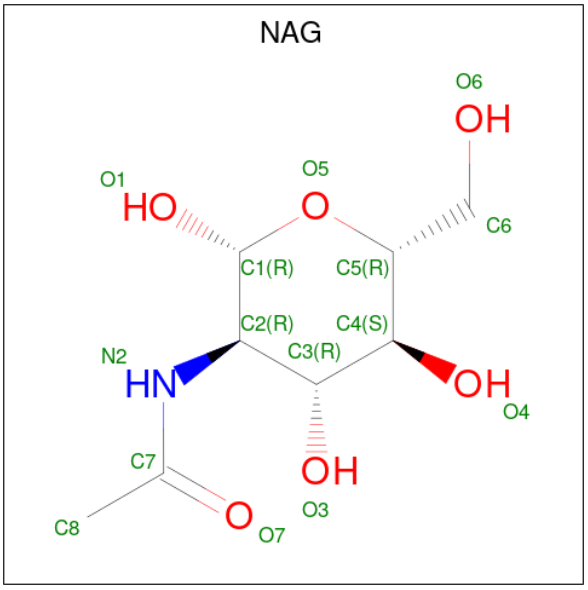
There are 4 unique types of molecules in this entry. The entry contains 8826 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 EP-cadherin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	540	Total 4191	C 2635	N 695	O 850	S 11	0	0
1	B	540	Total 4191	C 2635	N 695	O 850	S 11	0	0

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0

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Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0

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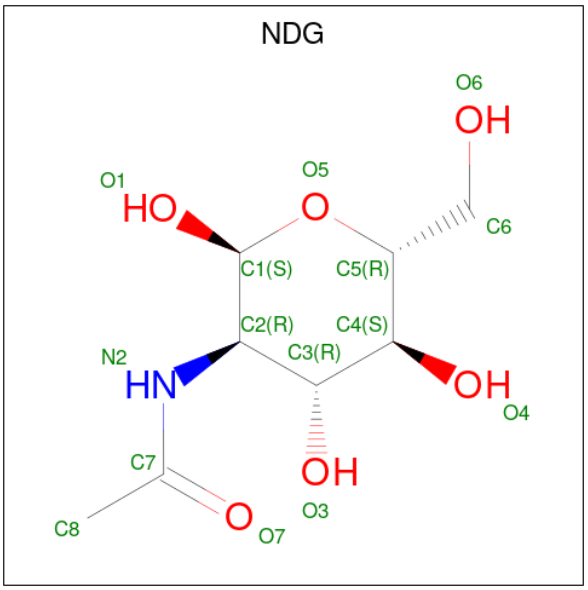
Mol	Chain	Residues	Atoms	AltConf
2	B	1	Total C N O 14 8 1 5	0

- Molecule 3 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total C N O 14 8 1 5	0
3	A	1	Total C N O 14 8 1 5	0
3	B	1	Total C N O 14 8 1 5	0
3	B	1	Total C N O 14 8 1 5	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

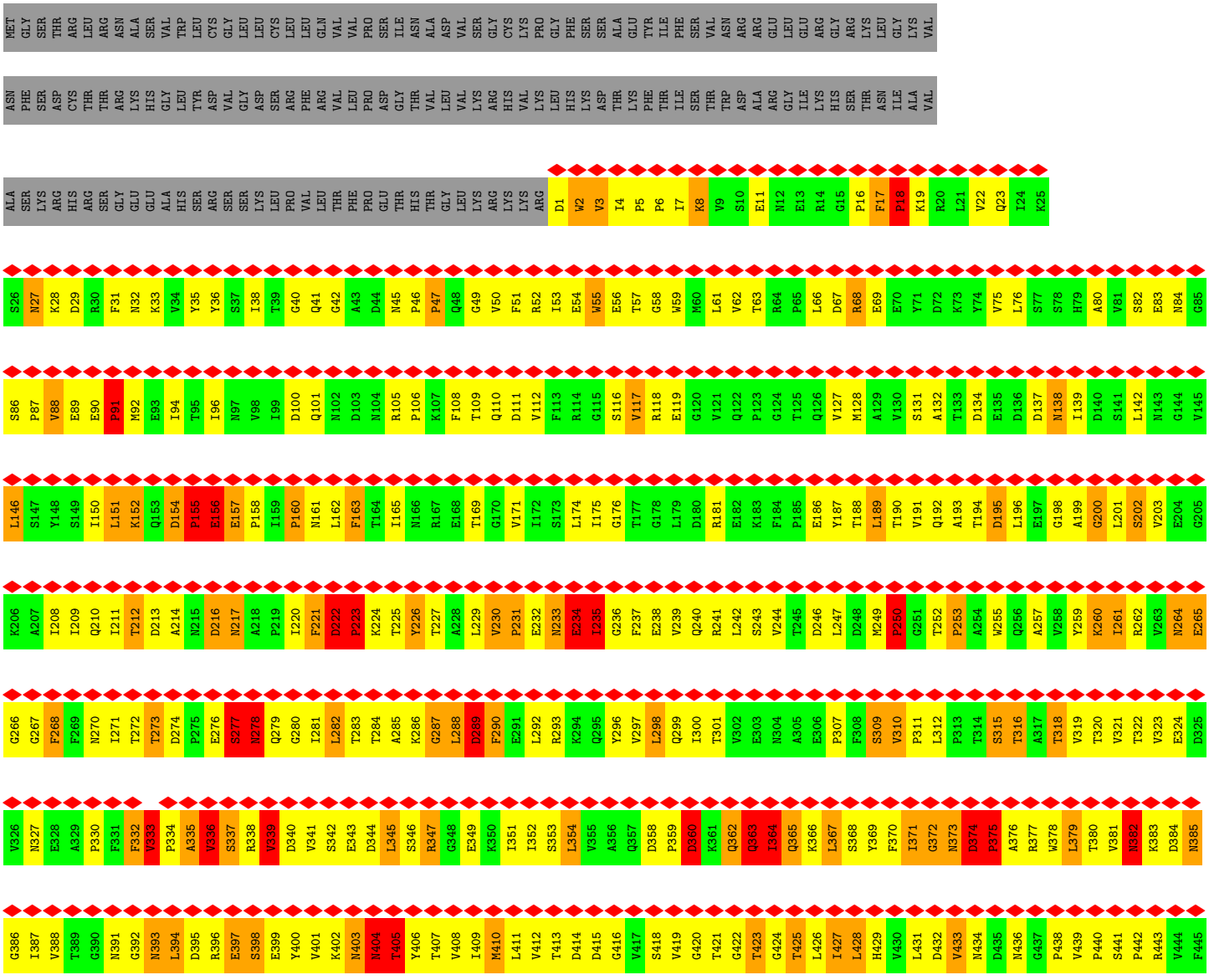
Mol	Chain	Residues	Atoms	AltConf
4	A	12	Total Ca 12 12	0
4	B	12	Total Ca 12 12	0

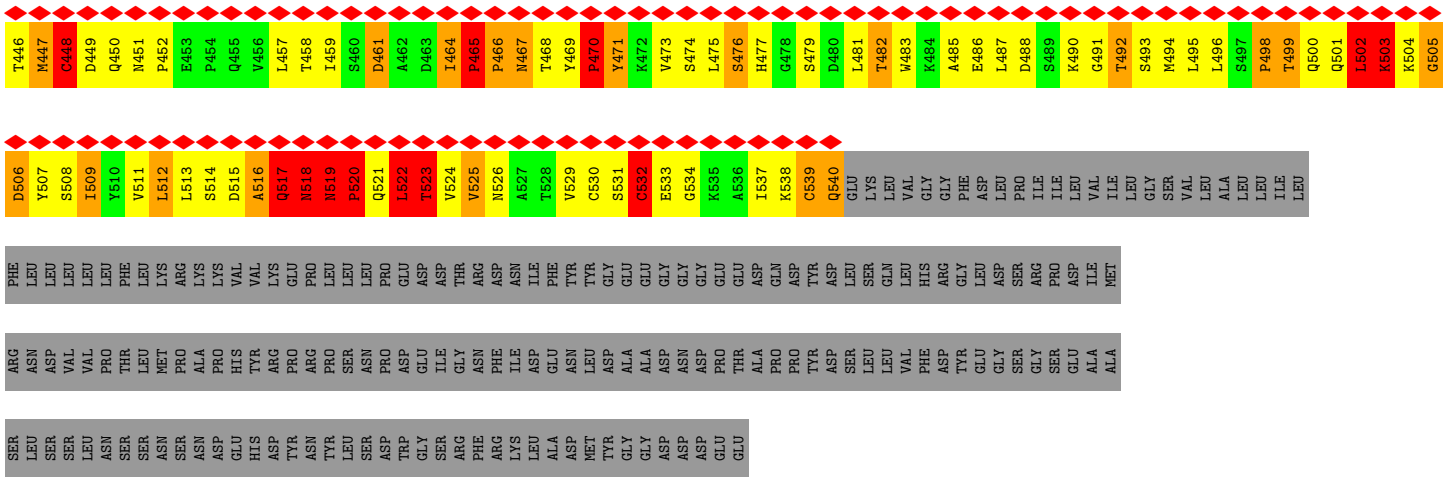
3 Residue-property plots (i)

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: EP-cadherin

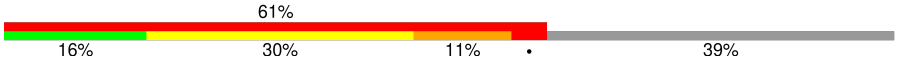
Chain A:

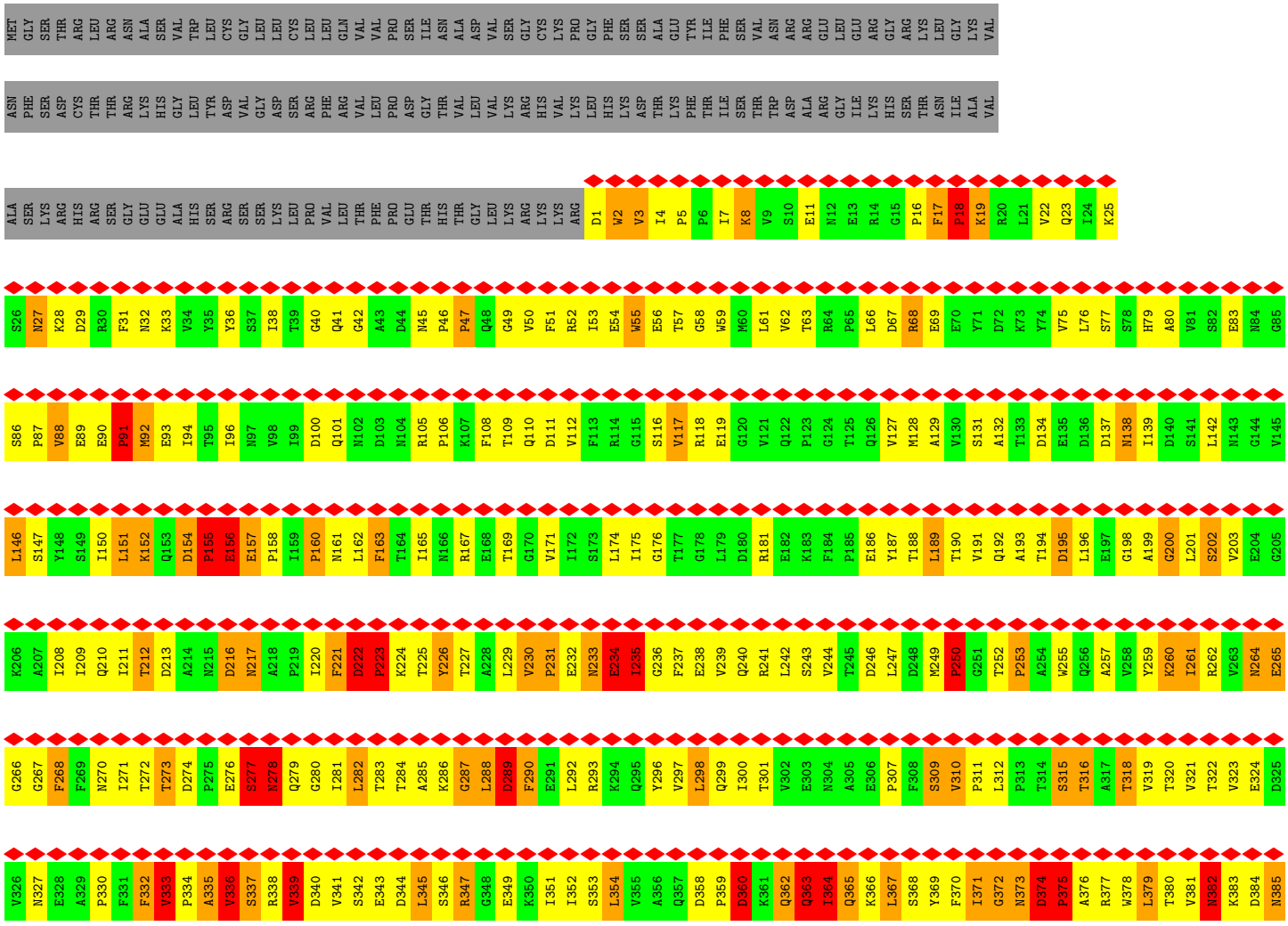


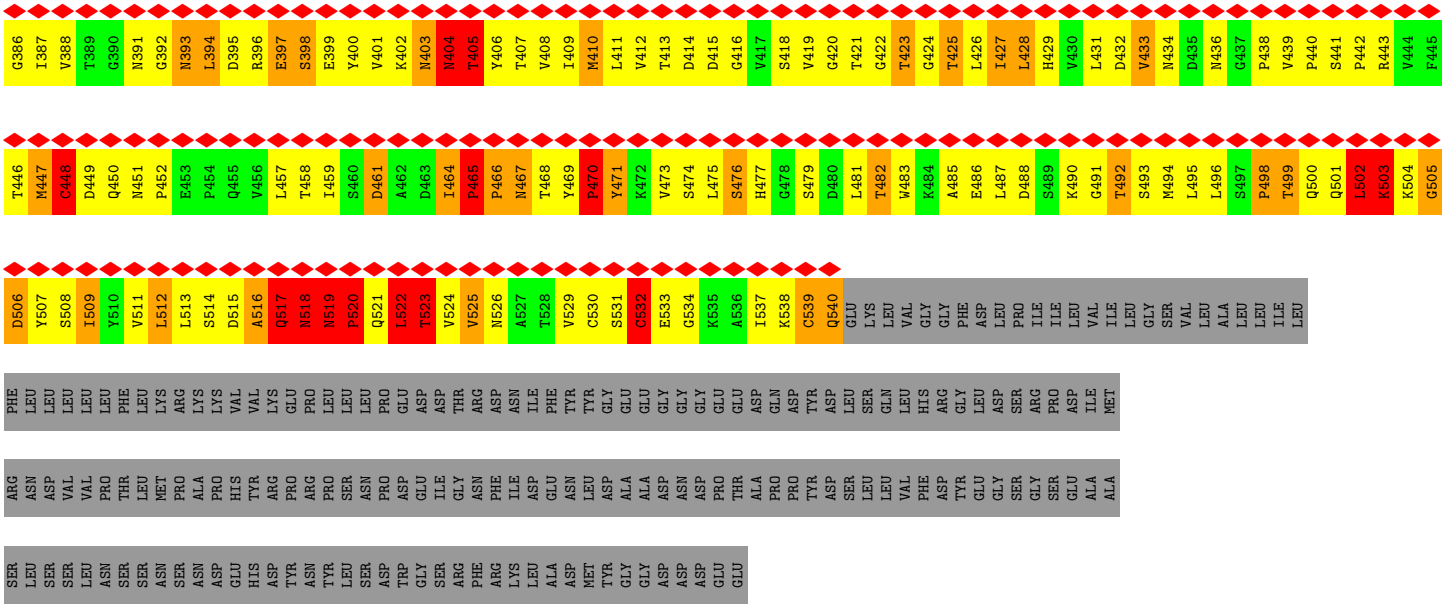


- Molecule 1: EP-cadherin

Chain B:






G386 I387 V388 T389 G390 N391 G392 N393 L394 D395 R396 E397 S398 E399 Y400 V401 K402 N403 N404 T405 Y406 T407 V408 I409 M410 L411 V412 T413 D414 D415 G416 V417 S418 V419 G420 T421 G422 T423 G424 T425 L426 I427 L428 H429 V430 L431 D432 V433 N434 D435 N436 G437 P438 V439 P440 S441 P442 R443 V444 F445
T446 M447 C448 D449 Q450 N451 P452 E453 P454 Q455 V456 L457 T458 I459 S460 D461 A462 D463 I464 P465 P466 N467 T468 Y469 P470 Y471 K472 V473 S474 L475 S476 H477 G478 S479 D480 L481 T482 W483 K484 A485 E486 L487 D488 S489 K490 G491 T492 S493 M494 L495 L496 S497 P498 T499 Q500 Q501 L502 K503 K504 G505
D506 Y507 S508 I509 Y510 V511 L512 L513 S514 D515 A516 Q517 N518 N519 P520 Q521 L522 T523 V524 V525 N526 A527 T528 V529 C530 S531 C532 E533 G534 K535 A536 I537 K538 C539 Q540 GLU LYS LEU VAL GLY GLY PHE ASP LEU PRO ILE ILE LEU VAL ILE LEU GLY SER VAL LEU ALA LEU LEU ILE LEU
PHE LEU LEU LEU LEU LEU PHE LEU LYS ARG LYS LYS VAL VAL LYS GLU PRO LEU LEU LEU PRO GLU ASP ASP THR ARG ASP ASN ILE PHE TYR TYR GLY GLU GLU GLY GLY GLY GLU GLU ASP GLN ASP TYR ASP LEU SER GLN LEU HIS ARG GLY LEU ASP SER ARG PRO ASP ILE MET
ARG ASN ASP VAL VAL PRO THR LEU MET PRO ALA PRO HIS TYR ARG PRO ARG PRO SER ASN PRO ASP GLU ILE GLY ASN PHE ILE ASP GLU ASN LEU ASP ALA ALA ASP ASN ASP PRO THR ALA PRO PRO TYR ASP SER LEU LEU VAL PHE ASP TYR GLU GLY SER GLY SER GLU ALA ALA
SER LEU SER SER LEU ASN SER SER SER ASN SER ASN ASP GLU HIS ASP TYR ASN TYR LEU SER ASP TRP GLY SER ARG PHE ARG LYS LEU ALA ASP MET TYR GLY GLY ASP ASP ASP GLU GLU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	Not provided	
Resolution determination method	Not provided	
CTF correction method	no CTF correction. Imaging at underfocus 0.4 micron with CM200FEG microscope at 50,000 magnification	Depositor
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	1200	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	500	Depositor
Magnification	68276	Depositor
Image detector	GENERIC GATAN	Depositor
Maximum voxel value	2603.000	Depositor
Minimum voxel value	-1866.000	Depositor
Average voxel value	1323.980	Depositor
Voxel value standard deviation	218.755	Depositor
Recommended contour level	1760	Depositor
Tomogram size (Å)	3720.19, 3720.19, 617.61	wwPDB
Tomogram dimensions	512, 512, 85	wwPDB
Tomogram angles (°)	90, 90, 90	wwPDB
Grid spacing (Å)	7.266, 7.266, 7.266	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: CA, NAG, NDG

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	0.70	8/4276 (0.2%)	1.44	81/5839 (1.4%)
1	B	0.70	8/4276 (0.2%)	1.39	79/5839 (1.4%)
All	All	0.70	16/8552 (0.2%)	1.42	160/11678 (1.4%)

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	1	4
1	B	0	4
All	All	1	8

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	335	ALA	CA-CB	-8.37	1.34	1.52
1	B	335	ALA	CA-CB	-8.33	1.34	1.52
1	A	539	CYS	CB-SG	8.17	1.96	1.82
1	B	539	CYS	CB-SG	8.15	1.96	1.82
1	B	223	PRO	CG-CD	7.02	1.73	1.50

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	490	LYS	N-CA-CB	-28.44	59.41	110.60
1	A	520	PRO	CA-C-N	-13.30	87.95	117.20
1	B	520	PRO	CA-C-N	-13.28	87.99	117.20
1	B	290	PHE	N-CA-C	12.73	145.38	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	235	ILE	N-CA-C	12.72	145.34	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	490	LYS	CA

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	PHE	Sidechain
1	A	18	PRO	Mainchain
1	A	222	ASP	Mainchain
1	A	520	PRO	Mainchain
1	B	17	PHE	Sidechain

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	A	4191	0	4085	709	0
1	B	4191	0	4090	721	0
2	A	182	0	169	94	0
2	B	182	0	169	93	0
3	A	28	0	24	9	0
3	B	28	0	24	9	0
4	A	12	0	0	0	0
4	B	12	0	0	0	0
All	All	8826	0	8561	1395	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 80.

The worst 5 of 1395 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:B:464:ILE:HD12	1:B:465:PRO:CD	1.30	1.58
1:A:464:ILE:HD12	1:A:465:PRO:CD	1.30	1.55
1:A:87:PRO:CG	1:B:89:GLU:HB3	1.16	1.54
1:B:464:ILE:CD1	1:B:465:PRO:HD2	1.50	1.41
1:A:464:ILE:CD1	1:A:465:PRO:HD2	1.50	1.37

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	A	538/880 (61%)	401 (74%)	92 (17%)	45 (8%)	0	9
1	B	538/880 (61%)	401 (74%)	92 (17%)	45 (8%)	0	9
All	All	1076/1760 (61%)	802 (74%)	184 (17%)	90 (8%)	1	9

5 of 90 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	91	PRO
1	A	155	PRO
1	A	235	ILE
1	A	347	ARG
1	A	363	GLN

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	A	480/779 (62%)	381 (79%)	99 (21%)	1 6
1	B	480/779 (62%)	381 (79%)	99 (21%)	1 6
All	All	960/1558 (62%)	762 (79%)	198 (21%)	3 6

5 of 198 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	156	GLU
1	B	310	VAL
1	B	195	ASP
1	B	250	PRO
1	B	345	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	104	ASN
1	B	264	ASN
1	B	110	GLN
1	B	217	ASN
1	B	299	GLN

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)

Of 54 ligands modelled in this entry, 24 are monoatomic - leaving 30 for Mogul analysis.

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	$\#\|Z\| > 2$
2	NAG	B	812	1	14,14,15	0.84	1 (7%)	17,19,21	0.76	1 (5%)
2	NAG	A	807	1	14,14,15	0.65	0	17,19,21	1.19	2 (11%)
2	NAG	A	812	1	14,14,15	0.83	1 (7%)	17,19,21	0.76	1 (5%)
2	NAG	B	808	1	14,14,15	0.67	0	17,19,21	0.70	0
2	NAG	A	904	1	14,14,15	0.76	1 (7%)	17,19,21	0.70	1 (5%)
2	NAG	A	801	1	14,14,15	0.70	0	17,19,21	0.97	1 (5%)
2	NAG	B	810	1	14,14,15	0.66	0	17,19,21	1.33	4 (23%)
2	NAG	B	805	1	14,14,15	0.71	0	17,19,21	1.06	1 (5%)
2	NAG	A	902	1	14,14,15	1.13	1 (7%)	17,19,21	1.09	2 (11%)
2	NAG	B	806	1	14,14,15	0.56	0	17,19,21	1.39	3 (17%)
3	NDG	A	804	1	14,14,15	0.65	0	17,19,21	0.78	0
2	NAG	A	810	1	14,14,15	0.67	0	17,19,21	1.33	4 (23%)
2	NAG	A	803	1	14,14,15	0.99	1 (7%)	17,19,21	1.15	2 (11%)
2	NAG	B	807	1	14,14,15	0.64	0	17,19,21	1.19	2 (11%)
2	NAG	B	904	1	14,14,15	0.77	1 (7%)	17,19,21	0.70	1 (5%)
2	NAG	B	809	1	14,14,15	0.77	1 (7%)	17,19,21	0.94	0
2	NAG	B	801	1	14,14,15	0.70	0	17,19,21	0.98	1 (5%)
2	NAG	A	903	1	14,14,15	0.55	0	17,19,21	0.79	0
2	NAG	A	802	1	14,14,15	0.76	1 (7%)	17,19,21	0.85	0
2	NAG	A	809	1	14,14,15	0.75	0	17,19,21	0.94	0
2	NAG	B	803	1	14,14,15	0.99	1 (7%)	17,19,21	1.16	2 (11%)
2	NAG	B	802	1	14,14,15	0.77	1 (7%)	17,19,21	0.85	0
3	NDG	B	804	1	14,14,15	0.64	0	17,19,21	0.78	0
3	NDG	B	811	1	14,14,15	0.86	0	17,19,21	1.97	1 (5%)
2	NAG	A	805	1	14,14,15	0.71	0	17,19,21	1.06	1 (5%)
2	NAG	A	808	1	14,14,15	0.65	0	17,19,21	0.70	0
2	NAG	B	903	1	14,14,15	0.55	0	17,19,21	0.79	0
2	NAG	A	806	1	14,14,15	0.56	0	17,19,21	1.39	3 (17%)
3	NDG	A	811	1	14,14,15	0.88	0	17,19,21	1.96	1 (5%)
2	NAG	B	902	1	14,14,15	1.12	1 (7%)	17,19,21	1.09	1 (5%)

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
2	NAG	B	812	1	-	4/6/23/26	0/1/1/1
2	NAG	A	807	1	-	5/6/23/26	0/1/1/1
2	NAG	A	812	1	-	4/6/23/26	0/1/1/1
2	NAG	B	808	1	-	3/6/23/26	0/1/1/1
2	NAG	A	904	1	-	3/6/23/26	0/1/1/1
2	NAG	A	801	1	-	4/6/23/26	0/1/1/1
2	NAG	B	810	1	-	3/6/23/26	0/1/1/1
2	NAG	B	805	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	902	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	806	1	1/1/5/7	2/6/23/26	0/1/1/1
3	NDG	A	804	1	-	0/6/23/26	0/1/1/1
2	NAG	A	810	1	-	3/6/23/26	0/1/1/1
2	NAG	A	803	1	-	2/6/23/26	0/1/1/1
2	NAG	B	807	1	-	5/6/23/26	0/1/1/1
2	NAG	B	904	1	-	3/6/23/26	0/1/1/1
2	NAG	B	809	1	-	2/6/23/26	0/1/1/1
2	NAG	B	801	1	-	4/6/23/26	0/1/1/1
2	NAG	A	903	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	802	1	-	2/6/23/26	0/1/1/1
2	NAG	A	809	1	-	2/6/23/26	0/1/1/1
2	NAG	B	802	1	-	2/6/23/26	0/1/1/1
2	NAG	B	803	1	-	2/6/23/26	0/1/1/1
3	NDG	B	804	1	-	0/6/23/26	0/1/1/1
3	NDG	B	811	1	-	2/6/23/26	0/1/1/1
2	NAG	A	805	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	808	1	-	3/6/23/26	0/1/1/1
2	NAG	B	903	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	806	1	1/1/5/7	2/6/23/26	0/1/1/1
3	NDG	A	811	1	-	2/6/23/26	0/1/1/1
2	NAG	B	902	1	1/1/5/7	2/6/23/26	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	902	NAG	C1-C2	3.38	1.57	1.52
2	B	902	NAG	C1-C2	3.31	1.56	1.52
2	B	803	NAG	O5-C5	2.62	1.48	1.43
2	A	803	NAG	O5-C5	2.62	1.48	1.43
2	B	904	NAG	C1-C2	-2.41	1.49	1.52

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	811	NDG	C2-N2-C7	-7.45	112.92	122.90
3	A	811	NDG	C2-N2-C7	-7.42	112.95	122.90
2	A	806	NAG	C2-N2-C7	-3.63	118.04	122.90
2	B	806	NAG	C2-N2-C7	-3.62	118.05	122.90
2	B	805	NAG	C2-N2-C7	-3.20	118.61	122.90

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	805	NAG	C1
2	A	806	NAG	C1
2	A	902	NAG	C1
2	A	903	NAG	C1
2	B	805	NAG	C1

5 of 76 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	807	NAG	C3-C2-N2-C7
2	A	808	NAG	C1-C2-N2-C7
2	A	810	NAG	C1-C2-N2-C7
2	A	812	NAG	C1-C2-N2-C7
2	A	902	NAG	C3-C2-N2-C7

There are no ring outliers.

26 monomers are involved in 205 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	812	NAG	3	0
2	A	807	NAG	17	0
2	A	812	NAG	3	0
2	B	808	NAG	2	0
2	A	904	NAG	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	NAG	22	0
2	B	810	NAG	13	0
2	B	805	NAG	7	0
2	A	902	NAG	8	0
2	B	806	NAG	12	0
3	A	804	NDG	2	0
2	A	810	NAG	13	0
2	A	803	NAG	4	0
2	B	807	NAG	16	0
2	B	904	NAG	8	0
2	B	809	NAG	8	0
2	B	801	NAG	22	0
2	A	809	NAG	8	0
2	B	803	NAG	4	0
3	B	804	NDG	2	0
3	B	811	NDG	7	0
2	A	805	NAG	7	0
2	A	808	NAG	2	0
2	A	806	NAG	12	0
3	A	811	NDG	7	0
2	B	902	NAG	8	0

5.7 Other polymers (i)

There are no such residues in this entry.

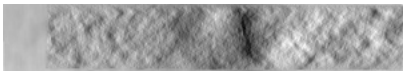
5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Tomogram visualisation

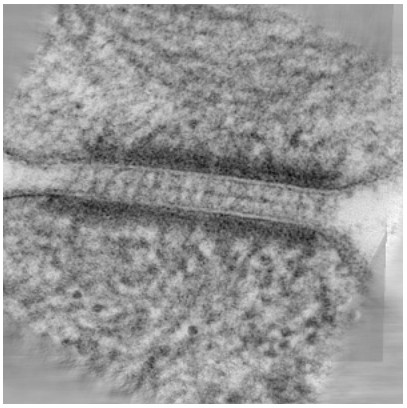
This section contains visualisations of the EMDB entry EMD-1052. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

6.1 Orthogonal projections



X

Y

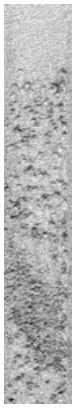


Z

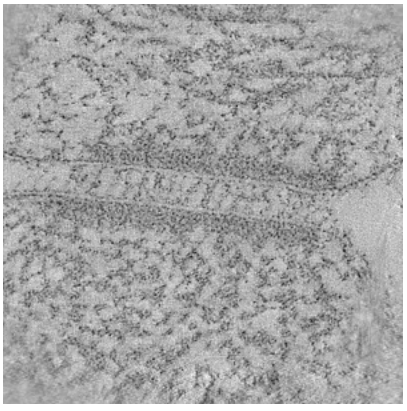
The images above show the tomogram projected in three orthogonal directions.

6.2 Central slices

X Index: 256



Y Index: 256

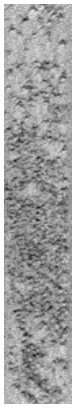


Z Index: 42

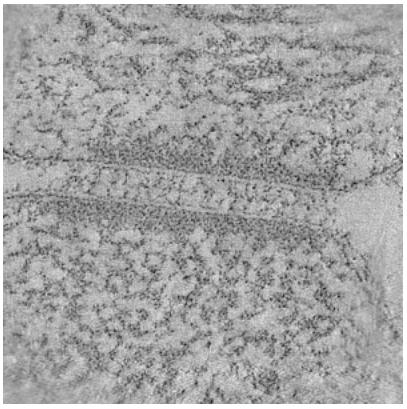
The images above show central slices of the tomogram in three orthogonal directions.

6.3 Largest variance slices (i)

X Index: 243



Y Index: 315



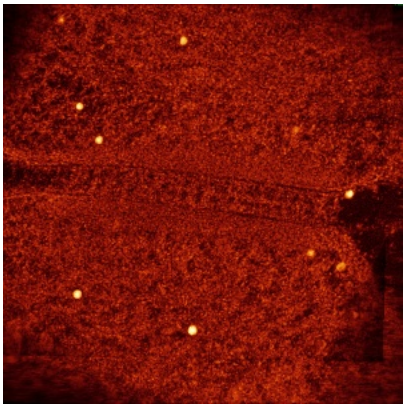
Z Index: 39

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

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

X

Y



Z

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

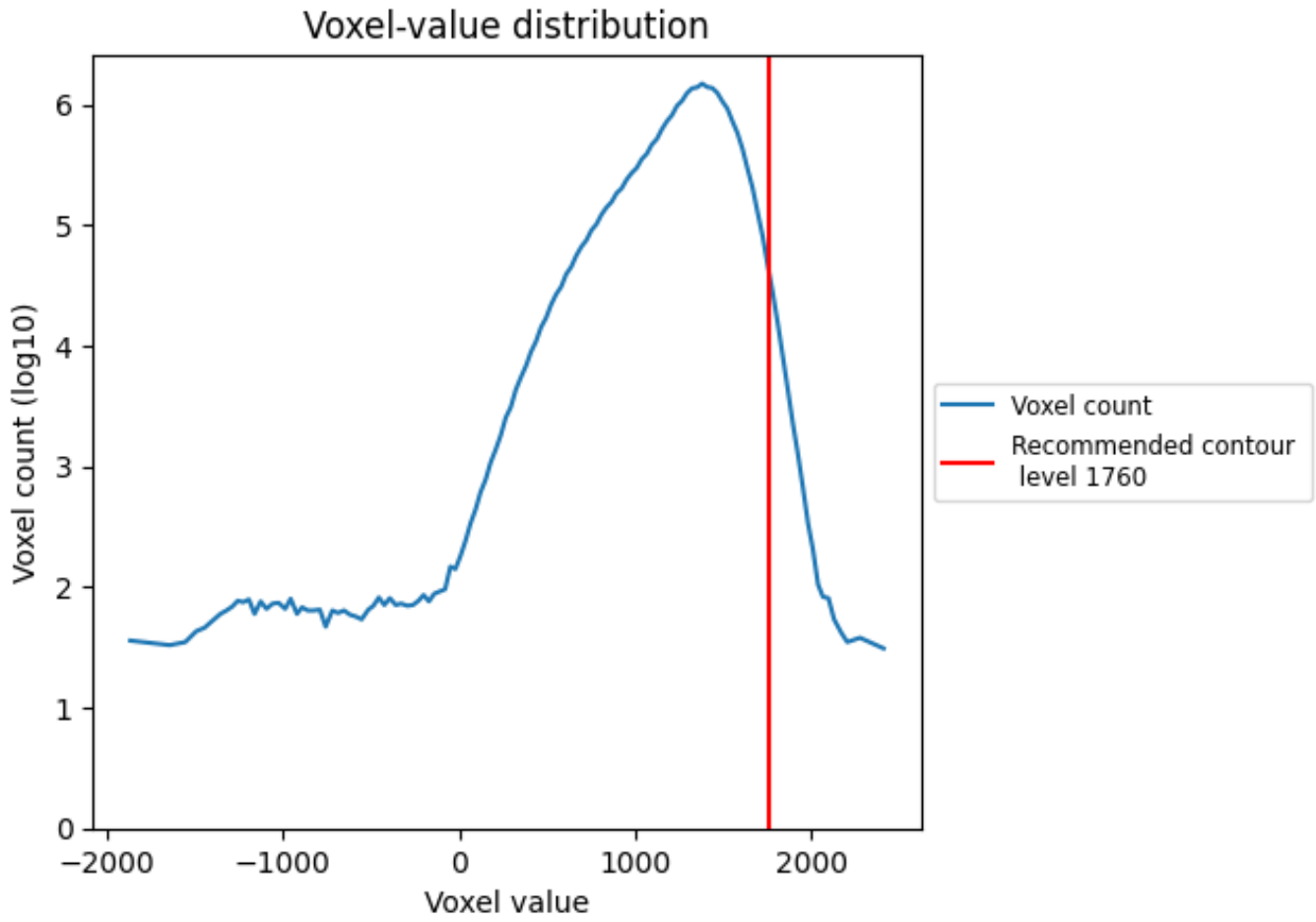
6.5 Mask visualisation (i)

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

7 Tomogram analysis

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

7.1 Voxel-value distribution



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.

8 Map-model fit

This section contains information regarding the fit between EMDB map EMD-1052 and PDB model 1Q5A. Per-residue inclusion information can be found in section 3 on page 7.

8.1 Map-model overlay

This section was not generated.

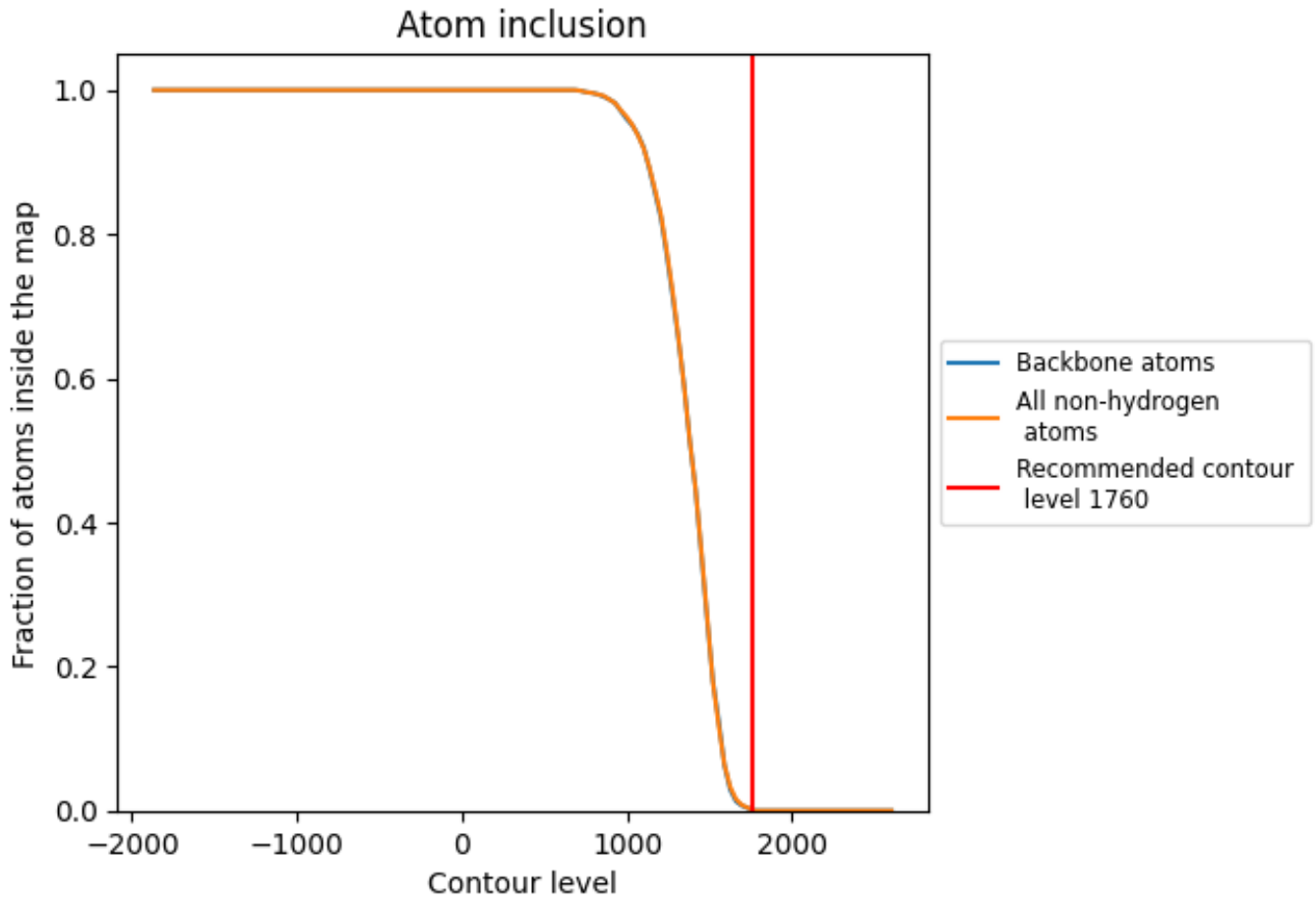
8.2 Q-score mapped to coordinate model

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.

8.3 Atom inclusion mapped to coordinate model

This section was not generated.

8.4 Atom inclusion (i)



At the recommended contour level, 0% of all backbone atoms, 0% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (1760) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0010	0.0050
A	0.0020	0.0070
B	0.0000	0.0030