



Full wwPDB EM Validation Report ⓘ

May 26, 2025 – 10:47 PM EDT

PDB ID : 8DDW / pdb_00008ddw
EMDB ID : EMD-27344
Title : cryo-EM structure of TRPM3 ion channel in complex with Gbg, tethered by ALFA-nanobody
Authors : Zhao, C.; MacKinnon, R.
Deposited on : 2022-06-19
Resolution : 4.70 Å(reported)

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

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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

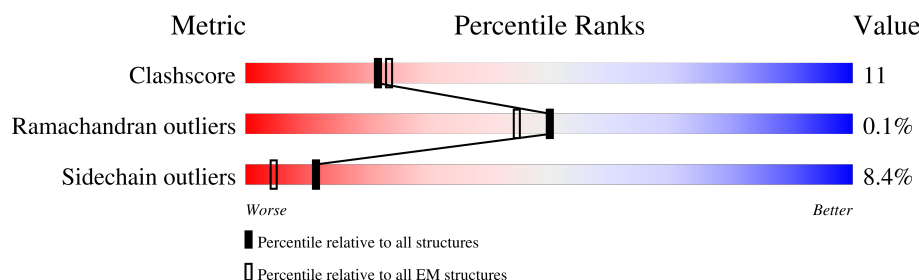
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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 $\leq 5\%$. 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	1371	<div> <div>12%</div> <div>36%</div> <div>13%</div> <div>•</div> <div>49%</div> </div>
1	B	1371	<div> <div>20%</div> <div>35%</div> <div>15%</div> <div>•</div> <div>49%</div> </div>
1	C	1371	<div> <div>18%</div> <div>36%</div> <div>14%</div> <div>•</div> <div>49%</div> </div>
1	D	1371	<div> <div>12%</div> <div>37%</div> <div>13%</div> <div>•</div> <div>48%</div> </div>
2	E	17	<div> <div>12%</div> <div>82%</div> <div>18%</div> </div>
2	F	17	<div> <div>18%</div> <div>94%</div> <div>6%</div> </div>
2	G	17	<div> <div>24%</div> <div>76%</div> <div>24%</div> </div>
2	H	17	<div> <div>18%</div> <div>88%</div> <div>12%</div> </div>

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Mol	Chain	Length	Quality of chain
3	I	339	<div> <div>50%</div> <div>55%</div> <div>42%</div> <div>..</div> </div>
4	J	70	<div> <div>40%</div> <div>53%</div> <div>23%</div> <div>6%</div> <div>19%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 25869 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 Transient receptor potential cation channel, subfamily M, member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	695	Total	C	N	O	S	0	0
			5576	3553	972	1014	37		
1	B	695	Total	C	N	O	S	0	0
			5576	3553	972	1014	37		
1	C	695	Total	C	N	O	S	0	0
			5576	3553	972	1014	37		
1	D	719	Total	C	N	O	S	0	0
			5765	3673	1003	1051	38		

- Molecule 2 is a protein called Unidentified segment at the N-terminus of TRPM3.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	E	17	Total	C	N	O	0	0
			85	51	17	17		
2	F	17	Total	C	N	O	0	0
			85	51	17	17		
2	G	17	Total	C	N	O	0	0
			85	51	17	17		
2	H	17	Total	C	N	O	0	0
			85	51	17	17		

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	337	Total	C	N	O	S	2	0
			2598	1603	466	506	23		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	57	Total	C	N	O	S	0	0
			438	274	77	84	3		

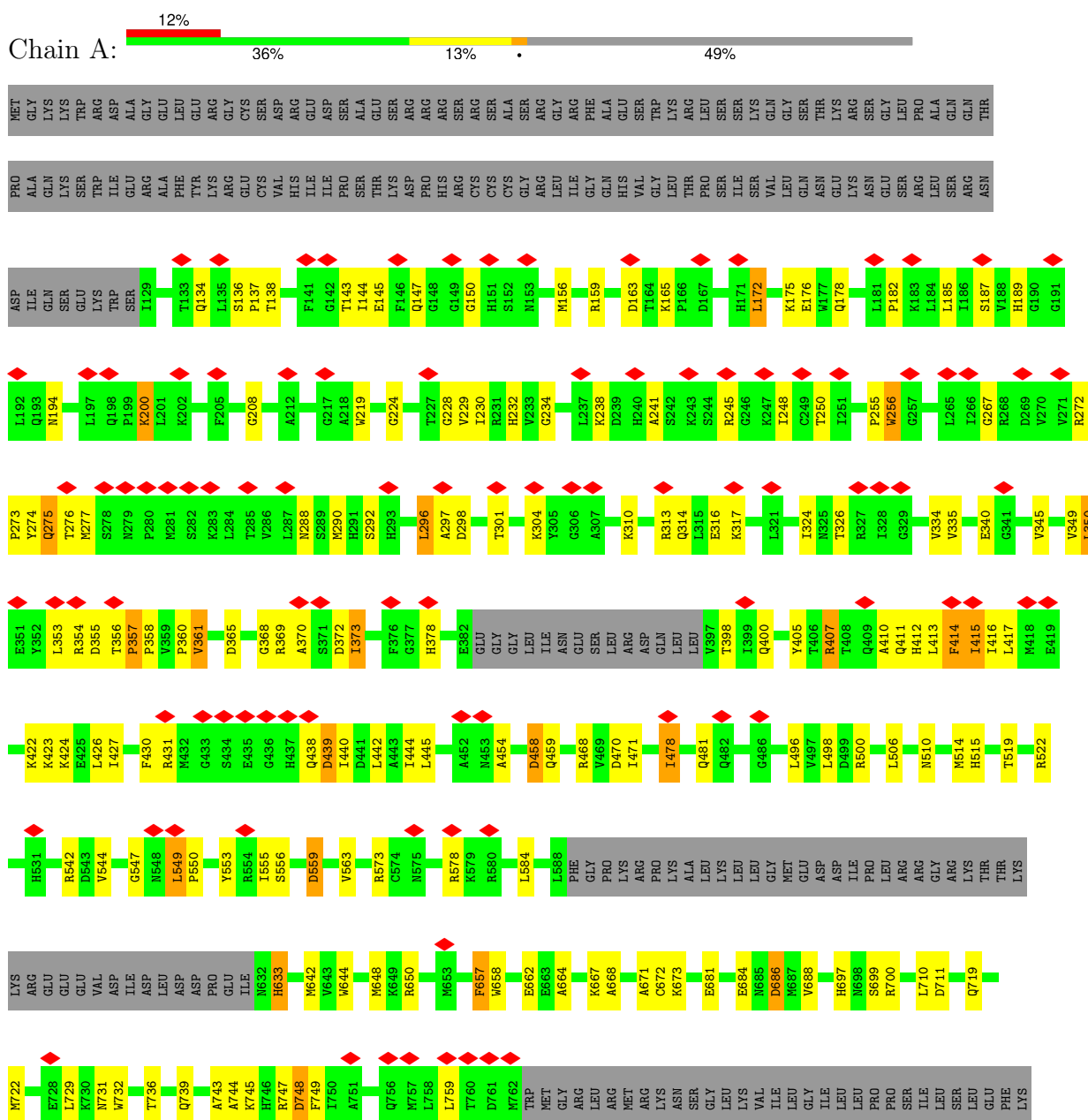
There is a discrepancy between the modelled and reference sequences:

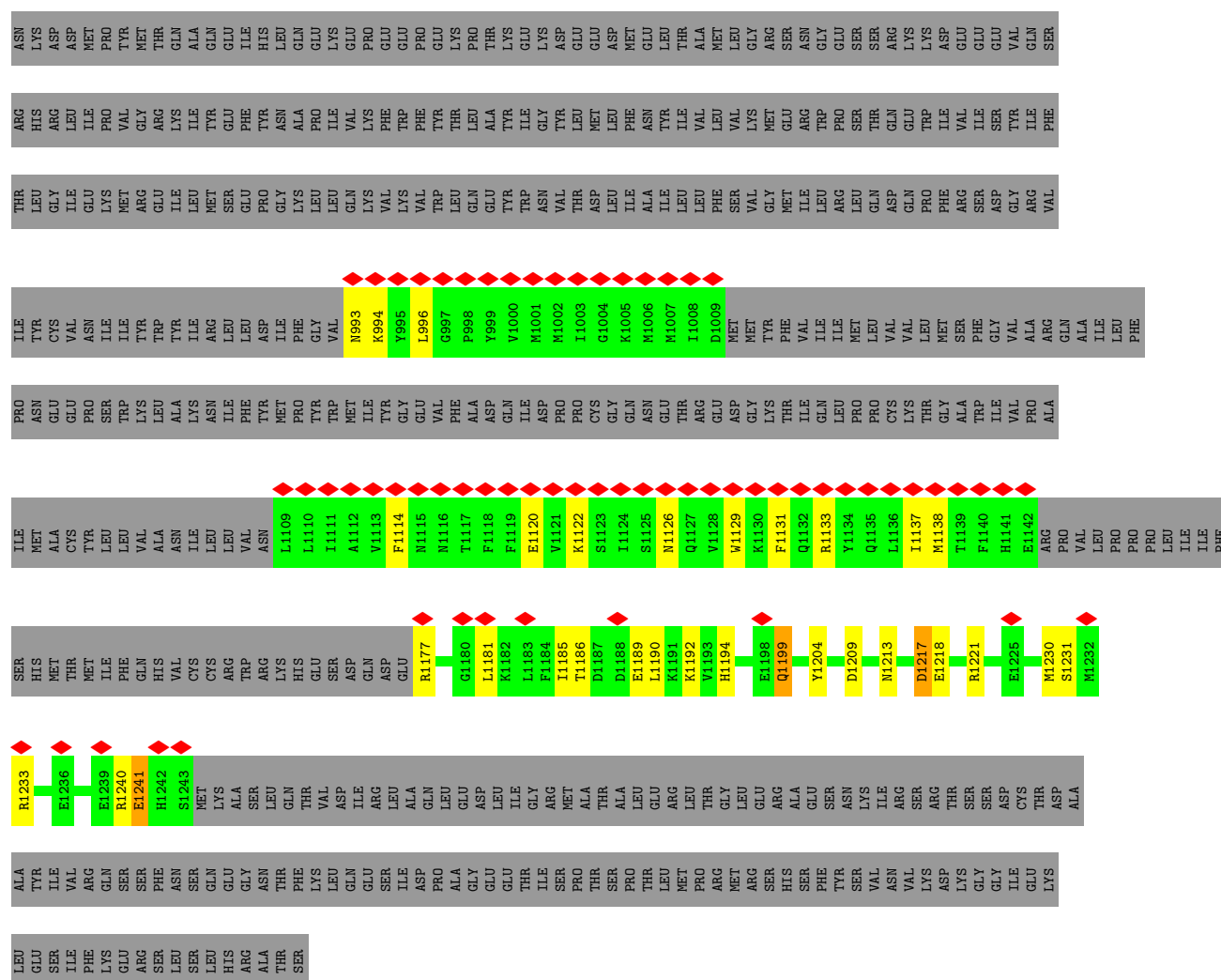
Chain	Residue	Modelled	Actual	Comment	Reference
J	68	SER	CYS	engineered mutation	UNP P59768

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: Transient receptor potential cation channel, subfamily M, member 3








SER HIS
GLY SER
PHE TYR
TRP LYS
VAL ASP
ASN VAL
GLY ASP
LYS ASP
LYS GLY
GLY ILE
ILE LYS
LYS LEU
GLU LEU
SER ILE
PHE SER
LYS PHE
GLU LYS
ARG ARG
SER LEU
SER SER
SER LEU
HIS HIS
ALA ARG
THR ALA
SER SER

- Molecule 1: Transient receptor potential cation channel, subfamily M, member 3

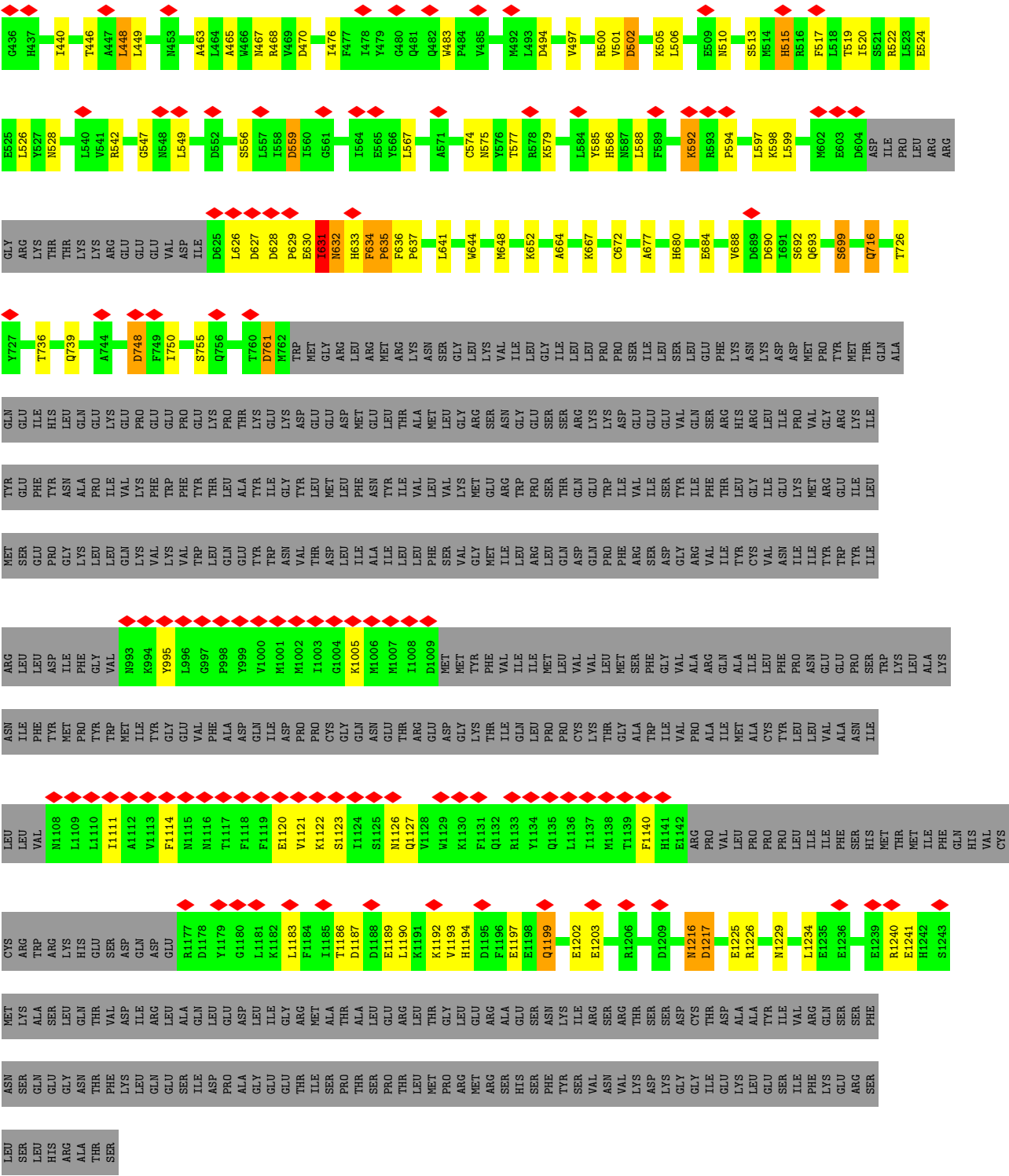
Chain C: 

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ASP ASP
ALA VAL
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ASP PHE
LYS TYR
LYS ARG
GLY ILE
CYS CYS
SER SER
VAL ASP
HIS ARG
GLU LEU
ILE ILE
PRO SER
SER ALA
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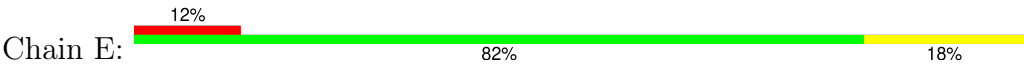
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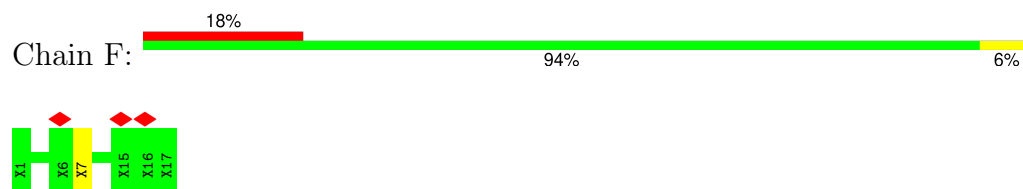
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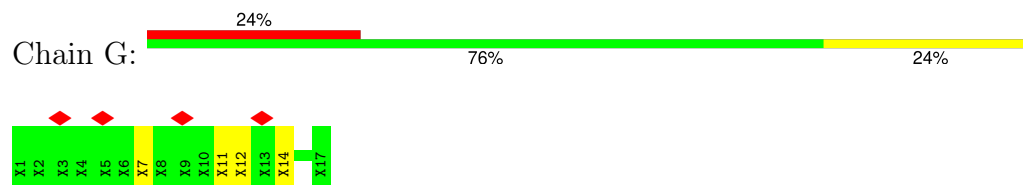
• Molecule 2: Unidentified segment at the N-terminus of TRPM3



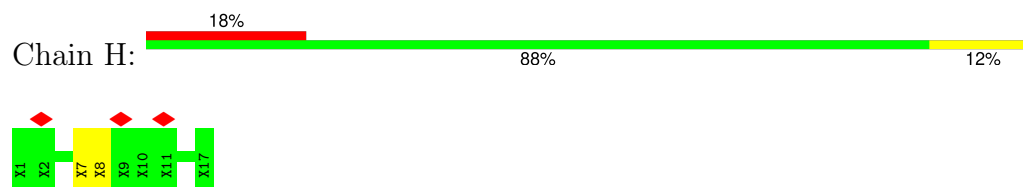
- Molecule 2: Unidentified segment at the N-terminus of TRPM3



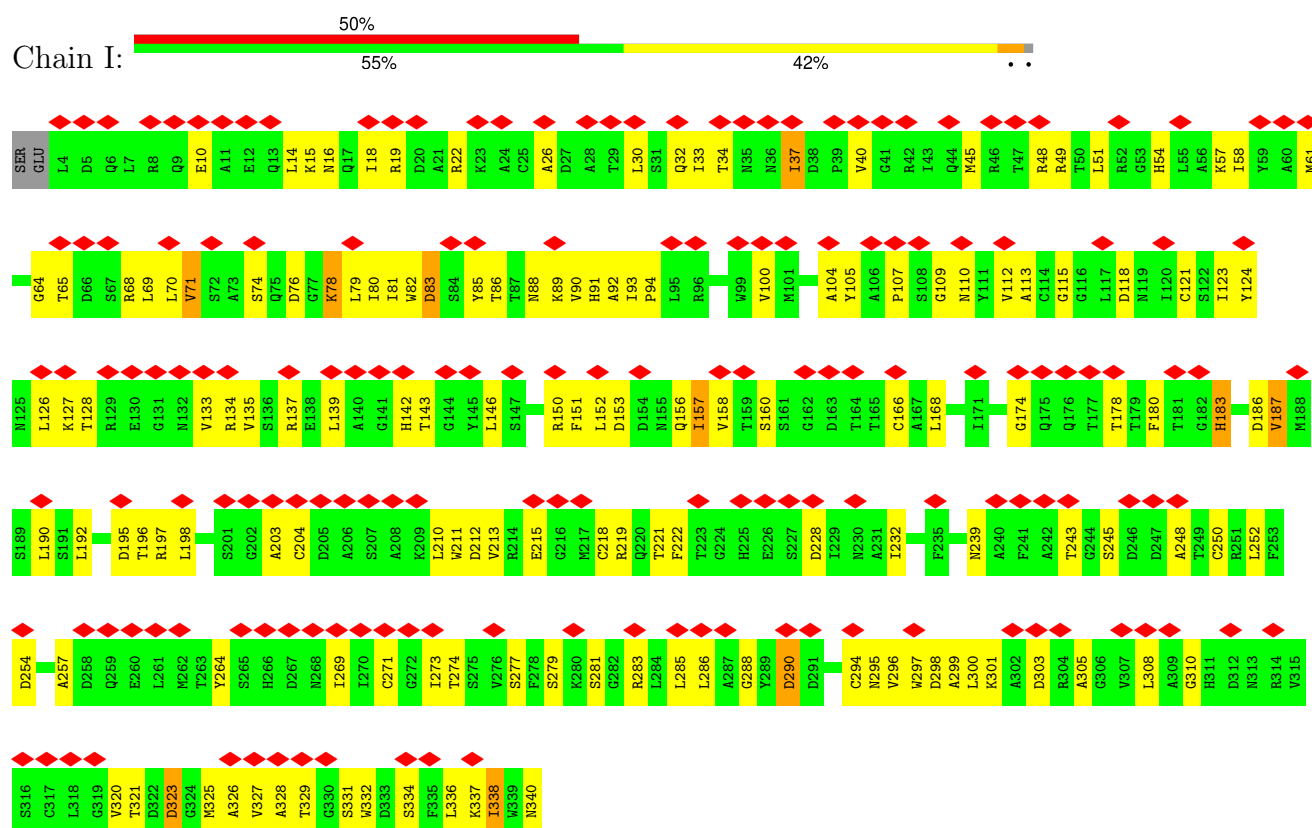
- Molecule 2: Unidentified segment at the N-terminus of TRPM3



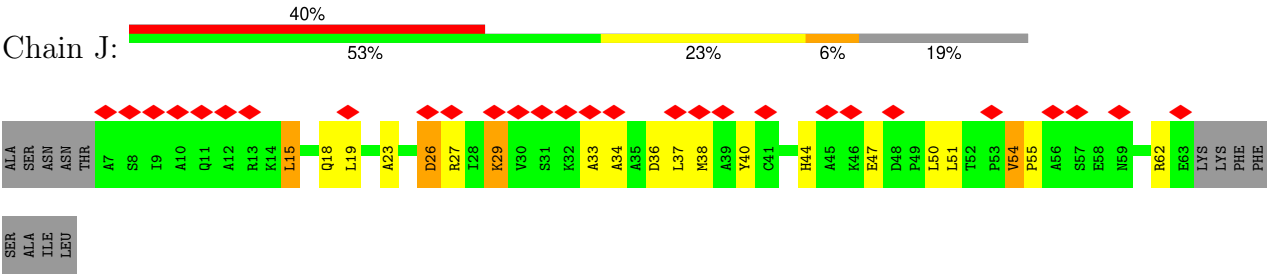
- Molecule 2: Unidentified segment at the N-terminus of TRPM3



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	62171	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 ($e^-/\text{\AA}^2$)	51.4	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.041	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	0.14	0/5686	0.31	0/7667
1	B	0.13	0/5686	0.29	0/7667
1	C	0.13	0/5686	0.30	0/7667
1	D	0.19	0/5879	0.35	1/7927 (0.0%)
3	I	0.13	0/2651	0.34	0/3593
4	J	0.17	0/444	0.41	0/599
All	All	0.15	0/26032	0.32	1/35120 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	632	ASN	N-CA-C	-8.57	99.89	111.54

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	A	5576	0	5602	122	0
1	B	5576	0	5602	113	0
1	C	5576	0	5602	122	0
1	D	5765	0	5793	142	0
2	E	85	0	21	3	0
2	F	85	0	23	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	85	0	23	4	0
2	H	85	0	19	2	0
3	I	2598	0	2509	96	0
4	J	438	0	447	16	0
All	All	25869	0	25641	586	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 11.

All (586) 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:D:629:PRO:HD2	1:D:631:ILE:HD13	1.52	0.89
1:A:356:THR:HB	1:A:357:PRO:HD3	1.59	0.82
1:D:520:ILE:N	1:D:632:ASN:HD21	1.83	0.76
3:I:54:HIS:HB2	3:I:334:SER:HB2	1.67	0.75
1:D:520:ILE:H	1:D:632:ASN:CG	1.95	0.74
1:A:496:LEU:O	1:A:650:ARG:NH1	2.23	0.72
1:D:205:PHE:HA	1:D:440:ILE:HG13	1.73	0.71
1:B:205:PHE:HA	1:B:440:ILE:HG13	1.73	0.71
1:A:439:ASP:OD1	1:A:439:ASP:N	2.24	0.70
1:D:520:ILE:H	1:D:632:ASN:ND2	1.90	0.70
3:I:51:LEU:HB3	3:I:54:HIS:HE1	1.57	0.70
3:I:252:LEU:HD22	3:I:299:ALA:HB1	1.73	0.70
1:D:407:ARG:HB2	1:D:411:GLN:HB2	1.76	0.68
1:D:726:THR:HB	1:D:1183:LEU:HB2	1.76	0.67
1:A:355:ASP:CG	1:A:357:PRO:HD2	2.20	0.67
1:C:750:ILE:O	1:C:756:GLN:NE2	2.28	0.66
1:D:629:PRO:O	1:D:631:ILE:N	2.29	0.66
1:B:1217:ASP:OD1	1:B:1217:ASP:N	2.28	0.66
1:A:185:LEU:HB3	1:A:334:VAL:HG22	1.76	0.66
1:D:629:PRO:O	1:D:630:GLU:HB2	1.95	0.66
1:C:1005:LYS:HD2	1:C:1121:VAL:HG13	1.78	0.65
3:I:160:SER:HB3	3:I:190:LEU:HD23	1.78	0.65
1:D:229:VAL:HG11	1:D:339:VAL:HB	1.76	0.65
1:B:458:ASP:OD1	1:B:458:ASP:N	2.30	0.65
1:B:346:ILE:HD12	1:B:374:LEU:HD21	1.78	0.65
1:C:502:ASP:OD1	1:C:502:ASP:N	2.28	0.65
1:B:250:THR:HB	1:B:292:SER:H	1.61	0.65
1:D:631:ILE:HG23	1:D:632:ASN:N	2.10	0.64
1:A:573:ARG:HH21	1:A:578:ARG:HD3	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:54:VAL:HG22	4:J:55:PRO:HD2	1.79	0.64
1:C:325:ASN:O	1:C:327:ARG:NH1	2.30	0.64
1:A:350:LEU:HD22	1:A:354:ARG:HH11	1.63	0.64
3:I:239:ASN:ND2	4:J:36:ASP:OD2	2.31	0.64
1:A:136:SER:O	2:E:8:UNK:N	2.32	0.63
1:B:573:ARG:HB3	1:B:578:ARG:HH22	1.63	0.63
1:D:506:LEU:O	1:D:510:ASN:ND2	2.31	0.63
1:C:664:ALA:HA	1:C:667:LYS:HD3	1.79	0.63
1:A:498:LEU:O	1:A:500:ARG:NH1	2.30	0.63
1:B:208:GLY:HA3	1:B:440:ILE:HB	1.80	0.63
1:D:517:PHE:O	1:D:522:ARG:NH1	2.32	0.63
1:D:634:PHE:N	1:D:634:PHE:CD1	2.67	0.63
1:A:407:ARG:HG3	1:A:411:GLN:HB2	1.80	0.63
1:B:498:LEU:O	1:B:500:ARG:NH1	2.30	0.63
1:A:506:LEU:O	1:A:510:ASN:ND2	2.31	0.62
3:I:166:CYS:HB2	3:I:180:PHE:HB2	1.80	0.62
1:B:559:ASP:OD1	1:B:559:ASP:N	2.33	0.62
3:I:64:GLY:N	3:I:69:LEU:O	2.33	0.62
1:B:197:LEU:HD11	1:B:202:LYS:HB3	1.80	0.62
1:D:136:SER:O	2:H:8:UNK:N	2.33	0.62
3:I:104:ALA:HB3	3:I:113:ALA:HB3	1.81	0.62
3:I:51:LEU:HD23	3:I:336:LEU:HB3	1.80	0.62
1:A:335:VAL:HG23	1:A:360:PRO:HG2	1.82	0.61
3:I:45:MET:HE2	3:I:308:LEU:HD21	1.81	0.61
1:A:137:PRO:HA	2:E:7:UNK:HA	1.82	0.61
1:A:743:ALA:O	1:A:745:LYS:NZ	2.33	0.61
1:C:313:ARG:NH1	1:C:313:ARG:O	2.33	0.61
1:B:651:GLN:HE21	1:B:655:LEU:HG	1.65	0.61
1:C:556:SER:OG	1:C:559:ASP:OD1	2.18	0.61
1:D:559:ASP:OD1	1:D:559:ASP:N	2.31	0.61
1:B:502:ASP:OD1	1:B:502:ASP:N	2.34	0.61
1:C:573:ARG:HE	1:C:578:ARG:HH21	1.49	0.61
1:D:502:ASP:OD1	1:D:502:ASP:N	2.32	0.61
1:D:520:ILE:N	1:D:632:ASN:ND2	2.48	0.61
1:C:1221:ARG:NH1	1:C:1225:GLU:OE2	2.34	0.61
1:A:559:ASP:N	1:A:559:ASP:OD1	2.33	0.60
1:D:634:PHE:O	1:D:636:PHE:N	2.34	0.60
1:A:355:ASP:O	1:A:356:THR:C	2.45	0.60
1:A:445:LEU:HD23	1:A:471:ILE:HG13	1.83	0.60
1:B:1142:GLU:HA	1:B:1177:ARG:HH22	1.67	0.60
1:D:644:TRP:NE1	1:D:648:MET:SD	2.74	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:218:CYS:O	4:J:18:GLN:NE2	2.35	0.60
1:D:333:PRO:HB2	1:D:448:LEU:HD22	1.83	0.60
1:A:145:GLU:HG3	1:A:273:PRO:HA	1.82	0.60
1:B:313:ARG:HG3	1:B:317:LYS:HE2	1.84	0.60
1:B:496:LEU:O	1:B:650:ARG:NH1	2.34	0.60
1:A:1122:LYS:O	1:A:1126:ASN:ND2	2.34	0.60
3:I:115:GLY:HA3	3:I:146:LEU:HD23	1.84	0.60
1:B:524:GLU:O	1:B:528:ASN:ND2	2.32	0.59
1:A:224:GLY:H	1:A:230:ILE:HD13	1.67	0.59
1:A:1240:ARG:NH1	1:D:1241:GLU:OE1	2.36	0.59
1:D:397:VAL:N	1:D:400:GLN:OE1	2.35	0.59
1:C:690:ASP:OD1	1:C:690:ASP:N	2.29	0.59
3:I:48:ARG:NE	3:I:340:ASN:OD1	2.31	0.59
1:A:248:ILE:O	1:A:292:SER:OG	2.20	0.59
1:B:1133:ARG:HH21	1:B:1137:ILE:HD11	1.67	0.59
1:D:1217:ASP:N	1:D:1217:ASP:OD1	2.32	0.59
1:A:353:LEU:HD13	1:A:423:LYS:HB2	1.84	0.59
1:B:1122:LYS:O	1:B:1126:ASN:ND2	2.36	0.59
1:C:748:ASP:N	1:C:748:ASP:OD1	2.35	0.59
1:D:594:PRO:HB2	1:D:597:LEU:HB2	1.85	0.58
1:D:716:GLN:NE2	1:D:1199:GLN:OE1	2.32	0.58
1:D:267:GLY:H	1:D:272:ARG:HH11	1.50	0.58
1:C:402:THR:OG1	1:C:409:GLN:OE1	2.22	0.58
1:A:1241:GLU:OE1	1:B:1240:ARG:NH2	2.35	0.58
1:A:644:TRP:NE1	1:A:648:MET:SD	2.77	0.58
1:A:658:TRP:HE1	1:A:668:ALA:HB2	1.69	0.58
3:I:80:ILE:HA	3:I:92:ALA:HA	1.84	0.58
3:I:187:VAL:HA	3:I:203:ALA:HA	1.86	0.58
1:A:255:PRO:HA	1:A:297:ALA:HB3	1.85	0.58
1:C:257:GLY:HA3	1:C:302:THR:HA	1.85	0.58
1:C:506:LEU:O	1:C:510:ASN:ND2	2.31	0.58
1:C:719:GLN:HA	1:C:722:MET:HE2	1.85	0.58
1:D:342:GLY:H	1:D:345:VAL:HB	1.69	0.58
1:B:439:ASP:HB2	1:B:442:LEU:HB2	1.85	0.58
1:B:493:LEU:HB2	1:B:522:ARG:HE	1.69	0.58
1:D:629:PRO:C	1:D:631:ILE:N	2.61	0.58
1:B:1221:ARG:NH1	1:B:1225:GLU:OE2	2.37	0.58
1:D:313:ARG:NH2	1:D:355:ASP:OD2	2.36	0.58
1:A:187:SER:OG	1:A:189:HIS:NE2	2.35	0.57
1:B:189:HIS:NE2	1:B:352:TYR:OH	2.34	0.57
1:A:194:ASN:HA	1:A:228:GLY:H	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:542:ARG:O	1:C:547:GLY:N	2.37	0.57
1:C:697:HIS:HD2	1:C:700:ARG:HH12	1.51	0.57
3:I:310:GLY:O	3:I:337:LYS:NZ	2.37	0.57
1:C:1225:GLU:O	1:C:1229:ASN:ND2	2.38	0.57
3:I:121:CYS:HB3	3:I:139:LEU:HB2	1.86	0.57
4:J:34:ALA:O	4:J:38:MET:N	2.33	0.57
1:C:365:ASP:HB3	1:C:431:ARG:HH22	1.69	0.57
1:D:1186:THR:HG22	1:D:1189:GLU:HG2	1.86	0.57
1:D:1190:LEU:O	1:D:1194:HIS:ND1	2.38	0.57
1:B:144:ILE:HG22	1:B:272:ARG:HB2	1.86	0.57
1:D:630:GLU:O	1:D:631:ILE:HG22	2.04	0.56
1:C:458:ASP:OD1	1:C:458:ASP:N	2.37	0.56
1:A:163:ASP:O	1:A:165:LYS:NZ	2.39	0.56
1:A:313:ARG:O	1:A:313:ARG:NH1	2.39	0.56
1:A:993:ASN:OD1	1:A:996:LEU:N	2.36	0.56
3:I:250:CYS:HB3	3:I:264:TYR:HB2	1.86	0.56
1:D:631:ILE:O	1:D:633:HIS:ND1	2.39	0.56
4:J:29:LYS:O	4:J:33:ALA:N	2.37	0.56
1:A:143:THR:OG1	1:A:156:MET:SD	2.63	0.56
1:B:144:ILE:HG13	1:B:155:ALA:HB3	1.88	0.56
1:B:173:MET:HB3	1:B:179:LEU:HD12	1.87	0.56
1:B:692:SER:O	1:B:696:ASN:ND2	2.38	0.56
1:D:632:ASN:C	1:D:632:ASN:HD22	2.13	0.56
1:B:664:ALA:N	1:B:1197:GLU:OE2	2.38	0.56
1:C:221:PHE:O	1:C:312:ARG:NH2	2.38	0.56
1:A:748:ASP:OD1	1:A:748:ASP:N	2.36	0.56
1:B:336:ALA:HB3	1:B:361:VAL:HG22	1.86	0.56
1:C:565:GLU:OE2	1:C:577:THR:OG1	2.19	0.56
1:C:1241:GLU:OE1	1:D:1240:ARG:NH2	2.38	0.56
1:D:574:CYS:SG	1:D:575:ASN:N	2.79	0.56
3:I:76:ASP:HB2	3:I:78:LYS:HE3	1.86	0.56
3:I:137:ARG:HH21	3:I:174:GLY:HA3	1.70	0.56
1:D:299:ASN:OD1	1:D:299:ASN:N	2.39	0.56
3:I:248:ALA:HB1	3:I:269:ILE:HG22	1.88	0.56
1:C:159:ARG:HA	1:C:296:LEU:HB2	1.88	0.56
1:B:994:LYS:NZ	1:B:995:TYR:OH	2.39	0.55
1:C:672:CYS:HG	1:C:699:SER:HG	1.40	0.55
3:I:326:ALA:HA	4:J:50:LEU:HD21	1.87	0.55
3:I:126:LEU:HA	3:I:133:VAL:HG22	1.89	0.55
3:I:128:THR:HG21	3:I:134:ARG:HG2	1.88	0.55
3:I:279:SER:OG	3:I:283:ARG:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1122:LYS:O	1:C:1126:ASN:ND2	2.40	0.55
1:A:430:PHE:HE1	1:A:438:GLN:HA	1.71	0.55
1:B:137:PRO:HA	2:F:7:UNK:HA	1.88	0.55
1:D:238:LYS:HB2	1:D:290:MET:HG3	1.89	0.55
4:J:23:ALA:HA	4:J:27:ARG:HH22	1.72	0.55
1:A:208:GLY:HA3	1:A:440:ILE:HB	1.89	0.55
1:B:275:GLN:NE2	1:B:277:MET:O	2.34	0.55
1:C:175:LYS:O	1:C:178:GLN:NE2	2.39	0.55
3:I:254:ASP:OD2	3:I:257:ALA:N	2.40	0.55
1:B:577:THR:O	1:B:579:LYS:NZ	2.40	0.55
1:A:672:CYS:SG	1:A:699:SER:OG	2.57	0.55
1:B:473:ARG:HB2	1:B:506:LEU:HD21	1.89	0.55
1:D:265:LEU:HA	1:D:272:ARG:HD3	1.87	0.55
3:I:271:CYS:HB3	3:I:290:ASP:HB2	1.89	0.55
1:D:577:THR:O	1:D:579:LYS:NZ	2.39	0.54
1:C:1181:LEU:HG	1:C:1182:LYS:HG3	1.90	0.54
1:B:335:VAL:HB	1:B:448:LEU:HD21	1.88	0.54
1:C:712:GLN:HG2	1:C:1204:TYR:HB2	1.88	0.54
1:D:257:GLY:O	1:D:262:GLN:NE2	2.40	0.54
1:D:631:ILE:O	1:D:632:ASN:C	2.50	0.54
1:D:1189:GLU:HA	1:D:1192:LYS:HD3	1.88	0.54
3:I:83:ASP:N	3:I:88:ASN:O	2.39	0.54
1:A:241:ALA:O	1:B:1206:ARG:NH1	2.38	0.54
1:B:175:LYS:O	1:B:178:GLN:NE2	2.41	0.54
1:A:175:LYS:O	1:A:178:GLN:NE2	2.41	0.54
1:D:172:LEU:HD12	1:D:176:GLU:HB2	1.89	0.54
3:I:195:ASP:HB2	3:I:197:ARG:HH11	1.73	0.54
1:B:194:ASN:OD1	1:B:231:ARG:NH1	2.40	0.54
1:D:183:LYS:NZ	1:D:465:ALA:O	2.39	0.54
1:D:748:ASP:OD1	1:D:748:ASP:N	2.33	0.54
1:A:439:ASP:HB2	1:A:442:LEU:HB2	1.90	0.54
1:A:697:HIS:HD2	1:A:700:ARG:HH12	1.55	0.54
1:C:413:LEU:HB3	1:C:416:ILE:HD11	1.90	0.54
1:D:592:LYS:NZ	1:D:594:PRO:O	2.41	0.54
3:I:331:SER:OG	3:I:332:TRP:N	2.39	0.54
1:A:454:ALA:O	1:A:459:GLN:NE2	2.41	0.54
1:B:468:ARG:NH2	1:B:470:ASP:OD2	2.40	0.54
1:D:185:LEU:HB3	1:D:334:VAL:HG22	1.90	0.54
1:D:208:GLY:HA3	1:D:440:ILE:HB	1.89	0.54
3:I:180:PHE:HZ	3:I:213:VAL:HA	1.73	0.54
1:C:255:PRO:HG2	1:C:258:ILE:HG13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:112:VAL:HG23	3:I:126:LEU:HD11	1.89	0.53
3:I:285:LEU:O	3:I:297:TRP:N	2.41	0.53
1:A:256:TRP:HB2	1:A:296:LEU:HB3	1.90	0.53
1:B:401:LYS:HZ1	1:B:413:LEU:HD12	1.73	0.53
1:C:711:ASP:HA	1:C:752:HIS:HE2	1.72	0.53
3:I:61:MET:HE2	3:I:336:LEU:HD11	1.89	0.53
1:C:353:LEU:HB3	1:C:423:LYS:HD2	1.90	0.53
1:D:634:PHE:O	1:D:637:PRO:HD3	2.08	0.53
1:C:565:GLU:OE2	1:C:574:CYS:N	2.39	0.53
1:D:137:PRO:HA	2:H:7:UNK:HA	1.90	0.53
3:I:298:ASP:HB3	3:I:303:ASP:H	1.74	0.53
1:C:172:LEU:HD12	1:C:176:GLU:HB2	1.89	0.53
1:C:582:ARG:O	1:C:586:HIS:HB2	2.08	0.53
1:D:353:LEU:HB3	1:D:423:LYS:HD2	1.91	0.53
1:C:349:VAL:HG23	1:C:361:VAL:HG21	1.91	0.53
3:I:232:ILE:HA	3:I:243:THR:HA	1.91	0.53
1:A:234:GLY:HA3	1:A:288:ASN:HD21	1.73	0.53
1:B:407:ARG:HG2	1:B:410:ALA:HB3	1.91	0.53
1:D:664:ALA:N	1:D:1197:GLU:OE2	2.41	0.53
3:I:40:VAL:HG22	3:I:303:ASP:HB3	1.92	0.52
1:D:690:ASP:HA	1:D:693:GLN:HE21	1.72	0.52
3:I:83:ASP:OD2	3:I:86:THR:OG1	2.23	0.52
1:A:250:THR:HB	1:A:292:SER:H	1.75	0.52
1:C:470:ASP:OD1	1:C:470:ASP:N	2.42	0.52
1:C:350:LEU:HD13	1:C:354:ARG:HH22	1.74	0.52
3:I:33:ILE:HG22	3:I:34:THR:HG23	1.91	0.52
1:C:137:PRO:HA	2:G:7:UNK:HA	1.92	0.52
1:D:258:ILE:HA	1:D:303:GLY:HA2	1.92	0.52
1:D:627:ASP:O	1:D:628:ASP:HB3	2.10	0.52
1:A:349:VAL:HG23	1:A:361:VAL:HG21	1.92	0.52
1:B:398:THR:HA	1:B:414:PHE:HE2	1.75	0.52
3:I:15:LYS:HD3	3:I:19:ARG:HE	1.73	0.52
1:D:224:GLY:O	1:D:288:ASN:N	2.36	0.51
1:A:550:PRO:HG2	1:A:553:TYR:HB2	1.92	0.51
1:A:1189:GLU:HA	1:A:1192:LYS:HD3	1.93	0.51
3:I:118:ASP:OD1	3:I:118:ASP:N	2.43	0.51
1:C:574:CYS:SG	1:C:575:ASN:N	2.83	0.51
1:C:761:ASP:OD1	1:C:761:ASP:N	2.42	0.51
3:I:281:SER:HA	4:J:40:TYR:CZ	2.46	0.51
3:I:121:CYS:O	3:I:139:LEU:N	2.44	0.51
1:A:411:GLN:HE22	1:A:413:LEU:HG	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:742:VAL:O	1:B:745:LYS:NZ	2.38	0.51
1:D:1005:LYS:HD2	1:D:1121:VAL:HG13	1.92	0.51
3:I:22:ARG:O	3:I:26:ALA:N	2.40	0.51
3:I:79:LEU:HB3	3:I:93:ILE:HB	1.92	0.51
1:B:141:PHE:O	1:B:269:ASP:N	2.40	0.50
1:C:719:GLN:HB3	1:C:723:LYS:HZ1	1.76	0.50
1:D:234:GLY:HA3	1:D:288:ASN:HD21	1.76	0.50
1:B:186:ILE:HB	1:B:220:ILE:HG12	1.93	0.50
1:B:574:CYS:SG	1:B:575:ASN:N	2.84	0.50
1:C:129:ILE:HD12	1:C:132:HIS:HB2	1.93	0.50
1:C:559:ASP:OD1	1:C:559:ASP:N	2.31	0.50
1:B:159:ARG:HA	1:B:296:LEU:HB2	1.93	0.50
3:I:57:LYS:HB3	3:I:332:TRP:CG	2.46	0.50
1:D:250:THR:HB	1:D:292:SER:H	1.76	0.50
3:I:69:LEU:HD21	3:I:81:ILE:HG23	1.93	0.50
1:B:157:TYR:OH	1:B:267:GLY:O	2.29	0.50
1:C:429:VAL:HB	1:C:431:ARG:HH21	1.76	0.50
3:I:198:LEU:HD23	3:I:212:ASP:HA	1.92	0.50
1:B:342:GLY:H	1:B:345:VAL:HB	1.76	0.50
1:C:323:LYS:HD3	1:C:331:GLY:HA2	1.93	0.50
1:C:419:GLU:O	1:C:423:LYS:NZ	2.45	0.50
1:D:201:LEU:HD21	1:D:366:GLY:HA3	1.93	0.50
3:I:37:ILE:HD12	3:I:283:ARG:HH22	1.75	0.50
3:I:151:PHE:HA	3:I:157:ILE:HA	1.93	0.50
1:D:221:PHE:O	1:D:312:ARG:NH2	2.45	0.49
1:B:277:MET:HB2	1:C:511:GLY:HA3	1.93	0.49
1:B:470:ASP:OD1	1:B:470:ASP:N	2.44	0.49
1:C:132:HIS:O	2:G:12:UNK:N	2.45	0.49
1:D:344:ASN:O	1:D:347:SER:OG	2.22	0.49
4:J:26:ASP:N	4:J:26:ASP:OD1	2.45	0.49
1:A:353:LEU:HD11	1:A:427:ILE:HD11	1.93	0.49
1:C:139:ASP:H	1:C:159:ARG:HD3	1.77	0.49
1:B:195:PHE:O	1:B:231:ARG:NH2	2.45	0.49
1:D:761:ASP:N	1:D:761:ASP:OD1	2.46	0.49
1:B:446:THR:HG22	1:B:475:GLN:HG3	1.95	0.49
1:C:254:ALA:O	1:C:297:ALA:N	2.45	0.49
1:D:166:PRO:HA	1:D:169:LEU:HD12	1.94	0.49
1:D:324:ILE:HG23	1:D:326:THR:H	1.78	0.49
3:I:239:ASN:HB2	4:J:37:LEU:HD21	1.93	0.49
4:J:44:HIS:ND1	4:J:47:GLU:OE2	2.46	0.49
4:J:47:GLU:N	4:J:47:GLU:OE1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:598:LYS:HG3	1:D:599:LEU:HD12	1.94	0.49
1:A:514:MET:HE3	1:A:657:PHE:HZ	1.77	0.49
1:A:664:ALA:HA	1:A:667:LYS:HD3	1.93	0.49
1:A:1241:GLU:HA	1:B:1240:ARG:HH12	1.77	0.49
1:B:1189:GLU:HA	1:B:1192:LYS:HD3	1.95	0.49
1:D:634:PHE:O	1:D:635:PRO:C	2.55	0.49
1:A:468:ARG:NH2	1:A:470:ASP:OD2	2.46	0.48
1:B:663:GLU:OE2	1:B:731:ASN:ND2	2.46	0.48
1:D:467:ASN:HB2	1:D:500:ARG:HH21	1.78	0.48
1:D:502:ASP:O	1:D:505:LYS:HG2	2.13	0.48
1:D:1122:LYS:O	1:D:1126:ASN:ND2	2.32	0.48
3:I:245:SER:H	3:I:273:ILE:HD12	1.78	0.48
3:I:48:ARG:NH2	3:I:340:ASN:O	2.46	0.48
1:A:398:THR:HB	1:A:414:PHE:HZ	1.78	0.48
1:D:664:ALA:HA	1:D:667:LYS:HD3	1.94	0.48
1:C:139:ASP:OD1	1:C:159:ARG:NH1	2.47	0.48
1:C:256:TRP:N	1:C:297:ALA:O	2.46	0.48
1:C:324:ILE:HG23	1:C:326:THR:H	1.79	0.48
1:A:697:HIS:CD2	1:A:700:ARG:HH22	2.31	0.48
1:C:363:VAL:O	1:C:430:PHE:N	2.46	0.48
1:D:630:GLU:HB3	1:D:633:HIS:HE1	1.79	0.48
1:A:407:ARG:HH12	1:A:410:ALA:HB3	1.78	0.48
1:A:673:LYS:HD3	1:A:744:ALA:HA	1.96	0.48
1:B:561:GLY:HA3	1:B:576:TYR:HB2	1.95	0.48
1:B:741:ALA:O	1:B:745:LYS:N	2.47	0.48
1:C:577:THR:HB	1:C:582:ARG:HH21	1.79	0.48
3:I:30:LEU:HD21	3:I:300:LEU:HG	1.94	0.48
1:A:1218:GLU:OE2	1:A:1221:ARG:NH2	2.44	0.48
1:A:458:ASP:N	1:A:458:ASP:OD1	2.45	0.48
1:B:496:LEU:HD11	1:B:514:MET:HE1	1.96	0.48
1:C:185:LEU:HD22	1:C:319:ILE:HG21	1.95	0.48
1:C:156:MET:SD	1:C:156:MET:N	2.86	0.47
1:C:198:GLN:NE2	1:C:199:PRO:O	2.47	0.47
1:B:256:TRP:N	1:B:297:ALA:O	2.46	0.47
1:B:745:LYS:HB3	1:B:747:ARG:HH12	1.78	0.47
1:C:697:HIS:CD2	1:C:700:ARG:HH22	2.32	0.47
1:D:1225:GLU:O	1:D:1229:ASN:ND2	2.47	0.47
1:A:519:THR:H	1:A:522:ARG:HB2	1.78	0.47
1:A:573:ARG:HE	1:A:578:ARG:NH1	2.12	0.47
1:A:1185:ILE:HG21	1:A:1190:LEU:HD13	1.95	0.47
1:C:431:ARG:HG3	1:C:434:SER:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:ILE:HA	1:D:335:VAL:HG12	1.96	0.47
1:A:400:GLN:OE1	1:A:400:GLN:N	2.45	0.47
1:D:230:ILE:O	1:D:288:ASN:ND2	2.48	0.47
1:D:319:ILE:HA	1:D:322:GLN:HG2	1.97	0.47
3:I:45:MET:HE3	3:I:296:VAL:HG21	1.96	0.47
1:A:313:ARG:NH1	1:A:317:LYS:HG3	2.30	0.47
1:A:358:PRO:HB2	1:A:426:LEU:HD12	1.96	0.47
1:B:260:GLU:OE2	1:B:279:ASN:ND2	2.48	0.47
1:D:140:ALA:HB3	1:D:159:ARG:HD3	1.95	0.47
1:D:250:THR:H	1:D:292:SER:HB2	1.80	0.47
3:I:68:ARG:HG3	3:I:85:TYR:CD1	2.49	0.47
1:D:182:PRO:HG3	1:D:219:TRP:CG	2.49	0.47
1:D:1187:ASP:OD1	1:D:1187:ASP:N	2.39	0.47
1:D:1216:ASN:OD1	1:D:1216:ASN:N	2.46	0.47
3:I:183:HIS:HD2	3:I:211:TRP:HE1	1.63	0.47
1:A:368:GLY:H	1:A:372:ASP:HB2	1.80	0.47
1:B:188:VAL:O	1:B:312:ARG:NH2	2.48	0.47
1:B:435:GLU:O	1:B:438:GLN:NE2	2.47	0.47
1:D:160:VAL:O	1:D:298:ASP:N	2.38	0.47
1:D:176:GLU:O	1:D:178:GLN:NE2	2.48	0.47
1:D:631:ILE:C	1:D:633:HIS:N	2.70	0.47
1:D:680:HIS:NE2	1:D:684:GLU:OE2	2.48	0.47
3:I:105:TYR:CE2	3:I:109:GLY:HA2	2.49	0.47
3:I:215:GLU:N	3:I:215:GLU:OE1	2.48	0.47
1:B:515:HIS:O	1:B:633:HIS:NE2	2.47	0.47
1:C:756:GLN:HE22	1:C:1130:LYS:HB3	1.80	0.47
1:C:1120:GLU:OE1	1:C:1120:GLU:N	2.43	0.47
1:D:370:ALA:O	1:D:373:ILE:HG12	2.15	0.47
1:C:754:CYS:HA	1:C:757:MET:HG2	1.95	0.47
1:D:353:LEU:HD13	1:D:423:LYS:HB2	1.97	0.47
1:D:634:PHE:C	1:D:636:PHE:N	2.73	0.47
1:A:147:GLN:N	1:A:274:TYR:O	2.37	0.46
1:D:197:LEU:HD11	1:D:202:LYS:HB3	1.97	0.46
1:A:144:ILE:HG22	1:A:272:ARG:HB2	1.97	0.46
1:A:200:LYS:HA	1:A:200:LYS:HD2	1.64	0.46
1:A:229:VAL:HA	1:A:232:HIS:HD2	1.79	0.46
1:B:431:ARG:HE	1:B:434:SER:HB3	1.80	0.46
1:C:544:VAL:HG21	1:C:563:VAL:HG22	1.96	0.46
1:A:542:ARG:HG3	1:A:547:GLY:HA2	1.97	0.46
1:B:299:ASN:OD1	1:B:299:ASN:N	2.49	0.46
3:I:49:ARG:NH2	4:J:62:ARG:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:THR:HB	1:A:304:LYS:HG3	1.97	0.46
1:B:452:ALA:HB3	1:B:459:GLN:HE21	1.80	0.46
1:D:313:ARG:O	1:D:313:ARG:NH1	2.49	0.46
1:D:402:THR:OG1	1:D:409:GLN:NE2	2.48	0.46
3:I:158:VAL:HG22	3:I:168:LEU:HD13	1.97	0.46
3:I:264:TYR:OH	3:I:299:ALA:O	2.19	0.46
1:B:748:ASP:OD1	1:B:748:ASP:N	2.49	0.46
1:C:129:ILE:HD13	2:G:14:UNK:HA	1.98	0.46
1:D:631:ILE:CG2	1:D:632:ASN:N	2.79	0.46
1:D:1111:ILE:HA	1:D:1114:PHE:HB2	1.97	0.46
1:B:226:ASN:HB2	1:B:288:ASN:HA	1.98	0.46
1:C:1217:ASP:OD1	1:C:1217:ASP:N	2.47	0.46
3:I:281:SER:HB3	4:J:44:HIS:HD2	1.80	0.46
1:D:468:ARG:NH2	1:D:470:ASP:OD2	2.49	0.46
1:A:356:THR:O	1:A:358:PRO:HD3	2.15	0.46
1:A:642:MET:HE2	1:A:671:ALA:HB2	1.96	0.46
1:C:194:ASN:OD1	1:C:231:ARG:NH1	2.49	0.46
3:I:10:GLU:O	3:I:14:LEU:N	2.39	0.46
3:I:110:ASN:HD22	3:I:127:LYS:HD3	1.81	0.46
1:A:1177:ARG:HG3	1:A:1181:LEU:HD23	1.97	0.46
1:D:494:ASP:HA	1:D:497:VAL:HG22	1.98	0.46
1:D:513:SER:OG	1:D:515:HIS:ND1	2.28	0.46
3:I:150:ARG:HB3	3:I:192:LEU:HD11	1.97	0.46
1:A:378:HIS:CE1	1:A:424:LYS:HB2	2.51	0.45
1:C:519:THR:HG23	1:C:522:ARG:HD2	1.98	0.45
3:I:65:THR:HG21	3:I:107:PRO:HA	1.99	0.45
1:B:328:ILE:HG13	1:B:458:ASP:HA	1.98	0.45
1:C:139:ASP:OD1	1:C:139:ASP:N	2.49	0.45
1:B:171:HIS:O	1:B:175:LYS:HB2	2.16	0.45
1:C:245:ARG:NE	1:D:1203:GLU:OE1	2.49	0.45
1:D:182:PRO:HD3	1:D:219:TRP:CE2	2.51	0.45
3:I:37:ILE:HG13	3:I:301:LYS:HZ2	1.82	0.45
3:I:210:LEU:HB2	3:I:222:PHE:HE2	1.82	0.45
1:A:159:ARG:NH2	1:A:298:ASP:OD2	2.44	0.45
1:A:310:LYS:O	1:A:314:GLN:HG2	2.17	0.45
1:B:350:LEU:O	1:B:354:ARG:N	2.40	0.45
1:D:238:LYS:HA	1:D:290:MET:HE2	1.99	0.45
1:D:567:LEU:HD22	1:D:677:ALA:HB1	1.98	0.45
3:I:328:ALA:HB2	3:I:338:ILE:HG23	1.98	0.45
1:B:556:SER:OG	1:B:559:ASP:OD1	2.23	0.45
1:D:497:VAL:HG12	1:D:526:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:156:GLN:HG3	3:I:168:LEU:HD11	1.97	0.45
1:C:208:GLY:HA2	1:C:441:ASP:HB2	1.99	0.45
1:C:1198:GLU:HA	1:C:1201:ILE:HG22	1.99	0.45
1:D:146:PHE:HD2	1:D:153:ASN:HB3	1.82	0.45
1:D:190:GLY:HA2	1:D:339:VAL:O	2.17	0.45
1:D:672:CYS:O	1:D:699:SER:OG	2.35	0.45
3:I:204:CYS:HA	3:I:228:ASP:HA	1.98	0.45
1:A:747:ARG:HG2	1:A:1131:PHE:CG	2.52	0.45
1:D:542:ARG:HG3	1:D:547:GLY:HA2	1.99	0.45
1:D:631:ILE:HD12	1:D:631:ILE:HA	1.70	0.45
1:B:1229:ASN:HA	1:B:1232:MET:HE3	1.99	0.44
1:C:185:LEU:HD22	1:C:319:ILE:HD12	2.00	0.44
3:I:16:ASN:OD1	3:I:19:ARG:NH2	2.50	0.44
3:I:152:LEU:HB2	3:I:156:GLN:HB3	1.99	0.44
1:A:1231:SER:HB2	1:B:1230:MET:HE2	1.99	0.44
1:C:747:ARG:HG2	1:C:1131:PHE:CG	2.52	0.44
1:C:750:ILE:O	1:C:755:SER:OG	2.35	0.44
1:D:159:ARG:HA	1:D:296:LEU:HB2	1.99	0.44
1:D:520:ILE:HG13	1:D:632:ASN:ND2	2.31	0.44
1:B:538:TYR:HD1	1:B:555:ILE:HD11	1.83	0.44
1:C:153:ASN:ND2	1:C:291:HIS:O	2.38	0.44
1:D:417:LEU:HA	1:D:420:CYS:HB3	1.97	0.44
1:D:520:ILE:N	1:D:632:ASN:OD1	2.40	0.44
1:A:729:LEU:HB3	1:A:732:TRP:CD1	2.52	0.44
1:B:439:ASP:OD1	1:B:439:ASP:N	2.50	0.44
1:B:1196:PHE:O	1:B:1199:GLN:HG2	2.17	0.44
1:C:256:TRP:NE1	1:C:262:GLN:OE1	2.50	0.44
1:C:335:VAL:HB	1:C:448:LEU:HD21	1.98	0.44
1:C:350:LEU:O	1:C:354:ARG:N	2.50	0.44
1:C:690:ASP:O	1:C:693:GLN:HG2	2.17	0.44
1:D:183:LYS:HG2	1:D:324:ILE:HD11	2.00	0.44
1:D:470:ASP:OD1	1:D:470:ASP:N	2.51	0.44
1:A:314:GLN:HA	1:A:317:LYS:HD2	2.00	0.44
1:D:641:LEU:HD23	1:D:641:LEU:HA	1.85	0.44
3:I:283:ARG:HG2	4:J:51:LEU:HD22	1.98	0.44
1:A:356:THR:HB	1:A:357:PRO:CD	2.41	0.44
1:B:356:THR:HB	1:B:357:PRO:HD3	2.00	0.44
1:B:1228:GLU:HB2	1:C:1226:ARG:NH1	2.33	0.44
1:D:631:ILE:O	1:D:633:HIS:CG	2.71	0.44
3:I:294[B]:CYS:SG	3:I:295:ASN:N	2.90	0.44
1:A:729:LEU:HB3	1:A:732:TRP:HD1	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1199:GLN:HE21	1:A:1199:GLN:HB3	1.57	0.44
1:A:1230:MET:HG3	1:D:1234:LEU:HD22	1.99	0.44
1:C:313:ARG:NH1	1:C:316:GLU:HB2	2.33	0.44
1:C:1185:ILE:HD12	1:C:1185:ILE:HA	1.85	0.44
3:I:274:THR:N	3:I:288:GLY:O	2.40	0.44
1:A:150:GLY:HA3	1:B:509:GLU:HG2	2.00	0.43
1:A:275:GLN:NE2	1:A:277:MET:H	2.16	0.43
1:C:230:ILE:HA	1:C:233:VAL:HG22	2.00	0.43
3:I:286:LEU:HD21	3:I:327:VAL:HG21	2.00	0.43
1:C:1001:MET:HE2	1:C:1001:MET:HB3	1.94	0.43
1:A:134:GLN:N	2:E:10:UNK:O	2.36	0.43
1:A:229:VAL:HA	1:A:232:HIS:CD2	2.54	0.43
1:A:422:LYS:HD2	1:A:423:LYS:HZ2	1.82	0.43
1:A:994:LYS:HA	1:A:1129:TRP:CZ2	2.53	0.43
3:I:37:ILE:H	3:I:37:ILE:HG12	1.43	0.43
1:A:759:LEU:HB3	1:A:1137:ILE:HD12	2.00	0.43
1:B:340:GLU:HA	1:B:367:SER:HB3	2.00	0.43
1:B:541:VAL:HG22	1:B:563:VAL:HG21	2.01	0.43
1:C:1228:GLU:HB2	1:D:1226:ARG:NH1	2.34	0.43
1:D:519:THR:HB	1:D:632:ASN:OD1	2.18	0.43
3:I:210:LEU:HB3	3:I:219:ARG:HB2	2.00	0.43
1:A:245:ARG:HE	1:B:1206:ARG:HG2	1.82	0.43
1:B:368:GLY:H	1:B:372:ASP:HB2	1.82	0.43
1:B:542:ARG:O	1:B:547:GLY:N	2.51	0.43
1:D:170:LEU:HD22	1:D:318:HIS:CE1	2.53	0.43
3:I:34:THR:HB	3:I:37:ILE:HD11	2.00	0.43
3:I:107:PRO:HG2	3:I:153:ASP:HA	1.99	0.43
1:B:501:VAL:HG21	1:B:652:LYS:HG2	2.01	0.43
1:C:746:HIS:HE1	1:C:748:ASP:HB2	1.83	0.43
3:I:79:LEU:N	3:I:93:ILE:O	2.36	0.43
1:A:415:ILE:HD13	1:A:415:ILE:H	1.83	0.43
1:C:183:LYS:HD3	1:C:465:ALA:HB1	2.01	0.43
1:D:221:PHE:HE1	1:D:251:ILE:HD12	1.83	0.43
1:A:1209:ASP:O	1:A:1213:ASN:ND2	2.38	0.43
1:B:187:SER:OG	1:B:189:HIS:NE2	2.45	0.43
1:B:1185:ILE:HD12	1:B:1185:ILE:HA	1.93	0.43
1:D:476:ILE:HG22	1:D:483:TRP:HH2	1.83	0.43
1:D:501:VAL:HG21	1:D:652:LYS:HG2	2.01	0.43
1:A:544:VAL:HG21	1:A:563:VAL:HG22	2.00	0.43
1:B:578:ARG:HA	1:B:578:ARG:HD3	1.77	0.43
3:I:323:ASP:HB2	3:I:325:MET:HG3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:LYS:HA	1:A:290:MET:HE2	2.01	0.43
1:B:328:ILE:HD11	1:B:457:PRO:HB2	2.01	0.43
1:B:516:ARG:HA	1:B:633:HIS:CE1	2.54	0.43
3:I:328:ALA:HA	3:I:338:ILE:HA	2.01	0.43
1:A:335:VAL:HG11	1:A:444:ILE:HG23	2.01	0.42
1:B:370:ALA:HA	1:B:373:ILE:HG23	2.01	0.42
1:D:256:TRP:HB3	1:D:298:ASP:HA	2.01	0.42
3:I:57:LYS:HB3	3:I:332:TRP:CD2	2.54	0.42
1:A:313:ARG:NH1	1:A:316:GLU:HB2	2.34	0.42
1:B:131:LYS:HD3	1:B:131:LYS:HA	1.83	0.42
1:B:172:LEU:HD12	1:B:176:GLU:HB2	2.01	0.42
1:D:628:ASP:HB2	1:D:631:ILE:HB	2.01	0.42
3:I:320:VAL:HG22	3:I:327:VAL:HG12	2.01	0.42
1:A:172:LEU:HG	1:A:176:GLU:HB2	2.00	0.42
1:C:437:HIS:NE2	1:C:446:THR:HG21	2.35	0.42
1:C:257:GLY:HA2	1:C:262:GLN:NE2	2.34	0.42
1:C:489:GLU:HB3	1:C:522:ARG:NH2	2.34	0.42
1:D:446:THR:HA	1:D:449:LEU:HB2	2.01	0.42
1:D:736:THR:OG1	1:D:739:GLN:NE2	2.52	0.42
3:I:58:ILE:HG12	3:I:74:SER:HB2	2.01	0.42
3:I:82:TRP:HA	3:I:89:LYS:HA	2.00	0.42
3:I:180:PHE:CD2	3:I:211:TRP:HB3	2.55	0.42
1:A:515:HIS:O	1:A:633:HIS:NE2	2.52	0.42
1:B:250:THR:H	1:B:292:SER:HB2	1.84	0.42
1:C:1187:ASP:OD1	1:C:1187:ASP:N	2.52	0.42
3:I:124:TYR:HA	3:I:135:VAL:HA	2.00	0.42
1:A:478:ILE:HG13	1:A:481:GLN:NE2	2.34	0.42
1:A:686:ASP:OD1	1:A:686:ASP:N	2.53	0.42
1:B:191:GLY:H	1:B:341:GLY:H	1.67	0.42
1:C:641:LEU:HB3	1:C:657:PHE:CD2	2.55	0.42
1:A:340:GLU:CD	1:A:369:ARG:HB2	2.45	0.42
1:A:697:HIS:CD2	1:A:700:ARG:HH12	2.37	0.42
1:B:398:THR:HA	1:B:414:PHE:CE2	2.54	0.42
1:B:224:GLY:H	1:B:230:ILE:HD13	1.84	0.42
1:C:313:ARG:NH1	1:C:317:LYS:HG3	2.35	0.42
1:C:636:PHE:HB3	1:C:639:HIS:ND1	2.34	0.42
1:D:404:THR:HG22	1:D:408:THR:HA	2.02	0.42
1:D:524:GLU:OE2	1:D:585:TYR:OH	2.33	0.42
1:A:736:THR:OG1	1:A:739:GLN:NE2	2.53	0.42
1:C:165:LYS:HA	1:C:166:PRO:HD3	1.92	0.42
1:B:349:VAL:HG23	1:B:361:VAL:HG21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:697:HIS:CD2	1:B:700:ARG:HH12	2.37	0.42
1:C:182:PRO:HG3	1:C:219:TRP:CD2	2.54	0.41
1:C:370:ALA:O	1:C:373:ILE:HG12	2.20	0.41
3:I:329:THR:N	3:I:337:LYS:O	2.40	0.41
1:B:133:THR:HG21	1:B:300:GLY:HA3	2.02	0.41
1:B:407:ARG:HB3	1:B:411:GLN:HB2	2.02	0.41
1:C:245:ARG:NH2	1:D:1203:GLU:OE2	2.52	0.41
1:D:524:GLU:O	1:D:528:ASN:ND2	2.40	0.41
1:A:365:ASP:CG	1:A:431:ARG:HA	2.44	0.41
1:B:425:GLU:H	1:B:425:GLU:CD	2.28	0.41
1:C:729:LEU:HD23	1:C:729:LEU:HA	1.96	0.41
1:C:762:MET:H	1:C:762:MET:HE3	1.86	0.41
1:D:313:ARG:NH1	1:D:317:LYS:HG3	2.36	0.41
1:A:267:GLY:H	1:A:272:ARG:NH1	2.19	0.41
1:B:736:THR:N	1:B:739:GLN:OE1	2.53	0.41
1:C:353:LEU:HD22	1:C:423:LYS:HB2	2.03	0.41
1:C:757:MET:HE3	1:C:757:MET:HB2	1.97	0.41
1:A:182:PRO:HD3	1:A:219:TRP:CE2	2.56	0.41
1:B:1234:LEU:HD21	1:C:1233:ARG:HB3	2.01	0.41
1:D:167:ASP:OD1	1:D:168:LEU:N	2.53	0.41
1:D:463:ALA:O	1:D:467:ASN:N	2.54	0.41
1:B:657:PHE:HD1	1:B:657:PHE:HA	1.76	0.41
3:I:78:LYS:HA	3:I:94:PRO:HA	2.03	0.41
1:B:583:THR:O	1:B:587:ASN:N	2.51	0.41
1:C:281:MET:N	1:C:281:MET:SD	2.94	0.41
1:C:310:LYS:O	1:C:314:GLN:HG2	2.21	0.41
1:C:998:PRO:O	1:C:1002:MET:HG3	2.21	0.41
1:D:404:THR:HA	1:D:408:THR:HA	2.03	0.41
1:D:634:PHE:H	1:D:634:PHE:HD1	1.66	0.41
1:A:553:TYR:CE2	1:A:555:ILE:HA	2.56	0.41
1:A:573:ARG:NH2	1:A:578:ARG:HD3	2.34	0.41
1:A:1233:ARG:HB3	1:D:1234:LEU:HD21	2.03	0.41
1:B:447:ALA:HA	1:B:450:LYS:HG2	2.03	0.41
1:B:1231:SER:HB2	1:C:1230:MET:HE2	2.03	0.41
1:C:313:ARG:HA	1:C:313:ARG:HD2	1.86	0.41
1:D:424:LYS:HA	1:D:427:ILE:HG13	2.02	0.41
1:D:1123:SER:O	1:D:1127:GLN:HG2	2.21	0.41
1:A:710:LEU:HD22	1:A:749:PHE:CZ	2.56	0.41
1:B:993:ASN:HB3	1:B:996:LEU:HB2	2.03	0.41
1:C:141:PHE:HB2	1:C:158:VAL:HG22	2.03	0.41
1:C:250:THR:H	1:C:292:SER:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:464:LEU:O	1:C:500:ARG:NH2	2.54	0.41
3:I:71:VAL:HG23	3:I:79:LEU:HG	2.03	0.41
1:A:324:ILE:HG23	1:A:326:THR:H	1.85	0.40
1:A:370:ALA:HA	1:A:373:ILE:HG23	2.02	0.40
1:A:470:ASP:OD1	1:A:470:ASP:N	2.52	0.40
1:C:165:LYS:HA	1:C:165:LYS:HD3	1.85	0.40
1:C:369:ARG:HG3	1:C:370:ALA:H	1.86	0.40
3:I:183:HIS:CD2	3:I:211:TRP:HE1	2.39	0.40
4:J:15:LEU:O	4:J:19:LEU:N	2.49	0.40
1:A:1129:TRP:CH2	1:A:1133:ARG:HD2	2.57	0.40
1:A:1217:ASP:OD1	1:A:1217:ASP:N	2.54	0.40
1:C:133:THR:HA	2:G:11:UNK:HA	2.03	0.40
1:C:224:GLY:H	1:C:230:ILE:HD13	1.85	0.40
1:C:523:LEU:HA	1:C:526:LEU:HD12	2.03	0.40
1:C:532:GLY:HA3	1:C:650:ARG:HH21	1.85	0.40
3:I:296:VAL:HB	3:I:305:ALA:HB3	2.02	0.40
1:B:556:SER:N	1:B:559:ASP:OD2	2.54	0.40
1:D:369:ARG:HA	1:D:369:ARG:HD3	1.86	0.40
1:A:542:ARG:HD3	1:A:549:LEU:HD21	2.04	0.40
1:A:681:GLU:O	1:A:684:GLU:HG2	2.20	0.40
1:C:747:ARG:HE	1:C:1128:VAL:HA	1.86	0.40
1:C:747:ARG:HH21	1:C:1128:VAL:HG13	1.87	0.40
1:D:631:ILE:HG13	1:D:632:ASN:H	1.87	0.40
1:D:750:ILE:O	1:D:755:SER:OG	2.40	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	A	683/1371 (50%)	646 (95%)	36 (5%)	1 (0%)	48 83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	683/1371 (50%)	653 (96%)	30 (4%)	0	100	100
1	C	683/1371 (50%)	650 (95%)	33 (5%)	0	100	100
1	D	707/1371 (52%)	670 (95%)	35 (5%)	2 (0%)	37	72
3	I	337/339 (99%)	308 (91%)	29 (9%)	0	100	100
4	J	55/70 (79%)	47 (86%)	8 (14%)	0	100	100
All	All	3148/5893 (53%)	2974 (94%)	171 (5%)	3 (0%)	50	83

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	631	ILE
1	D	635	PRO
1	A	357	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	610/1219 (50%)	566 (93%)	44 (7%)	12	32
1	B	610/1219 (50%)	549 (90%)	61 (10%)	6	21
1	C	610/1219 (50%)	562 (92%)	48 (8%)	10	29
1	D	631/1219 (52%)	580 (92%)	51 (8%)	9	29
3	I	282/282 (100%)	257 (91%)	25 (9%)	8	25
4	J	46/57 (81%)	42 (91%)	4 (9%)	8	26
All	All	2789/5215 (54%)	2556 (92%)	233 (8%)	11	28

All (233) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	138	THR
1	A	172	LEU
1	A	200	LYS

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Mol	Chain	Res	Type
1	A	256	TRP
1	A	275	GLN
1	A	276	THR
1	A	296	LEU
1	A	345	VAL
1	A	350	LEU
1	A	361	VAL
1	A	373	ILE
1	A	405	TYR
1	A	407	ARG
1	A	412	HIS
1	A	414	PHE
1	A	415	ILE
1	A	416	ILE
1	A	417	LEU
1	A	439	ASP
1	A	458	ASP
1	A	478	ILE
1	A	549	LEU
1	A	556	SER
1	A	559	ASP
1	A	584	LEU
1	A	633	HIS
1	A	657	PHE
1	A	662	GLU
1	A	686	ASP
1	A	688	VAL
1	A	711	ASP
1	A	719	GLN
1	A	722	MET
1	A	731	ASN
1	A	748	ASP
1	A	1114	PHE
1	A	1120	GLU
1	A	1138	MET
1	A	1186	THR
1	A	1194	HIS
1	A	1199	GLN
1	A	1204	TYR
1	A	1217	ASP
1	A	1241	GLU
1	B	130	SER

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Mol	Chain	Res	Type
1	B	163	ASP
1	B	175	LYS
1	B	192	LEU
1	B	227	THR
1	B	245	ARG
1	B	258	ILE
1	B	266	ILE
1	B	275	GLN
1	B	318	HIS
1	B	327	ARG
1	B	328	ILE
1	B	344	ASN
1	B	347	SER
1	B	350	LEU
1	B	369	ARG
1	B	373	ILE
1	B	412	HIS
1	B	413	LEU
1	B	414	PHE
1	B	415	ILE
1	B	423	LYS
1	B	439	ASP
1	B	445	LEU
1	B	450	LYS
1	B	458	ASP
1	B	462	LEU
1	B	481	GLN
1	B	490	GLN
1	B	502	ASP
1	B	506	LEU
1	B	516	ARG
1	B	518	LEU
1	B	519	THR
1	B	529	THR
1	B	549	LEU
1	B	559	ASP
1	B	584	LEU
1	B	586	HIS
1	B	632	ASN
1	B	633	HIS
1	B	648	MET
1	B	657	PHE

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Mol	Chain	Res	Type
1	B	687	MET
1	B	688	VAL
1	B	693	GLN
1	B	705	LEU
1	B	719	GLN
1	B	724	LEU
1	B	731	ASN
1	B	762	MET
1	B	999	TYR
1	B	1111	ILE
1	B	1135	GLN
1	B	1183	LEU
1	B	1186	THR
1	B	1190	LEU
1	B	1199	GLN
1	B	1216	ASN
1	B	1217	ASP
1	B	1239	GLU
1	C	138	THR
1	C	160	VAL
1	C	167	ASP
1	C	193	GLN
1	C	197	LEU
1	C	200	LYS
1	C	205	PHE
1	C	227	THR
1	C	271	VAL
1	C	279	ASN
1	C	287	LEU
1	C	291	HIS
1	C	294	PHE
1	C	319	ILE
1	C	350	LEU
1	C	373	ILE
1	C	407	ARG
1	C	412	HIS
1	C	413	LEU
1	C	414	PHE
1	C	431	ARG
1	C	440	ILE
1	C	458	ASP
1	C	478	ILE

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Mol	Chain	Res	Type
1	C	479	TYR
1	C	502	ASP
1	C	517	PHE
1	C	537	LEU
1	C	539	HIS
1	C	557	LEU
1	C	559	ASP
1	C	578	ARG
1	C	633	HIS
1	C	648	MET
1	C	681	GLU
1	C	690	ASP
1	C	726	THR
1	C	731	ASN
1	C	748	ASP
1	C	761	ASP
1	C	762	MET
1	C	1137	ILE
1	C	1140	PHE
1	C	1142	GLU
1	C	1186	THR
1	C	1199	GLN
1	C	1206	ARG
1	C	1232	MET
1	D	131	LYS
1	D	143	THR
1	D	170	LEU
1	D	171	HIS
1	D	172	LEU
1	D	192	LEU
1	D	205	PHE
1	D	214	MET
1	D	222	THR
1	D	229	VAL
1	D	235	ASP
1	D	261	ASN
1	D	276	THR
1	D	299	ASN
1	D	330	GLN
1	D	339	VAL
1	D	344	ASN
1	D	345	VAL

Continued on next page...

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Mol	Chain	Res	Type
1	D	350	LEU
1	D	397	VAL
1	D	411	GLN
1	D	412	HIS
1	D	415	ILE
1	D	416	ILE
1	D	417	LEU
1	D	448	LEU
1	D	502	ASP
1	D	515	HIS
1	D	549	LEU
1	D	556	SER
1	D	559	ASP
1	D	586	HIS
1	D	588	LEU
1	D	592	LYS
1	D	626	LEU
1	D	631	ILE
1	D	634	PHE
1	D	688	VAL
1	D	692	SER
1	D	699	SER
1	D	716	GLN
1	D	748	ASP
1	D	761	ASP
1	D	995	TYR
1	D	1120	GLU
1	D	1140	PHE
1	D	1193	VAL
1	D	1199	GLN
1	D	1202	GLU
1	D	1216	ASN
1	D	1217	ASP
3	I	18	ILE
3	I	32	GLN
3	I	37	ILE
3	I	70	LEU
3	I	71	VAL
3	I	78	LYS
3	I	83	ASP
3	I	90	VAL
3	I	91	HIS

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Mol	Chain	Res	Type
3	I	100	VAL
3	I	123	ILE
3	I	142	HIS
3	I	143	THR
3	I	157	ILE
3	I	178	THR
3	I	183	HIS
3	I	186	ASP
3	I	187	VAL
3	I	196	THR
3	I	221	THR
3	I	277	SER
3	I	290	ASP
3	I	321	THR
3	I	323	ASP
3	I	338	ILE
4	J	15	LEU
4	J	26	ASP
4	J	29	LYS
4	J	54	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (74) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	HIS
1	A	193	GLN
1	A	198	GLN
1	A	261	ASN
1	A	275	GLN
1	A	288	ASN
1	A	378	HIS
1	A	490	GLN
1	A	535	ASN
1	A	539	HIS
1	A	575	ASN
1	A	696	ASN
1	A	697	HIS
1	A	716	GLN
1	A	719	GLN
1	A	739	GLN
1	A	1116	ASN
1	A	1199	GLN

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Mol	Chain	Res	Type
1	B	132	HIS
1	B	134	GLN
1	B	178	GLN
1	B	198	GLN
1	B	232	HIS
1	B	293	HIS
1	B	314	GLN
1	B	378	HIS
1	B	453	ASN
1	B	459	GLN
1	B	587	ASN
1	B	680	HIS
1	B	697	HIS
1	B	719	GLN
1	B	731	ASN
1	B	1194	HIS
1	B	1199	GLN
1	B	1242	HIS
1	C	178	GLN
1	C	279	ASN
1	C	288	ASN
1	C	314	GLN
1	C	378	HIS
1	C	481	GLN
1	C	659	GLN
1	C	697	HIS
1	C	698	ASN
1	C	712	GLN
1	C	716	GLN
1	C	719	GLN
1	C	731	ASN
1	C	746	HIS
1	C	756	GLN
1	C	1115	ASN
1	C	1126	ASN
1	C	1135	GLN
1	D	153	ASN
1	D	171	HIS
1	D	178	GLN
1	D	262	GLN
1	D	314	GLN
1	D	318	HIS

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Mol	Chain	Res	Type
1	D	409	GLN
1	D	548	ASN
1	D	575	ASN
1	D	659	GLN
1	D	693	GLN
1	D	696	ASN
1	D	719	GLN
1	D	731	ASN
1	D	739	GLN
1	D	1108	ASN
1	D	1116	ASN
3	I	44	GLN
3	I	91	HIS
3	I	220	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](#)

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.

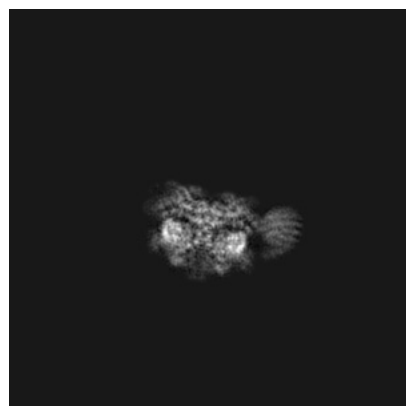
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27344. These allow visual inspection of the internal detail of the map and identification of artifacts.

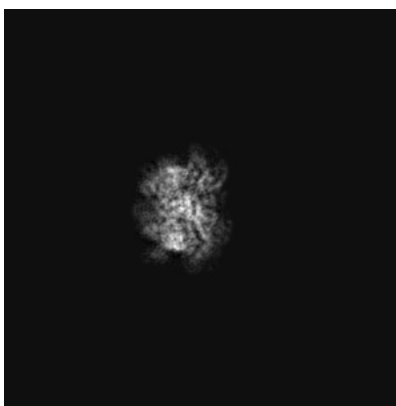
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

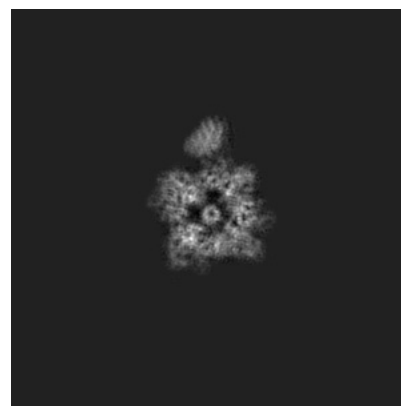
6.1.1 Primary map



X

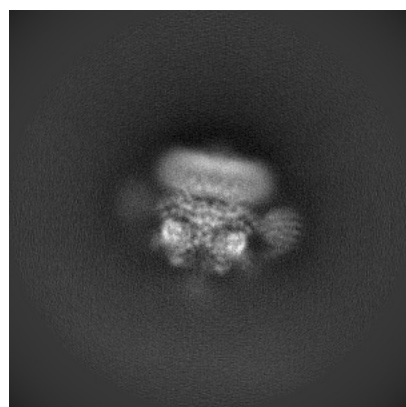


Y

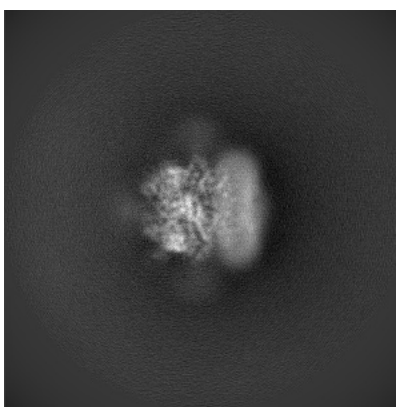


Z

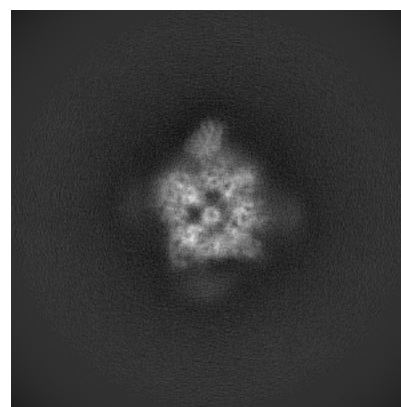
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

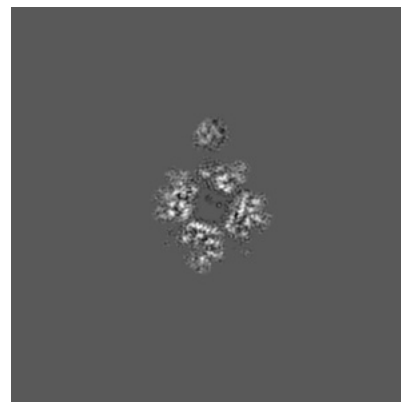
6.2.1 Primary map



X Index: 224

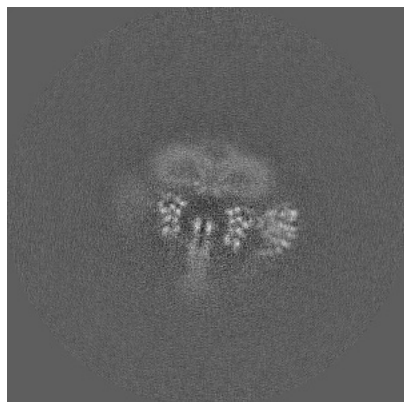


Y Index: 224

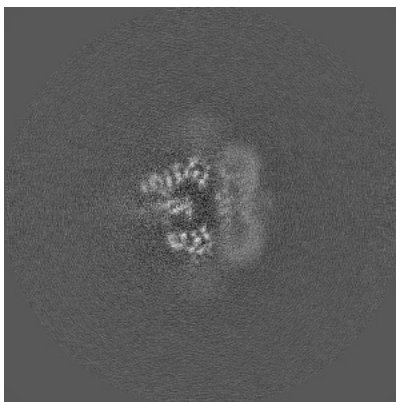


Z Index: 224

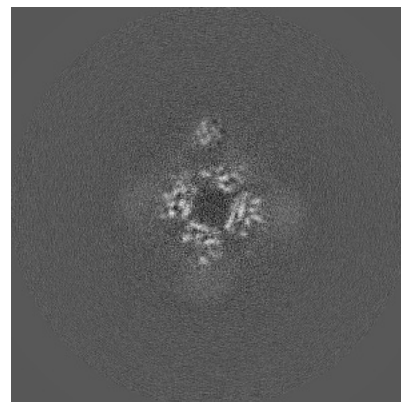
6.2.2 Raw map



X Index: 224



Y Index: 224

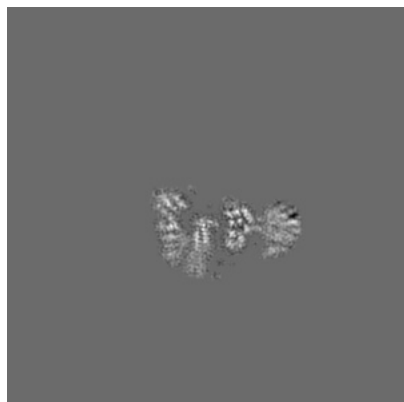


Z Index: 224

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

6.3 Largest variance slices [i](#)

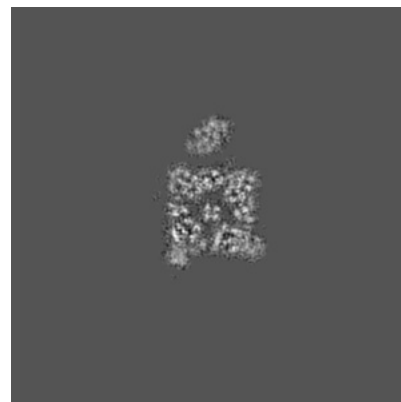
6.3.1 Primary map



X Index: 229

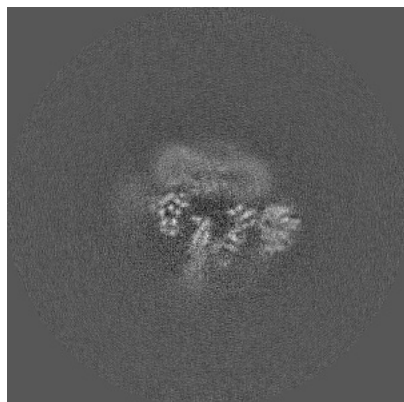


Y Index: 191

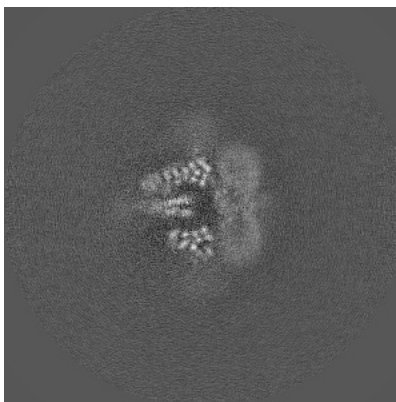


Z Index: 190

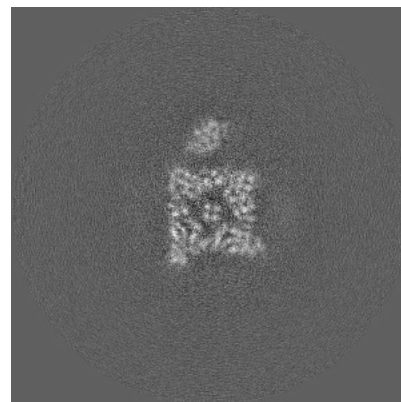
6.3.2 Raw map



X Index: 219



Y Index: 221

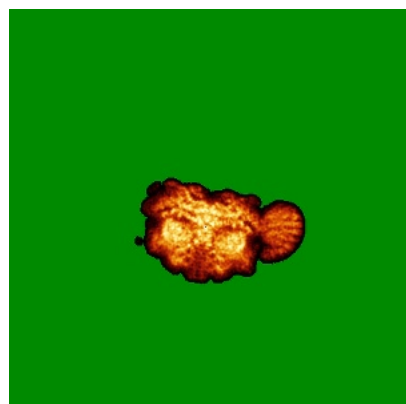


Z Index: 192

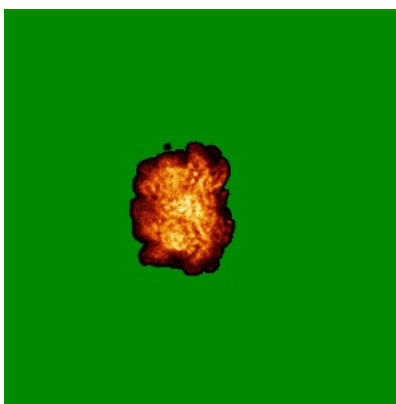
The images above show the largest variance slices of the map in three orthogonal directions.

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

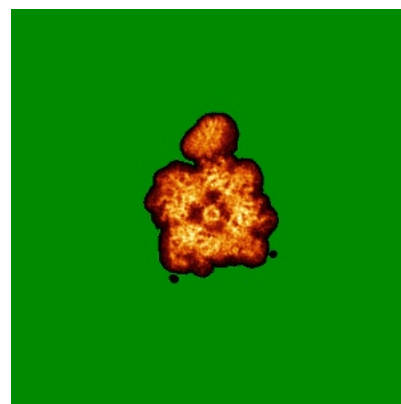
6.4.1 Primary map



X

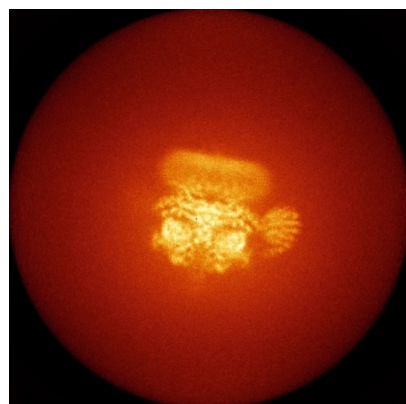


Y

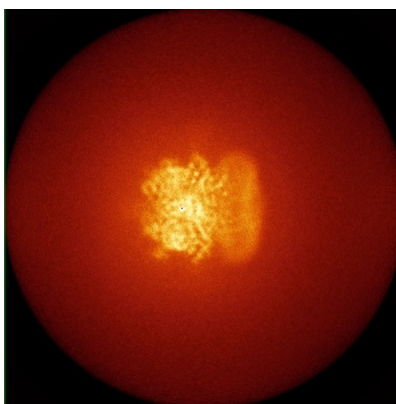


Z

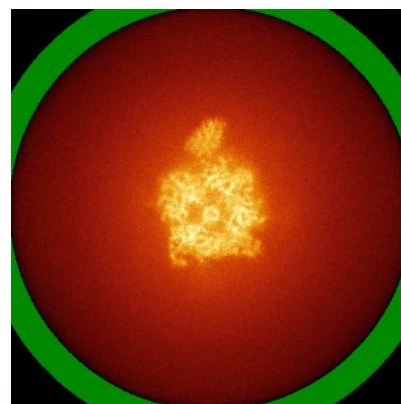
6.4.2 Raw map



X



Y

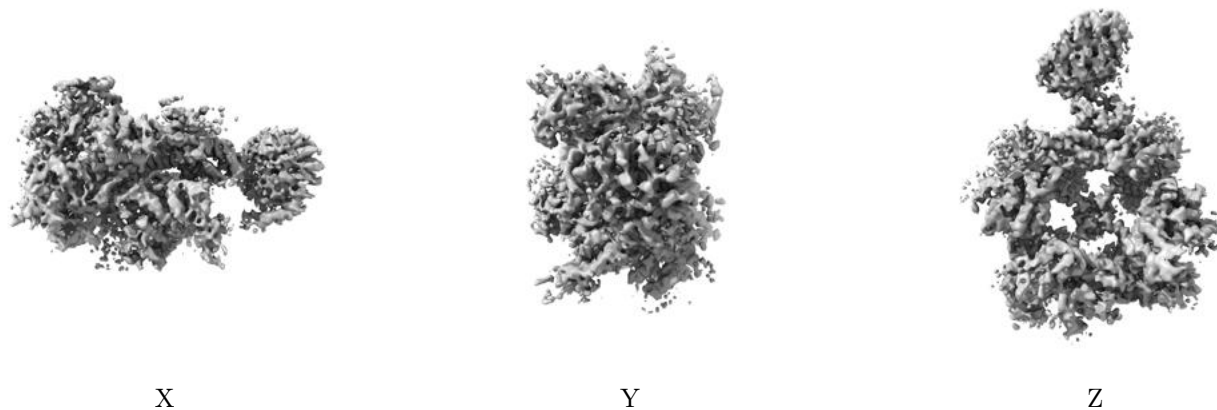


Z

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

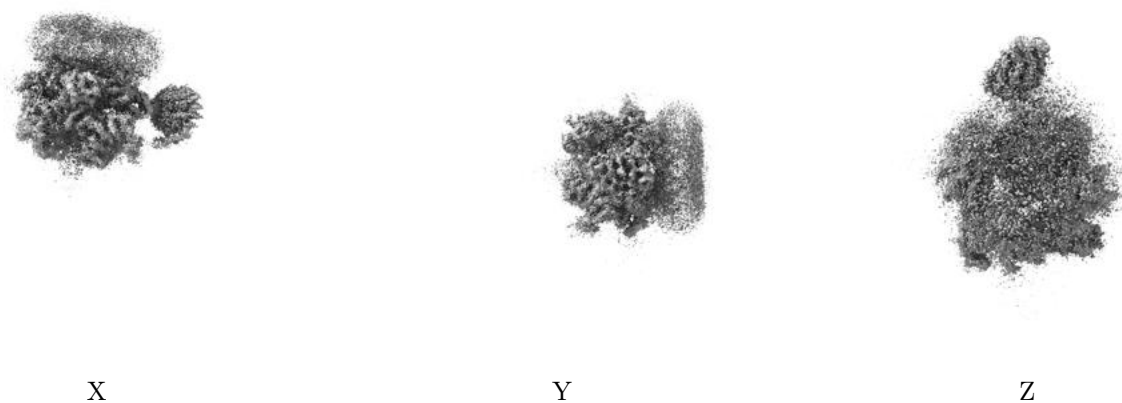
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

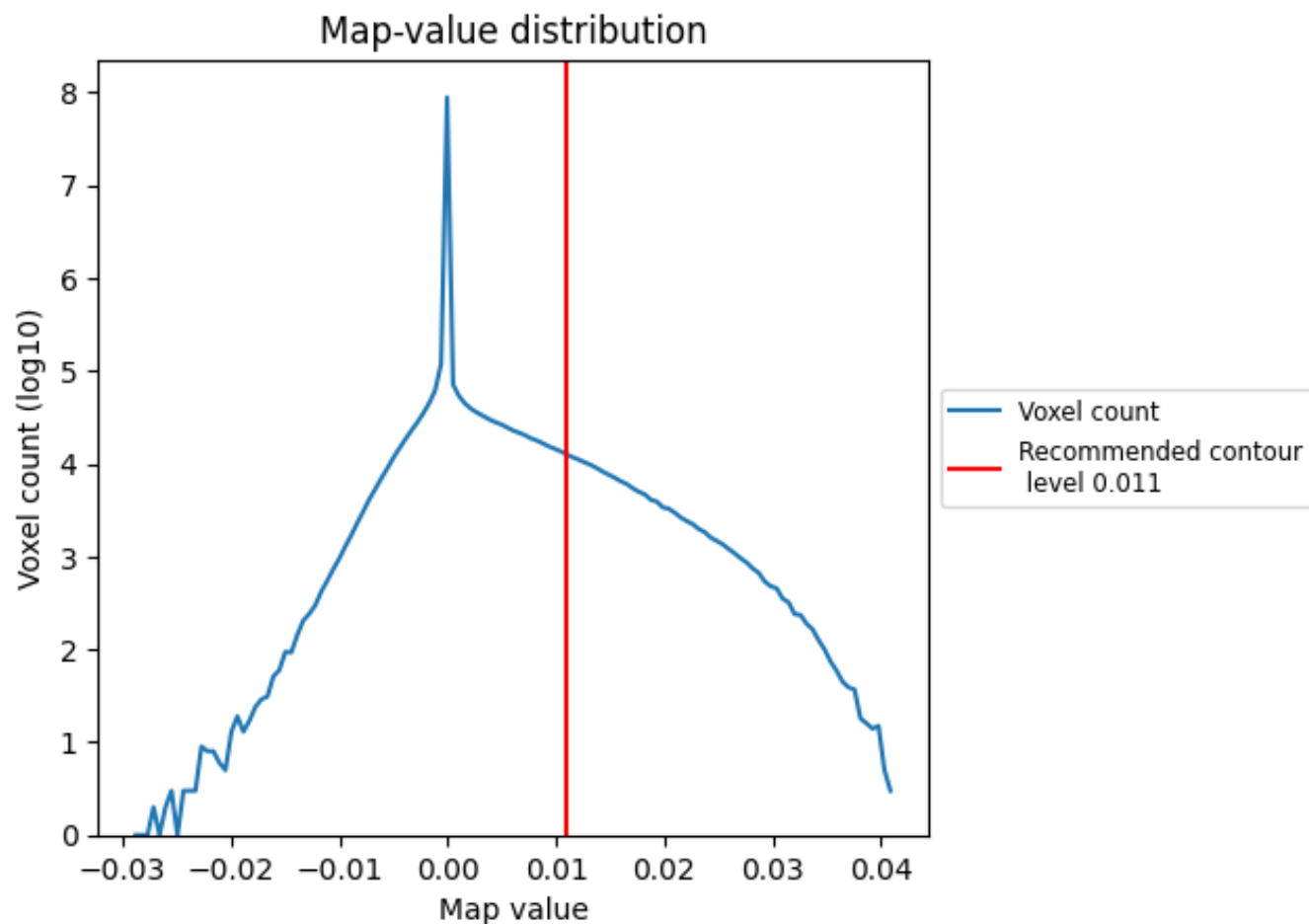
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

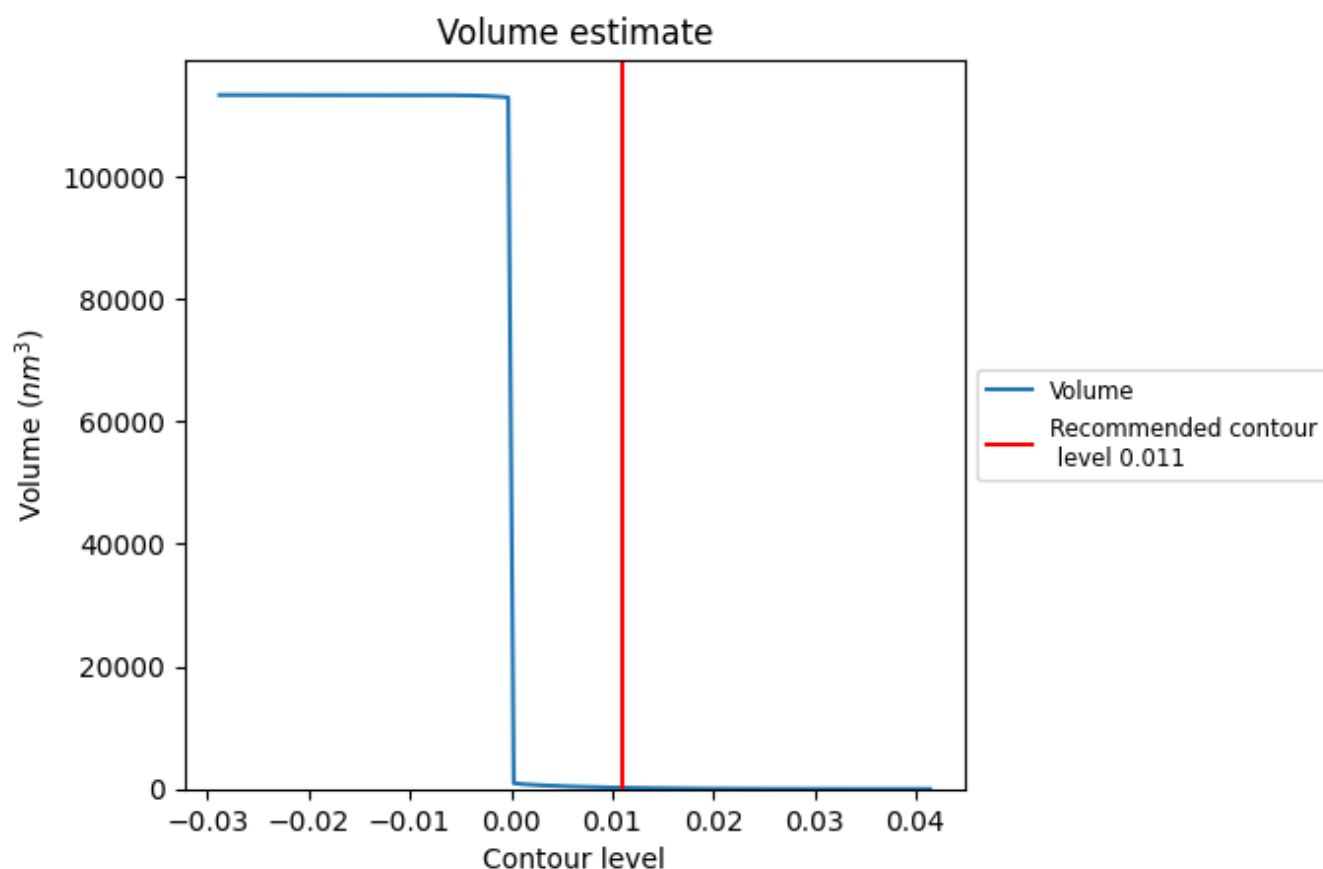
This section contains the results of statistical analysis of the map.

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.

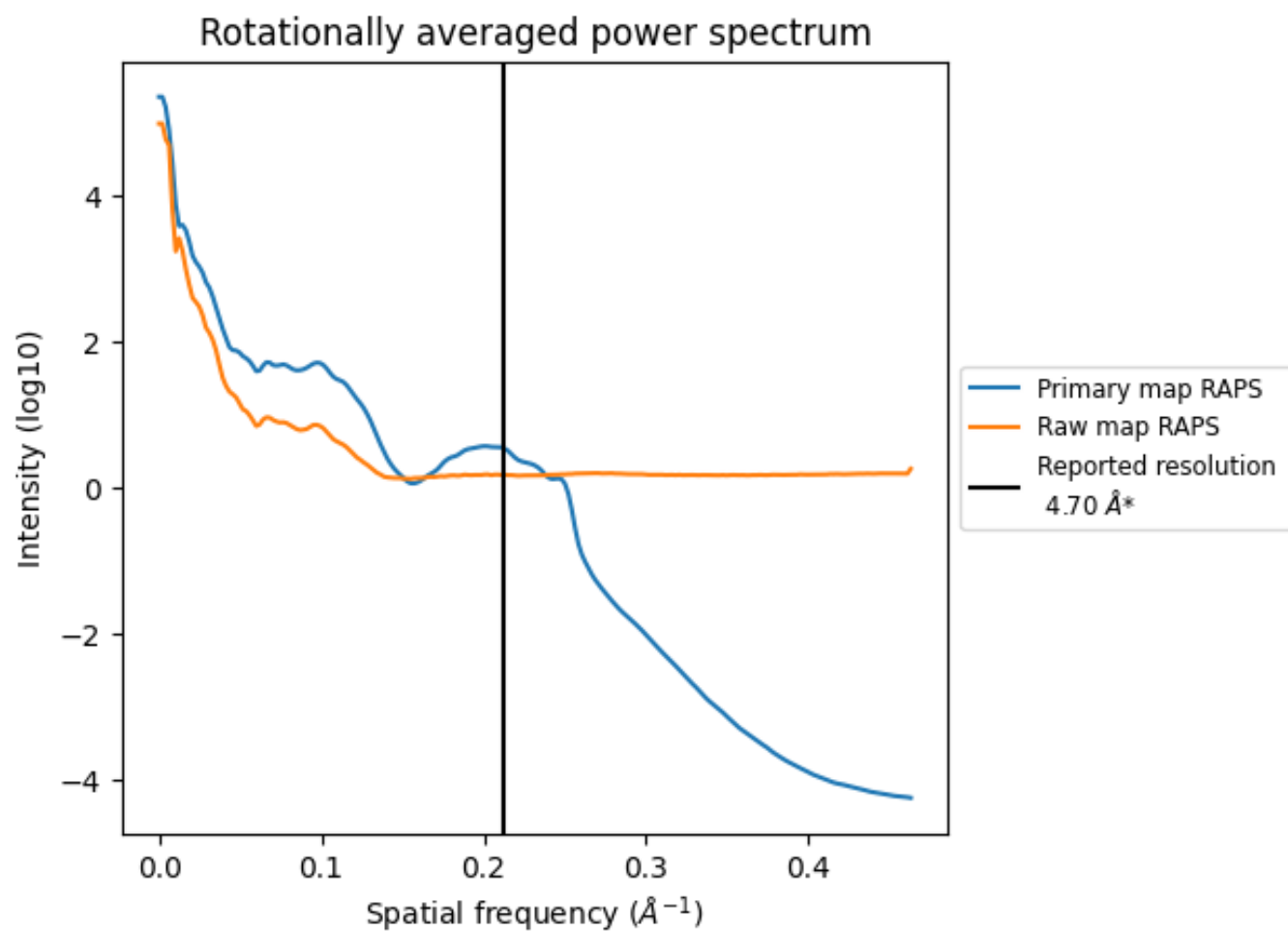
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 198 nm³; this corresponds to an approximate mass of 179 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 ⓘ

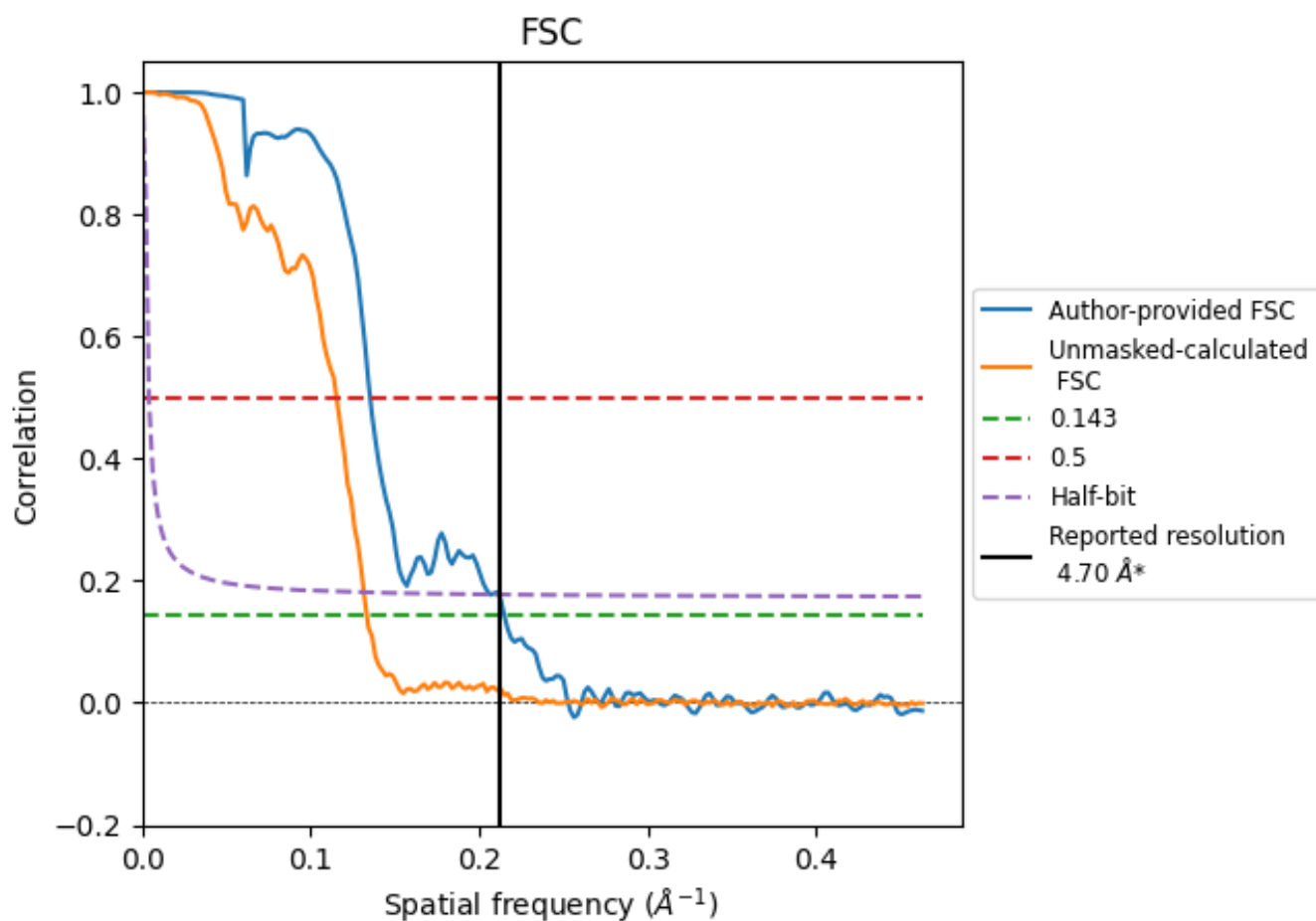


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 \AA^{-1}

8.2 Resolution estimates [i](#)

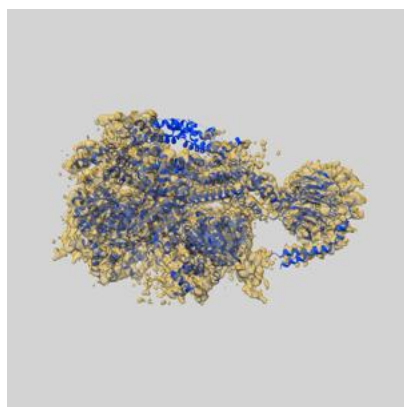
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.65	7.39	4.84
Unmasked-calculated*	7.50	8.67	7.60

*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 7.50 differs from the reported value 4.7 by more than 10 %

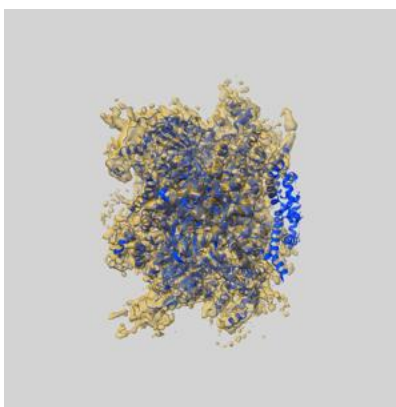
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27344 and PDB model 8DDW. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

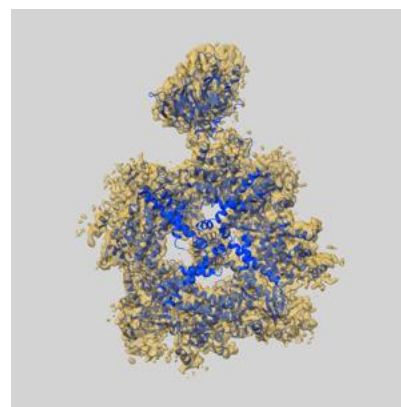
9.1 Map-model overlay [i](#)



X



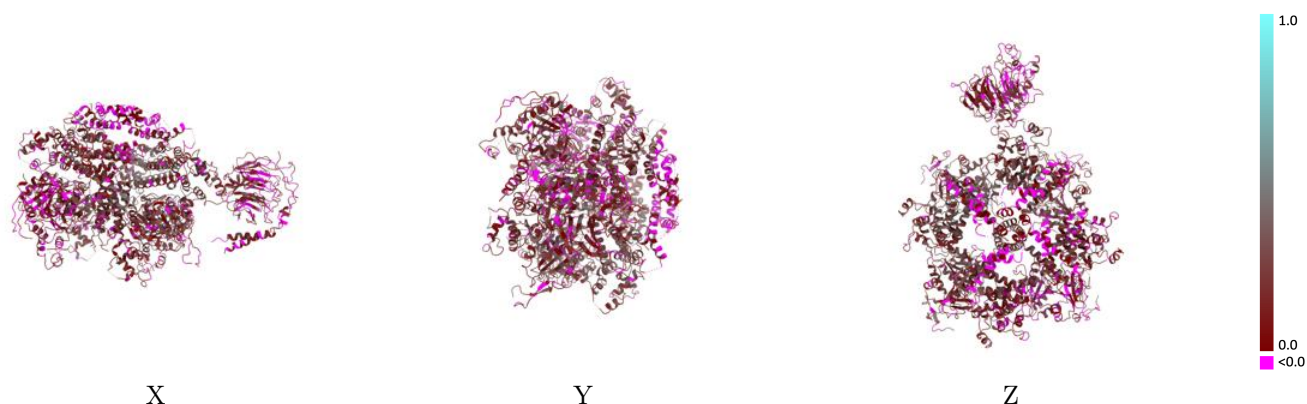
Y



Z

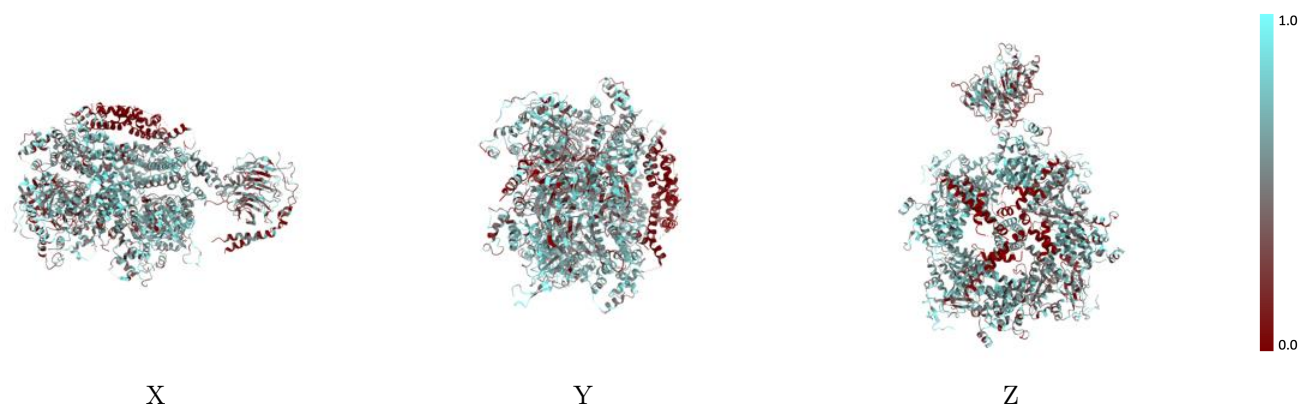
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



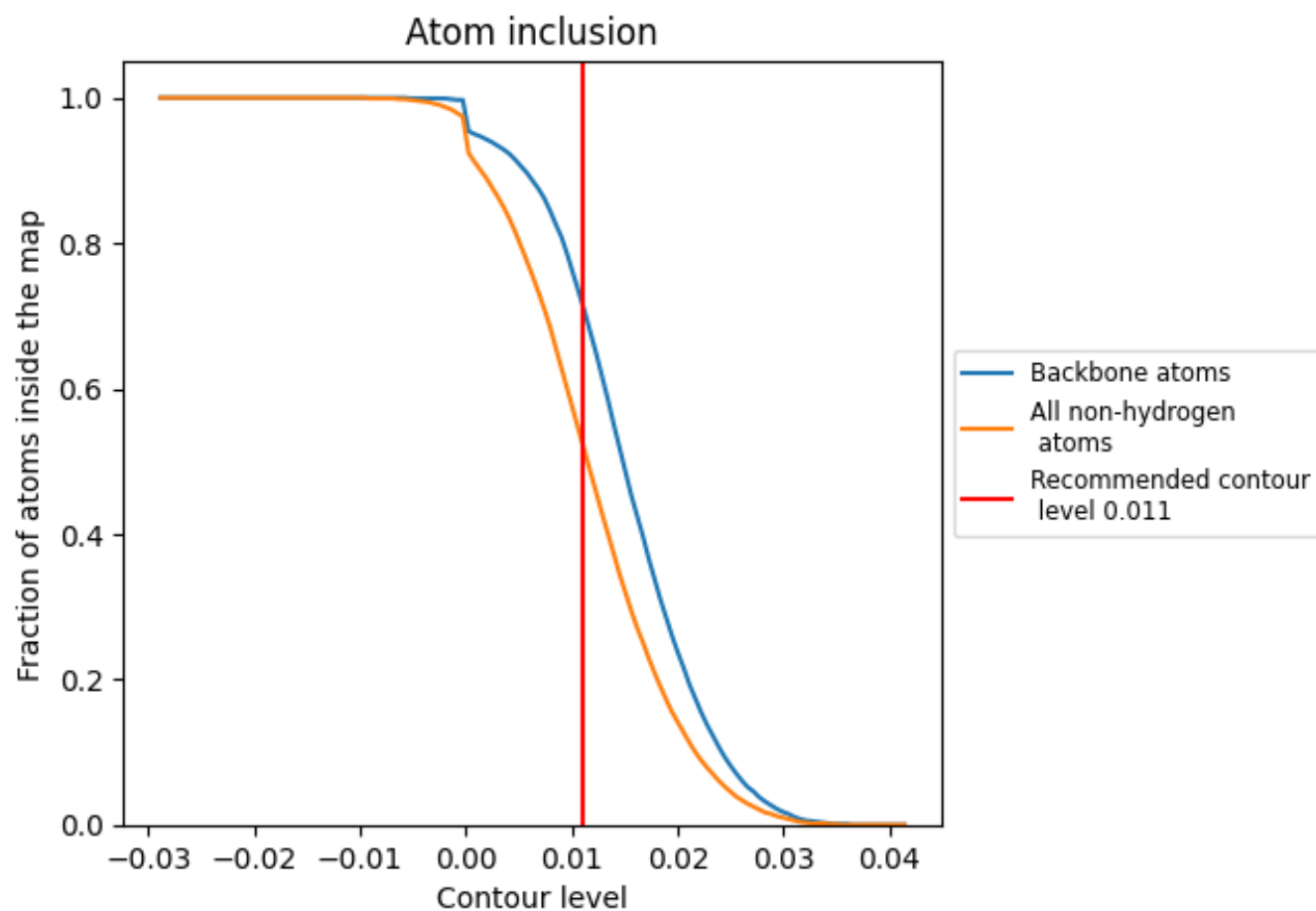
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 52% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5250	<div></div> 0.1690
A	<div></div> 0.5760	<div></div> 0.2050
B	<div></div> 0.4770	<div></div> 0.1300
C	<div></div> 0.5200	<div></div> 0.1530
D	<div></div> 0.5680	<div></div> 0.2240
E	<div></div> 0.7650	<div></div> 0.1670
F	<div></div> 0.7060	<div></div> 0.1190
G	<div></div> 0.7060	<div></div> 0.0980
H	<div></div> 0.8120	<div></div> 0.1370
I	<div></div> 0.4260	<div></div> 0.1060
J	<div></div> 0.4200	<div></div> 0.1040

1.0

0.0

<0.0