Full wwPDB EM Validation Report ⓘ

Aug 9, 2026 – 04:23 PM JST

PDB ID	:	23SG / pdb_000023sg
EMDB ID	:	EMD-69208
Title	:	The composite Cryo-EM structure of bacteriophage RAN69 pre-ejectosome-portal complex
Authors	:	Ruan, Z.; Hu, H.; Wang, A.; Shao, Q.; Li, X.; Xie, L.; Sun, Z.; Yu, J.; Fang, Q.
Deposited on	:	2026-02-15
Resolution	:	3.00 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ 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:

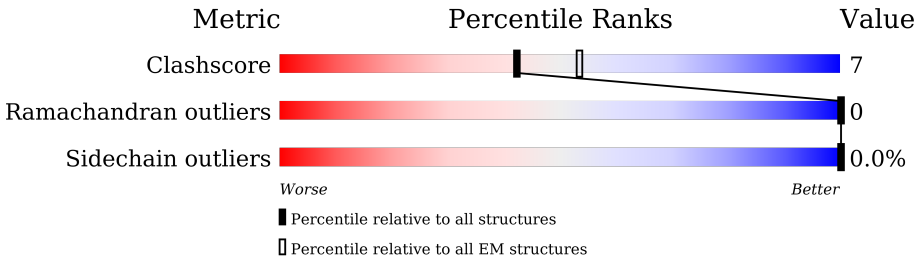
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

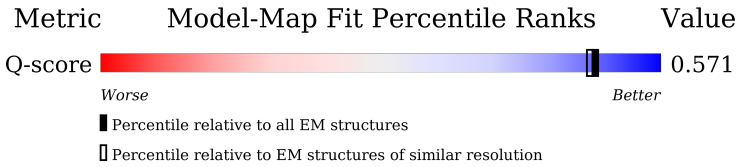
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 Å.

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





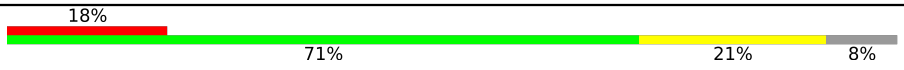
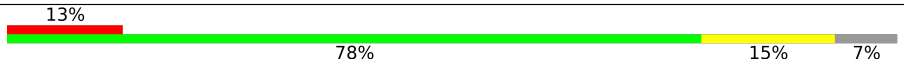
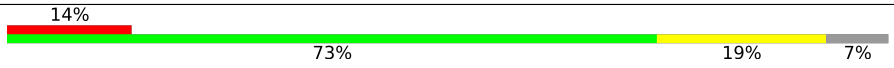
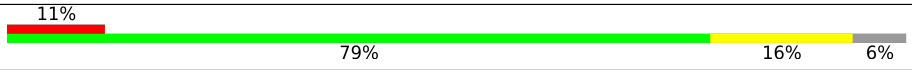
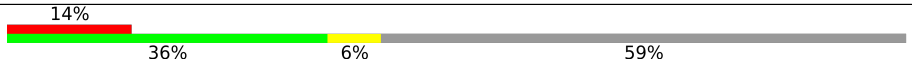
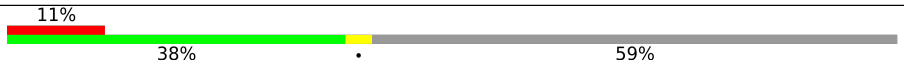
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	G	893	9% 77% 13% 10%
1	N	893	7% 78% 12% 10%
2	X	195	28% 67% 8% 25%
2	a	195	27% 61% 11% 28%

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Mol	Chain	Length	Quality of chain
3	S	1239	
4	A	531	
4	D	531	
4	d	531	
5	g	87	
5	m	87	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 35335 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 gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	806	Total	C	N	O	S	0	0
			6173	3795	1105	1248	25		
1	G	807	Total	C	N	O	S	0	0
			6179	3800	1108	1246	25		

- Molecule 2 is a protein called gp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	146	Total	C	N	O	S	0	0
			1109	688	198	218	5		
2	a	140	Total	C	N	O	S	0	0
			1079	669	191	213	6		

- Molecule 3 is a protein called gp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	1135	Total	C	N	O	S	0	0
			8748	5443	1580	1678	47		

- Molecule 4 is a protein called portal gp19.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	501	Total	C	N	O	S	0	0
			3883	2442	655	779	7		
4	A	492	Total	C	N	O	S	0	0
			3822	2407	643	765	7		
4	D	492	Total	C	N	O	S	0	0
			3822	2407	643	765	7		

- Molecule 5 is a protein called gp20.

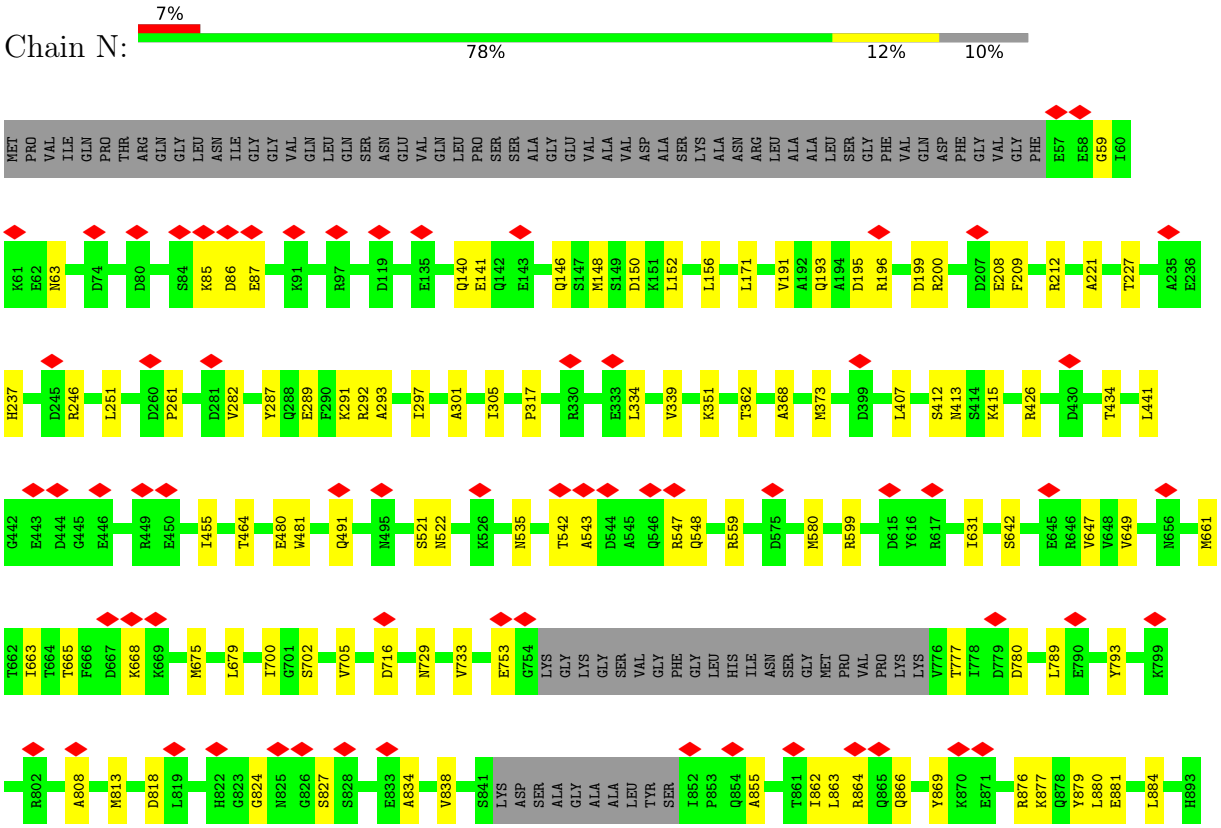
Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	36	Total	C	N	O	S	0	0
			260	160	50	49	1		
5	g	36	Total	C	N	O	S	0	0
			260	160	50	49	1		

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.

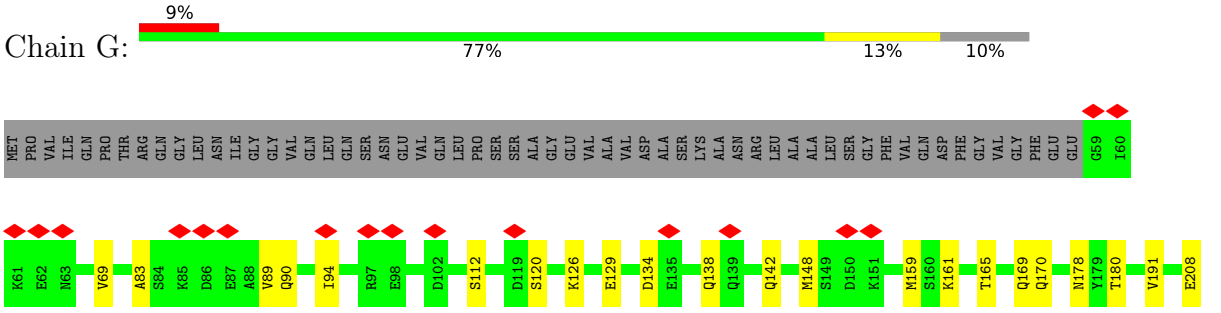
- Molecule 1: gp11

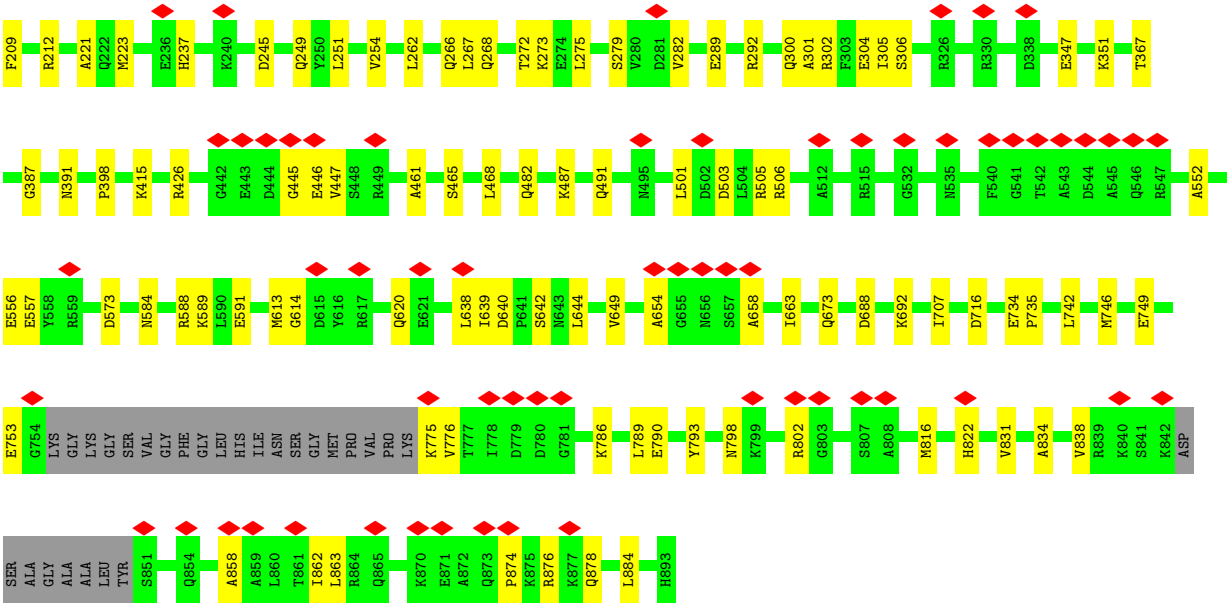
Chain N:



- Molecule 1: gp11

Chain G:

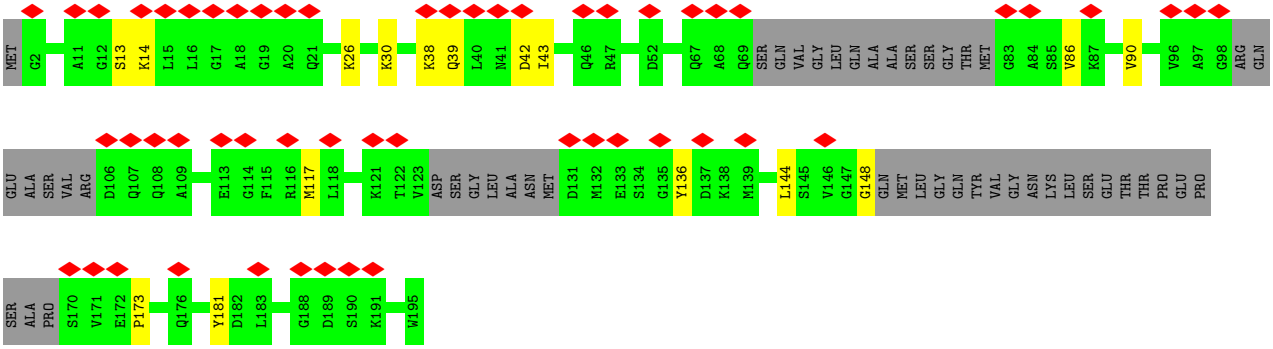




• Molecule 2: gp12

Chain X:

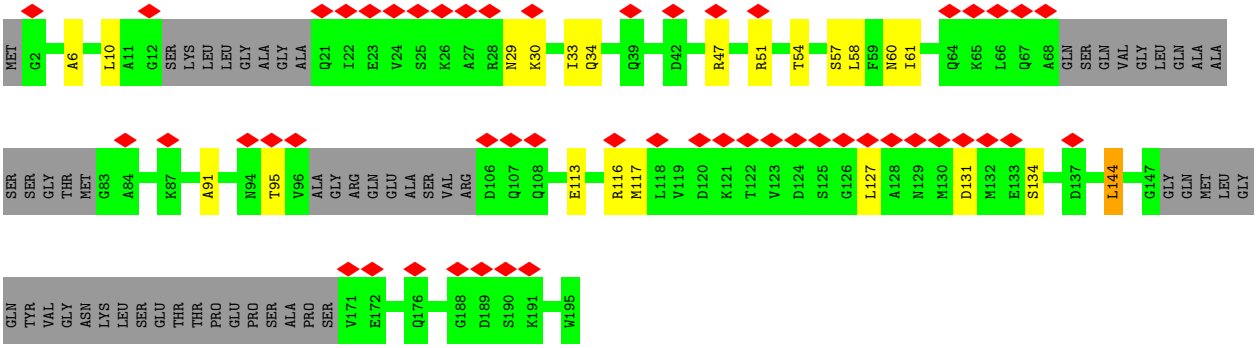




• Molecule 2: gp12

Chain a:





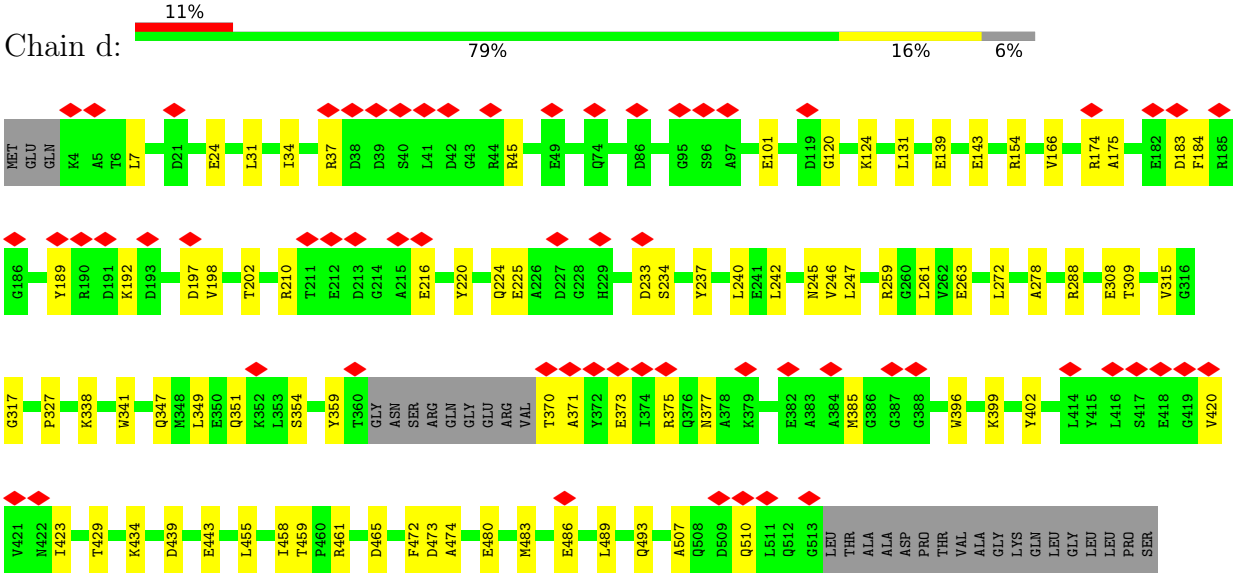
• Molecule 3: gp10

Chain S:



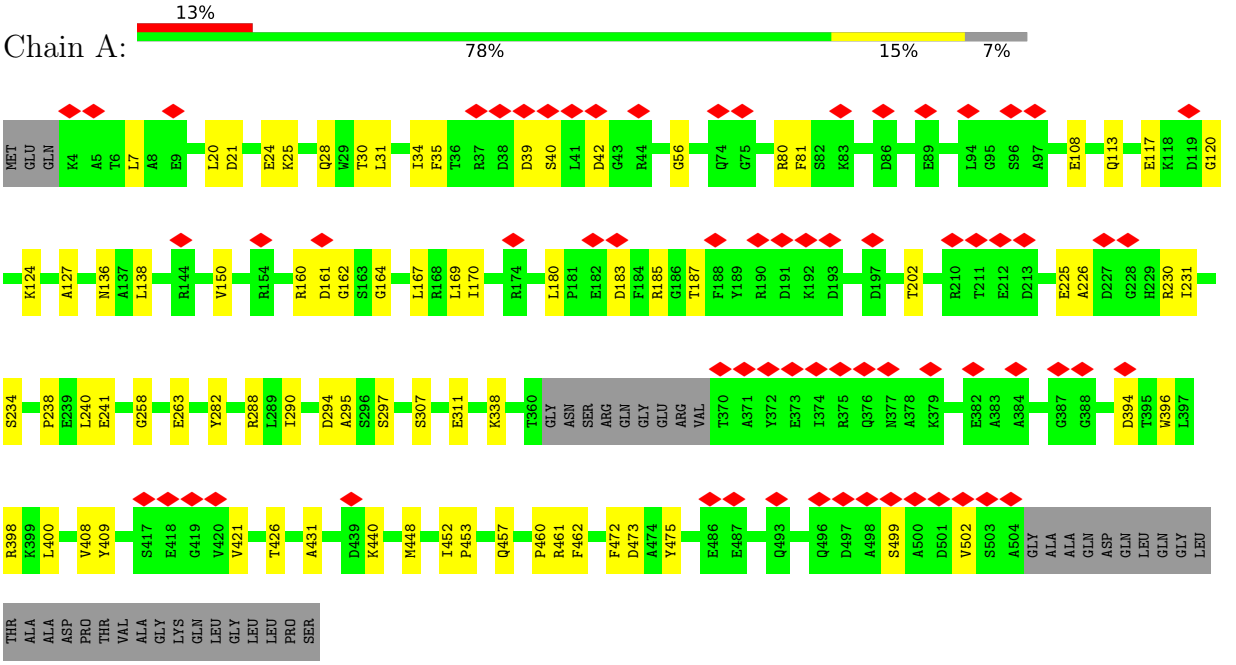
• Molecule 4: portal gp19

Chain d:



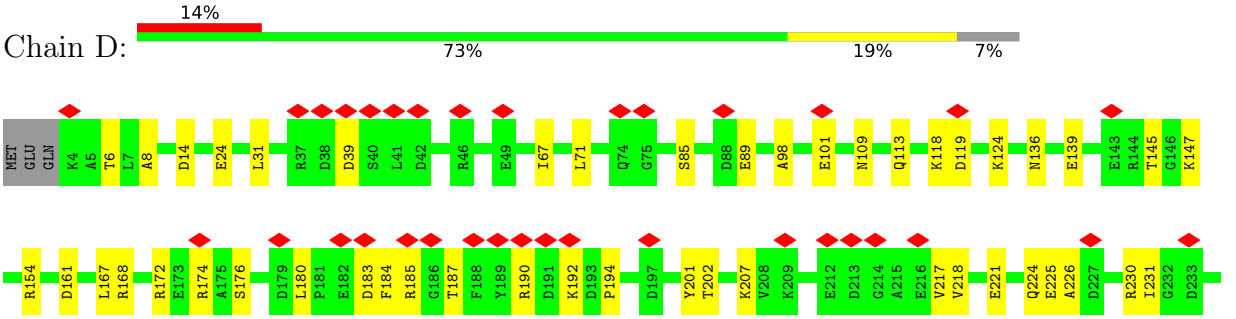
• Molecule 4: portal gp19

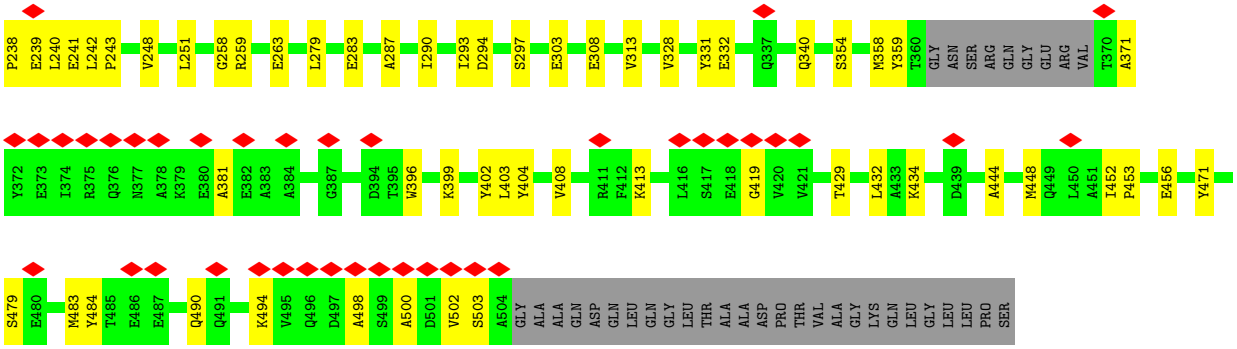
Chain A:



• Molecule 4: portal gp19

Chain D:

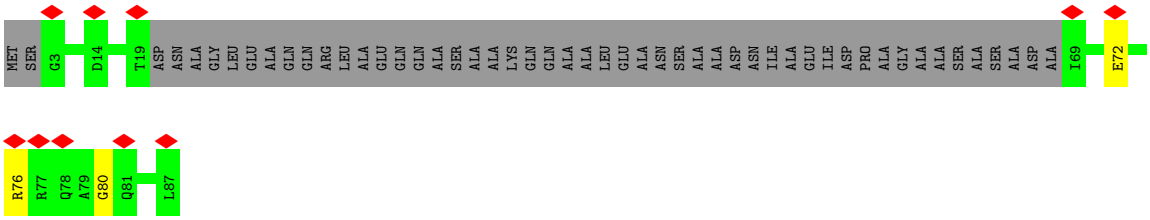




- Molecule 5: gp20

Chain m:

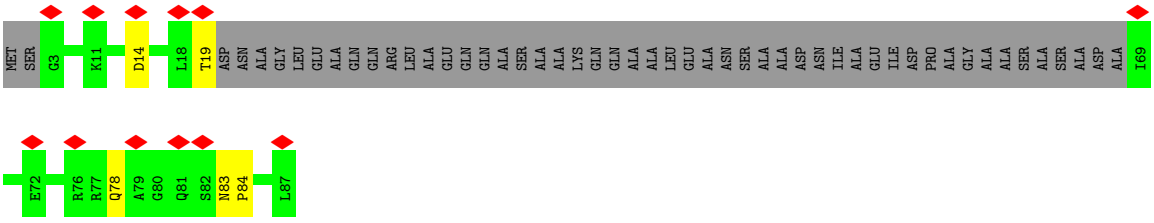




- Molecule 5: gp20

Chain g:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25878	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	13.135	Depositor
Minimum map value	-7.616	Depositor
Average map value	-0.061	Depositor
Map value standard deviation	0.983	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	342.72003, 342.72003, 342.72003	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	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	G	0.12	0/6264	0.26	0/8454
1	N	0.14	0/6258	0.27	0/8448
2	X	0.23	0/1120	0.39	0/1504
2	a	0.24	0/1090	0.42	0/1465
3	S	0.12	0/8896	0.27	0/12028
4	A	0.11	0/3888	0.27	0/5263
4	D	0.11	0/3888	0.26	0/5263
4	d	0.12	0/3949	0.28	0/5345
5	g	0.11	0/259	0.31	0/341
5	m	0.11	0/259	0.33	0/341
All	All	0.13	0/35871	0.28	0/48452

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	G	6179	0	6059	76	0
1	N	6173	0	6040	71	0
2	X	1109	0	1091	11	0
2	a	1079	0	1054	20	0
3	S	8748	0	8636	160	0
4	A	3822	0	3737	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	3822	0	3737	64	0
4	d	3883	0	3792	59	0
5	g	260	0	282	7	0
5	m	260	0	282	2	0
All	All	35335	0	34710	472	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 7.

All (472) 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)
3:S:403:GLN:NE2	3:S:426:MET:SD	2.51	0.82
3:S:35:ASP:OD2	3:S:659:ARG:NH1	2.20	0.75
3:S:747:TRP:HE3	3:S:847:LEU:HD23	1.52	0.74
3:S:855:ASN:HA	3:S:858:LYS:HE3	1.69	0.74
3:S:1129:LEU:HA	3:S:1132:ILE:HD12	1.69	0.73
1:N:59:GLY:O	1:N:63:ASN:ND2	2.22	0.73
2:a:30:LYS:O	2:a:34:GLN:NE2	2.22	0.73
3:S:1018:VAL:HG13	3:S:1076:MET:HE3	1.73	0.71
1:G:347:GLU:HG2	1:G:351:LYS:HE2	1.73	0.70
3:S:550:ARG:NH2	3:S:558:SER:OG	2.25	0.69
4:A:226:ALA:HB2	4:A:231:ILE:HD11	1.74	0.68
3:S:45:ALA:HB2	3:S:109:GLU:HB2	1.76	0.68
3:S:996:ALA:O	3:S:1000:VAL:HG13	1.94	0.68
1:N:818:ASP:OD2	1:N:876:ARG:NH1	2.27	0.67
1:N:412:SER:O	1:N:415:LYS:NZ	2.28	0.67
3:S:654:SER:O	3:S:659:ARG:NH2	2.28	0.67
1:G:816:MET:HE1	1:G:831:VAL:HG23	1.77	0.67
4:d:473:ASP:HB2	4:D:101:GLU:HB3	1.75	0.67
3:S:600:LEU:HB2	3:S:990:THR:HG21	1.77	0.66
4:d:338:LYS:NZ	4:D:332:GLU:OE1	2.29	0.66
1:N:777:THR:H	1:N:780:ASP:HB2	1.61	0.66
3:S:329:ARG:NH2	3:S:497:GLU:OE2	2.29	0.65
4:d:37:ARG:HD3	4:d:154:ARG:HH12	1.62	0.64
4:D:448:MET:HG2	4:D:471:TYR:CD2	2.33	0.63
1:N:261:PRO:HD3	1:N:297:ILE:HD11	1.81	0.63
1:N:808:ALA:HB1	1:N:813:MET:HE2	1.79	0.63
3:S:615:ASP:OD2	3:S:619:ARG:NH1	2.32	0.63
3:S:951:GLU:HG3	3:S:1150:MET:HE3	1.79	0.63
3:S:629:ASP:OD1	3:S:798:ARG:NH2	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S:877:PHE:HB2	3:S:883:PRO:HG3	1.80	0.63
4:D:259:ARG:NH1	4:D:263:GLU:OE2	2.31	0.62
2:a:30:LYS:HG2	2:a:34:GLN:HE22	1.63	0.62
3:S:533:ARG:NH1	3:S:1178:GLN:OE1	2.33	0.62
3:S:375:ALA:O	3:S:379:GLU:HG3	1.99	0.62
4:d:259:ARG:NH1	4:d:263:GLU:OE2	2.31	0.61
1:G:789:LEU:HD23	1:G:793:TYR:HD2	1.65	0.61
3:S:44:ARG:NH1	3:S:109:GLU:OE1	2.34	0.61
2:a:91:ALA:O	2:a:95:THR:HG23	2.01	0.61
1:N:547:ARG:NH2	1:G:613:MET:SD	2.74	0.60
4:d:24:GLU:OE2	4:d:154:ARG:NH2	2.34	0.60
3:S:39:VAL:HG13	3:S:76:ARG:HD3	1.83	0.60
4:d:210:ARG:NH1	4:d:216:GLU:OE1	2.34	0.60
3:S:44:ARG:HD3	3:S:64:ALA:HB2	1.83	0.60
1:G:191:VAL:HG13	1:G:237:HIS:HB2	1.84	0.60
1:G:138:GLN:O	1:G:142:GLN:HG2	2.01	0.60
3:S:760:LEU:HD12	3:S:773:ILE:HG23	1.83	0.59
3:S:727:VAL:HG21	3:S:776:PHE:HE2	1.67	0.59
4:D:14:ASP:OD2	4:D:168:ARG:NH2	2.34	0.59
3:S:276:ASN:HD22	3:S:321:ALA:HB3	1.68	0.59
4:d:459:THR:HG22	4:d:461:ARG:H	1.68	0.59
3:S:1159:ARG:NE	3:S:1163:GLU:OE1	2.36	0.58
4:A:230:ARG:HH22	4:A:234:SER:HB3	1.66	0.58
1:N:548:GLN:NE2	1:G:614:GLY:O	2.35	0.58
3:S:39:VAL:HG11	3:S:73:ALA:HA	1.85	0.58
3:S:601:SER:HA	3:S:605:HIS:HB2	1.85	0.58
4:d:261:LEU:HD22	4:d:385:MET:HE1	1.85	0.58
1:G:245:ASP:O	1:G:249:GLN:HG3	2.03	0.58
4:D:303:GLU:HB2	4:D:313:VAL:HG23	1.85	0.58
4:d:7:LEU:HD12	4:d:225:GLU:HB2	1.85	0.58
1:N:227:THR:HB	1:G:170:GLN:HG2	1.86	0.58
1:G:649:VAL:HG22	1:G:663:ILE:HG22	1.85	0.58
4:D:176:SER:OG	4:D:194:PRO:O	2.20	0.58
1:G:557:GLU:OE1	1:G:588:ARG:NH2	2.35	0.58
1:N:522:ASN:OD1	1:N:559:ARG:NH2	2.36	0.58
4:d:480:GLU:HG3	4:D:98:ALA:HB2	1.86	0.58
4:D:293:ILE:HG12	4:D:328:VAL:HG22	1.85	0.58
2:a:29:ASN:O	2:a:33:ILE:HG12	2.04	0.57
2:X:144:LEU:HD12	1:G:169:GLN:OE1	2.03	0.57
3:S:962:GLN:NE2	3:S:1012:ASN:O	2.29	0.57
1:G:654:ALA:HB3	1:G:658:ALA:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:661:MET:HG2	1:N:679:LEU:HD21	1.86	0.57
3:S:733:ASP:O	3:S:737:ASN:ND2	2.36	0.57
1:G:468:LEU:HD13	1:G:620:GLN:HB3	1.86	0.57
4:D:444:ALA:O	4:D:448:MET:HG3	2.05	0.57
2:X:136:TYR:CD1	1:G:180:THR:HG23	2.39	0.57
3:S:110:GLU:OE1	3:S:134:ARG:NH2	2.37	0.57
4:d:45:ARG:NH2	4:A:263:GLU:OE1	2.38	0.57
1:N:863:LEU:HD22	1:N:884:LEU:HD22	1.85	0.57
4:d:439:ASP:O	4:d:443:GLU:HG3	2.04	0.57
4:A:80:ARG:NH1	4:A:108:GLU:OE1	2.38	0.57
4:D:139:GLU:OE1	4:D:396:TRP:NE1	2.34	0.57
3:S:285:HIS:O	3:S:289:GLN:HG3	2.04	0.56
3:S:948:ASP:OD1	3:S:949:MET:N	2.38	0.56
4:A:453:PRO:O	4:A:457:GLN:HG2	2.06	0.56
4:D:24:GLU:OE2	4:D:154:ARG:NH2	2.38	0.56
1:G:306:SER:HB2	5:g:84:PRO:HG2	1.86	0.56
1:N:191:VAL:HG23	1:N:237:HIS:HB2	1.88	0.56
2:X:86:VAL:O	2:X:90:VAL:HG23	2.06	0.56
1:G:863:LEU:HD22	1:G:884:LEU:HD22	1.87	0.56
1:N:193:GLN:OE1	1:N:196:ARG:NH2	2.39	0.56
3:S:949:MET:HG2	3:S:952:ARG:HH21	1.70	0.56
1:G:351:LYS:HZ2	5:g:84:PRO:HB3	1.71	0.56
4:d:242:LEU:O	4:d:399:LYS:NZ	2.36	0.56
4:D:354:SER:HB3	4:D:359:TYR:HB3	1.88	0.55
1:G:822:HIS:O	1:G:822:HIS:ND1	2.39	0.55
2:a:144:LEU:HD11	1:G:223:MET:HE2	1.87	0.55
4:d:166:VAL:HG21	4:d:246:VAL:HG21	1.88	0.55
3:S:759:LEU:O	3:S:763:MET:HG3	2.07	0.55
1:G:398:PRO:O	1:G:426:ARG:NH2	2.40	0.55
4:A:40:SER:OG	4:A:42:ASP:O	2.22	0.55
4:A:120:GLY:O	4:A:124:LYS:HG2	2.06	0.55
3:S:272:VAL:HG12	3:S:354:GLU:HA	1.89	0.55
4:d:288:ARG:HG2	4:D:308:GLU:HG3	1.89	0.55
3:S:757:ASP:HB2	3:S:760:LEU:HD23	1.89	0.54
4:D:207:LYS:NZ	4:D:221:GLU:OE1	2.33	0.54
1:G:552:ALA:O	1:G:556:GLU:HG2	2.07	0.54
1:N:195:ASP:OD1	1:N:246:ARG:NH2	2.30	0.54
2:a:61:ILE:HG21	4:d:486:GLU:HB2	1.90	0.54
3:S:1126:TRP:HB2	3:S:1228:PRO:HG3	1.89	0.54
1:G:289:GLU:OE1	1:G:292:ARG:NH2	2.37	0.54
4:A:80:ARG:HG2	4:A:431:ALA:HB1	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:307:SER:HB2	4:A:311:GLU:HB2	1.89	0.54
1:N:642:SER:O	1:N:668:LYS:NZ	2.40	0.54
4:A:180:LEU:O	4:A:185:ARG:NH1	2.41	0.54
4:d:474:ALA:HA	4:D:434:LYS:HB3	1.88	0.54
1:N:864:ARG:NE	1:N:881:GLU:OE1	2.38	0.54
4:D:294:ASP:HB3	4:D:297:SER:HB3	1.89	0.54
3:S:1136:GLN:NE2	3:S:1176:LEU:O	2.41	0.54
1:G:688:ASP:OD2	1:G:692:LYS:NZ	2.41	0.53
4:d:434:LYS:NZ	4:A:473:ASP:OD2	2.34	0.53
1:N:491:GLN:OE1	1:N:535:ASN:ND2	2.38	0.53
1:G:367:THR:HG21	1:G:707:ILE:HG21	1.90	0.53
4:d:373:GLU:OE2	4:d:377:ASN:ND2	2.42	0.53
4:D:180:LEU:O	4:D:185:ARG:NH1	2.42	0.53
3:S:734:GLY:HA3	3:S:766:ALA:HB1	1.90	0.53
3:S:709:ARG:HG2	3:S:724:VAL:HG12	1.90	0.53
2:X:42:ASP:OD1	2:X:43:ILE:N	2.42	0.53
3:S:305:LEU:HA	3:S:308:ILE:HG12	1.91	0.52
3:S:140:MET:HE2	3:S:1218:LYS:HD3	1.90	0.52
1:G:209:PHE:CD1	1:G:221:ALA:HB1	2.45	0.52
1:G:120:SER:OG	1:G:178:ASN:ND2	2.43	0.52
1:G:798:ASN:O	1:G:802:ARG:HG3	2.10	0.52
1:N:317:PRO:HD3	1:N:362:THR:HG22	1.90	0.52
1:G:351:LYS:NZ	5:g:84:PRO:HB3	2.24	0.52
3:S:406:LEU:HD21	3:S:452:VAL:HG11	1.92	0.52
4:D:358:MET:SD	4:D:381:ALA:HA	2.50	0.52
4:D:39:ASP:OD2	4:D:174:ARG:NH1	2.42	0.52
4:D:183:ASP:O	4:D:187:THR:HG22	2.09	0.52
1:N:464:THR:HB	5:g:83:ASN:ND2	2.25	0.52
1:N:480:GLU:HG2	1:N:481:TRP:CD1	2.45	0.51
4:d:370:THR:OG1	4:d:371:ALA:N	2.42	0.51
1:G:482:GLN:OE1	1:G:584:ASN:ND2	2.42	0.51
5:g:14:ASP:OD1	5:g:19:THR:OG1	2.24	0.51
3:S:398:ARG:NH2	3:S:459:ALA:O	2.43	0.51
1:N:86:ASP:OD1	1:N:87:GLU:N	2.44	0.51
4:D:202:THR:HB	4:D:224:GLN:HG2	1.92	0.51
4:D:279:LEU:O	4:D:283:GLU:HG3	2.10	0.51
3:S:431:ALA:O	3:S:487:SER:OG	2.29	0.51
1:N:209:PHE:CD1	1:N:221:ALA:HB1	2.46	0.51
2:a:60:ASN:ND2	4:D:484:TYR:OH	2.44	0.51
3:S:1205:ASP:O	3:S:1208:THR:OG1	2.28	0.51
4:d:174:ARG:HB2	4:A:162:GLY:HA3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S:577:MET:HE2	3:S:660:TRP:CD1	2.46	0.51
4:A:20:LEU:HD13	4:A:35:PHE:HZ	1.75	0.51
1:N:729:ASN:HD21	1:N:733:VAL:HB	1.75	0.50
3:S:252:GLY:HA3	3:S:256:ARG:HH11	1.76	0.50
4:d:272:LEU:HD13	4:d:349:LEU:HD22	1.93	0.50
3:S:265:VAL:HA	3:S:360:THR:HG22	1.94	0.50
3:S:664:MET:HE1	3:S:829:TYR:OH	2.11	0.50
3:S:57:SER:HB2	3:S:60:ASP:HB2	1.93	0.50
4:d:101:GLU:HB3	4:A:473:ASP:HB2	1.93	0.50
4:A:448:MET:HE1	4:A:472:PHE:CE1	2.46	0.50
1:N:407:LEU:HD22	1:N:426:ARG:HH11	1.77	0.50
4:A:136:ASN:OD1	4:A:258:GLY:N	2.36	0.50
4:D:136:ASN:OD1	4:D:258:GLY:N	2.41	0.50
1:N:293:ALA:O	1:N:297:ILE:HG13	2.11	0.50
1:N:543:ALA:HB2	1:G:387:GLY:HA2	1.94	0.50
2:a:58:LEU:HD22	4:d:489:LEU:HD23	1.93	0.50
4:D:172:ARG:HG3	4:D:201:TYR:CE2	2.47	0.49
4:D:183:ASP:OD1	4:D:184:PHE:N	2.42	0.49
4:D:85:SER:O	4:D:89:GLU:HG3	2.13	0.49
3:S:924:MET:HG3	3:S:1161:VAL:HG22	1.94	0.49
3:S:615:ASP:O	3:S:619:ARG:HG3	2.12	0.49
3:S:661:HIS:CE1	3:S:677:LYS:HB2	2.47	0.49
3:S:1174:ILE:HD13	3:S:1199:LEU:HD13	1.94	0.49
1:N:599:ARG:HD2	1:N:647:VAL:HB	1.95	0.49
3:S:813:ARG:NH1	3:S:815:GLN:OE1	2.46	0.49
3:S:1092:PHE:HB2	3:S:1095:PHE:HD2	1.76	0.49
1:G:786:LYS:HG2	1:G:790:GLU:OE2	2.12	0.49
1:G:640:ASP:OD2	1:G:642:SER:OG	2.26	0.49
2:X:181:TYR:OH	1:G:159:MET:O	2.27	0.49
1:G:874:PRO:O	1:G:878:GLN:HG2	2.13	0.49
4:d:472:PHE:HE2	4:d:483:MET:HE3	1.77	0.49
4:D:225:GLU:OE2	4:D:230:ARG:NH2	2.45	0.49
3:S:544:GLY:HA2	3:S:861:VAL:HG22	1.94	0.49
4:A:39:ASP:OD1	4:A:40:SER:N	2.46	0.49
4:d:197:ASP:OD1	4:d:197:ASP:N	2.46	0.48
4:d:458:ILE:HD13	4:D:452:ILE:HD12	1.95	0.48
4:d:507:ALA:O	4:d:510:GLN:HG3	2.12	0.48
4:A:288:ARG:HE	4:A:290:ILE:HD11	1.77	0.48
4:d:341:TRP:HZ3	4:D:340:GLN:HG3	1.78	0.48
4:D:479:SER:HB3	4:D:483:MET:HG3	1.94	0.48
4:D:118:LYS:NZ	4:D:145:THR:O	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S:1088:GLU:OE2	3:S:1090:SER:HB2	2.14	0.48
1:G:347:GLU:OE2	5:g:78:GLN:NE2	2.47	0.48
4:A:230:ARG:NH2	4:A:234:SER:HB3	2.28	0.48
1:N:152:LEU:HD23	1:N:156:LEU:HD11	1.96	0.48
3:S:943:VAL:HG22	3:S:949:MET:HE2	1.96	0.48
1:G:445:GLY:O	1:G:505:ARG:NH2	2.47	0.48
4:d:31:LEU:O	4:d:34:ILE:HG22	2.14	0.48
1:N:287:TYR:O	1:N:291:LYS:HG2	2.14	0.47
4:D:217:VAL:HG13	4:D:419:GLY:HA2	1.94	0.47
1:N:199:ASP:OD1	1:N:200:ARG:N	2.47	0.47
3:S:389:LEU:HB3	3:S:395:LEU:HD23	1.96	0.47
3:S:1163:GLU:OE2	3:S:1163:GLU:N	2.48	0.47
2:X:38:LYS:HB2	2:X:38:LYS:HE3	1.66	0.47
3:S:423:PRO:HD2	3:S:424:HIS:H	1.79	0.47
1:G:262:LEU:O	1:G:266:GLN:HG3	2.12	0.47
1:G:300:GLN:O	1:G:304:GLU:HG3	2.14	0.47
4:A:161:ASP:HB3	4:A:167:LEU:HD11	1.96	0.47
4:A:499:SER:HA	4:A:502:VAL:HG12	1.97	0.47
1:G:858:ALA:O	1:G:862:ILE:HG12	2.15	0.47
4:A:24:GLU:OE2	4:A:28:GLN:NE2	2.33	0.47
4:D:448:MET:HG2	4:D:471:TYR:HD2	1.79	0.47
1:N:522:ASN:HD21	3:S:138:ARG:HD3	1.79	0.47
3:S:389:LEU:HD23	3:S:427:LEU:HD12	1.96	0.47
3:S:750:LEU:HD12	3:S:879:LEU:HD13	1.97	0.47
1:G:834:ALA:O	1:G:838:VAL:HG23	2.14	0.47
1:N:869:TYR:CZ	1:N:877:LYS:HG2	2.50	0.47
3:S:1018:VAL:HG22	3:S:1076:MET:HG2	1.97	0.47
3:S:1092:PHE:HB2	3:S:1095:PHE:CD2	2.50	0.47
4:A:282:TYR:CE1	4:A:338:LYS:HD3	2.50	0.47
4:D:453:PRO:HA	4:D:456:GLU:HG2	1.97	0.47
3:S:613:ARG:NH1	3:S:617:GLU:OE1	2.47	0.47
1:N:631:ILE:HG23	1:N:663:ILE:HD13	1.97	0.47
2:X:148:GLY:HA2	2:X:173:PRO:HD2	1.97	0.47
3:S:515:ASN:OD1	3:S:516:GLU:N	2.48	0.47
4:d:183:ASP:OD1	4:d:184:PHE:N	2.48	0.47
1:N:879:TYR:HD1	1:N:880:LEU:HD22	1.80	0.46
3:S:707:LEU:HD22	3:S:812:MET:HE2	1.96	0.46
3:S:1146:ALA:O	3:S:1150:MET:HG3	2.15	0.46
1:G:90:GLN:O	1:G:94:ILE:HG12	2.15	0.46
4:d:120:GLY:O	4:d:124:LYS:HG2	2.15	0.46
4:d:233:ASP:OD1	4:d:234:SER:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:240:LEU:HD11	4:D:402:TYR:CD2	2.50	0.46
3:S:262:MET:HE1	3:S:365:LEU:HD13	1.98	0.46
3:S:475:ASP:O	3:S:479:THR:HG23	2.15	0.46
1:G:461:ALA:O	1:G:465:SER:HB2	2.15	0.46
4:A:183:ASP:O	4:A:187:THR:HG22	2.16	0.46
1:N:301:ALA:O	1:N:305:ILE:HG12	2.16	0.46
1:N:789:LEU:HD23	1:N:793:TYR:HD2	1.81	0.46
1:N:716:ASP:OD2	1:N:753:GLU:N	2.47	0.46
1:G:301:ALA:O	1:G:305:ILE:HG12	2.16	0.46
1:N:212:ARG:NH2	1:G:178:ASN:OD1	2.30	0.46
3:S:849:THR:O	3:S:853:MET:HG3	2.16	0.46
3:S:877:PHE:CD2	3:S:892:LEU:HD22	2.51	0.46
1:G:589:LYS:NZ	1:G:591:GLU:OE2	2.44	0.46
2:a:113:GLU:OE1	2:a:116:ARG:NH2	2.43	0.46
3:S:1132:ILE:HG21	3:S:1177:LEU:HD21	1.98	0.46
1:G:749:GLU:OE2	1:G:876:ARG:NH1	2.35	0.46
1:N:208:GLU:O	1:N:212:ARG:HG2	2.16	0.46
1:N:838:VAL:HG22	1:N:855:ALA:HB1	1.98	0.46
3:S:273:GLN:HA	3:S:354:GLU:HG3	1.97	0.46
3:S:277:VAL:HA	3:S:320:MET:SD	2.56	0.46
3:S:953:LEU:HD23	3:S:1146:ALA:HB2	1.97	0.46
3:S:1232:ILE:O	3:S:1236:PHE:HB2	2.15	0.46
1:G:638:LEU:HD21	1:G:673:GLN:HG2	1.98	0.46
4:d:139:GLU:OE1	4:d:396:TRP:NE1	2.40	0.46
4:D:109:ASN:O	4:D:113:GLN:HG2	2.16	0.46
4:D:242:LEU:HD12	4:D:243:PRO:HD2	1.98	0.46
3:S:287:VAL:HG21	3:S:317:PHE:CD2	2.51	0.46
3:S:1213:ILE:O	3:S:1217:THR:HG23	2.16	0.46
1:G:775:LYS:HG3	1:G:776:VAL:HG13	1.97	0.46
4:d:24:GLU:OE1	4:d:37:ARG:NH2	2.49	0.46
1:N:434:THR:HG21	1:N:455:ILE:HG13	1.97	0.45
1:N:521:SER:O	1:N:559:ARG:NH1	2.48	0.45
1:G:161:LYS:O	1:G:165:THR:HG23	2.16	0.45
2:a:54:THR:HG21	4:d:493:GLN:HB2	1.99	0.45
3:S:974:ALA:HB2	3:S:1077:MET:CE	2.47	0.45
2:X:117:MET:HB2	1:G:191:VAL:HG11	1.98	0.45
3:S:38:GLY:HA3	3:S:113:TYR:HA	1.99	0.45
3:S:1133:MET:HE2	3:S:1137:PHE:CE1	2.52	0.45
4:D:371:ALA:HB1	4:D:432:LEU:HD23	1.98	0.45
1:N:368:ALA:HA	1:N:373:MET:HE3	1.98	0.45
2:a:6:ALA:O	2:a:10:LEU:HG	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:220:TYR:O	4:d:237:TYR:N	2.48	0.45
3:S:280:VAL:HG22	3:S:319:LEU:HB2	1.98	0.45
3:S:312:VAL:HG13	3:S:312:VAL:O	2.17	0.45
4:d:202:THR:HG23	4:d:224:GLN:HG2	1.98	0.45
4:d:347:GLN:O	4:d:351:GLN:HG2	2.17	0.45
4:d:420:VAL:HG22	4:D:145:THR:HG22	1.98	0.45
4:A:170:ILE:HA	4:A:202:THR:O	2.15	0.45
2:a:61:ILE:HD11	4:A:461:ARG:HD3	1.99	0.45
3:S:1064:GLU:HG2	3:S:1065:LEU:N	2.31	0.45
4:D:6:THR:HG22	4:D:8:ALA:H	1.81	0.45
1:N:351:LYS:HG3	5:m:80:GLY:O	2.17	0.45
2:a:54:THR:O	2:a:58:LEU:HD23	2.16	0.45
3:S:848:LYS:O	3:S:852:THR:HG23	2.16	0.45
3:S:936:TRP:HA	3:S:939:GLU:HG2	1.99	0.45
1:G:208:GLU:O	1:G:212:ARG:HG2	2.17	0.45
2:a:47:ARG:HG2	2:a:51:ARG:HE	1.81	0.45
2:a:113:GLU:O	2:a:117:MET:HG3	2.16	0.45
3:S:664:MET:HE2	3:S:833:MET:HE3	1.99	0.45
4:A:81:PHE:N	4:A:108:GLU:OE2	2.36	0.45
3:S:1129:LEU:HD22	3:S:1228:PRO:HG2	1.99	0.45
4:A:240:LEU:HD11	4:A:421:VAL:HG11	1.99	0.45
4:D:242:LEU:O	4:D:399:LYS:NZ	2.49	0.45
2:a:51:ARG:HH22	4:D:503:SER:CB	2.30	0.44
3:S:555:ASP:HB3	3:S:562:ARG:HB2	1.99	0.44
1:G:447:VAL:HG23	1:G:501:LEU:HD22	1.98	0.44
4:d:315:VAL:HG21	4:d:327:PRO:HG3	1.99	0.44
4:d:375:ARG:HG2	4:d:429:THR:HG23	1.99	0.44
4:D:161:ASP:HB3	4:D:167:LEU:HD11	1.99	0.44
3:S:1133:MET:SD	3:S:1228:PRO:HB2	2.58	0.44
4:d:143:GLU:OE2	4:d:237:TYR:OH	2.29	0.44
4:d:317:GLY:HA3	4:A:295:ALA:HB3	1.99	0.44
4:D:67:ILE:O	4:D:71:LEU:HB2	2.17	0.44
1:N:334:LEU:HD22	1:N:339:VAL:HG21	1.98	0.44
3:S:273:GLN:O	3:S:322:GLY:HA2	2.17	0.44
3:S:622:HIS:CD2	3:S:815:GLN:HE21	2.35	0.44
4:A:408:VAL:HG13	4:A:409:TYR:CD2	2.53	0.44
3:S:692:ARG:NH2	3:S:1067:MET:SD	2.91	0.44
3:S:1211:MET:HE2	3:S:1216:PHE:HA	2.00	0.44
1:G:639:ILE:HD13	1:G:644:LEU:HD13	1.99	0.44
4:A:127:ALA:HB2	4:A:150:VAL:HG11	2.00	0.44
4:D:218:VAL:HB	4:D:239:GLU:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:415:LYS:HD3	1:N:415:LYS:HA	1.81	0.44
3:S:284:ALA:O	3:S:288:THR:HG23	2.18	0.44
3:S:320:MET:HE1	3:S:328:ALA:HA	1.99	0.44
3:S:389:LEU:HD21	3:S:424:HIS:HA	1.98	0.44
3:S:986:TRP:CE2	3:S:1117:LEU:HD11	2.53	0.44
3:S:1073:GLY:O	3:S:1077:MET:HG2	2.18	0.44
4:D:248:VAL:HG11	4:D:251:LEU:HD21	1.99	0.44
1:N:146:GLN:NE2	1:N:150:ASP:OD2	2.51	0.44
4:d:220:TYR:N	4:d:237:TYR:O	2.51	0.44
2:a:131:ASP:HB3	2:a:134:SER:HB2	1.99	0.44
3:S:317:PHE:CD1	3:S:345:VAL:HB	2.53	0.44
4:A:452:ILE:HG23	4:A:462:PHE:HE2	1.83	0.44
5:m:72:GLU:O	5:m:76:ARG:HG3	2.18	0.44
1:N:261:PRO:HD3	1:N:297:ILE:CD1	2.45	0.43
1:N:631:ILE:HG12	1:N:663:ILE:HD11	2.00	0.43
2:X:39:GLN:O	2:X:43:ILE:HG12	2.18	0.43
3:S:350:PRO:HG3	3:S:369:ASP:OD1	2.17	0.43
3:S:727:VAL:HG21	3:S:776:PHE:CE2	2.51	0.43
4:A:21:ASP:O	4:A:25:LYS:HG2	2.18	0.43
4:A:294:ASP:HB3	4:A:297:SER:HB3	2.00	0.43
1:N:85:LYS:HE3	1:N:85:LYS:HB2	1.86	0.43
3:S:1140:MET:HG2	3:S:1168:MET:HB2	1.99	0.43
4:d:37:ARG:NE	4:d:154:ARG:HH22	2.16	0.43
4:d:354:SER:HB3	4:d:359:TYR:HB3	1.99	0.43
1:G:83:ALA:HA	1:G:89:VAL:HG23	2.00	0.43
1:G:134:ASP:O	1:G:138:GLN:HG2	2.18	0.43
4:A:440:LYS:HD3	4:A:475:TYR:O	2.19	0.43
1:G:734:GLU:OE2	1:G:735:PRO:HD2	2.18	0.43
1:G:503:ASP:OD1	1:G:506:ARG:NH2	2.52	0.43
1:G:716:ASP:HB2	1:G:753:GLU:OE1	2.18	0.43
4:d:37:ARG:HD3	4:d:154:ARG:NH1	2.31	0.43
4:d:465:ASP:HB3	4:A:461:ARG:HH21	1.84	0.43
1:N:413:ASN:OD1	1:G:302:ARG:HD2	2.18	0.43
3:S:618:SER:HA	3:S:820:THR:HB	2.01	0.43
1:G:273:LYS:HB3	1:G:273:LYS:HE2	1.77	0.43
1:N:148:MET:HE3	1:N:148:MET:HB3	1.94	0.43
1:N:647:VAL:HG22	1:N:665:THR:HG22	2.00	0.43
3:S:504:ARG:O	3:S:508:GLU:HG3	2.19	0.43
3:S:692:ARG:HB2	3:S:1067:MET:HE1	2.01	0.43
4:A:160:ARG:NH1	4:A:164:GLY:O	2.39	0.43
4:D:238:PRO:HD2	4:D:241:GLU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:g:83:ASN:OD1	5:g:84:PRO:HD2	2.19	0.43
2:a:57:SER:OG	4:A:460:PRO:HD2	2.19	0.43
3:S:106:PRO:HB2	3:S:111:ILE:HG13	2.01	0.43
3:S:970:PHE:CZ	3:S:1073:GLY:HA3	2.54	0.43
3:S:120:ARG:NH2	3:S:121:GLU:OE2	2.52	0.43
3:S:566:VAL:HG11	3:S:839:MET:HE2	2.01	0.43
3:S:1018:VAL:HG21	3:S:1077:MET:SD	2.59	0.43
4:d:245:ASN:OD1	4:d:399:LYS:HG2	2.19	0.43
4:D:190:ARG:HH11	4:D:192:LYS:HD3	1.84	0.43
1:N:140:GLN:NE2	1:N:141:GLU:HG2	2.34	0.43
1:N:649:VAL:HG12	1:N:661:MET:HE3	2.01	0.42
3:S:258:LEU:O	3:S:262:MET:HG2	2.19	0.42
1:G:112:SER:HB3	1:G:148:MET:HE1	2.01	0.42
4:D:124:LYS:NZ	4:D:139:GLU:OE2	2.41	0.42
1:N:480:GLU:HA	1:N:580:MET:HE2	2.01	0.42
3:S:211:ILE:HD13	3:S:915:THR:HG23	2.02	0.42
3:S:411:ASN:OD1	3:S:411:ASN:N	2.53	0.42
1:G:268:GLN:O	1:G:272:THR:HG23	2.19	0.42
1:G:275:LEU:HB2	1:G:279:SER:HB3	2.00	0.42
4:d:189:TYR:HD1	4:d:192:LYS:HG3	1.84	0.42
4:A:426:THR:HG23	4:A:431:ALA:HA	2.01	0.42
3:S:633:ASN:OD1	3:S:796:ARG:NH1	2.52	0.42
3:S:1200:LEU:O	3:S:1204:GLN:HG2	2.19	0.42
1:N:834:ALA:O	1:N:838:VAL:HG23	2.20	0.42
4:D:404:TYR:O	4:D:408:VAL:HG23	2.19	0.42
4:D:413:LYS:HE2	4:D:413:LYS:HB3	1.77	0.42
4:D:429:THR:HA	4:D:432:LEU:HD13	2.01	0.42
2:X:26:LYS:O	2:X:30:LYS:HG2	2.20	0.42
3:S:1137:PHE:CE1	3:S:1168:MET:HE1	2.54	0.42
1:N:862:ILE:O	1:N:866:GLN:HG2	2.19	0.42
3:S:335:ASN:HB3	3:S:337:ASP:OD1	2.20	0.42
3:S:1064:GLU:O	3:S:1068:GLN:HG2	2.20	0.42
3:S:1171:ILE:HG23	3:S:1199:LEU:HD21	2.01	0.42
4:D:403:LEU:HD23	4:D:403:LEU:HA	1.90	0.42
4:D:500:ALA:O	4:D:503:SER:HB3	2.20	0.42
1:N:824:GLY:H	1:N:827:SER:HB3	1.85	0.42
3:S:613:ARG:O	3:S:617:GLU:HG3	2.20	0.42
1:N:542:THR:OG1	1:G:391:ASN:HB2	2.19	0.42
1:N:702:SER:O	1:N:705:VAL:HG23	2.20	0.42
3:S:501:ASP:OD2	3:S:1158:ARG:NH2	2.53	0.42
3:S:1115:LYS:O	3:S:1119:ARG:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:278:ALA:HB2	4:D:287:ALA:HB1	2.02	0.42
4:D:498:ALA:O	4:D:502:VAL:HG23	2.19	0.42
1:N:877:LYS:O	1:N:881:GLU:HG2	2.19	0.41
3:S:299:ARG:O	3:S:303:VAL:HG23	2.20	0.41
1:G:573:ASP:OD2	1:G:573:ASP:N	2.48	0.41
4:d:308:GLU:HG3	4:d:309:THR:HG23	2.01	0.41
4:A:113:GLN:O	4:A:117:GLU:HG3	2.20	0.41
3:S:754:MET:SD	3:S:836:ARG:HB3	2.60	0.41
3:S:974:ALA:HB3	3:S:1011:VAL:HG13	2.01	0.41
3:S:1159:ARG:O	3:S:1162:THR:N	2.53	0.41
1:G:251:LEU:HD12	1:G:282:VAL:HG21	2.01	0.41
4:D:31:LEU:HD23	4:D:31:LEU:HA	1.91	0.41
4:D:290:ILE:HB	4:D:331:TYR:HB3	2.02	0.41
3:S:85:PRO:HB3	3:S:118:ALA:HB1	2.01	0.41
3:S:205:ILE:HA	3:S:208:VAL:HG12	2.02	0.41
4:A:448:MET:HG2	4:A:452:ILE:HD12	2.02	0.41
1:N:251:LEU:HD12	1:N:282:VAL:HG21	2.01	0.41
1:N:289:GLU:O	1:N:292:ARG:HG3	2.20	0.41
3:S:905:LYS:HE3	3:S:905:LYS:HB3	1.89	0.41
1:G:742:LEU:HG	1:G:746:MET:HE3	2.02	0.41
4:D:119:ASP:HB2	4:D:147:LYS:HE2	2.02	0.41
1:N:152:LEU:HB3	1:G:69:VAL:HG21	2.02	0.41
3:S:318:THR:N	3:S:345:VAL:O	2.40	0.41
3:S:888:LEU:N	3:S:889:PRO:HD2	2.35	0.41
3:S:935:PRO:HA	3:S:938:LYS:HE3	2.03	0.41
1:G:302:ARG:NH2	1:G:347:GLU:OE2	2.53	0.41
4:d:131:LEU:HD11	4:d:247:LEU:HB3	2.02	0.41
2:a:51:ARG:HG2	4:d:493:GLN:NE2	2.35	0.41
3:S:136:ARG:O	3:S:140:MET:HG3	2.20	0.41
3:S:362:GLY:O	3:S:366:ARG:HG3	2.20	0.41
3:S:929:ARG:O	3:S:933:GLU:HG3	2.20	0.41
3:S:1107:SER:HA	3:S:1110:VAL:HG12	2.01	0.41
4:d:240:LEU:HD23	4:d:240:LEU:HA	1.92	0.41
2:X:13:SER:OG	2:X:14:LYS:N	2.53	0.41
3:S:113:TYR:CZ	3:S:126:ARG:HG2	2.55	0.41
3:S:248:THR:HG22	3:S:267:ALA:HB3	2.02	0.41
3:S:983:GLN:HB3	3:S:985:PRO:HD2	2.03	0.41
4:A:30:THR:HG22	4:A:56:GLY:HA3	2.02	0.41
1:N:675:MET:HB3	3:S:214:LEU:HB2	2.03	0.41
3:S:687:SER:HB3	3:S:690:LYS:HG2	2.02	0.41
3:S:1212:ASP:OD1	3:S:1215:THR:OG1	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:126:LYS:HA	1:G:129:GLU:HG2	2.02	0.41
1:G:487:LYS:HE3	1:G:491:GLN:HE22	1.85	0.41
4:A:396:TRP:O	4:A:400:LEU:HG	2.21	0.41
1:N:152:LEU:HD22	1:N:171:LEU:HD11	2.03	0.41
1:N:441:LEU:HD23	1:N:441:LEU:HA	1.89	0.41
3:S:297:LEU:HD13	3:S:305:LEU:HD21	2.02	0.41
3:S:308:ILE:O	3:S:312:VAL:HG12	2.21	0.41
3:S:498:PHE:HB3	3:S:914:ASP:CG	2.46	0.41
3:S:628:TYR:CE2	3:S:632:LEU:HD11	2.56	0.41
3:S:877:PHE:CE2	3:S:892:LEU:HD22	2.56	0.41
4:d:175:ALA:O	4:d:198:VAL:N	2.53	0.41
4:A:31:LEU:O	4:A:34:ILE:HG22	2.20	0.41
1:G:415:LYS:HA	1:G:415:LYS:HD3	1.90	0.41
1:G:446:GLU:OE1	1:G:446:GLU:N	2.54	0.41
4:D:490:GLN:O	4:D:494:LYS:HG2	2.21	0.41
3:S:1043:ARG:HD2	3:S:1043:ARG:HA	1.75	0.40
4:A:238:PRO:HD2	4:A:241:GLU:HB2	2.03	0.40
3:S:832:ARG:HA	3:S:880:GLY:HA3	2.03	0.40
3:S:1105:PHE:CZ	3:S:1139:LEU:HB2	2.56	0.40
1:G:254:VAL:HG12	1:G:267:LEU:HD11	2.03	0.40
4:A:7:LEU:HD13	4:A:225:GLU:CD	2.47	0.40
4:A:394:ASP:O	4:A:398:ARG:HB2	2.21	0.40
3:S:641:GLU:HG3	3:S:643:ASP:OD1	2.22	0.40
3:S:1116:ILE:HG12	3:S:1235:ASN:ND2	2.37	0.40
4:d:455:LEU:HD21	4:D:448:MET:HE1	2.03	0.40
1:N:542:THR:OG1	1:G:387:GLY:O	2.39	0.40
1:N:700:ILE:HD13	1:N:700:ILE:HA	1.97	0.40
2:a:127:LEU:H	2:a:127:LEU:HD23	1.86	0.40
3:S:1017:ILE:HD11	3:S:1102:ILE:HB	2.03	0.40
4:d:402:TYR:OH	4:d:423:ILE:O	2.29	0.40
4:D:226:ALA:HB2	4:D:231:ILE:HD11	2.04	0.40
3:S:952:ARG:HD2	3:S:1020:ASP:OD1	2.21	0.40
4:A:138:LEU:HD11	4:A:169:LEU:HD21	2.03	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	G	801/893 (90%)	794 (99%)	7 (1%)	0	100	100
1	N	800/893 (90%)	792 (99%)	8 (1%)	0	100	100
2	X	136/195 (70%)	131 (96%)	5 (4%)	0	100	100
2	a	130/195 (67%)	126 (97%)	4 (3%)	0	100	100
3	S	1127/1239 (91%)	1102 (98%)	25 (2%)	0	100	100
4	A	488/531 (92%)	477 (98%)	11 (2%)	0	100	100
4	D	488/531 (92%)	477 (98%)	11 (2%)	0	100	100
4	d	497/531 (94%)	487 (98%)	10 (2%)	0	100	100
5	g	32/87 (37%)	32 (100%)	0	0	100	100
5	m	32/87 (37%)	32 (100%)	0	0	100	100
All	All	4531/5182 (87%)	4450 (98%)	81 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	650/714 (91%)	650 (100%)	0	100	100
1	N	649/714 (91%)	649 (100%)	0	100	100
2	X	114/153 (74%)	114 (100%)	0	100	100
2	a	113/153 (74%)	112 (99%)	1 (1%)	70	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	S	906/978 (93%)	906 (100%)	0	100	100
4	A	403/431 (94%)	403 (100%)	0	100	100
4	D	403/431 (94%)	403 (100%)	0	100	100
4	d	408/431 (95%)	408 (100%)	0	100	100
5	g	27/58 (47%)	27 (100%)	0	100	100
5	m	27/58 (47%)	27 (100%)	0	100	100
All	All	3700/4121 (90%)	3699 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	a	144	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	N	259	GLN
1	N	278	ASN
1	N	610	GLN
1	N	622	GLN
1	N	673	GLN
1	N	704	GLN
1	N	800	GLN
1	N	820	ASN
2	X	46	GLN
2	X	94	ASN
2	X	108	GLN
2	a	34	GLN
2	a	60	ASN
3	S	115	HIS
3	S	338	ASN
3	S	446	GLN
3	S	622	HIS
3	S	855	ASN
3	S	977	ASN
3	S	1106	GLN
3	S	1122	ASN
1	G	63	ASN
1	G	139	GLN

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Mol	Chain	Res	Type
1	G	144	HIS
1	G	170	GLN
1	G	183	GLN
1	G	256	GLN
1	G	319	GLN
1	G	451	ASN
1	G	584	ASN
1	G	622	GLN
1	G	659	GLN
1	G	744	ASN
4	d	508	GLN
4	A	250	ASN
4	A	422	ASN
4	A	488	GLN
4	A	493	GLN
4	D	126	GLN
4	D	281	ASN
4	D	446	GLN
5	g	81	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

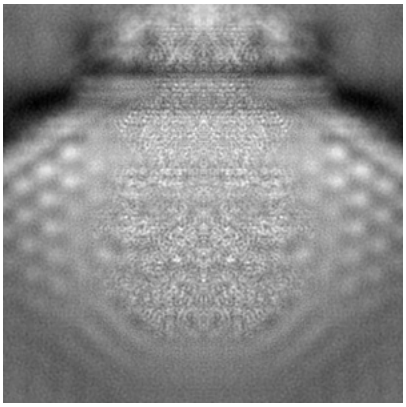
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-69208. These allow visual inspection of the internal detail of the map and identification of artifacts.

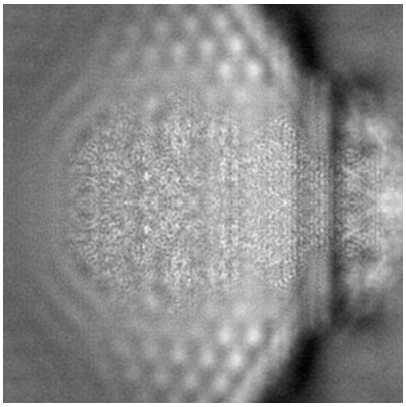
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

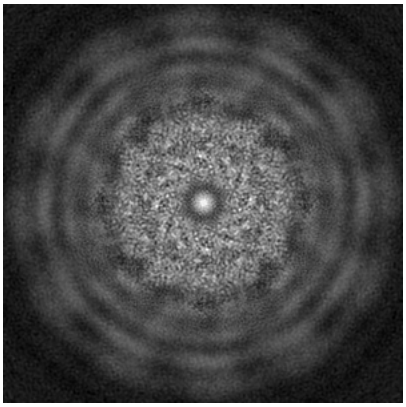
6.1.1 Primary map



X



Y

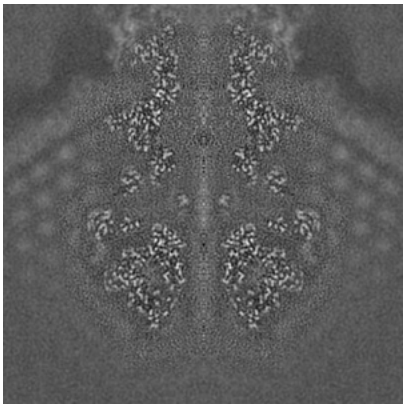


Z

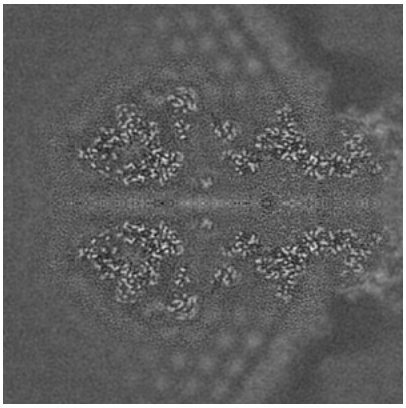
The images above show the map projected in three orthogonal directions.

6.2 Central slices

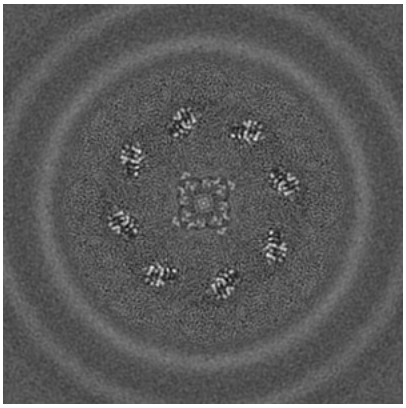
6.2.1 Primary map



X Index: 144



Y Index: 144

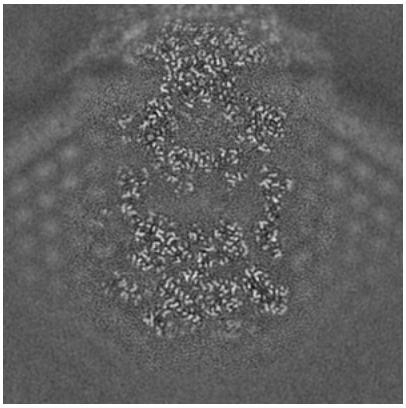


Z Index: 144

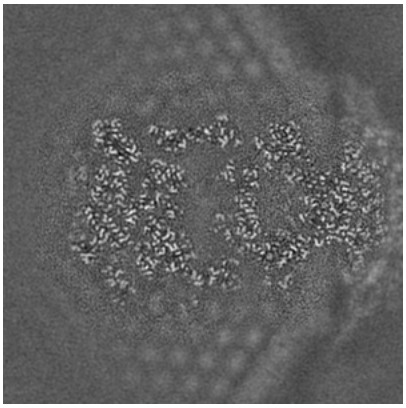
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

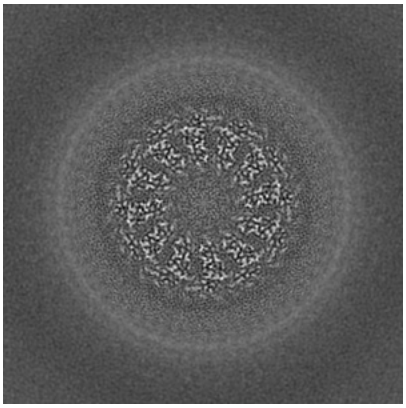
6.3.1 Primary map



X Index: 167



Y Index: 121

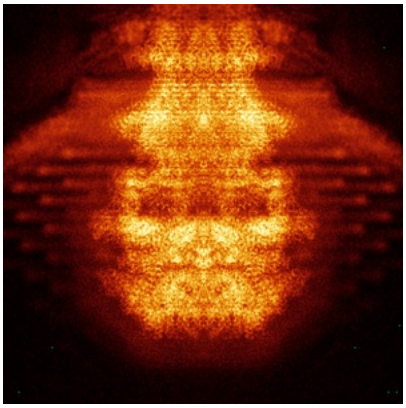


Z Index: 206

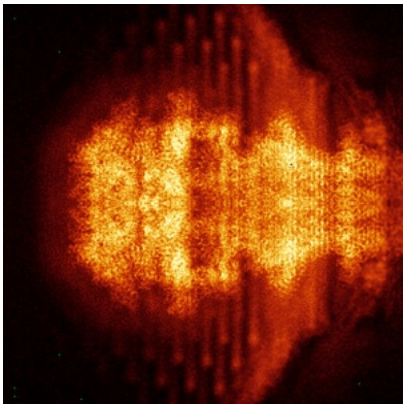
The images above show the largest variance slices of the map in three orthogonal directions.

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

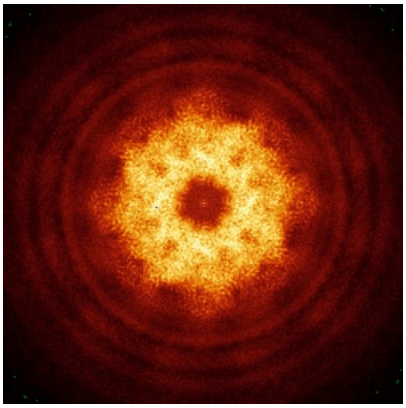
6.4.1 Primary map



X



Y

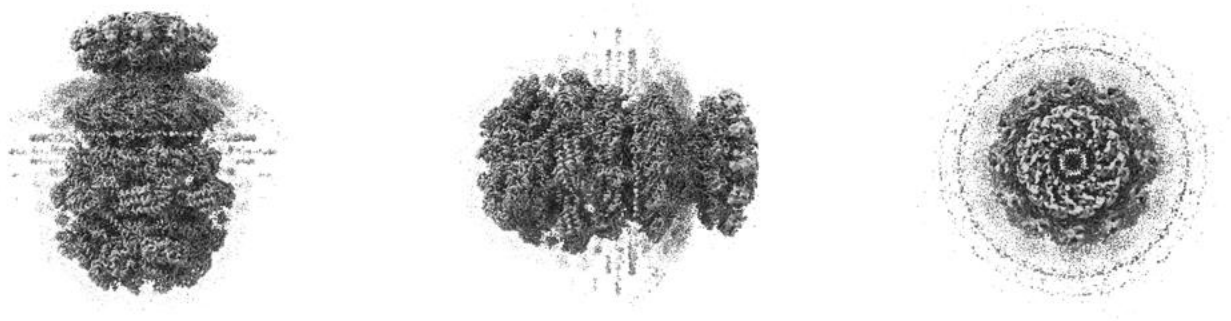


Z

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 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

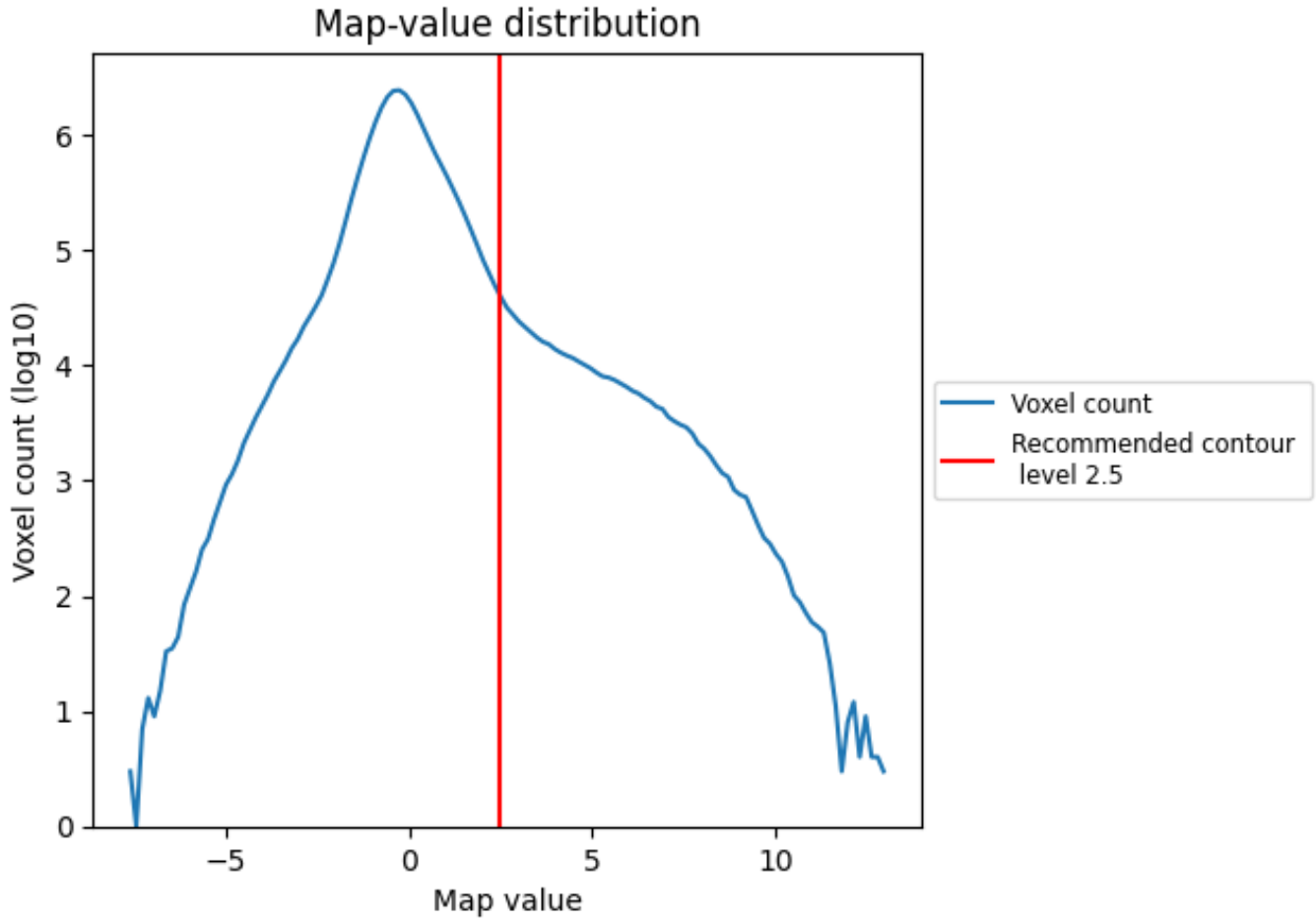
6.6 Mask visualisation (i)

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

7 Map analysis

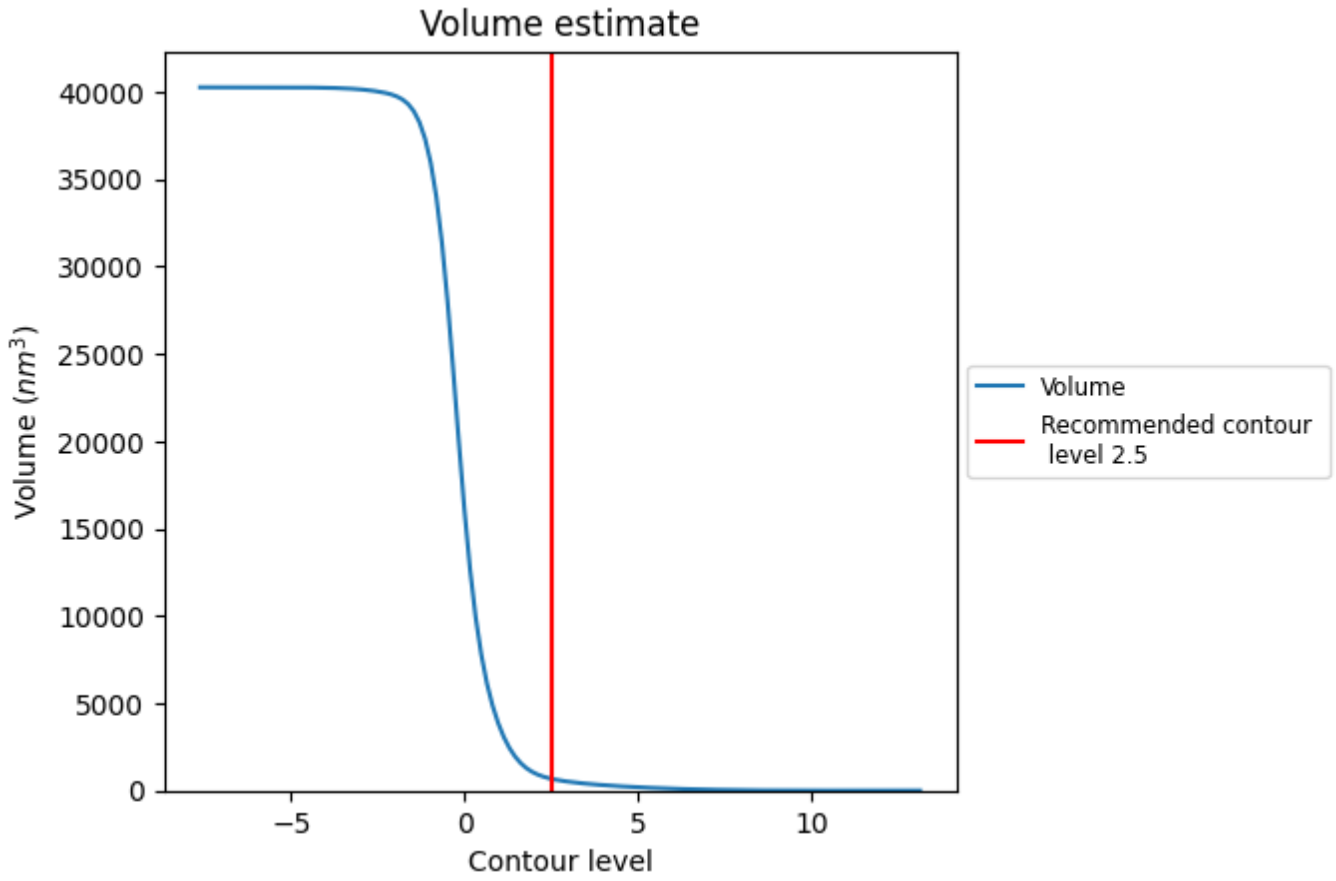
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

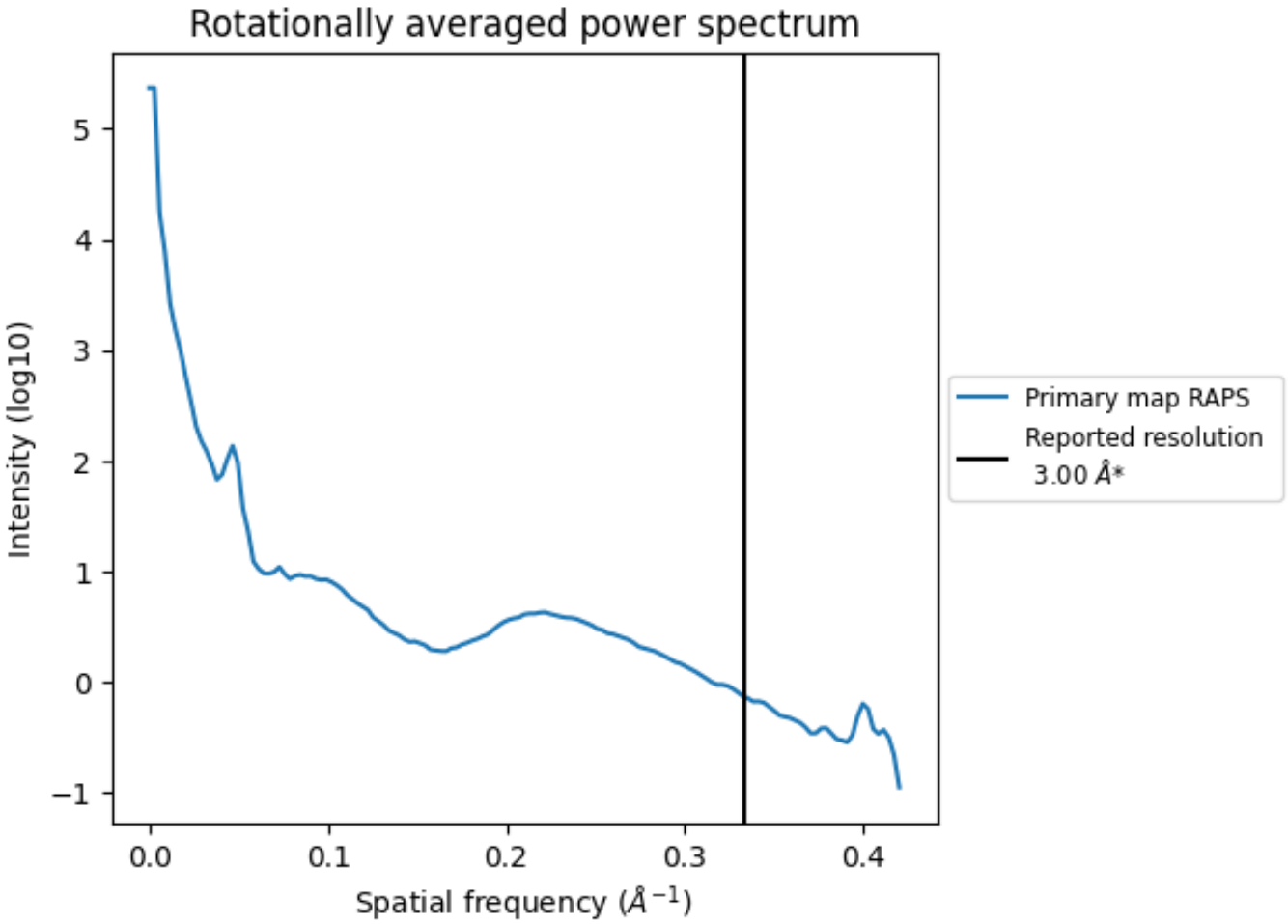
7.2 Volume estimate (i)



The volume at the recommended contour level is 679 nm^3; this corresponds to an approximate mass of 614 kDa.

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

7.3 Rotationally averaged power spectrum (i)



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

8 Fourier-Shell correlation (i)

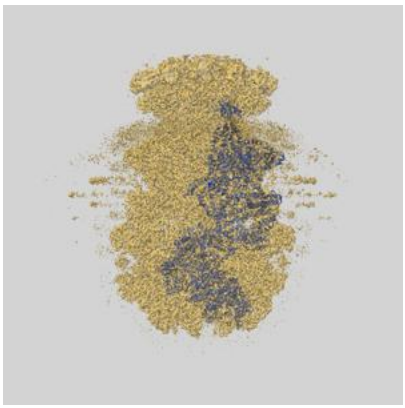
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

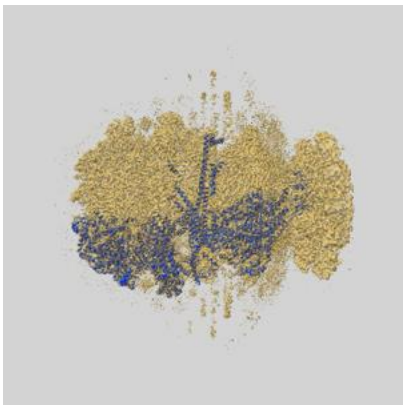
This section contains information regarding the fit between EMDB map EMD-69208 and PDB model 23SG. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

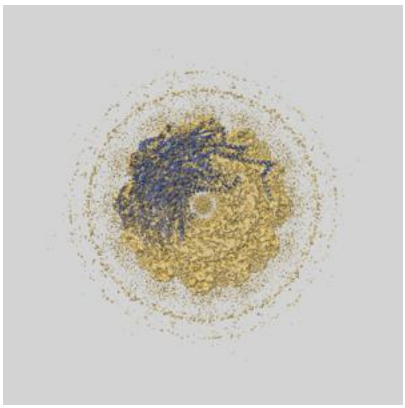
9.1.1 Map-model overlay



X

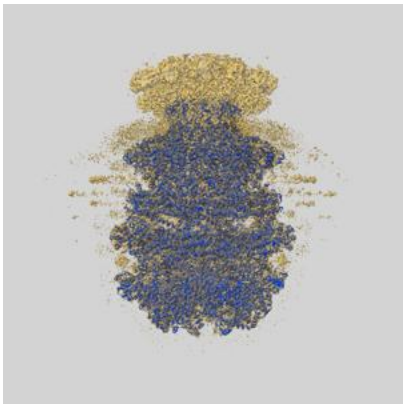


Y

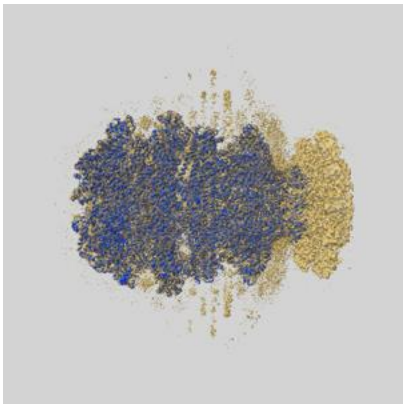


Z

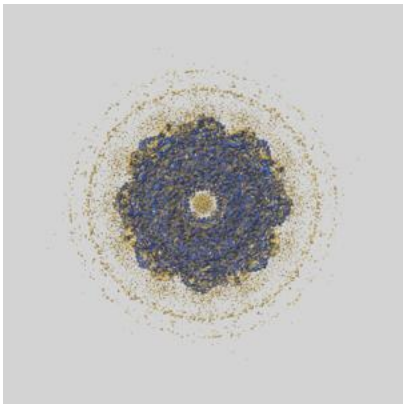
9.1.2 Map-model assembly overlay



X



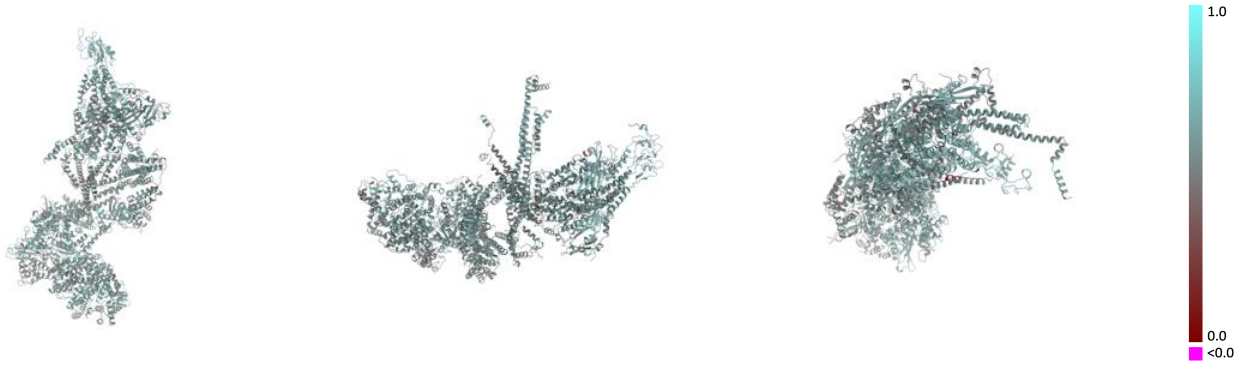
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

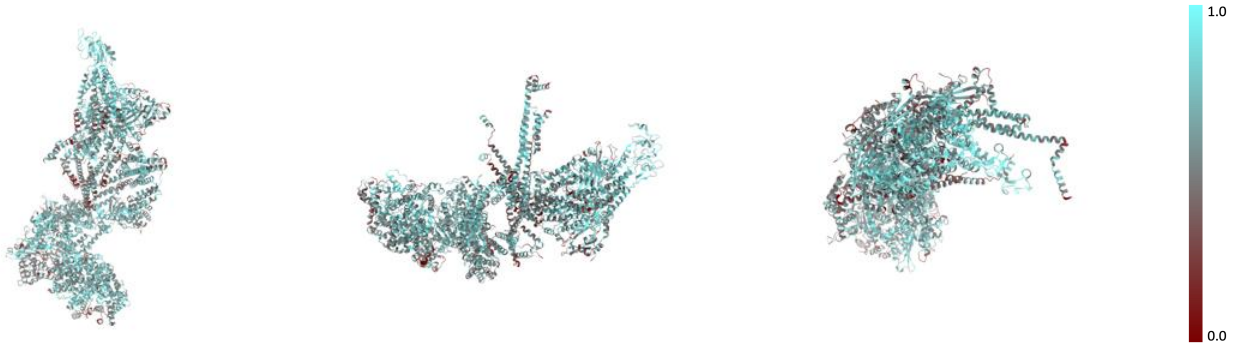
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

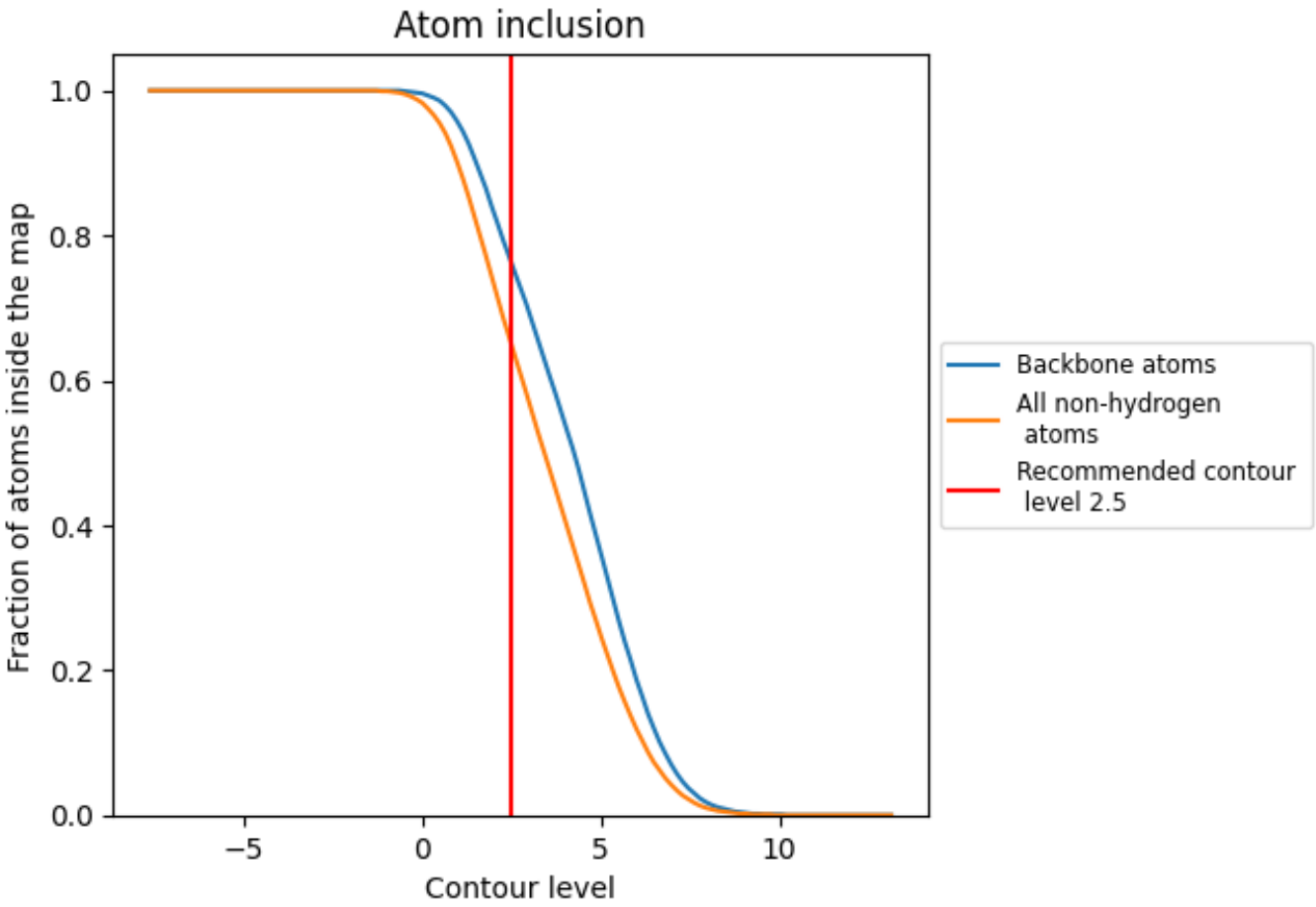
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 65% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6500	0.5710
A	0.6730	0.5820
D	0.6590	0.5780
G	0.6800	0.5760
N	0.6900	0.5810
S	0.6220	0.5610
X	0.4780	0.5200
a	0.4800	0.5170
d	0.6790	0.5820
g	0.5390	0.5730
m	0.5390	0.5500

