



wwPDB EM Validation Summary Report ⓘ

May 18, 2026 – 01:58 PM JST

PDB ID : 23SG / pdb_000023sg
EMDB ID : EMD-69208
Title : The composite Cryo-EM structure of bacteriophage RAN69 pre-ejectosome-p
ortal 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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

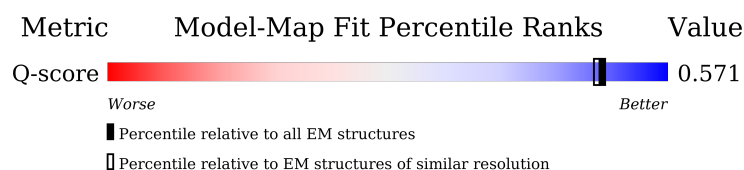
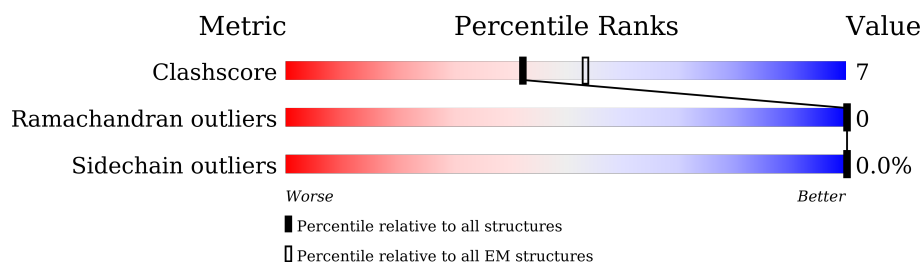
1 Overall quality at a glance

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.



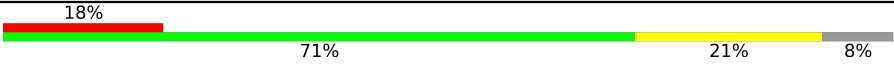

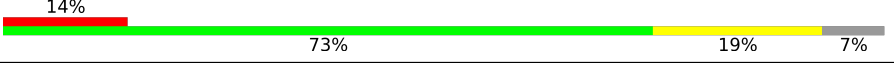
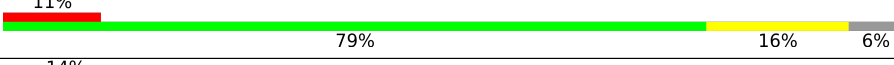


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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 $\leq 5\%$. 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	G	893	<div> <div>9%</div> <div>77%</div> <div>13%</div> <div>10%</div> </div>
1	N	893	<div> <div>7%</div> <div>78%</div> <div>12%</div> <div>10%</div> </div>
2	X	195	<div> <div>28%</div> <div>67%</div> <div>8%</div> <div>25%</div> </div>
2	a	195	<div> <div>27%</div> <div>61%</div> <div>11%</div> <div>28%</div> </div>

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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		

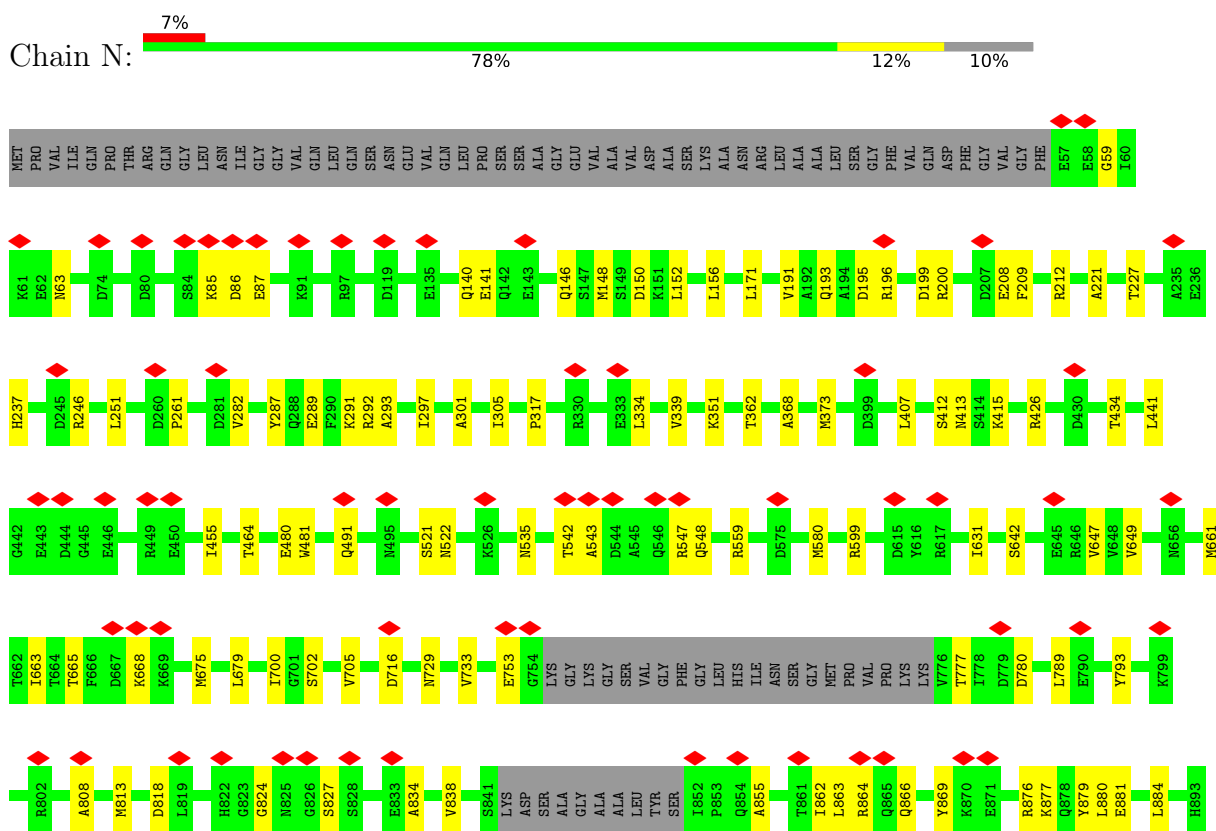
- Molecule 5 is a protein called gp20.

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

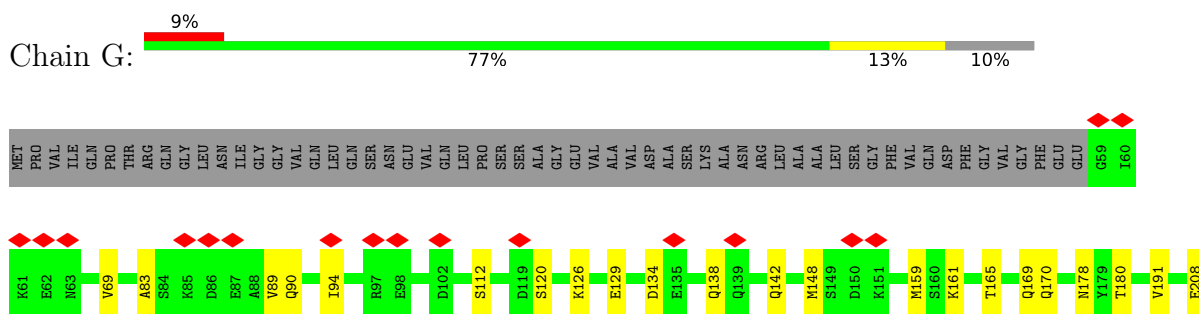
3 Residue-property plots

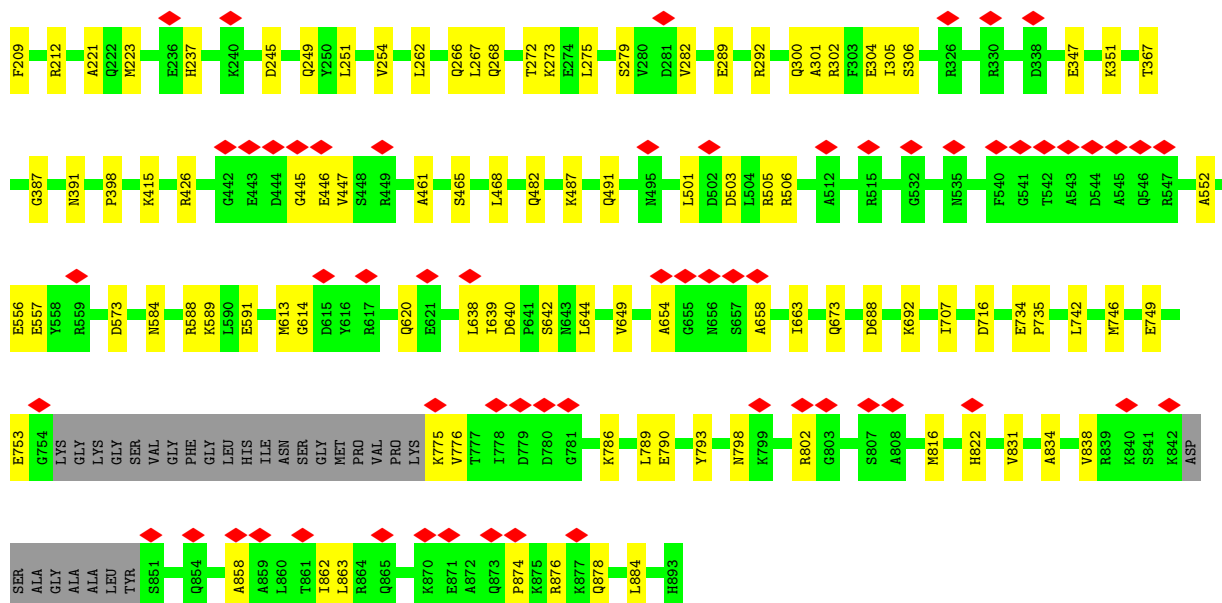
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: gp11

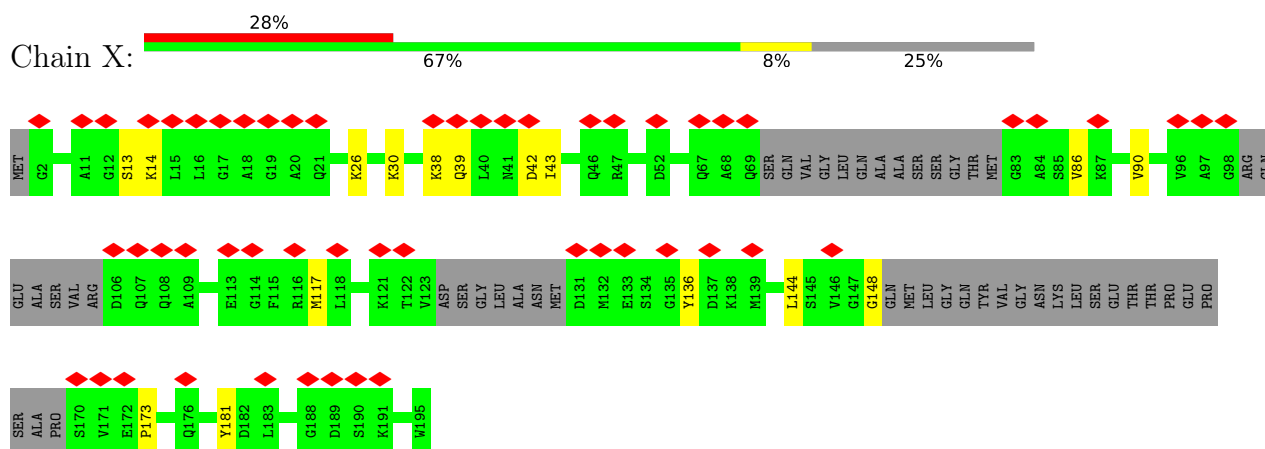


• Molecule 1: gp11

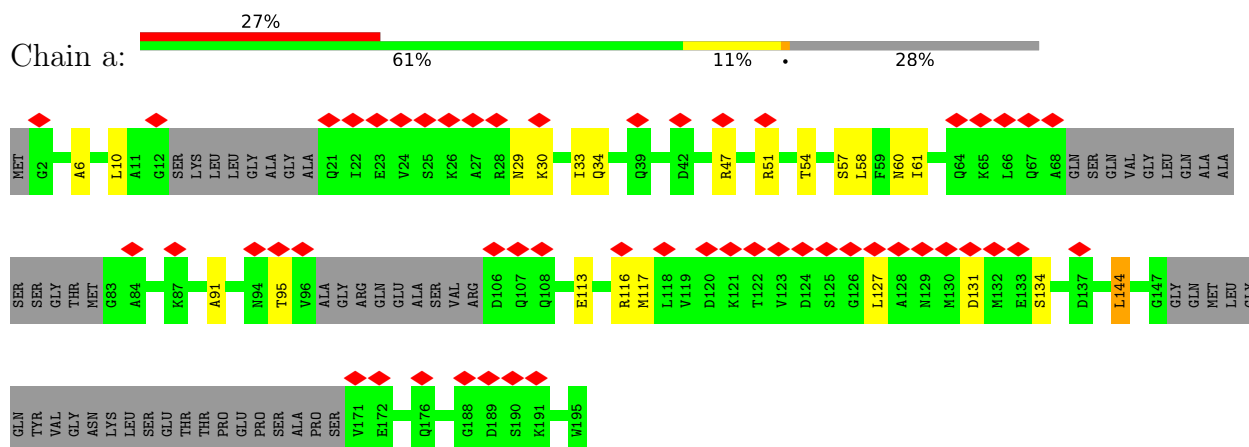




• Molecule 2: gp12



• Molecule 2: gp12

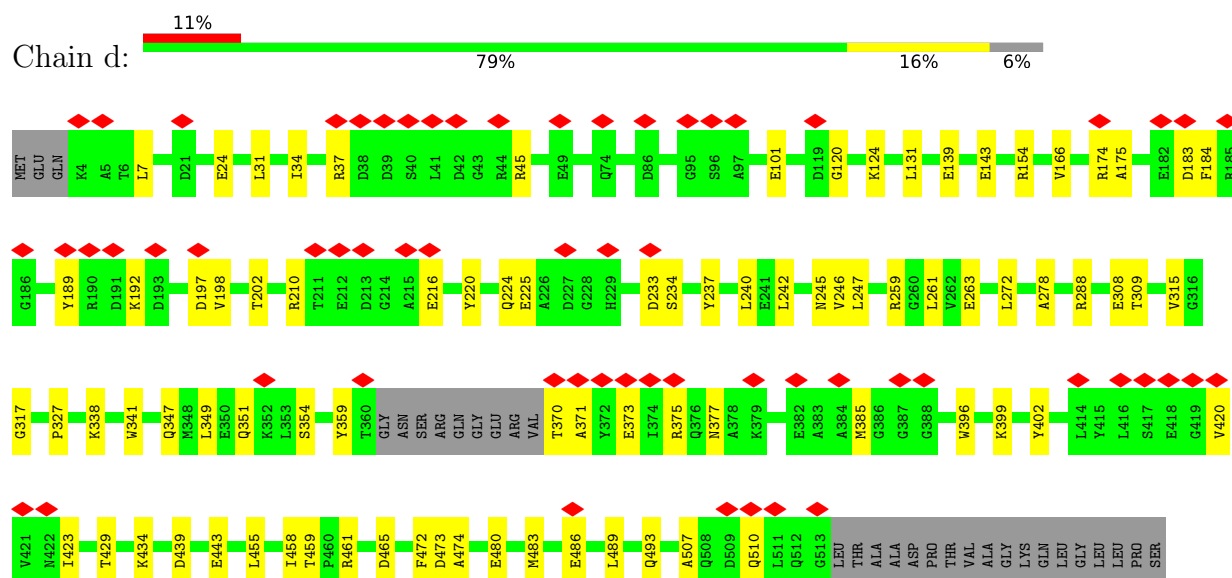


• Molecule 3: gp10

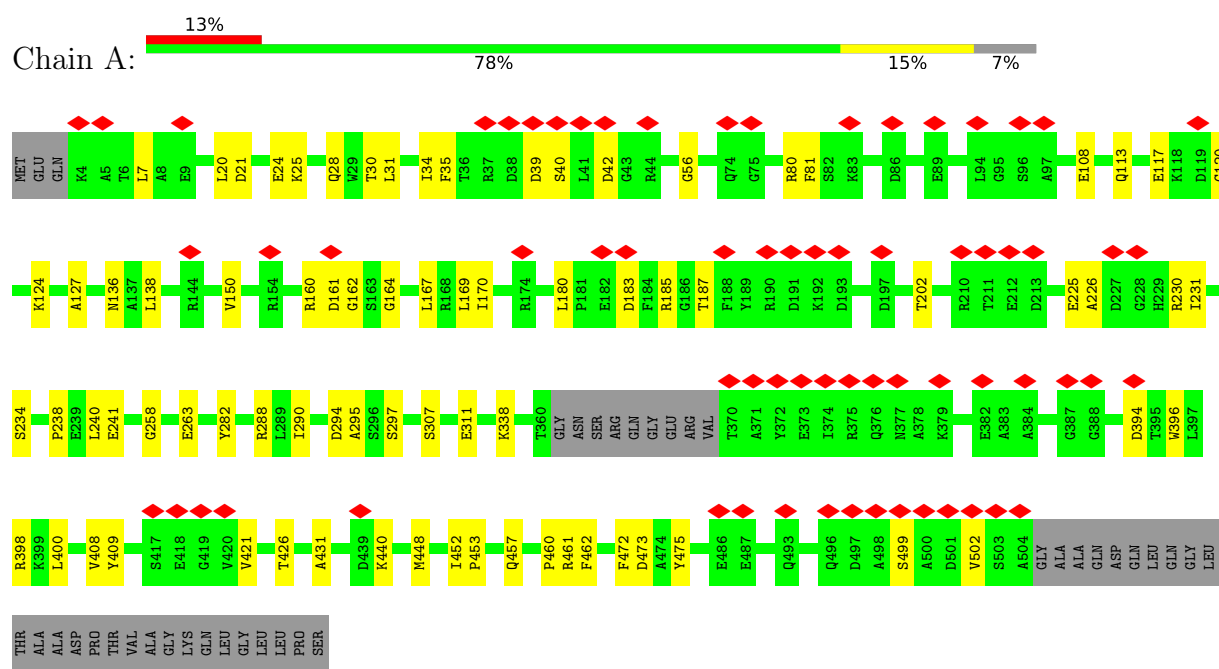


MET	ALA	GLN	PHE	LEU	ASN	GLN	GLU	PRO	ASN	ALA	PRO	GLN	GLU	LYS	ASP	SER	SER	ALA	GLY	LYS	ALA	THR	THR	LEU	LYS	PRO	ALA	ALA	PRO	PRO	SER	SER	VAL	D30	W31	N32	D33	A34	D35	D36	G37	G38	V39	R44	A45	T53	P54	A55	T56	S57	A58	G59	D60	S61	A64	A73	R76	P85
P106	E109	E110	I111	E112	Y113	A118	S119	R120	E121	D124	Y125	R126	R134	N135	R136	D137	R138	M139	M140	S141	ASP	ASN	VAL	ALA	GLY	VAL	VAL	ALA	ALA	GLY	MET	LEU	LEU	ASP	ASP	SER	PRO	PHE	ILE	ILE	ALA	ALA	GLY	ILE	ALA	ALA	GLY	ARG	THR	GLY	LEU	ALA						
VAL	ARG	SER	ALA	ILE	ARG	E264	E265	L266	A267	V272	Q273	N276	V277	V280	K283	A284	H285	H286	T287	T288	Q289	S293	T294	G295	T296	L297	T298	R299	G300	Q301	E302	V303	L304	L305	D306	A307	I308	E309	P310	V311	V312	R313	D314	V315	D316	F317	T318	M320	A321	G322	T323	D324	A328	R329				
N335	P336	D337	N338	E425	M426	L427	A431	V345	P350	A351	E354	G355	T360	V361	G362	L365	R366	A367	A368	D369	A370	A375	E379	R387	A388	L389	D390	A391	D392	P393	S394	L395	V396	E397	R398	L399	K400	Q403	E404	H405	L406	A410	N411	L412	K413	G414	E415	Y418										
D422	P423	H424	E425	M426	L427	A431	R442	S445	Q446	T447	A448	K450	S451	V452	L453	A459	Q462	A463	F464	G465	I466	THR	ALA	ARG	GLY	SER	S472	L473	D474	D475	T479	F480	E481	K485	W486	S487	E497	F498	D501	B504	E508	L511	R512	E513	Q514													
N515	E516	F517	R533	D539	G544	S545	E546	D547	R550	D555	S558	R562	V566	M577	L600	S601	H605	R613	A614	D615	L616	E617	S618	R619	H622	Y628	D629	L632	N633	E641	A642	D643	S654	R659	W660	H661	M664	L670	D671																			
D672	A673	D674	V675	L676	K677	S687	K690	L691	R692	E697	L707	F708	R709	D714	N718	I719	E720	P721	E722	V723	V724	V727	D733	G734	N737	G738	R739	A740	A741	G742	G744	F745	M746	W747	R748	G749	L750	I751	W752	G753	M754	S755	E756	D757	E758	L759	W760	G761	A762									
M763	R764	M765	A766	S769	D770	S771	A772	I773	M774	S775	F776	A777	A778	ALA	ASN	LEU	ARG	SER	SER	GLY	THR	ALA	ASN	PRO	ALA	ARG	ASN	LEU	ARG	H795	R796	L797	R798	M806	M812	R813	M814	Q815	T820	Y829	R832	M833	R836	M839	S845	D846	L847	K848	T849	L850								
E851	T852	M853	L854	N855	A856	S857	K858	H859	S860	V861	A862	N863	P864	E865	R869	F877	L878	L879	G880	G881	M882	P883	A884	D885	A886	N887	L888	P889	D890	M891	L892	R893	K905	D914	T915	N924	R929	E933	Q934	P935	W936	F937	K938	E939	Y943	D948	M949	S950	E951	R952								
L953	R958	Q962	R963	F970	A974	Q983	T1116	P985	W986	T990	A996	V1000	V1011	N1012	I1017	V1018	A1019	D1020	E1031	K1038	D1042	R1043	E1053	N1056	P1057	E1064	L1065	Q1066	M1067	Q1068	G1073	M1076	M1077	D1078	E1088	L1089	S1090	H1091	F1092	A1093																		
Q1094	F1095	I1102	F1105	Q1106	S1107	V1110	K1115	T1116	L1117	P1118	R1119	W1126	L1129	T1132	M1133	Q1136	F1137	P1138	L1139	M1140	A1146	M1150	D1151	G1152	K1153	D1154	T1155	D1156	T1157	R1158	L1159	L1160	V1161	T1162	E1163	M1168	T1171	T1174	S1175	L1176	L1177	Q1178	L1199	L1200														
Q1204	D1205	T1208	M1211	D1212	I1213	K1214	T1215	F1216	T1217	K1218	I1223	Q1224	P1228	I1232	N1236	F1236	G1237	ASP	ASP																																							

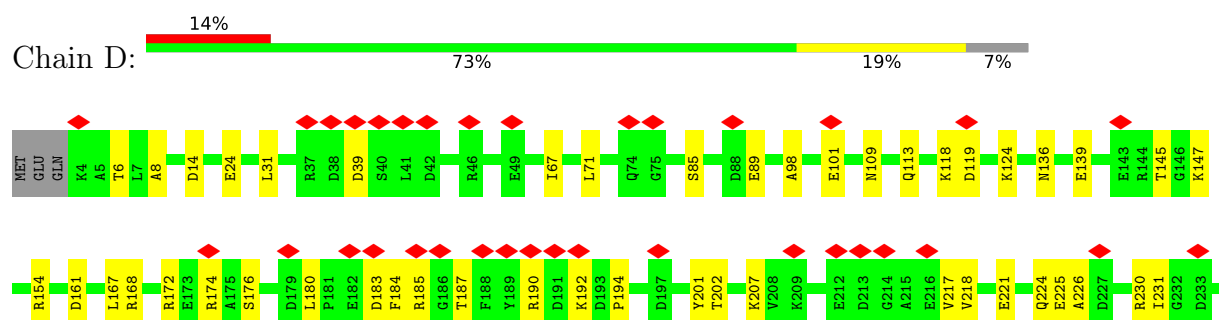
- Molecule 4: portal gp19

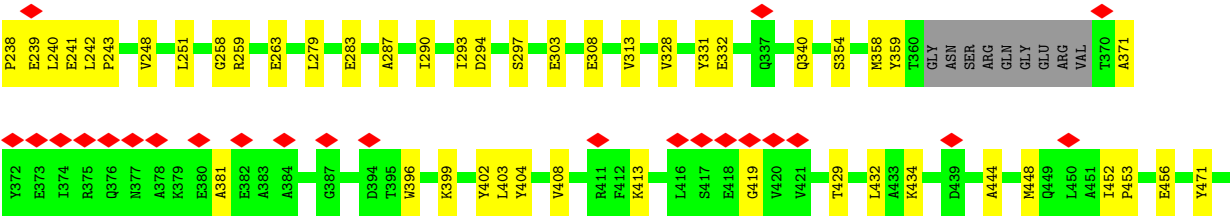


- Molecule 4: portal gp19

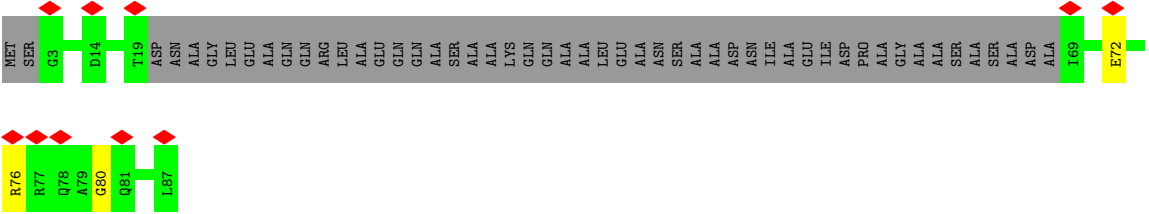


- Molecule 4: portal gp19

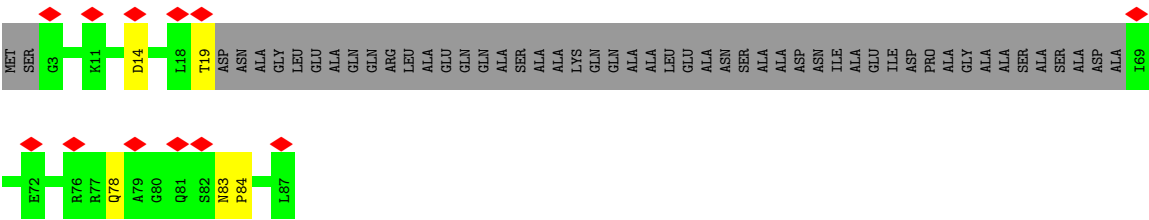
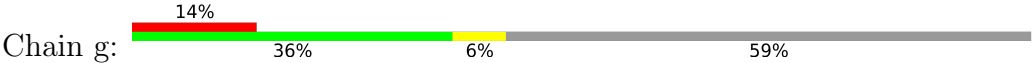




• Molecule 5: gp20



• Molecule 5: gp20



4 Experimental information

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 ($e^-/\text{\AA}^2$)	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 [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	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 [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	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.

The worst 5 of 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

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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
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. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	451	ASN
4	A	422	ASN
1	G	584	ASN
1	G	744	ASN
4	A	493	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.

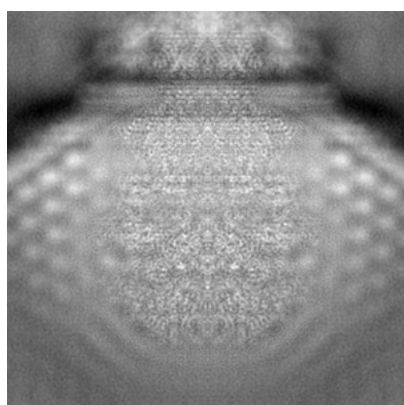
6 Map visualisation [i](#)

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

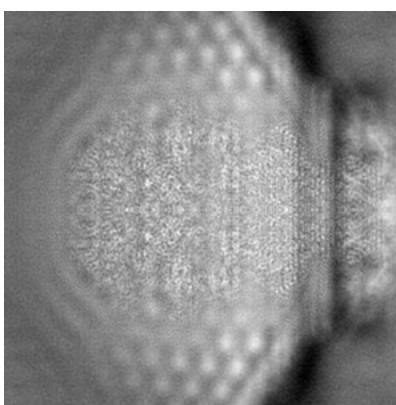
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

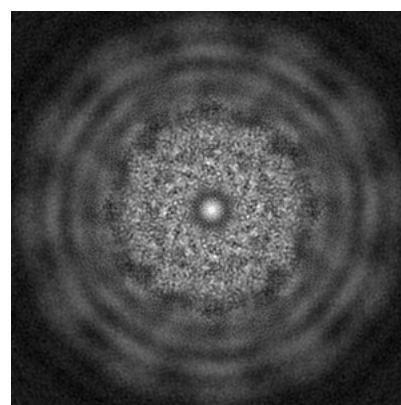
6.1.1 Primary map



X



Y

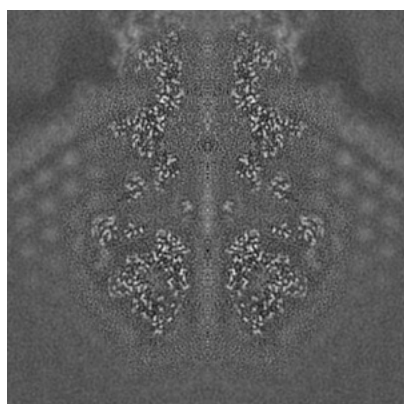


Z

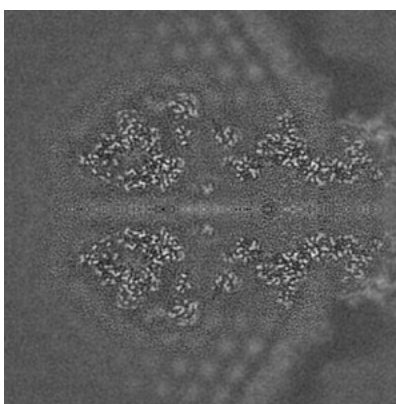
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

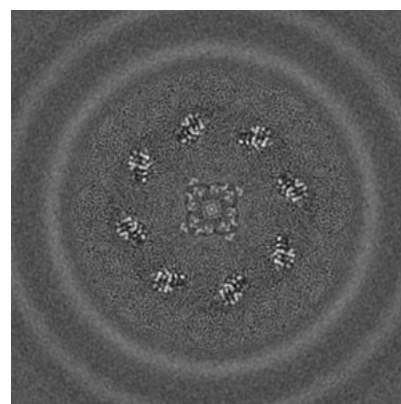
6.2.1 Primary map



X Index: 144



Y Index: 144

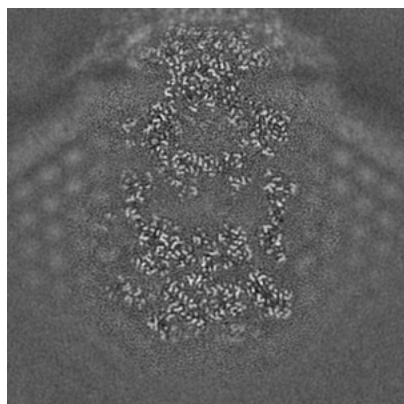


Z Index: 144

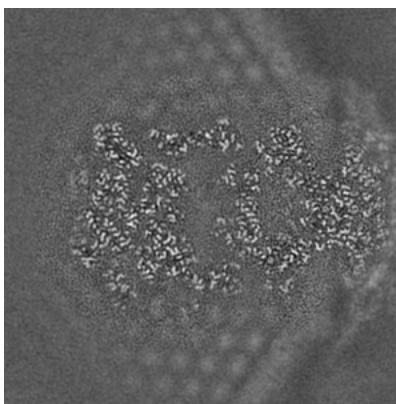
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

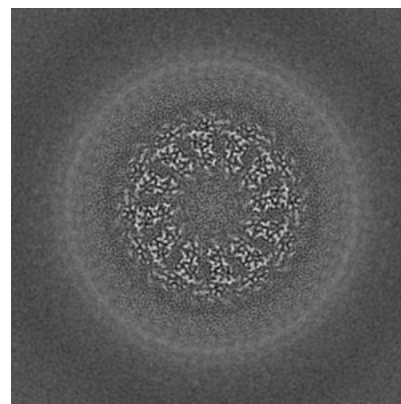
6.3.1 Primary map



X Index: 167



Y Index: 121

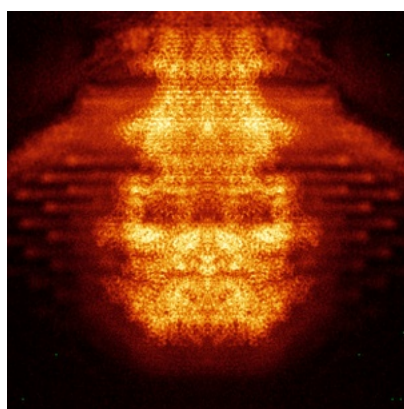


Z Index: 206

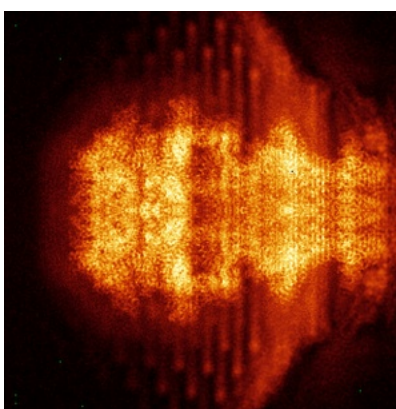
The images above show the largest variance slices of the map in three orthogonal directions.

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

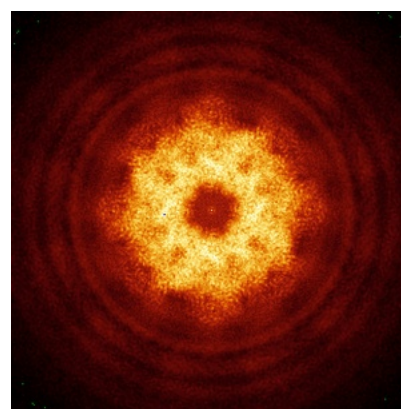
6.4.1 Primary map



X



Y

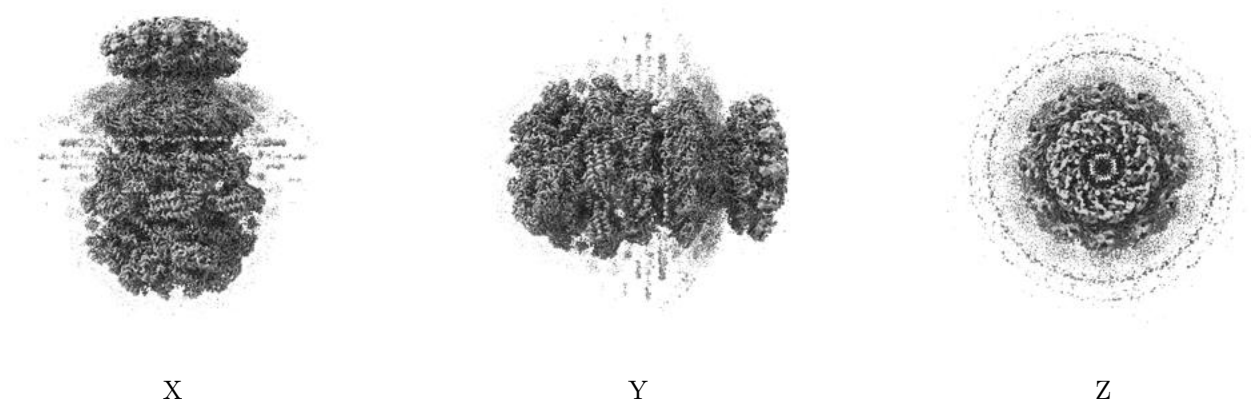


Z

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



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.

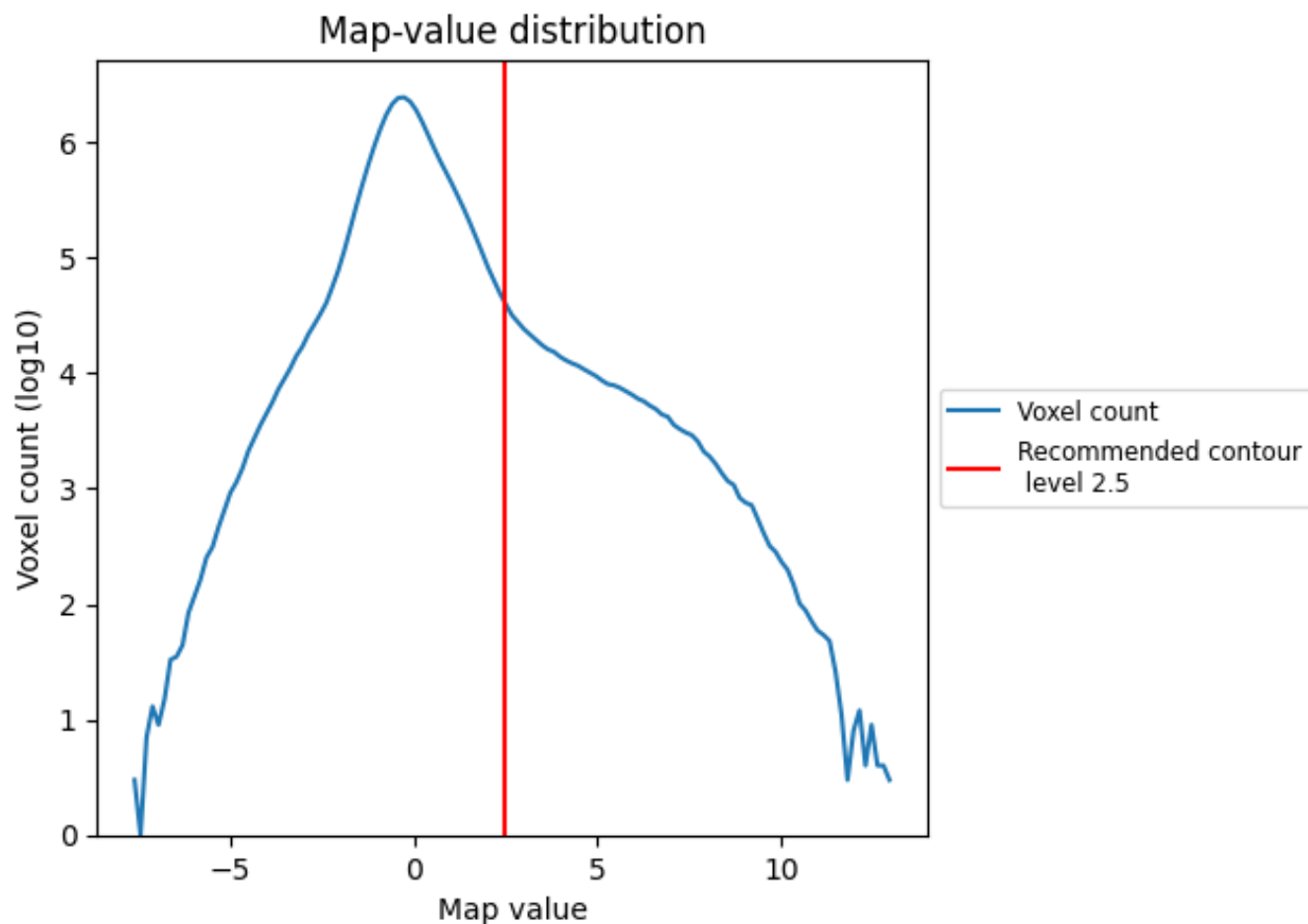
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

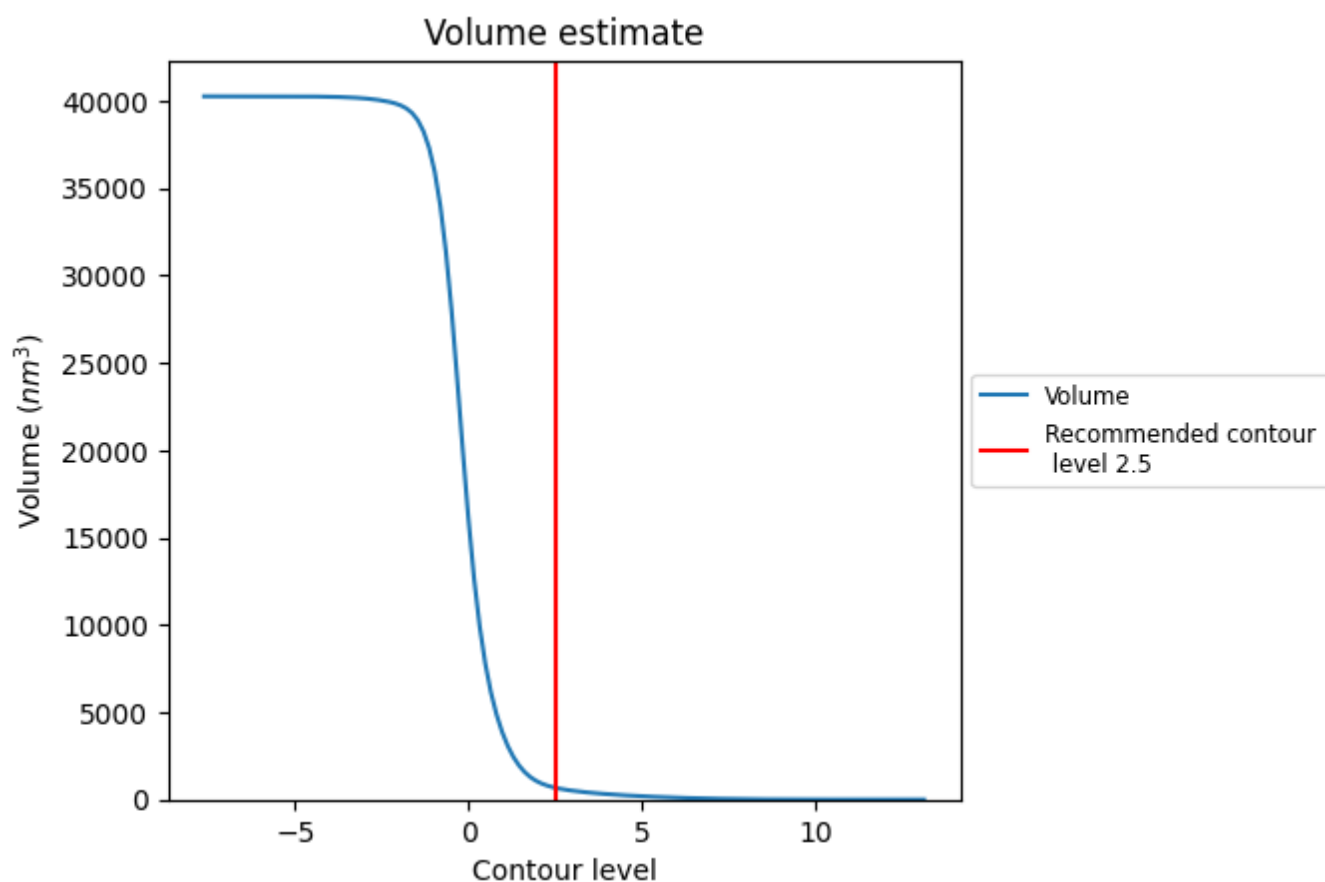
This section contains the results of statistical analysis of the map.

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.

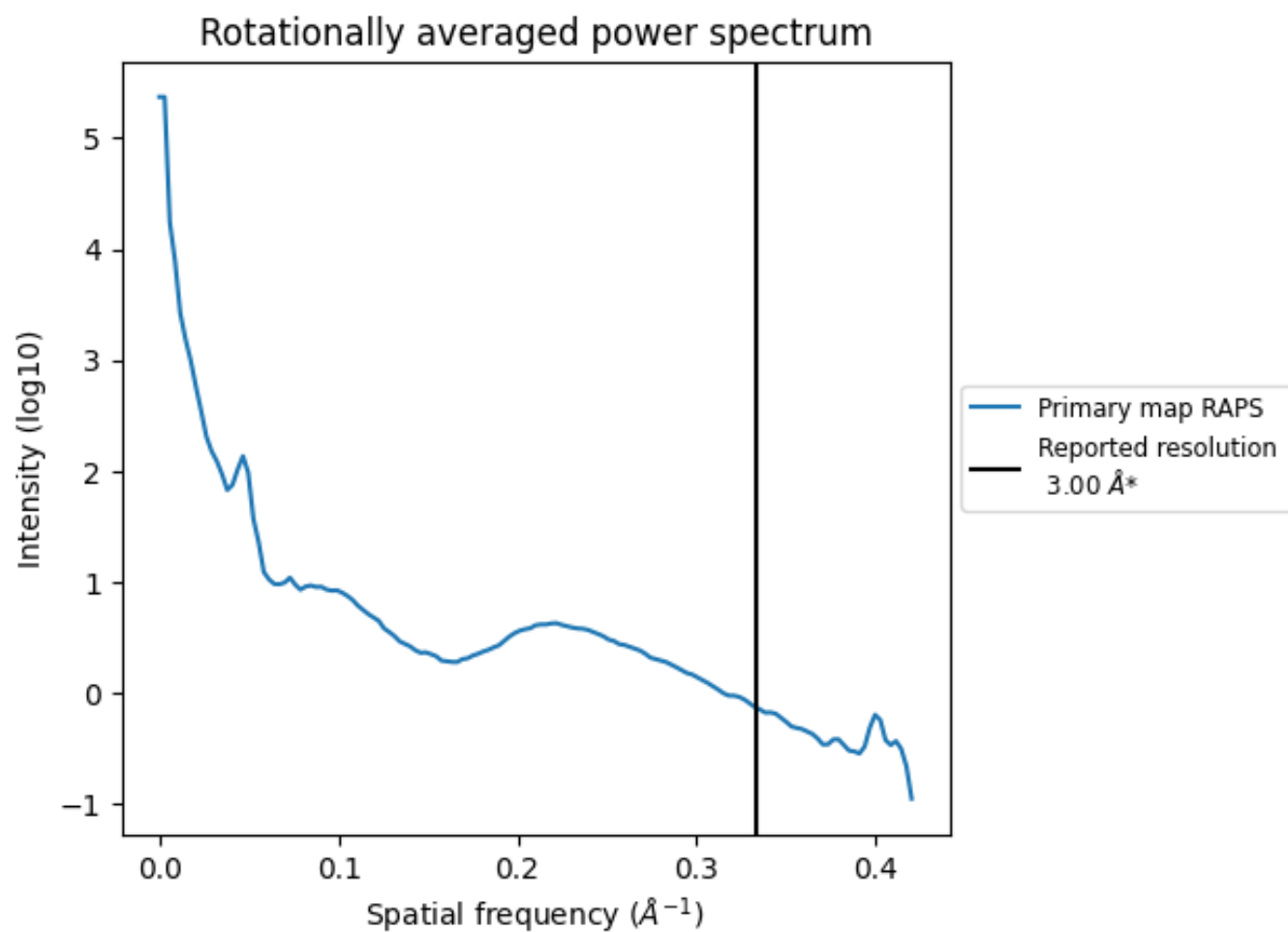
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 679 nm³; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation

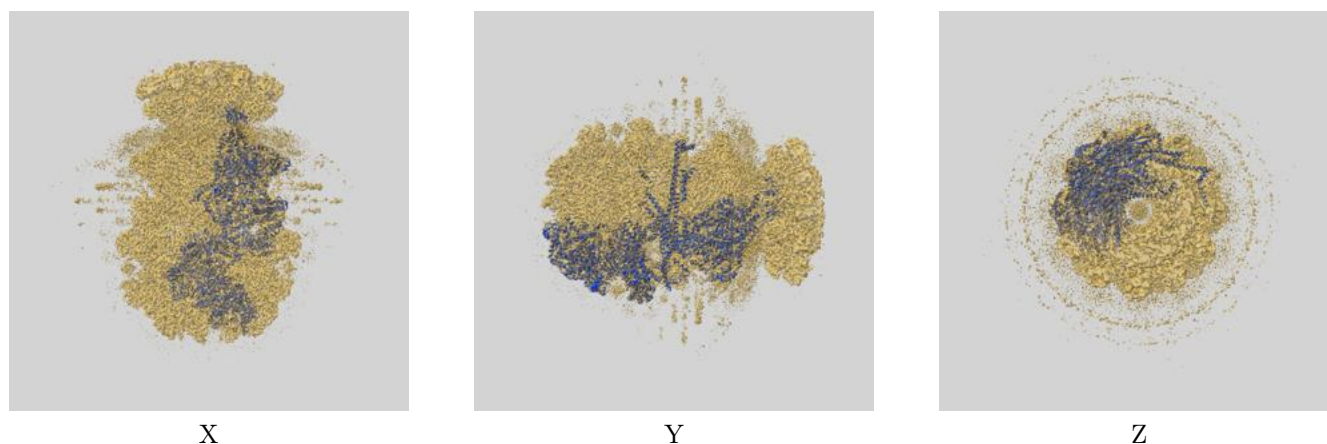
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit ⓘ

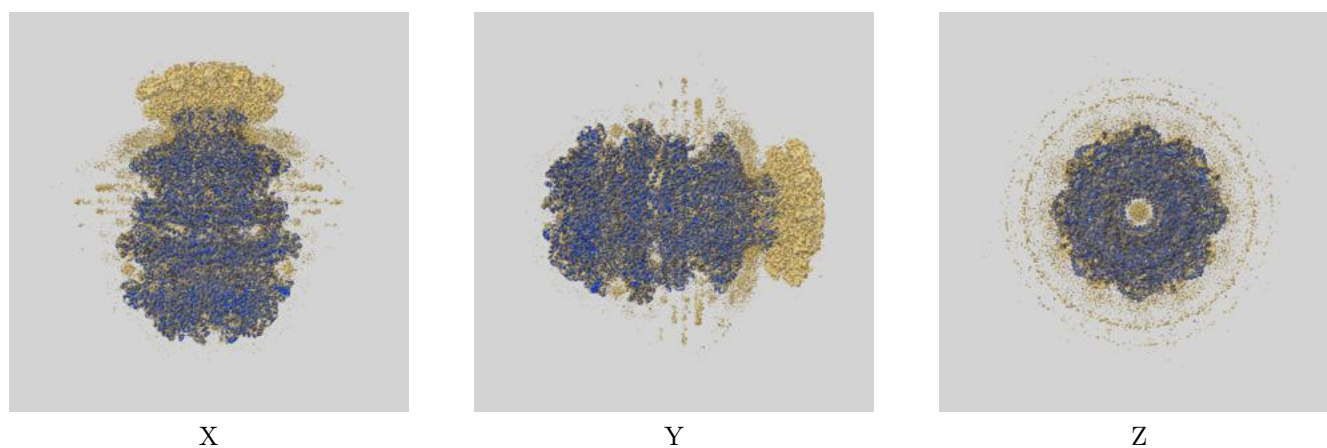
This section contains information regarding the fit between EMDB map EMD-69208 and PDB model 23SG. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

9.1.1 Map-model overlay ⓘ

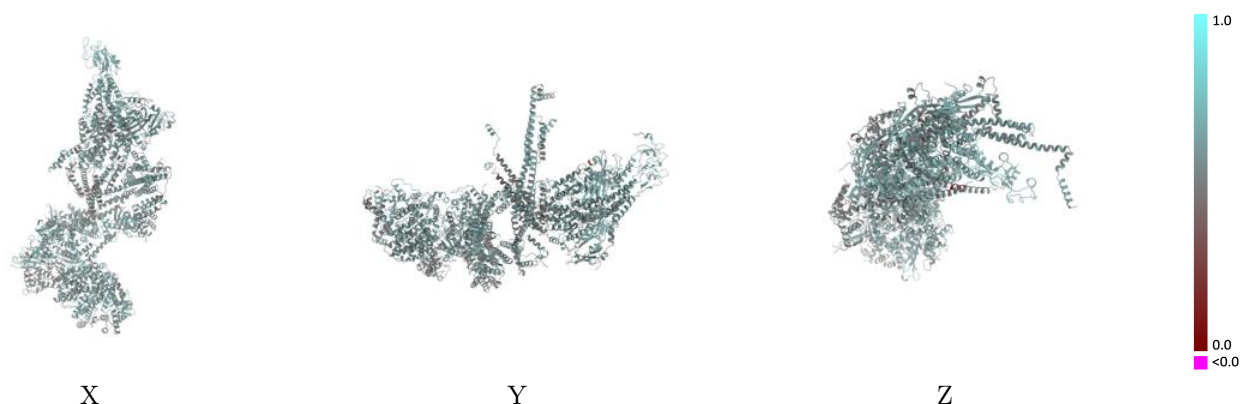


9.1.2 Map-model assembly overlay ⓘ



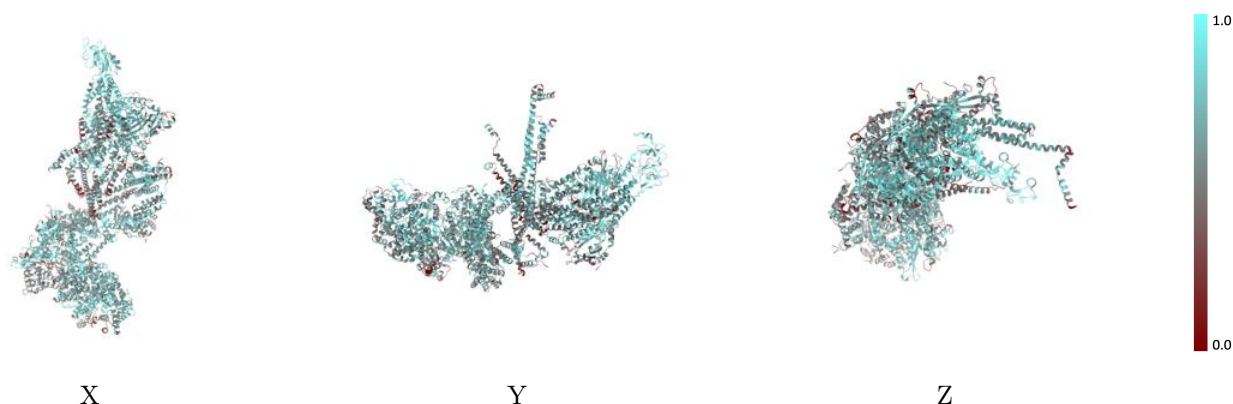
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



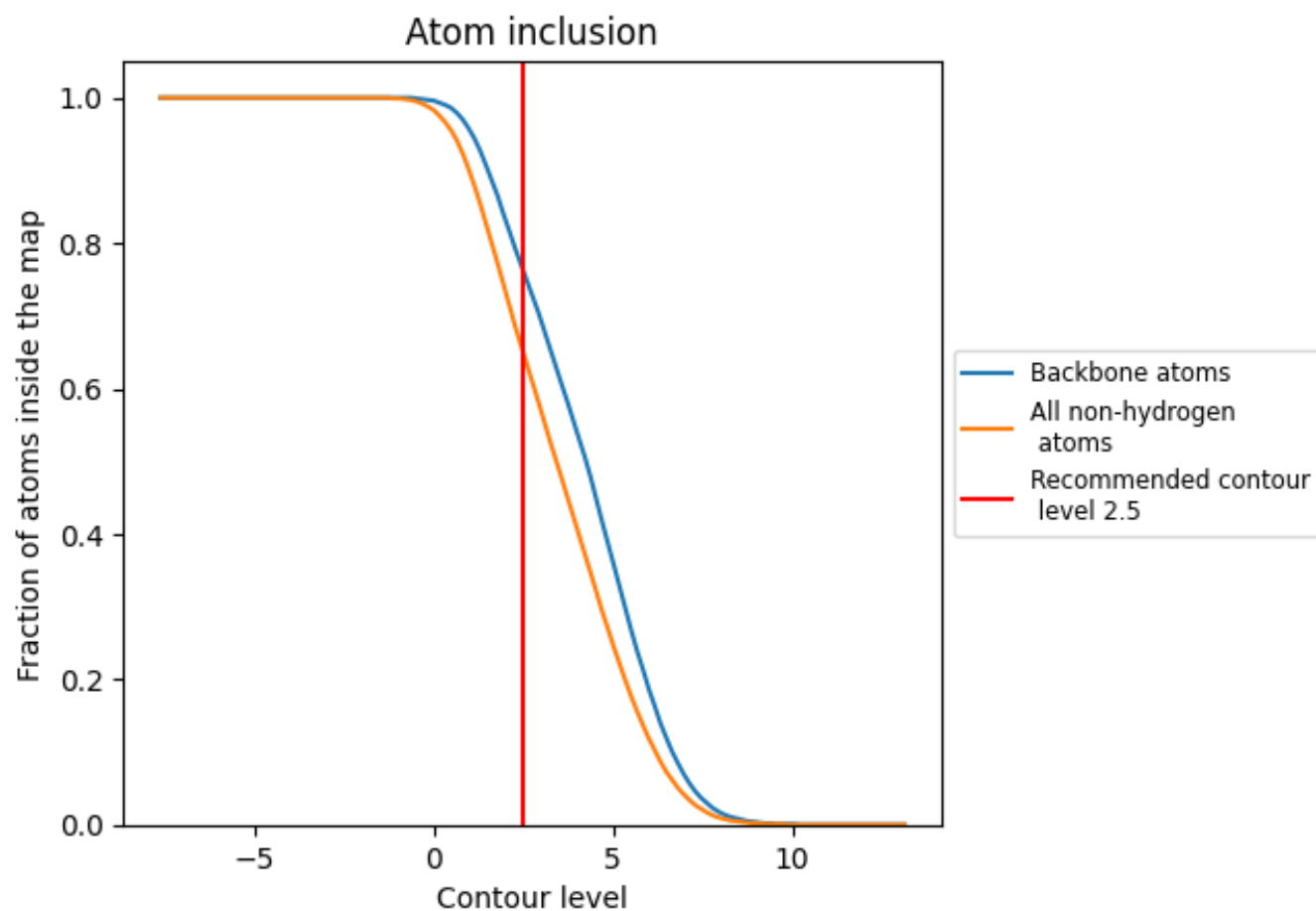
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (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	<div></div> 0.6500	<div></div> 0.5710
A	<div></div> 0.6730	<div></div> 0.5820
D	<div></div> 0.6590	<div></div> 0.5780
G	<div></div> 0.6800	<div></div> 0.5760
N	<div></div> 0.6900	<div></div> 0.5810
S	<div></div> 0.6220	<div></div> 0.5610
X	<div></div> 0.4780	<div></div> 0.5200
a	<div></div> 0.4800	<div></div> 0.5170
d	<div></div> 0.6790	<div></div> 0.5820
g	<div></div> 0.5390	<div></div> 0.5730
m	<div></div> 0.5390	<div></div> 0.5500

1.0

0.0

<0.0