



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:58 AM UTC

PDB ID : 6YLF / pdb_00006ylf
EMDB ID : EMD-10837
Title : Rix1-Rea1 pre-60S particle - Rea1, body 3 (rigid body refinement, composite structure of Rea1 ring and tail)
Authors : Kater, L.; Beckmann, R.
Deposited on : 2020-04-07
Resolution : 4.20 Å (reported)
Based on initial models : 6OR5, 6HYD, 6QTA, 6HYP

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

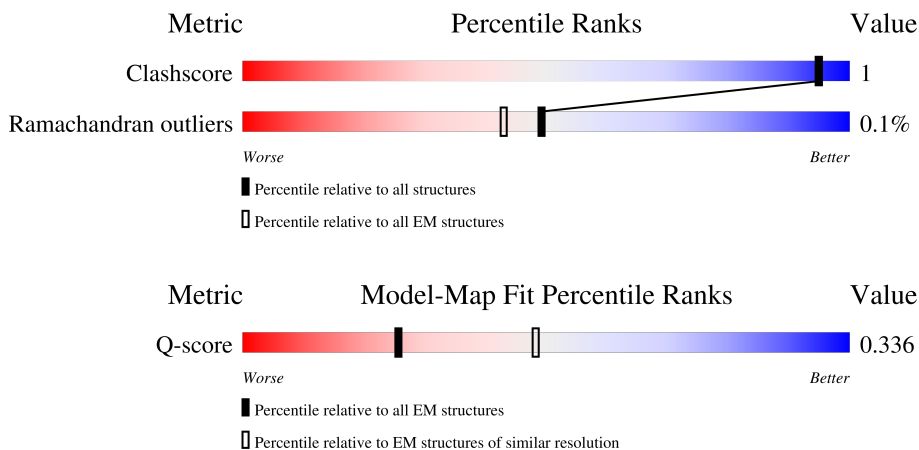
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	AP1	4910	
2	xP1	515	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18362 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 Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	AP1	3629	Total	C	N	O	0	0
			18010	10752	3629	3629		

- Molecule 2 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	xP1	71	Total	C	N	O	0	0
			352	210	71	71		

- Molecule 1: Midasin



PRO	ASP	TYR	GLU	ASP	THR	ALA	LEU	VAL	THR	THR	ASN	GLU	LYS	ASP	ILE	SER	PRO	GLU	N3202	T3274	VAL	PHE	GLY	ASN	I3280	V3305	L3309	K3310	Q3311	A3338	S3359	S3360	F3417	VAL	SER	GLU	GLU	LYS	LYS	GLU	THR	ALA	PRO	N3427	A3511	D3515	V3516	Y3557	SER	ASN																
L2595	E2764	LYS	ASN	ALA	LYS	LEU	THR	THR	SER	F2772	V2785	S2789	T2861	E2862	E2863	K2864	T2865	V2871	E2875	D2966	P2969	Q2970	S2971	P2972	S3038	D3068	G3105	Q3156	GLU	GLU	ASN	GLU	GLU	LYS	LYS	SER	ASN	MET	PHE	LYS	PHE	ASN	ASP	ASN	SER	ASP	ASP	Y3174	F3182																	
S2058	Q2095	V2096	D2097	P2147	E2148	K2149	D2152	N2158	L2164	E2178	E2182	T2185	K2186	E2187	A2188	S2189	V2190	L2216	C2217	S2218	P2219	S2220	S2227	E2230	S2234	I2237	ASN	GLU	CYS	SER	GLN	GLU	ASP	GLY	Q2246	P2247	C2267	S2270	R2271	A2272	F2289	GLU	LEU																							
GLY	GLU	ASN	ILE	ASP	PHE	VAL	GLY	ILE	LYS	ILE	LYS	LEU	ASN	GLU	P2322	D2323	I2357	Y2415	A2418	Q2427	L2428	N2443	R2470	N2474	T2491	D2492	E2493	L2494	T2495	A2503	F2504	N2505	Q2506	R2507	K2510	N2511	T2512	P2513	C2539	T2560	A2561																									
GLN	ASP	GLU	VAL	GLY	MET	PHE	LYS	PRO	ARG	PHE	PRO	ASP	ALA	SER	SER	F1719	N1720	A1723	A1727	S1728	R1735	P1742	P1749	G1750	N1766	S1774	E1775	L1779	F1783	G1784	A1785	ASP	ALA	PRO	GLY	GLU	ARG	SER	GLY	GLU	THR	LEU	H1798																							
S1578	R1579	L1580	A1588	F1598	G1599	K1600	LYS	LEU	GLY	GLY	M1606	A1607	T1608	N1625	K1626	V1627	M1644	L1650	G1651	T1652	K1666	S1667	L1668	ARG	THR	GLU	CYS	ILE	ILE	GLN	LEU	LYS	LEU	CYS	GLY	ASP	LEU	GLU	LEU	GLN	GLN	ILE	GLU	THR	LEU	ILE	VAL	THR																		
V1508	L1509	E1510	P1511	E1512	R1513	S1514	L1515	L1516	L1517	A1518	E1519	GLN	SER	S1523	D1524	S1525	L1526	V1527	T1528	A1529	S1530	E1531	N1532	F1533	Q1534	F1535	F1536	A1537	P1541	G1542	G1543	D1544	Y1545	G1546	K1547	K1548	E1549	L1550	R1555	N1556	R1557	F1558	T1559	E1560	P1564	S1565	M1566	E1567	D1568	F1569	N1570	N1573	S1577													
LEU	GLN	GLN	TYR	SER	LYS	SER	ASN	ASN	ILE	ALA	GLU	ASP	VAL	GLN	LEU	GLU	ILE	GLN	LYS	LEU	ARG	ASP	SER	LEU	PHE	E1473	W1474	S1475	D1476	G1477	P1478	R1484	T1485	G1486	N1487	F1488	F1489	L1490	L1491	D1492	E1493	I1494	S1495	L1496	A1497	D1498	D1499	S1500	V1501	L1502	E1503															
T1370	G1371	C1372	G1373	K1374	Q1379	Q1383	L1389	I1390	T1391	L1392	H1395	Q1396	R1397	T1398	E1399	T1400	G1401	D1402	G1405	A1406	ARG	PRO	VAL	ARG	ASN	GLU	LYS	ILE	GLN	TYR	LYS	LEU	ILE	ALA	ASN	ASP	GLN	VAL	LEU	PHE	E1473	W1474	S1475	D1476	G1477	P1478	R1484	T1485	G1486	N1487	F1488	F1489	L1490	L1491	D1492	E1493	I1494	S1495	L1496	A1497	D1498	D1499	S1500	V1501	L1502	E1503
F1262	E1263	F1275	A1278	LEU	ARG	ASP	ALA	V1283	L1295	L1296	R1299	T1302	P1303	E1314	K1318	VAL	LYS	LEU	ASP	MET	ASP	GLN	TYR	ALA	SER	LEU	GLU	LYS	L1335	S1340	V1341	T1342	W1343	M1347	R1348	L1358	K1359	N1360	K1361	E1362	P1363	V1364	V1367	G1368	E1369																					
V1181	V1182	H1183	P1184	L1189	L1190	F1191	A1192	N1195	P1196	P1197	G1198	I1199	G1202	R1203	K1204	I1205	A1209	E1216	D1220	D1221	D1225	E1226	L1227	E1228	I1229	I1230	R1234	C1235	Q1236	I1237	Y1241	K1244	I1245	V1246	E1247	VAL	TYR	ARG	GLN	LEU	SER	ILE	GLU	ARG	SER	ALA	R1260	L1261																		
Q1116	E1117	Y1118	L1119	GLY	THR	TYR	VAL	THR	THR	ASP	ASP	THR	GLY	LYS	LEU	SER	PHE	LYS	GLU	G1135	V1136	L1137	V1138	E1139	R1142	K1143	W1146	I1147	V1148	L1149	D1150	L1154	A1155	P1156	T1157	D1158	V1159	L1160	E1161	A1162	L1163	M1164	L1167	D1168	D1169	M1170	R1171	E1172	L1173	F1174	I1175	P1176	E1177	T1178	Q1179	E1180										

CYS	SER	GLY	THR	TRP	ILE	ALA	HIS
SER	GLY	HIS	MET	VAL	TRP	THR	GLY
GLY	VAL	PHE	LEU	ASN	ASP	THR	SER
GLY	ALA	LEU	THR	HIS	THR	SER	THR
LYS	SER	TRP	ASN	LEU	VAL	MET	ILE
ASP	VAL	ASN	SER	SER	SER	ASP	LEU
LYS	TYR	PRO	PRO	LEU	ARG	THR	CYS
MET	GLN	LEU	LEU	SER	VAL	THR	SER
VAL	VAL	LYS	THR	THR	CYS	ILE	ALA
ARG	ALA	SER	ASP	ASN	GLN	ARG	PHE
LEU	LEU	THR	THR	TYR	THR	LEU	ALA
TRP	SER	LYS	LYS	ALA	THR	TRP	ALA
THR	SER	PRO	PRO	LEU	MET	ASP	PRO
HIS	ASP	ILE	ILE	MET	THR	ASP	HIS
	ASP	ASP	ASP	GLY	THR	THR	THR
	CYS	CYS	ARG	GLY	HIS	LYS	VAL
	ARG	ARG	ARG	THR	ASN	GLN	LYS
	LEU	LEU	MET	ALA	HIS	GLY	ARG
	LEU	THR	THR	PHE	ASN	GLN	MET
	VAL	GLY	GLY	ASP	SER	CYS	VAL
	SER	SER	HIS	HIS	VAL	LEU	THR
	CYS	CYS	GLN	THR	SER	GLY	GLY
	LYS	LYS	LEU	LYS	VAL	ALA	ALA
	ASP	ASP	VAL	LYS	LEU	LYS	GLY
	THR	THR	ASN	PRO	TRP	ARG	ASN
	LEU	VAL	VAL	SER	GLY	GLY	THR
	LYS	LYS	ALA	THR	THR	THR	ALA
	VAL	VAL	PHE	VAL	VAL	HIS	ALA
	ASP	ASP	THR	GLY	ARG	LEU	VAL
	ARG	ARG	TYR	ILE	SER	THR	THR
	LYS	LYS	ILE	ASP	GLU	PRO	GLU
	VAL	VAL	ALA	ASN	ARG	GLU	MET
	LEU	LEU	ALA	THR	THR	ILE	HIS
	ASP	ASP	SER	THR	ASP	ILE	THR
	GLU	LEU	PHE	LYS	ARG	VAL	THR
	VAL	PRO	ASP	ILE	VAL	VAL	GLY
	TYR	THR	ASN	CYS	TRP	LYS	LYS
	ASP	LYS	ILE	LYS	ASP	PRO	ASN
	GLY	GLY	LYS	ILE	GLY	GLY	TYR
	HIS	HIS	THR	THR	GLY	THR	ASN
	ASP	ASP	LYS	ASN	ASN	SER	TRP
	GLY	GLY	THR	SER	LYS	VAL	VAL
	VAL	VAL	THR	GLN	PRO	GLY	LEU
	TYR	THR	GLY	ARG	LEU	CYS	VAL
	VAL	VAL	ARG	CYS	THR	VAL	PHE
	ASP	ASP	ASP	ILE	ASN	VAL	LYS
	THR	THR	THR	THR	THR	THR	THR
	LYS	LYS	THR	ALA	THR	THR	GLY
	ARG	ARG	PHE	ASP	HIS	GLI	ARG
	VAL	VAL	THR	ASP	VAL	VAL	SER
	GLY	GLY	THR	THR	THR	THR	SER
	ASP	ASP	THR	THR	THR	THR	SER
	VAL	VAL	THR	THR	THR	THR	ALA
	ALA	ALA	LYS	ILE	ILE	ILE	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	55397	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.143	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	370.65, 370.65, 370.65	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	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	AP1	0.30	0/17970	0.68	3/25013 (0.0%)
2	xP1	0.26	0/346	0.56	0/473
All	All	0.30	0/18316	0.68	3/25486 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AP1	0	14

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	AP1	3567	PRO	N-CA-CB	7.94	111.14	102.72
1	AP1	3594	PRO	N-CA-CB	7.11	110.72	103.25
1	AP1	255	ILE	CA-C-O	-5.47	114.64	120.39

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AP1	223	LEU	Peptide
1	AP1	406	GLU	Peptide
1	AP1	947	ASN	Peptide
1	AP1	948	THR	Peptide
1	AP1	95	ILE	Peptide

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	AP1	18010	0	7839	27	0
2	xP1	352	0	145	1	0
All	All	18362	0	7984	28	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 1.

The worst 5 of 28 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:AP1:263:LYS:HA	1:AP1:274:LYS:O	1.74	0.87
1:AP1:263:LYS:CA	1:AP1:274:LYS:O	2.40	0.69
1:AP1:263:LYS:CB	1:AP1:274:LYS:O	2.45	0.65
1:AP1:1779:LEU:O	1:AP1:1783:PHE:N	2.30	0.64
1:AP1:2178:GLU:O	1:AP1:2182:GLU:N	2.37	0.57

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	AP1	3549/4910 (72%)	3232 (91%)	313 (9%)	4 (0%)	48	82
2	xP1	59/515 (12%)	53 (90%)	6 (10%)	0	100	100
All	All	3608/5425 (66%)	3285 (91%)	319 (9%)	4 (0%)	49	82

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AP1	241	PRO
1	AP1	3594	PRO
1	AP1	280	ASP
1	AP1	948	THR

5.3.2 Protein sidechains [i](#)

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

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AP1	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AP1	3595:LEU	C	3599:ARG	N	4.97
1	AP1	3575:LEU	C	3579:VAL	N	3.43
1	AP1	3587:MET	C	3591:ARG	N	3.23

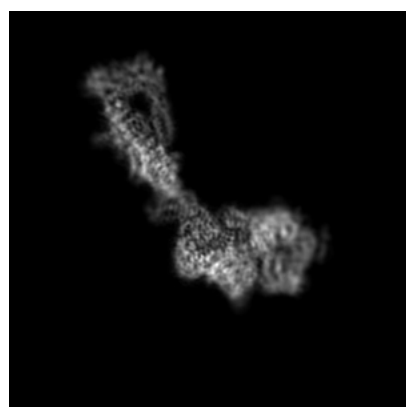
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10837. These allow visual inspection of the internal detail of the map and identification of artifacts.

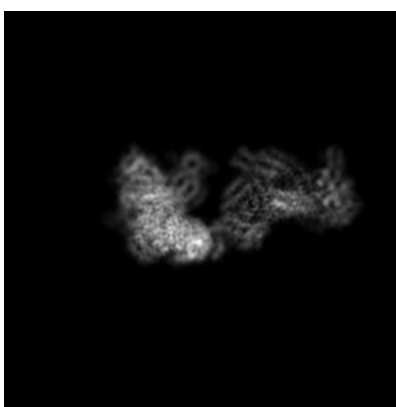
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

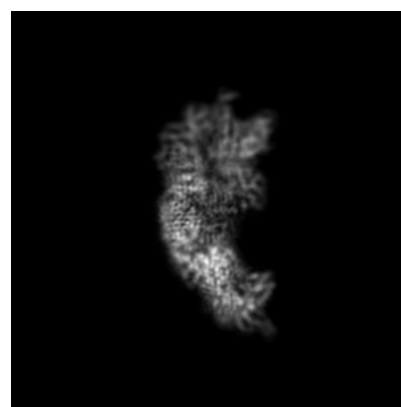
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

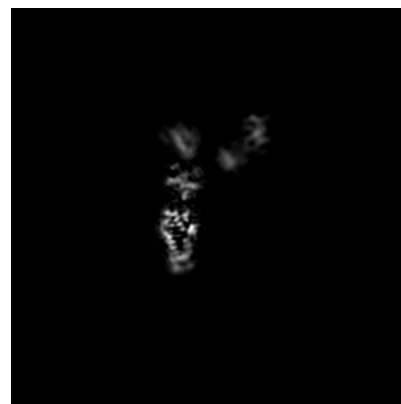
6.2.1 Primary map



X Index: 175



Y Index: 175



Z Index: 175

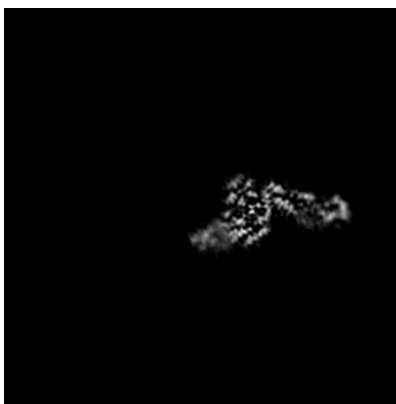
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

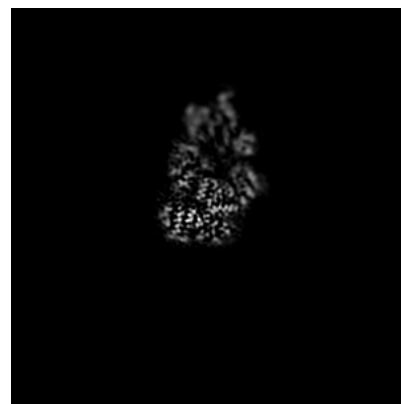
6.3.1 Primary map



X Index: 188



Y Index: 132

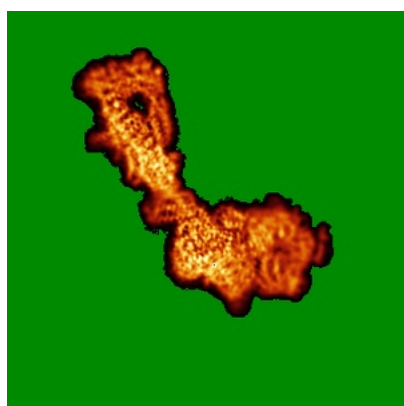


Z Index: 133

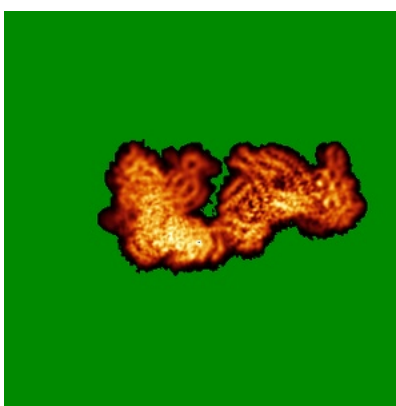
The images above show the largest variance slices of the map in three orthogonal directions.

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

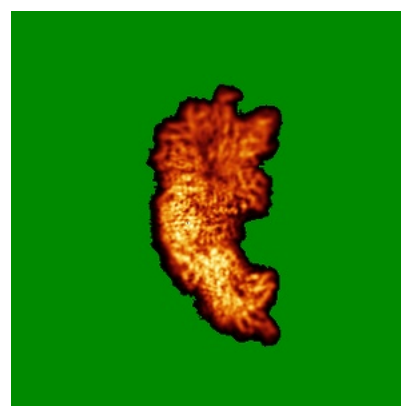
6.4.1 Primary map



X



Y

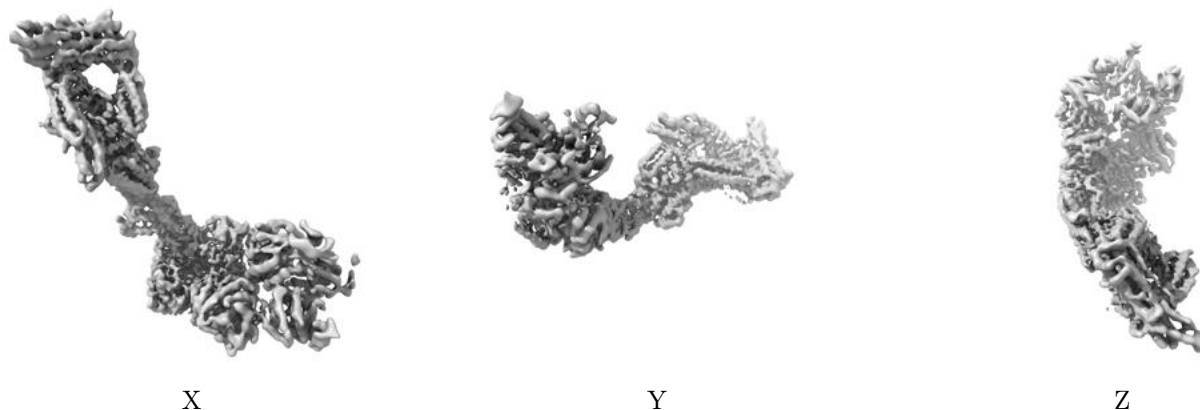


Z

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

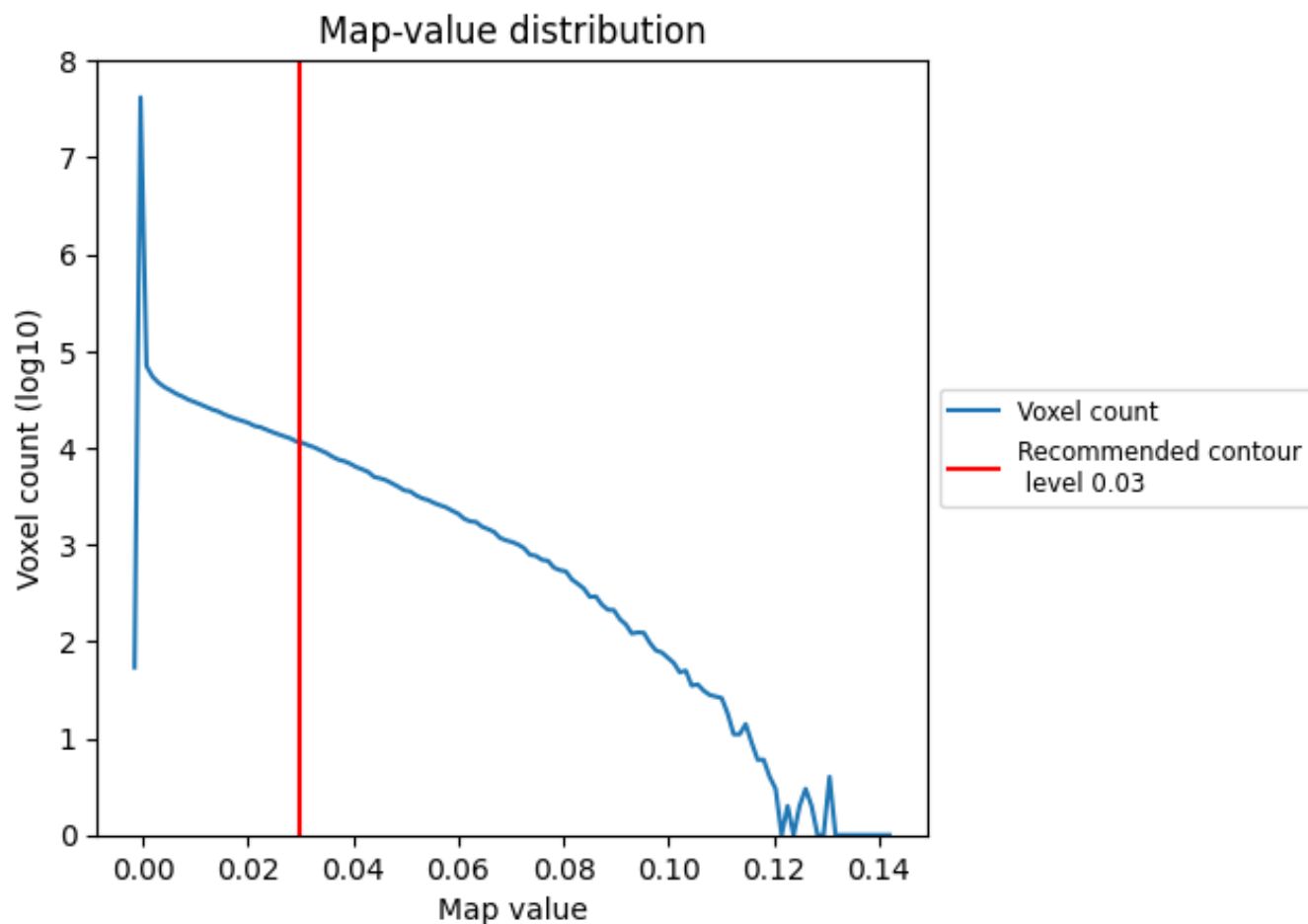
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

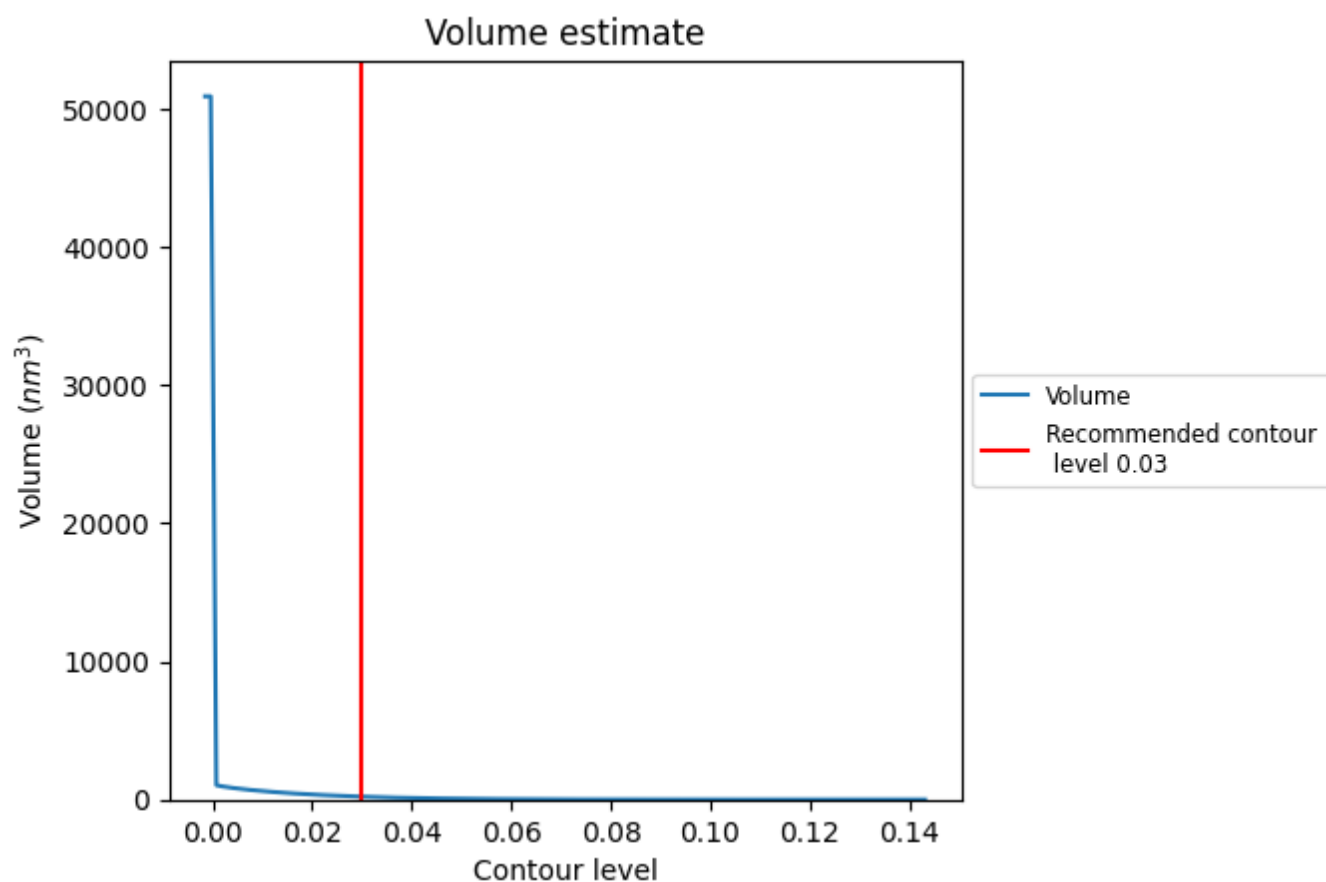
This section contains the results of statistical analysis of the map.

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.

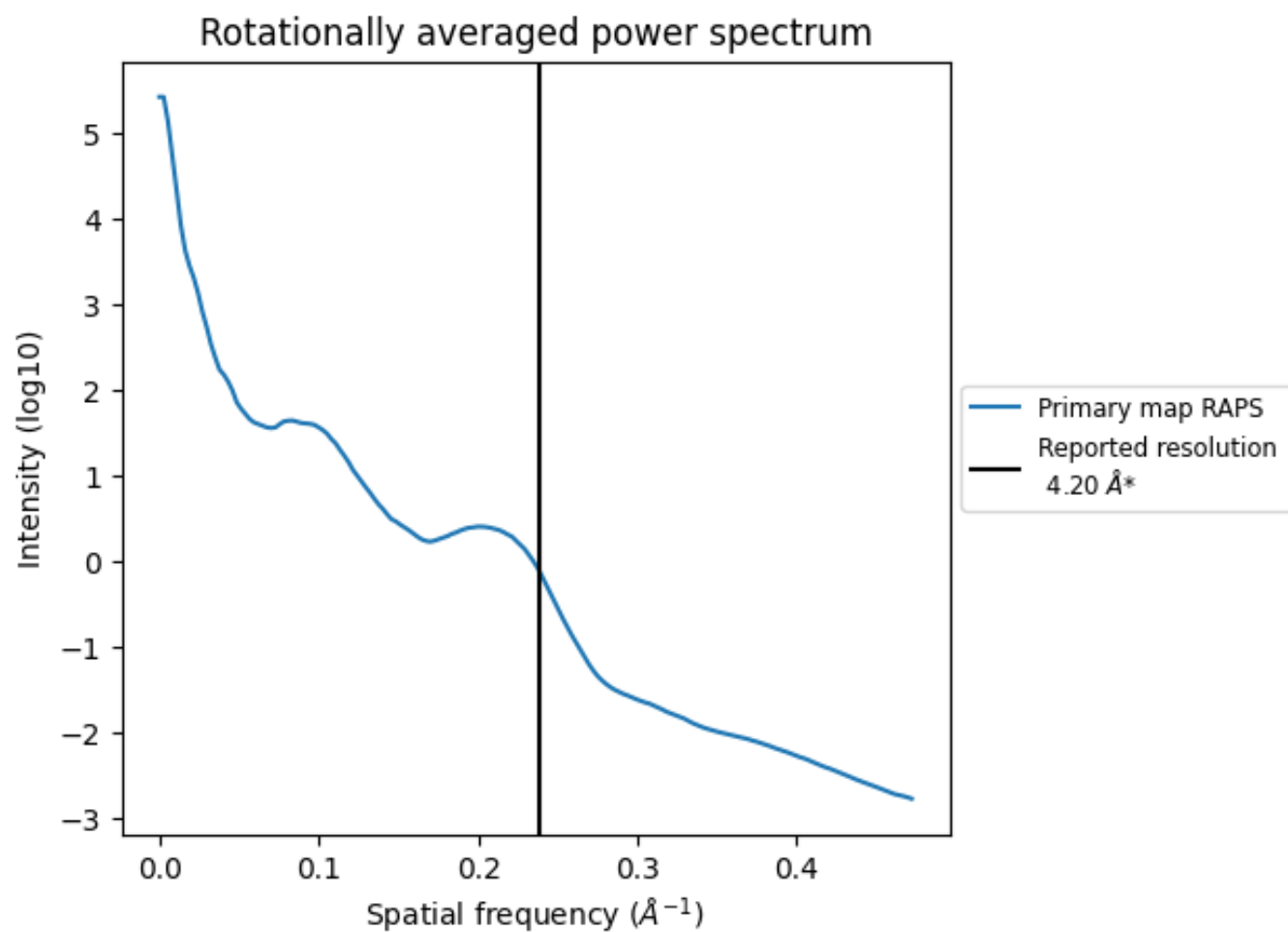
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 210 nm^3 ; this corresponds to an approximate mass of 189 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 0.238 Å⁻¹

8 Fourier-Shell correlation

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

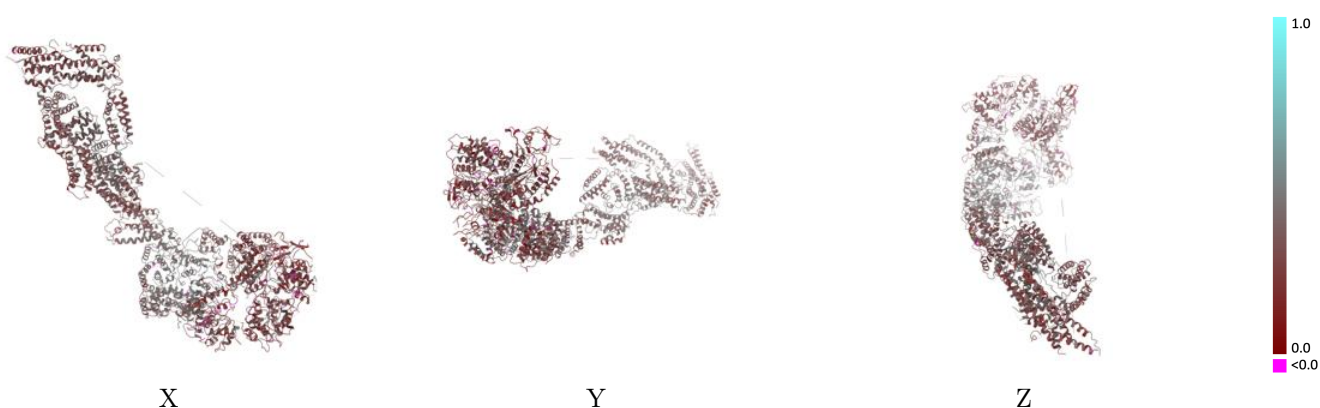
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10837 and PDB model 6YLF. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

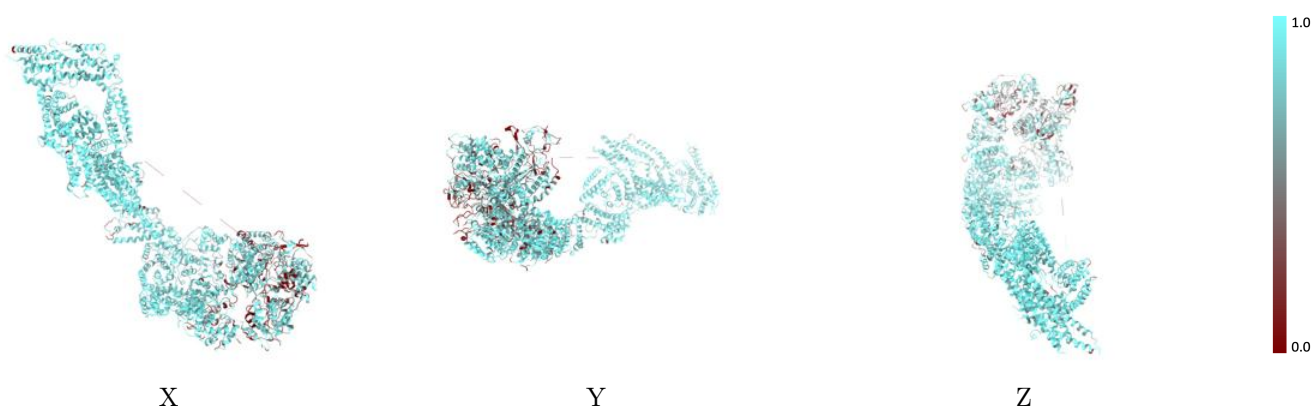
This section was not generated.

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



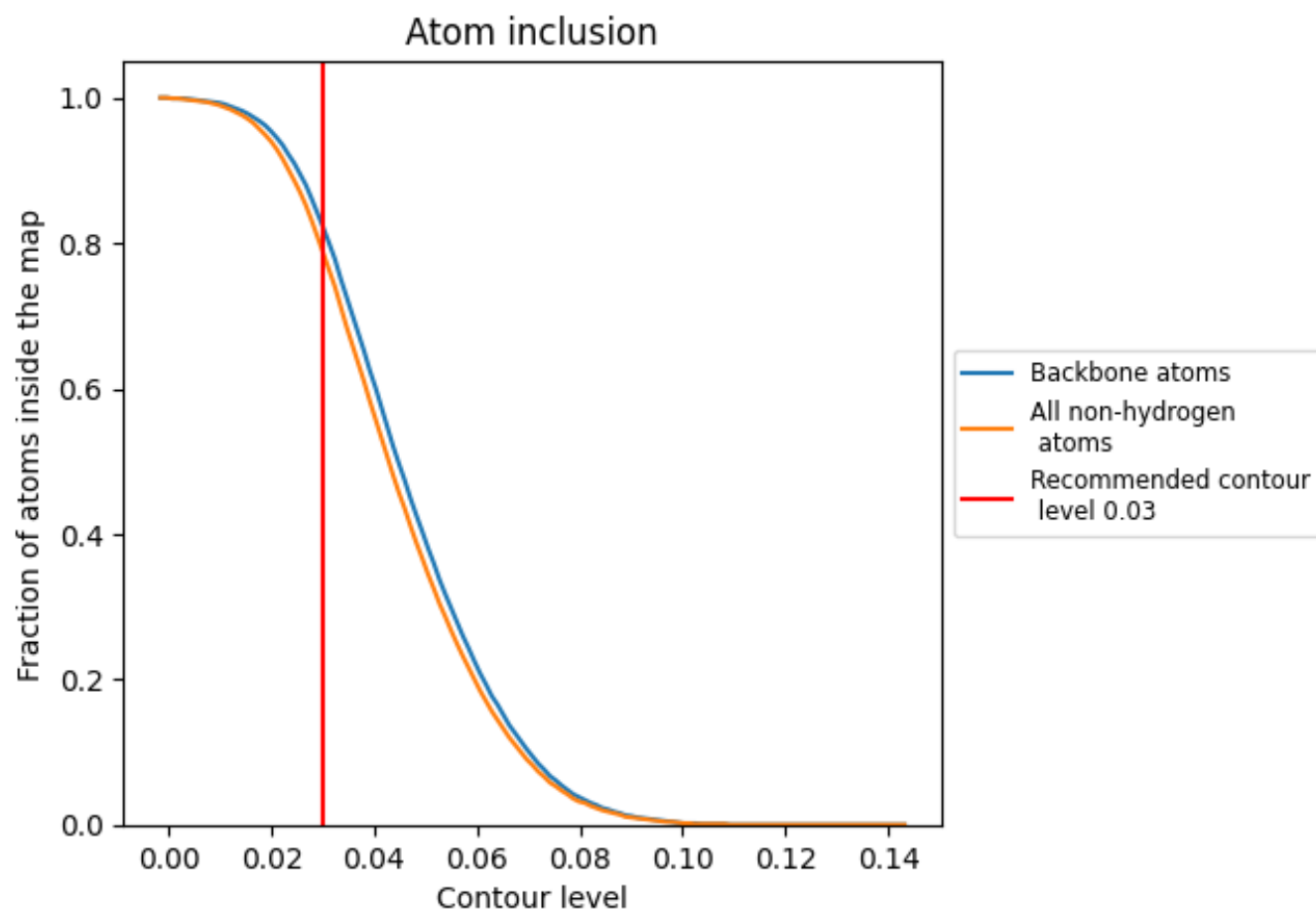
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 79% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7890	0.3360
AP1	0.7950	0.3380
xP1	0.4800	0.2400

