



wwPDB EM Validation Summary Report ⓘ

Mar 3, 2025 – 04:39 PM JST

PDB ID : 9L3W
EMDB ID : EMD-62793
Title : Cryo-EM structure of the chemokine-like receptor 1 in complex with chemerin and Gi1
Authors : Zhu, Y.; He, M.; Wu, B.; Zhao, Q.
Deposited on : 2024-12-19
Resolution : 3.50 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.2

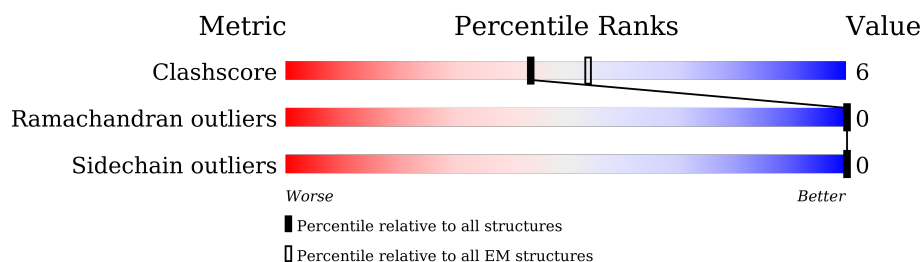
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	354	
2	B	340	
3	C	71	
4	L	137	
5	R	419	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7262 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 Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	205	Total	C	N	O	S	0	0
			1572	1007	259	293	13		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	CYS	SER	engineered mutation	UNP P63096
A	202	THR	GLY	engineered mutation	UNP P63096
A	203	ALA	GLY	engineered mutation	UNP P63096
A	245	ALA	GLU	engineered mutation	UNP P63096
A	326	SER	ALA	engineered mutation	UNP P63096

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	335	Total	C	N	O	S	0	0
			2487	1542	437	487	21		

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	54	Total	C	N	O	S	0	0
			353	224	63	64	2		

- Molecule 4 is a protein called Retinoic acid receptor responder protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	108	Total	C	N	O	S	0	0
			732	467	123	136	6		

- Molecule 5 is a protein called Chemerin-like receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	281	Total	C	N	O	S	0	0
			2118	1411	347	342	18		

There are 46 discrepancies between the modelled and reference sequences:

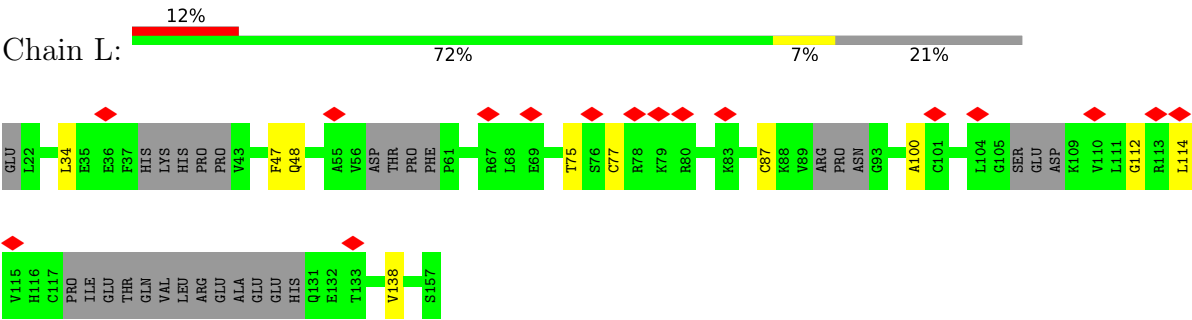
Chain	Residue	Modelled	Actual	Comment	Reference
R	374	GLU	-	expression tag	UNP Q99788
R	375	PHE	-	expression tag	UNP Q99788
R	376	LEU	-	expression tag	UNP Q99788
R	377	GLU	-	expression tag	UNP Q99788
R	378	VAL	-	expression tag	UNP Q99788
R	379	LEU	-	expression tag	UNP Q99788
R	380	PHE	-	expression tag	UNP Q99788
R	381	GLN	-	expression tag	UNP Q99788
R	382	GLY	-	expression tag	UNP Q99788
R	383	PRO	-	expression tag	UNP Q99788
R	384	TRP	-	expression tag	UNP Q99788
R	385	SER	-	expression tag	UNP Q99788
R	386	HIS	-	expression tag	UNP Q99788
R	387	PRO	-	expression tag	UNP Q99788
R	388	GLN	-	expression tag	UNP Q99788
R	389	PHE	-	expression tag	UNP Q99788
R	390	GLU	-	expression tag	UNP Q99788
R	391	LYS	-	expression tag	UNP Q99788
R	392	GLY	-	expression tag	UNP Q99788
R	393	GLY	-	expression tag	UNP Q99788
R	394	GLY	-	expression tag	UNP Q99788
R	395	SER	-	expression tag	UNP Q99788
R	396	GLY	-	expression tag	UNP Q99788
R	397	GLY	-	expression tag	UNP Q99788
R	398	GLY	-	expression tag	UNP Q99788
R	399	SER	-	expression tag	UNP Q99788
R	400	GLY	-	expression tag	UNP Q99788
R	401	GLY	-	expression tag	UNP Q99788
R	402	SER	-	expression tag	UNP Q99788
R	403	ALA	-	expression tag	UNP Q99788
R	404	TRP	-	expression tag	UNP Q99788
R	405	SER	-	expression tag	UNP Q99788
R	406	HIS	-	expression tag	UNP Q99788
R	407	PRO	-	expression tag	UNP Q99788
R	408	GLN	-	expression tag	UNP Q99788
R	409	PHE	-	expression tag	UNP Q99788
R	410	GLU	-	expression tag	UNP Q99788

Continued on next page...

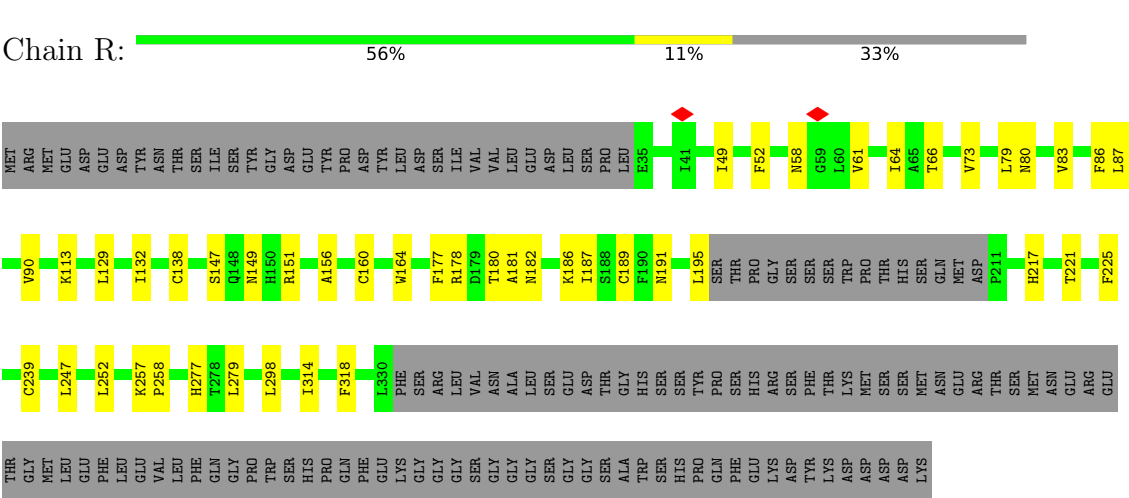
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	411	LYS	-	expression tag	UNP Q99788
R	412	ASP	-	expression tag	UNP Q99788
R	413	TYR	-	expression tag	UNP Q99788
R	414	LYS	-	expression tag	UNP Q99788
R	415	ASP	-	expression tag	UNP Q99788
R	416	ASP	-	expression tag	UNP Q99788
R	417	ASP	-	expression tag	UNP Q99788
R	418	ASP	-	expression tag	UNP Q99788
R	419	LYS	-	expression tag	UNP Q99788

● Molecule 4: Retinoic acid receptor responder protein 2



● Molecule 5: Chemerin-like receptor 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	89786	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.317	Depositor
Minimum map value	-2.172	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.071	Depositor
Recommended contour level	0.4	Depositor
Map size (\AA)	274.176, 274.176, 274.176	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.071, 1.071, 1.071	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.24	0/1597	0.41	0/2154
2	B	0.24	0/2534	0.51	0/3448
3	C	0.24	0/359	0.41	0/494
4	L	0.24	0/741	0.44	0/1004
5	R	0.24	0/2174	0.43	0/2969
All	All	0.24	0/7405	0.45	0/10069

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	A	1572	0	1482	21	0
2	B	2487	0	2331	38	0
3	C	353	0	312	4	0
4	L	732	0	629	5	0
5	R	2118	0	2097	31	0
All	All	7262	0	6851	89	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 6.

The worst 5 of 89 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)
2:B:271:CYS:HB2	2:B:290:ASP:HB2	1.74	0.70
1:A:196:PHE:HE2	1:A:339:VAL:HG21	1.58	0.69
2:B:161:SER:OG	2:B:163:ASP:OD1	2.12	0.68
5:R:80:ASN:ND2	5:R:160:CYS:SG	2.67	0.67
4:L:48:GLN:HB2	4:L:75:THR:HG21	1.76	0.67

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	195/354 (55%)	192 (98%)	3 (2%)	0	100	100
2	B	333/340 (98%)	325 (98%)	8 (2%)	0	100	100
3	C	52/71 (73%)	52 (100%)	0	0	100	100
4	L	96/137 (70%)	94 (98%)	2 (2%)	0	100	100
5	R	277/419 (66%)	261 (94%)	16 (6%)	0	100	100
All	All	953/1321 (72%)	924 (97%)	29 (3%)	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	A	161/306 (53%)	161 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	258/283 (91%)	258 (100%)	0	100	100
3	C	27/58 (47%)	27 (100%)	0	100	100
4	L	64/121 (53%)	64 (100%)	0	100	100
5	R	217/375 (58%)	217 (100%)	0	100	100
All	All	727/1143 (64%)	727 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
4	L	153	GLN
5	R	80	ASN
5	R	217	HIS

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 ⓘ

There are no chain breaks in this entry.

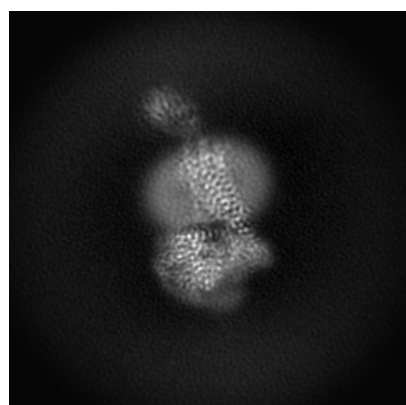
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62793. These allow visual inspection of the internal detail of the map and identification of artifacts.

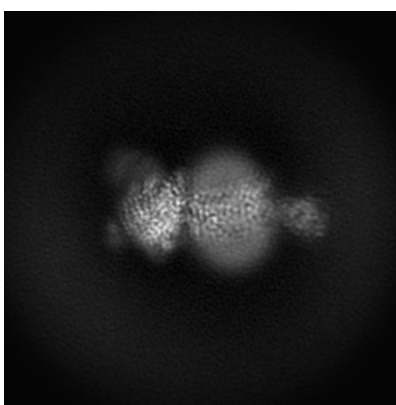
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

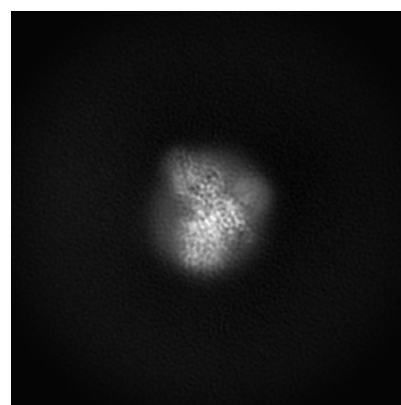
6.1.1 Primary map



X



Y

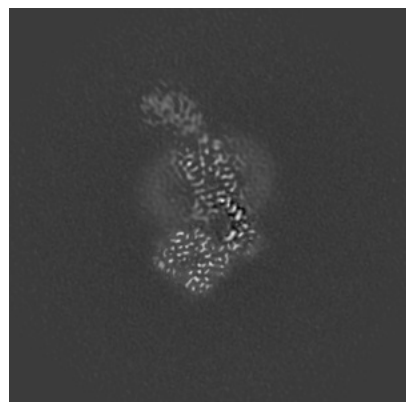


Z

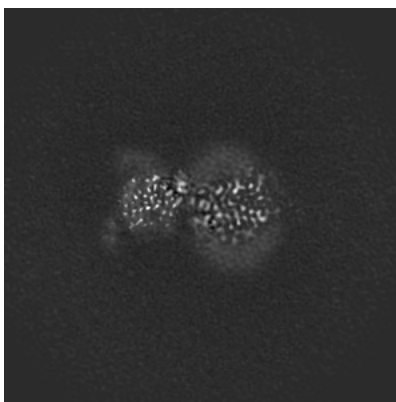
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

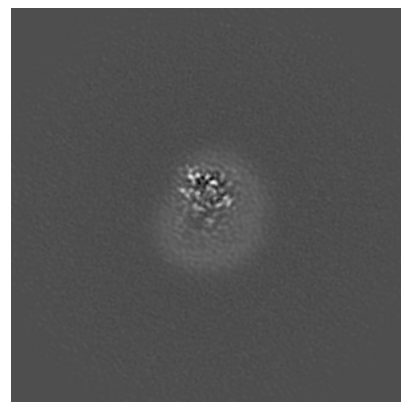
6.2.1 Primary map



X Index: 128



Y Index: 128

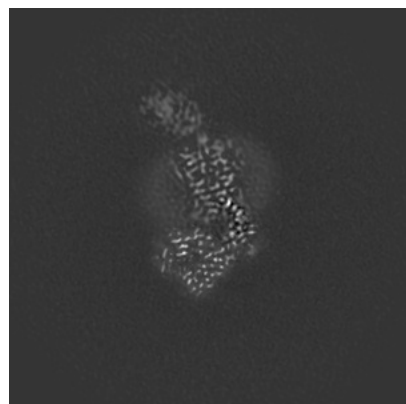


Z Index: 128

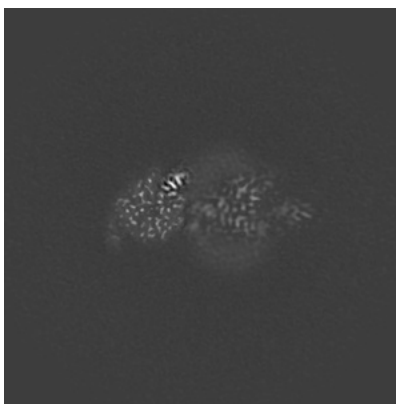
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

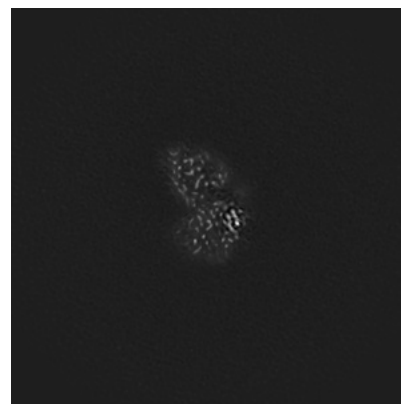
6.3.1 Primary map



X Index: 129



Y Index: 119

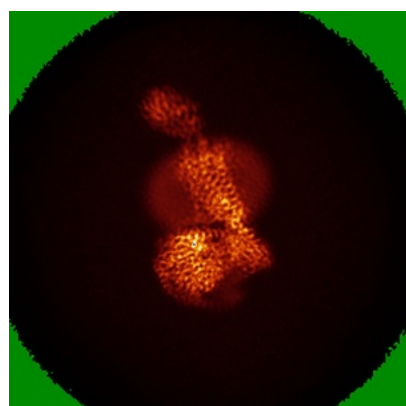


Z Index: 105

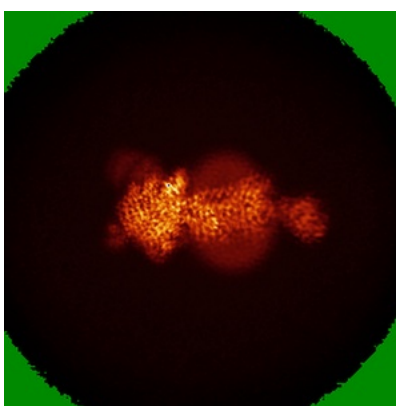
The images above show the largest variance slices of the map in three orthogonal directions.

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

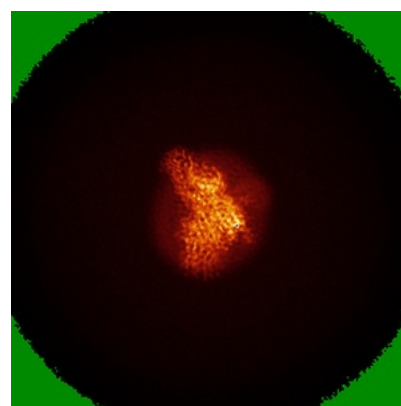
6.4.1 Primary map



X



Y

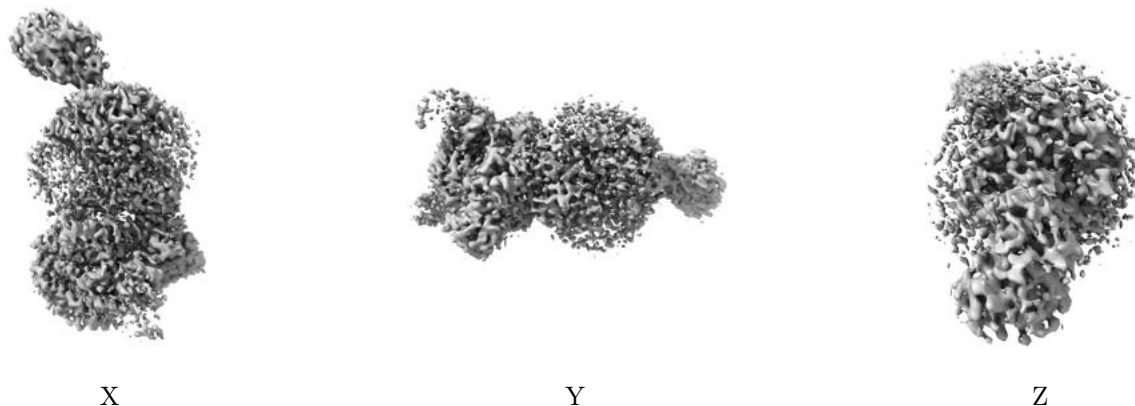


Z

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

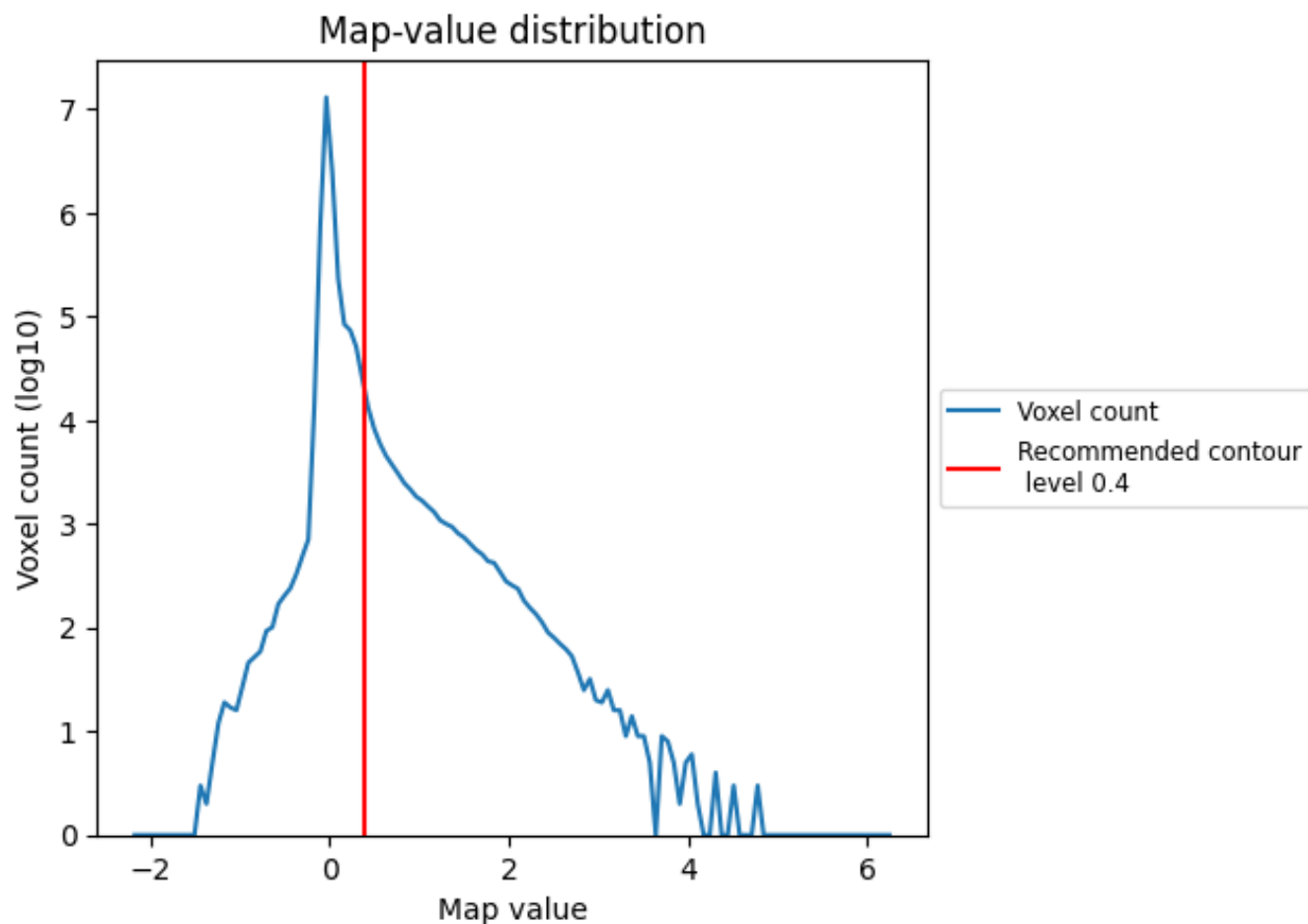
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

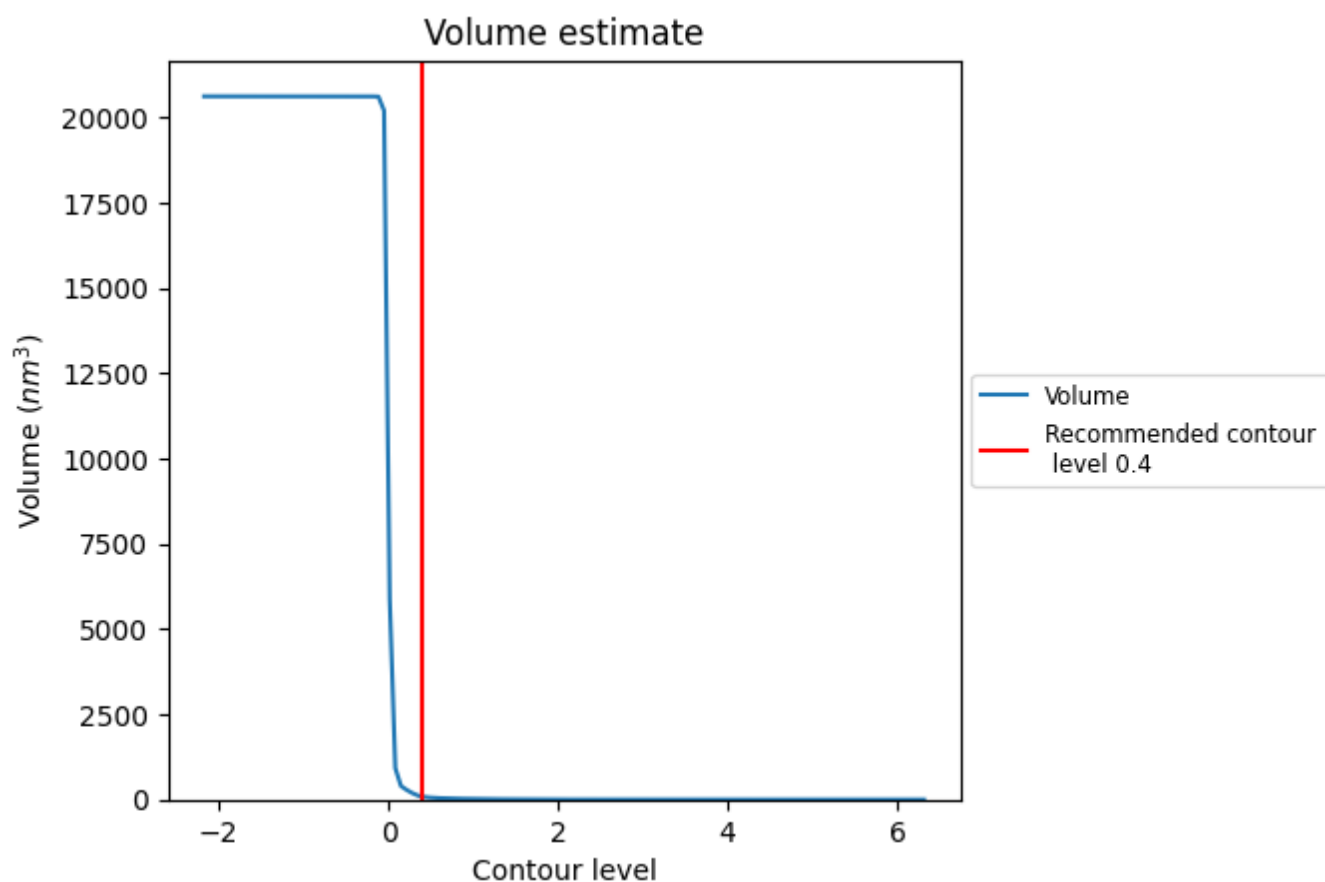
This section contains the results of statistical analysis of the map.

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.

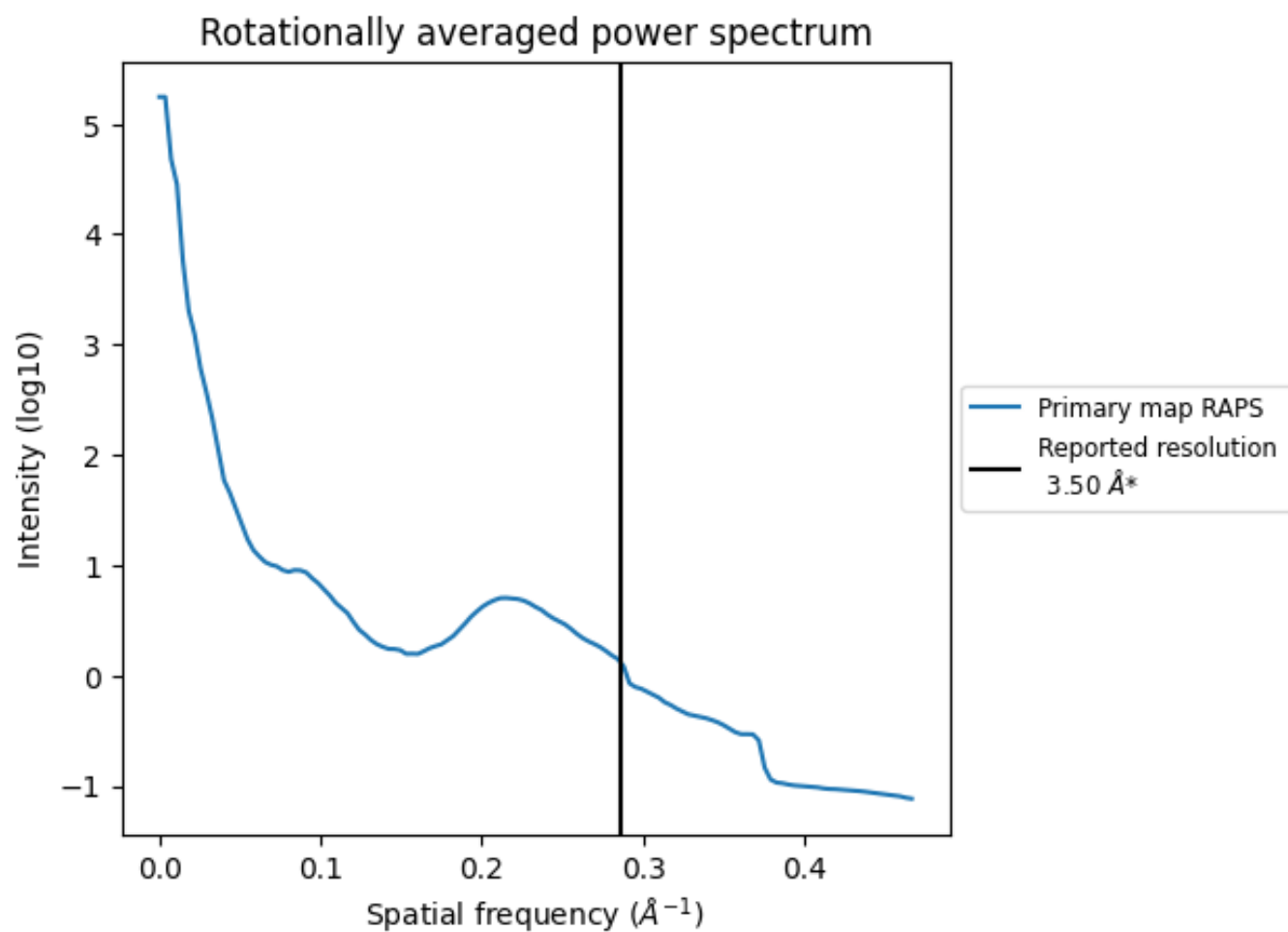
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 88 nm^3 ; this corresponds to an approximate mass of 80 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 0.286 Å⁻¹

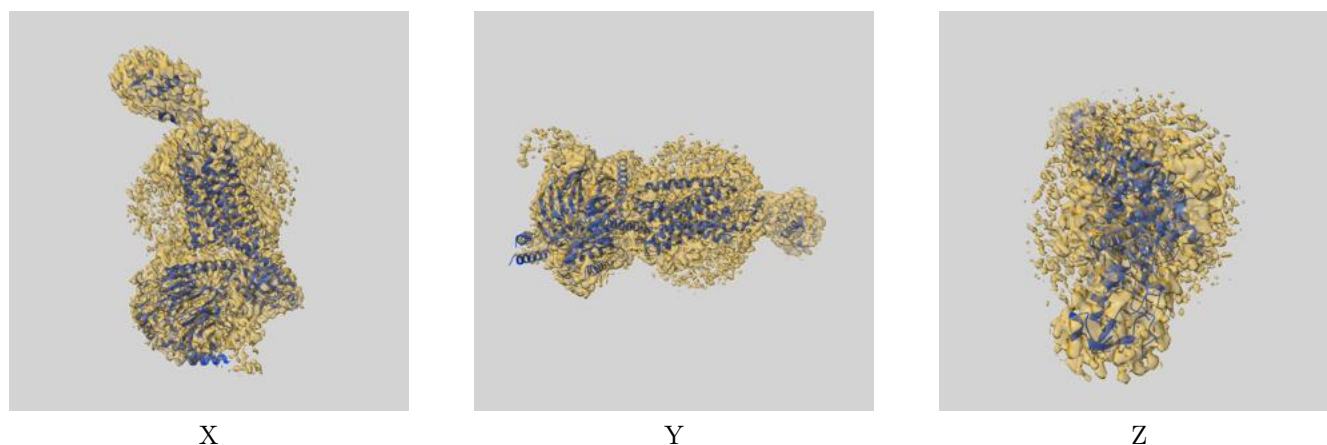
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

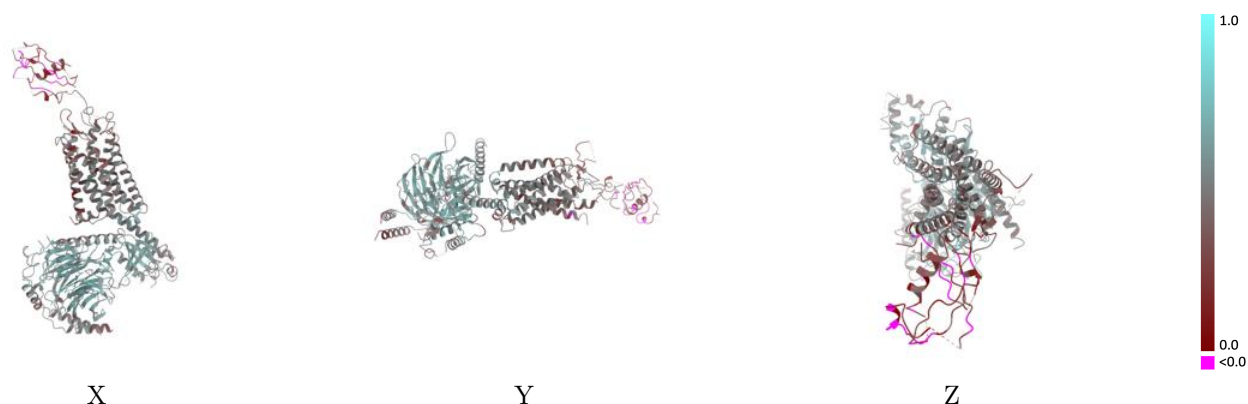
This section contains information regarding the fit between EMDB map EMD-62793 and PDB model 9L3W. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



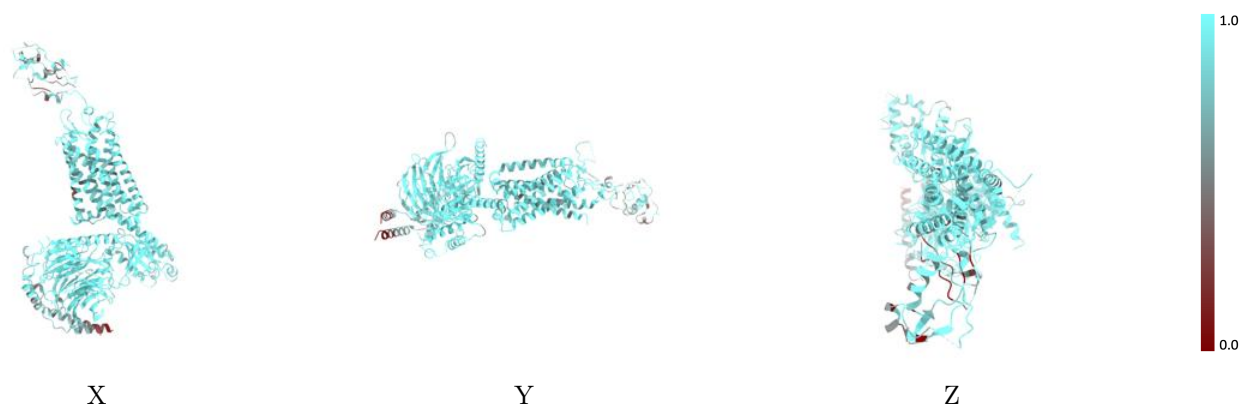
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



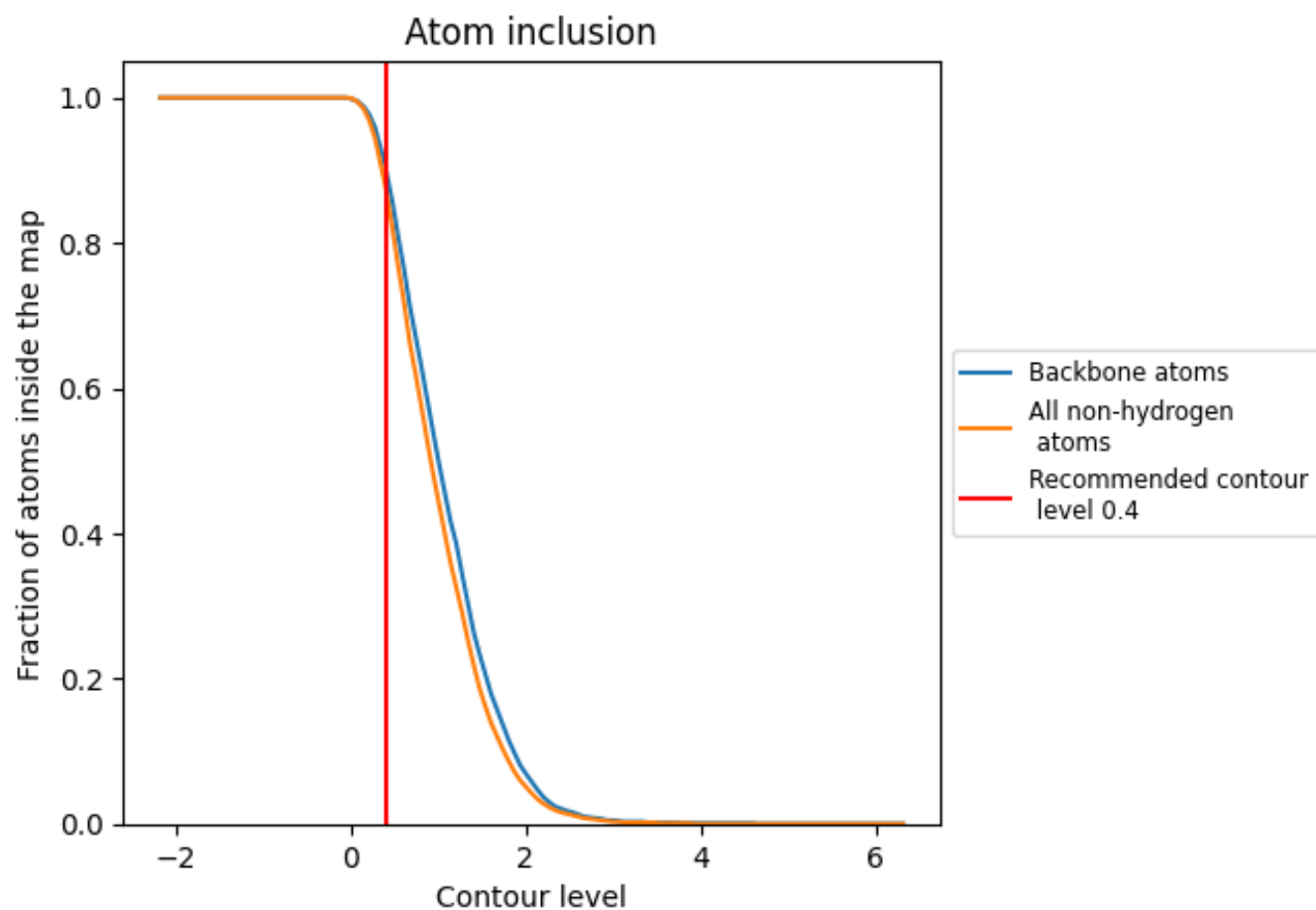
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8780	<div></div> 0.4790
A	<div></div> 0.9210	<div></div> 0.5230
B	<div></div> 0.9110	<div></div> 0.5600
C	<div></div> 0.7170	<div></div> 0.4950
L	<div></div> 0.7180	<div></div> 0.2140
R	<div></div> 0.8910	<div></div> 0.4390

