WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB EM Validation Summary Report (i)

May 17, 2025 – 04:28 PM EDT

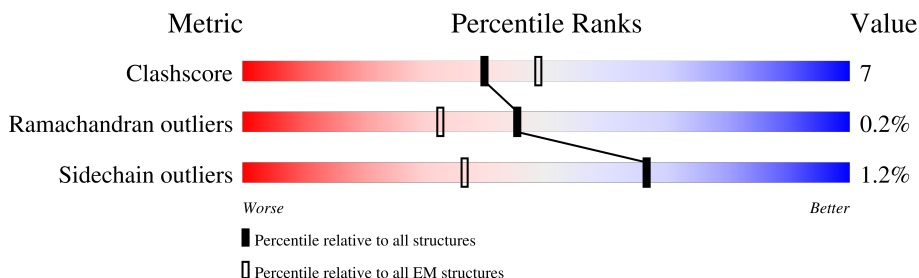|		
PDB ID	:	6D7S / pdb_00006d7s
EMDB ID	:	EMD-7824
Title	:	Cryo-EM structure of human TRPV6-Y467A in amphipols
Authors	:	Singh, A.K.; Saotome, K.; McGoldrick, L.L.; Sobolevsky, A.I.
Deposited on	:	2018-04-25
Resolution	:	4.34 Å(reported)

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 4.34 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	Percentile Ranks	Value
Clashscore		7
Ramachandran outliers		0.2%
Sidechain outliers		1.2%

Worse   *Better*

■ Percentile relative to all structures

▯ Percentile relative to all EM structures

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 <=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	742	17% · 63% 16% · 20%
1	B	742	16% · 63% 17% · 20%
1	C	742	14% · 63% 16% · 20%
1	D	742	16% · 64% 16% · 20%

2 Entry composition ⓘ

There is only 1 type of molecule in this entry. The entry contains 19018 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Transient receptor potential cation channel subfamily V member 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	593	Total	C	N	O	S	0	0
			4755	3070	805	841	39		
1	B	593	Total	C	N	O	S	0	0
			4753	3070	803	841	39		
1	C	593	Total	C	N	O	S	0	0
			4755	3070	805	841	39		
1	D	593	Total	C	N	O	S	0	0
			4755	3070	805	841	39		

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	467	ALA	TYR	engineered mutation	UNP Q9H1D0
A	726	LEU	-	expression tag	UNP Q9H1D0
A	727	VAL	-	expression tag	UNP Q9H1D0
A	728	PRO	-	expression tag	UNP Q9H1D0
A	729	ARG	-	expression tag	UNP Q9H1D0
A	730	GLY	-	expression tag	UNP Q9H1D0
A	731	SER	-	expression tag	UNP Q9H1D0
A	732	ALA	-	expression tag	UNP Q9H1D0
A	733	ALA	-	expression tag	UNP Q9H1D0
A	734	ALA	-	expression tag	UNP Q9H1D0
A	735	TRP	-	expression tag	UNP Q9H1D0
A	736	SER	-	expression tag	UNP Q9H1D0
A	737	HIS	-	expression tag	UNP Q9H1D0
A	738	PRO	-	expression tag	UNP Q9H1D0
A	739	GLN	-	expression tag	UNP Q9H1D0
A	740	PHE	-	expression tag	UNP Q9H1D0
A	741	GLU	-	expression tag	UNP Q9H1D0
A	742	LYS	-	expression tag	UNP Q9H1D0
B	467	ALA	TYR	engineered mutation	UNP Q9H1D0
B	726	LEU	-	expression tag	UNP Q9H1D0
B	727	VAL	-	expression tag	UNP Q9H1D0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	728	PRO	-	expression tag	UNP Q9H1D0
B	729	ARG	-	expression tag	UNP Q9H1D0
B	730	GLY	-	expression tag	UNP Q9H1D0
B	731	SER	-	expression tag	UNP Q9H1D0
B	732	ALA	-	expression tag	UNP Q9H1D0
B	733	ALA	-	expression tag	UNP Q9H1D0
B	734	ALA	-	expression tag	UNP Q9H1D0
B	735	TRP	-	expression tag	UNP Q9H1D0
B	736	SER	-	expression tag	UNP Q9H1D0
B	737	HIS	-	expression tag	UNP Q9H1D0
B	738	PRO	-	expression tag	UNP Q9H1D0
B	739	GLN	-	expression tag	UNP Q9H1D0
B	740	PHE	-	expression tag	UNP Q9H1D0
B	741	GLU	-	expression tag	UNP Q9H1D0
B	742	LYS	-	expression tag	UNP Q9H1D0
C	467	ALA	TYR	engineered mutation	UNP Q9H1D0
C	726	LEU	-	expression tag	UNP Q9H1D0
C	727	VAL	-	expression tag	UNP Q9H1D0
C	728	PRO	-	expression tag	UNP Q9H1D0
C	729	ARG	-	expression tag	UNP Q9H1D0
C	730	GLY	-	expression tag	UNP Q9H1D0
C	731	SER	-	expression tag	UNP Q9H1D0
C	732	ALA	-	expression tag	UNP Q9H1D0
C	733	ALA	-	expression tag	UNP Q9H1D0
C	734	ALA	-	expression tag	UNP Q9H1D0
C	735	TRP	-	expression tag	UNP Q9H1D0
C	736	SER	-	expression tag	UNP Q9H1D0
C	737	HIS	-	expression tag	UNP Q9H1D0
C	738	PRO	-	expression tag	UNP Q9H1D0
C	739	GLN	-	expression tag	UNP Q9H1D0
C	740	PHE	-	expression tag	UNP Q9H1D0
C	741	GLU	-	expression tag	UNP Q9H1D0
C	742	LYS	-	expression tag	UNP Q9H1D0
D	467	ALA	TYR	engineered mutation	UNP Q9H1D0
D	726	LEU	-	expression tag	UNP Q9H1D0
D	727	VAL	-	expression tag	UNP Q9H1D0
D	728	PRO	-	expression tag	UNP Q9H1D0
D	729	ARG	-	expression tag	UNP Q9H1D0
D	730	GLY	-	expression tag	UNP Q9H1D0
D	731	SER	-	expression tag	UNP Q9H1D0
D	732	ALA	-	expression tag	UNP Q9H1D0
D	733	ALA	-	expression tag	UNP Q9H1D0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	734	ALA	-	expression tag	UNP Q9H1D0
D	735	TRP	-	expression tag	UNP Q9H1D0
D	736	SER	-	expression tag	UNP Q9H1D0
D	737	HIS	-	expression tag	UNP Q9H1D0
D	738	PRO	-	expression tag	UNP Q9H1D0
D	739	GLN	-	expression tag	UNP Q9H1D0
D	740	PHE	-	expression tag	UNP Q9H1D0
D	741	GLU	-	expression tag	UNP Q9H1D0
D	742	LYS	-	expression tag	UNP Q9H1D0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Transient receptor potential cation channel subfamily V member 6

Chain A:

• Molecule 1: Transient receptor potential cation channel subfamily V member 6

Chain B:

• Molecule 1: Transient receptor potential cation channel subfamily V member 6

Chain C:

14%

63%   16%   20%

• Molecule 1: Transient receptor potential cation channel subfamily V member 6

Chain D:

4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	115126	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/Å^2)$	67.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.145	Depositor
Minimum map value	-0.074	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	199.92, 199.92, 199.92	wwPDB
Map dimensions	204, 204, 204	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.98, 0.98, 0.98	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	A	0.34	0/4863	0.69	6/6599 (0.1%)
1	B	0.34	0/4859	0.69	6/6589 (0.1%)
1	C	0.34	0/4863	0.69	6/6599 (0.1%)
1	D	0.34	0/4863	0.69	6/6599 (0.1%)
All	All	0.34	0/19448	0.69	24/26386 (0.1%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	223	ASP	CA-C-N	6.53	129.35	120.54
1	D	223	ASP	C-N-CA	6.53	129.35	120.54
1	A	223	ASP	CA-C-N	6.51	129.33	120.54
1	A	223	ASP	C-N-CA	6.51	129.33	120.54
1	C	223	ASP	CA-C-N	6.49	129.31	120.54

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	A	4755	0	4812	68	0
1	B	4753	0	4808	74	0
1	C	4755	0	4812	71	0
1	D	4755	0	4812	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	19018	0	19244	262	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 262 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:B:342:CYS:C	1:B:343:PHE:CA	2.41	0.93
1:B:343:PHE:C	1:B:344:THR:CA	2.43	0.92
1:B:273:LEU:HD11	1:C:160:ILE:HG12	1.66	0.77
1:C:273:LEU:HD11	1:D:160:ILE:HG12	1.72	0.71
1:A:273:LEU:HD11	1:B:160:ILE:HG12	1.72	0.69

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	A	589/742 (79%)	517 (88%)	71 (12%)	1 (0%)	44	78
1	B	586/742 (79%)	514 (88%)	71 (12%)	1 (0%)	44	78
1	C	589/742 (79%)	517 (88%)	71 (12%)	1 (0%)	44	78
1	D	589/742 (79%)	517 (88%)	71 (12%)	1 (0%)	44	78
All	All	2353/2968 (79%)	2065 (88%)	284 (12%)	4 (0%)	45	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	351	PRO

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Mol	Chain	Res	Type
1	B	351	PRO
1	C	351	PRO
1	D	351	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	515/645 (80%)	509 (99%)	6 (1%)	67	79
1	B	513/645 (80%)	507 (99%)	6 (1%)	67	79
1	C	515/645 (80%)	509 (99%)	6 (1%)	67	79
1	D	515/645 (80%)	509 (99%)	6 (1%)	67	79
All	All	2058/2580 (80%)	2034 (99%)	24 (1%)	66	79

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	452	VAL
1	C	625	LEU
1	C	520	LEU
1	D	160	ILE
1	B	160	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	522	HIS
1	D	208	ASN
1	C	546	ASN
1	D	36	GLN
1	D	365	ASN

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-7824. 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 |
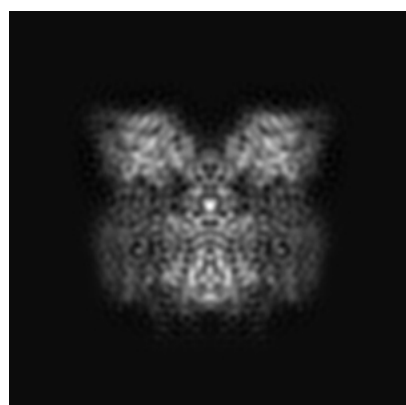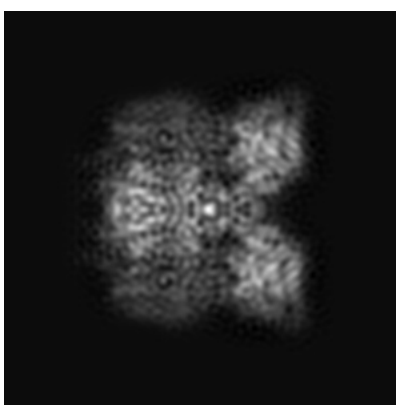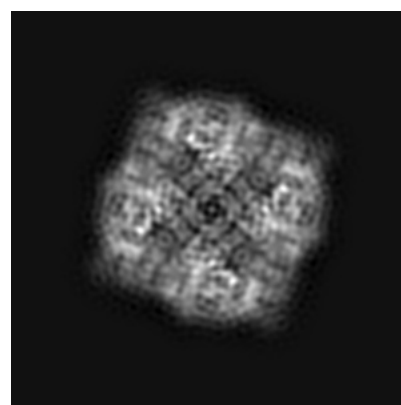
The images above show the map projected in three orthogonal directions.

6.2   Central slices (i)

6.2.1   Primary map
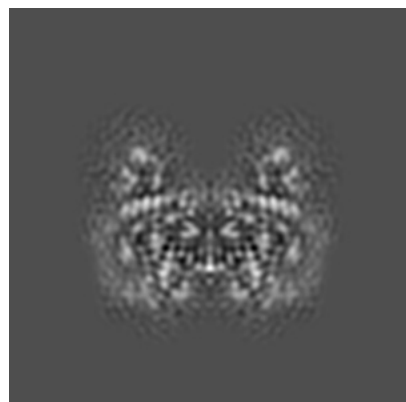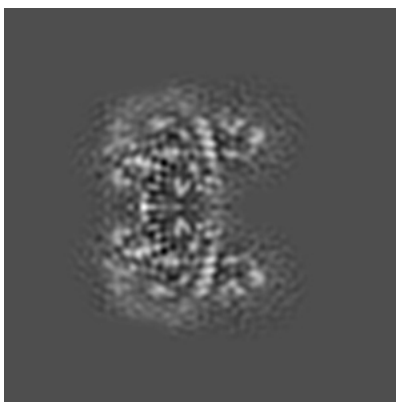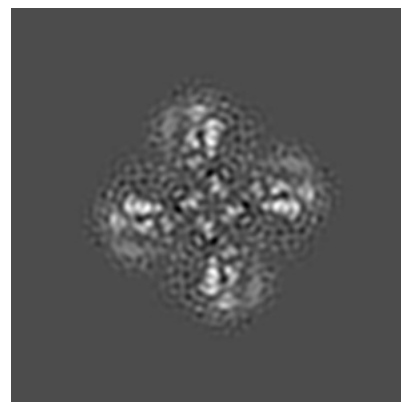
| X Index: 102 | Y Index: 102 | Z Index: 102 |

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

6.3 Largest variance slices ⓘ
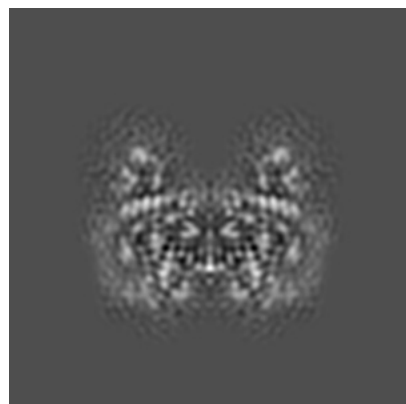
6.3.1 Primary map
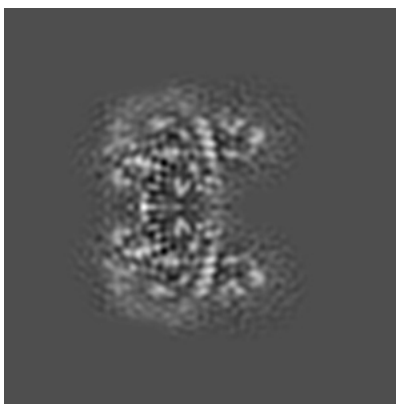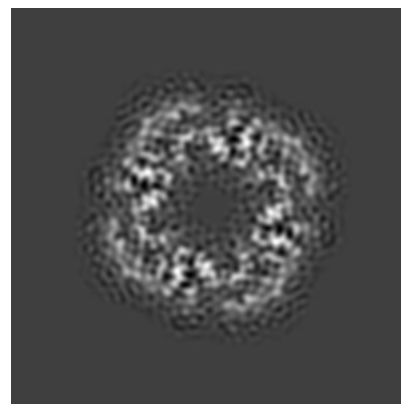
| X Index: 102 | Y Index: 102 | Z Index: 127 |

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

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

6.4.1 Primary map

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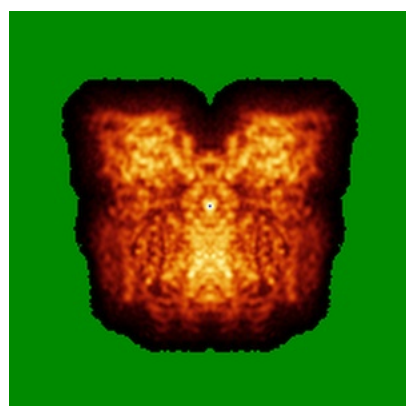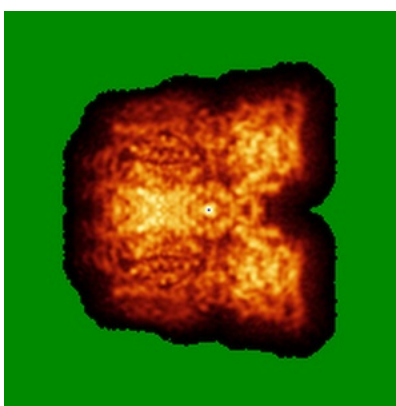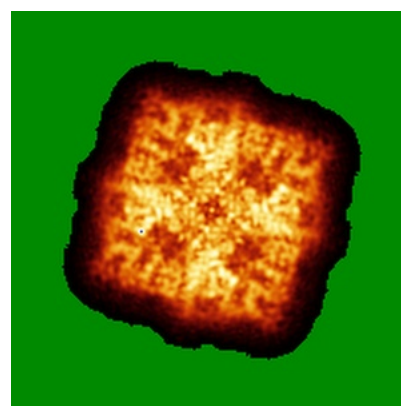
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views ⓘ

6.5.1 Primary map

| X | Y | Z |
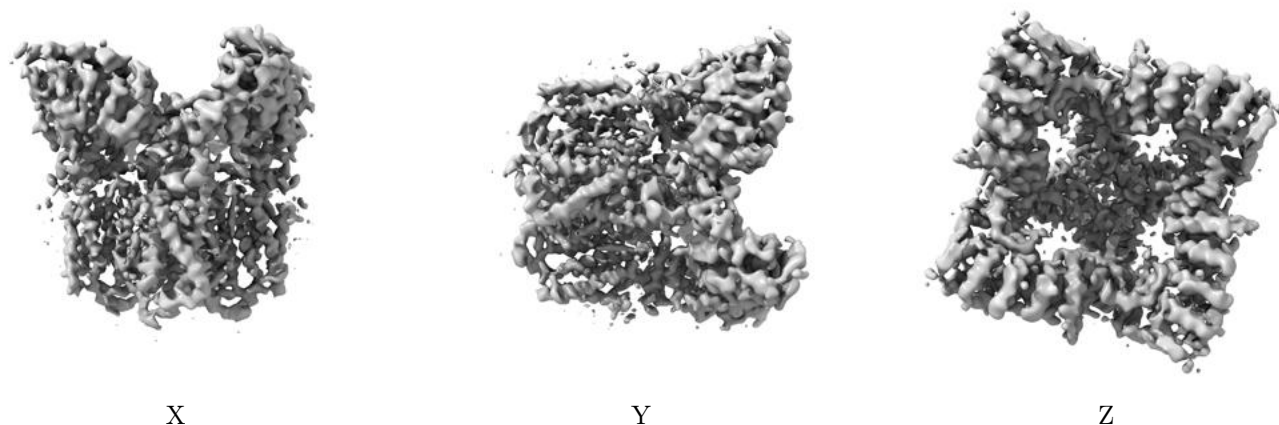
The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.6 Mask visualisation ⓘ

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 ⓘ
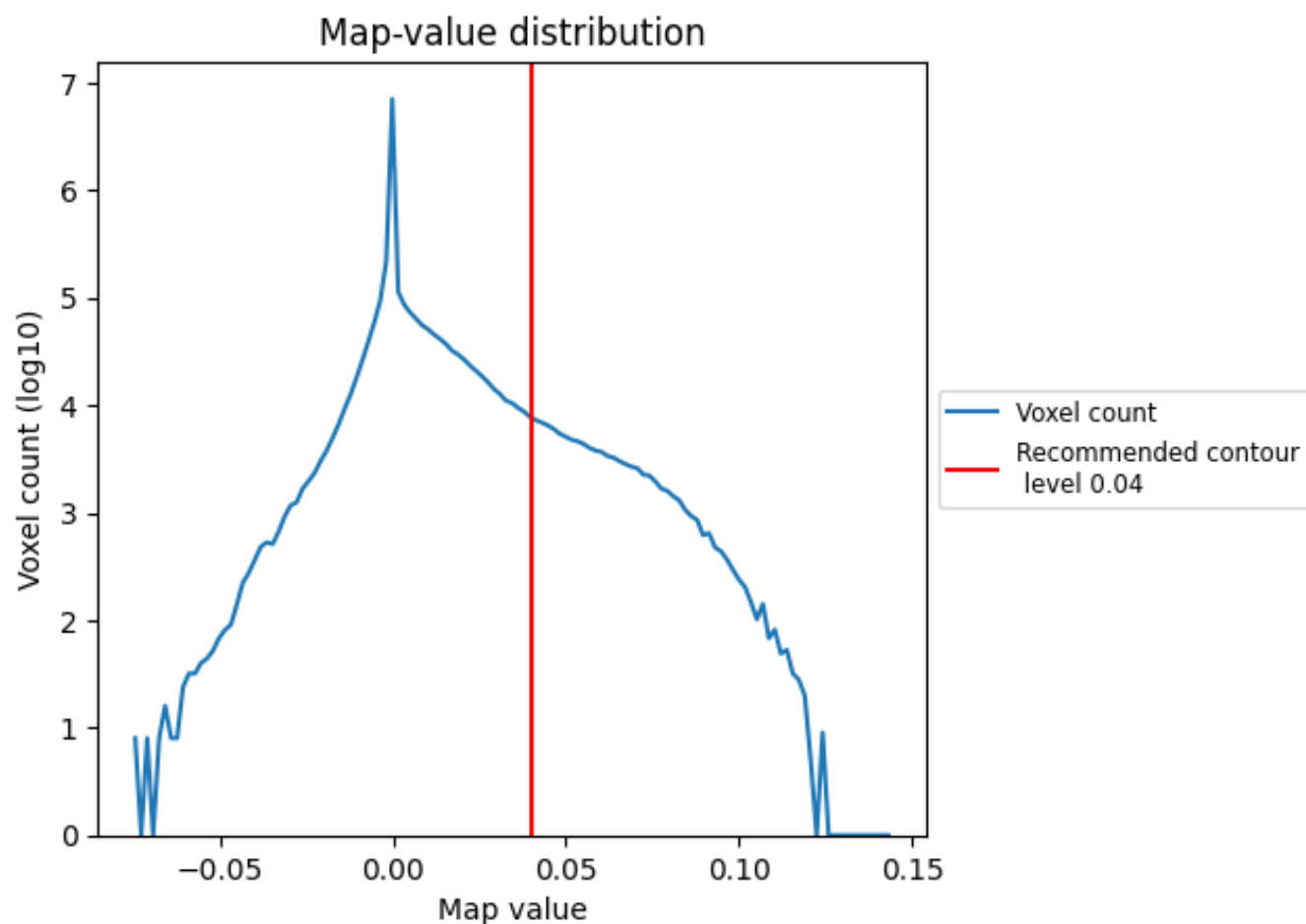
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2   Volume estimate ⓘ
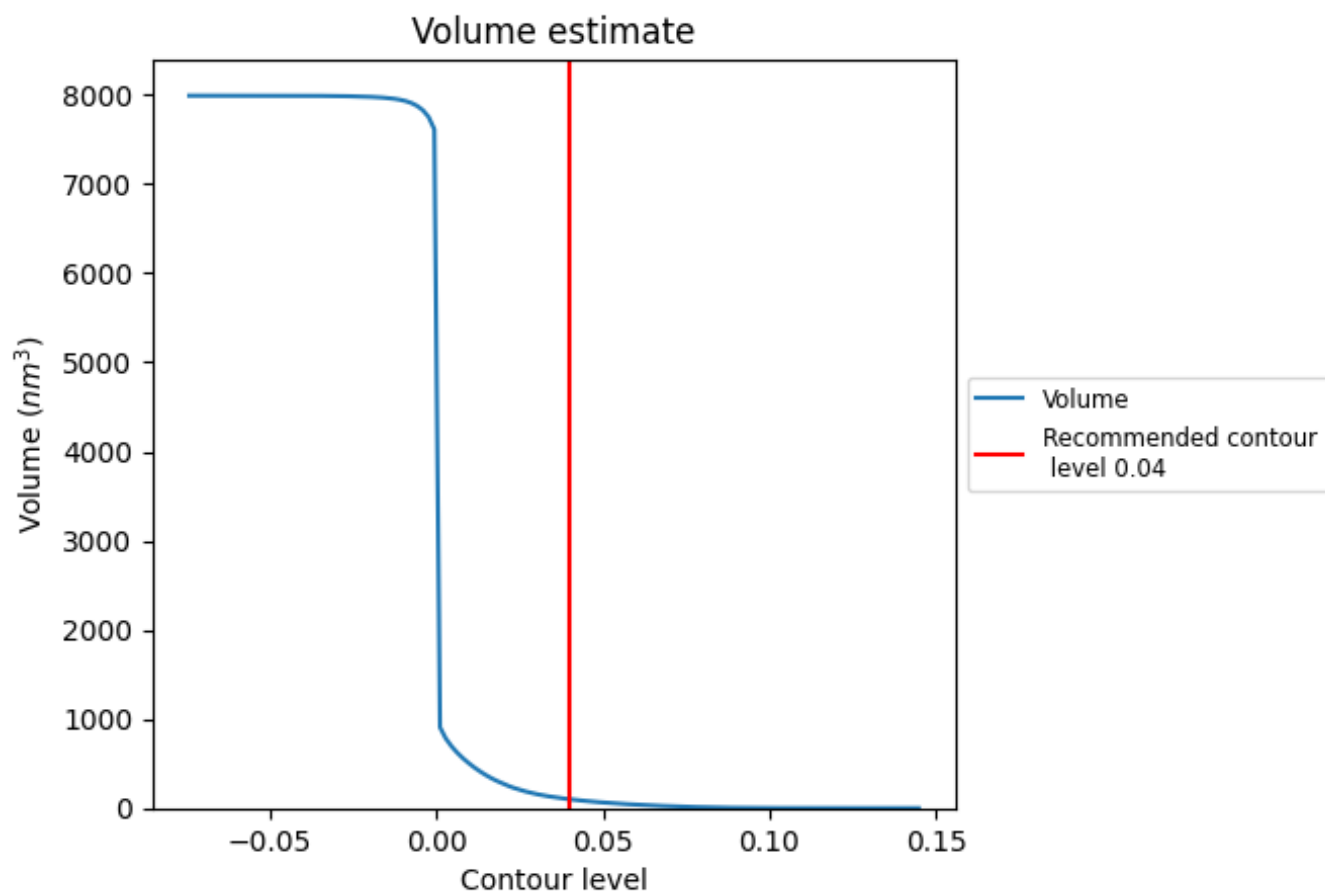
The volume at the recommended contour level is 99 nm^3; this corresponds to an approximate mass of 90 kDa.

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 ⓘ
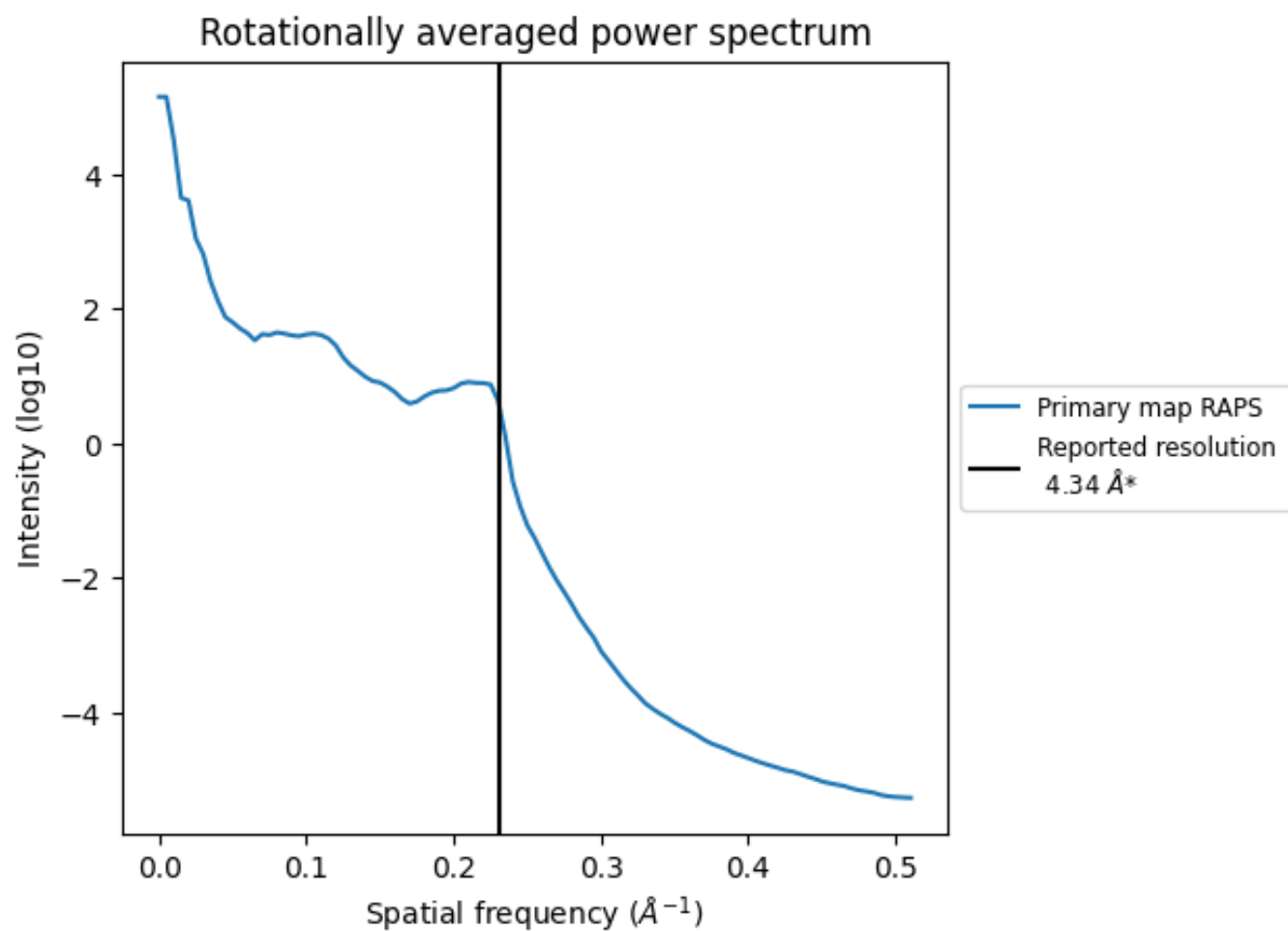
*Reported resolution corresponds to spatial frequency of 0.230 Å^{-1}

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-7824 and PDB model 6D7S. Per-residue inclusion information can be found in section 3 on page 6.
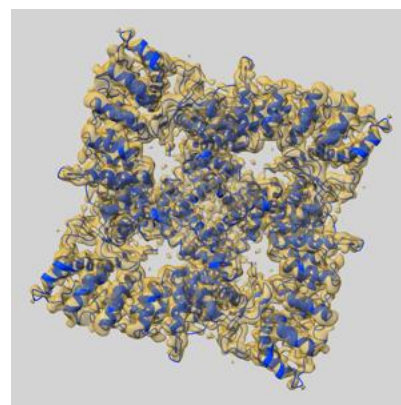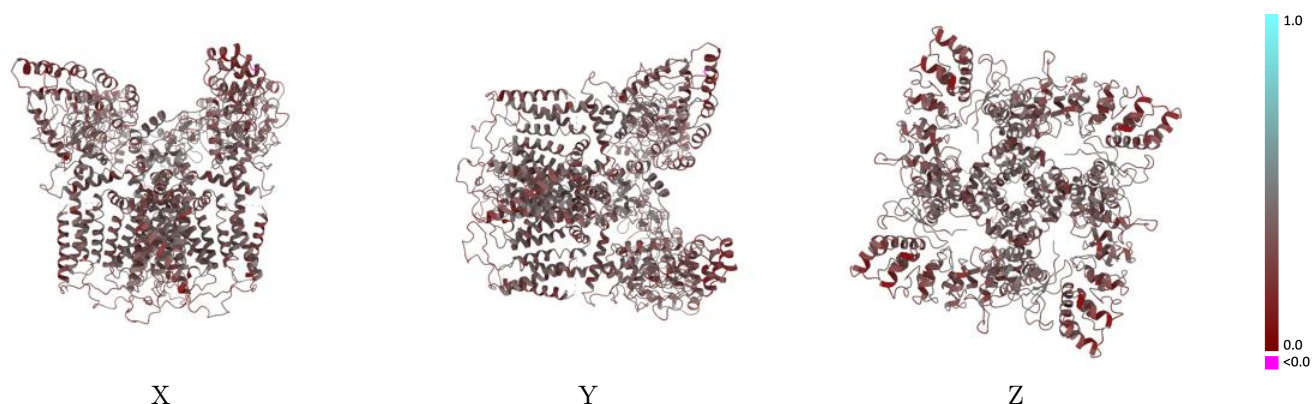
9.1   Map-model overlay ⓘ
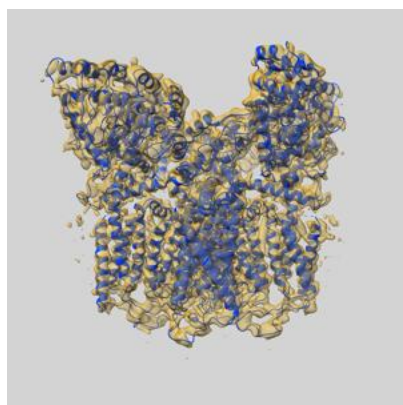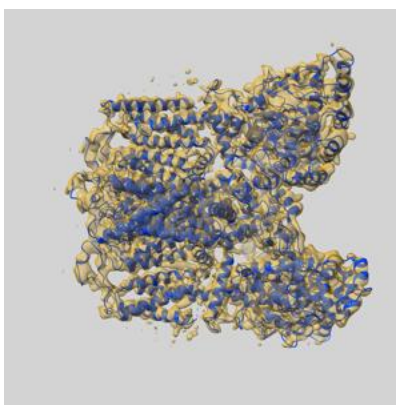
X   Y   Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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 ⓘ


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 ⓘ
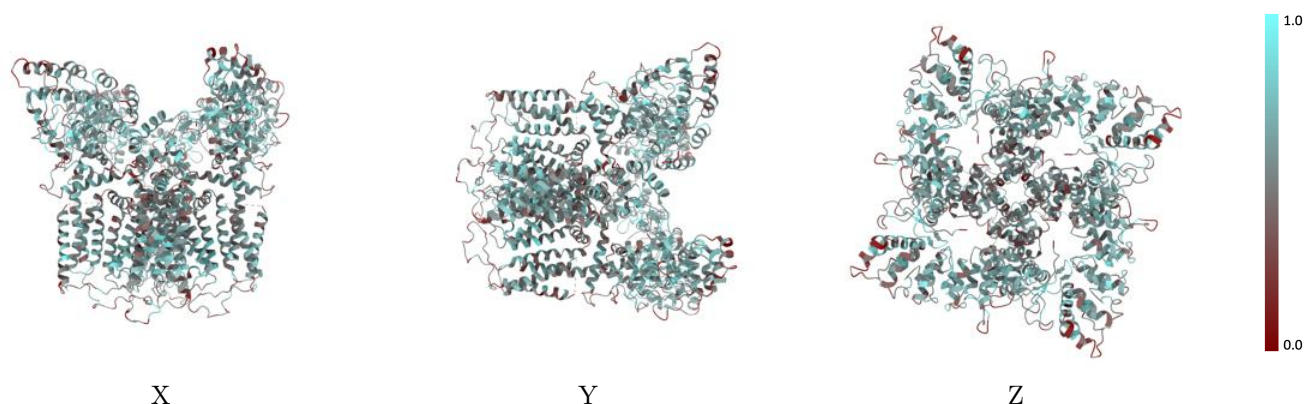
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion ⓘ
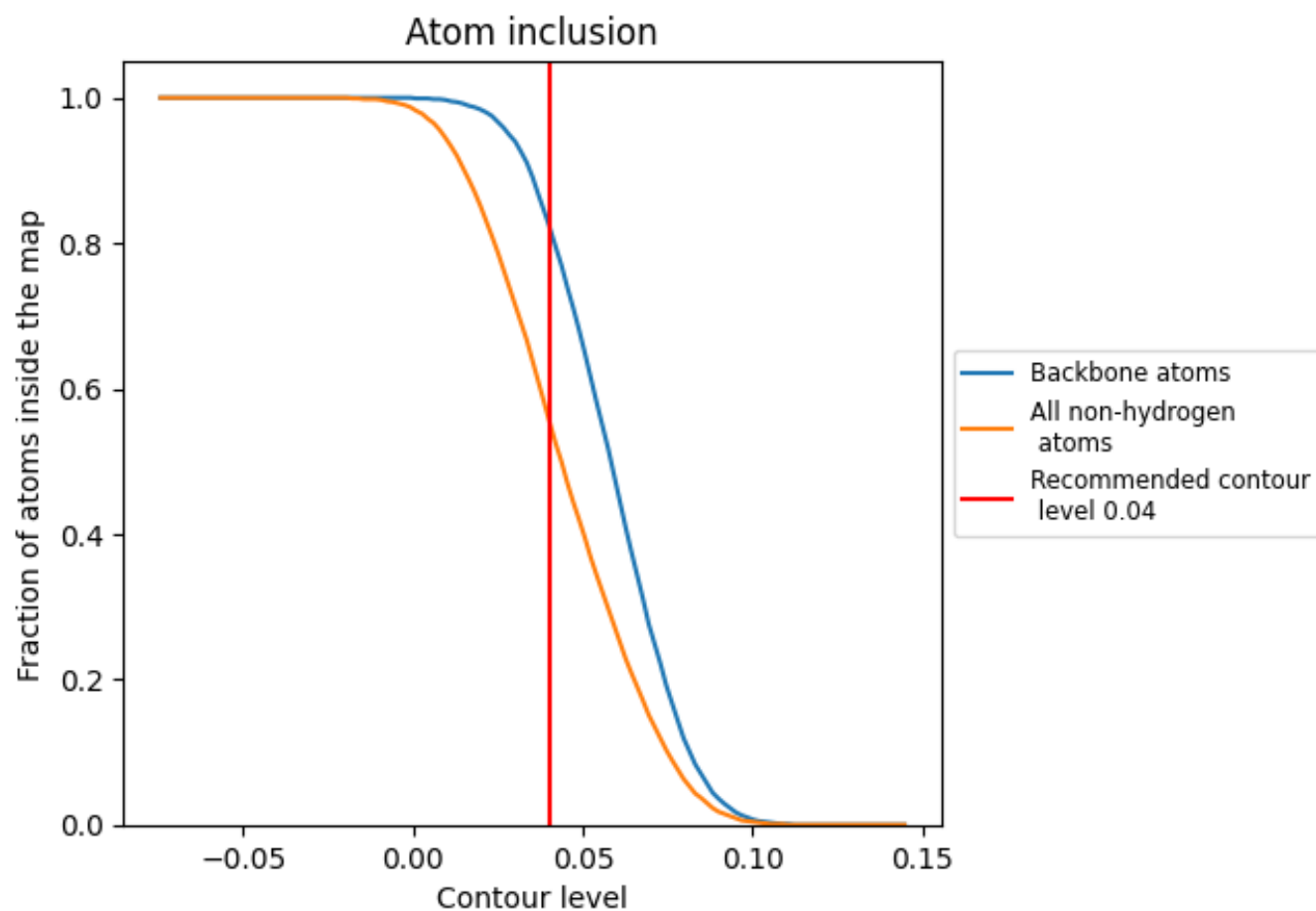
At the recommended contour level, 83% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5580	0.3390
A	0.5570	0.3370
B	0.5590	0.3400
C	0.5590	0.3410
D	0.5550	0.3400

1.0

0.0
<0.0