



## wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 06:23 PM JST

PDB ID : 7W6T  
EMDB ID : EMD-32335  
Title : CryoEM structure of human KChIP1-Kv4.3-DPP6 complex  
Authors : Ma, D.M.; Guo, J.T.  
Deposited on : 2021-12-02  
Resolution : 3.85 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
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) : 2.39

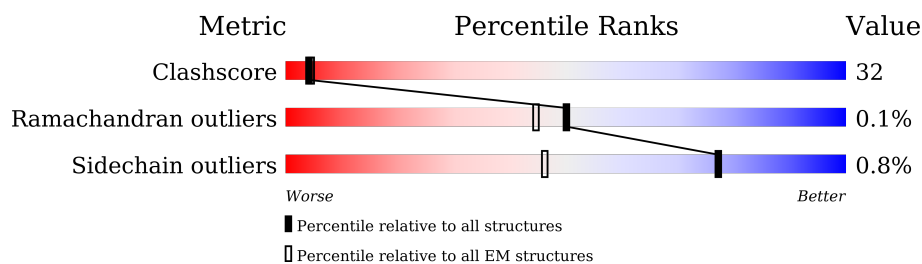
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.85 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  $\geq 3$ , 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	228	<div> <div>19%</div> <div>40%</div> <div>38%</div> <div>21%</div> </div>
1	C	228	<div> <div>5%</div> <div>29%</div> <div>49%</div> <div>21%</div> </div>
1	E	228	<div> <div>17%</div> <div>40%</div> <div>39%</div> <div>21%</div> </div>
1	G	228	<div> <div>10%</div> <div>38%</div> <div>40%</div> <div>21%</div> </div>
2	B	636	<div> <div>34%</div> <div>34%</div> <div>32%</div> </div>
2	D	636	<div> <div>31%</div> <div>37%</div> <div>32%</div> </div>
2	F	636	<div> <div>36%</div> <div>32%</div> <div>32%</div> </div>
2	H	636	<div> <div>35%</div> <div>32%</div> <div>32%</div> </div>

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Mol	Chain	Length	Quality of chain
3	I	873	<div><div></div><div>32%53%14%</div></div>
3	J	873	<div><div>7%</div><div>32%53%14%</div></div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 31768 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 Kv channel-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	179	Total	C	N	O	S	0	0
			1474	942	240	284	8		
1	C	179	Total	C	N	O	S	0	0
			1474	942	240	284	8		
1	E	179	Total	C	N	O	S	0	0
			1474	942	240	284	8		
1	G	179	Total	C	N	O	S	0	0
			1474	942	240	284	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q9NZI2
C	0	SER	-	expression tag	UNP Q9NZI2
E	0	SER	-	expression tag	UNP Q9NZI2
G	0	SER	-	expression tag	UNP Q9NZI2

- Molecule 2 is a protein called Isoform 2 of Potassium voltage-gated channel subfamily D member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	430	Total	C	N	O	S	0	0
			3456	2245	579	607	25		
2	D	430	Total	C	N	O	S	0	0
			3456	2245	579	607	25		
2	F	430	Total	C	N	O	S	0	0
			3456	2245	579	607	25		
2	H	430	Total	C	N	O	S	0	0
			3456	2245	579	607	25		

- Molecule 3 is a protein called Dipeptidyl aminopeptidase-like protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	749	Total	C	N	O	S	0	0
			6024	3842	1025	1134	23		
3	J	749	Total	C	N	O	S	0	0
			6024	3842	1025	1134	23		

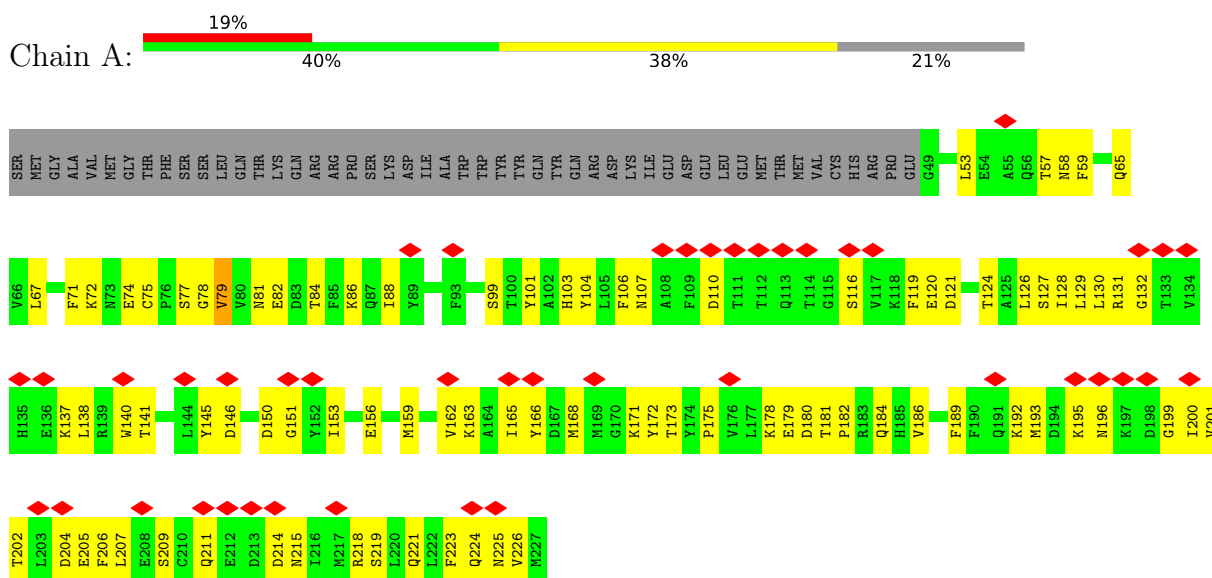
There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	805	LEU	-	expression tag	UNP E9PWX1
I	806	GLU	-	expression tag	UNP E9PWX1
I	807	GLY	-	expression tag	UNP E9PWX1
I	808	GLY	-	expression tag	UNP E9PWX1
I	809	SER	-	expression tag	UNP E9PWX1
I	810	SER	-	expression tag	UNP E9PWX1
I	811	ASP	-	expression tag	UNP E9PWX1
I	812	TYR	-	expression tag	UNP E9PWX1
I	813	LYS	-	expression tag	UNP E9PWX1
I	814	ASP	-	expression tag	UNP E9PWX1
I	815	ASP	-	expression tag	UNP E9PWX1
I	816	ASP	-	expression tag	UNP E9PWX1
I	817	ASP	-	expression tag	UNP E9PWX1
I	818	LYS	-	expression tag	UNP E9PWX1
J	805	LEU	-	expression tag	UNP E9PWX1
J	806	GLU	-	expression tag	UNP E9PWX1
J	807	GLY	-	expression tag	UNP E9PWX1
J	808	GLY	-	expression tag	UNP E9PWX1
J	809	SER	-	expression tag	UNP E9PWX1
J	810	SER	-	expression tag	UNP E9PWX1
J	811	ASP	-	expression tag	UNP E9PWX1
J	812	TYR	-	expression tag	UNP E9PWX1
J	813	LYS	-	expression tag	UNP E9PWX1
J	814	ASP	-	expression tag	UNP E9PWX1
J	815	ASP	-	expression tag	UNP E9PWX1
J	816	ASP	-	expression tag	UNP E9PWX1
J	817	ASP	-	expression tag	UNP E9PWX1
J	818	LYS	-	expression tag	UNP E9PWX1

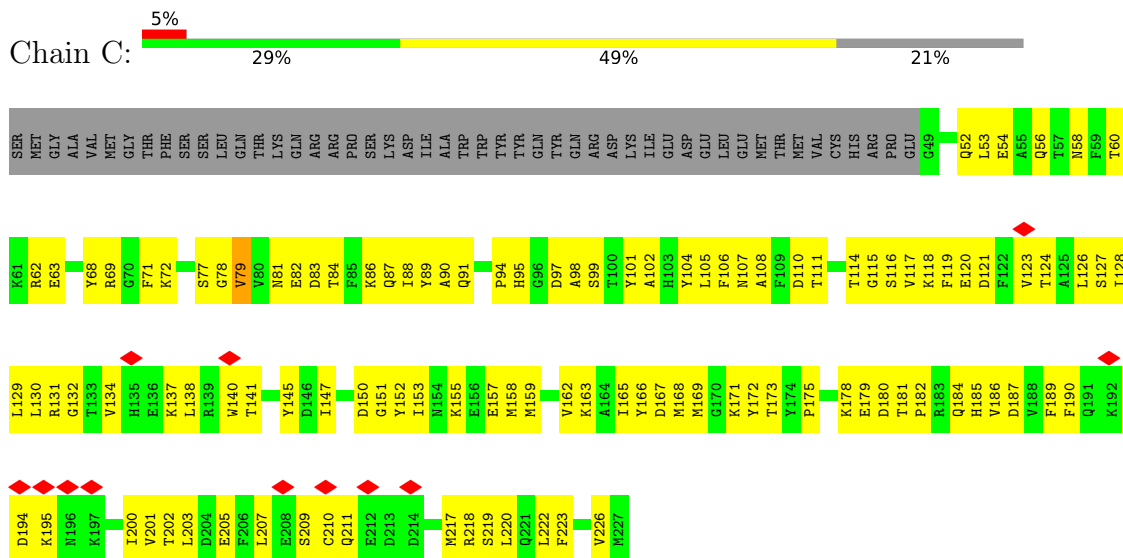
### 3 Residue-property plots

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.

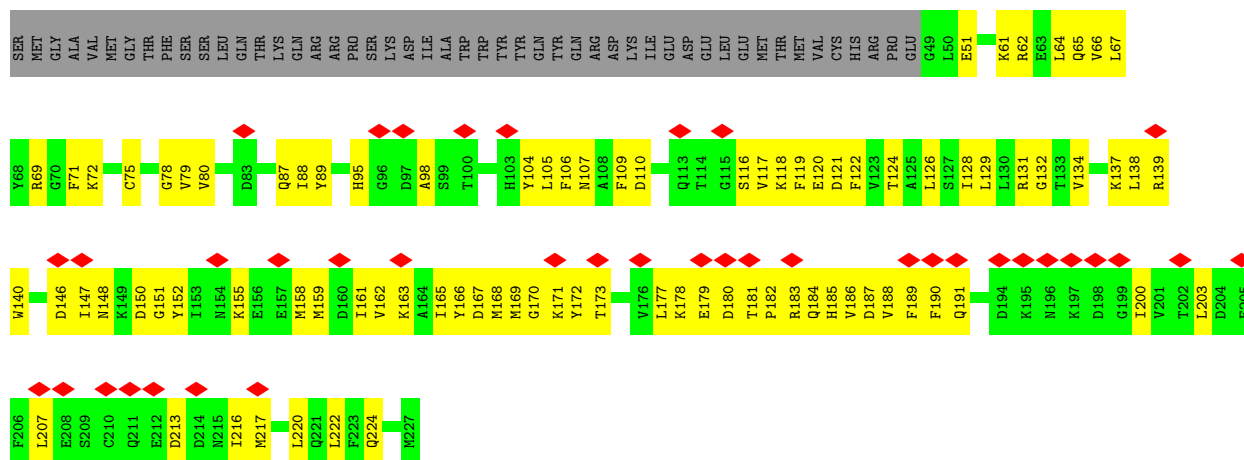
- Molecule 1: Kv channel-interacting protein 1



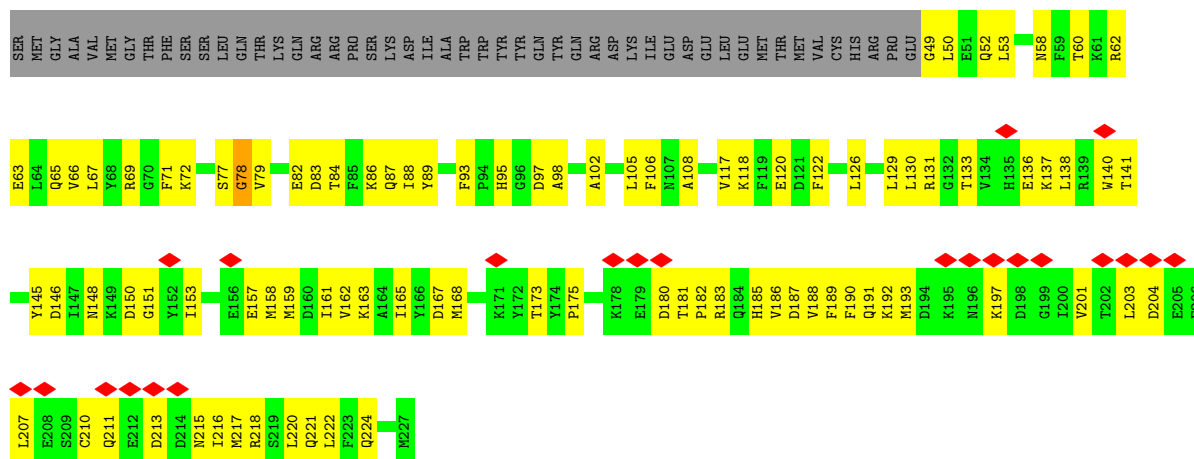
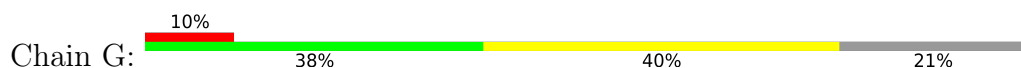
- Molecule 1: Kv channel-interacting protein 1



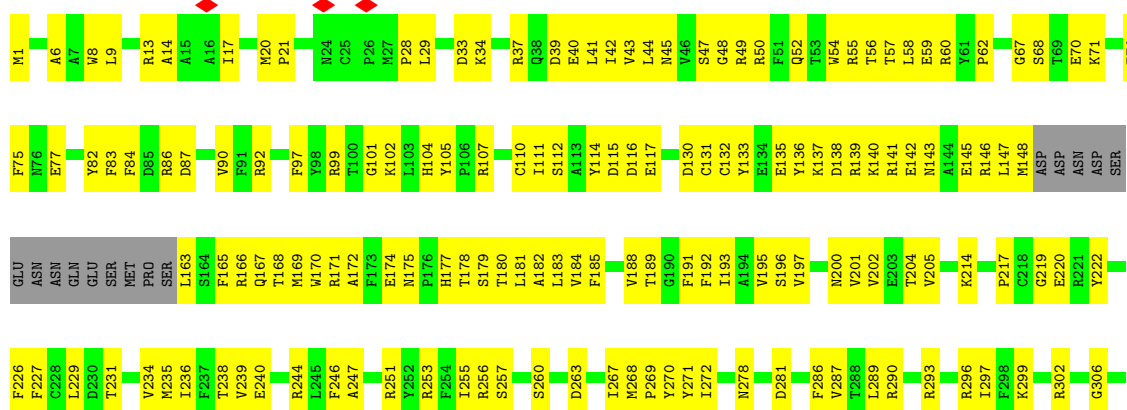
- Molecule 1: Kv channel-interacting protein 1



• Molecule 1: Kv channel-interacting protein 1



• Molecule 2: Isoform 2 of Potassium voltage-gated channel subfamily D member 3



I309	S407	S470	ARG	GLN
L310	R408	L471	ARG	ILE
G311	I409	I472	SER	THR
Y312	Y410	I473	LYS	THR
T313	H411	S474	LYS	ALA
L314	Q414	H476	THR	ILE
K315	R415	H477	THR	ILE
E320	K418	H478	HIS	SER
L324	L419	L479	LEU	ILE
M330	R420	L480	PRO	PRO
A331	A421	H481	ASN	THR
I332	K424	L483	SER	PRO
I333	A425	E484	LEU	ALA
I334	R426	T486	PRO	LEU
V338	LEU	T487	THR	THR
Y341	ALA	ASN	LEU	GLY
S347	ARG	HIS	ARG	GLU
A348	ILE	GLU	SER	SER
I354	VAL	PHE	MET	ARG
F358	ALA	ILE	GLN	ILE
I362	ALA	ASP	GLU	PRO
M365	LYS	THR	LEU	PRO
L368	THR	SER	SER	ALA
G369	GLY	THR	GLN	ASN
Y370	LEU	GLU	ILE	THR
G371	LYS	SER	PRO	ASN
D372	ARG	MET	SER	ILE
M373	ASN	GLN	LEU	ALA
K381	GLY	ASN	THR	SER
I382	ASN	TYR	THR	ASN
S385	ALA	ARG	VAL	VAL
I386	LEU	SER	LYS	LYS
C387	GLU	PRO	SER	VAL
S388	LEU	SER	LEU	VAL
V392	THR	THR	LYS	VAL
L397	THR	ASP	ALA	SER
P398	PRO	ASP	ASP	THR
V399	GLU	GLY	GLY	HIS
P400	GLU	ARG	LEU	PRO
V401	GLU	ARG	LEU	THR
T402	HIS	THR	THR	THR
V403	MET	THR	ASN	CYS
S404	GLY	THR	CYS	LYS
N405	LYS	THR	THR	THR
F406	THR	SER	SER	SER

- Molecule 2: Isoform 2 of Potassium voltage-gated channel subfamily D member 3

Chain D:  31% 37% 32%

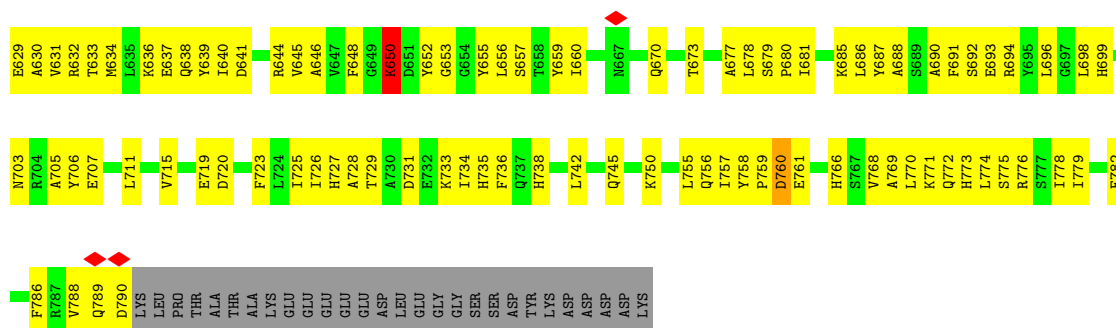
M1	K71	E145	V205	D281	P375	ASN	SER
A2	E72	R146	P206	F286	K376	GLY	THR
A3	F75	L147	G212	R290	T377	LEU	ARG
G4	N76	M148	S213	R291	G384	LEU	SER
A7	T79	ASP	K214	F292	S385	ASN	ASN
F11	K80	ASN	E215	R293	L386	ALA	SER
A12	E81	SER	L216	R294	C387	LEU	LEU
R13	Y82	GLU	E220	R295	S388	LEU	ALA
F19	F83	ASN	R221	R296	L389	THR	ASP
M20	F84	ASN	Y222	K299	S390	GLY	HIS
P21	D85	GLN	F226	F300	G391	THR	PRO
V22	R86	GLU	F227	S301	L393	PRO	LEU
A23	D87	MET	G228	R302	V394	GLU	ARG
Y24	F90	PRO	L229	H303	P397	GLU	THR
P26	F91	SER	D230	S304	L398	GLU	CYS
M27	R92	L163	T231	H305	P399	THR	THR
P28	C93	S164	V234	G306	V401	GLY	SER
L29	F94	F165	M235	L307	R408	THR	ARG
A30	N96	R166	I236	I309	Y409	THR	ARG
P31	F97	Q167	E240	T313	Y410	THR	LYS
A32	Y98	T168	V239	S319	H411	THR	THR
D33	R99	M169	E241	G322	Q412	THR	ILE
K34	T100	R171	L242	G323	S474	THR	HIS
N35	G101	A172	L243	F323	Q414	THR	ILE
K36	K102	F173	R244	F326	H476	THR	PRO
R37	L103	E174	L245	F326	H477	THR	ASN
Q38	H104	N175	A246	M330	K418	THR	SER
D39	Y105	P176	A247	I332	R419	THR	ASN
E40	P106	H177	A248	K420	A421	THR	ALA
V43	R107	T178	Y252	K423	Q422	THR	LEU
L44	E109	L180	R256	K424	K424	THR	ALA
N45	C110	L181	S257	A425	R426	THR	GLY
V46	I111	A182	L183	LEU	LEU	THR	GLU
S47	S112	L184	V258	E343	ARG	THR	ARG
Q48	A113	V184	M259	K344	ALA	THR	ARG
R49	Y114	F185	S260	S353	ILE	THR	PRO
R50	D115	Y186	I261	L354	ILE	THR	PRO
F51	D116	Y187	L262	P355	ARG	THR	PRO
Q52	E117	T188	V264	A356	THR	THR	ALA
T53	L118	T189	V265	K359	LYS	THR	ALA
W54	D130	F191	A266	Y360	GLY	THR	VAL
R55	C131	F192	L267	T361	GLY	THR	GLN
T56	Y133	I193	M268	I362	GLY	THR	ASN
E59	E134	A194	P269	V363	ASN	THR	ASN
R60	E135	V195	Y270	K365	ASN	THR	ASN
Y61	D138	V197	L272	T372	THR	THR	GLN
T64	R139	T199	G273	L274	LEU	THR	PRO
L65	K140	N200	T277	N278	LEU	THR	SER
L66	R141	V201	E202	M143	HIS	THR	ILE
G67	E142	E203	T204	A144	SER	THR	ALA
S68	M143	E203			LYS	THR	ALA
T69	E144				ASN	THR	ASN
E70					THR	THR	ASN

- Molecule 2: Isoform 2 of Potassium voltage-gated channel subfamily D member 3

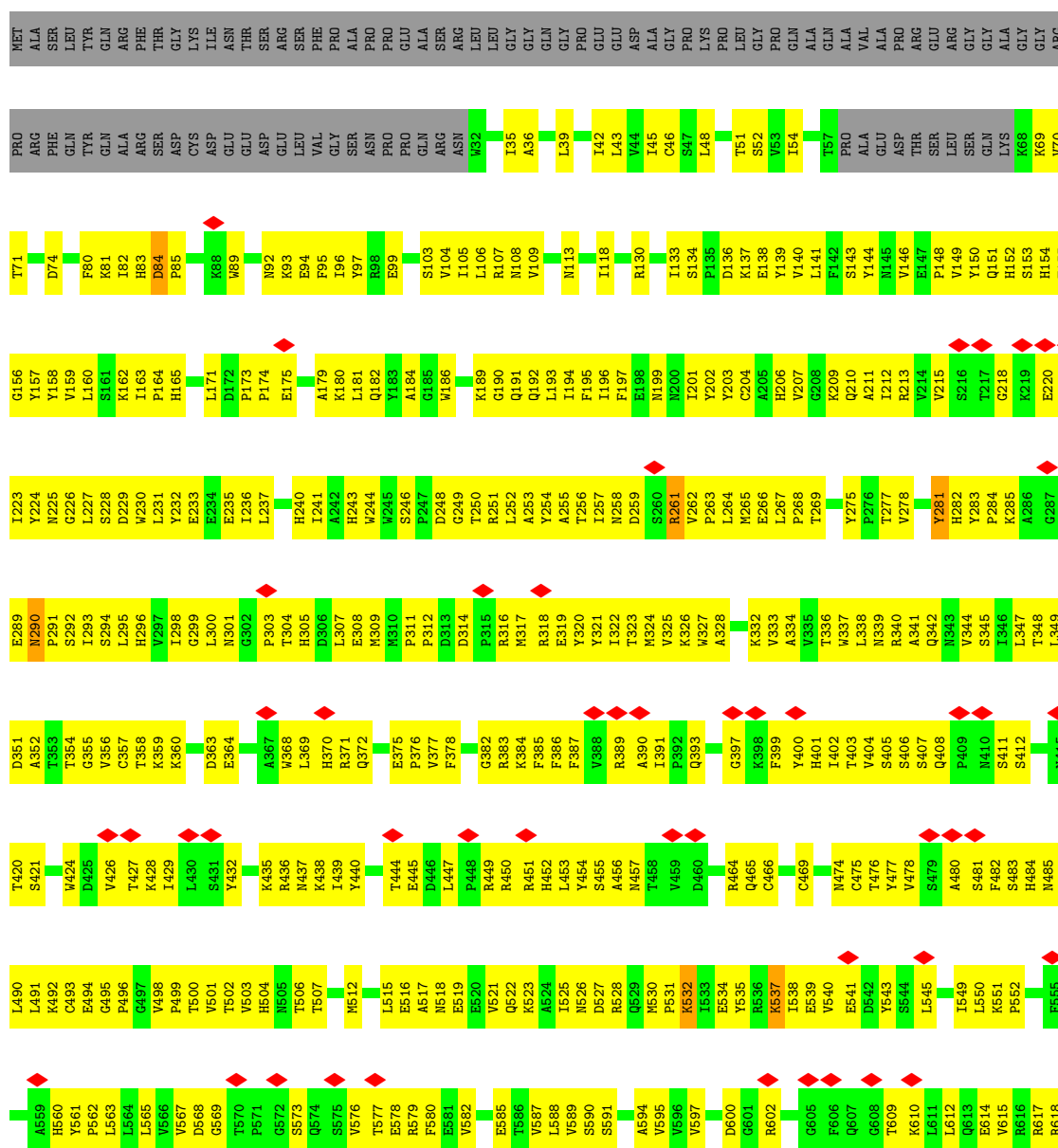








• Molecule 3: Dipeptidyl aminopeptidase-like protein 6



L622	E623	E624	K625	D626	Q627	M628	R632	T633	M634	L635	I640	D641	K642	T643	R644	V645	A646	V647	F648	G649	K650	D651	Y652	G653	G654	Y655	L656	S657	T658	Y659	I660	L661	P662	A663	K664	G665	E666	F672	T673	S676	A677	L678	S679	P680	I681	T682	D683	F684	K685	L686	Y687	A688	S689	A690	F691
S692	E693	R694	Y695	L696	G697	L698	H699	G700	L701	R704	A705	Y706	E707	K710	L711	A712	H713	R714	V715	L718	E719	D720	Q721	Q722	F723	L724	I725	I726	H727	A728	I729	A730	D731	E732	K733	I734	H735	F736	Q737	H738	I739	I743	T744	Q745	L746	I747	K750	A751	N752	Y753	S754	L755	Q756	I757	
Y758	P759	D760	E761	S762	H763	Y764	F765	L770	H773	L774	I778	F786	R787	V788	Q789	D790	LYS	LEU	PRO	THR	ALA	THR	ALA	LYS	GLU	GLU	GLU	GLU	ASP	LEU	GLU	GLY	GLY	SER	SER	ASP	ASP	TYR	LYS	ASP	ASP	ASP	ASP	LYS											

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	263176	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	65	Depositor
Minimum defocus (nm)	-1100	Depositor
Maximum defocus (nm)	-1300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.080	Depositor
Minimum map value	-0.457	Depositor
Average map value	-0.005	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.0956	Depositor
Map size ( $\text{\AA}$ )	273.78003, 273.78003, 273.78003	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.014, 1.014, 1.014	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	0.26	0/1506	0.44	0/2032
1	C	0.28	0/1506	0.47	0/2032
1	E	0.28	0/1506	0.48	0/2032
1	G	0.27	0/1506	0.47	0/2032
2	B	0.39	0/3544	0.47	0/4800
2	D	0.37	0/3544	0.46	0/4800
2	F	0.37	0/3544	0.47	0/4800
2	H	0.38	0/3544	0.47	0/4800
3	I	0.35	0/6171	0.54	0/8370
3	J	0.35	0/6171	0.53	0/8370
All	All	0.35	0/32542	0.50	0/44068

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	G	0	1
3	I	0	4
3	J	0	2
All	All	0	7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	78	GLY	Peptide
3	I	267	LEU	Peptide
3	I	285	LYS	Peptide

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Mol	Chain	Res	Type	Group
3	I	650	LYS	Peptide
3	I	760	ASP	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	A	1474	0	1415	72	0
1	C	1474	0	1415	104	0
1	E	1474	0	1415	73	0
1	G	1474	0	1415	75	0
2	B	3456	0	3462	200	0
2	D	3456	0	3462	226	0
2	F	3456	0	3462	182	0
2	H	3456	0	3462	192	0
3	I	6024	0	5922	528	0
3	J	6024	0	5922	516	0
All	All	31768	0	31352	2013	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 32.

The worst 5 of 2013 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:C:186:VAL:O	1:C:189:PHE:HB3	1.60	1.01
1:A:186:VAL:O	1:A:189:PHE:HB3	1.61	0.99
3:J:265:MET:HB2	3:J:283:TYR:HB2	1.42	0.98
3:J:92:ASN:HA	3:J:484:HIS:HB2	1.50	0.94
3:J:264:LEU:HA	3:J:282:HIS:HA	1.51	0.92

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	177/228 (78%)	165 (93%)	12 (7%)	0	100	100
1	C	177/228 (78%)	161 (91%)	15 (8%)	1 (1%)	22	57
1	E	177/228 (78%)	160 (90%)	17 (10%)	0	100	100
1	G	177/228 (78%)	164 (93%)	13 (7%)	0	100	100
2	B	424/636 (67%)	380 (90%)	44 (10%)	0	100	100
2	D	424/636 (67%)	383 (90%)	40 (9%)	1 (0%)	44	75
2	F	424/636 (67%)	379 (89%)	45 (11%)	0	100	100
2	H	424/636 (67%)	389 (92%)	35 (8%)	0	100	100
3	I	745/873 (85%)	656 (88%)	89 (12%)	0	100	100
3	J	745/873 (85%)	638 (86%)	107 (14%)	0	100	100
All	All	3894/5202 (75%)	3475 (89%)	417 (11%)	2 (0%)	50	80

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	484	GLU
1	C	79	VAL

### 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	162/208 (78%)	161 (99%)	1 (1%)	84	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	162/208 (78%)	162 (100%)	0	100	100
1	E	162/208 (78%)	161 (99%)	1 (1%)	84	88
1	G	162/208 (78%)	162 (100%)	0	100	100
2	B	374/560 (67%)	370 (99%)	4 (1%)	70	79
2	D	374/560 (67%)	371 (99%)	3 (1%)	79	84
2	F	374/560 (67%)	371 (99%)	3 (1%)	79	84
2	H	374/560 (67%)	370 (99%)	4 (1%)	70	79
3	I	667/766 (87%)	662 (99%)	5 (1%)	81	86
3	J	667/766 (87%)	660 (99%)	7 (1%)	73	81
All	All	3478/4604 (76%)	3450 (99%)	28 (1%)	77	84

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	214	LYS
3	J	764	TYR
3	I	450	ARG
3	J	532	LYS
3	I	97	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	206	HIS
3	I	638	GLN
3	J	522	GLN
3	I	225	ASN
3	I	437	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 [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.

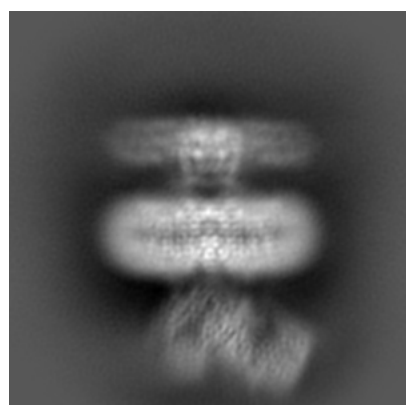
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32335. These allow visual inspection of the internal detail of the map and identification of artifacts.

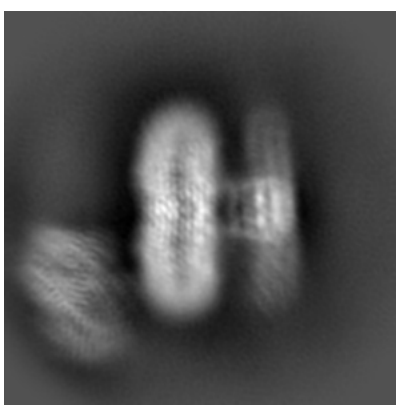
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

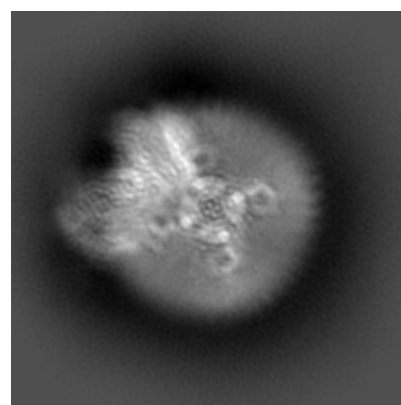
#### 6.1.1 Primary map



X



Y

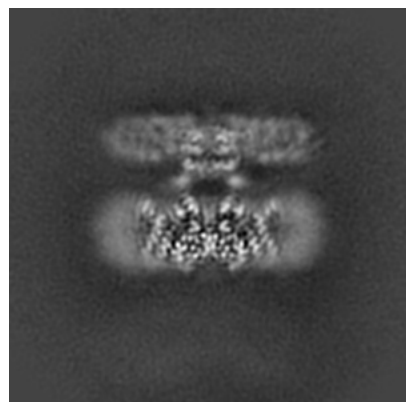


Z

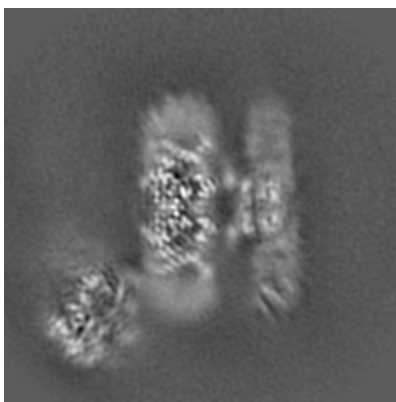
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

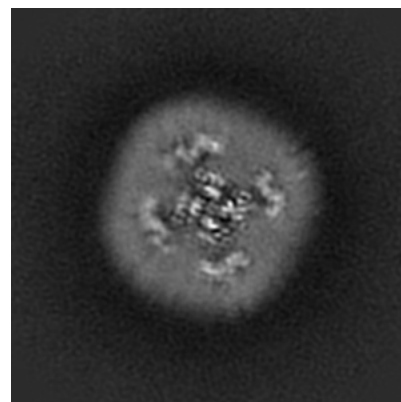
#### 6.2.1 Primary map



X Index: 135



Y Index: 135

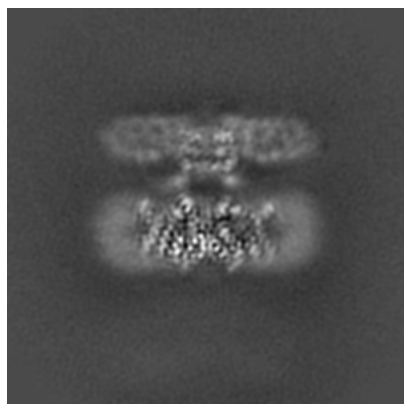


Z Index: 135

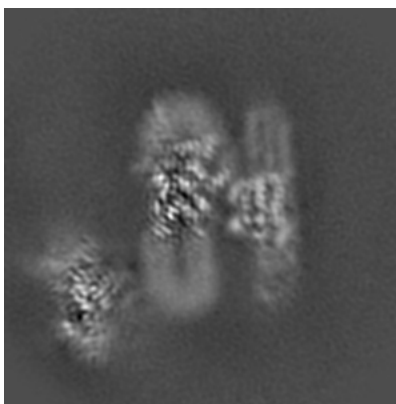
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

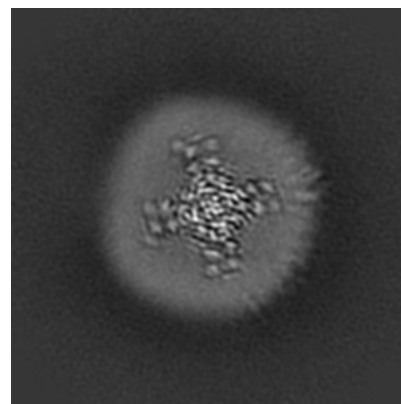
### 6.3.1 Primary map



X Index: 137



Y Index: 144



Z Index: 107

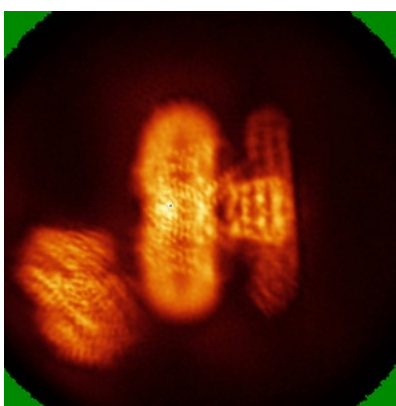
The images above show the largest variance slices of the map in three orthogonal directions.

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

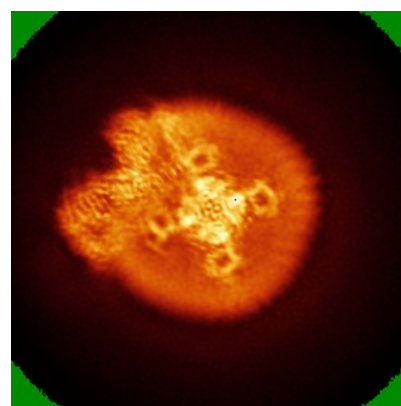
### 6.4.1 Primary map



X



Y

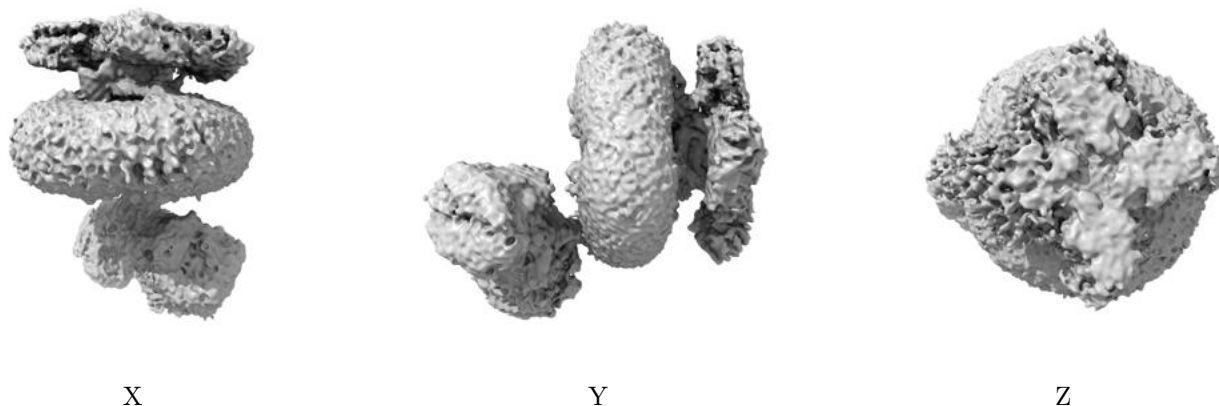


Z

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 0.0956. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

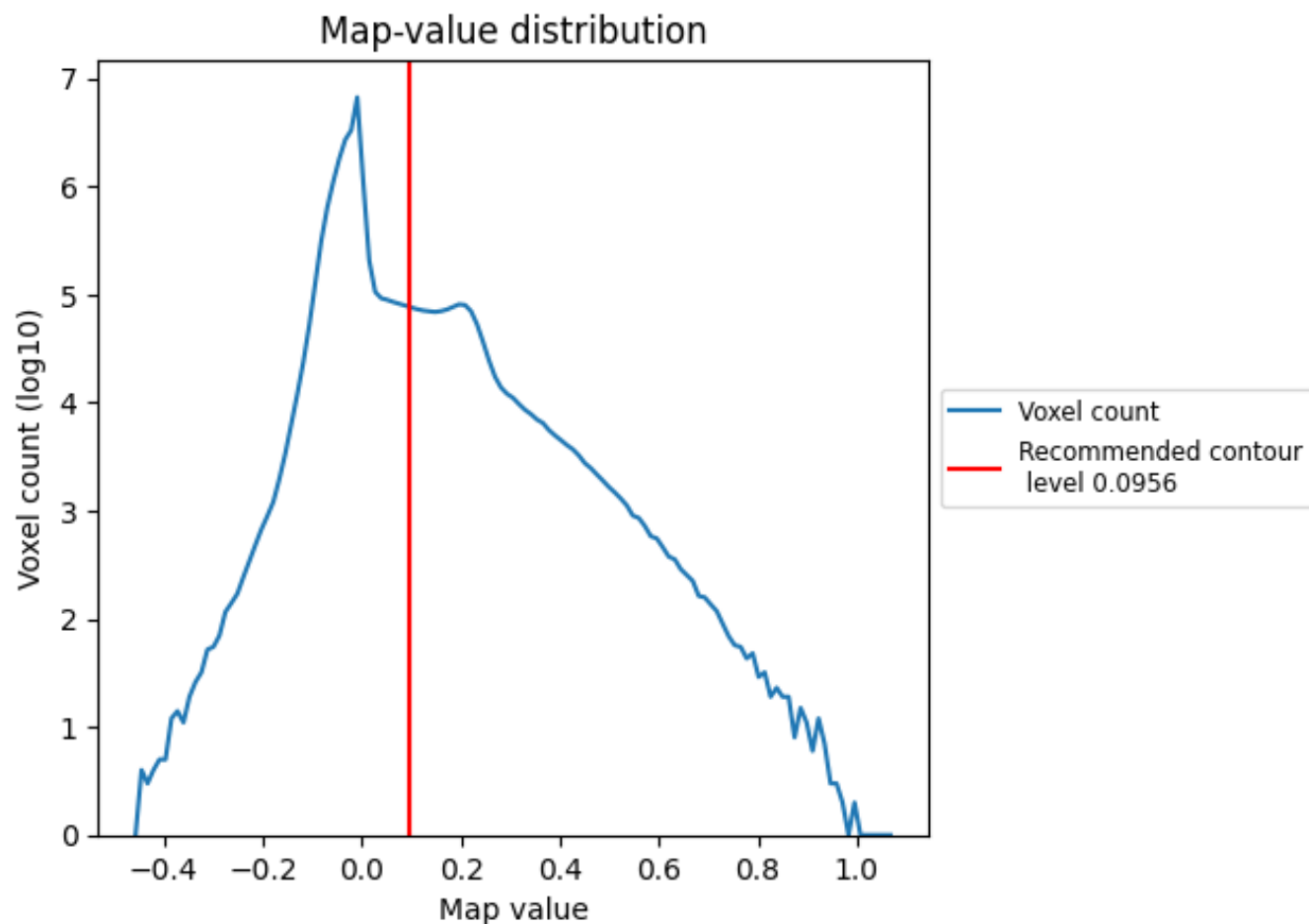
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

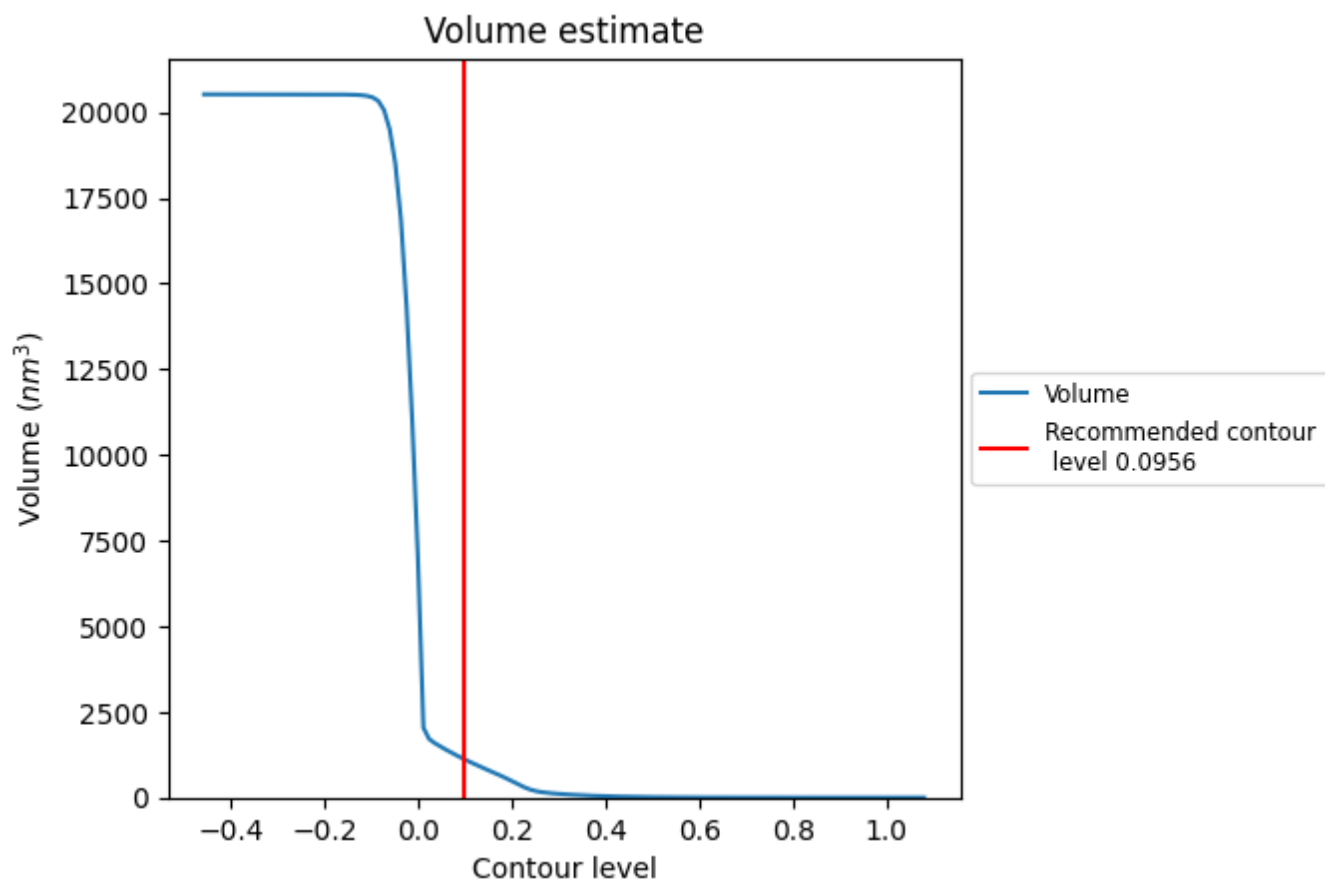
This section contains the results of statistical analysis of the map.

### 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.

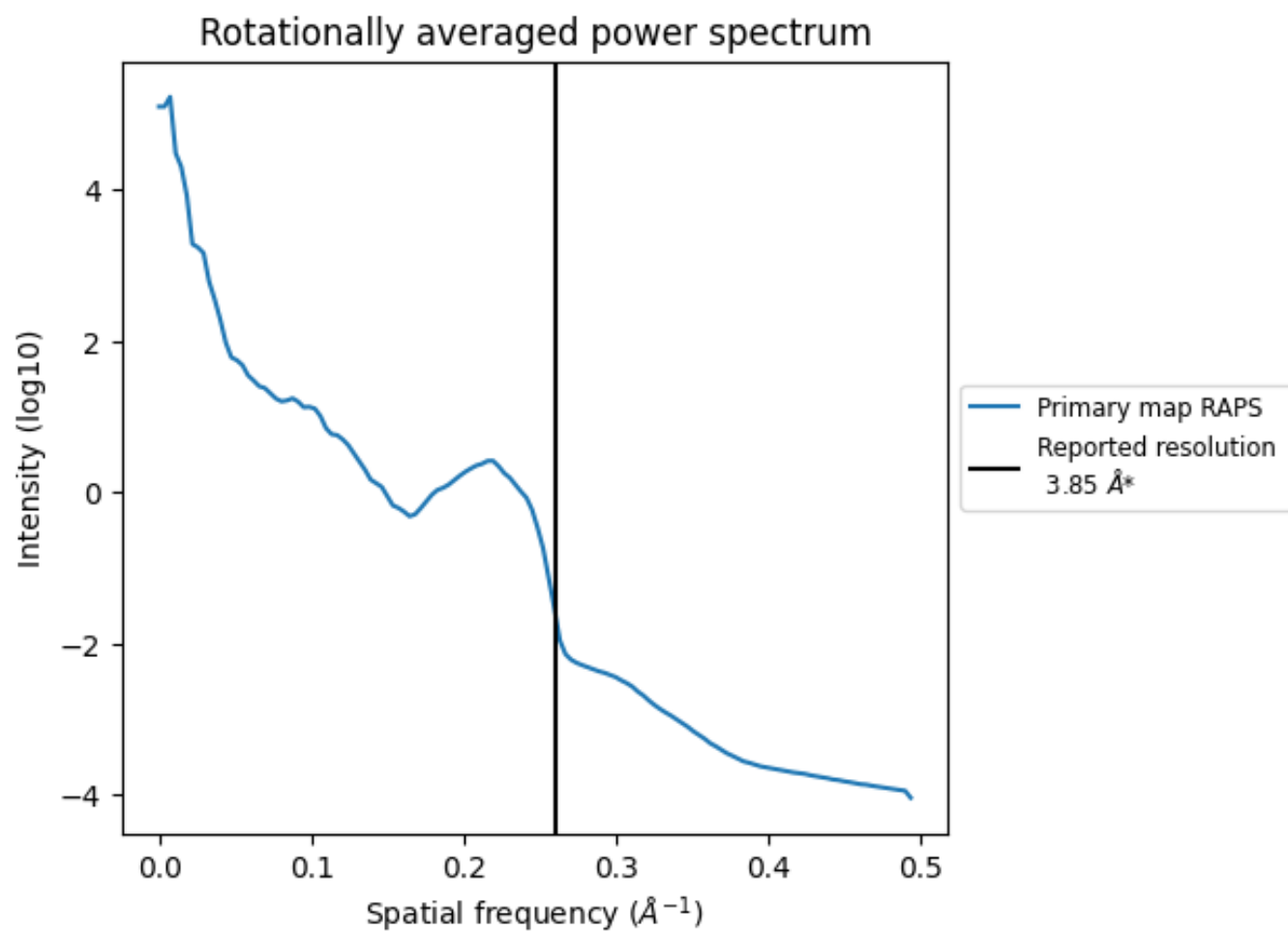
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1137  $\text{nm}^3$ ; this corresponds to an approximate mass of 1027 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 0.260 Å<sup>-1</sup>



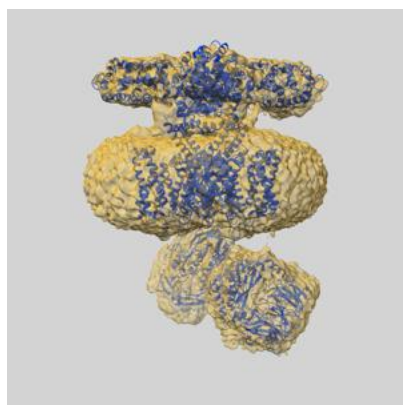
## 8 Fourier-Shell correlation

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

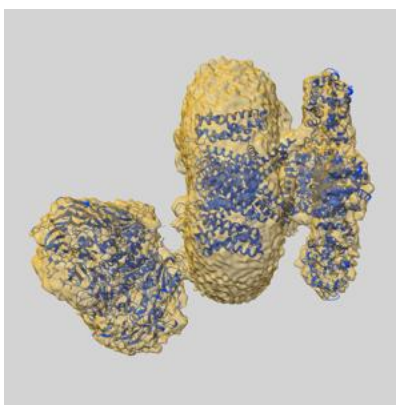
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32335 and PDB model 7W6T. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

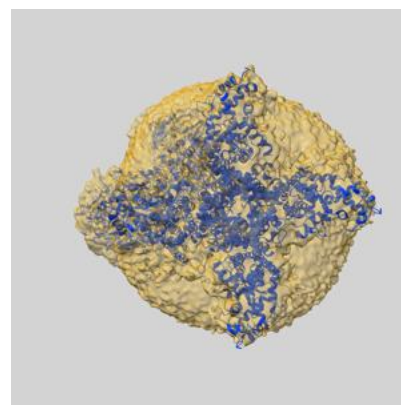
### 9.1 Map-model overlay [i](#)



X



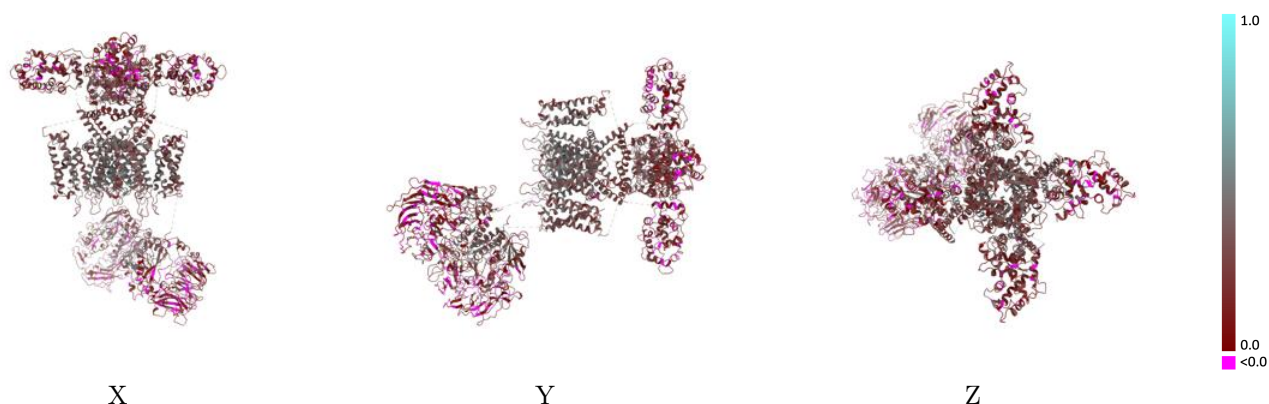
Y



Z

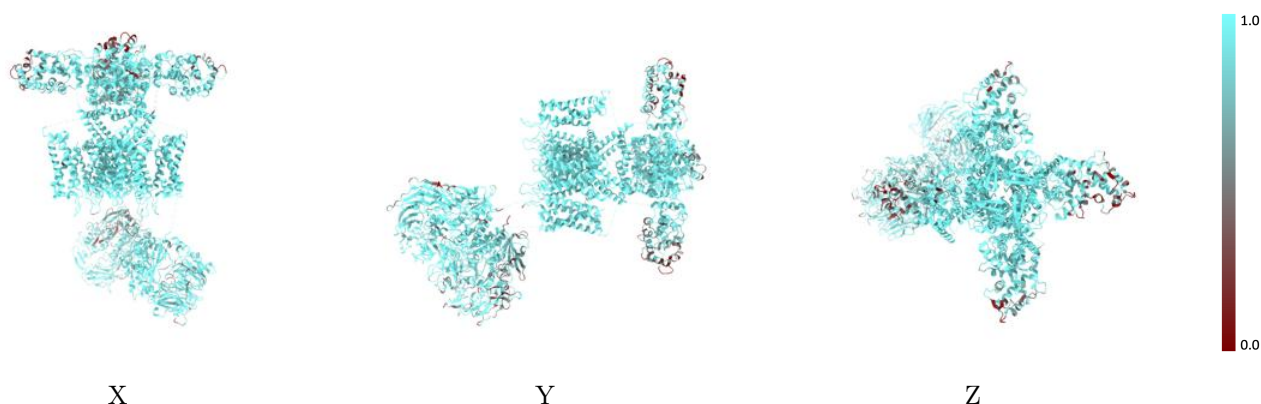
The images above show the 3D surface view of the map at the recommended contour level 0.0956 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



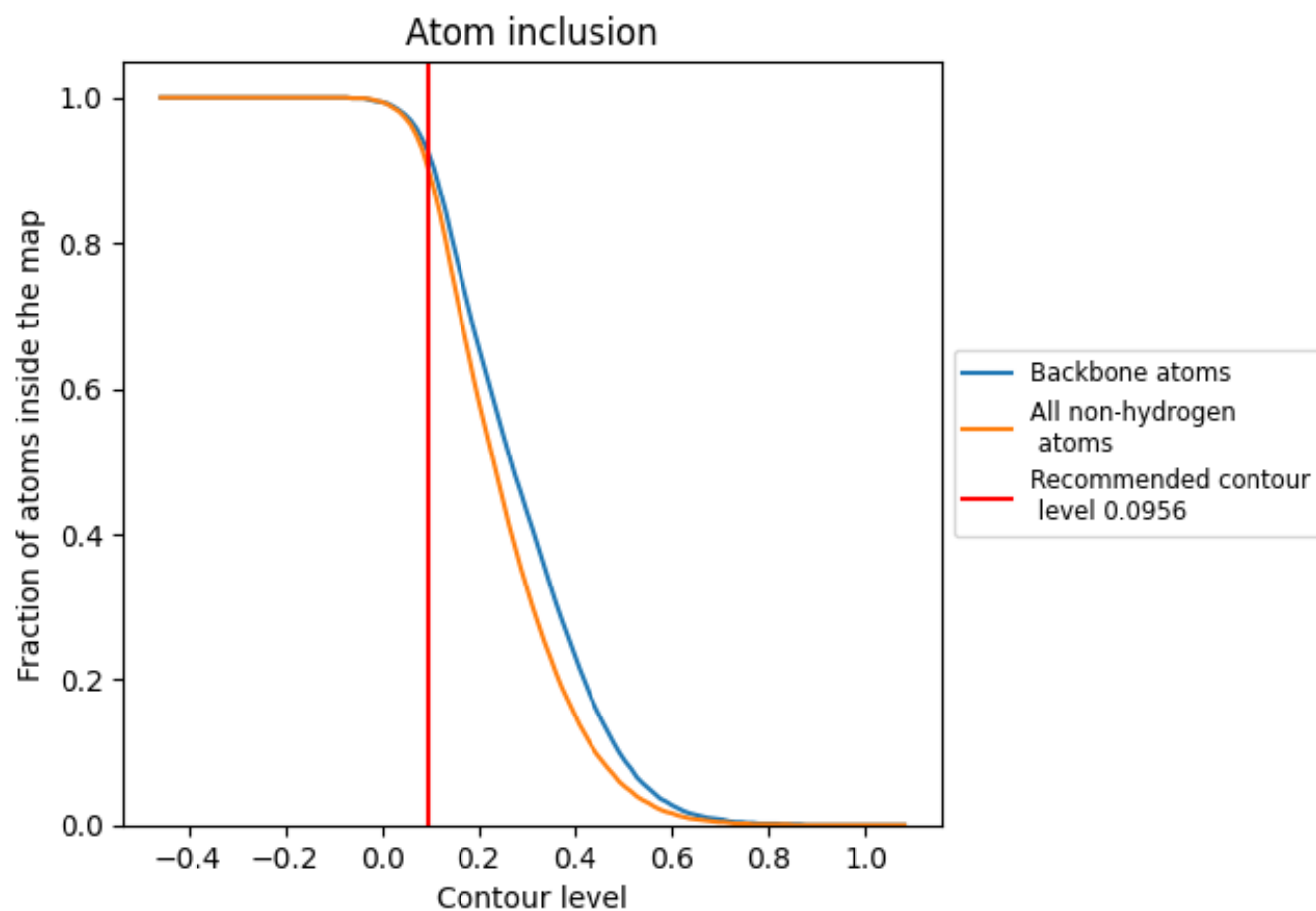
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0956).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.0956) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9020	<div></div> 0.2500
A	<div></div> 0.6920	<div></div> 0.1520
B	<div></div> 0.9770	<div></div> 0.3270
C	<div></div> 0.8610	<div></div> 0.1880
D	<div></div> 0.9800	<div></div> 0.3190
E	<div></div> 0.6780	<div></div> 0.1440
F	<div></div> 0.9740	<div></div> 0.3320
G	<div></div> 0.8020	<div></div> 0.1840
H	<div></div> 0.9770	<div></div> 0.3340
I	<div></div> 0.9330	<div></div> 0.1940
J	<div></div> 0.8440	<div></div> 0.2080

1.0

0.0

<0.0