



wwPDB EM Validation Summary Report ⓘ

Nov 12, 2022 – 05:45 PM EST

PDB ID : 6V4J
EMDB ID : EMD-21041
Title : Structure of TrkH-TrkA in complex with ATP
Authors : Zhou, M.; Zhang, H.
Deposited on : 2019-11-27
Resolution : 2.97 Å(reported)

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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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

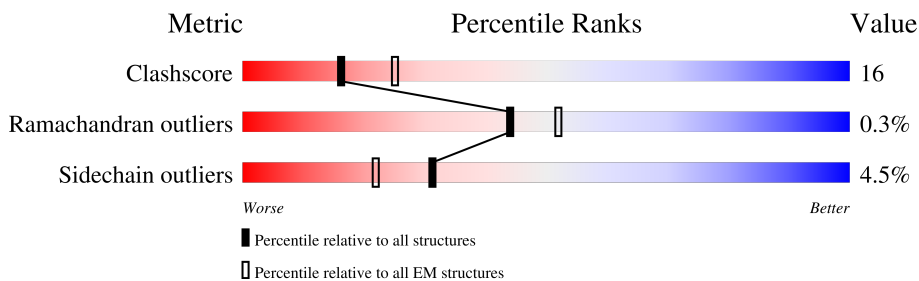
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.97 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	485	
1	B	485	
1	C	485	
1	D	485	
2	E	458	
2	F	458	
2	G	458	
2	H	458	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20637 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 Trk system potassium uptake protein TrkH.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	447	Total	C	N	O	S	0	0
			3450	2320	538	575	17		
1	B	434	Total	C	N	O	S	0	0
			3354	2256	524	557	17		
1	C	442	Total	C	N	O	S	0	0
			3414	2297	532	568	17		
1	D	438	Total	C	N	O	S	0	0
			3390	2282	528	563	17		

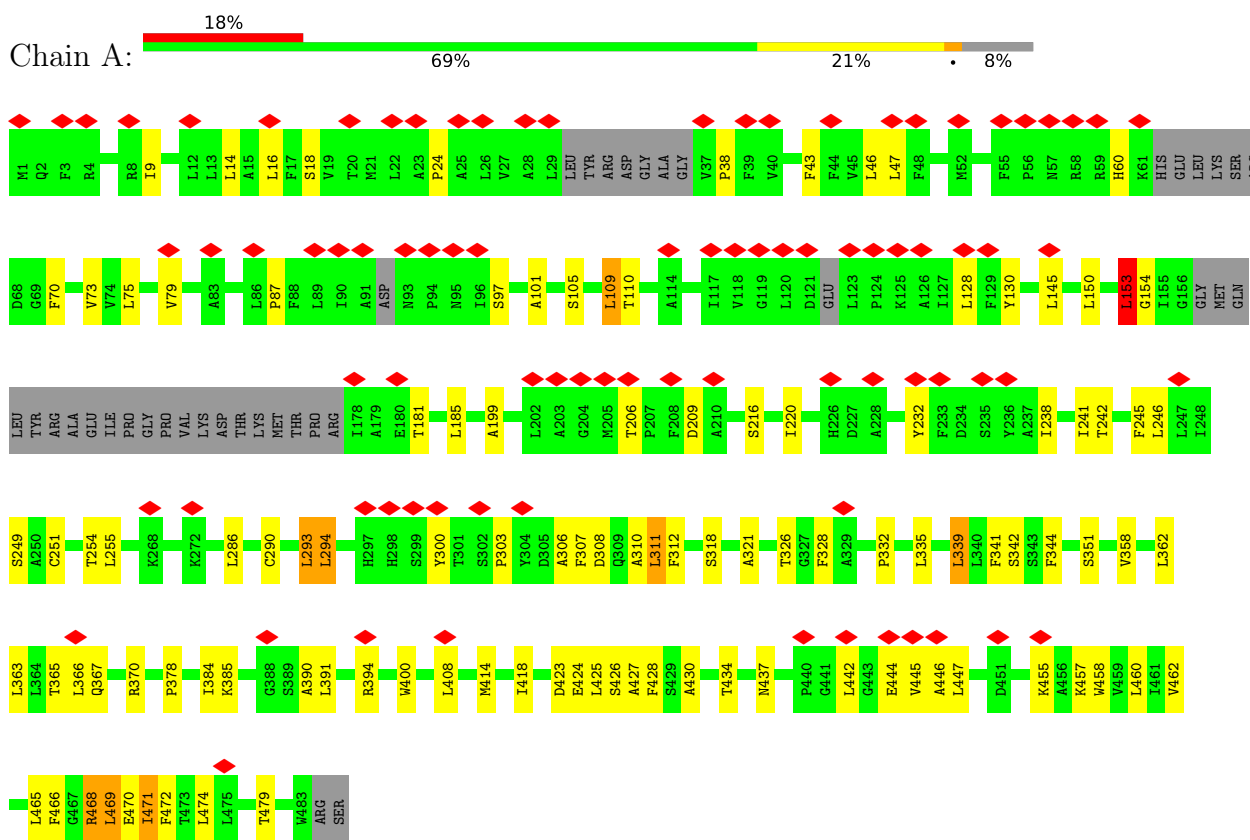
- Molecule 2 is a protein called Potassium uptake protein TrkA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	234	Total	C	N	O	S	0	0
			1748	1088	303	348	9		
2	F	234	Total	C	N	O	S	0	0
			1767	1099	307	351	10		
2	G	234	Total	C	N	O	S	0	0
			1753	1090	307	347	9		
2	H	234	Total	C	N	O	S	0	0
			1761	1094	307	351	9		

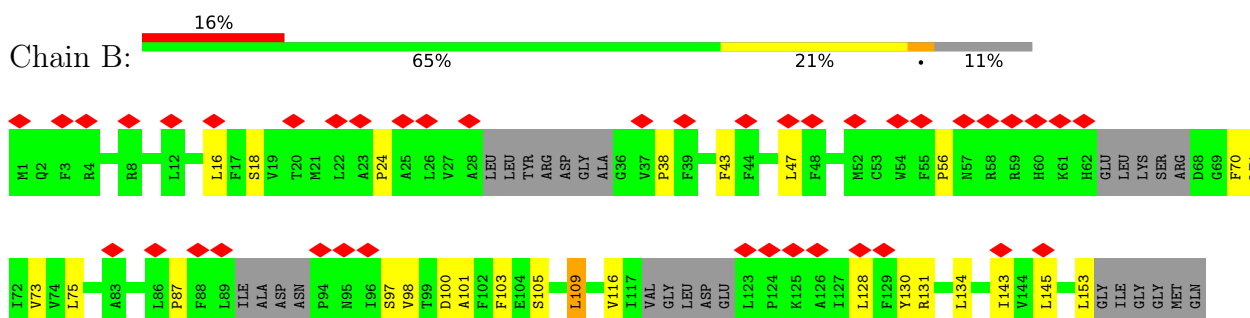
3 Residue-property plots

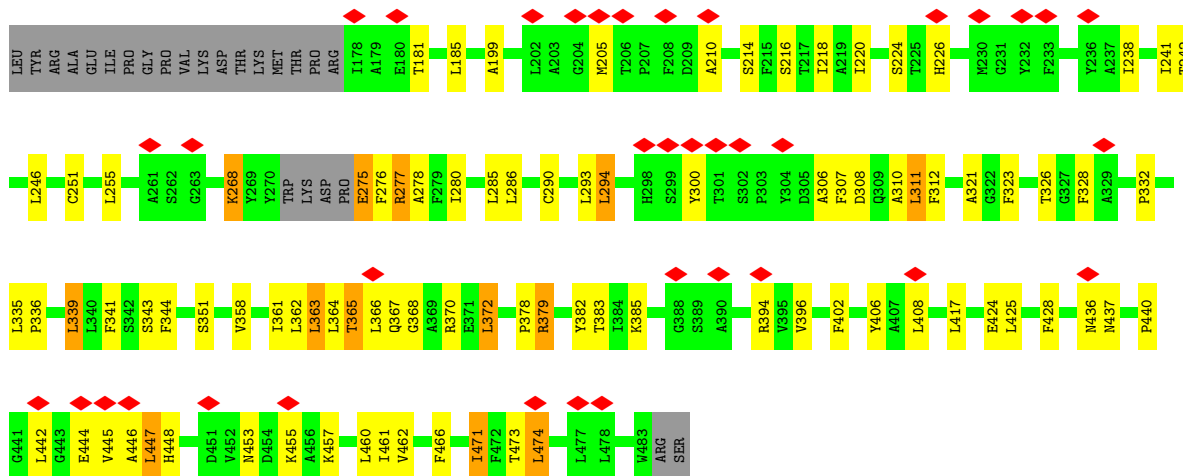
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

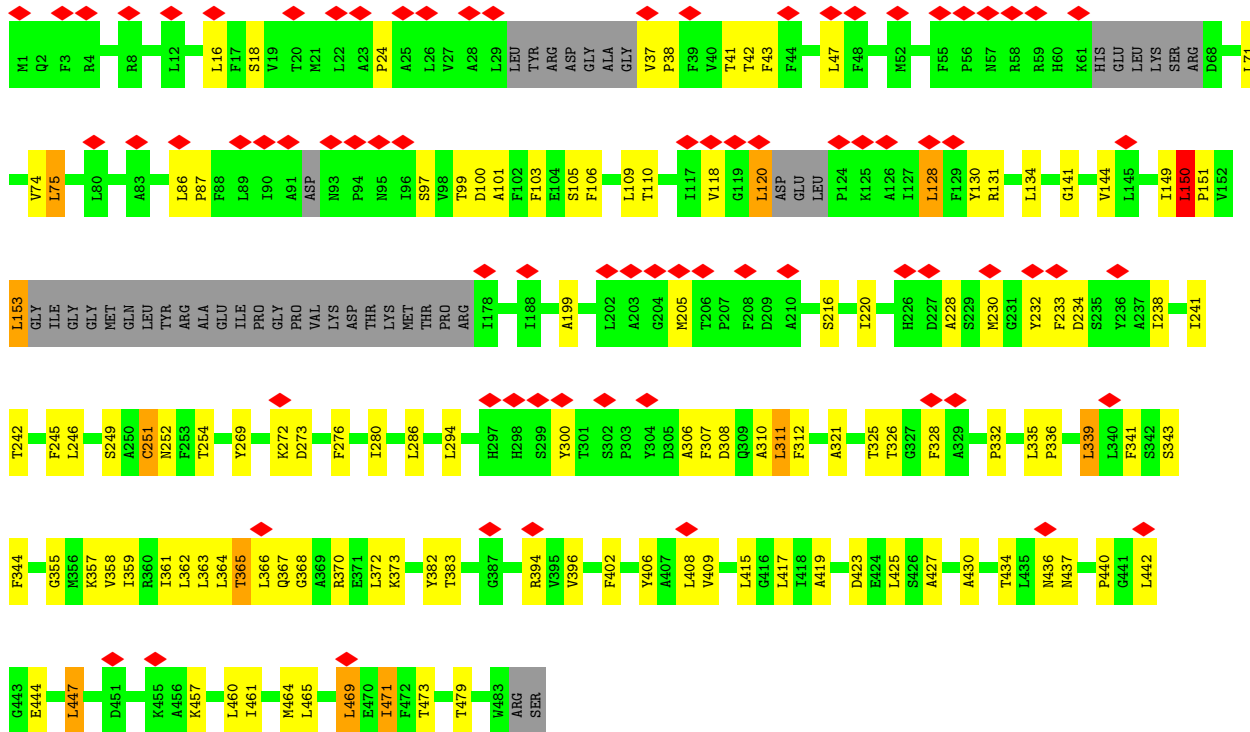


- Molecule 1: Trk system potassium uptake protein TrkH

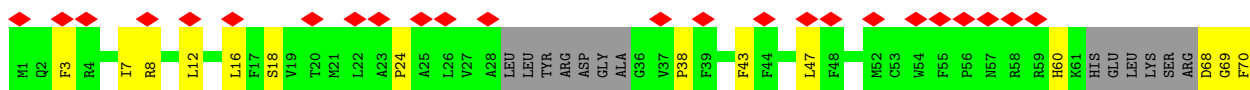


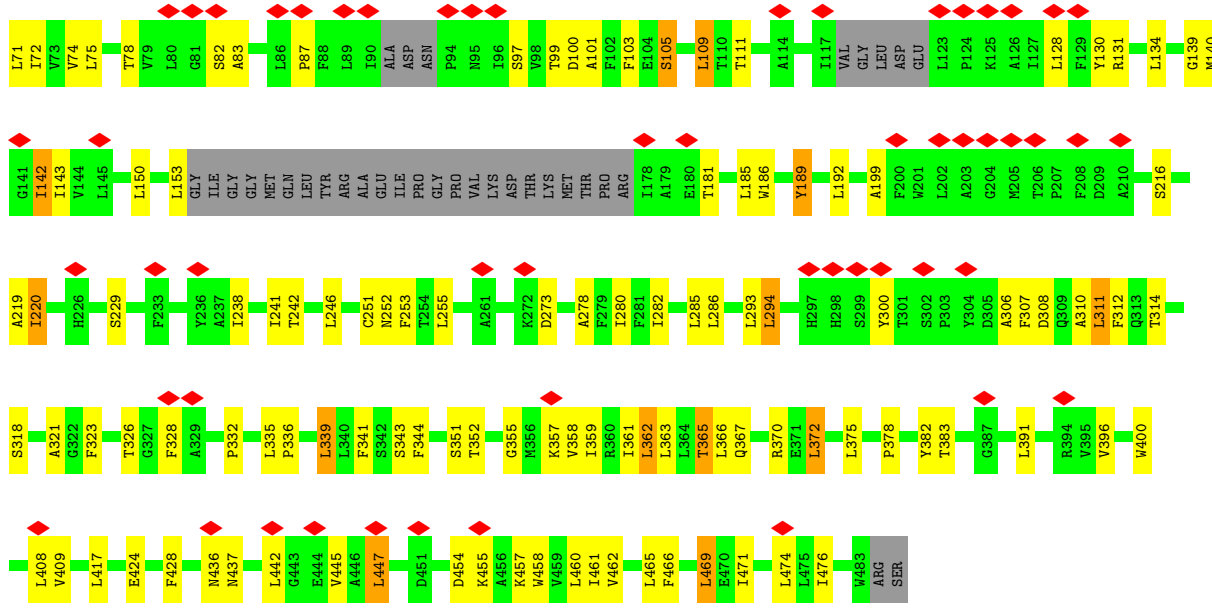


• Molecule 1: Trk system potassium uptake protein TrkH

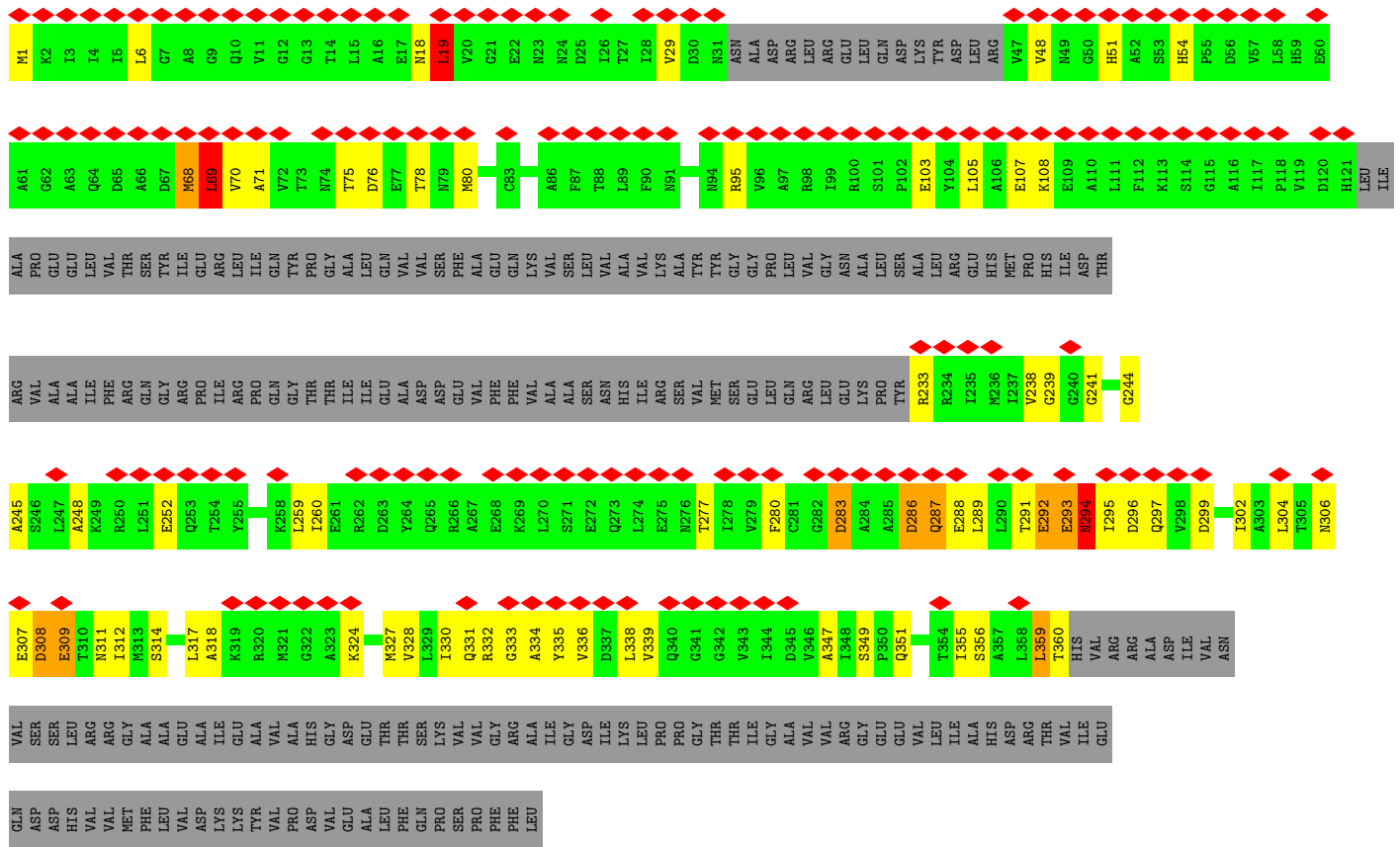
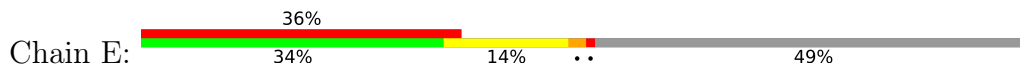


• Molecule 1: Trk system potassium uptake protein TrkH

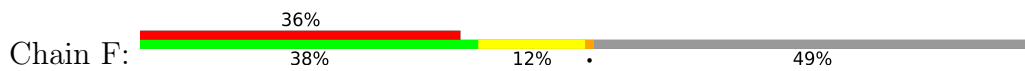




• Molecule 2: Potassium uptake protein TrkA

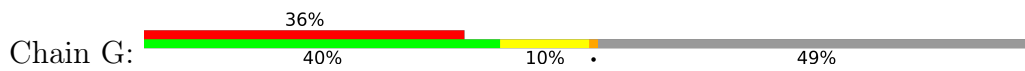


• Molecule 2: Potassium uptake protein TrkA

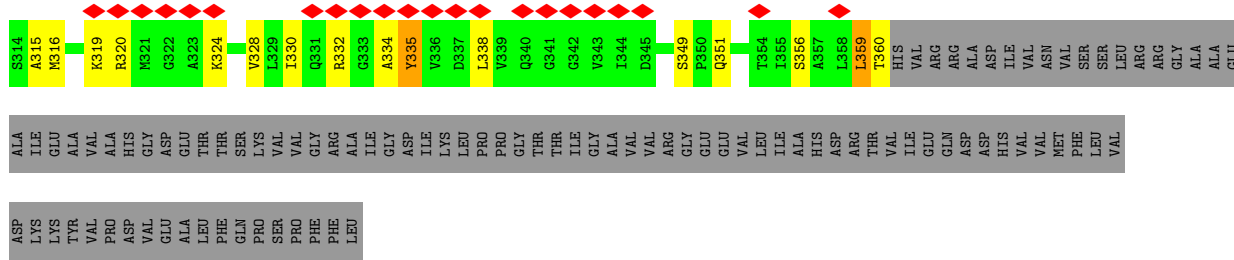


M1	K2	I3	I4	I5	L6	G7	A8	G9	Q10	V11	G12	G13	T14	L15	A16	E17	N18	L19	V20	G21	E22	N23	N24	D25	I26	T27	I28	V29	D30	N31	ASN	ALA	ASP	ARG	LEU	GLU	LYS	GLN	ASP	LYS	TYR	ASP	ARG	V47	V48	M49	G50	H51	A52	H54	P55	D56	V57	L58	H59	E60			
A61	G62	A63	Q64	D65	A66	D67	M68	L69	V70	A71	V72	T73	N74	T75	D76	E77	T78	N79	M80	C83	A86	F87	T88	L89	F90	N91	N94	R95	V96	A97	R98	I99	R100	LYS	ALA	LEU	PRO	TYR	E103	Y104	L105	A106	E107	K108	E109	A110	L111	F112	K113	S114	G115	I116	I117	P118	V119	D120	H121	LEU	ILE
ALA	PRO	GLU	GLU	LEU	VAL	THR	SER	TYR	ILE	GLU	PRO	GLY	THR	GLY	ALA	LEU	GLN	VAL	VAL	ASP	SER	PHE	ALA	ALA	GLY	GLN	GLY	TYR	GLY	PRO	PRO	LEU	VAL	ASN	ALA	LEU	PRO	TYR	ASP	ALA	LEU	ARG	GLU	GLU	HIS	HIS	MET	PRO	HIS	ILE	ASP	ASP	THR						
ARG	VAL	ALA	ALA	ILE	PHE	ARG	GLN	GLY	ARG	PRO	GLN	THR	THR	ILE	ILE	GLU	ALA	ASP	ASP	GLY	VAL	PHE	PHE	VAL	PHE	VAL	VAL	GLY	GLY	LEU	GLN	ARG	LEU	LYS	PRO	TYR	R233	R234	I235	M236	I237	V238	G239	G240	G241	N242	I243												
G244	A245	S246	L247	A248	K249	R250	L251	E252	Q253	T254	Y255	S256	V257	K258	L259	R262	D263	Y264	D265	R266	A267	K269	L270	S271	E272	Q273	L274	E275	M276	T277	I278	V279	F280	C281	G282	D283	A284	A285	D286	Q287	E288	L289	L290	T291	E292	E293	N294	I295	D296	Q297	V298	D299	I302	A303	L304	T305			
N306	E307	D308	E309	T310	N311	I312	M313	S314	A315	M316	L317	A318	K319	R320	M321	G322	A323	K324	K325	V326	M327	I330	Q331	R332	G333	A334	Y335	V336	D337	L338	V339	Q340	G341	G342	V343	I344	D345	T354	L358	L359	T360	HIS	VAL	ARG	ARG	VAL	ALA	ASP	ALA	ILE	VAL	ASN	VAL	SER	SER	LEU	ARG	ARG	
GLY	ALA	ALA	GLU	ILE	ALA	GLU	VAL	ALA	HIS	GLY	ASP	GLU	THR	THR	LYS	VAL	VAL	ARG	ALA	ILE	GLY	ASP	ILE	GLY	ILE	VAL	VAL	VAL	VAL	ARG	GLY	GLY	GLY	GLU	GLU	VAL	LEU	ILE	HIS	ASP	ASP	THR	THR	VAL	ILE	GLU	GLN	ASP	ASP	HIS	VAL	VAL							
MET	PHE	LEU	VAL	ASP	LYS	LYS	TYR	VAL	PRO	PRO	ASP	VAL	VAL	PHE	GLN	PRO	SER	PRO	PHE	PHE	LEU																																						

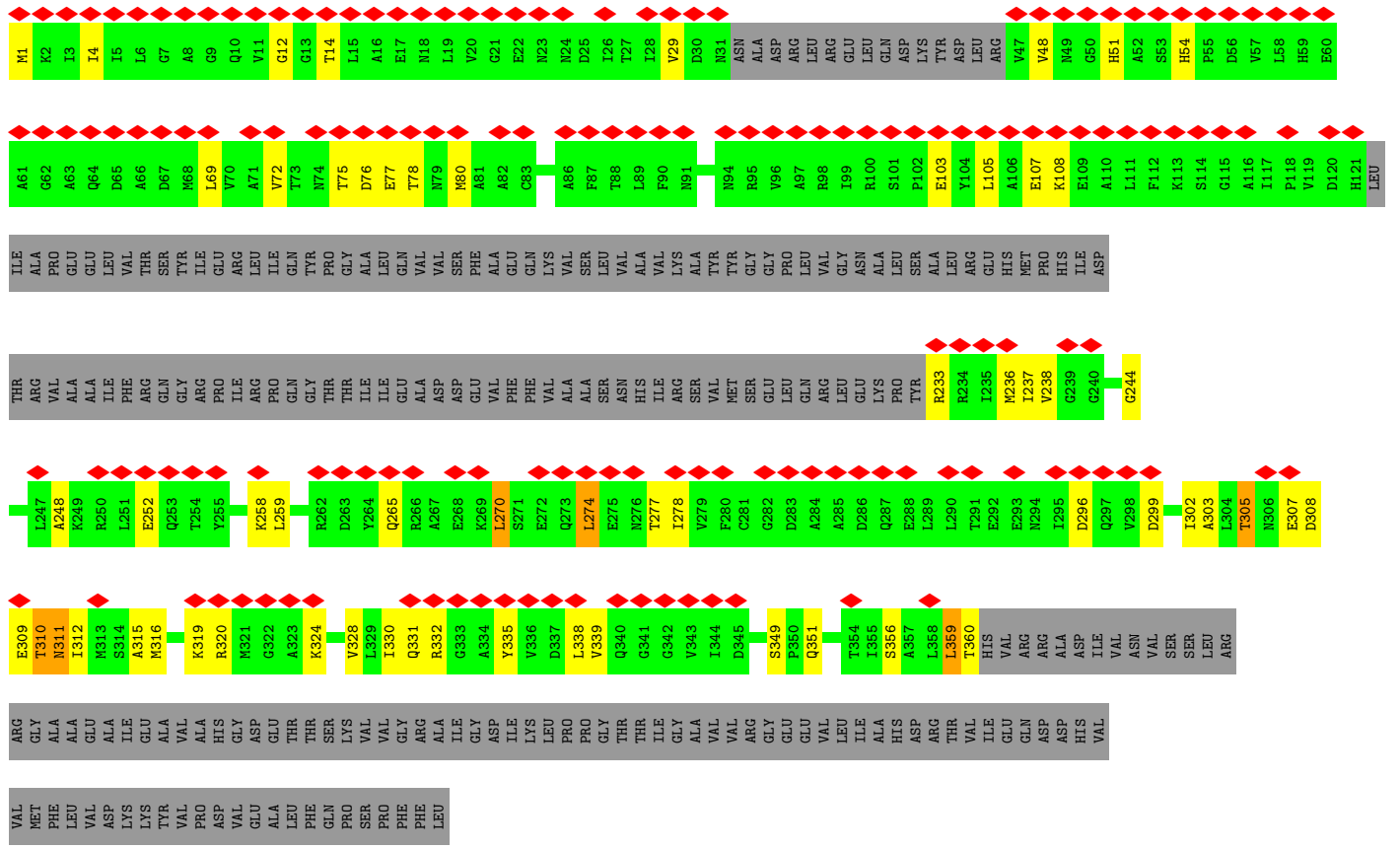
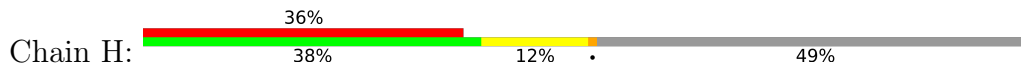
• Molecule 2: Potassium uptake protein TrkA



M1	K2	I3	I4	I5	L6	G7	A8	G9	Q10	V11	G12	G13	T14	L15	A16	E17	N18	L19	V20	G21	E22	N23	N24	D25	I26	T27	I28	V29	D30	N31	ASN	ALA	ASP	ARG	LEU	GLU	LYS	GLN	ASP	LYS	TYR	ASP	ARG	V47	V48	M49	G50	H51	A52	H54	P55	D56	V57	L58	H59	E60			
A61	G62	A63	Q64	D65	A66	D67	M68	L69	V70	A71	V72	T73	N74	T75	D76	E77	T78	N79	M80	C83	A86	F87	T88	L89	F90	N91	N94	R95	V96	A97	R98	I99	R100	LYS	ALA	LEU	PRO	TYR	E103	Y104	L105	A106	E107	K108	E109	A110	L111	F112	K113	S114	G115	I116	I117	P118	V119	D120	H121	LEU	ILE
ALA	PRO	GLU	GLU	LEU	VAL	THR	SER	TYR	ILE	GLU	PRO	GLY	THR	GLY	ALA	LEU	GLN	VAL	VAL	ASP	SER	PHE	ALA	ALA	GLY	GLN	GLY	TYR	GLY	PRO	PRO	LEU	VAL	ASN	ALA	LEU	PRO	TYR	ASP	ALA	LEU	ARG	GLU	HIS	HIS	MET	PRO	HIS	ILE	ASP	THR								
ARG	VAL	ALA	ALA	ILE	PHE	ARG	GLN	GLY	ARG	PRO	GLN	THR	THR	ILE	ILE	GLU	ALA	ASP	ASP	GLY	VAL	PHE	PHE	VAL	VAL	VAL	VAL	GLY	GLY	LEU	GLN	ARG	LEU	LYS	PRO	TYR	R233	R234	I235	M236	I237	V238	G239	G240	G241	A245													
R250	L251	E252	Q253	T254	Y255	R258	R262	D263	T264	Q265	R266	A267	E268	R269	L270	S271	E272	Q273	L274	E275	M276	T277	I278	V279	F280	C281	G282	D283	A284	A285	D286	Q287	E288	L289	L290	T291	E292	E293	N294	I295	D296	Q297	V298	D299	A303	L304	T305	N306	E307	D308	E309	T310	N311	I312	H313				
ALA	PRO	GLU	GLU	LEU	VAL	THR	SER	TYR	ILE	GLU	PRO	GLY	THR	GLY	ALA	LEU	GLN	VAL	VAL	ASP	SER	PHE	ALA	ALA	GLY	GLN	GLY	TYR	GLY	PRO	PRO	LEU	VAL	ASN	ALA	LEU	PRO	TYR	R233	R234	I235	M236	I237	V238	G239	G240	G241	A245											



● Molecule 2: Potassium uptake protein TrkA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72317	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	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	0.261	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (\AA)	273.24, 273.24, 273.24	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.242, 1.242, 1.242	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	0.48	0/3546	0.94	20/4831 (0.4%)
1	B	0.46	0/3447	0.92	16/4692 (0.3%)
1	C	0.47	0/3510	0.90	13/4783 (0.3%)
1	D	0.46	0/3486	0.89	17/4748 (0.4%)
2	E	0.82	4/1763 (0.2%)	1.19	12/2388 (0.5%)
2	F	0.38	0/1782	0.72	2/2411 (0.1%)
2	G	0.36	0/1768	0.72	3/2394 (0.1%)
2	H	0.35	0/1776	0.73	2/2404 (0.1%)
All	All	0.49	4/21078 (0.0%)	0.90	85/28651 (0.3%)

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	B	0	1
1	C	0	2
2	E	0	3
2	H	0	1
All	All	0	7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	69	LEU	C-N	-27.42	0.70	1.34
2	E	68	MET	C-N	10.03	1.57	1.34
2	E	18	ASN	C-N	-8.95	1.13	1.34
2	E	19	LEU	C-N	6.59	1.49	1.34

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	68	MET	O-C-N	-28.54	77.04	122.70
2	E	68	MET	CA-C-N	20.00	161.19	117.20
2	E	68	MET	C-N-CA	16.50	162.96	121.70
2	E	18	ASN	C-N-CA	-13.95	86.82	121.70
2	E	18	ASN	O-C-N	13.00	143.50	122.70

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	275	GLU	Peptide
1	C	118	VAL	Peptide
1	C	251	CYS	Peptide
2	E	19	LEU	Mainchain
2	E	68	MET	Mainchain

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	3450	0	3527	85	0
1	B	3354	0	3426	88	0
1	C	3414	0	3485	90	0
1	D	3390	0	3465	90	0
2	E	1748	0	1745	110	0
2	F	1767	0	1780	74	0
2	G	1753	0	1756	73	0
2	H	1761	0	1763	99	0
All	All	20637	0	20947	661	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 16.

The worst 5 of 661 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:G:332:ARG:HD2	2:G:335:TYR:CE2	1.24	1.65

Continued on next page...

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:332:ARG:HB3	2:G:335:TYR:CZ	1.33	1.59
2:G:332:ARG:CB	2:G:335:TYR:CZ	1.86	1.56
2:G:332:ARG:CD	2:G:335:TYR:HE2	0.94	1.56
1:A:425:LEU:HD23	1:A:444:GLU:CG	1.43	1.45

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	435/485 (90%)	415 (95%)	20 (5%)	0	100	100
1	B	420/485 (87%)	408 (97%)	11 (3%)	1 (0%)	47	80
1	C	430/485 (89%)	415 (96%)	14 (3%)	1 (0%)	47	80
1	D	426/485 (88%)	411 (96%)	14 (3%)	1 (0%)	47	80
2	E	228/458 (50%)	210 (92%)	14 (6%)	4 (2%)	8	35
2	F	228/458 (50%)	221 (97%)	7 (3%)	0	100	100
2	G	228/458 (50%)	214 (94%)	13 (6%)	1 (0%)	34	70
2	H	228/458 (50%)	215 (94%)	12 (5%)	1 (0%)	34	70
All	All	2623/3772 (70%)	2509 (96%)	105 (4%)	9 (0%)	44	74

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	69	LEU
2	E	294	ASN
2	H	311	ASN
2	E	292	GLU
2	G	311	ASN

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	363/395 (92%)	344 (95%)	19 (5%)	23	57
1	B	353/395 (89%)	334 (95%)	19 (5%)	22	55
1	C	359/395 (91%)	342 (95%)	17 (5%)	26	61
1	D	357/395 (90%)	337 (94%)	20 (6%)	21	54
2	E	185/378 (49%)	177 (96%)	8 (4%)	29	64
2	F	190/378 (50%)	180 (95%)	10 (5%)	22	56
2	G	186/378 (49%)	184 (99%)	2 (1%)	73	90
2	H	188/378 (50%)	185 (98%)	3 (2%)	62	85
All	All	2181/3092 (70%)	2083 (96%)	98 (4%)	31	62

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	105	SER
1	D	400	TRP
1	D	142	ILE
1	D	293	LEU
2	E	283	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	287	GLN
2	F	311	ASN
2	H	265	GLN
2	G	311	ASN
1	B	448	HIS

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 monosaccharides 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
2	E	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	18:ASN	C	19:LEU	N	1.13
1	E	69:LEU	C	70:VAL	N	0.71

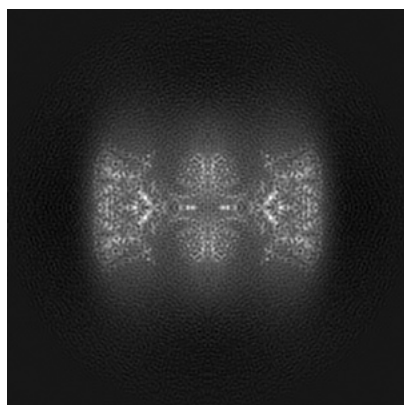
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21041. These allow visual inspection of the internal detail of the map and identification of artifacts.

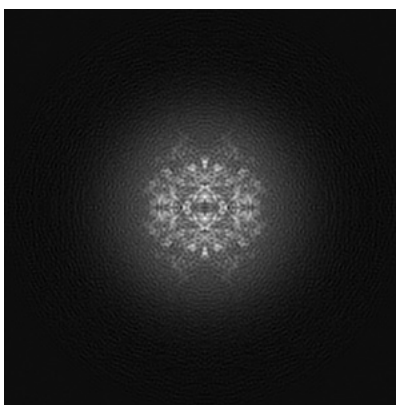
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

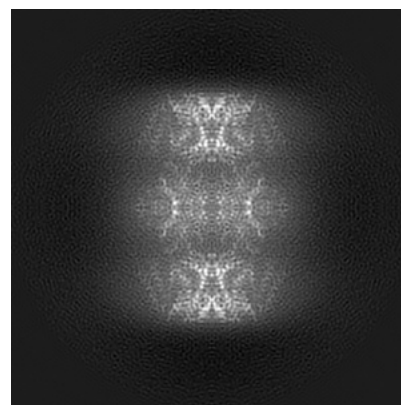
6.1.1 Primary map



X



Y

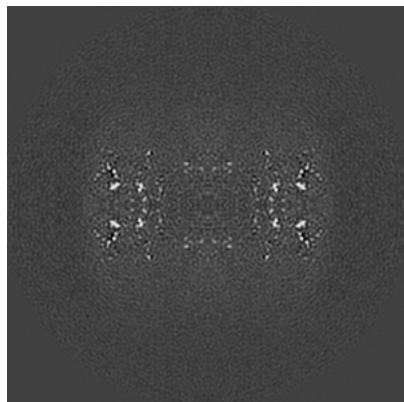


Z

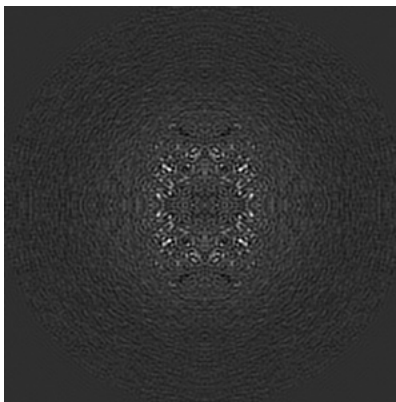
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

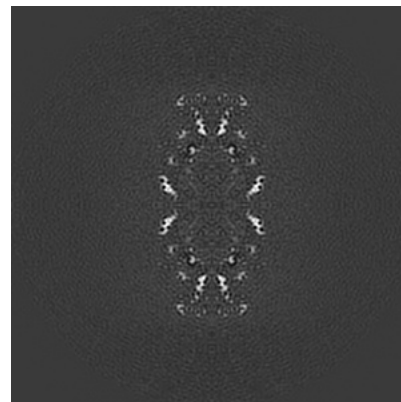
6.2.1 Primary map



X Index: 110



Y Index: 110

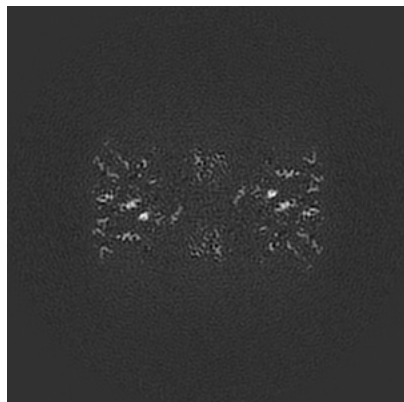


Z Index: 110

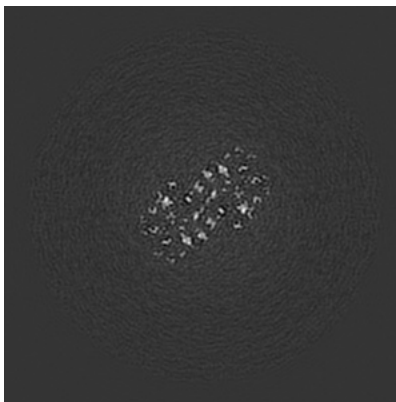
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

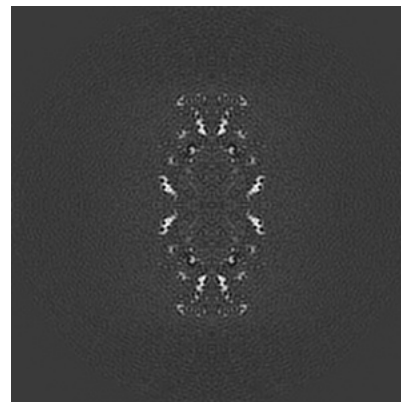
6.3.1 Primary map



X Index: 116



Y Index: 55

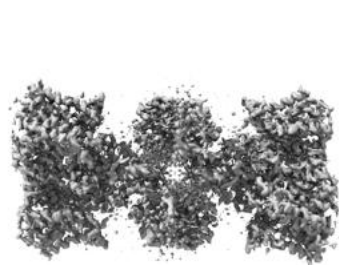


Z Index: 110

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

6.4 Orthogonal surface views [i](#)

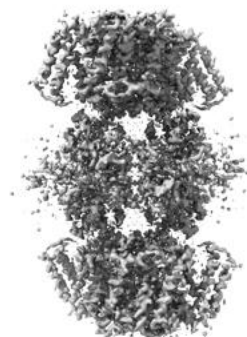
6.4.1 Primary map



X



Y



Z

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.

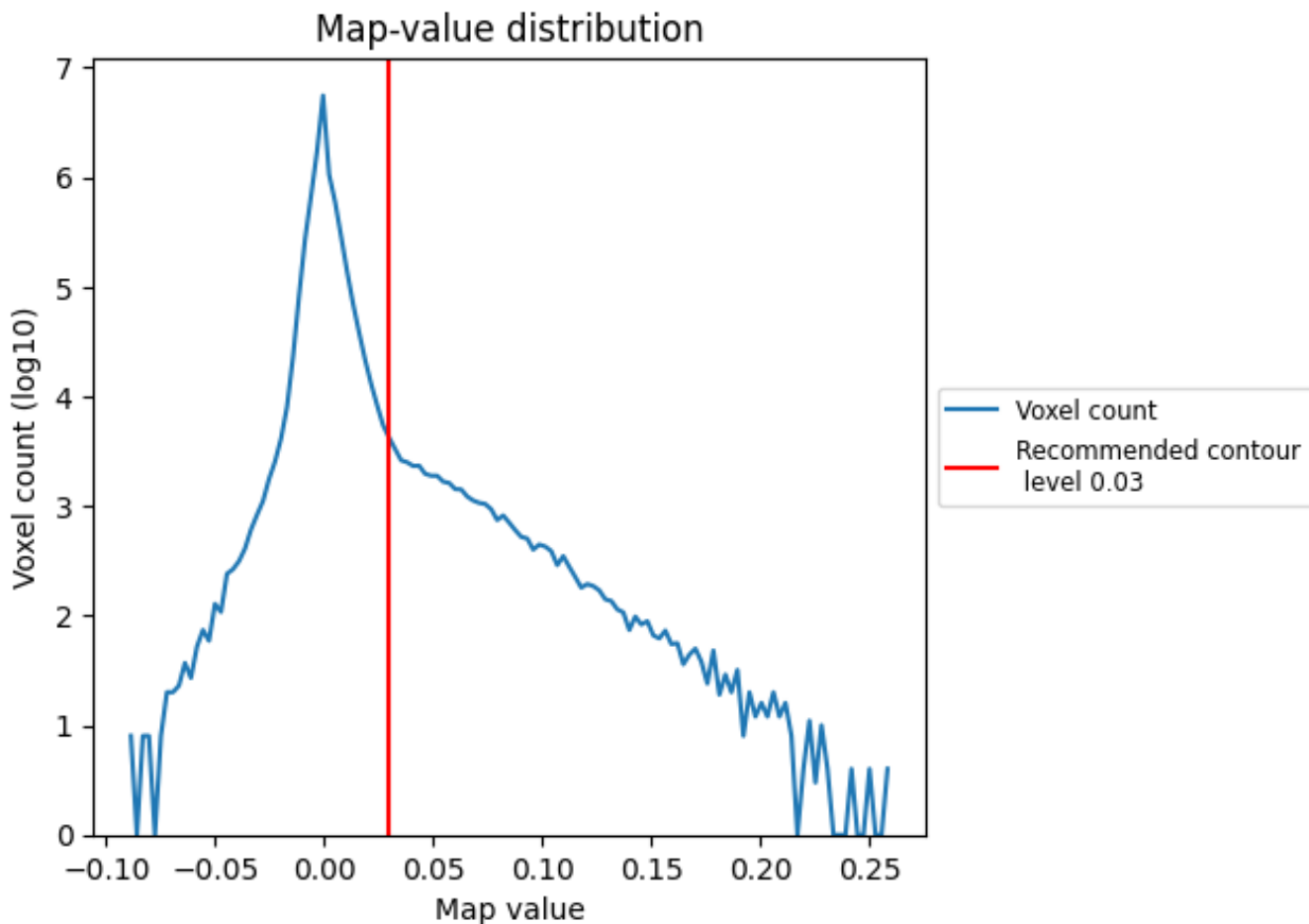
6.5 Mask visualisation

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

7 Map analysis [i](#)

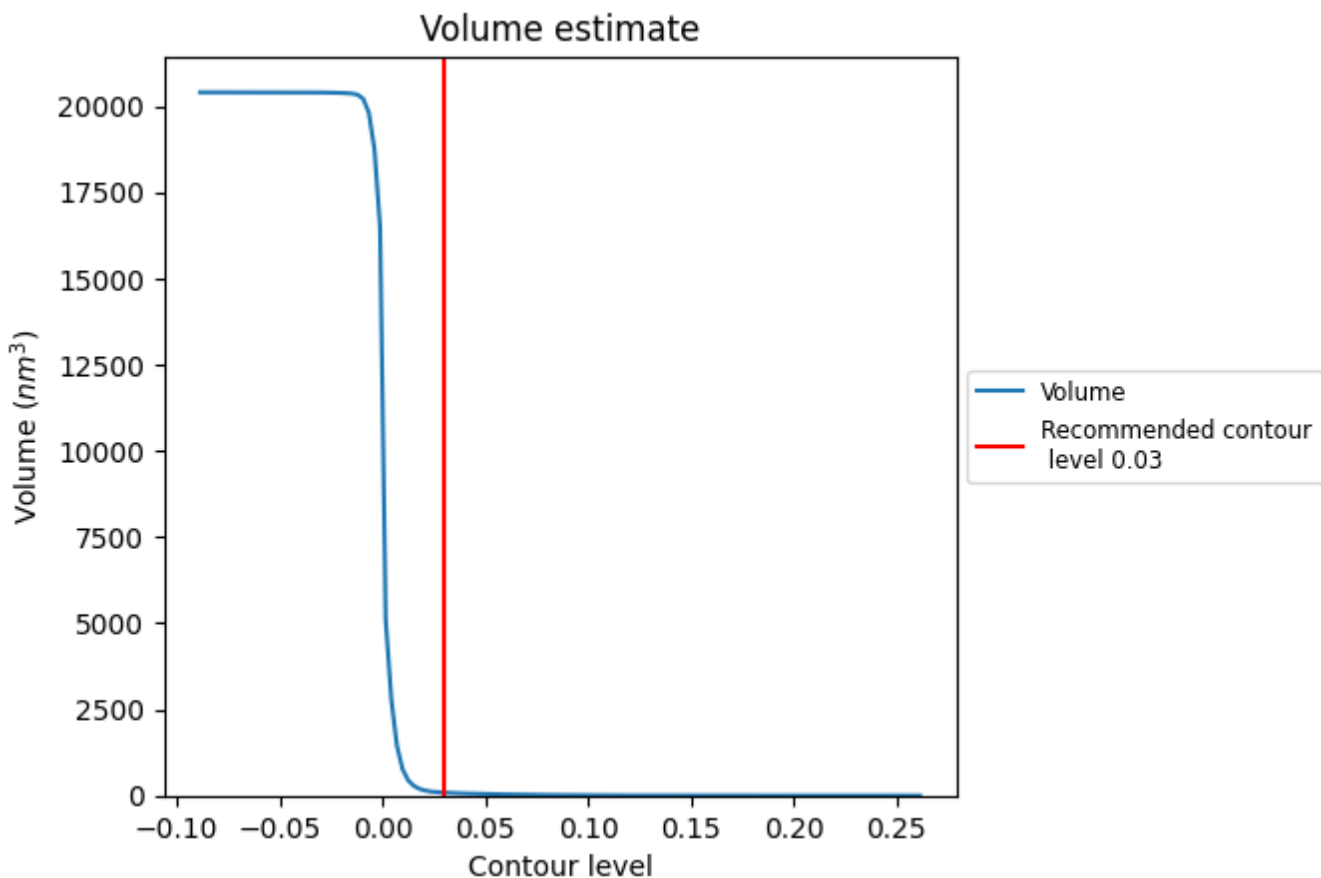
This section contains the results of statistical analysis of the map.

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.

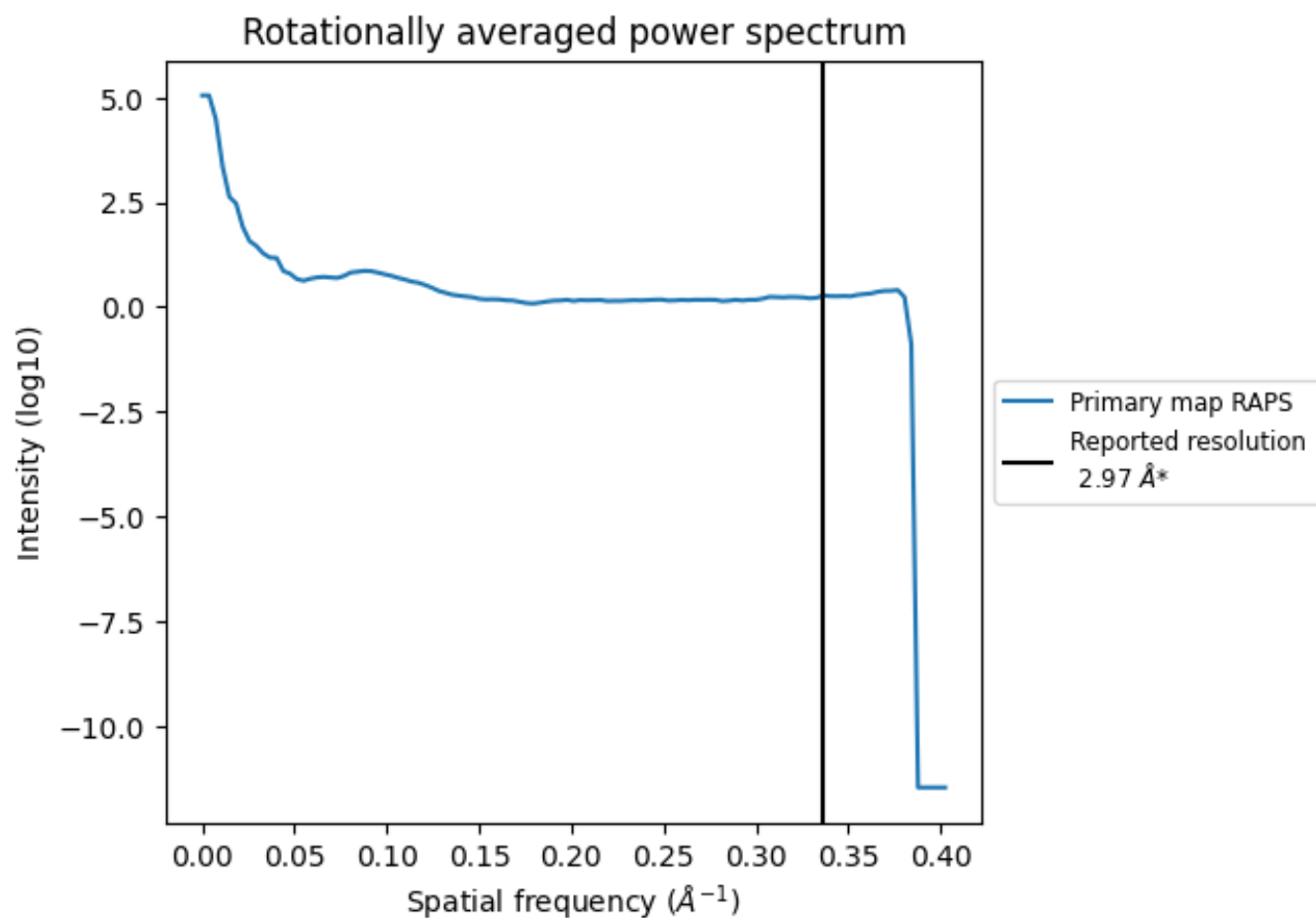
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 83 nm³; this corresponds to an approximate mass of 75 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.337 Å⁻¹

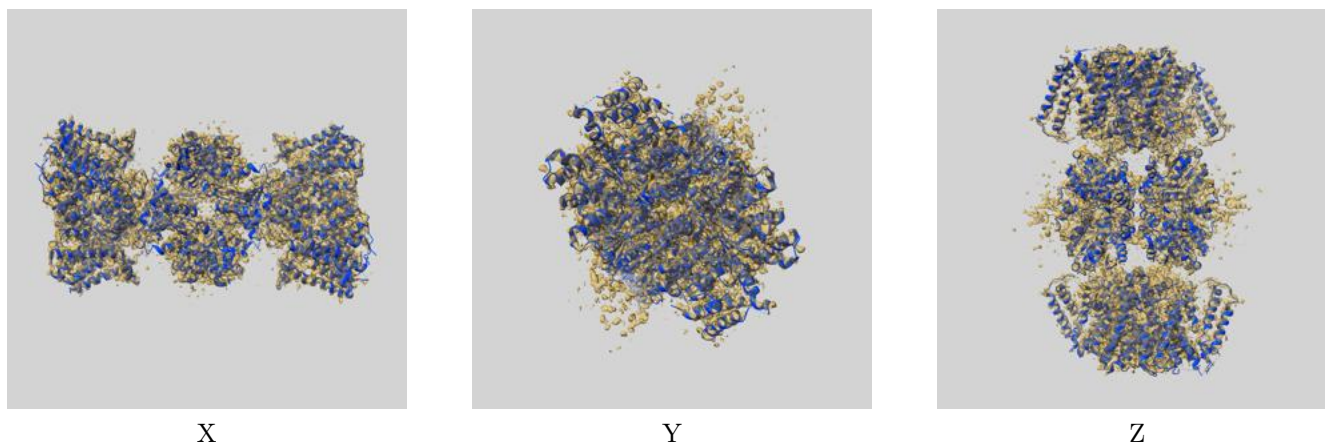
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

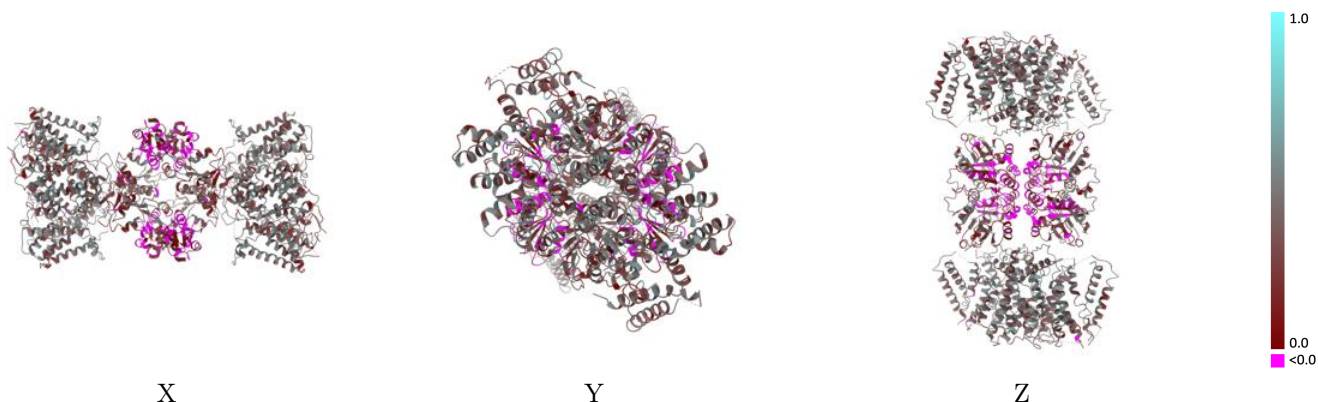
This section contains information regarding the fit between EMDB map EMD-21041 and PDB model 6V4J. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



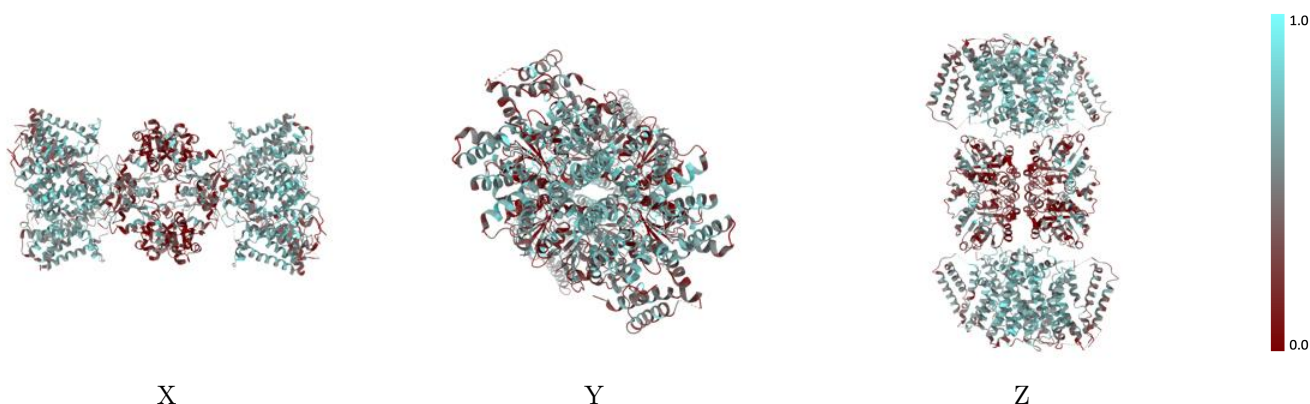
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



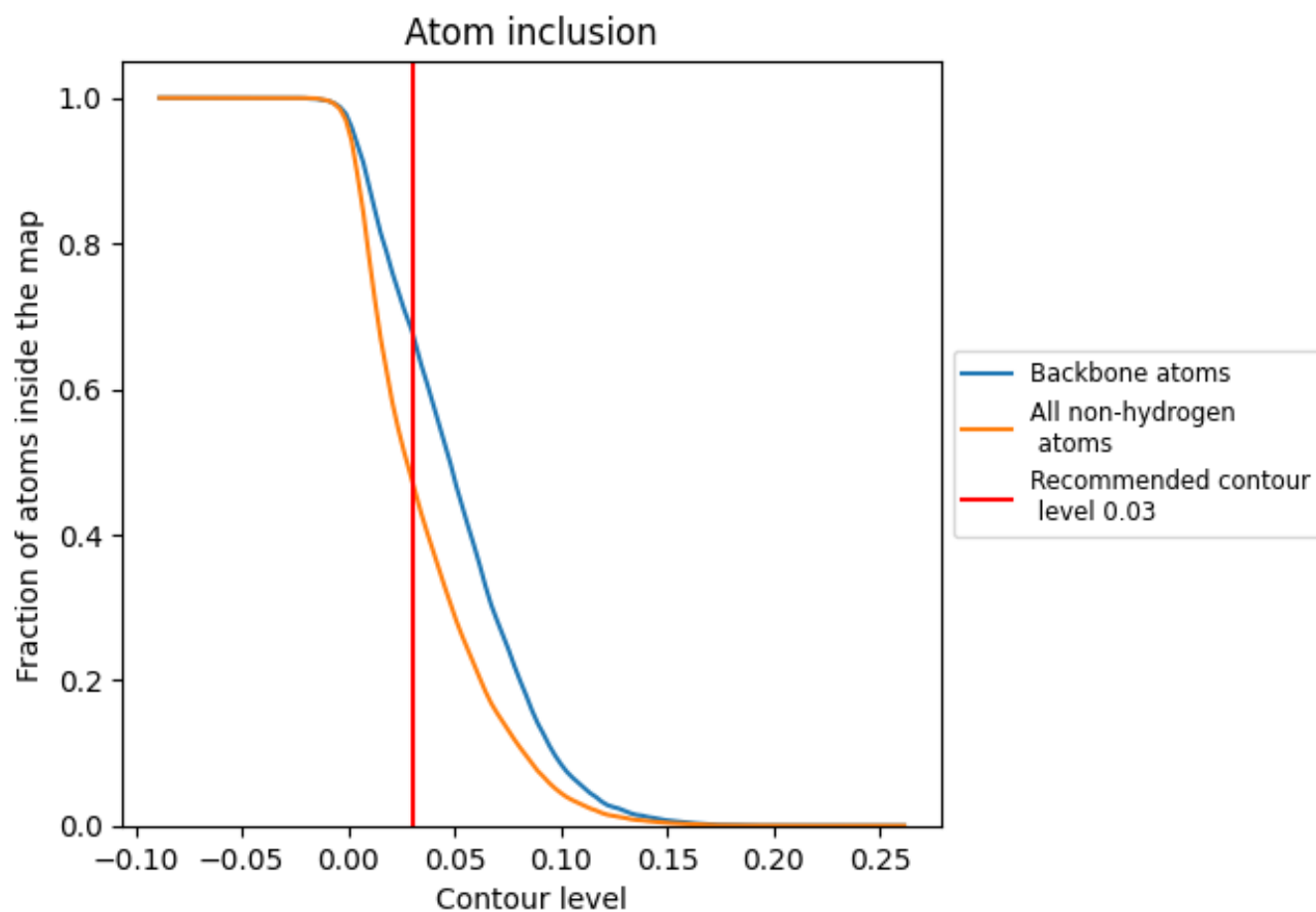
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).



















9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 47% 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	 0.4739	 0.3370
A	 0.5724	 0.4190
B	 0.5804	 0.4180
C	 0.5720	 0.4210
D	 0.5782	 0.4190
E	 0.2822	 0.1800
F	 0.2725	 0.1700
G	 0.2759	 0.1750
H	 0.2769	 0.1790

