



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:19 AM UTC

PDB ID : 7RG9 / pdb_00007rg9
EMDB ID : EMD-24445
Title : cryo-EM of human Glucagon-like peptide 1 receptor GLP-1R in apo form
Authors : Sun, B.; Kobilka, B.K.; Sloop, K.W.; Feng, D.; Kobilka, T.S.
Deposited on : 2021-07-14
Resolution : 3.20 Å (reported)
Based on initial model : 6VCB

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

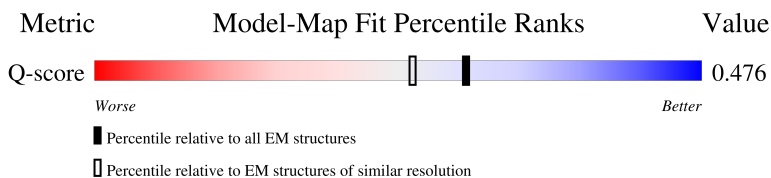
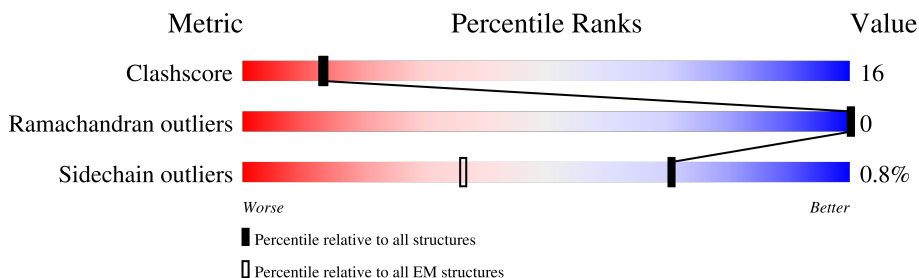
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	373	
2	B	350	
3	E	297	
4	G	71	

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Mol	Chain	Length	Quality of chain
5	N	160	9% 64% 16% • 20%
6	R	445	31% 40% 20% 40%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9769 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 Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	220	1792	1138	323	324	7	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	MET	-	initiating methionine	UNP P63092-2
A	9	GLY	-	expression tag	UNP P63092-2
A	10	CYS	-	expression tag	UNP P63092-2
A	11	THR	-	expression tag	UNP P63092-2
A	12	LEU	-	expression tag	UNP P63092-2
A	13	SER	-	expression tag	UNP P63092-2
A	14	ALA	-	expression tag	UNP P63092-2
A	15	GLU	-	expression tag	UNP P63092-2
A	16	ASP	-	expression tag	UNP P63092-2
A	17	LYS	-	expression tag	UNP P63092-2
A	18	ALA	-	expression tag	UNP P63092-2
A	19	ALA	-	expression tag	UNP P63092-2
A	20	VAL	-	expression tag	UNP P63092-2
A	21	GLU	-	expression tag	UNP P63092-2
A	22	ARG	-	expression tag	UNP P63092-2
A	23	SER	-	expression tag	UNP P63092-2
A	24	LYS	-	expression tag	UNP P63092-2
A	25	MET	-	expression tag	UNP P63092-2

- 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
			Total	C	N	O	S		
2	B	339	2581	1591	462	507	21	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	MET	-	expression tag	UNP P62873
B	-8	HIS	-	expression tag	UNP P62873
B	-7	HIS	-	expression tag	UNP P62873
B	-6	HIS	-	expression tag	UNP P62873
B	-5	HIS	-	expression tag	UNP P62873
B	-4	HIS	-	expression tag	UNP P62873
B	-3	HIS	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873

- Molecule 3 is a protein called Single-chain variable fragment 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	232	Total	C	N	O	S	0	0
			1783	1131	295	347	10		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	59	Total	C	N	O	S	0	0
			453	282	80	88	3		

- Molecule 5 is a protein called nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	N	128	Total	C	N	O	S	0	0
			967	601	169	191	6		

- Molecule 6 is a protein called Glucagon-like peptide 1 receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	268	Total	C	N	O	S	0	0
			2193	1480	348	354	11		

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-22	MET	-	initiating methionine	UNP P43220
R	-21	LYS	-	expression tag	UNP P43220

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-20	THR	-	expression tag	UNP P43220
R	-19	ILE	-	expression tag	UNP P43220
R	-18	ILE	-	expression tag	UNP P43220
R	-17	ALA	-	expression tag	UNP P43220
R	-16	LEU	-	expression tag	UNP P43220
R	-15	SER	-	expression tag	UNP P43220
R	-14	TYR	-	expression tag	UNP P43220
R	-13	ILE	-	expression tag	UNP P43220
R	-12	PHE	-	expression tag	UNP P43220
R	-11	CYS	-	expression tag	UNP P43220
R	-10	LEU	-	expression tag	UNP P43220
R	-9	VAL	-	expression tag	UNP P43220
R	-8	PHE	-	expression tag	UNP P43220
R	-7	ALA	-	expression tag	UNP P43220
R	-6	ASP	-	expression tag	UNP P43220
R	-5	TYR	-	expression tag	UNP P43220
R	-4	LYS	-	expression tag	UNP P43220
R	-3	ASP	-	expression tag	UNP P43220
R	-2	ASP	-	expression tag	UNP P43220
R	-1	ASP	-	expression tag	UNP P43220
R	0	ASP	-	expression tag	UNP P43220
R	1	ALA	-	expression tag	UNP P43220
R	2	ALA	-	expression tag	UNP P43220
R	3	ALA	-	expression tag	UNP P43220
R	4	GLY	-	expression tag	UNP P43220
R	5	GLY	-	expression tag	UNP P43220
R	6	SER	-	expression tag	UNP P43220
R	7	GLY	-	expression tag	UNP P43220
R	8	GLY	-	expression tag	UNP P43220
R	9	SER	-	expression tag	UNP P43220
R	10	LEU	-	expression tag	UNP P43220
R	11	GLU	-	expression tag	UNP P43220
R	12	VAL	-	expression tag	UNP P43220
R	13	LEU	-	expression tag	UNP P43220
R	14	PHE	-	expression tag	UNP P43220
R	15	GLN	-	expression tag	UNP P43220
R	16	GLY	-	expression tag	UNP P43220
R	17	PRO	-	expression tag	UNP P43220
R	18	GLY	-	expression tag	UNP P43220
R	19	GLY	-	expression tag	UNP P43220
R	20	SER	-	expression tag	UNP P43220
R	21	GLY	-	expression tag	UNP P43220

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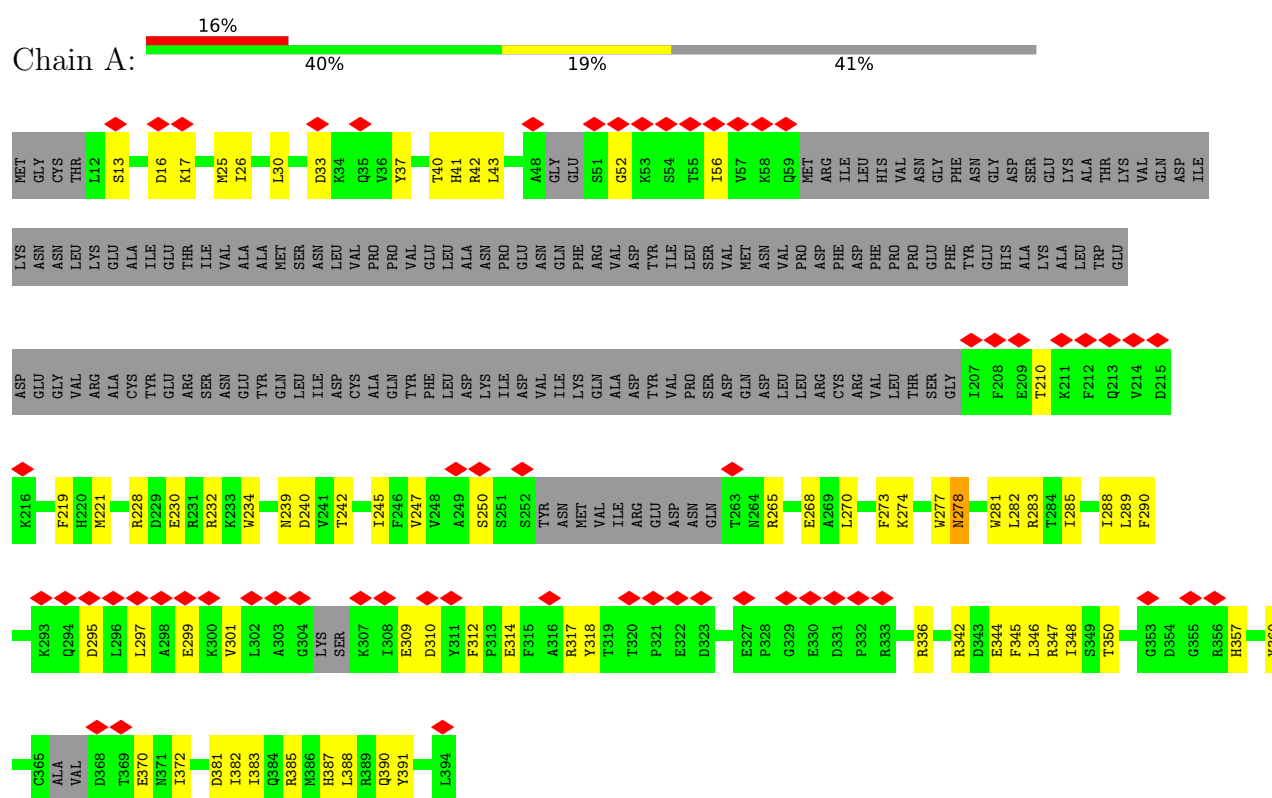
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Chain	Residue	Modelled	Actual	Comment	Reference
R	22	GLY	-	expression tag	UNP P43220
R	23	SER	-	expression tag	UNP P43220
R	260	PHE	LEU	conflict	UNP P43220

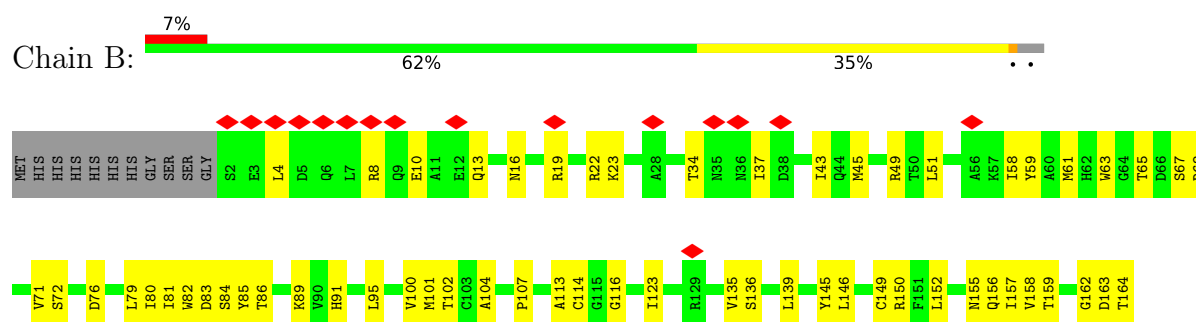
3 Residue-property plots

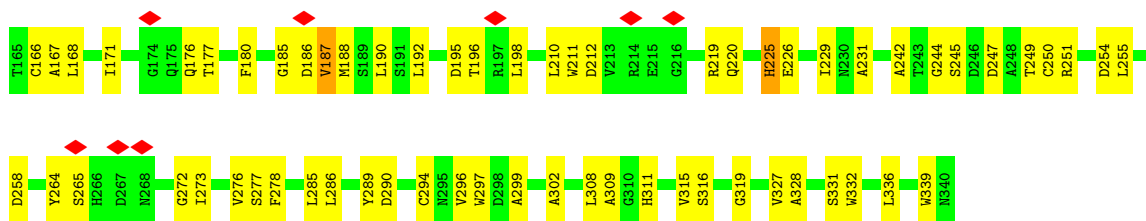
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

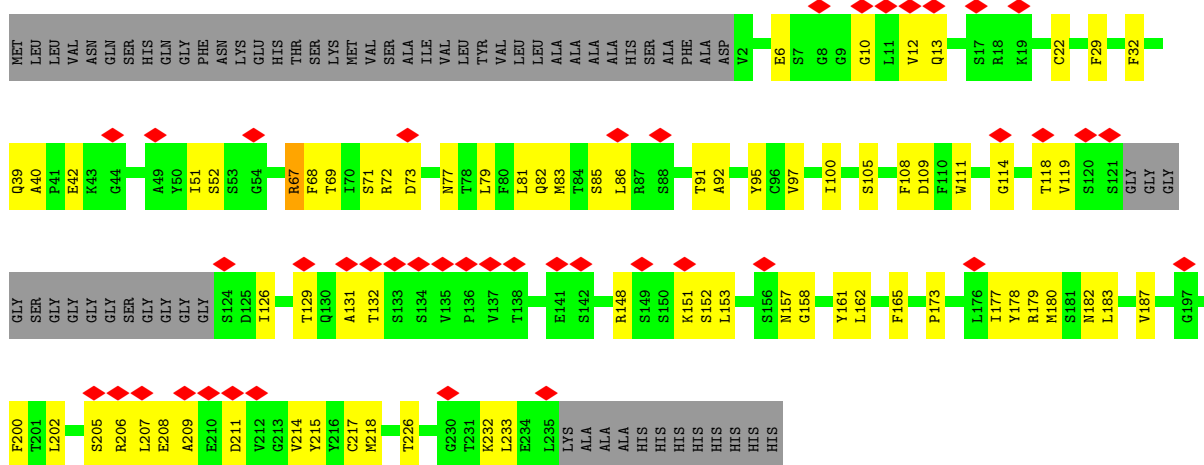


- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

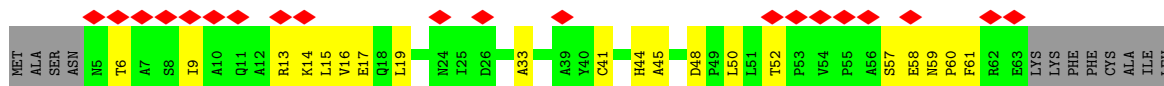




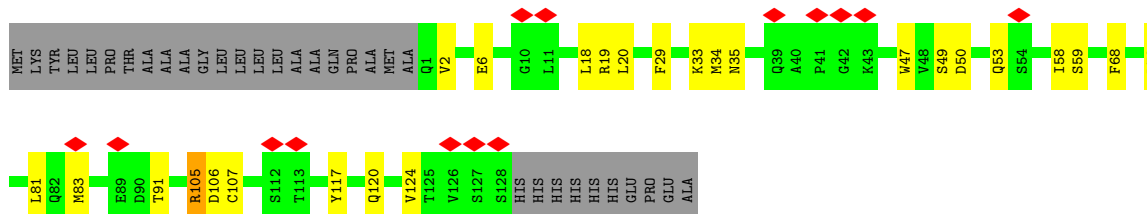
• Molecule 3: Single-chain variable fragment 16



• Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



• Molecule 5: nanobody 35



• Molecule 6: Glucagon-like peptide 1 receptor



V365	I366	F367	A368	F369	V370	M371	D372	E373	H374	A375	E376	G377	T378	L379	R380	F381	I382	K383	L384	F385	T386	L387	L388	S389	F390	F393	G394	G395	L396	N397	V398	A399	I400	C403	P404	N405	N406	M407	E408	V409	Q410	E411	E412	F413	E414	K415	E416	R421	LEU							
Y289	L290	E294	G295	C296	W297	T298	R299	N300	S301	N302	M303	N304	Y305	W306	I307	I308	I309	R310	L311	P312	I313	L314	V319	F321	L322	I323	F324	I328	C329	I330	V331	K336	L339	NET	CYS	LYS	THR	D344	I345	K346	C347	R348	L349	A350	K351	S352	T353	L354	L360	H363	E364					
D222	S223	L224	S225	C226	R227	L228	V229	F230	L231	L232	M233	Q234	Y235	C236	V237	A238	A239	Y242	W243	L244	L245	V246	E247	G248	V249	Y250	L251	F257	S258	V259	F260	S261	E262	Q263	W264	T265	F266	R267	L268	Y269	V270	S271	I272	V276	P277	L278	L279	F280	V281	V282	P283	W284	G285	I286	K288	
A158	L159	A164	I165	L166	L167	G168	F169	R170	H171	L172	H173	C174	T175	R176	M177	Y178	H179	H180	L181	M182	L183	F184	F187	I188	L189	R190	A191	L192	S193	V194	F195	I196	K197	D198	A199	A200	L201	K202	W203	M204	Y205	S206	T207	ALA	Y148	G150	G151	Y152	A153	L154	S155	F156	S157	Z219	Y220	Q221
LYS	TRP	ARG	GLU	TYR	ARG	PHE	CYS	THR	ALA	GLU	GLY	SER	LEU	THR	LEU	GLN	LYS	ASP	PRO	ASN	PRO	PRO	ALA	THR	ASP	LEU	TRP	LEU	TRP	LEU	TRP	LEU	TRP	LEU	TRP	VAL	ASN	VAL	SER	PRO	PRO	TRP	TYR	LEU	PRO	TRP	ALA	SER	SER	VAL	PRO	GLN				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	154469	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 ($e^-/\text{\AA}^2$)	53.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.103	Depositor
Minimum map value	-0.065	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.022	Depositor
Map size ($\text{\AA}$)	249.6, 249.6, 249.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.832, 0.832, 0.832	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	0.46	0/1824	0.52	0/2454
2	B	0.43	0/2627	0.57	2/3564 (0.1%)
3	E	0.46	0/1827	0.49	0/2477
4	G	0.49	0/459	0.66	0/620
5	N	0.47	0/987	0.59	2/1338 (0.1%)
6	R	0.56	0/2254	0.46	0/3065
All	All	0.48	0/9978	0.53	4/13518 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	76	ASP	N-CA-C	-6.71	105.06	113.18
2	B	187	VAL	CA-C-O	-5.47	114.78	121.13
5	N	105	ARG	N-CA-C	-5.41	105.99	112.59
5	N	106	ASP	N-CA-CB	-5.08	102.35	110.63

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	1792	0	1752	59	0
2	B	2581	0	2473	115	0
3	E	1783	0	1717	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	453	0	460	15	0
5	N	967	0	922	15	0
6	R	2193	0	2226	69	0
All	All	9769	0	9550	310	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 310 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:A:16:ASP:OD2	2:B:86:THR:HG21	1.65	0.96
6:R:299:ARG:NH1	6:R:300:ASN:OD1	2.03	0.91
4:G:57:SER:OG	4:G:58:GLU:OE1	1.92	0.86
1:A:16:ASP:OD2	2:B:86:THR:CG2	2.23	0.85
2:B:145:TYR:OH	2:B:188:MET:HE1	1.79	0.83

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	208/373 (56%)	195 (94%)	13 (6%)	0	100	100
2	B	337/350 (96%)	302 (90%)	35 (10%)	0	100	100
3	E	228/297 (77%)	212 (93%)	16 (7%)	0	100	100
4	G	57/71 (80%)	51 (90%)	6 (10%)	0	100	100
5	N	126/160 (79%)	117 (93%)	9 (7%)	0	100	100
6	R	262/445 (59%)	238 (91%)	24 (9%)	0	100	100
All	All	1218/1696 (72%)	1115 (92%)	103 (8%)	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	189/334 (57%)	188 (100%)	1 (0%)	81	85
2	B	277/291 (95%)	275 (99%)	2 (1%)	76	83
3	E	197/239 (82%)	195 (99%)	2 (1%)	68	80
4	G	48/58 (83%)	47 (98%)	1 (2%)	47	71
5	N	104/129 (81%)	102 (98%)	2 (2%)	50	73
6	R	232/389 (60%)	232 (100%)	0	100	100
All	All	1047/1440 (73%)	1039 (99%)	8 (1%)	70	82

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	N	105	ARG
5	N	6	GLU
3	E	233	LEU
3	E	67	ARG
4	G	44	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	88	ASN
2	B	183	HIS
2	B	266	HIS
2	B	268	ASN
5	N	77	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

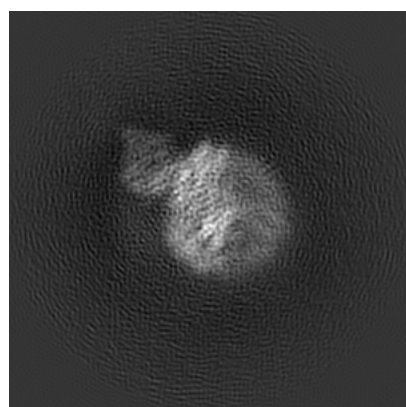
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24445. These allow visual inspection of the internal detail of the map and identification of artifacts.

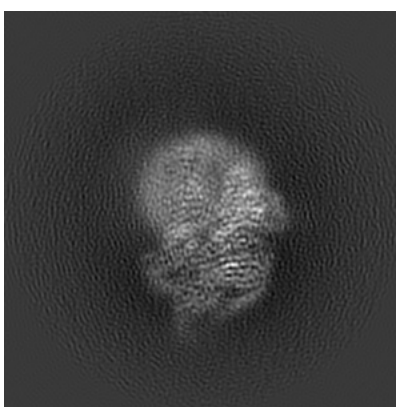
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

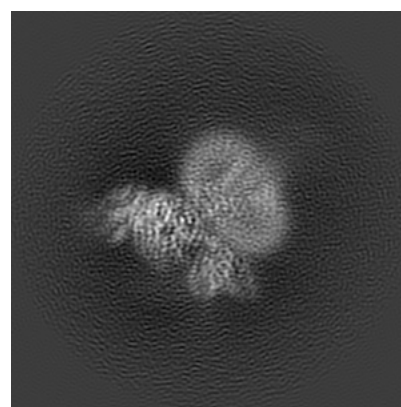
6.1.1 Primary map



X



Y



Z

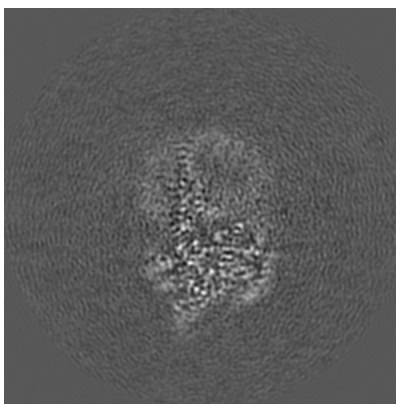
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

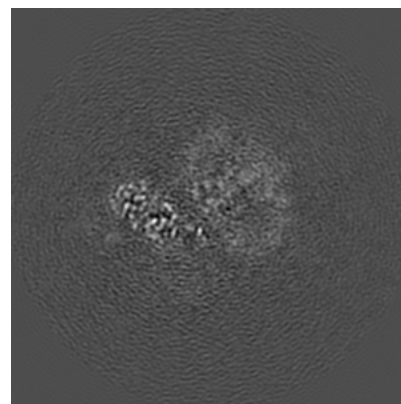
6.2.1 Primary map



X Index: 150



Y Index: 150

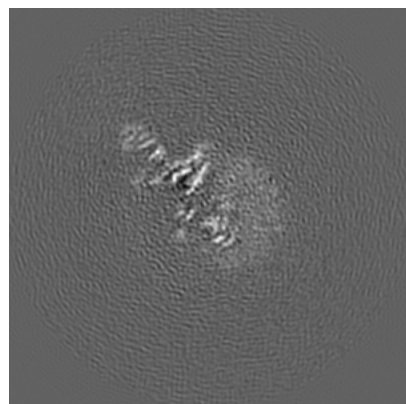


Z Index: 150

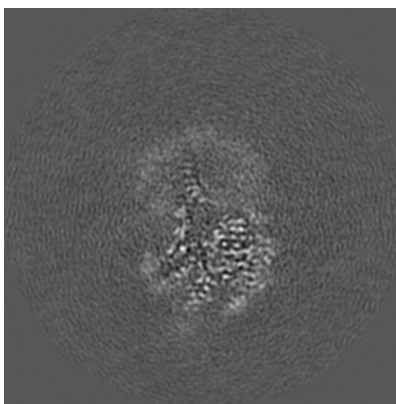
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

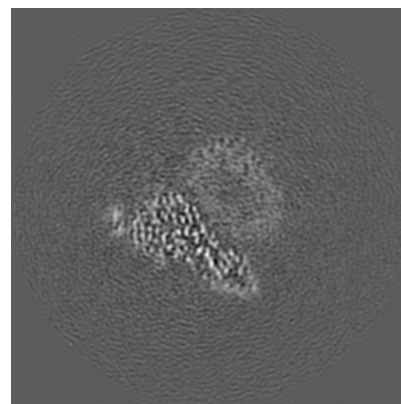
6.3.1 Primary map



X Index: 139



Y Index: 144

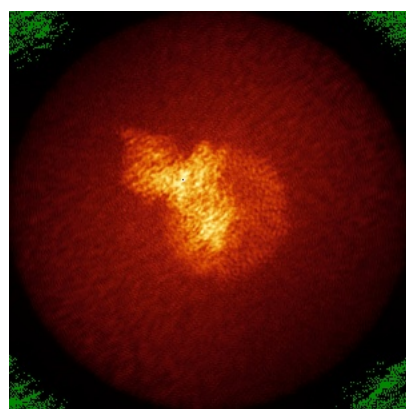


Z Index: 175

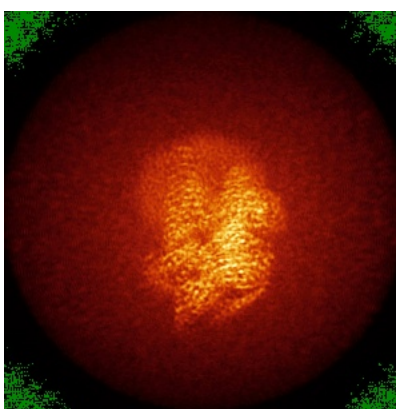
The images above show the largest variance slices of the map in three orthogonal directions.

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

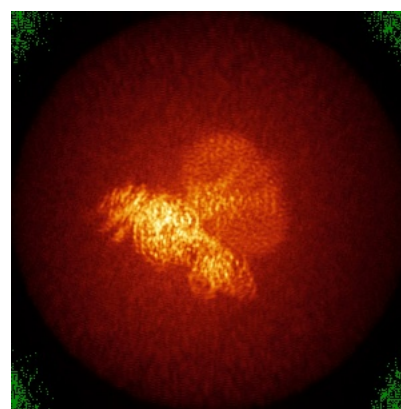
6.4.1 Primary map



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

This section was not generated.

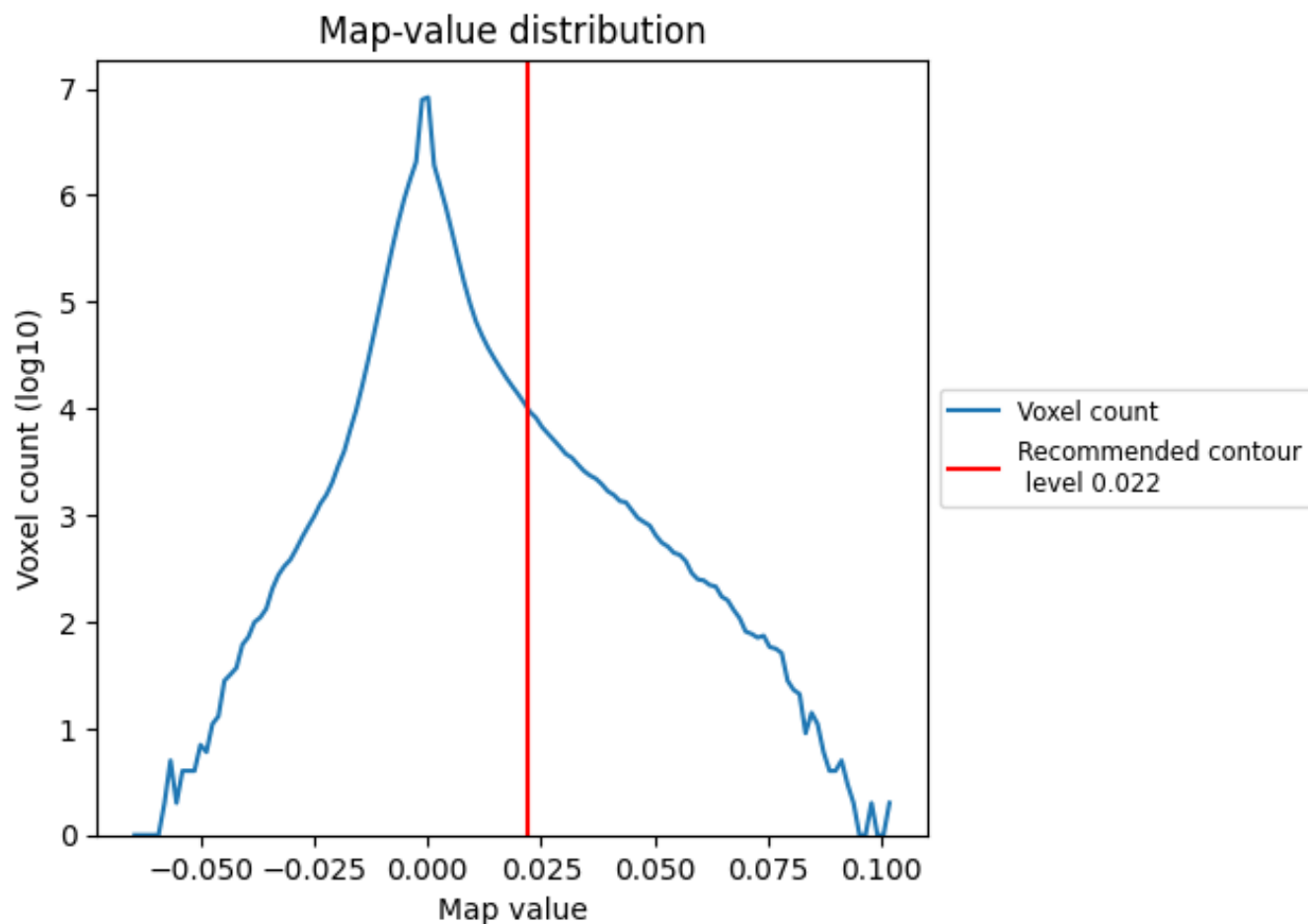
6.6 Mask visualisation

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

7 Map analysis [i](#)

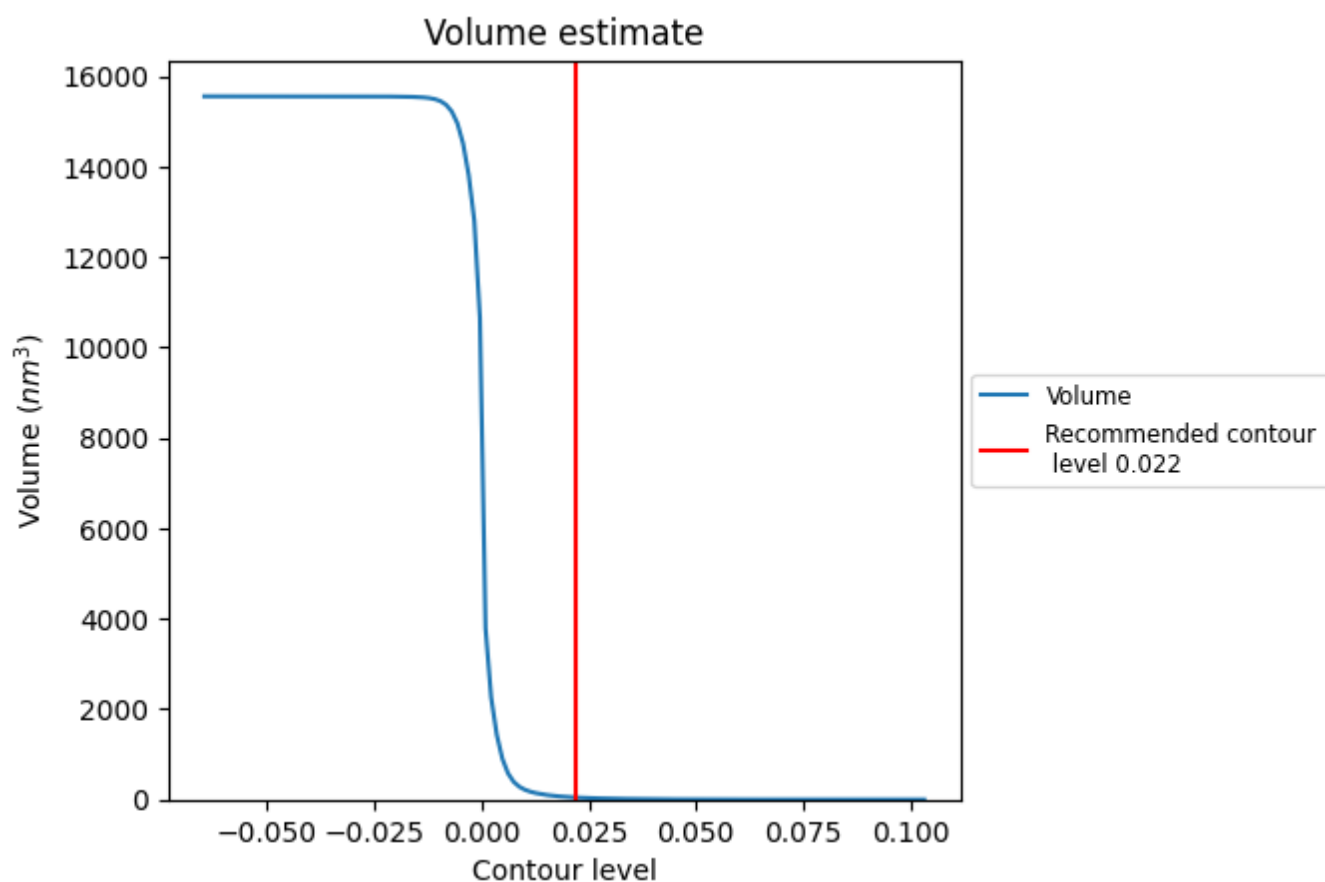
This section contains the results of statistical analysis of the map.

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.

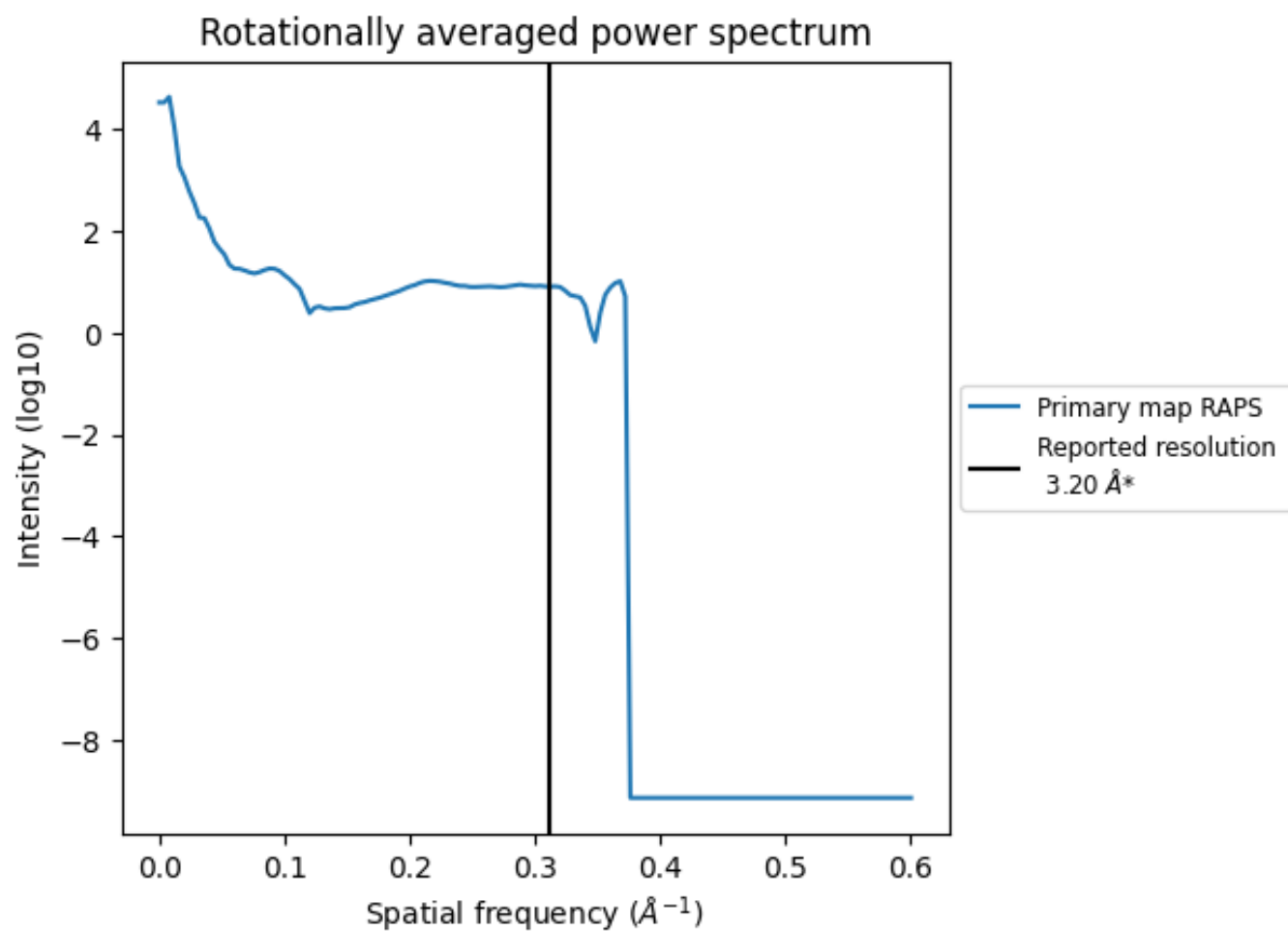
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 45 nm³; this corresponds to an approximate mass of 41 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 0.312 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-24445 and PDB model 7RG9. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

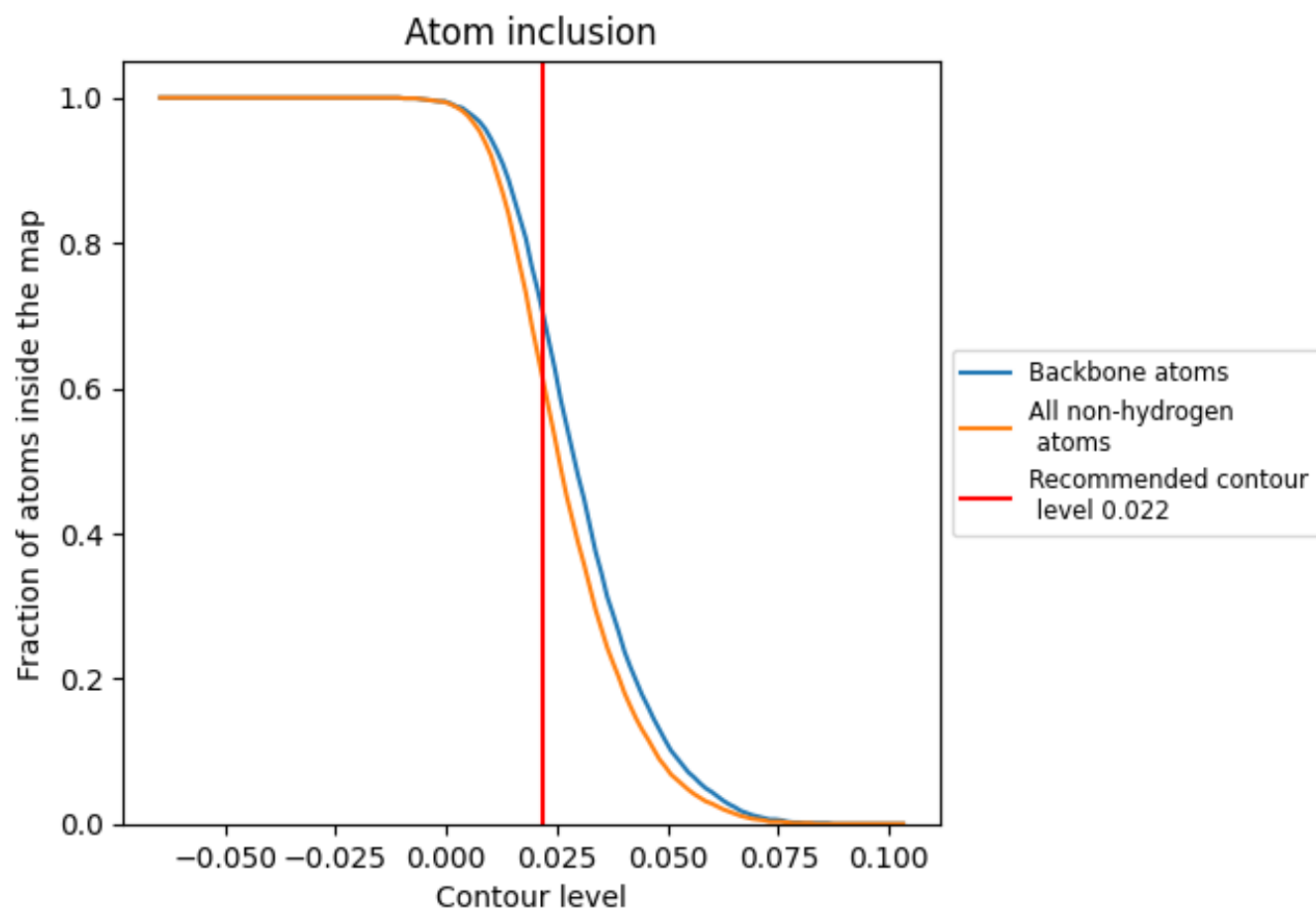


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 61% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6060	0.4760
A	0.5800	0.4750
B	0.7610	0.5180
E	0.6330	0.4960
G	0.5290	0.4490
N	0.6860	0.5110
R	0.4030	0.4020

