



## wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:08 AM UTC

PDB ID : 7DAG / pdb\_00007dag  
EMDB ID : EMD-30625  
Title : Vibrio cholera aldehyde-alcohol dehydrogenase  
Authors : Cho, S.; Cho, C.; Song, J.; Kim, G.  
Deposited on : 2020-10-16  
Resolution : 4.37 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:

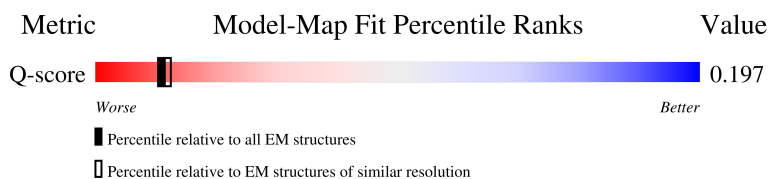
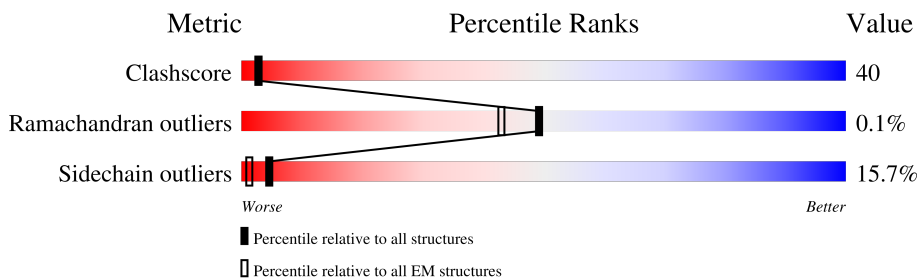
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 4.37 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	3738 ( 3.87 - 4.87 )

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	894	71% 
1	B	894	55% 
1	C	894	13% 
1	D	894	12% 

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Mol	Chain	Length	Quality of chain
1	E	894	<p>31% 34% 50% 11% . .</p>
1	F	894	<p>38% 35% 50% 11% . .</p>
1	G	894	<p>40% 20% 27% 53%</p>
1	H	894	<p>48% 27% 23% 50%</p>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 45976 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.

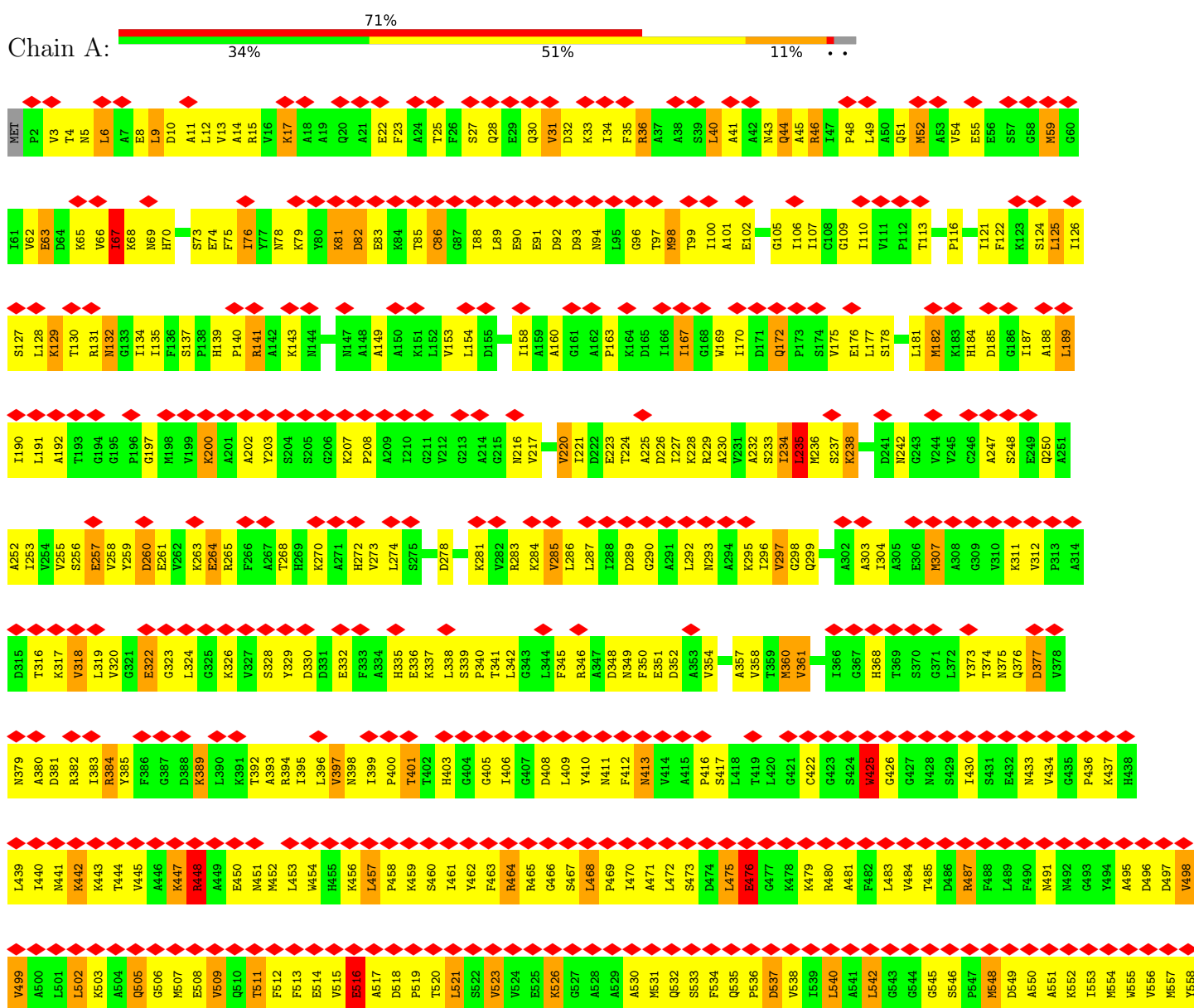
- Molecule 1 is a protein called Aldehyde-alcohol dehydrogenase.

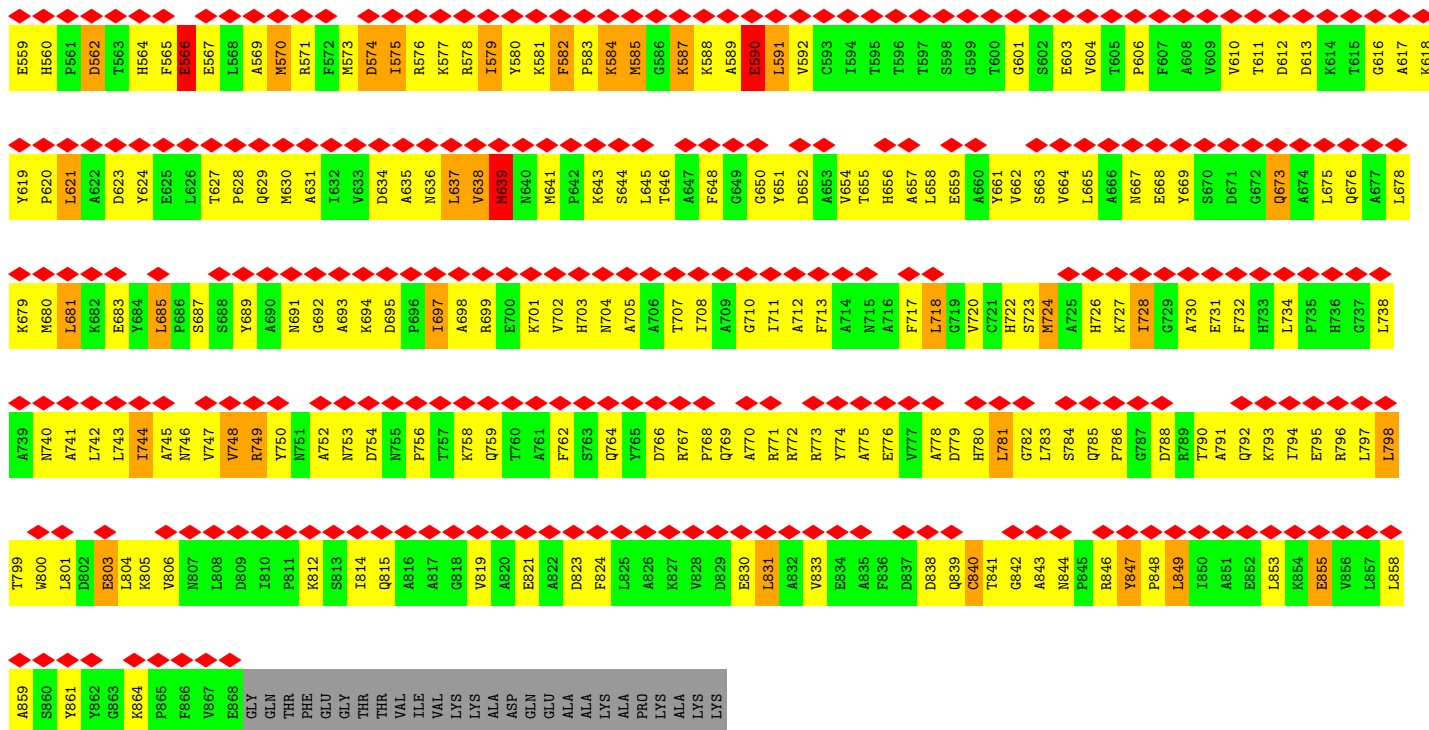
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	867	Total 6568	C 4174	N 1119	O 1246	S 29	0	0
1	B	867	Total 6568	C 4174	N 1119	O 1246	S 29	0	0
1	C	867	Total 6568	C 4174	N 1119	O 1246	S 29	0	0
1	D	867	Total 6568	C 4174	N 1119	O 1246	S 29	0	0
1	E	867	Total 6568	C 4174	N 1119	O 1246	S 29	0	0
1	F	867	Total 6568	C 4174	N 1119	O 1246	S 29	0	0
1	G	419	Total 3250	C 2078	N 547	O 608	S 17	0	0
1	H	448	Total 3318	C 2096	N 572	O 638	S 12	0	0

### 3 Residue-property plots

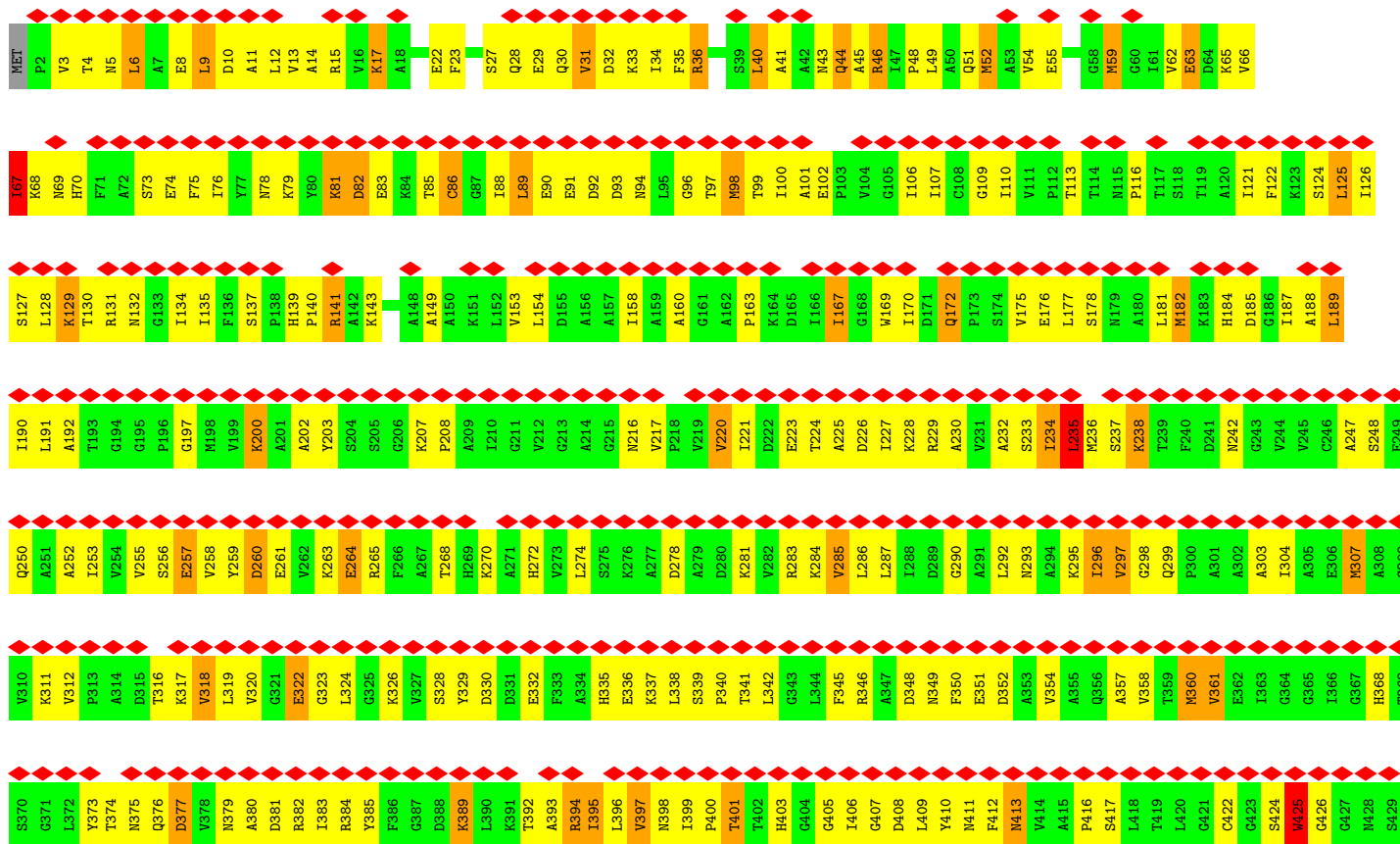
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

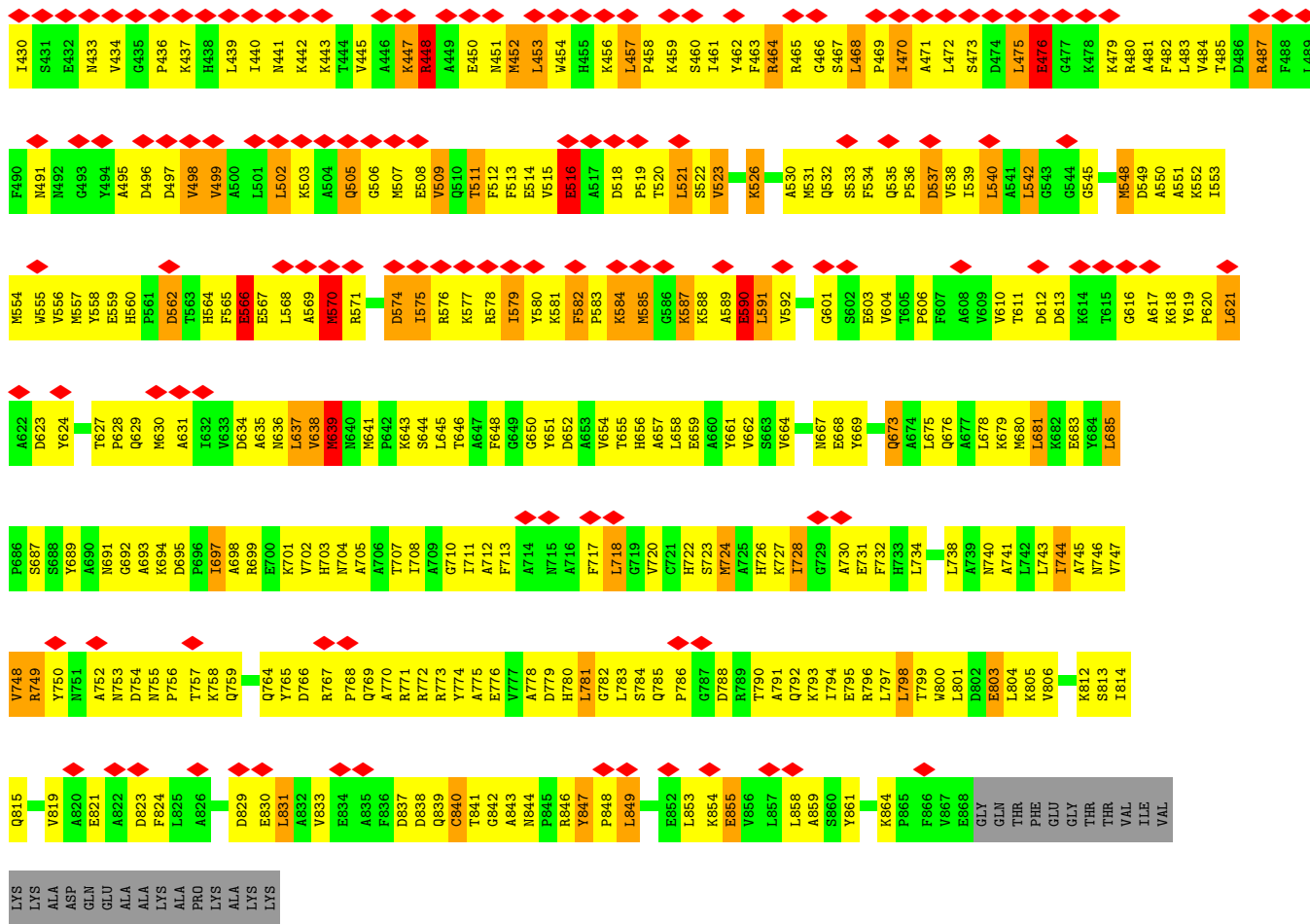
- Molecule 1: Aldehyde-alcohol dehydrogenase



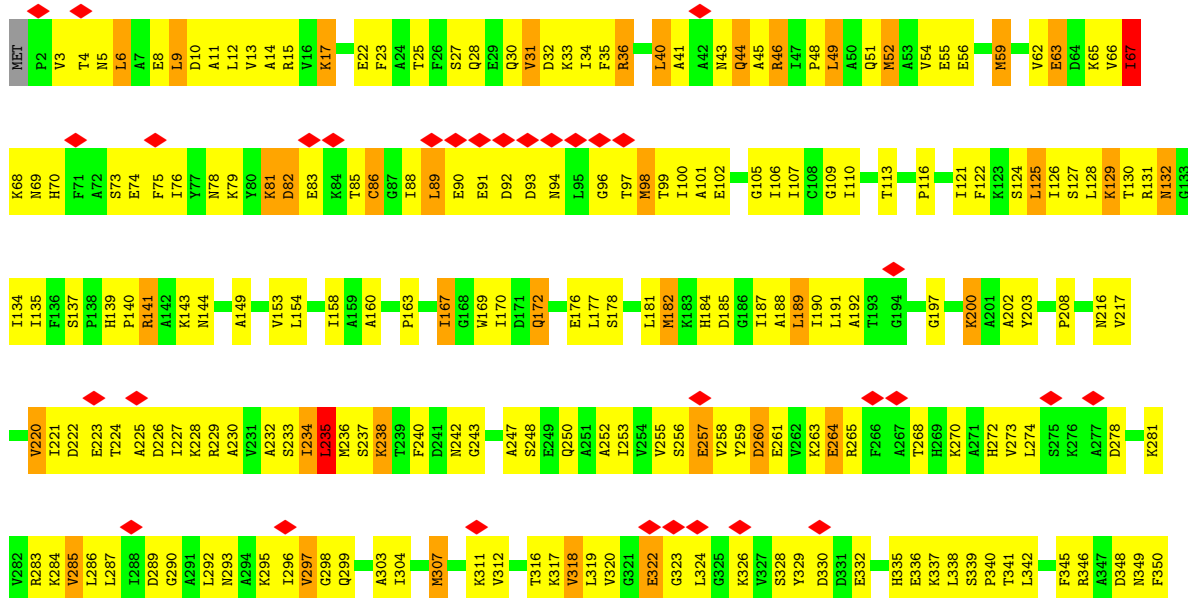


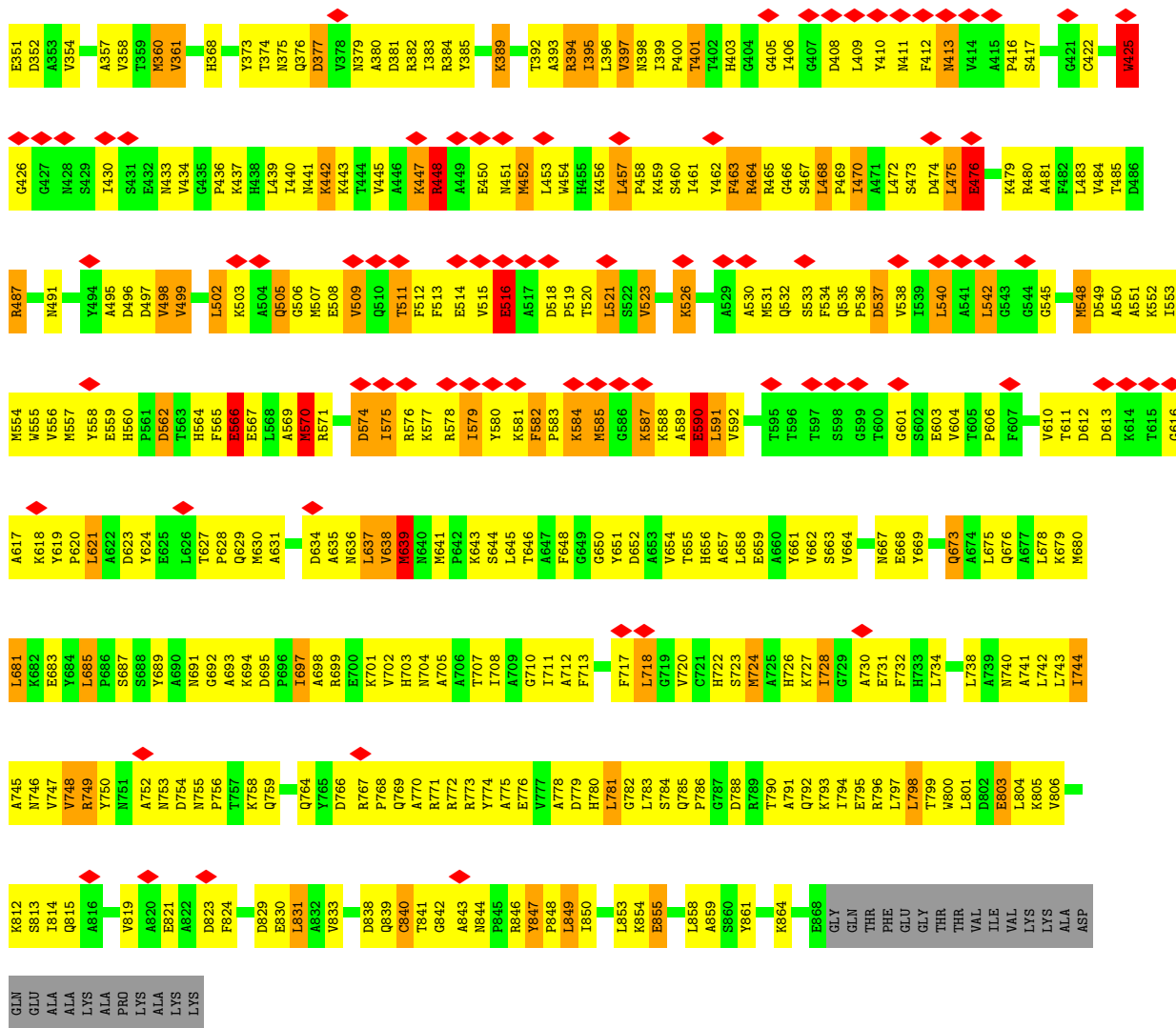
● Molecule 1: Aldehyde-alcohol dehydrogenase



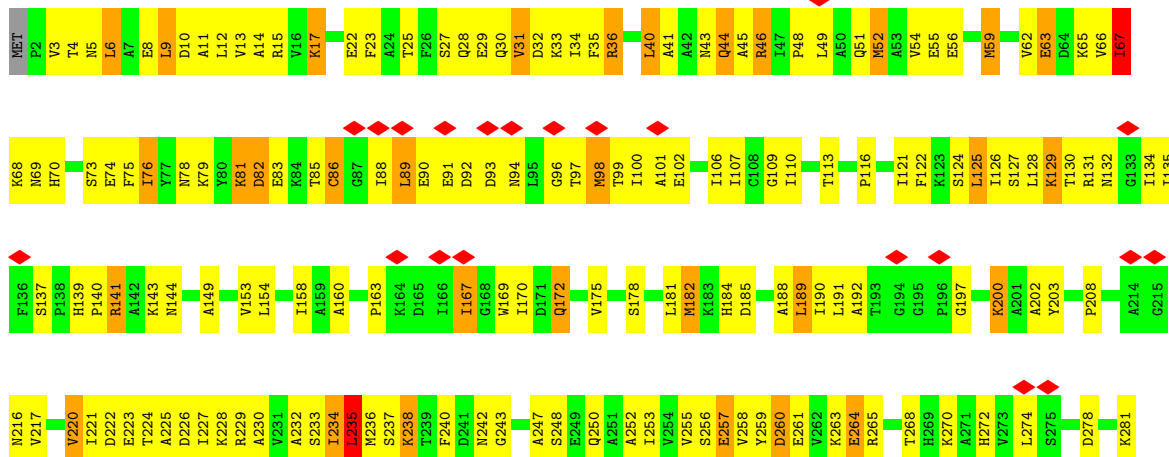


● Molecule 1: Aldehyde-alcohol dehydrogenase





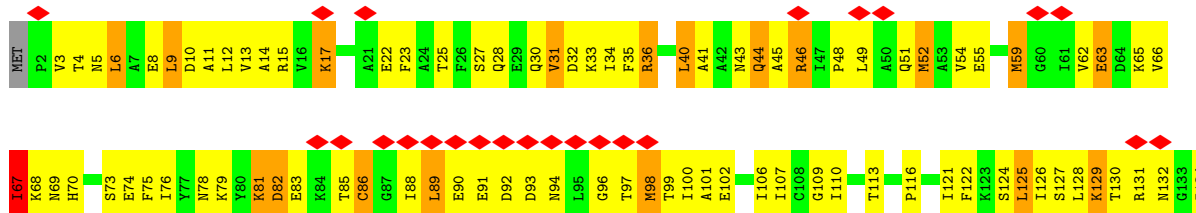
• Molecule 1: Aldehyde-alcohol dehydrogenase







● Molecule 1: Aldehyde-alcohol dehydrogenase







I61	I121	L181	D241	A303	E362	G423	LEU	GLY	SER	SER	LEU	ALA
V62	F122	M182	N242	A304	I363	S424	THR	GLY	VAL	MET	SER	ASN
E63	K123	K183	G243	I304	G364	S425	ASP	GLY	THR	ALA	GLN	PRO
D64	S124	H184	V244	A305	G367	G426	ARG	PRO	PHE	ASN	GLY	TYR
K65	L125	D185	V245	E306	H368	G427	PRO	ALA	VAL	GLU	ASP	PRO
V66	I126	G186	C246	M307	H369	N428	LEU	ASP	VAL	TYR	THR	ILE
I67	S127	G187	A247	A308	T369	S429	PHE	ALA	VAL	ASP	ALA	ALA
K68	L128	A188	S248	G309	S370	I430	ASN	ALA	THR	SER	THR	ALA
N69	K129	L189	E249	K310	G371	S431	LYS	LYS	ASP	GLY	GLN	LEU
H70	T130	I190	Q250	V311	L372	E432	GLY	ILE	ASP	ALA	LEU	LEU
F71	R131	A192	A251	K312	Y373	N433	ALA	THR	ALA	LEU	GLU	LEU
A72	M132	A193	A252	V313	T374	N434	ASP	VAL	GLN	GLN	ARG	VAL
S73	G133	T193	I253	P313	Q376	V435	VAL	TYR	ALA	ALA	LEU	LEU
E74	I134	G194	V254	A314	D377	G436	VAL	GLU	VAL	LYS	THR	ALA
F75	L135	G195	V255	D315	D378	K437	LEU	PRO	ALA	ALA	LEU	LEU
I76	F136	P196	S256	T316	V378	H438	LEU	ASP	ALA	LYS	ASP	TYR
Y77	S137	G197	E257	K317	N379	L439	LYS	THR	GLY	GLU	LEU	GLY
N78	P138	M198	V258	V318	A380	I440	ALA	HIS	TYR	TYR	LEU	LYS
K79	H139	V199	Y259	L319	D381	I441	GLN	PHE	LEU	LEU	LEU	PRO
Y80	P140	V199	Y259	L319	D381	I441	GLN	PHE	LEU	LEU	LEU	PRO
K81	R141	K200	D260	V320	R382	K442	MET	GLU	THR	SER	VAL	VAL
D82	A142	A201	E261	G321	I383	K443	GLU	LEU	PRO	SER	VAL	GLU
E83	K143	A202	V262	E322	R384	T444	VAL	ALA	THR	ALA	ARG	GLN
K84	K144	Y203	K263	G323	Y385	V445	THR	MET	ALA	ALA	ILE	GLN
T85	N144	S204	E264	L324	F386	A446	PHE	PHE	ILE	GLY	ALA	THR
C86	S145	S205	R265	G325	F387	K447	PHE	MET	VAL	ALA	ASP	GLY
G87	T146	G206	F266	G326	D388	R448	GLU	ASP	ASP	LYS	ILE	GLY
I88	N147	K207	A267	V327	K389	A449	VAL	ALA	ALA	PRO	ALA	THR
L89	A148	P208	T268	S328	K390	G450	ALA	ARG	LEU	THR	ILE	VAL
E90	A149	A209	H269	Y329	K391	G451	ALA	ILE	LEU	ALA	GLY	VAL
E91	K151	I210	K270	D330	T392	A452	THR	LYS	ASN	GLU	ALA	VAL
D92	L152	V212	A271	D331	R393	A453	THR	LYS	PRO	LEU	ALA	VAL
D93	V153	G213	G272	F332	R394	A454	THR	LYS	PRO	LEU	ALA	VAL
N94	L154	G214	V273	F333	I395	A455	THR	LYS	PRO	LEU	ALA	VAL
L95	D155	G215	S274	H334	L396	V397	THR	LYS	PRO	LEU	ALA	VAL
G96	A156	N216	S275	H335	V398	V398	THR	LYS	PRO	LEU	ALA	VAL
T97	A157	N216	K276	K336	I399	I399	THR	LYS	PRO	LEU	ALA	VAL
M98	I158	V217	A277	L337	P400	T401	THR	LYS	PRO	LEU	ALA	VAL
T99	A159	P218	D278	S338	T402	T402	THR	LYS	PRO	LEU	ALA	VAL
I100	A160	V219	A279	P340	H403	H403	THR	LYS	PRO	LEU	ALA	VAL
A101	G161	V220	D280	L342	G404	G404	THR	LYS	PRO	LEU	ALA	VAL
E102	P162	I221	K281	L344	G405	G405	THR	LYS	PRO	LEU	ALA	VAL
P103	P163	D222	R282	L344	I406	I406	THR	LYS	PRO	LEU	ALA	VAL
G104	K164	E223	R283	F345	G407	G407	THR	LYS	PRO	LEU	ALA	VAL
V105	D165	T224	K284	R346	D408	D408	THR	LYS	PRO	LEU	ALA	VAL
I106	I166	A225	V285	A347	L409	L409	THR	LYS	PRO	LEU	ALA	VAL
I107	I167	D226	L286	D348	Y410	Y410	THR	LYS	PRO	LEU	ALA	VAL
C108	I167	I227	L287	N349	M411	M411	THR	LYS	PRO	LEU	ALA	VAL
G109	G168	K228	I288	F350	F412	F412	THR	LYS	PRO	LEU	ALA	VAL
I110	M169	R229	D289	E351	M413	M413	THR	LYS	PRO	LEU	ALA	VAL
V111	I170	A230	G290	D352	V414	V414	THR	LYS	PRO	LEU	ALA	VAL
P112	D171	V231	M293	A353	A415	A415	THR	LYS	PRO	LEU	ALA	VAL
T113	Q172	A232	A294	V354	P416	P416	THR	LYS	PRO	LEU	ALA	VAL
T114	P173	S233	K295	A355	S417	S417	THR	LYS	PRO	LEU	ALA	VAL
T115	S174	I234	I296	Q356	L418	L418	THR	LYS	PRO	LEU	ALA	VAL
N116	V175	L235	V297	A357	T419	T419	THR	LYS	PRO	LEU	ALA	VAL
P117	E176	M236	G298	V358	L420	L420	THR	LYS	PRO	LEU	ALA	VAL
T117	L177	S237	G299	M360	G421	G421	THR	LYS	PRO	LEU	ALA	VAL
S118	S178	K238	Q299	M361	C422	C422	THR	LYS	PRO	LEU	ALA	VAL
N119	N179	T239	P300	V361			THR	LYS	PRO	LEU	ALA	VAL
A120	A180	F240	A301				THR	LYS	PRO	LEU	ALA	VAL

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	62417	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 ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.932	Depositor
Minimum map value	-0.331	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.31	Depositor
Map size (Å)	293.41998, 293.41998, 293.41998	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.863, 0.863, 0.863	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	0.37	0/6693	0.84	20/9077 (0.2%)
1	B	0.37	0/6693	0.84	20/9077 (0.2%)
1	C	0.37	0/6693	0.84	20/9077 (0.2%)
1	D	0.37	0/6693	0.84	20/9077 (0.2%)
1	E	0.37	0/6693	0.84	20/9077 (0.2%)
1	F	0.37	0/6693	0.84	20/9077 (0.2%)
1	G	0.29	0/3322	0.63	8/4505 (0.2%)
1	H	0.20	0/3370	0.46	0/4569
All	All	0.36	0/46850	0.81	128/63536 (0.2%)

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	A	0	6
1	B	0	6
1	C	0	6
1	D	0	6
1	E	0	6
1	F	0	6
1	G	0	1
All	All	0	37

There are no bond length outliers.

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	464	ARG	CB-CG-CD	14.04	143.58	111.30
1	D	464	ARG	CB-CG-CD	14.02	143.54	111.30
1	E	464	ARG	CB-CG-CD	14.01	143.52	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	464	ARG	CB-CG-CD	14.01	143.51	111.30
1	A	464	ARG	CB-CG-CD	14.00	143.50	111.30

There are no chirality outliers.

5 of 37 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	295	LYS	Peptide
1	A	425	TRP	Peptide
1	A	447	LYS	Peptide
1	A	59	MET	Peptide
1	A	90	GLU	Sidechain

## 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	6568	0	6618	577	0
1	B	6568	0	6618	591	0
1	C	6568	0	6618	555	0
1	D	6568	0	6618	550	0
1	E	6568	0	6618	557	0
1	F	6568	0	6618	554	0
1	G	3250	0	3233	260	0
1	H	3318	0	3384	185	0
All	All	45976	0	46325	3717	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 40.

The worst 5 of 3717 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:F:452:MET:HA	1:G:464:ARG:HH12	1.11	1.12
1:D:470:ILE:HD11	1:E:452:MET:HE2	1.06	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:567:GLU:O	1:D:571:ARG:HB3	1.64	0.98
1:E:75:PHE:O	1:E:79:LYS:HB2	1.63	0.98
1:B:567:GLU:O	1:B:571:ARG:HB3	1.64	0.98

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	865/894 (97%)	770 (89%)	94 (11%)	1 (0%)	48	83
1	B	865/894 (97%)	770 (89%)	94 (11%)	1 (0%)	48	83
1	C	865/894 (97%)	772 (89%)	92 (11%)	1 (0%)	48	83
1	D	865/894 (97%)	771 (89%)	93 (11%)	1 (0%)	48	83
1	E	865/894 (97%)	771 (89%)	93 (11%)	1 (0%)	48	83
1	F	865/894 (97%)	770 (89%)	94 (11%)	1 (0%)	48	83
1	G	417/894 (47%)	380 (91%)	37 (9%)	0	100	100
1	H	446/894 (50%)	421 (94%)	25 (6%)	0	100	100
All	All	6053/7152 (85%)	5425 (90%)	622 (10%)	6 (0%)	49	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	448	ARG
1	B	448	ARG
1	C	448	ARG
1	D	448	ARG
1	E	448	ARG

### 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	687/707 (97%)	561 (82%)	126 (18%)	2	10
1	B	687/707 (97%)	562 (82%)	125 (18%)	2	10
1	C	687/707 (97%)	561 (82%)	126 (18%)	2	10
1	D	687/707 (97%)	562 (82%)	125 (18%)	2	10
1	E	687/707 (97%)	561 (82%)	126 (18%)	2	10
1	F	687/707 (97%)	562 (82%)	125 (18%)	2	10
1	G	338/707 (48%)	338 (100%)	0	100	100
1	H	349/707 (49%)	349 (100%)	0	100	100
All	All	4809/5656 (85%)	4056 (84%)	753 (16%)	4	13

5 of 753 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	557	MET
1	E	498	VAL
1	D	591	LEU
1	D	554	MET
1	E	98	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	780	HIS
1	G	629	GLN
1	G	792	GLN
1	C	560	HIS
1	C	272	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 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.

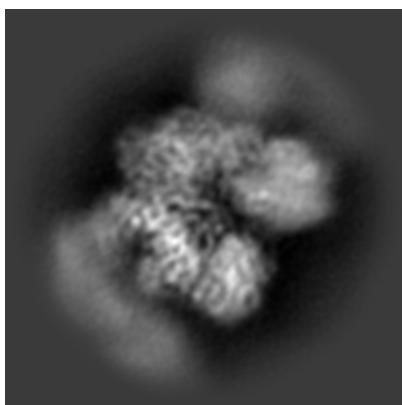
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30625. These allow visual inspection of the internal detail of the map and identification of artifacts.

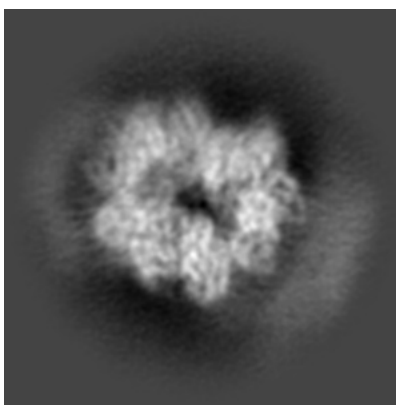
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

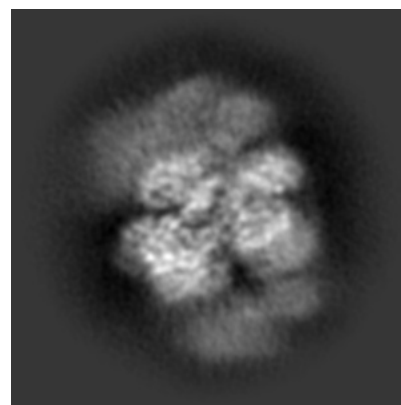
#### 6.1.1 Primary map



X



Y

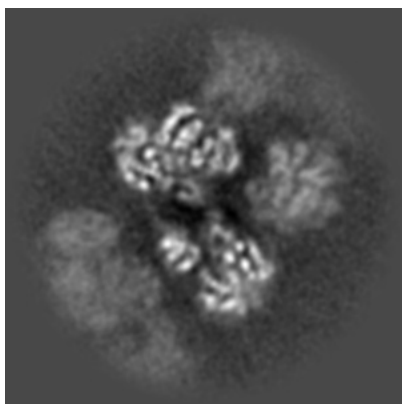


Z

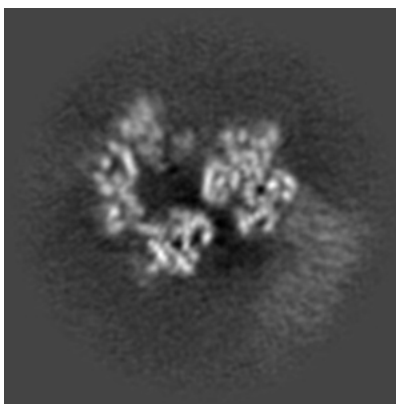
The images above show the map projected in three orthogonal directions.

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

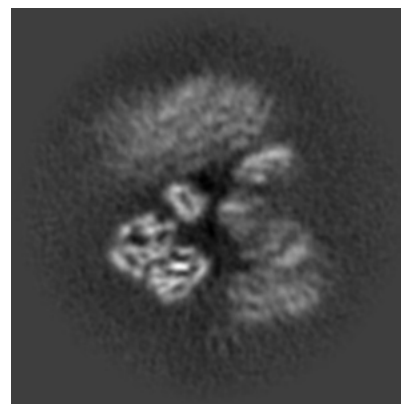
#### 6.2.1 Primary map



X Index: 170



Y Index: 170

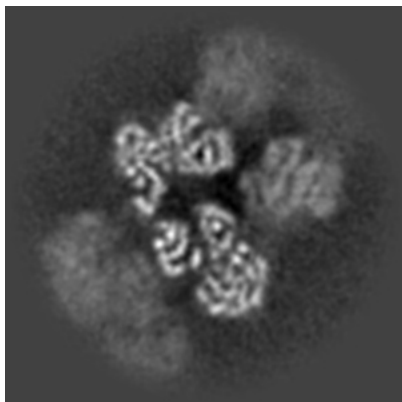


Z Index: 170

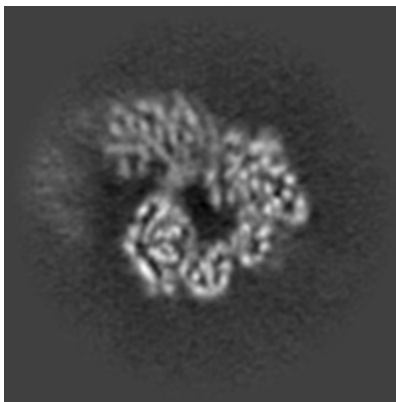
The images above show central slices of the map in three orthogonal directions.

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

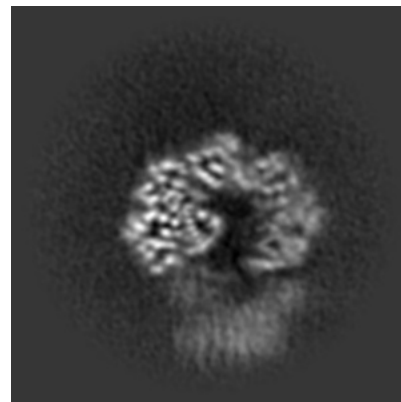
### 6.3.1 Primary map



X Index: 162



Y Index: 149

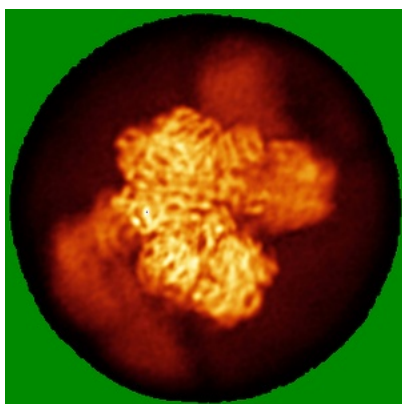


Z Index: 125

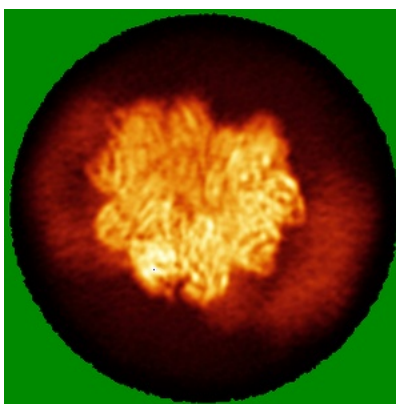
The images above show the largest variance slices of the map in three orthogonal directions.

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

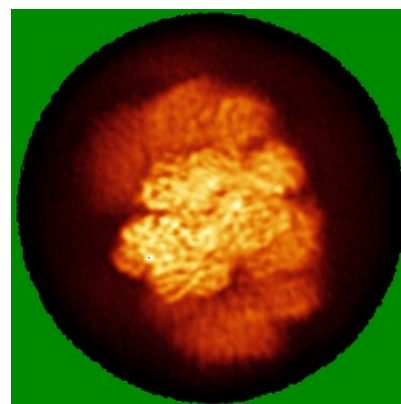
### 6.4.1 Primary map



X



Y

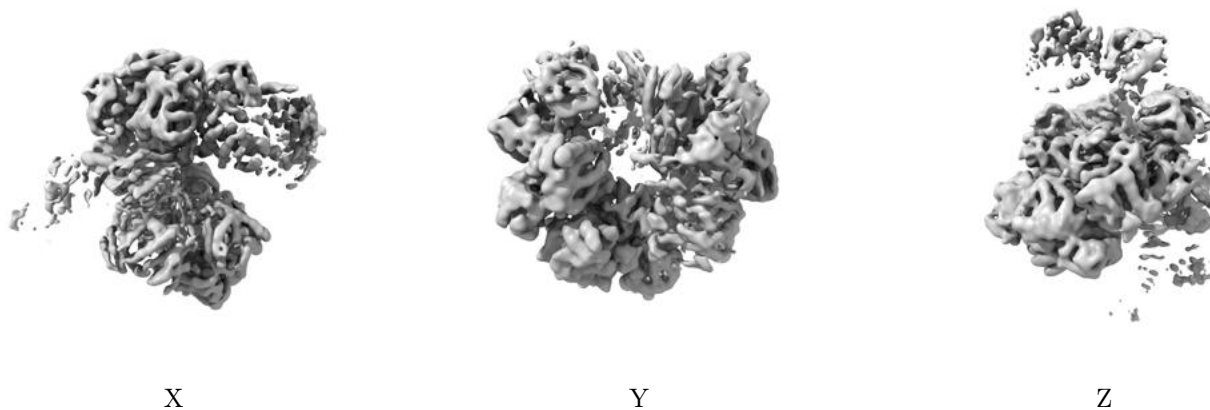


Z

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

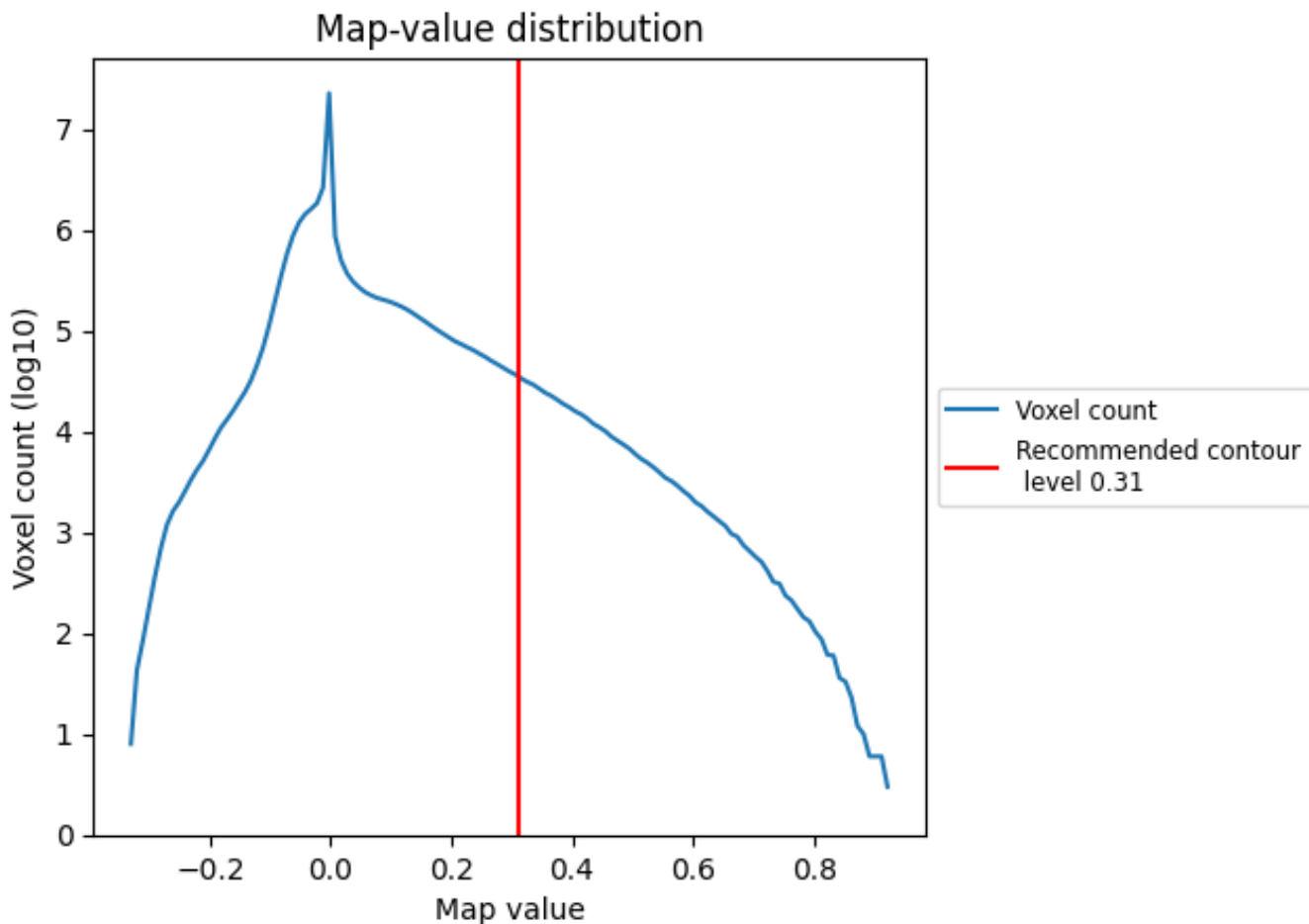
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

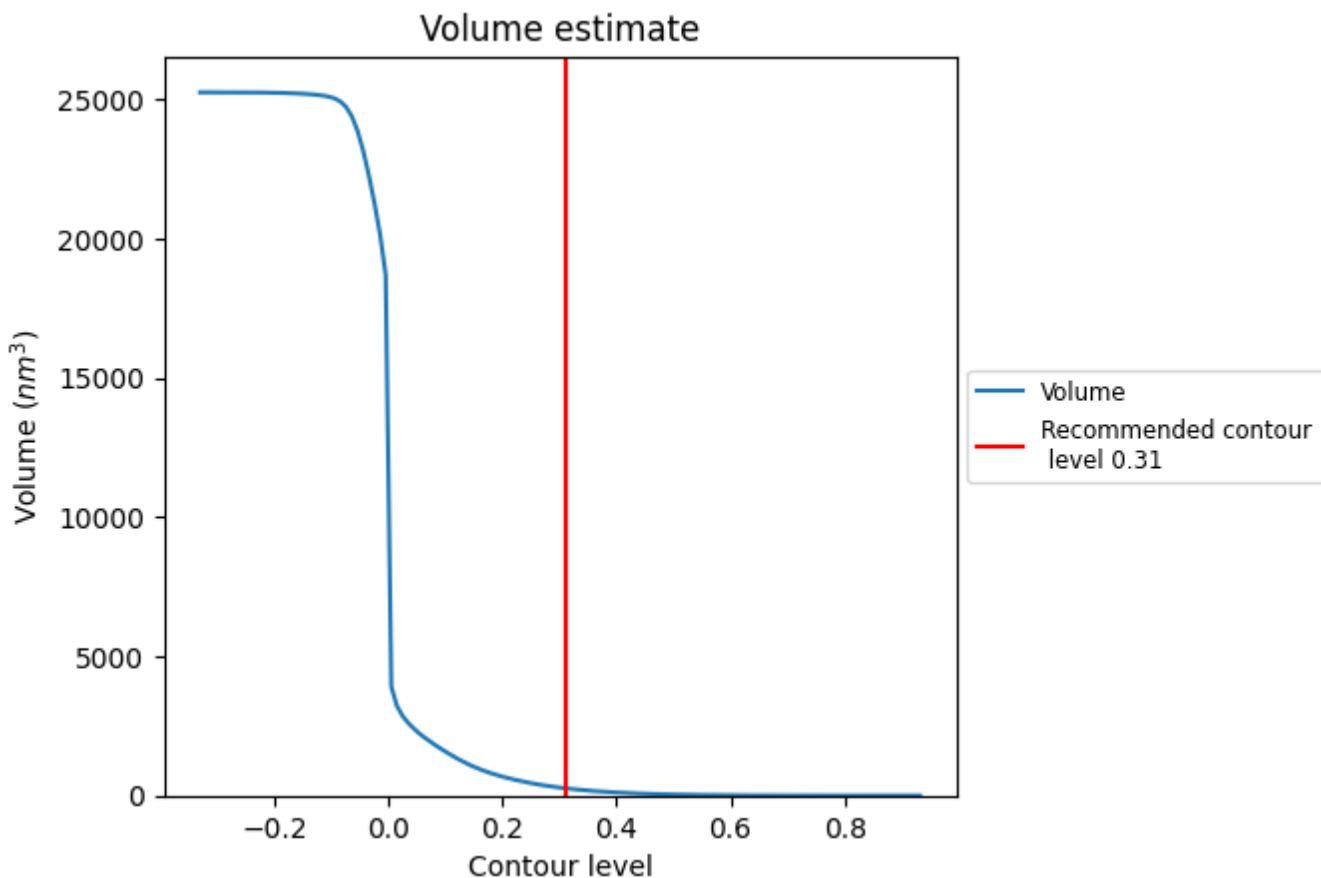
This section contains the results of statistical analysis of the map.

### 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.

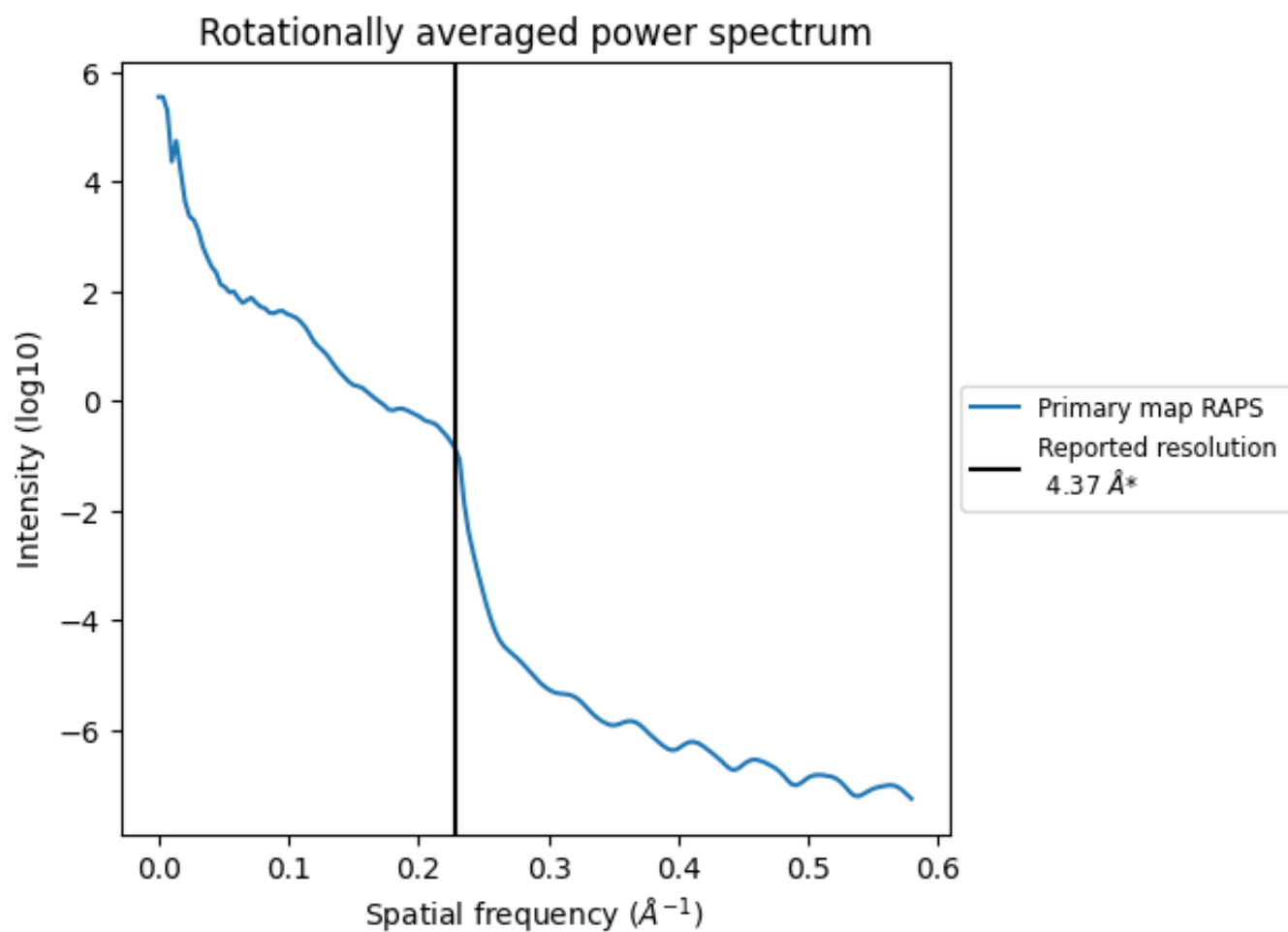
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 262 nm<sup>3</sup>; this corresponds to an approximate mass of 237 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  $0.229 \text{\AA}^{-1}$

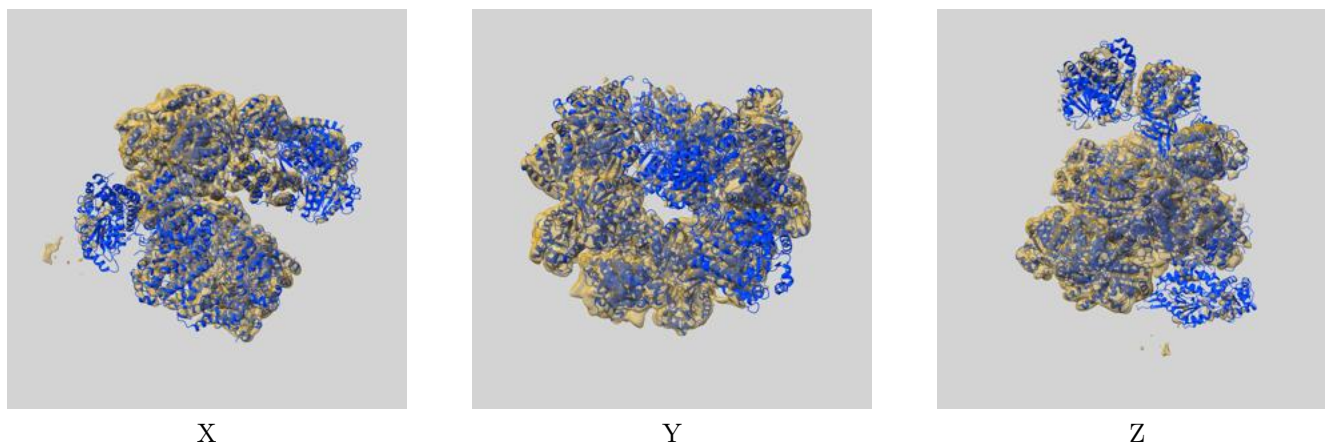
## 8 Fourier-Shell correlation

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

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

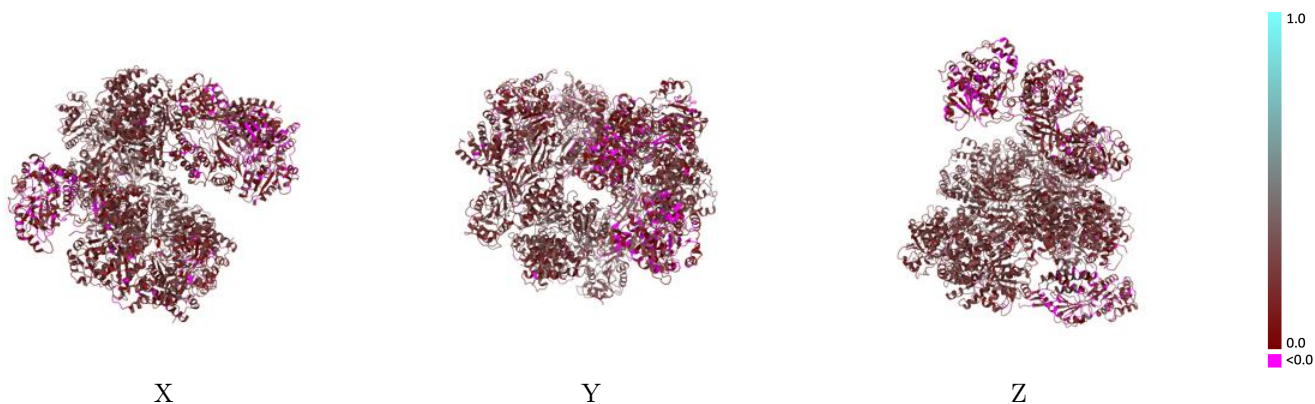
This section contains information regarding the fit between EMDB map EMD-30625 and PDB model 7DAG. Per-residue inclusion information can be found in section 3 on page 5.

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



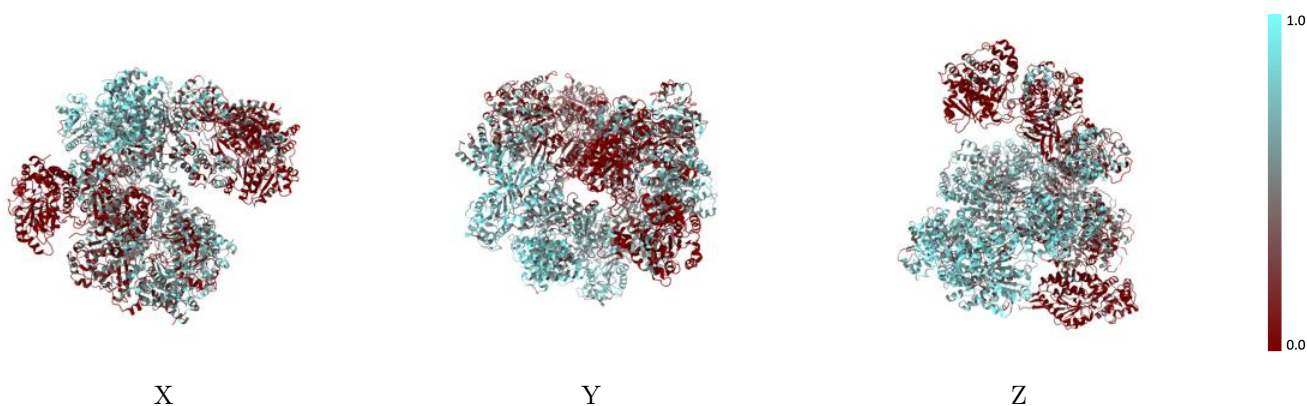
The images above show the 3D surface view of the map at the recommended contour level 0.31 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



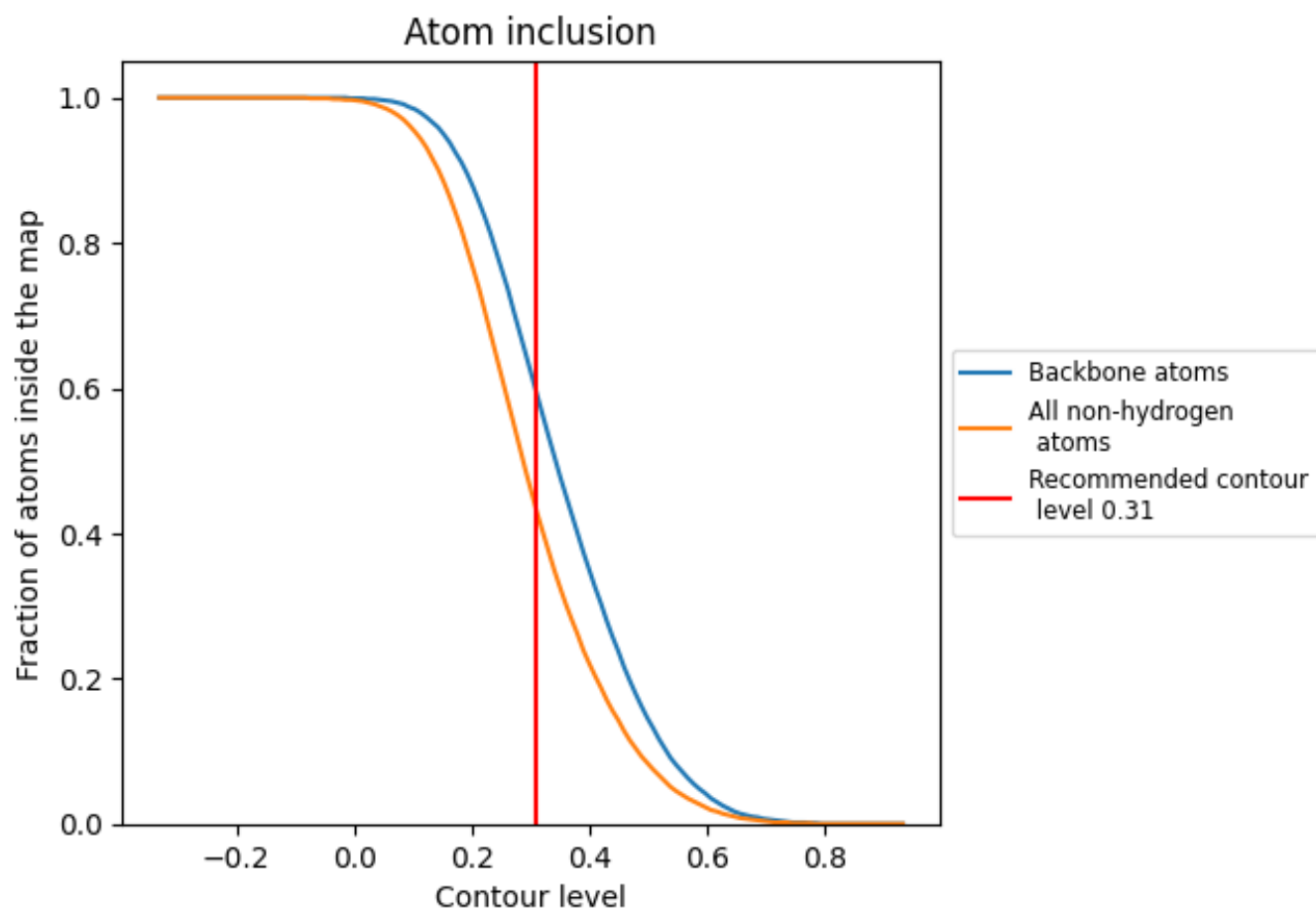
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.31).



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 43% 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 (0.31) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4310	 0.1970
A	 0.2300	 0.1290
B	 0.3540	 0.1930
C	 0.6610	 0.2430
D	 0.6820	 0.2390
E	 0.5310	 0.2110
F	 0.4650	 0.2120
G	 0.1490	 0.1980
H	 0.0410	 0.1080

