



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 11:19 PM UTC

PDB ID : 5O66 / pdb_00005o66
EMDB ID : EMD-8640
Title : Asymmetric AcrABZ-TolC
Authors : Du, D.; Luisi, B.F.
Deposited on : 2017-06-05
Resolution : 5.90 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

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:

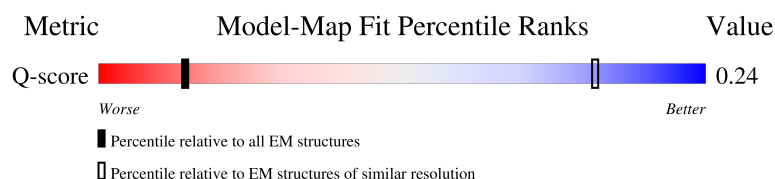
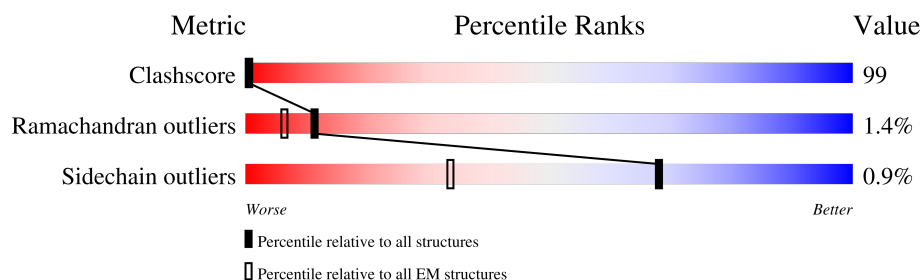
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 5.90 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	501 (5.40 - 6.40)

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	493	
1	B	493	
1	C	493	
2	D	373	

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Mol	Chain	Length	Quality of chain
2	E	373	
2	F	373	
2	G	373	
2	H	373	
2	I	373	
3	J	1049	
3	K	1049	
3	L	1049	
4	M	54	
4	N	54	
4	O	54	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 49671 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 Outer membrane protein TolC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	428	Total	C	N	O	S	0	0
			3304	2037	586	676	5		
1	B	428	Total	C	N	O	S	0	0
			3304	2037	586	676	5		
1	C	428	Total	C	N	O	S	0	0
			3304	2037	586	676	5		

- Molecule 2 is a protein called Multidrug efflux pump subunit AcrA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	340	Total	C	N	O	S	0	0
			2553	1591	451	506	5		
2	E	340	Total	C	N	O	S	0	0
			2553	1591	451	506	5		
2	F	340	Total	C	N	O	S	0	0
			2553	1591	451	506	5		
2	G	340	Total	C	N	O	S	0	0
			2553	1591	451	506	5		
2	H	340	Total	C	N	O	S	0	0
			2553	1591	451	506	5		
2	I	340	Total	C	N	O	S	0	0
			2553	1591	451	506	5		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	223	MET	PHE	conflict	UNP P0AE07
D	224	MET	LEU	conflict	UNP P0AE07
D	287	MET	LEU	conflict	UNP P0AE07
D	288	MET	LEU	conflict	UNP P0AE07
E	223	MET	PHE	conflict	UNP P0AE07
E	224	MET	LEU	conflict	UNP P0AE07
E	287	MET	LEU	conflict	UNP P0AE07

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Chain	Residue	Modelled	Actual	Comment	Reference
E	288	MET	LEU	conflict	UNP P0AE07
F	223	MET	PHE	conflict	UNP P0AE07
F	224	MET	LEU	conflict	UNP P0AE07
F	287	MET	LEU	conflict	UNP P0AE07
F	288	MET	LEU	conflict	UNP P0AE07
G	223	MET	PHE	conflict	UNP P0AE07
G	224	MET	LEU	conflict	UNP P0AE07
G	287	MET	LEU	conflict	UNP P0AE07
G	288	MET	LEU	conflict	UNP P0AE07
H	223	MET	PHE	conflict	UNP P0AE07
H	224	MET	LEU	conflict	UNP P0AE07
H	287	MET	LEU	conflict	UNP P0AE07
H	288	MET	LEU	conflict	UNP P0AE07
I	223	MET	PHE	conflict	UNP P0AE07
I	224	MET	LEU	conflict	UNP P0AE07
I	287	MET	LEU	conflict	UNP P0AE07
I	288	MET	LEU	conflict	UNP P0AE07

- Molecule 3 is a protein called Multidrug efflux pump subunit AcrB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	1044	Total	C	N	O	S	0	0
			7908	5086	1308	1470	44		
3	K	1033	Total	C	N	O	S	0	0
			7845	5049	1294	1458	44		
3	L	1033	Total	C	N	O	S	0	0
			7845	5049	1294	1458	44		

- Molecule 4 is a protein called Multidrug efflux pump accessory protein AcrZ.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	36	Total	C	N	O	S	0	0
			277	193	38	43	3		
4	N	37	Total	C	N	O	S	0	0
			283	196	39	45	3		
4	O	37	Total	C	N	O	S	0	0
			283	196	39	45	3		

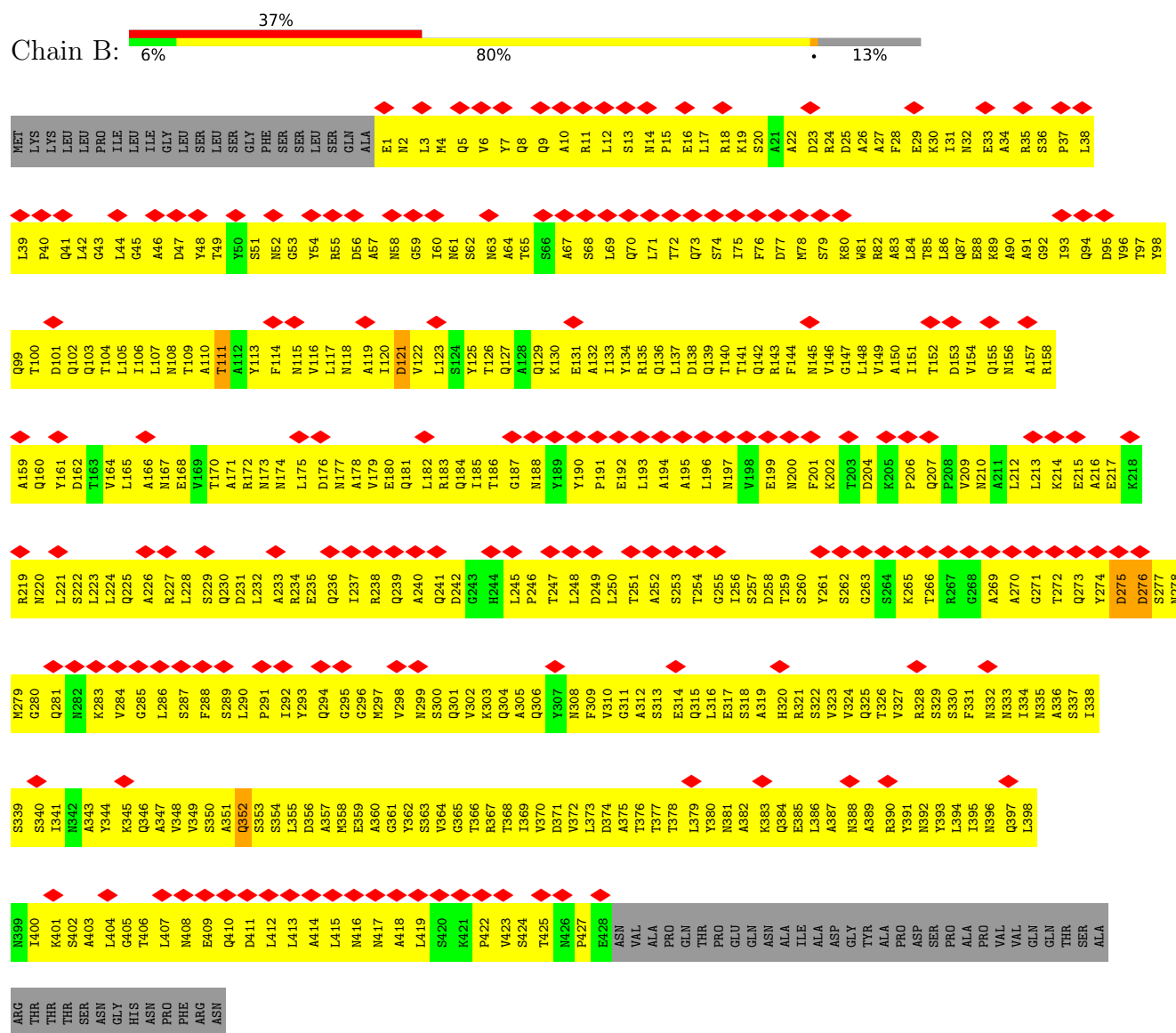
There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	50	HIS	-	expression tag	UNP P0AAX1

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Chain	Residue	Modelled	Actual	Comment	Reference
M	51	HIS	-	expression tag	UNP P0AAX1
M	52	HIS	-	expression tag	UNP P0AAX1
M	53	HIS	-	expression tag	UNP P0AAX1
M	54	HIS	-	expression tag	UNP P0AAX1
N	50	HIS	-	expression tag	UNP P0AAX1
N	51	HIS	-	expression tag	UNP P0AAX1
N	52	HIS	-	expression tag	UNP P0AAX1
N	53	HIS	-	expression tag	UNP P0AAX1
N	54	HIS	-	expression tag	UNP P0AAX1
O	50	HIS	-	expression tag	UNP P0AAX1
O	51	HIS	-	expression tag	UNP P0AAX1
O	52	HIS	-	expression tag	UNP P0AAX1
O	53	HIS	-	expression tag	UNP P0AAX1
O	54	HIS	-	expression tag	UNP P0AAX1

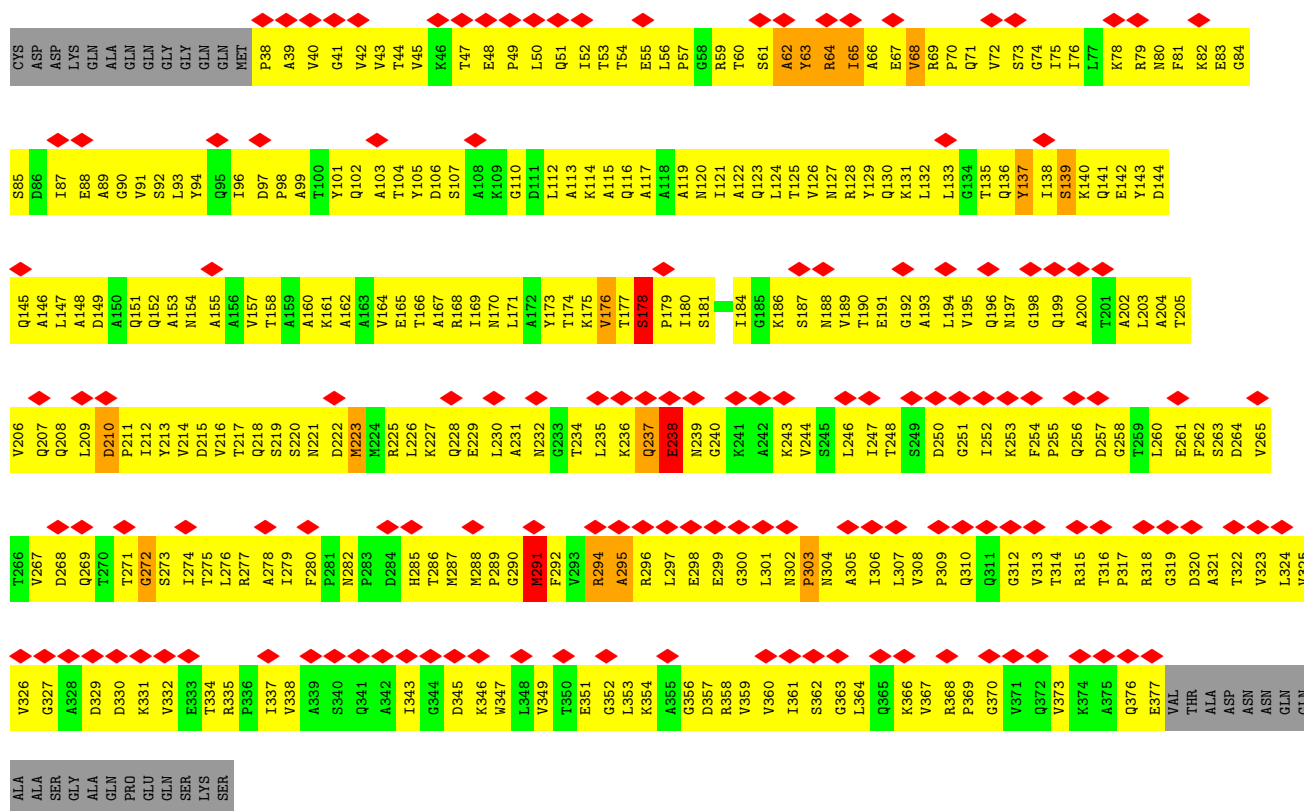


• Molecule 1: Outer membrane protein TolC



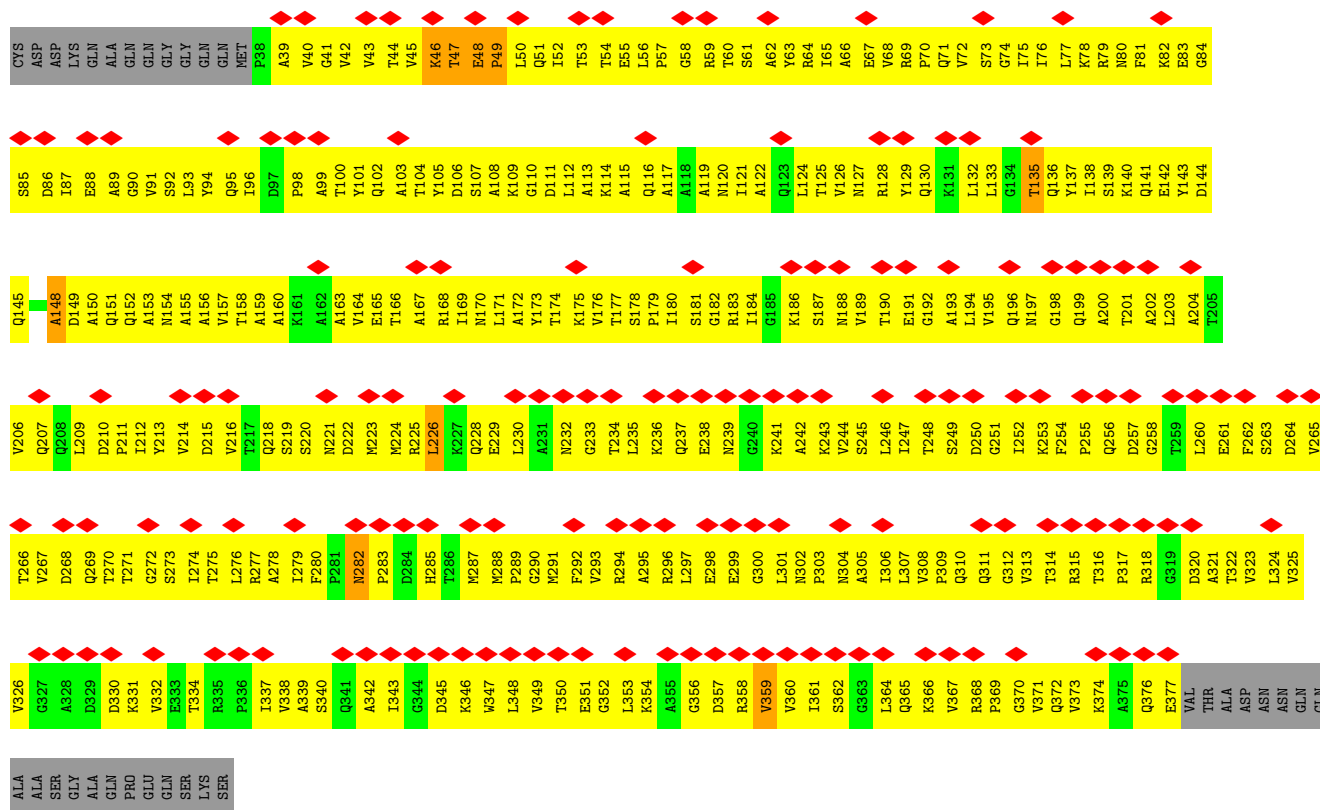


• Molecule 2: Multidrug efflux pump subunit AcrA

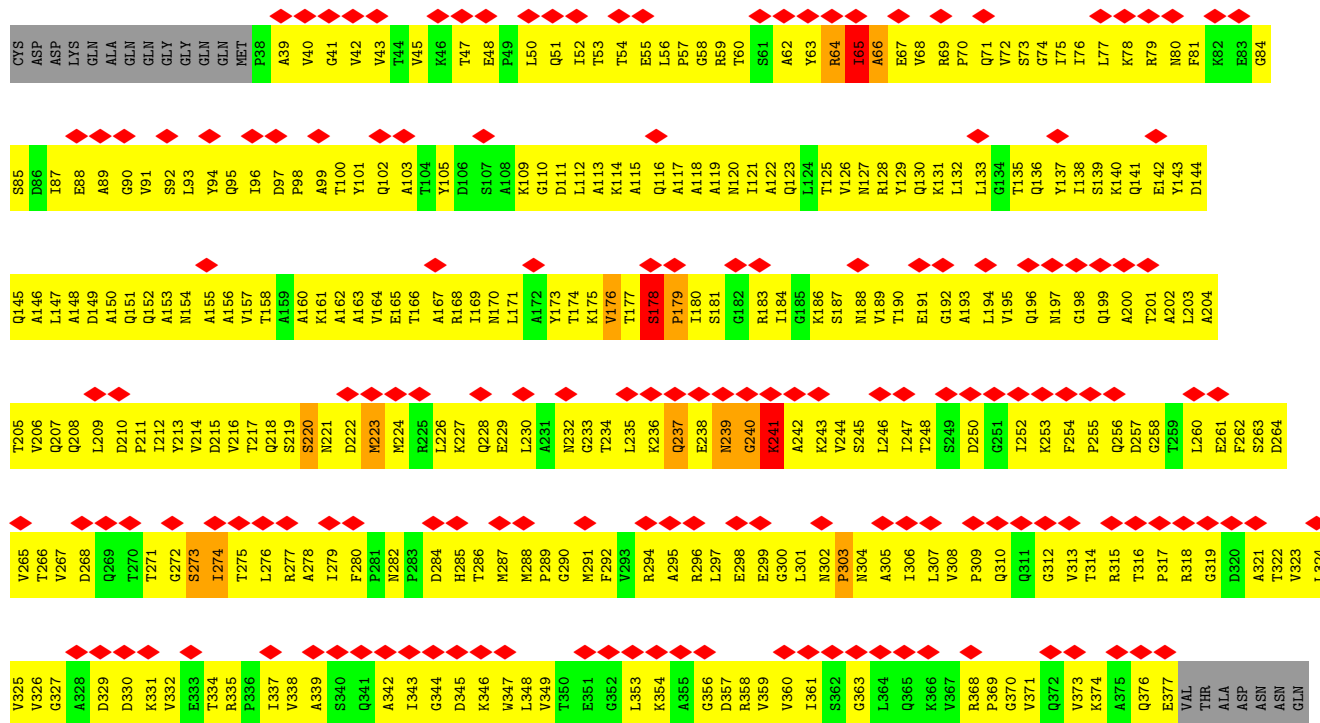


• Molecule 2: Multidrug efflux pump subunit AcrA



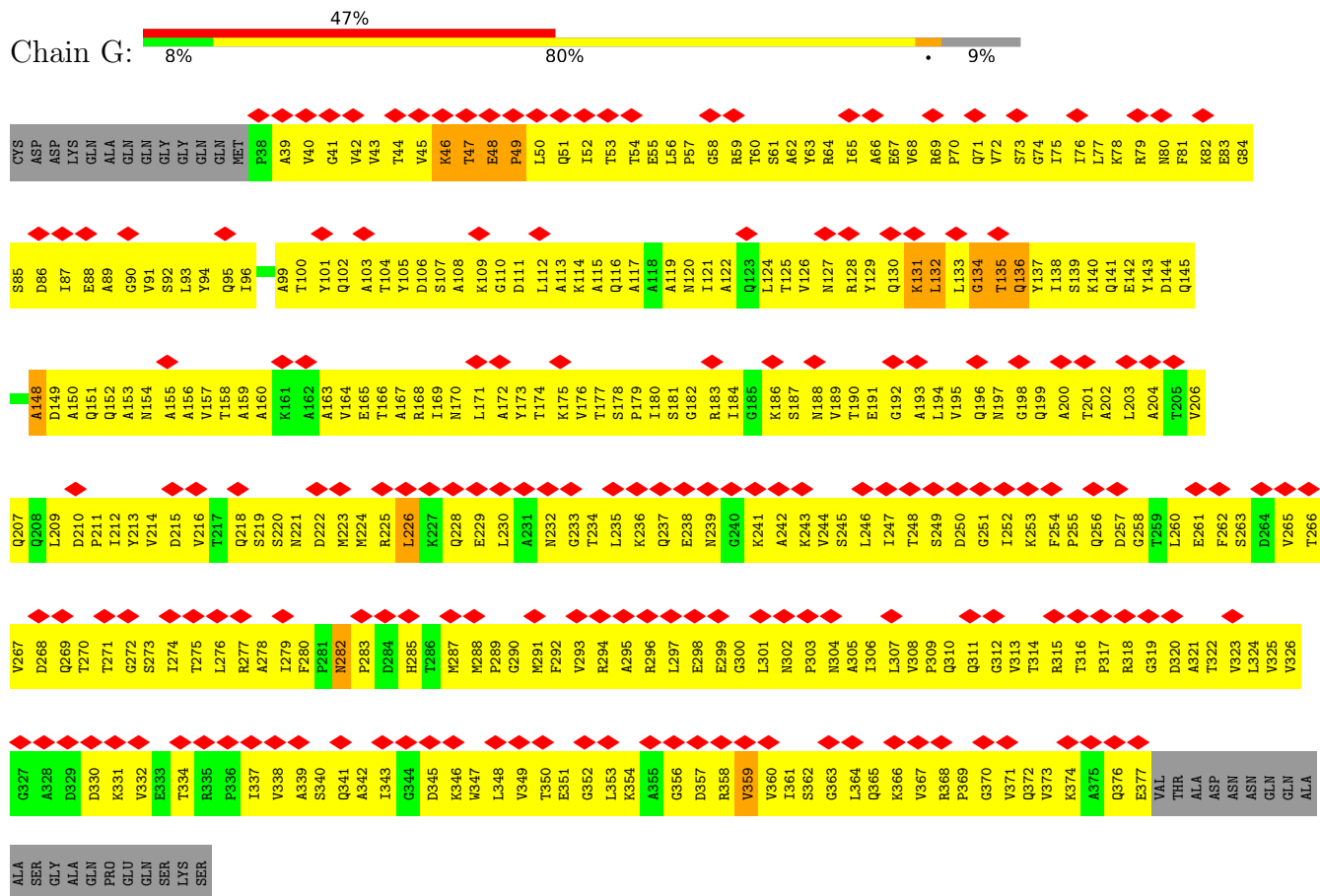


• Molecule 2: Multidrug efflux pump subunit AcrA

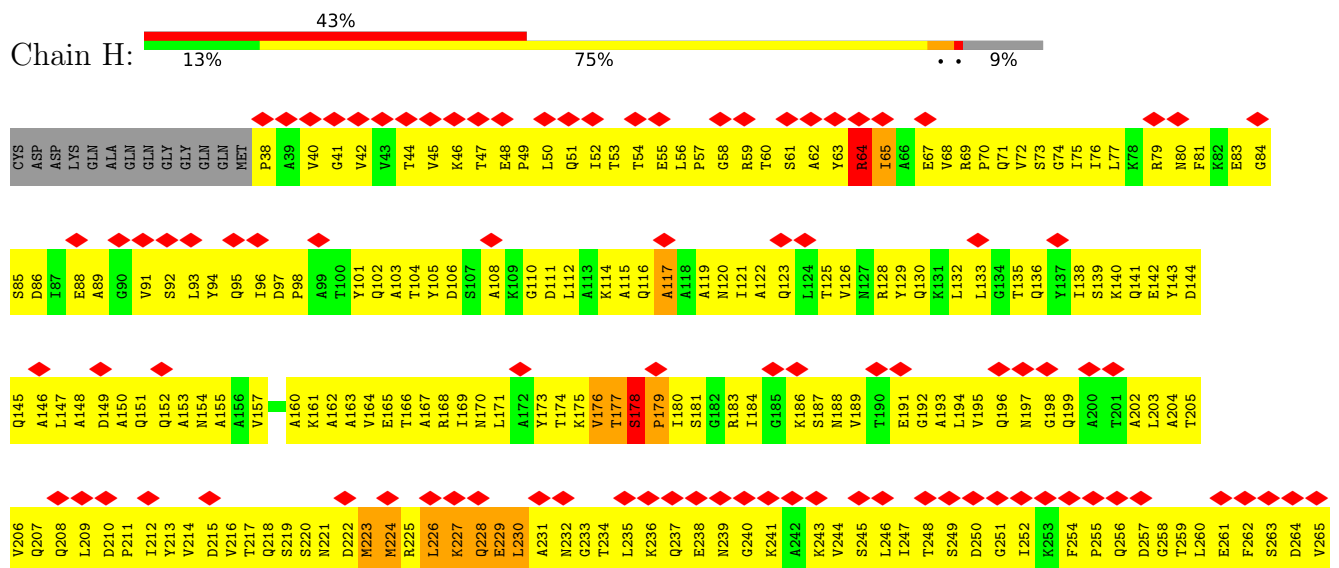


GLN
ALA
ALA
SER
GLY
ALA
ALA
GLN
PRO
GLU
GLN
SER
LYS
SER

• Molecule 2: Multidrug efflux pump subunit AcrA

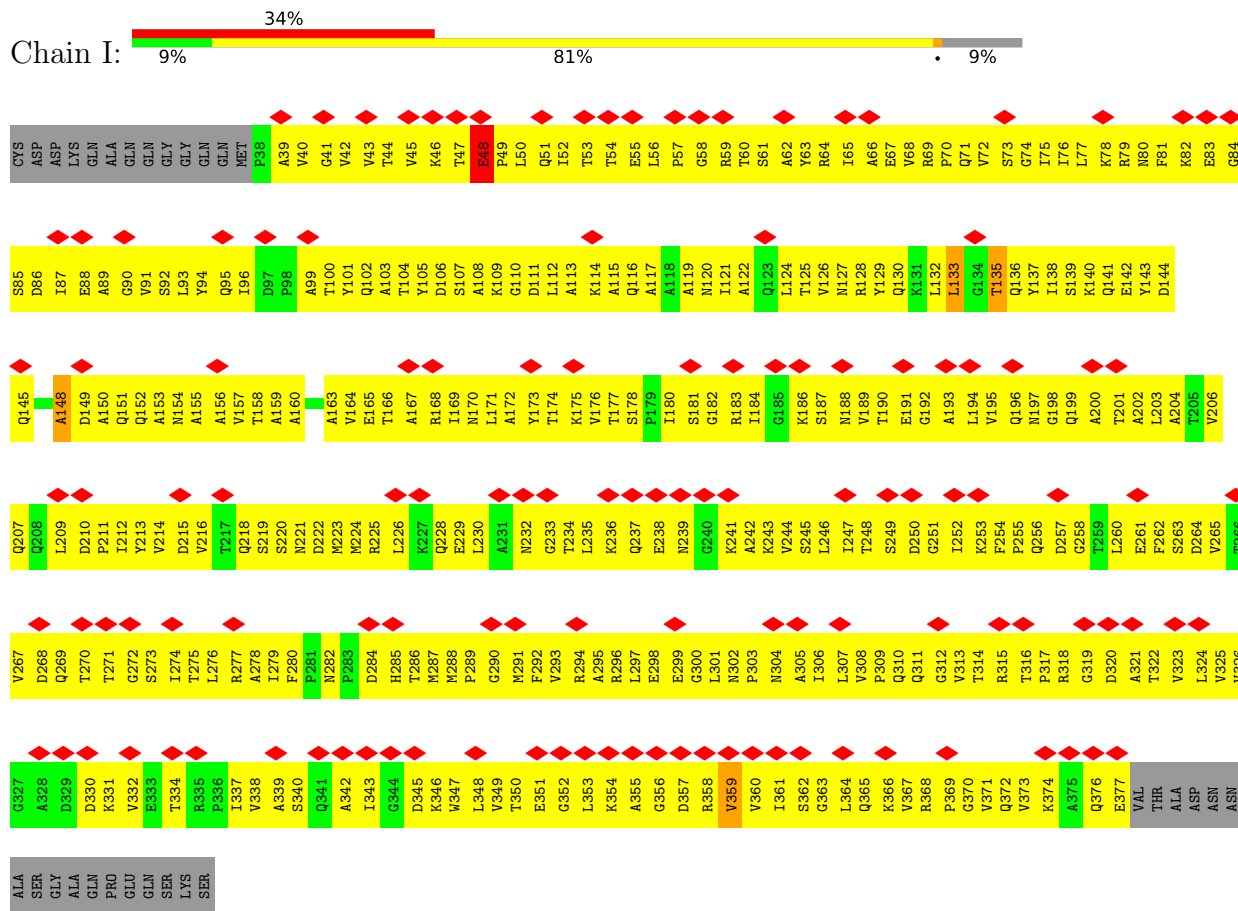


• Molecule 2: Multidrug efflux pump subunit AcrA

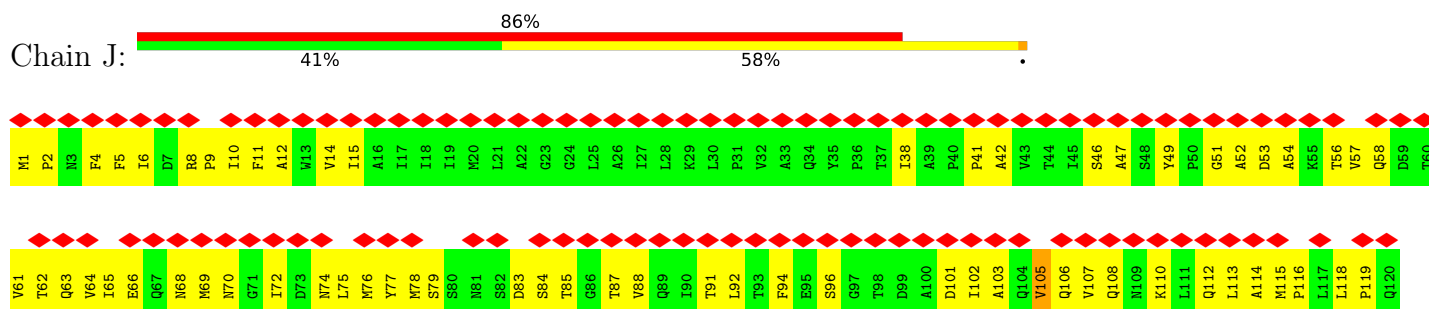




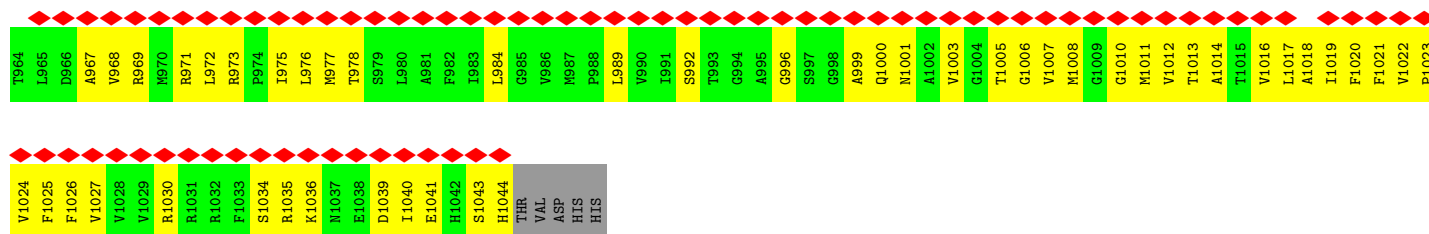
• Molecule 2: Multidrug efflux pump subunit AcrA



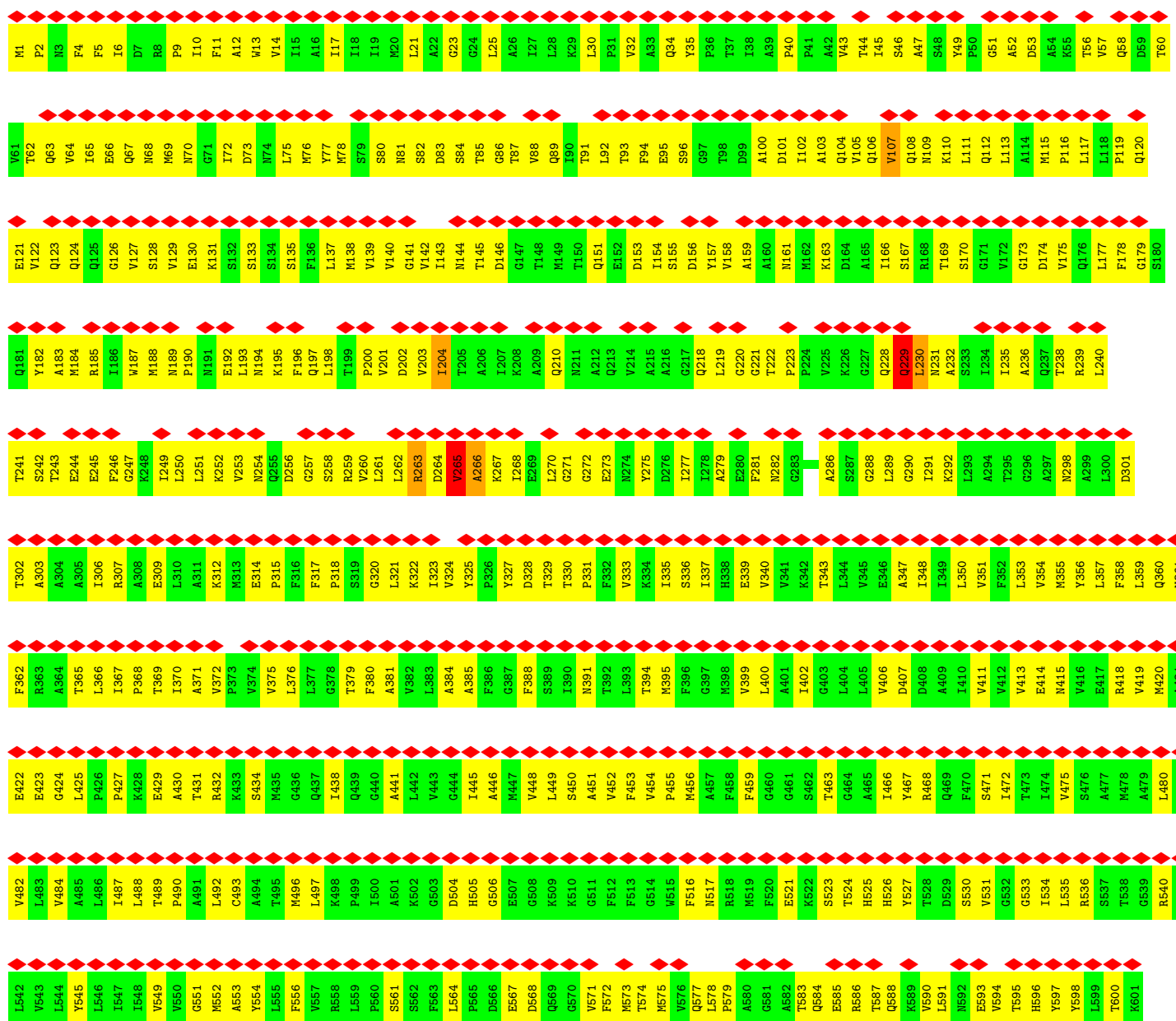
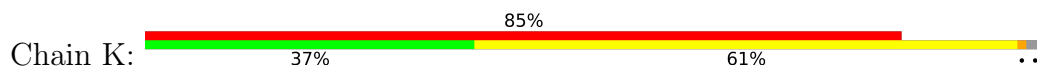
• Molecule 3: Multidrug efflux pump subunit AcrB

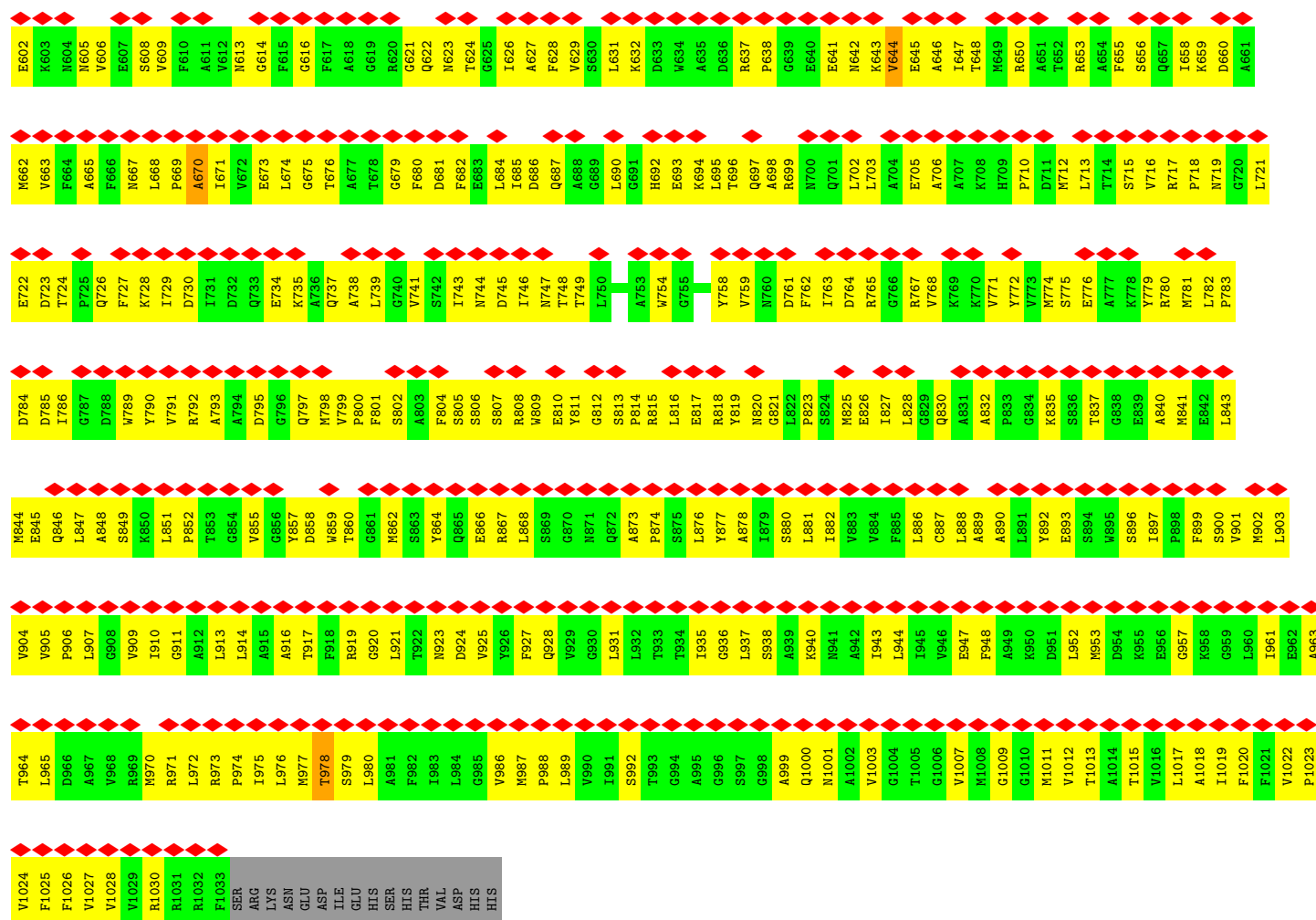




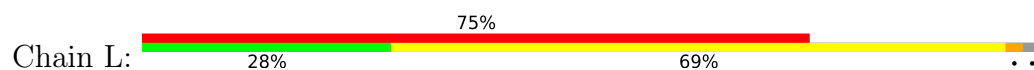


• Molecule 3: Multidrug efflux pump subunit AcrB

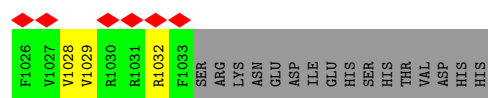




• Molecule 3: Multidrug efflux pump subunit AcrB



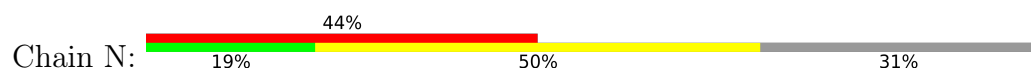
T964	L965	D966	A967	V968	R969	M970	R971	L972	R973	P974	I975	L976	M977	T978	S979	L980	A981	F982	I983	L984	G985	V986	M987	P988	L989	V990	V991	S992	T993	G994	A995	G996	S997	G998	A999	Q1000	N1001	A1002	A1003	G1004	T1005	G1006	V1007	M1011	V1012	T1013	A1014	T1015	V1016	L1017	A1018	I1019	E996	Q957	K958	F1021	V1022	P1023	V1024	F1025
D784	E845	Q846	A967	A848	S849	K850	L851	P852	T853	G854	A915	A916	T917	F918	R919	C920	L921	T922	N923	D924	V925	Y926	F927	Q928	V929	G930	L931	L932	T933	T934	I935	G936	L937	S938	A939	K940	N941	A942	I943	L944	V945	E947	F948	A949	K950	D951	L952	M953	D954	K955	E956	Q957	K958	F1021	V1022	P1023	V1024	F1025		
D784	D785	I786	G787	D788	W789	Y790	Y791	R792	A793	A794	D795	G796	Q797	T917	F918	R919	C920	L921	T922	N923	D924	V925	Y926	F927	Q928	V929	G930	L931	L932	T933	T934	I935	G936	L937	S938	A939	K940	N941	A942	I943	L944	V945	E947	F948	A949	K950	D951	L952	M953	D954	K955	E956	Q957	K958	F1021	V1022	P1023	V1024	F1025	
D723	T724	P725	Q726	F727	K728	I729	D730	Q733	E734	K735	A736	Q737	A738	L739	G740	V741	I743	N744	D745	L746	N747	T748	T749	L750	G751	A752	A753	K754	G755	G756	S757	Y758	F759	N760	D761	F762	I763	D764	R765	G766	R767	V768	K769	W770	V771	Y772	V773	M774	S775	E776	A777	K778	V779	W780	M781	L782	P783			
V663	F664	A665	F666	N667	L668	P669	A670	I671	V672	E673	L674	G675	T676	A677	T678	G679	F680	D681	F682	E683	L684	L685	D686	Q687	A688	G689	L690	D693	W694	A695	D696	R697	T696	Q697	A698	R699	W700	L702	L703	A704	E705	A706	A707	K708	H709	P710	D711	W712	L713	T714	S715	V716	R717	P718	W719	G720	L721	E722		
K603	N604	N605	V606	E607	S608	V609	F610	A611	V612	N613	G614	F615	G616	F617	A618	G619	R620	G621	Q622	N623	T624	G625	T626	F628	W629	S630	L631	K632	D633	W634	A635	D636	R637	Q639	E640	E641	N642	K643	V644	E645	A646	T647	T648	N649	R650	E651	Q652	T652	R653	A654	F655	S656	Q657	L658	K659	D660	A661	M662		
L542	V543	L483	V484	A485	L486	I487	L488	T489	P490	A491	L492	C493	A494	T495	M496	L497	K498	P499	I500	A501	K502	G503	D504	H506	G506	E507	G508	K509	K510	G511	F512	F513	G514	W515	F516	N517	R518	M519	F520	E521	K522	S523	T524	H525	W526	Y527	D528	S530	V531	G532	G533	I534	L535	R536	T538	E539	R540	Y541	E602	
E422	E423	G424	L425	P426	P427	K428	E429	A430	T431	L432	K433	A434	M435	G436	Q437	I438	Q439	P499	I500	A501	K502	G503	D504	H506	G506	E507	G508	K509	K510	G511	F512	F513	G514	W515	F516	N517	R518	M519	F520	E521	K522	S523	T524	H525	W526	Y527	D528	S530	V531	G532	G533	I534	L535	R536	T538	E539	R540	Y541	E602	
F362	R363	A364	T365	L366	I367	P368	T369	I370	A371	V372	P373	V374	V375	L376	L377	P318	S319	T379	F380	A381	V382	L383	A384	A385	F386	G387	F388	S389	I390	P391	T392	L393	T394	M395	F396	G397	M398	F399	E400	L401	A402	G403	L404	L405	V406	D407	A408	A409	I410	V411	V412	V413	E414	N415	V416	E417	R418	V419	M420	A421
T302	A303	A304	A305	I306	R307	A308	E309	L310	A311	K312	M313	E314	P315	F316	F317	P318	S319	T379	F380	A381	V382	L383	A384	A385	F386	G387	F388	S389	I390	P391	T392	L393	T394	M395	F396	G397	M398	F399	E400	L401	A402	G403	L404	L405	V406	D407	A408	A409	I410	V411	V412	V413	E414	N415	V416	E417	R418	V419	M420	A421
S242	T243	E244	E245	F246	G247	K248	I249	L250	L251	K252	V253	N254	Q255	D256	G257	R258	V259	L260	L261	L262	R263	D264	V265	A266	K267	I268	E269	L270	G271	G272	E273	N274	Y275	D276	I277	I278	A279	E280	F281	N282	Q283	Q284	P285	A286	S287	G288	L289	G290	K292	L293	A294	T295	Q296	N298	A299	L300	D301			



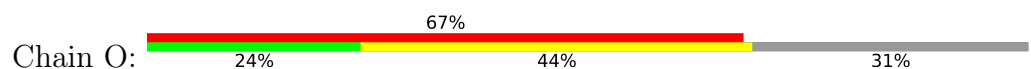
● Molecule 4: Multidrug efflux pump accessory protein AcrZ



● Molecule 4: Multidrug efflux pump accessory protein AcrZ



● Molecule 4: Multidrug efflux pump accessory protein AcrZ



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26950	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	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	0.143	Depositor
Minimum map value	-0.084	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	414.72, 414.72, 414.72	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.62, 1.62, 1.62	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	0.36	0/3345	0.60	0/4544
1	B	0.38	0/3345	0.60	0/4544
1	C	0.38	0/3345	0.60	0/4544
2	D	0.43	1/2585 (0.0%)	0.75	2/3512 (0.1%)
2	E	0.47	0/2585	0.74	4/3512 (0.1%)
2	F	0.40	0/2585	0.72	1/3512 (0.0%)
2	G	0.47	0/2585	0.74	4/3512 (0.1%)
2	H	0.40	0/2585	0.74	2/3512 (0.1%)
2	I	0.44	0/2585	0.71	2/3512 (0.1%)
3	J	0.52	2/8060 (0.0%)	0.66	3/10947 (0.0%)
3	K	0.50	0/7995	0.64	0/10859
3	L	0.59	4/7995 (0.1%)	0.71	4/10859 (0.0%)
4	M	0.42	0/281	0.57	0/380
4	N	0.42	0/287	0.67	0/388
4	O	0.39	0/287	0.60	0/388
All	All	0.47	7/50450 (0.0%)	0.68	22/68525 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	283	GLY	C-N	-7.23	1.18	1.33
3	J	126	GLY	C-N	-6.75	1.25	1.33
3	L	256	ASP	CA-C	-6.58	1.43	1.52
3	L	586	ARG	CZ-NH1	5.69	1.40	1.32
3	J	211	ASN	CA-CB	-5.48	1.45	1.53

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	586	ARG	NE-CZ-NH2	-10.60	109.66	119.20
2	D	319	GLY	N-CA-C	-6.96	106.80	115.08
3	J	616	GLY	N-CA-C	-6.64	101.39	111.42
2	D	272	GLY	N-CA-C	-6.27	106.42	115.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	227	LYS	N-CA-C	-5.97	104.78	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3304	0	3251	946	0
1	B	3304	0	3254	1053	0
1	C	3304	0	3254	1030	0
2	D	2553	0	2607	814	0
2	E	2553	0	2610	884	0
2	F	2553	0	2608	796	0
2	G	2553	0	2610	880	0
2	H	2553	0	2610	748	0
2	I	2553	0	2610	949	0
3	J	7908	0	8018	745	0
3	K	7845	0	7990	790	0
3	L	7845	0	7989	1067	0
4	M	277	0	313	23	0
4	N	283	0	318	28	0
4	O	283	0	318	29	0
All	All	49671	0	50360	9915	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 99.

The worst 5 of 9915 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)
3:J:865:GLN:CG	3:J:868:LEU:HD11	1.23	1.65
2:H:63:TYR:CG	2:H:64:ARG:HD2	1.25	1.65
2:H:63:TYR:CB	2:H:64:ARG:HD2	1.28	1.62
2:H:93:LEU:H	2:H:176:VAL:CG1	1.07	1.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:63:TYR:CB	2:H:64:ARG:HB2	1.31	1.57

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	426/493 (86%)	371 (87%)	46 (11%)	9 (2%)	5	29
1	B	426/493 (86%)	377 (88%)	44 (10%)	5 (1%)	10	43
1	C	426/493 (86%)	378 (89%)	44 (10%)	4 (1%)	14	50
2	D	338/373 (91%)	296 (88%)	31 (9%)	11 (3%)	3	21
2	E	338/373 (91%)	287 (85%)	45 (13%)	6 (2%)	6	34
2	F	338/373 (91%)	294 (87%)	34 (10%)	10 (3%)	3	22
2	G	338/373 (91%)	283 (84%)	47 (14%)	8 (2%)	4	27
2	H	338/373 (91%)	302 (89%)	29 (9%)	7 (2%)	5	29
2	I	338/373 (91%)	288 (85%)	48 (14%)	2 (1%)	21	59
3	J	1042/1049 (99%)	971 (93%)	64 (6%)	7 (1%)	18	56
3	K	1031/1049 (98%)	982 (95%)	41 (4%)	8 (1%)	16	54
3	L	1031/1049 (98%)	953 (92%)	64 (6%)	14 (1%)	9	40
4	M	34/54 (63%)	32 (94%)	2 (6%)	0	100	100
4	N	35/54 (65%)	33 (94%)	2 (6%)	0	100	100
4	O	35/54 (65%)	33 (94%)	2 (6%)	0	100	100
All	All	6514/7026 (93%)	5880 (90%)	543 (8%)	91 (1%)	11	40

5 of 91 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	ILE
1	A	77	ASP
2	D	62	ALA
2	D	137	TYR
2	D	178	SER

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	358/412 (87%)	357 (100%)	1 (0%)	86	85
1	B	358/412 (87%)	358 (100%)	0	100	100
1	C	358/412 (87%)	357 (100%)	1 (0%)	86	85
2	D	274/299 (92%)	266 (97%)	8 (3%)	37	58
2	E	274/299 (92%)	272 (99%)	2 (1%)	76	81
2	F	274/299 (92%)	266 (97%)	8 (3%)	37	58
2	G	274/299 (92%)	270 (98%)	4 (2%)	57	71
2	H	274/299 (92%)	266 (97%)	8 (3%)	37	58
2	I	274/299 (92%)	270 (98%)	4 (2%)	57	71
3	J	840/855 (98%)	836 (100%)	4 (0%)	81	83
3	K	838/855 (98%)	834 (100%)	4 (0%)	81	83
3	L	838/855 (98%)	833 (99%)	5 (1%)	78	82
4	M	31/46 (67%)	31 (100%)	0	100	100
4	N	32/46 (70%)	32 (100%)	0	100	100
4	O	32/46 (70%)	32 (100%)	0	100	100
All	All	5329/5733 (93%)	5280 (99%)	49 (1%)	68	78

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	223	MET
2	I	135	THR

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Mol	Chain	Res	Type
2	H	224	MET
2	I	46	LYS
3	J	218	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
3	K	605	ASN
3	K	719	ASN
3	L	254	ASN
1	C	332	ASN
1	C	320	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	283:GLY	C	284:GLN	N	1.18

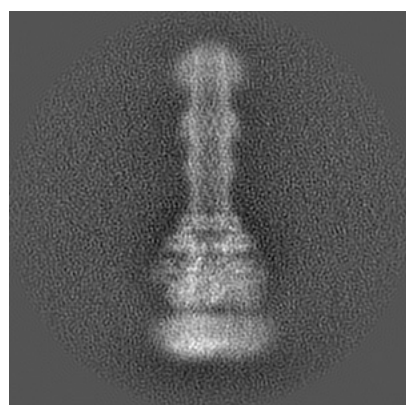
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8640. These allow visual inspection of the internal detail of the map and identification of artifacts.

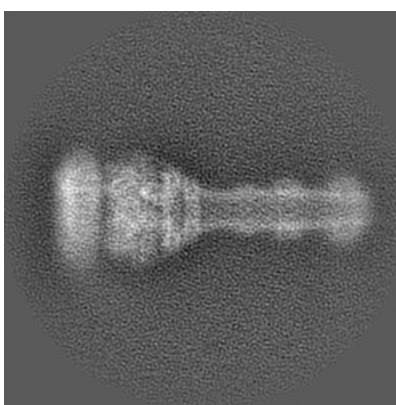
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

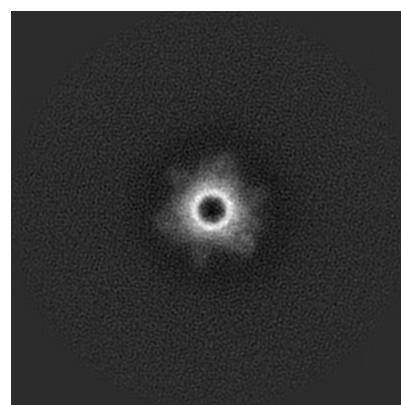
6.1.1 Primary map



X



Y

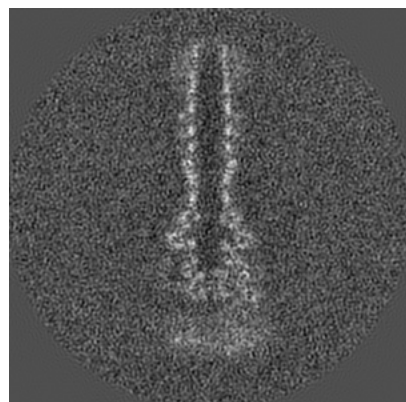


Z

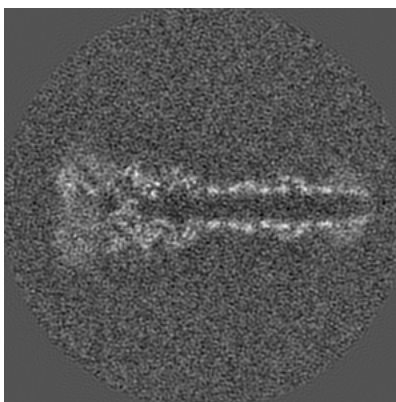
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

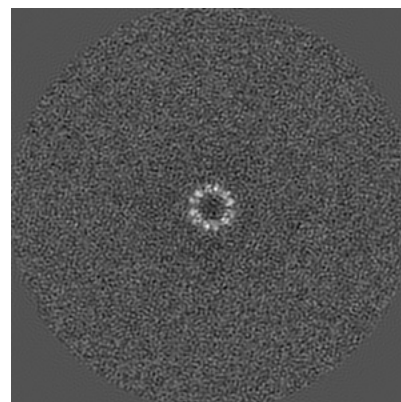
6.2.1 Primary map



X Index: 128



Y Index: 128

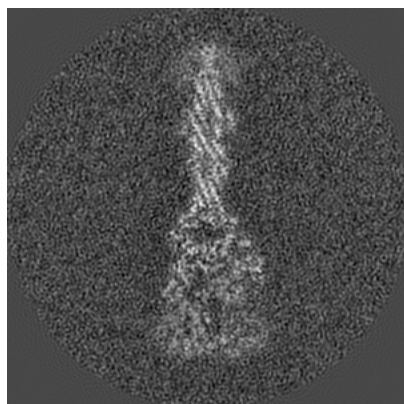


Z Index: 128

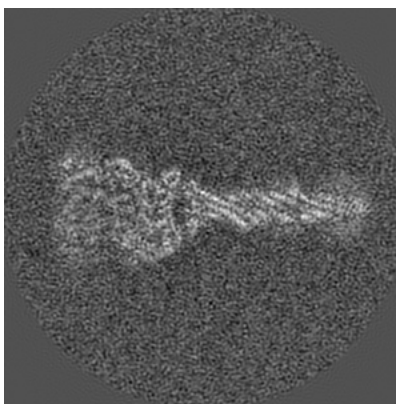
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

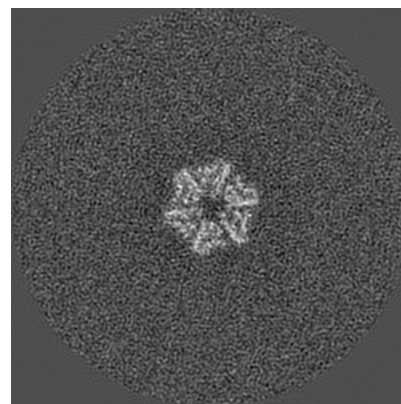
6.3.1 Primary map



X Index: 138



Y Index: 118

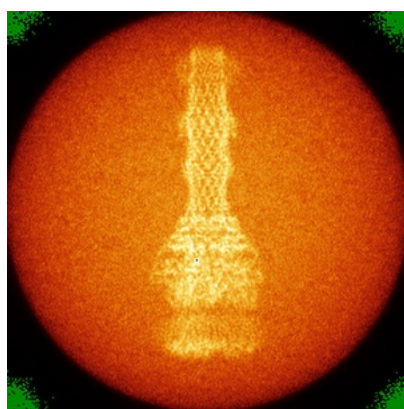


Z Index: 105

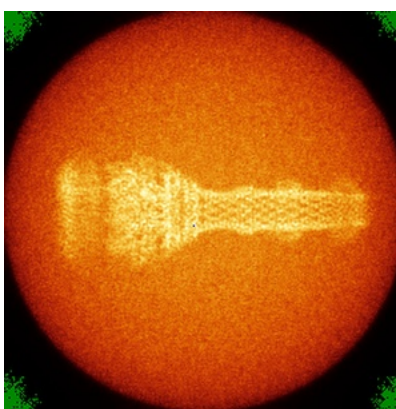
The images above show the largest variance slices of the map in three orthogonal directions.

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

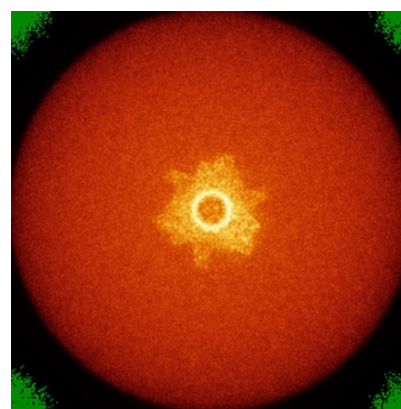
6.4.1 Primary map



X



Y

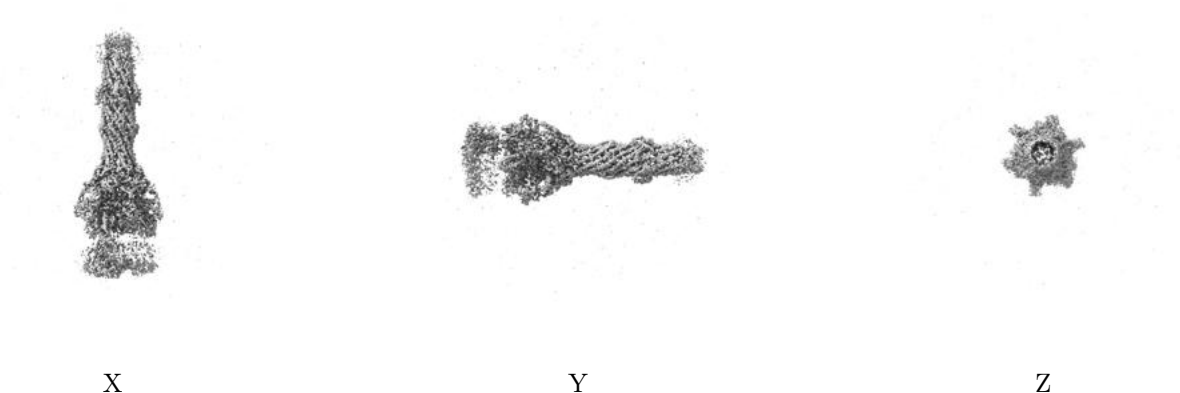


Z

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

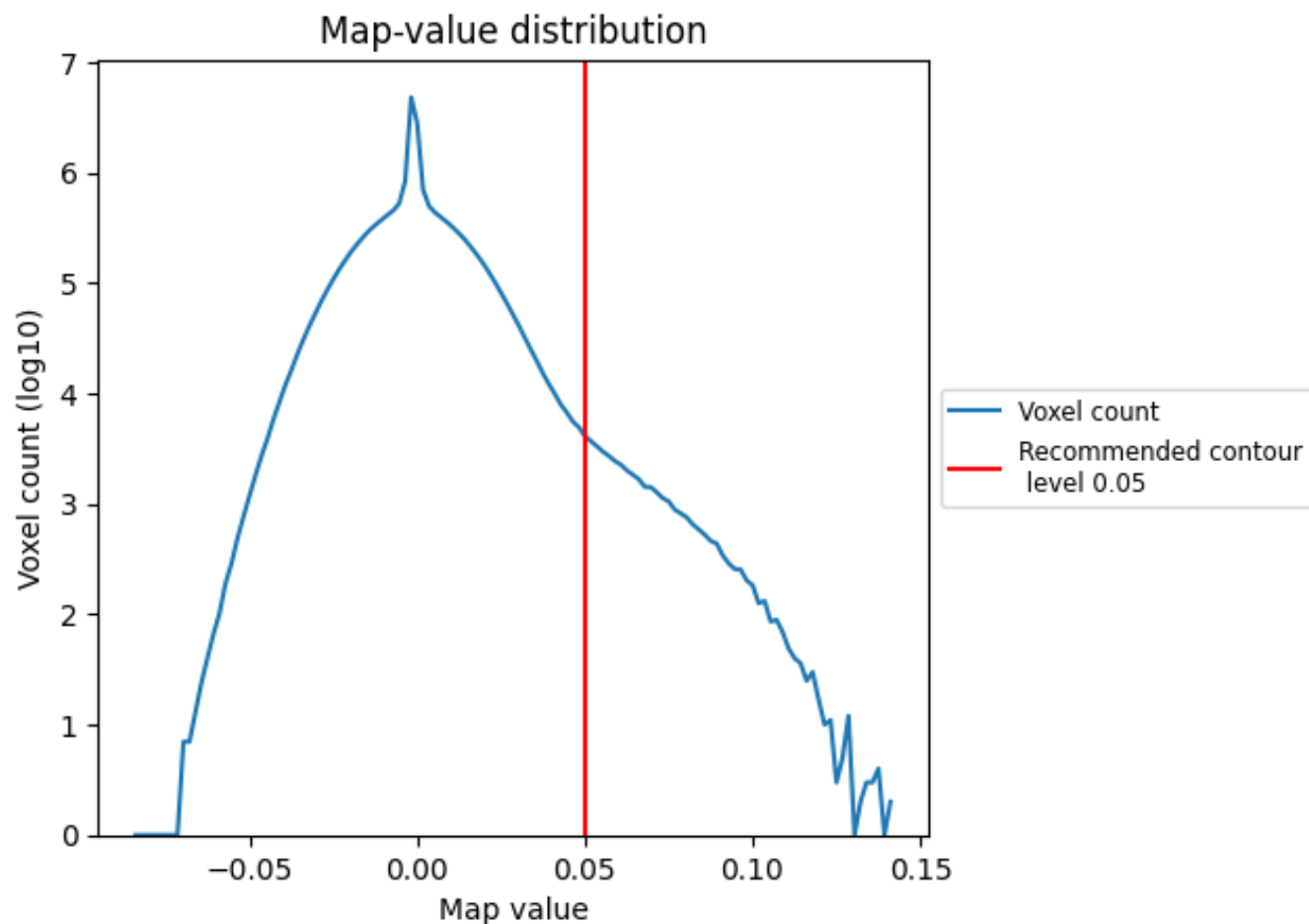
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

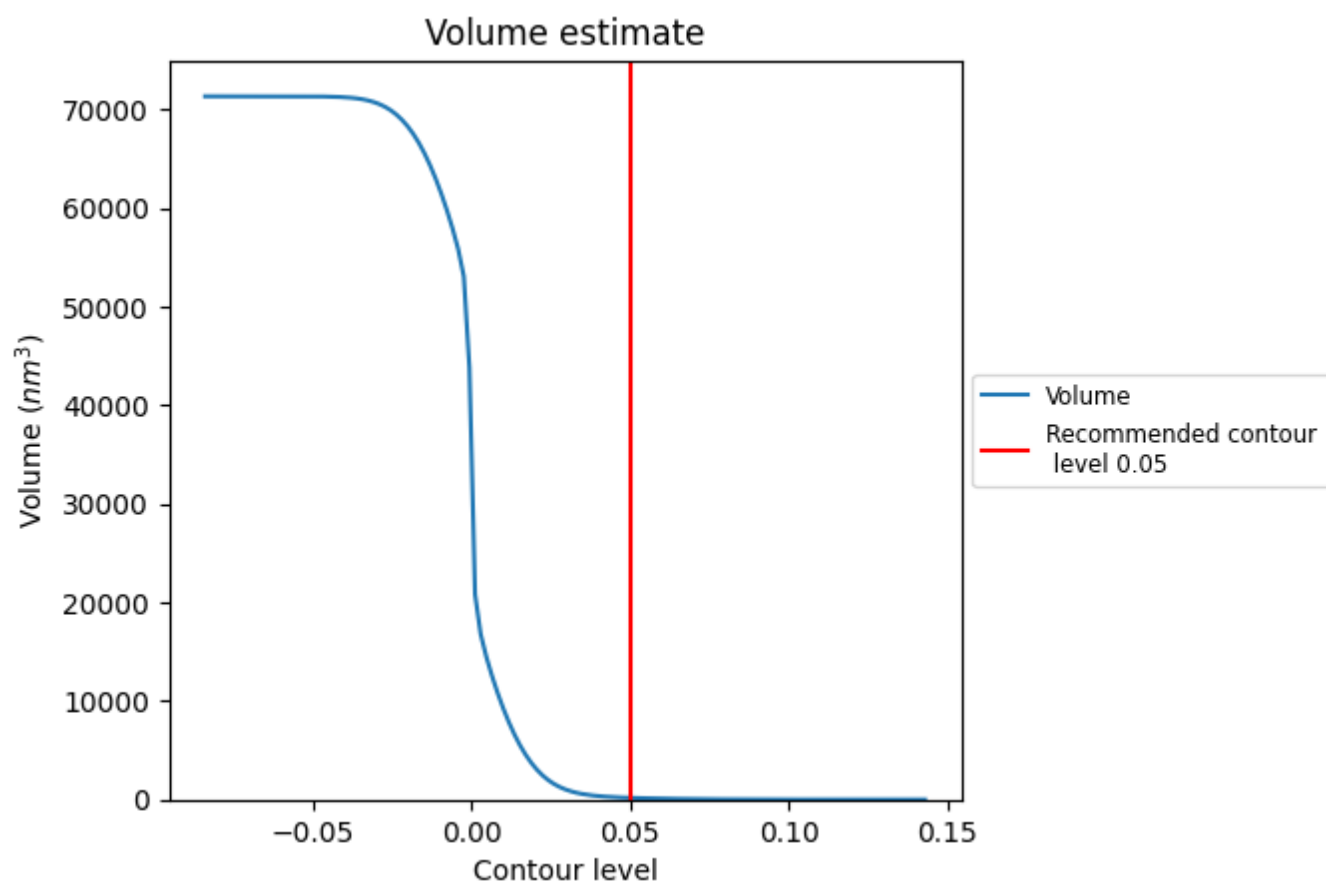
This section contains the results of statistical analysis of the map.

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.

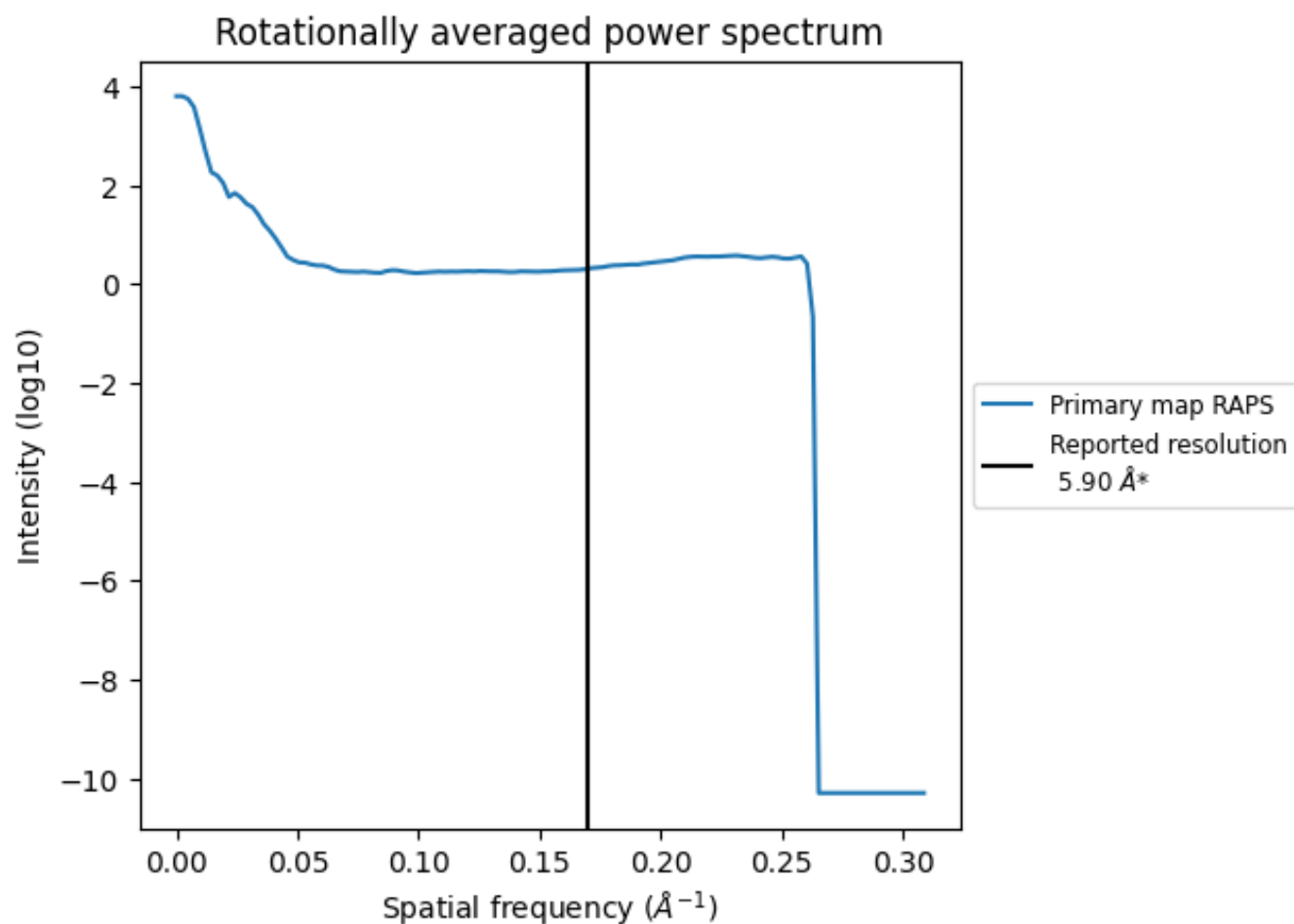
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 175 nm³; this corresponds to an approximate mass of 158 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 ⓘ

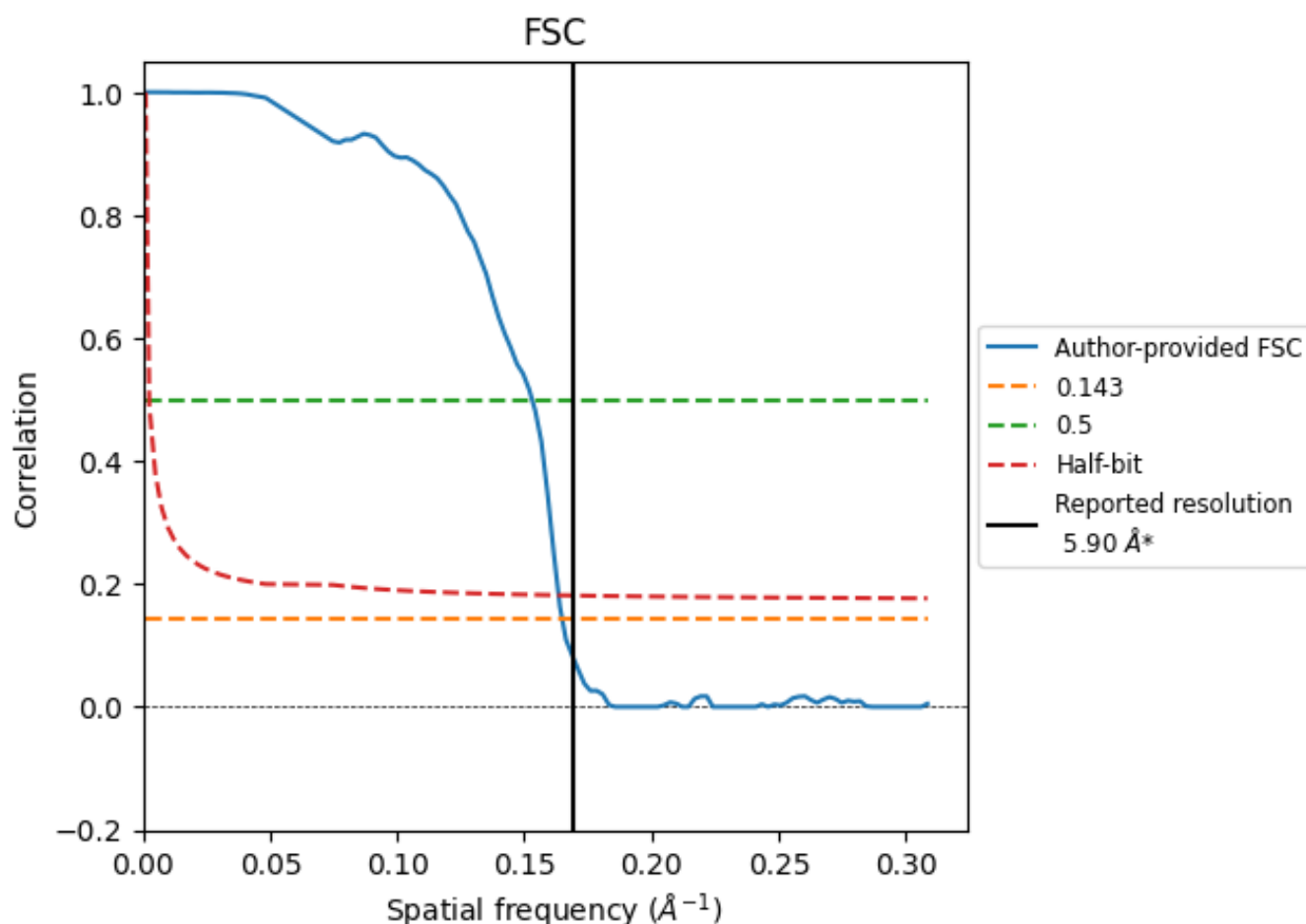


*Reported resolution corresponds to spatial frequency of 0.169 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.169 Å⁻¹

8.2 Resolution estimates [i](#)

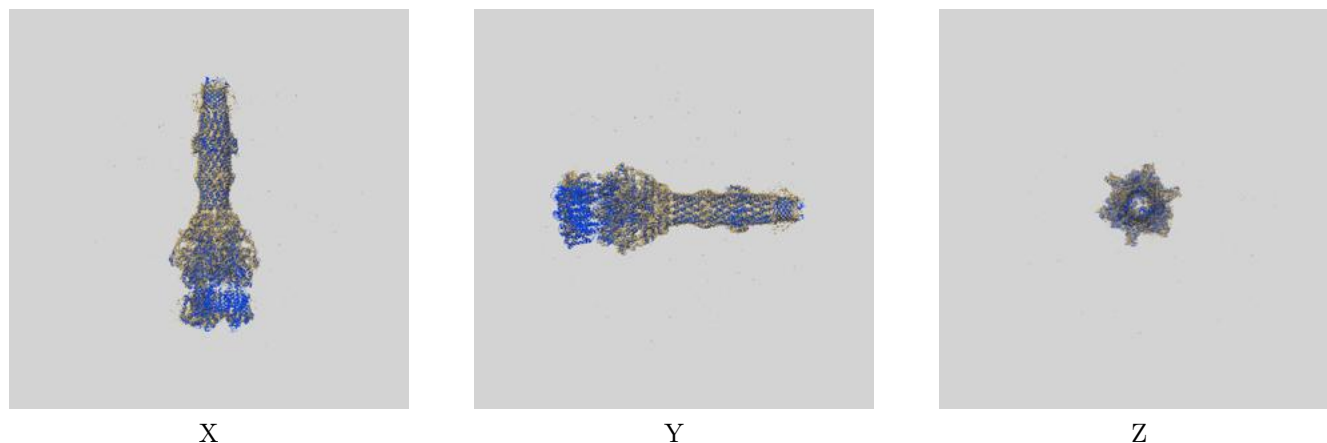
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.90	-	-
Author-provided FSC curve	6.06	6.54	6.12
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

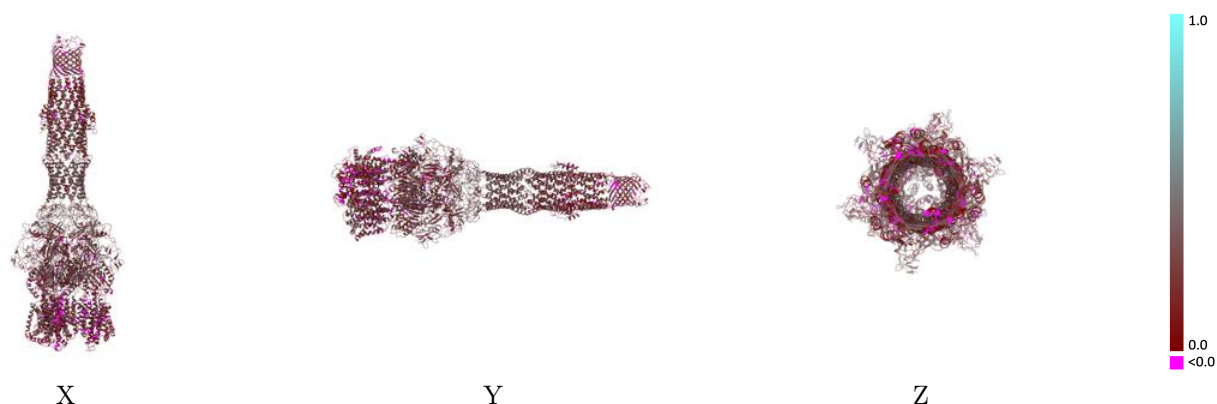
This section contains information regarding the fit between EMDB map EMD-8640 and PDB model 5O66. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



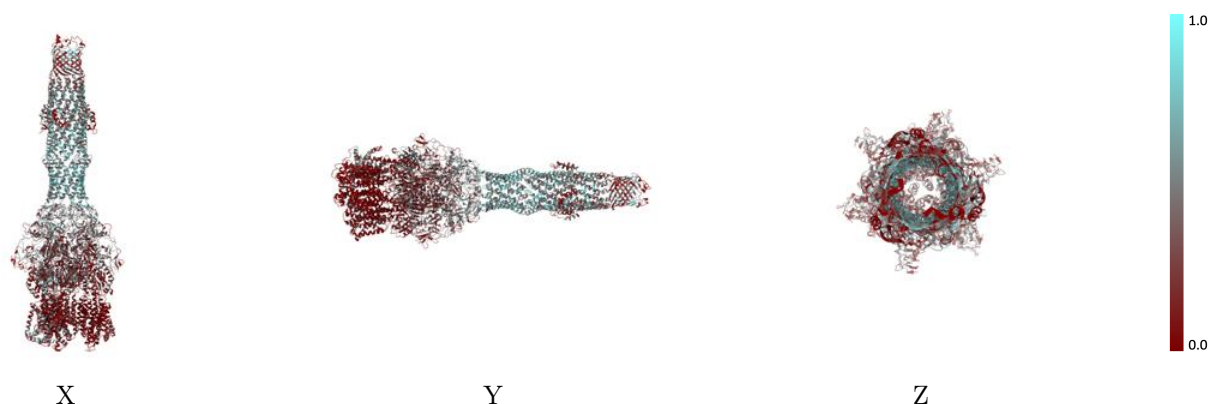
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



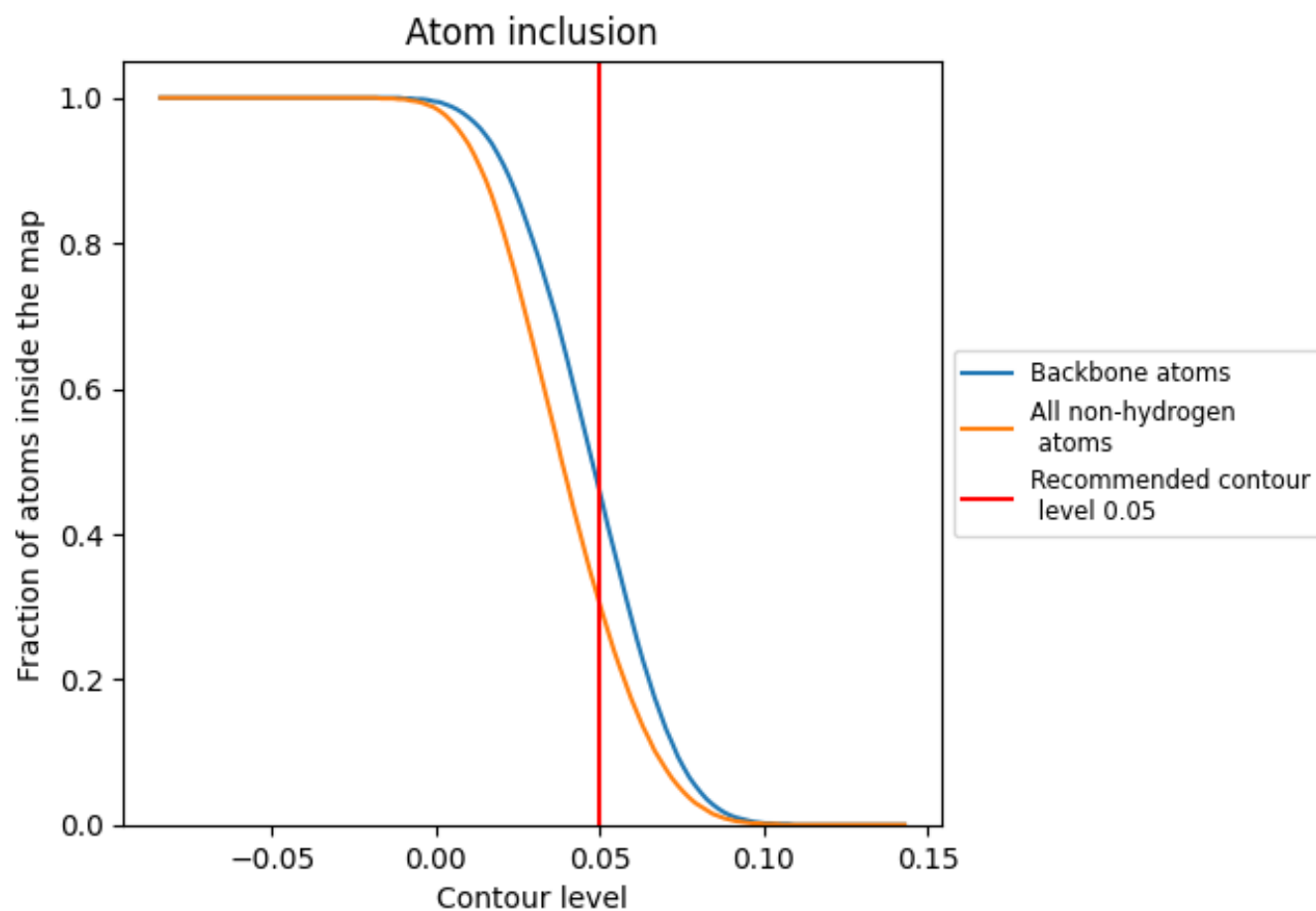
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 46% of all backbone atoms, 30% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3040	0.2400
A	0.4250	0.2250
B	0.4210	0.2100
C	0.4140	0.2190
D	0.4220	0.3200
E	0.4150	0.2910
F	0.4050	0.3040
G	0.3920	0.2740
H	0.4070	0.3180
I	0.4620	0.2920
J	0.1640	0.2060
K	0.1510	0.2220
L	0.2510	0.2070
M	0.0800	0.2000
N	0.2770	0.1970
O	0.0710	0.1850

1.0

0.0

<0.0