



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 09:51 pm GMT

PDB ID : 8BD7
EMDB ID : EMD-15977
Title : IFTB1 subcomplex of anterograde Intraflagellar transport trains (*Chlamydomonas reinhardtii*)
Authors : Lacey, S.E.; Foster, H.E.; Pigino, G.
Deposited on : 2022-10-18
Resolution : 9.90 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:

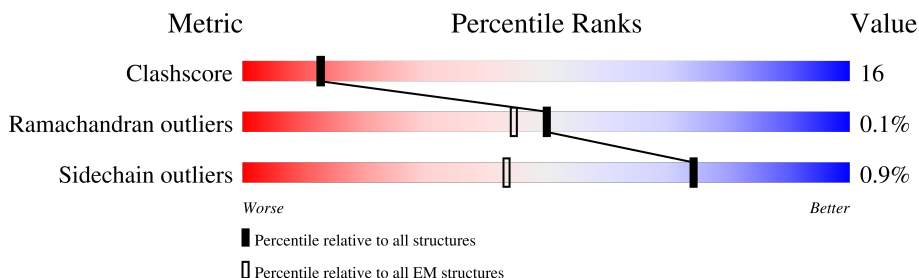
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.90 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.



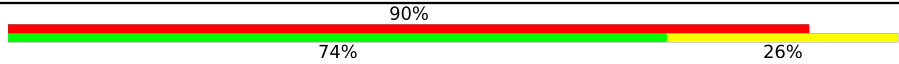
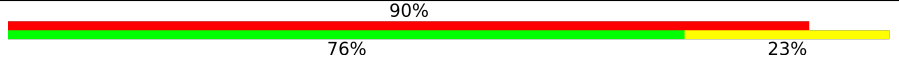
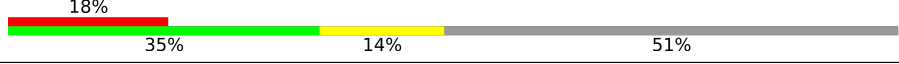



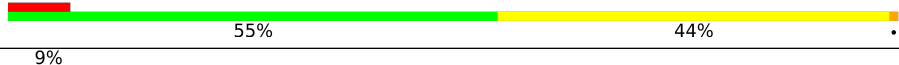

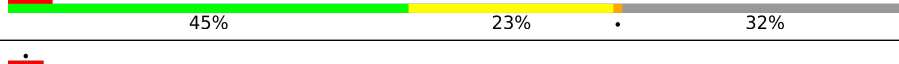
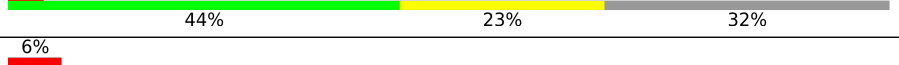




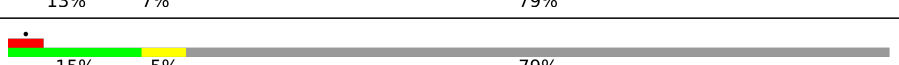
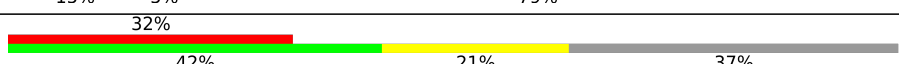
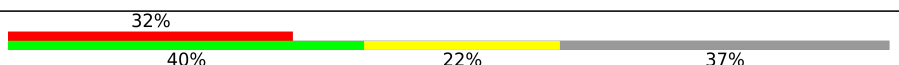

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	782	10% (Poor fit) 38% (0 outliers), 30% (1 outlier), 31% (2+ outliers) 31% (Not modelled)
1	H	782	10% (Poor fit) 37% (0 outliers), 31% (1 outlier), 31% (2+ outliers) 31% (Not modelled)
2	B	454	34% (0 outliers), 61% (1 outlier), 38% (2+ outliers) 38% (Not modelled)
2	J	454	35% (0 outliers), 64% (1 outlier), 36% (2+ outliers) 36% (Not modelled)
3	C	647	18% (Poor fit) 62% (0 outliers), 33% (1 outlier), 5% (2+ outliers) 5% (Not modelled)
3	K	647	21% (Poor fit) 62% (0 outliers), 34% (1 outlier), 5% (2+ outliers) 5% (Not modelled)
4	D	344	27% (Poor fit) 26% (0 outliers), 13% (1 outlier), 61% (2+ outliers) 61% (Not modelled)
4	N	344	28% (Poor fit) 25% (0 outliers), 13% (1 outlier), 61% (2+ outliers) 61% (Not modelled)

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Mol	Chain	Length	Quality of chain
5	E	555	
5	O	555	
6	F	683	
6	P	683	
7	G	641	
7	Q	641	
8	I	765	
8	R	765	
9	L	443	
9	T	443	
10	M	469	
10	U	469	
11	W	135	
11	Y	135	
12	X	510	
12	Z	510	
13	S	1755	
13	V	1755	

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 86268 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 IFT88.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	539	Total	C	N	O	S	0	0
			4337	2747	762	795	33		
1	H	539	Total	C	N	O	S	0	0
			4337	2747	762	795	33		

- Molecule 2 is a protein called Osm-6-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	454	Total	C	N	O	S	0	0
			3553	2269	591	680	13		
2	J	454	Total	C	N	O	S	0	0
			3553	2269	591	680	13		

- Molecule 3 is a protein called IFT70.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	619	Total	C	N	O	S	0	0
			4978	3171	826	948	33		
3	K	619	Total	C	N	O	S	0	0
			4978	3171	826	948	33		

- Molecule 4 is a protein called Intraflagellar transport protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	133	Total	C	N	O	S	0	0
			1045	666	172	197	10		
4	N	133	Total	C	N	O	S	0	0
			1045	666	172	197	10		

- Molecule 5 is a protein called Intraflagellar transport protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	555	Total	C	N	O	S	0	0
			4465	2855	763	820	27		
5	O	555	Total	C	N	O	S	0	0
			4465	2855	763	820	27		

- Molecule 6 is a protein called Intraflagellar transport protein 81.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	335	Total	C	N	O	S	0	0
			2701	1692	476	526	7		
6	P	335	Total	C	N	O	S	0	0
			2701	1692	476	526	7		

- Molecule 7 is a protein called Intraflagellar transport protein 74.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	205	Total	C	N	O	S	0	0
			1674	1023	302	342	7		
7	Q	205	Total	C	N	O	S	0	0
			1674	1023	302	342	7		

- Molecule 8 is a protein called Intraflagellar transport protein 80.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	765	Total	C	N	O	S	0	0
			6025	3807	1053	1132	33		
8	R	765	Total	C	N	O	S	0	0
			6025	3807	1053	1132	33		

- Molecule 9 is a protein called Clusterin-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	303	Total	C	N	O	S	0	0
			2472	1547	439	476	10		
9	T	303	Total	C	N	O	S	0	0
			2472	1547	439	476	10		

- Molecule 10 is a protein called Intraflagellar transport protein 57.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	164	Total	C	N	O	S	0	0
			1328	812	247	264	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	U	164	Total	C	N	O	S	0	0
			1328	812	247	264	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	356	ALA	PHE	conflict	UNP Q2XQY7
U	356	ALA	PHE	conflict	UNP Q2XQY7

- Molecule 11 is a protein called Intraflagellar transport particle protein IFT20.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	W	114	Total	C	N	O	S	0	0
			919	562	166	187	4		
11	Y	114	Total	C	N	O	S	0	0
			919	562	166	187	4		

- Molecule 12 is a protein called IFT54.

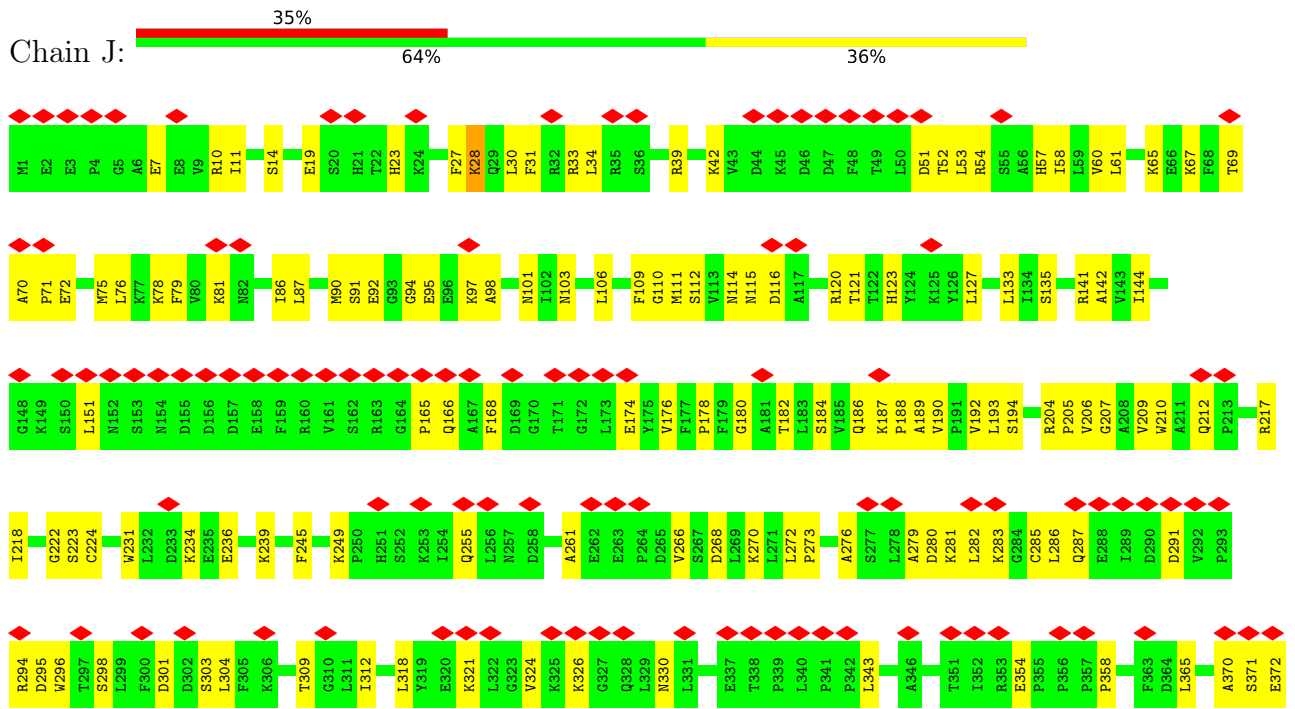
Mol	Chain	Residues	Atoms					AltConf	Trace
12	X	106	Total	C	N	O	S	0	0
			849	524	155	164	6		
12	Z	106	Total	C	N	O	S	0	0
			849	524	155	164	6		

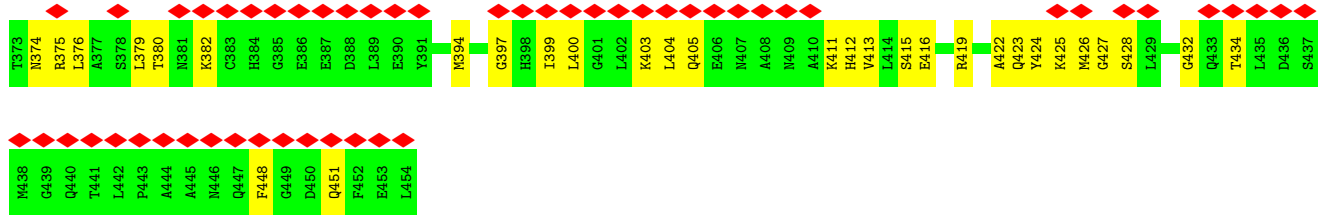
- Molecule 13 is a protein called Intraflagellar transport protein 172.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	1104	Total	C	N	O	S	0	0
			8788	5556	1532	1656	44		
13	V	1104	Total	C	N	O	S	0	0
			8788	5556	1532	1656	44		

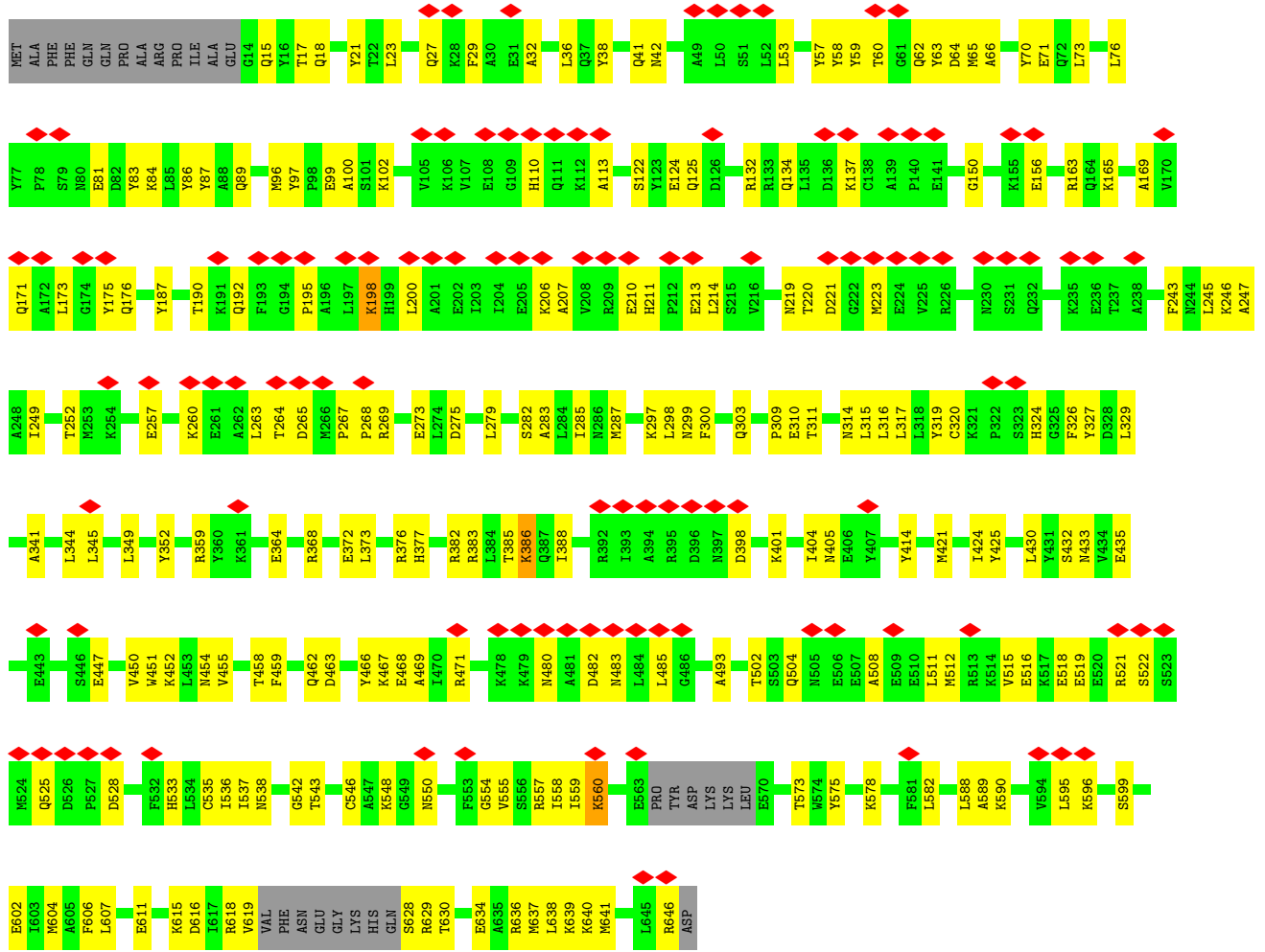


• Molecule 2: Osm-6-like protein

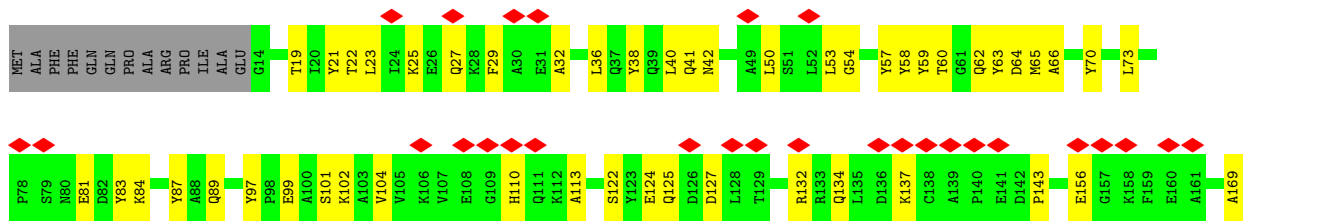


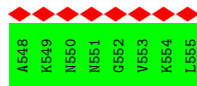
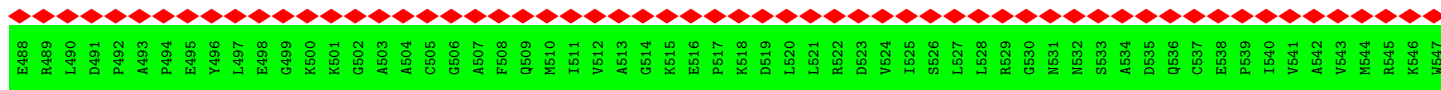


• Molecule 3: IFT70

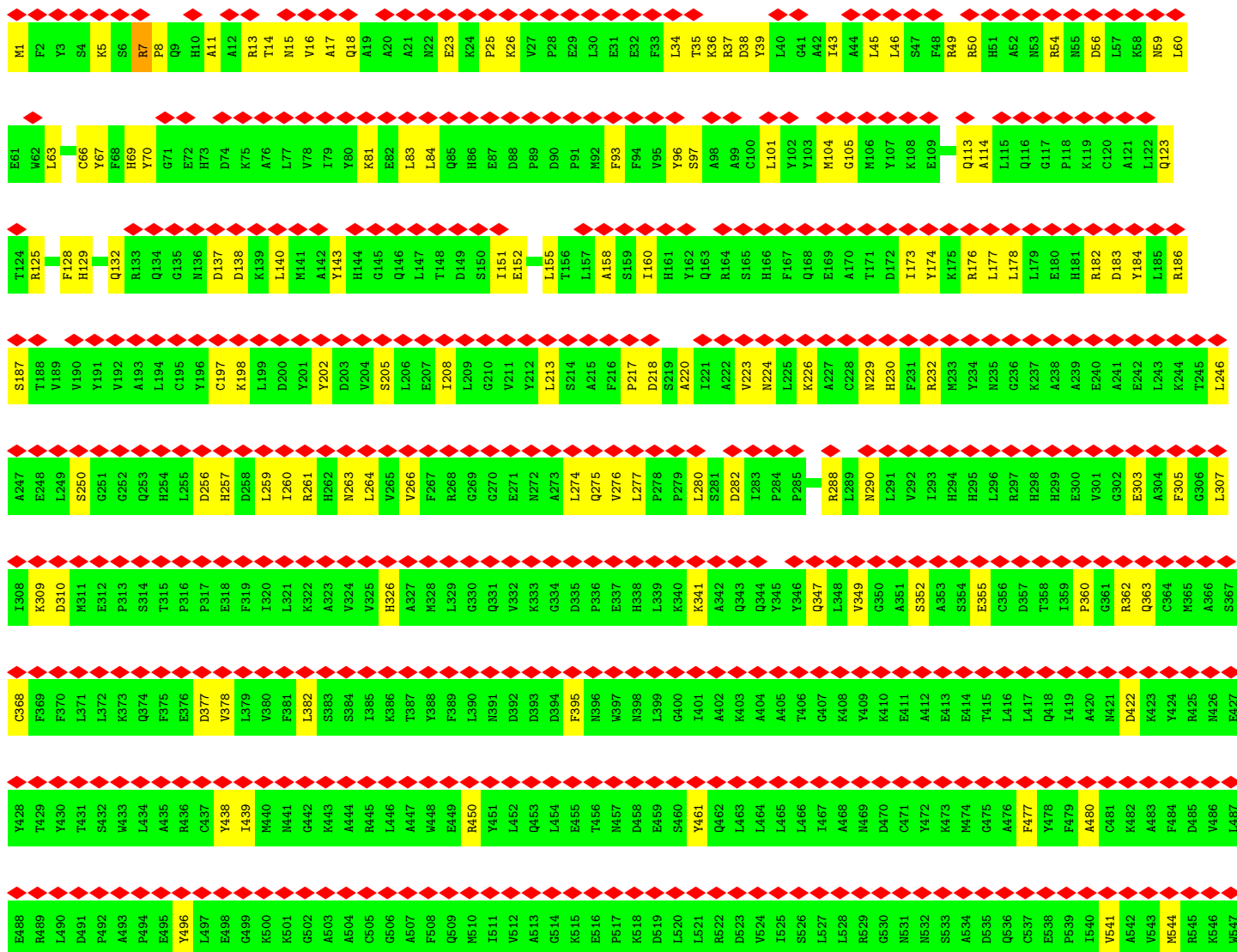
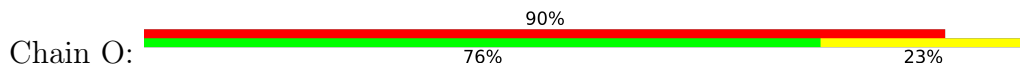


• Molecule 3: IFT70

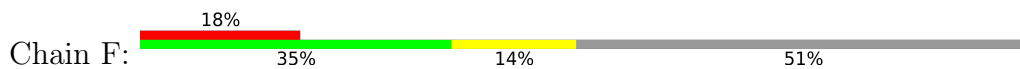


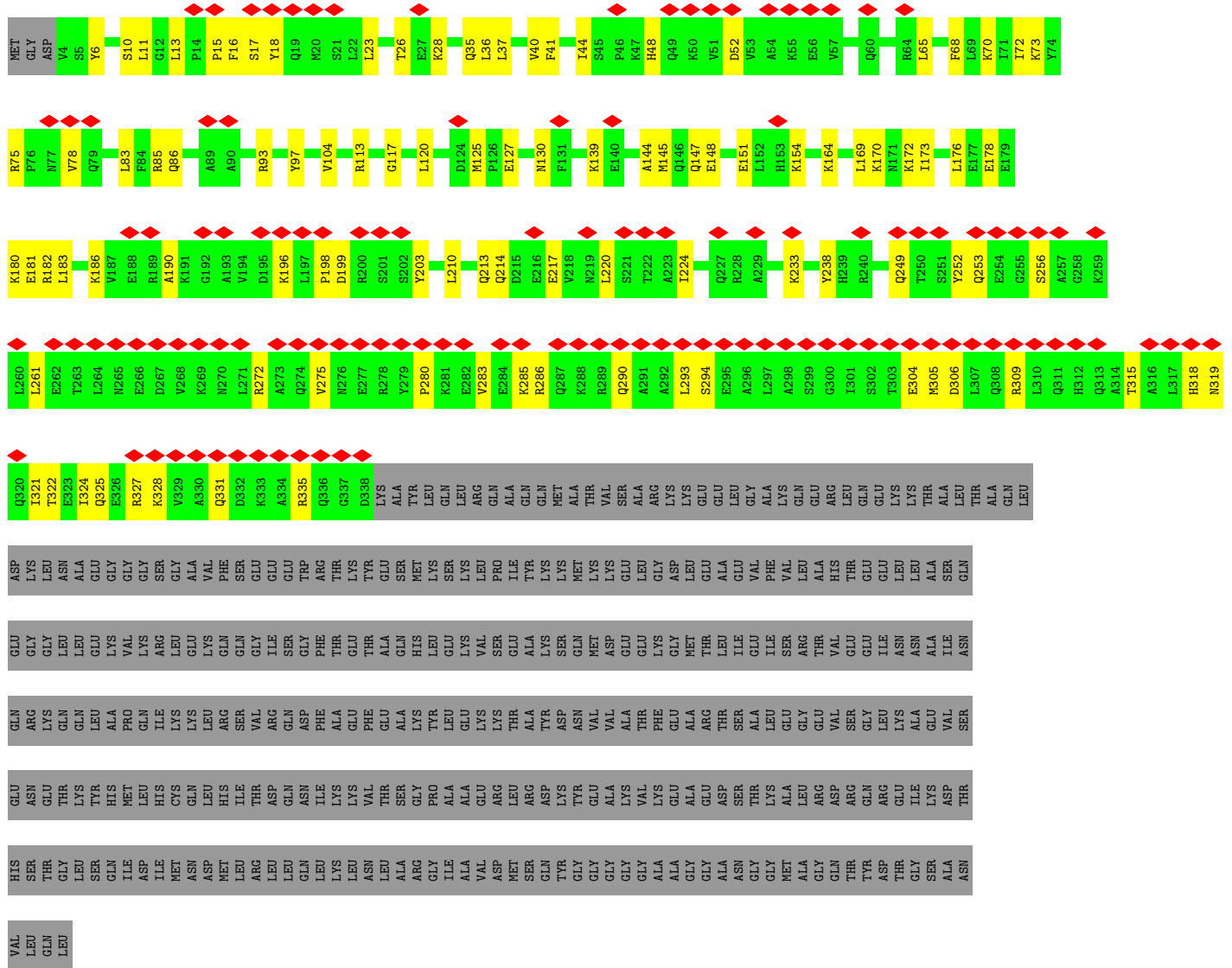


• Molecule 5: Intraflagellar transport protein 56

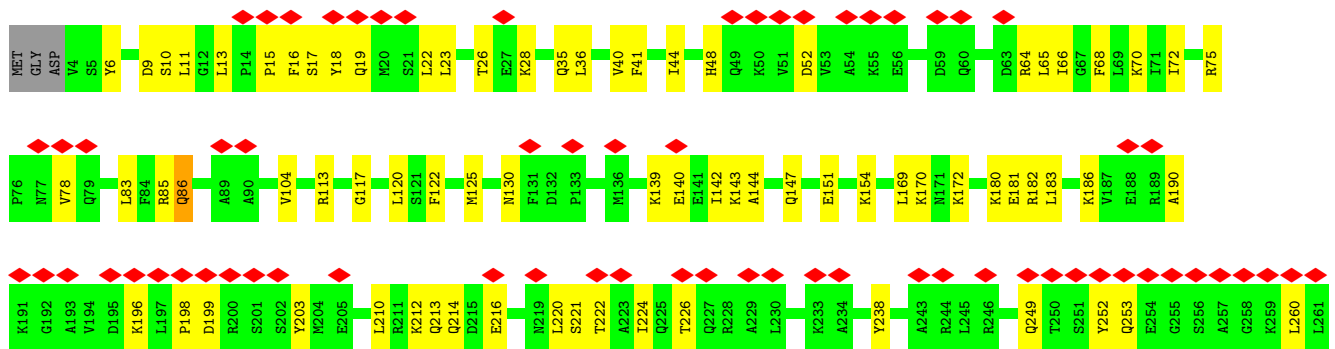
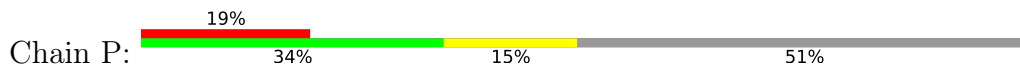


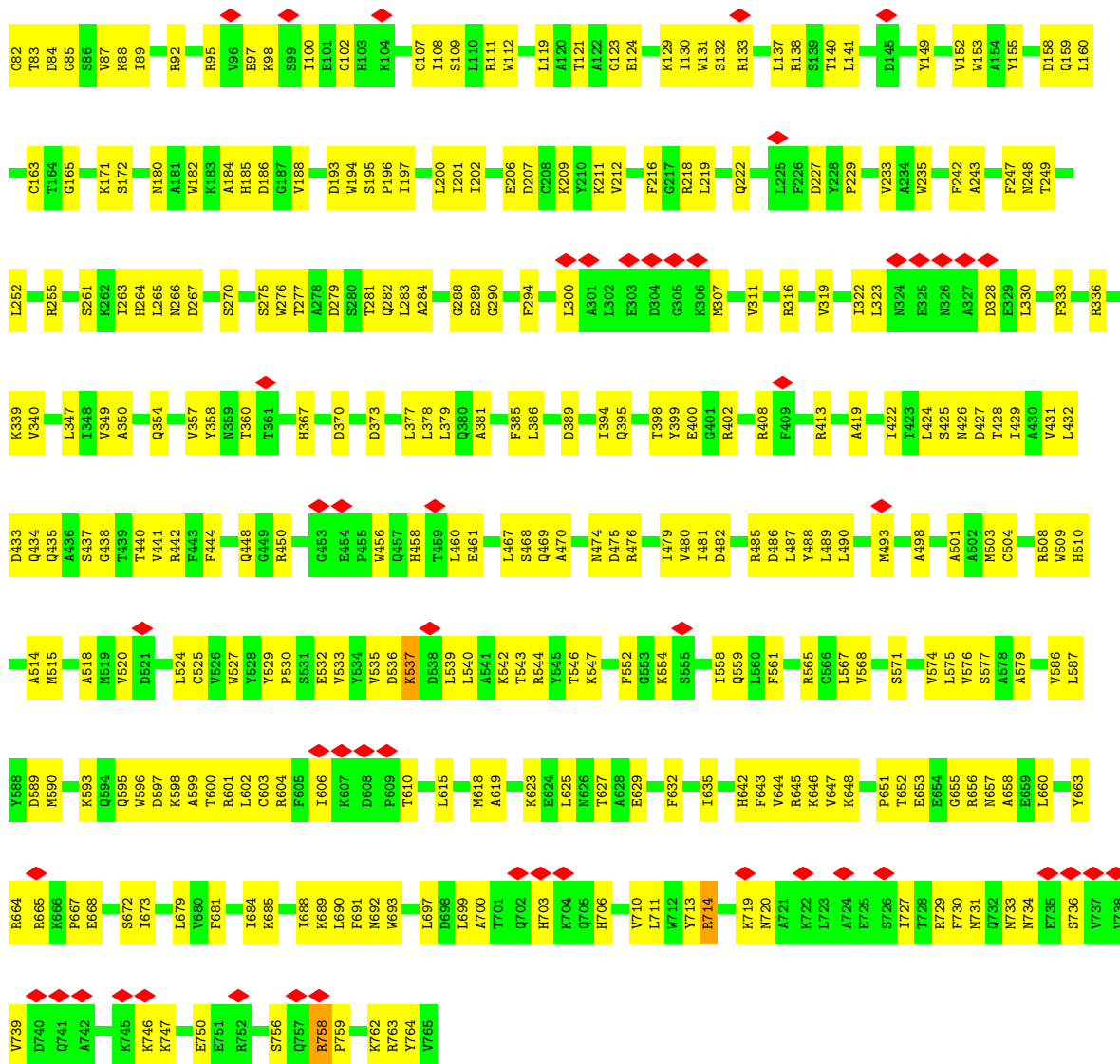
• Molecule 6: Intraflagellar transport protein 81



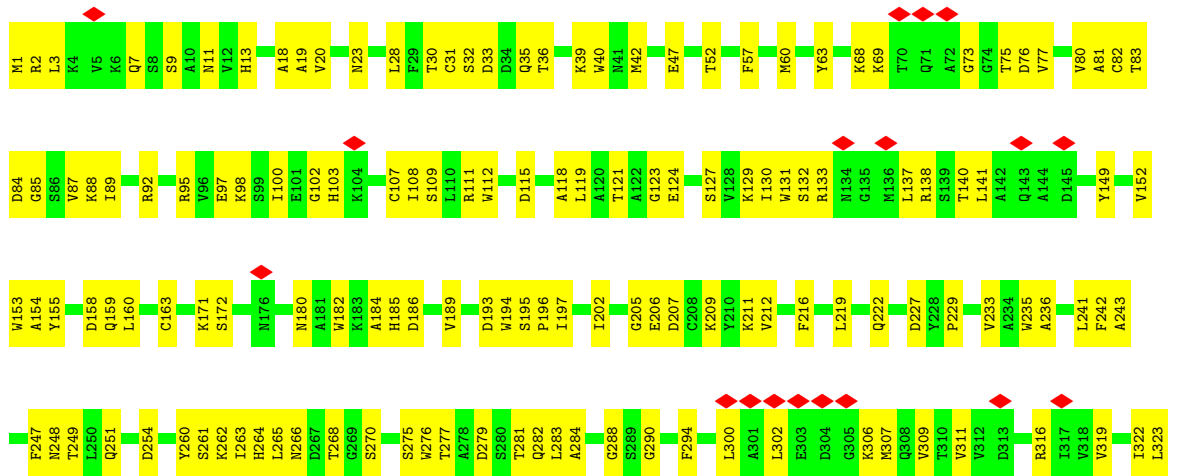


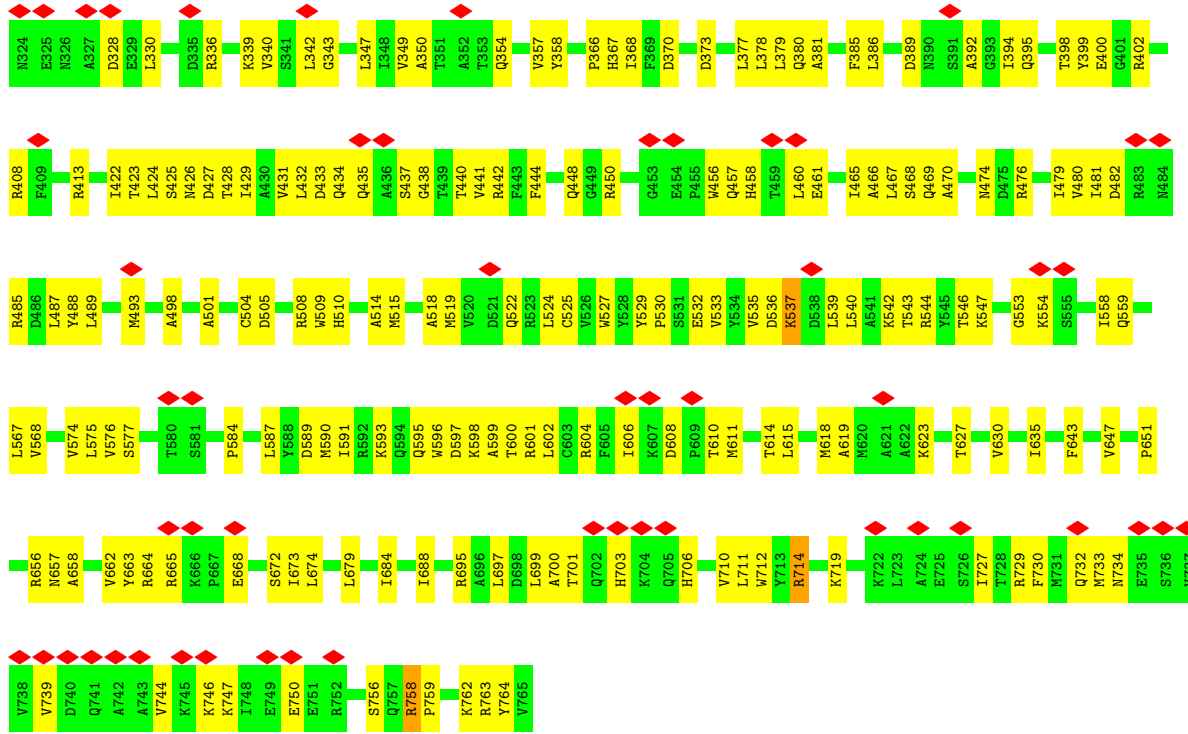
● Molecule 6: Intraflagellar transport protein 81



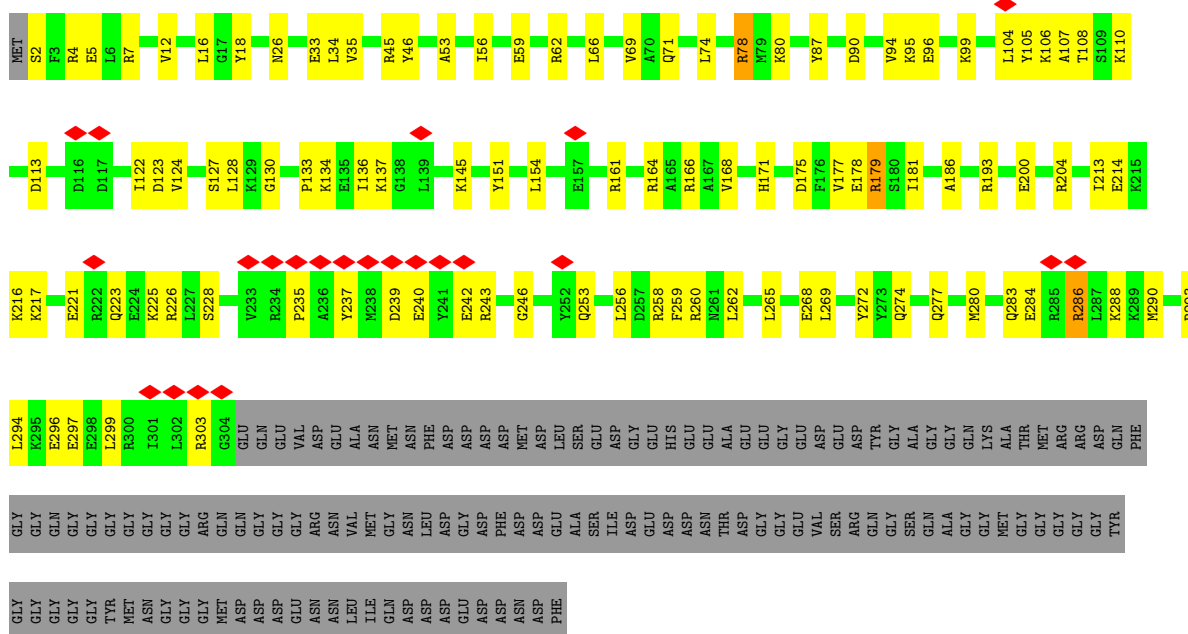


● Molecule 8: Intraflagellar transport protein 80





• Molecule 9: Clusterin-associated protein 1



• Molecule 9: Clusterin-associated protein 1



A987	A988	B989	K990	E993	A994	E995	K996	A997	Y998	L999	A1000	A1001	G1002	G1003	D1004	D1005	V1006	D1007	K1008	A1011	M1012	Y1013	K1014	R1015	M1016	K1017	M1018	Y1019	G1020	Q1021	M1022	I1023	R1024	L1025	V1026	T1027	Q1028	K1031	E1032	K1033	Y1034	P1035	E1036	A1037	H1038	T1041	A1042	Q1043	Q1044	E1046	E1048	L1051								
M916	F917	Y918	F919	R920	R921	A922	R923	R924	R925	Y926	E927	F928	T929	G930	L931	E932	E933	E934	R937	Y938	Y939	A942	A945	R946	D947	E950	R954	A955	G956	K957	W958	E959	A960	A961	Q962	R963	V964	A965	R966	G967	Y968	L969	T970	E971	E972	Y973	M974	K981	A982	A983	E984	F985	E986							
B850	R851	A855	E856	W857	L858	L860	E861	E862	E863	W864	W867	L868	Y869	T870	Y871	K872	Q873	M874	D875	A876	A877	L878	R879	H880	F881	L882	E883	S884	G885	A886	T887	L888	K889	K892	T895	D896	C897	R898	Q899	F900	A901	K902	A903	A904	G905	I906	I907	E908	Y909	L910	D911	P912	A915							
G780	G781	L782	R785	Q788	V789	W790	M791	S792	V793	H794	Y795	V796	W797	W798	D799	P800	A801	L802	L803	D804	L807	A808	S809	L810	A811	K812	A813	C814	L815	Y816	E817	Y823	M826	S827	R828	S829	S830	Q834	S835	Y836	R837	R838	G839	H840	A841	Y842	R843	K844	A845	T846	D847	L848	A849							
F621	L624	T625	P626	E627	D631	W632	L635	A636	E637	D638	N639	L645	W646	T647	A648	E649	R650	C651	Y652	L655	W656	L658	F663	L664	V667	Q673	A676	E677	G679	C680	C681	C682	T683	D684	A685	A690	M691	M692	A693	Q694	K697	G698	M699																	
L527	C530	D531	V536	P537	W541	Q545	S546	N548	N549	L550	V554	S555	M564	F565	P566	I567	K568	U571	R576	H577	N578	H579	R580	T581	E582	D586	E587	G588	L589	N590	L596	D597	E598	L600	L601	Q610	Q611	L513	H514	L515	S519	G520	R523																	
S445	V448	Q449	E450	A451	R452	G453	L454	S458	D466	L467	Q468	T469	W470	R471	L472	Q473	D474	L475	M476	A477	P478	T482	L483	A484	M487	H488	D489	T490	D493	W494	L495	M498	Q499	R500	G501	H502	H503	B507	D508	H511	H512	L513	H514	L515	G519	G520														
L373	I374	A375	R376	Y379	T380	L381	M382	G383	D385	L386	D387	T388	G389	L391	S392	P395	W396	D397	S398	D399	G400	S401	E402	H405	F406	A407	M408	E409	R410	V411	C412	M413	V414	H415	Y416	L420	H421	I422	V423	G426	R427	M428	L431	R435	M440	P441	Y442	L443	I444											
P301	M306	T307	V308	G309	S310	M311	T312	G313	A314	V315	D316	M317	Y318	D319	A320	C321	V322	K323	R324	H325	G329	E332	F333	T334	Y335	V336	S337	K338	S339	A340	V341	I342	V343	K344	K347	T348	G349	M350	R351	I352	A353	L354	K355	S356	V357	Y358	G359	Y360	E361	I362	E363	K364	R371	Y372						
N241	N242	D243	E244	R245	R246	E247	F248	T249	T250	C251	A252	F253	N254	P255	S256	G257	D258	T259	V260	V261	H262	S263	C264	Y265	P266	R267	F268	Y269	M270	Y271	G212	S213	C214	I215	A216	A217	A218	G219	N220	D221	N222	R223	Y224	V225	F226	Y227	D228	L229	N230	G231	Y232	R233	E233	L234	R235	S236	F237	M238	Y239	K300
I181	W182	K183	F184	M185	F186	P187	A188	E189	E190	G191	G192	T193	P194	T195	S196	S197	Q198	L199	V200	V201	H202	S203	C204	Y205	P206	Y207	S208	L209	G210	W211	G212	S213	C214	I215	A216	A217	A218	G219	N220	D221	N222	R223	Y224	V225	F226	Y227	D228	L229	N230	G231	Y232	R233	E233	L234	R235	S236	F237	M238	Y239	K300
W121	P122	K123	D124	R125	P126	N127	E128	V129	V130	F131	G132	L133	A134	D135	G136	K137	V138	R139	L140	G141	M142	L143	K144	N145	M146	K147	S148	Y149	T150	C151	Y152	A153	H154	P155	E156	M157	S158	Y159	V160	V161	A162	L163	A164	S165	S166	L167	N168	G169	Q170	N171	V172	L173	S174	G175	H176	M177	D178	G179	A180	

TYR	K1094	Y1029	A960	I896	Y823	T764	T683	E608	R523	L443	R371	S304	N241
ALA	Q1095	R1030	A961	D896	E824	G755	D684	D609	L527	I444	Y372	S304	N242
MET	V1096	K1031	R962	C897	H825	Q756	A685	A446	C530	A446	L373	T307	D243
PHE	A1097	E1032	R963	R898	R826	E757	V688	V447	Q530	V447	I374	V308	E244
LEU	A1098	K1033	V964	Q899	R828	E758	R689	V448	Q531	V449	A375	G309	E245
ASP	A1099	V1034	A965	F900	S829	Q759	V688	Q449	V536	Q449	A376	S310	R246
GLU	W1100	P1035	R966	A901	Q834	V763	R689	E450	R690	E450	A377	M311	E247
ARG	A1101	V1035	G967	K902	Q835	R766	M691	A451	A615	A451	A378	M311	F248
PHE	L1102	H1038	Y968	A903	R837	E767	A695	R452	V616	R452	A379	T312	T249
ALA	T1103	I1041	T970	A904	R838	E768	Q694	G453	G453	G453	A380	G313	T250
GLU	L1104	A1042	E971	I906	Q839	Q769	N696	I454	I454	I454	A381	G313	T251
ALA	L1104	S972	S972	I907	H840	Q770	N696	E620	P621	P621	A382	A314	C251
GLU	GLY	Q1043	Y978	E908	A841	Y770	Q698	P621	Q621	Q621	A383	V315	A252
ALA	GLY	Q1043	R843	V909	H842	L774	S702	L624	L624	L624	A384	D316	A253
GLU	ASP	Q1044	R843	L910	L774	L774	Y702	L624	L624	L624	A385	M317	F253
PHE	ASP	Q1044	A980	D911	K844	K844	L706	E627	E627	E627	A386	Y318	N254
ILE	GLY	L1045	K881	P912	A845	L846	L706	E627	E627	E627	A387	D319	P255
SER	ALA	E1046	K881	P912	A846	L846	L706	E627	E627	E627	A388	A320	S256
ALA	GLN	V1047	A982	A915	D847	L848	A708	Q631	Q631	Q631	A389	K323	D258
GLY	LEU	L1048	E984	M916	L848	L778	A708	Q632	Q632	Q632	A390	R324	T259
PRO	LEU	E1048	E984	P917	A849	G780	Q709	Q632	Q632	Q632	A391	H325	V260
LYS	LYS	E1053	F985	Y918	R850	G781	G710	L635	L635	L635	A392	K328	F262
LYS	LYS	A1054	E986	F919	R851	L782	G710	L635	L635	L635	A393	G329	G263
GLU	MET	A1054	E986	R920	E852	L782	G710	L635	L635	L635	A394	F331	T264
ALA	GLY	E1055	A987	R921	F853	L782	G710	L635	L635	L635	A395	F332	Y265
ASP	LEU	K1056	A987	R922	F853	L782	G710	L635	L635	L635	A396	F333	Y266
MET	LEU	H1057	H989	A923	R854	P783	G710	L635	L635	L635	A397	T334	N266
TYR	ASP	F1058	K990	A923	R854	P783	G710	L635	L635	L635	A398	Y335	R267
MET	ALA	V1059	E993	Q924	V857	A787	L716	Q638	Q638	Q638	A399	V336	F268
HIS	ILE	A1060	A994	R925	V857	A787	L716	Q638	Q638	Q638	A400	S337	Y269
ASN	GLU	V1061	E995	Y926	V857	A787	L716	Q638	Q638	Q638	A401	K338	M270
GLN	TYR	A1061	E995	Y926	V857	A787	L716	Q638	Q638	Q638	A402	S338	Y271
ASP	ALA	K1062	K996	T928	E861	V790	D721	A641	A641	A641	A403	S339	T272
TRP	VAL	D1063	K996	T929	E861	V790	D721	A641	A641	A641	A404	A340	T273
ASP	GLU	A1064	E997	Q930	E862	V793	H723	A643	A643	A643	A405	V341	F274
ALA	SER	V1065	E998	A931	E862	V793	H723	A643	A643	A643	A406	I342	N274
ALA	GLY	K1065	E999	A931	E862	V793	H723	A643	A643	A643	A407	I343	L275
MET	ALA	S1066	A1000	L932	V857	A787	L716	Q638	Q638	Q638	A408	I344	Q276
ARG	PHE	A1067	A1001	E934	V857	A787	L716	Q638	Q638	Q638	A409	I345	Q277
ALA	ALA	V1068	A1001	E934	V857	A787	L716	Q638	Q638	Q638	A410	I346	R277
GLU	ALA	Q1069	D1067	R937	V857	A787	L716	Q638	Q638	Q638	A411	I347	N278
ARG	GLU	M1070	K1008	Y939	V857	A787	L716	Q638	Q638	Q638	A412	I348	D279
ASP	THR	Y1071	K1008	Y939	V857	A787	L716	Q638	Q638	Q638	A413	I349	W280
PRO	THR	R1072	A1011	A942	V857	A787	L716	Q638	Q638	Q638	A414	I350	E281
THR	ARG	Q1073	M1012	D943	V857	A787	L716	Q638	Q638	Q638	A415	I351	E282
MET	ALA	Y1074	Y1013	M944	V857	A787	L716	Q638	Q638	Q638	A416	I352	A283
VAL	ALA	K1014	A945	A945	V857	A787	L716	Q638	Q638	Q638	A417	I353	G284
SER	ALA	R1015	R946	R946	V857	A787	L716	Q638	Q638	Q638	A418	I354	H285
GLU	ALA	M1016	D947	D947	V857	A787	L716	Q638	Q638	Q638	A419	I355	K286
ILE	HIS	W1077	F881	F881	V857	A787	L716	Q638	Q638	Q638	A420	I356	Q287
LEU	LEU	D1079	M1017	E950	V857	A787	L716	Q638	Q638	Q638	A421	I357	I288
SER	PRO	A1080	Y1019	S953	V857	A787	L716	Q638	Q638	Q638	A422	I358	D289
GLN	GLU	L1081	D1020	R954	V857	A787	L716	Q638	Q638	Q638	A423	I359	N290
ALA	VAL	R1082	Q1021	A955	V857	A787	L716	Q638	Q638	Q638	A424	I360	F291
HIS	HIS	Y1083	M1022	A955	V857	A787	L716	Q638	Q638	Q638	A425	I361	Y292
LEU	LEU	A1084	I1023	K957	V857	A787	L716	Q638	Q638	Q638	A426	I362	A293
LYS	LYS	K1085	R1024	W958	V857	A787	L716	Q638	Q638	Q638	A427	I363	V294
ALA	ALA	V1086	L1025	E959	V857	A787	L716	Q638	Q638	Q638	A428	I364	S295
TYR	TYR	Y1087	V1026	E959	V857	A787	L716	Q638	Q638	Q638	A429	I365	A296
GLU	GLU	G1088	T1027	E959	V857	A787	L716	Q638	Q638	Q638	A430	I366	A297
GLU	GLU	G1089	T1027	E959	V857	A787	L716	Q638	Q638	Q638	A431	I367	S298
ALA	ALA	N1090	V1090	E959	V857	A787	L716	Q638	Q638	Q638	A432	I368	A299
ALA	ALA	A1092	S1093	E959	V857	A787	L716	Q638	Q638	Q638	A433	I369	A300
ALA	ALA	S1093	S1093	E959	V857	A787	L716	Q638	Q638	Q638	A434	I370	S301

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	18216	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Warp/Relion/M - CTF Refinement in M	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	104	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.372	Depositor
Minimum map value	-0.388	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.466	Depositor
Map size (\AA)	775.68, 775.68, 775.68	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	3.03, 3.03, 3.03	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	0.30	0/4423	0.60	0/5956
1	H	0.32	1/4423 (0.0%)	0.62	0/5956
2	B	0.28	0/3635	0.57	0/4918
2	J	0.28	0/3635	0.59	0/4918
3	C	0.28	0/5080	0.56	0/6863
3	K	0.27	0/5080	0.57	0/6863
4	D	0.29	0/1068	0.61	0/1441
4	N	0.29	0/1068	0.62	0/1441
5	E	0.26	0/4570	0.52	0/6180
5	O	0.25	0/4570	0.51	0/6180
6	F	0.29	0/2740	0.62	0/3688
6	P	0.29	0/2740	0.64	0/3688
7	G	0.30	0/1687	0.65	0/2257
7	Q	0.33	0/1687	0.66	0/2257
8	I	0.28	0/6147	0.57	0/8333
8	R	0.27	0/6147	0.58	0/8333
9	L	0.28	0/2504	0.63	0/3356
9	T	0.35	2/2504 (0.1%)	0.65	0/3356
10	M	0.25	0/1343	0.59	0/1804
10	U	0.27	0/1343	0.60	0/1804
11	W	0.42	1/922 (0.1%)	0.64	0/1226
11	Y	0.33	0/922	0.62	0/1226
12	X	0.32	0/857	0.66	0/1144
12	Z	0.32	0/857	0.65	0/1144
13	S	0.27	0/8979	0.55	0/12160
13	V	0.28	0/8979	0.55	0/12160
All	All	0.29	4/87910 (0.0%)	0.58	0/118652

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	W	56	ASP	C-N	8.35	1.53	1.34
9	T	72	VAL	C-N	6.69	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	T	268	GLU	C-N	-5.12	1.22	1.34
1	H	262	ILE	C-N	5.06	1.45	1.34

There are no bond angle outliers.

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	4337	0	4306	191	0
1	H	4337	0	4306	201	0
2	B	3553	0	3523	158	0
2	J	3553	0	3523	146	0
3	C	4978	0	4912	161	0
3	K	4978	0	4912	154	0
4	D	1045	0	1039	44	0
4	N	1045	0	1039	44	0
5	E	4465	0	4396	109	0
5	O	4465	0	4396	93	0
6	F	2701	0	2731	81	0
6	P	2701	0	2731	80	0
7	G	1674	0	1673	46	0
7	Q	1674	0	1673	52	0
8	I	6025	0	5988	279	0
8	R	6025	0	5988	255	0
9	L	2472	0	2484	109	0
9	T	2472	0	2484	100	0
10	M	1328	0	1322	50	0
10	U	1328	0	1322	50	0
11	W	919	0	936	67	0
11	Y	919	0	936	52	0
12	X	849	0	863	49	0
12	Z	849	0	863	40	0
13	S	8788	0	8605	238	0
13	V	8788	0	8605	287	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	86268	0	85556	2793	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 2793 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)
9:L:136:ILE:HG21	12:X:410:GLU:CD	1.18	1.45
9:L:136:ILE:CG2	12:X:410:GLU:CD	1.98	1.30
9:L:136:ILE:HG21	12:X:410:GLU:OE2	1.21	1.27
9:L:136:ILE:CG2	12:X:410:GLU:OE1	2.02	1.07
9:T:133:PRO:HA	9:T:136:ILE:HG22	1.32	1.06

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	535/782 (68%)	472 (88%)	61 (11%)	2 (0%)	30	68
1	H	535/782 (68%)	474 (89%)	57 (11%)	4 (1%)	19	57
2	B	452/454 (100%)	391 (86%)	60 (13%)	1 (0%)	44	78
2	J	452/454 (100%)	393 (87%)	58 (13%)	1 (0%)	44	78
3	C	613/647 (95%)	580 (95%)	33 (5%)	0	100	100
3	K	613/647 (95%)	582 (95%)	31 (5%)	0	100	100
4	D	131/344 (38%)	116 (88%)	15 (12%)	0	100	100
4	N	131/344 (38%)	117 (89%)	14 (11%)	0	100	100
5	E	553/555 (100%)	508 (92%)	45 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	O	553/555 (100%)	513 (93%)	40 (7%)	0	100	100
6	F	333/683 (49%)	324 (97%)	9 (3%)	0	100	100
6	P	333/683 (49%)	323 (97%)	10 (3%)	0	100	100
7	G	203/641 (32%)	192 (95%)	11 (5%)	0	100	100
7	Q	203/641 (32%)	191 (94%)	12 (6%)	0	100	100
8	I	763/765 (100%)	697 (91%)	65 (8%)	1 (0%)	48	83
8	R	763/765 (100%)	704 (92%)	58 (8%)	1 (0%)	48	83
9	L	301/443 (68%)	279 (93%)	22 (7%)	0	100	100
9	T	301/443 (68%)	276 (92%)	25 (8%)	0	100	100
10	M	162/469 (34%)	158 (98%)	4 (2%)	0	100	100
10	U	162/469 (34%)	158 (98%)	4 (2%)	0	100	100
11	W	112/135 (83%)	112 (100%)	0	0	100	100
11	Y	112/135 (83%)	112 (100%)	0	0	100	100
12	X	104/510 (20%)	104 (100%)	0	0	100	100
12	Z	104/510 (20%)	102 (98%)	2 (2%)	0	100	100
13	S	1102/1755 (63%)	1034 (94%)	67 (6%)	1 (0%)	48	83
13	V	1102/1755 (63%)	1030 (94%)	72 (6%)	0	100	100
All	All	10728/16366 (66%)	9942 (93%)	775 (7%)	11 (0%)	50	83

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	629	MET
1	H	629	MET
1	A	431	GLU
1	H	304	TYR
1	H	305	ALA

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	457/627 (73%)	451 (99%)	6 (1%)	65	77
1	H	457/627 (73%)	451 (99%)	6 (1%)	65	77
2	B	388/388 (100%)	384 (99%)	4 (1%)	73	82
2	J	388/388 (100%)	386 (100%)	2 (0%)	86	89
3	C	534/558 (96%)	529 (99%)	5 (1%)	75	83
3	K	534/558 (96%)	530 (99%)	4 (1%)	81	87
4	D	114/288 (40%)	114 (100%)	0	100	100
4	N	114/288 (40%)	114 (100%)	0	100	100
5	E	469/469 (100%)	467 (100%)	2 (0%)	89	91
5	O	469/469 (100%)	467 (100%)	2 (0%)	89	91
6	F	296/581 (51%)	294 (99%)	2 (1%)	81	87
6	P	296/581 (51%)	294 (99%)	2 (1%)	81	87
7	G	185/526 (35%)	185 (100%)	0	100	100
7	Q	185/526 (35%)	185 (100%)	0	100	100
8	I	648/648 (100%)	641 (99%)	7 (1%)	70	80
8	R	648/648 (100%)	642 (99%)	6 (1%)	75	83
9	L	261/358 (73%)	258 (99%)	3 (1%)	70	80
9	T	261/358 (73%)	258 (99%)	3 (1%)	70	80
10	M	144/380 (38%)	139 (96%)	5 (4%)	31	51
10	U	144/380 (38%)	139 (96%)	5 (4%)	31	51
11	W	101/120 (84%)	100 (99%)	1 (1%)	73	82
11	Y	101/120 (84%)	101 (100%)	0	100	100
12	X	90/401 (22%)	89 (99%)	1 (1%)	70	80
12	Z	90/401 (22%)	89 (99%)	1 (1%)	70	80
13	S	915/1431 (64%)	905 (99%)	10 (1%)	70	80
13	V	915/1431 (64%)	906 (99%)	9 (1%)	73	82
All	All	9204/13550 (68%)	9118 (99%)	86 (1%)	74	83

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	K	560	LYS
10	U	322	LYS
5	O	362	ARG

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Mol	Chain	Res	Type
8	R	719	LYS
10	U	430	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
4	N	322	ASN
8	R	595	GLN
5	O	224	ASN
6	P	214	GLN
9	T	274	GLN

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.

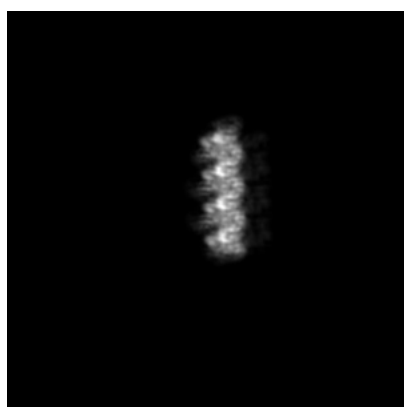
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15977. These allow visual inspection of the internal detail of the map and identification of artifacts.

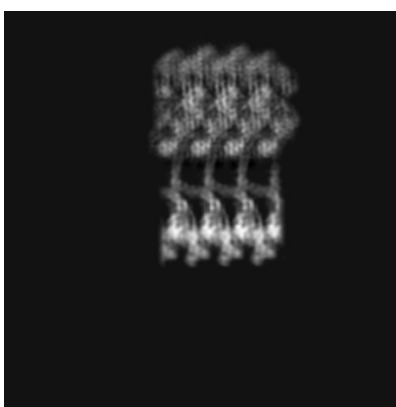
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

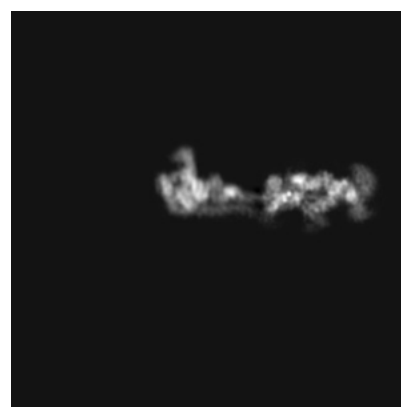
6.1.1 Primary map



X



Y

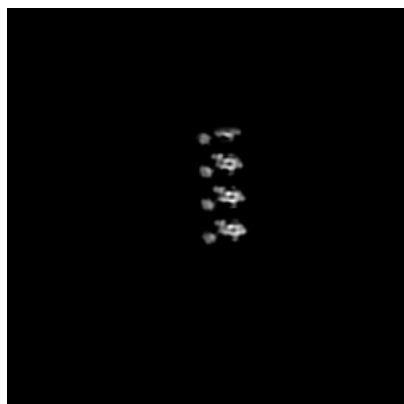


Z

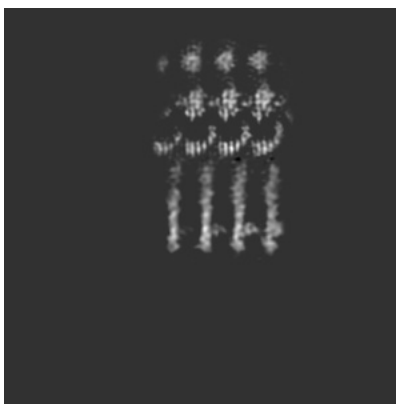
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 128



Y Index: 128

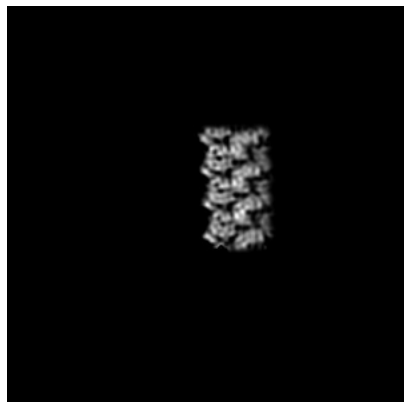


Z Index: 128

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: 113



Y Index: 138

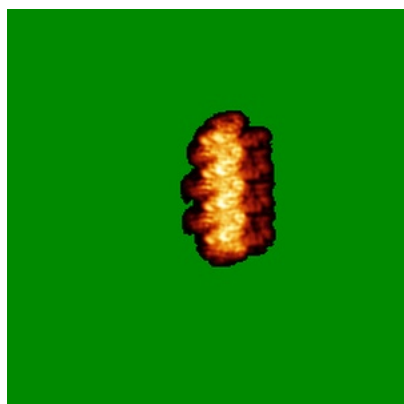


Z Index: 130

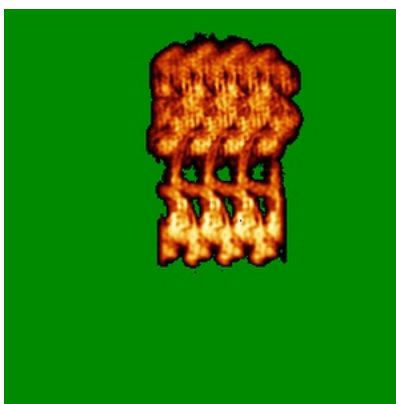
The images above show the largest variance slices of the map in three orthogonal directions.

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

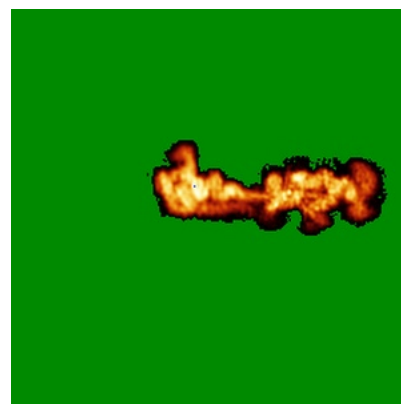
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.466. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

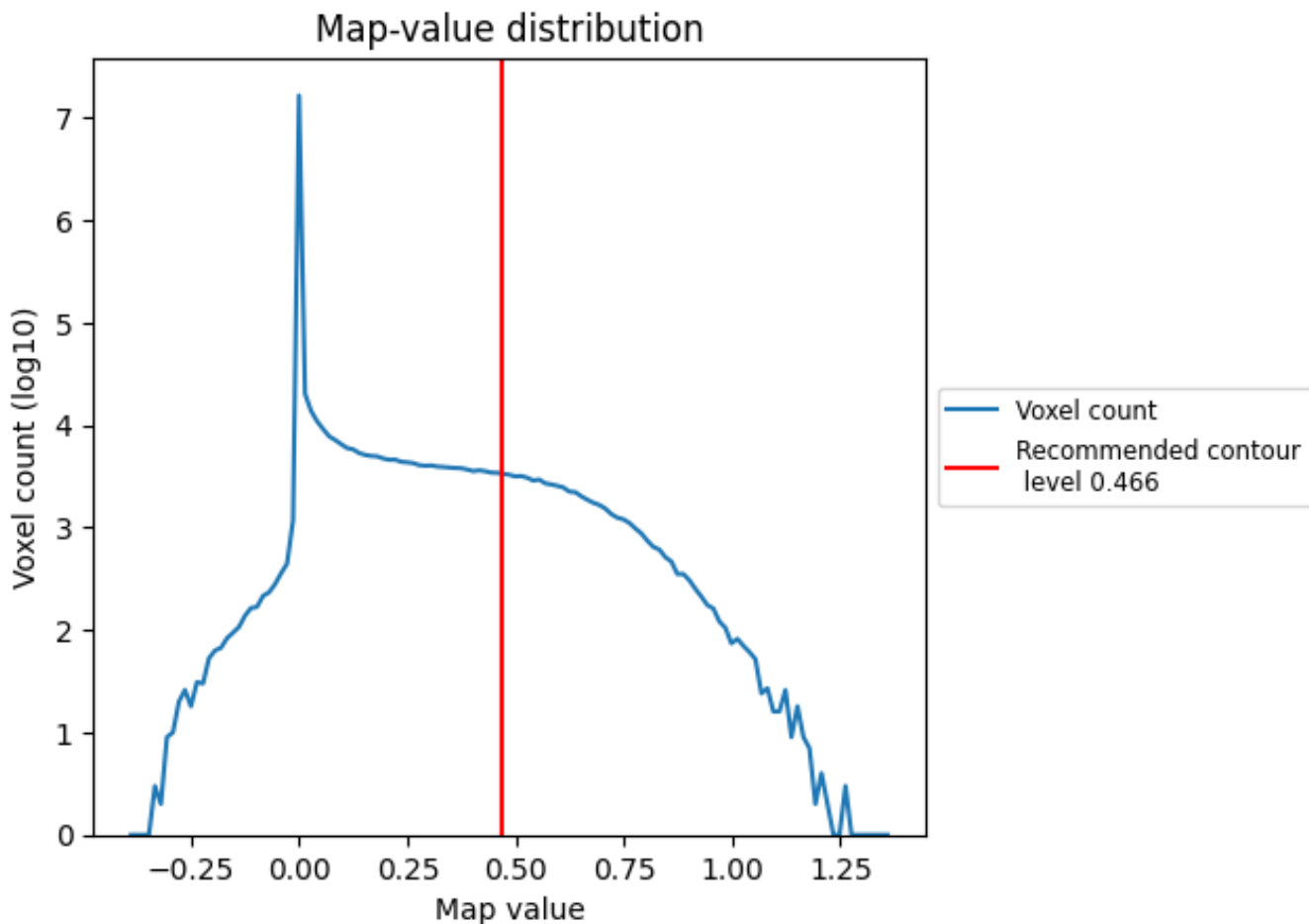
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

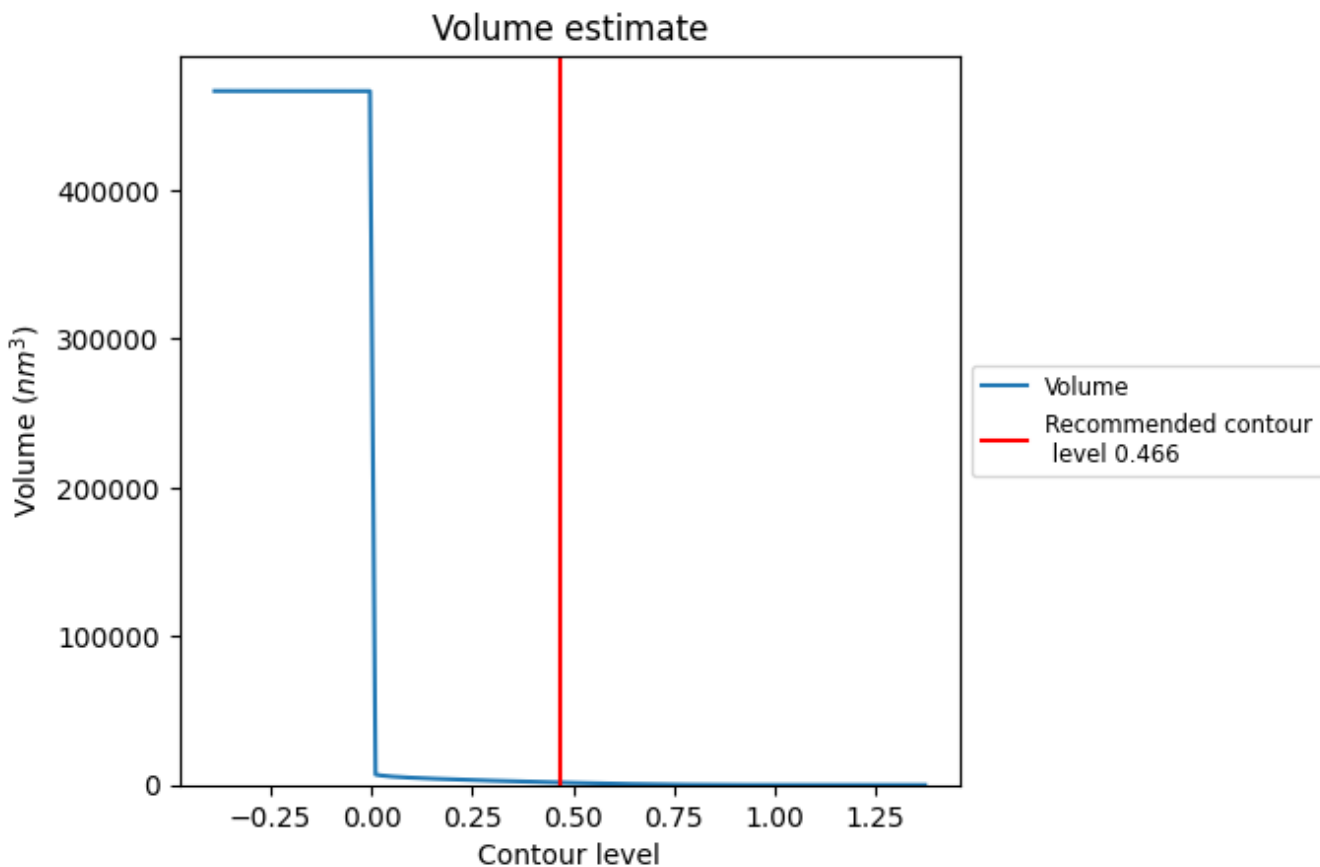
This section contains the results of statistical analysis of the map.

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.

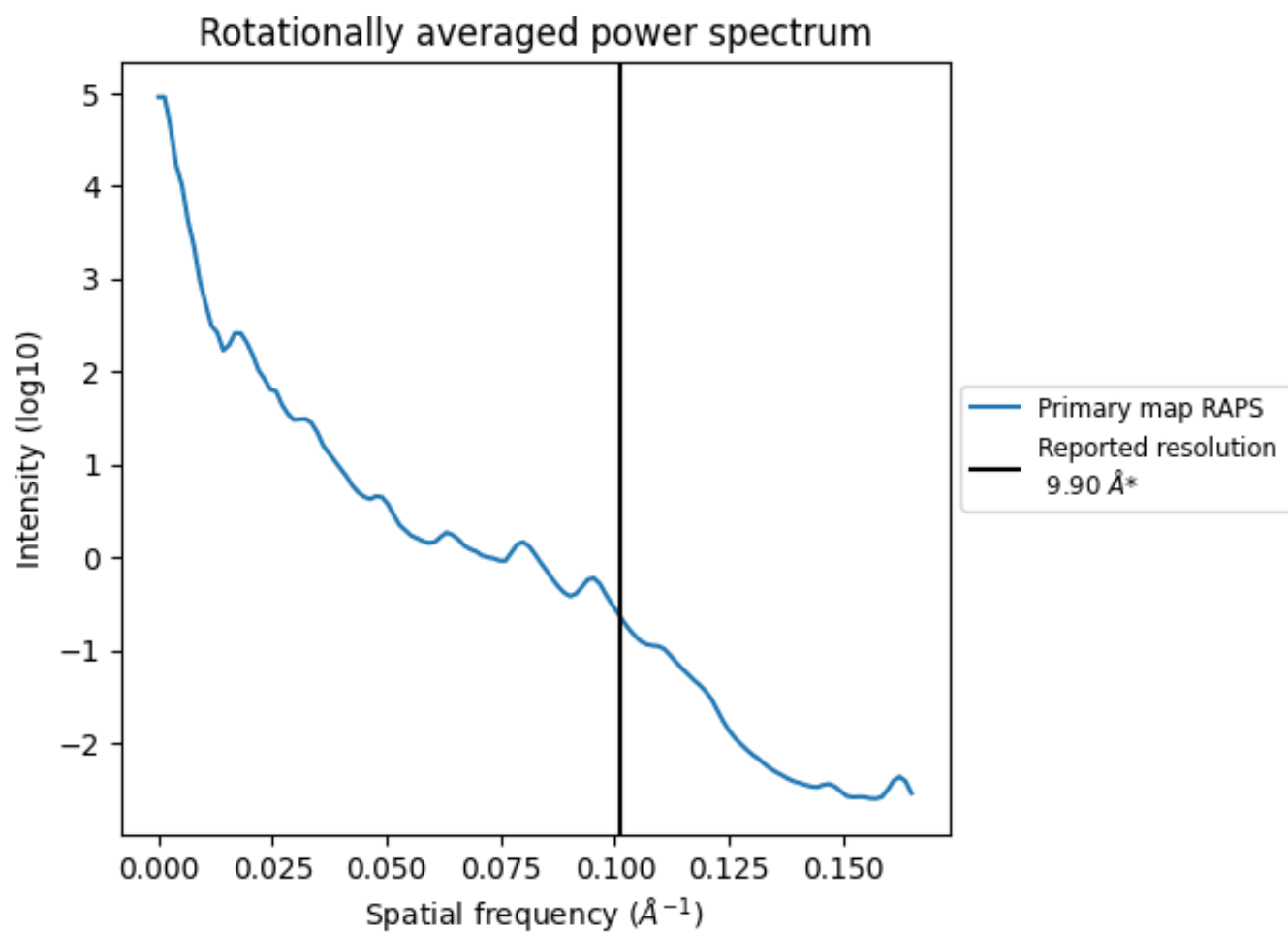
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1645 nm³; this corresponds to an approximate mass of 1486 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 0.101 Å⁻¹

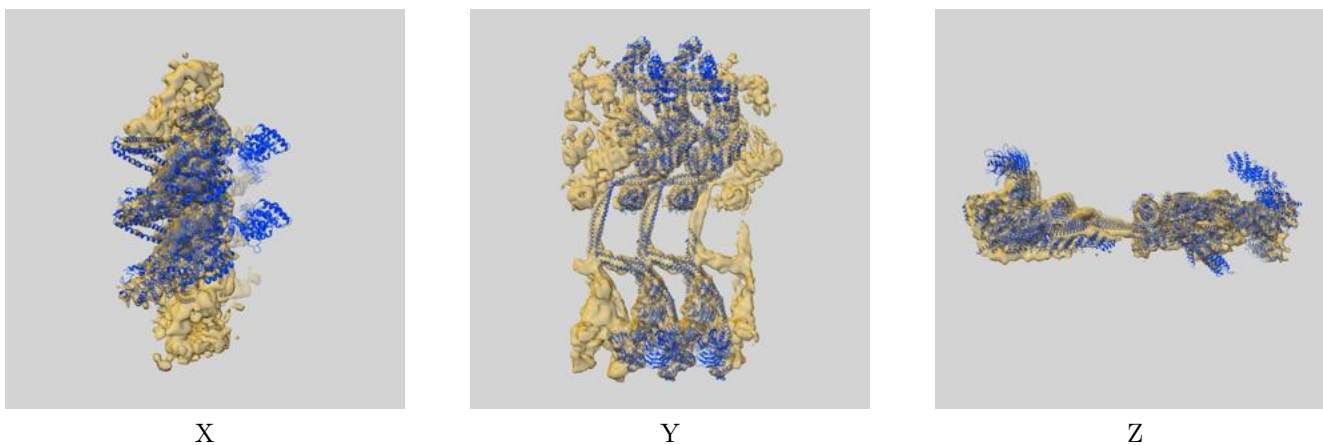
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

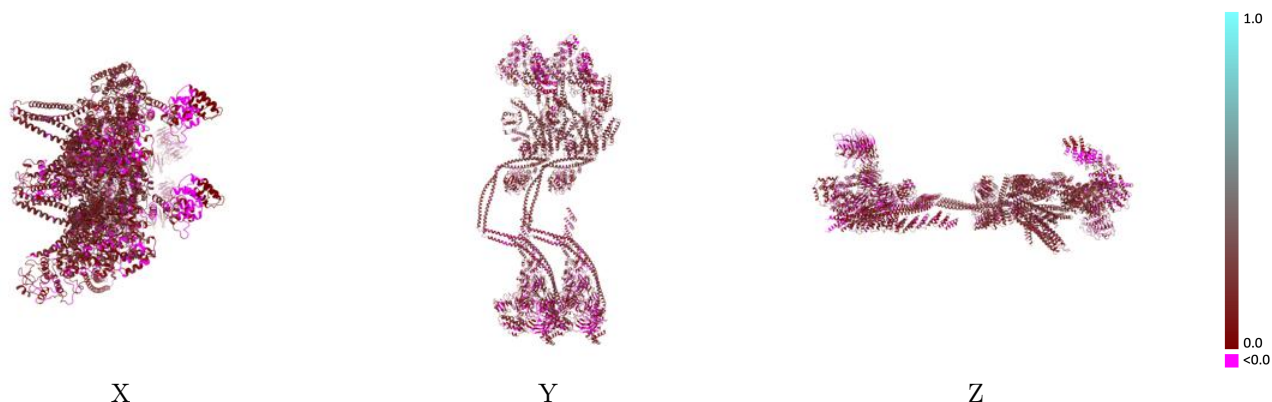
This section contains information regarding the fit between EMDB map EMD-15977 and PDB model 8BD7. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



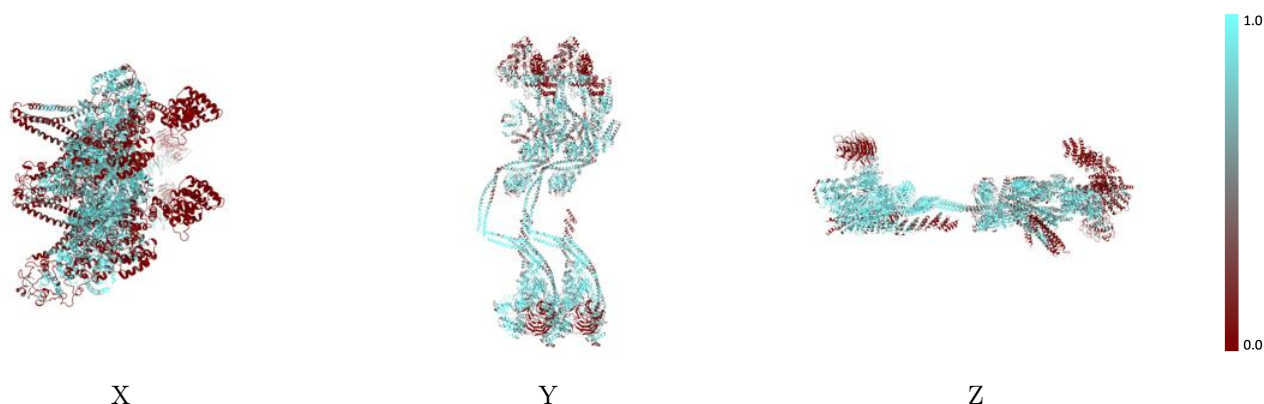
The images above show the 3D surface view of the map at the recommended contour level 0.466 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



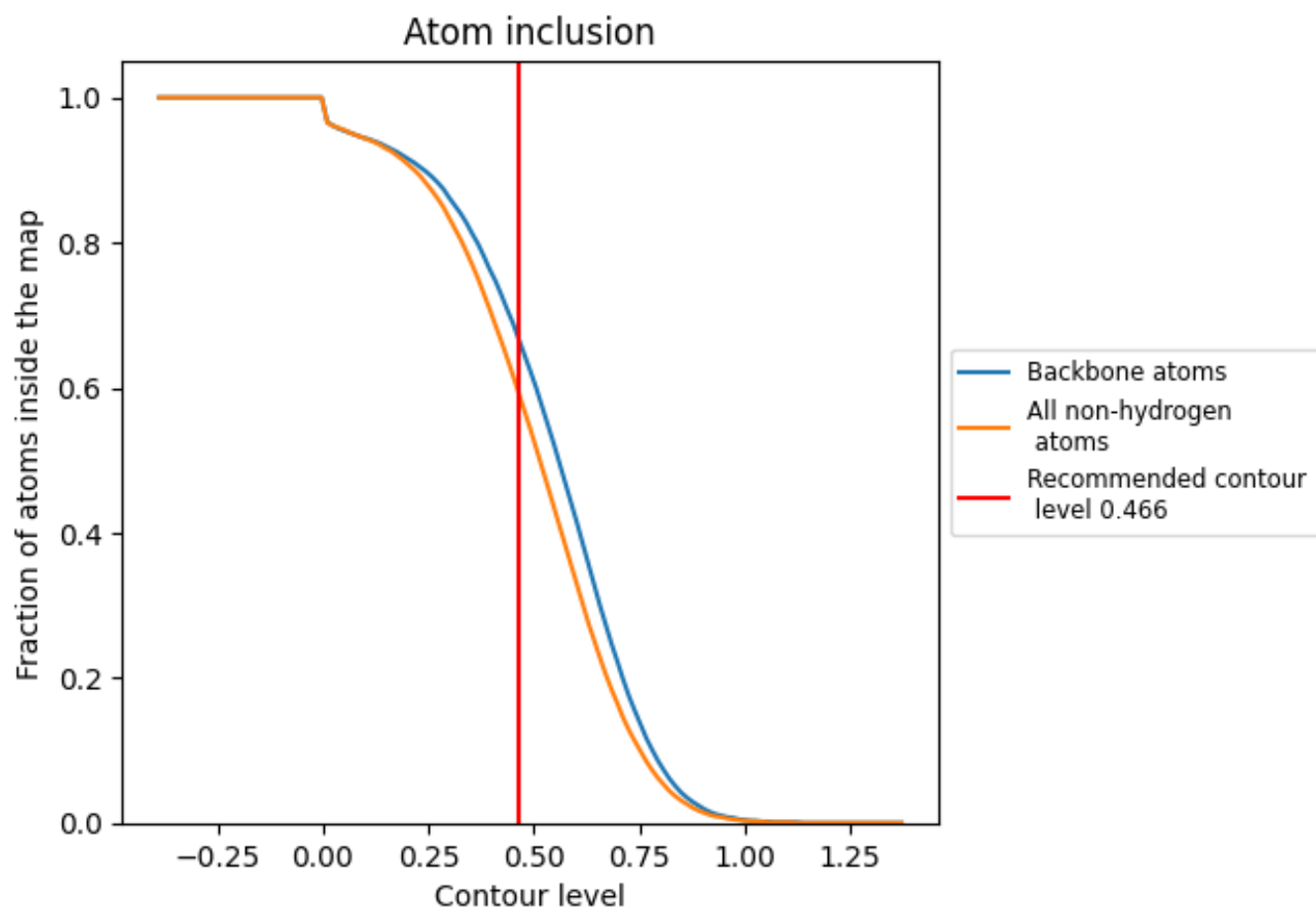
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.466).























































9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 59% 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 (0.466) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5900	 0.1160
A	 0.7580	 0.1590
B	 0.5930	 0.1360
C	 0.7070	 0.1610
D	 0.2980	 0.0960
E	 0.1130	 0.0420
F	 0.5210	 0.1690
G	 0.4670	 0.1840
H	 0.7500	 0.1580
I	 0.8760	 0.1030
J	 0.5710	 0.1220
K	 0.6770	 0.1590
L	 0.8300	 0.1370
M	 0.7730	 0.1540
N	 0.2730	 0.0760
O	 0.0990	 0.0410
P	 0.5200	 0.1620
Q	 0.4430	 0.1720
R	 0.8590	 0.0980
S	 0.4670	 0.0810
T	 0.8340	 0.1350
U	 0.7860	 0.1600
V	 0.4690	 0.0790
W	 0.7630	 0.1070
X	 0.6990	 0.1260
Y	 0.7600	 0.1010
Z	 0.7260	 0.1260

