



# wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 12:32 PM UTC

PDB ID : 8BD7 / pdb\_00008bd7  
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](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:

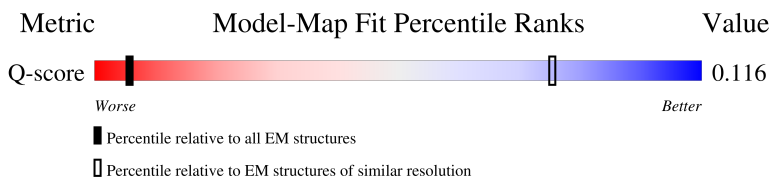
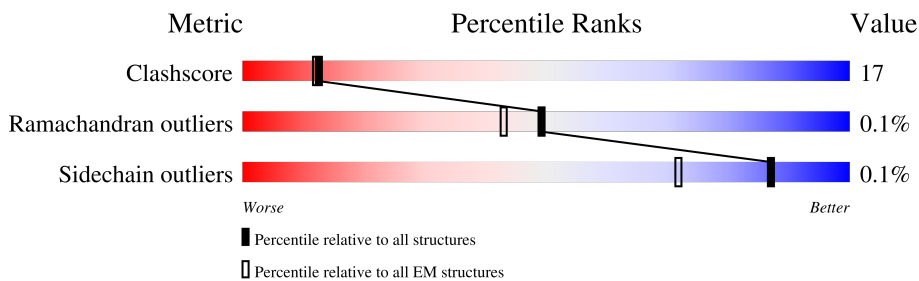
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	149 ( 9.40 - 10.40 )

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  $\geq 3$ , 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	782	<p>10% (Poor fit), 38% (0 outliers), 31% (1 outlier), 31% (2+ outliers)</p>
1	H	782	<p>10% (Poor fit), 37% (0 outliers), 31% (1 outlier), 31% (2+ outliers)</p>
2	B	454	<p>34% (Poor fit), 62% (0 outliers), 38% (1 outlier)</p>
2	J	454	<p>35% (Poor fit), 63% (0 outliers), 37% (1 outlier)</p>

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Mol	Chain	Length	Quality of chain
3	C	647	18% 61% 35%
3	K	647	21% 61% 34%
4	D	344	27% 25% 14% 61%
4	N	344	28% 25% 14% 61%
5	E	555	90% 74% 26%
5	O	555	90% 75% 25%
6	F	683	18% 35% 14% 51%
6	P	683	19% 34% 15% 51%
7	G	641	15% 22% 10% 68%
7	Q	641	15% 21% 11% 68%
8	I	765	7% 55% 45%
8	R	765	9% 57% 43%
9	L	443	5% 45% 24% 32%
9	T	443	• 44% 24% 32%
10	M	469	6% 22% 13% 65%
10	U	469	• 23% 12% 65%
11	W	135	13% 47% 37% • 16%
11	Y	135	16% 44% 40% 16%
12	X	510	5% 14% 7% 79%
12	Z	510	• 15% 6% 79%
13	S	1755	32% 41% 22% 37%
13	V	1755	32% 40% 23% 37%

## 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		

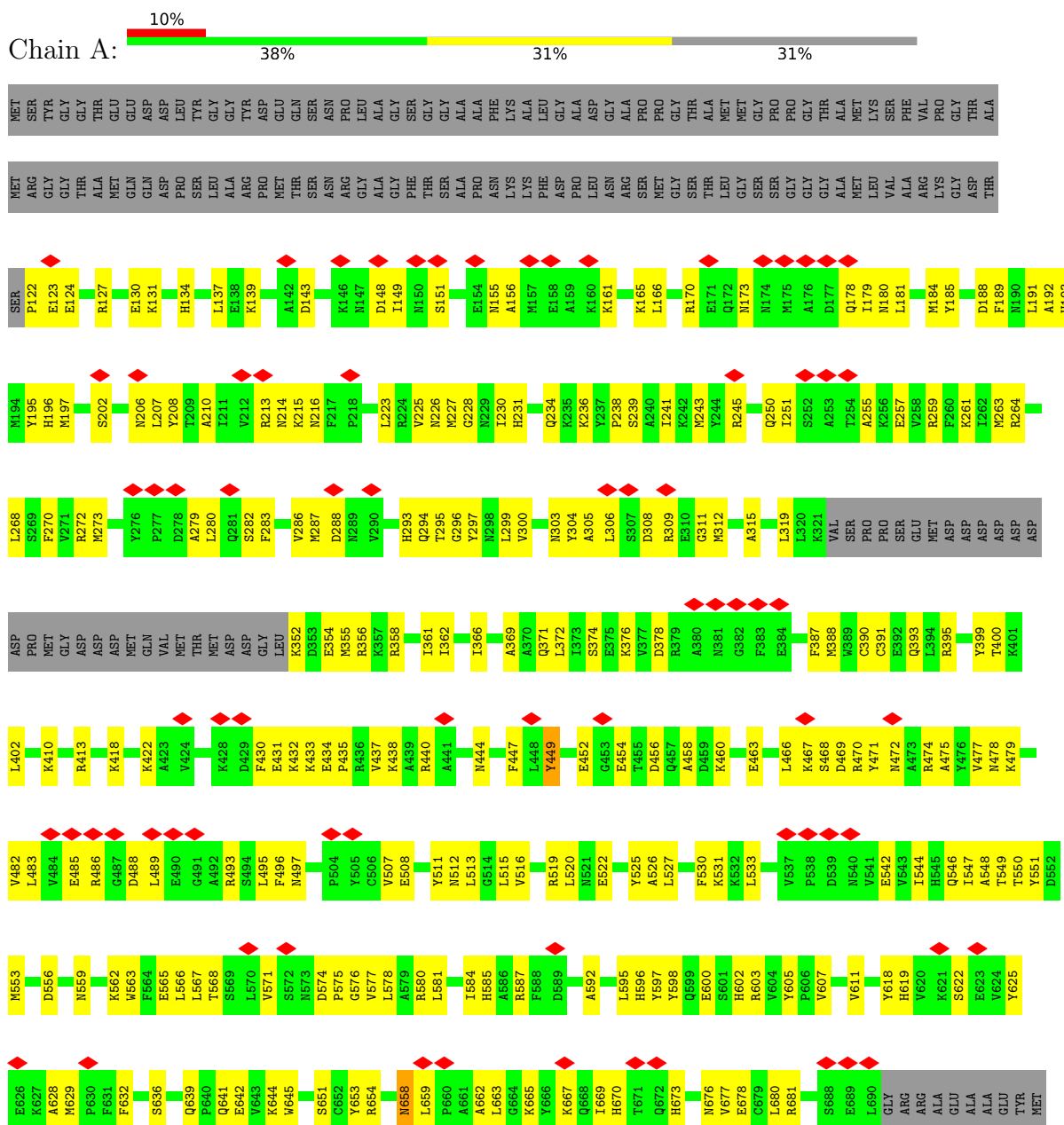
- Molecule 13 is a protein called Intraflagellar transport protein 172.

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		

### 3 Residue-property plots

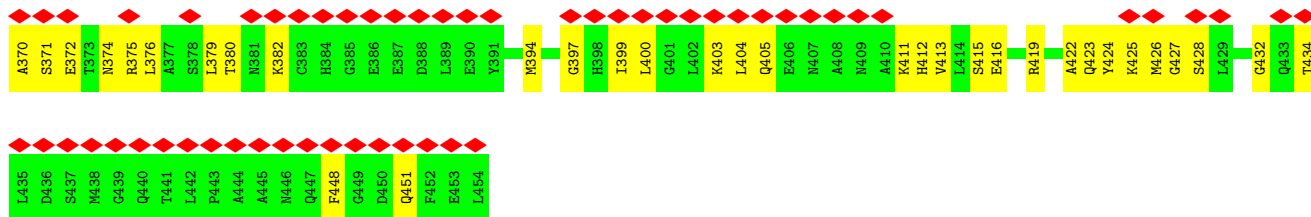
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: IFT88

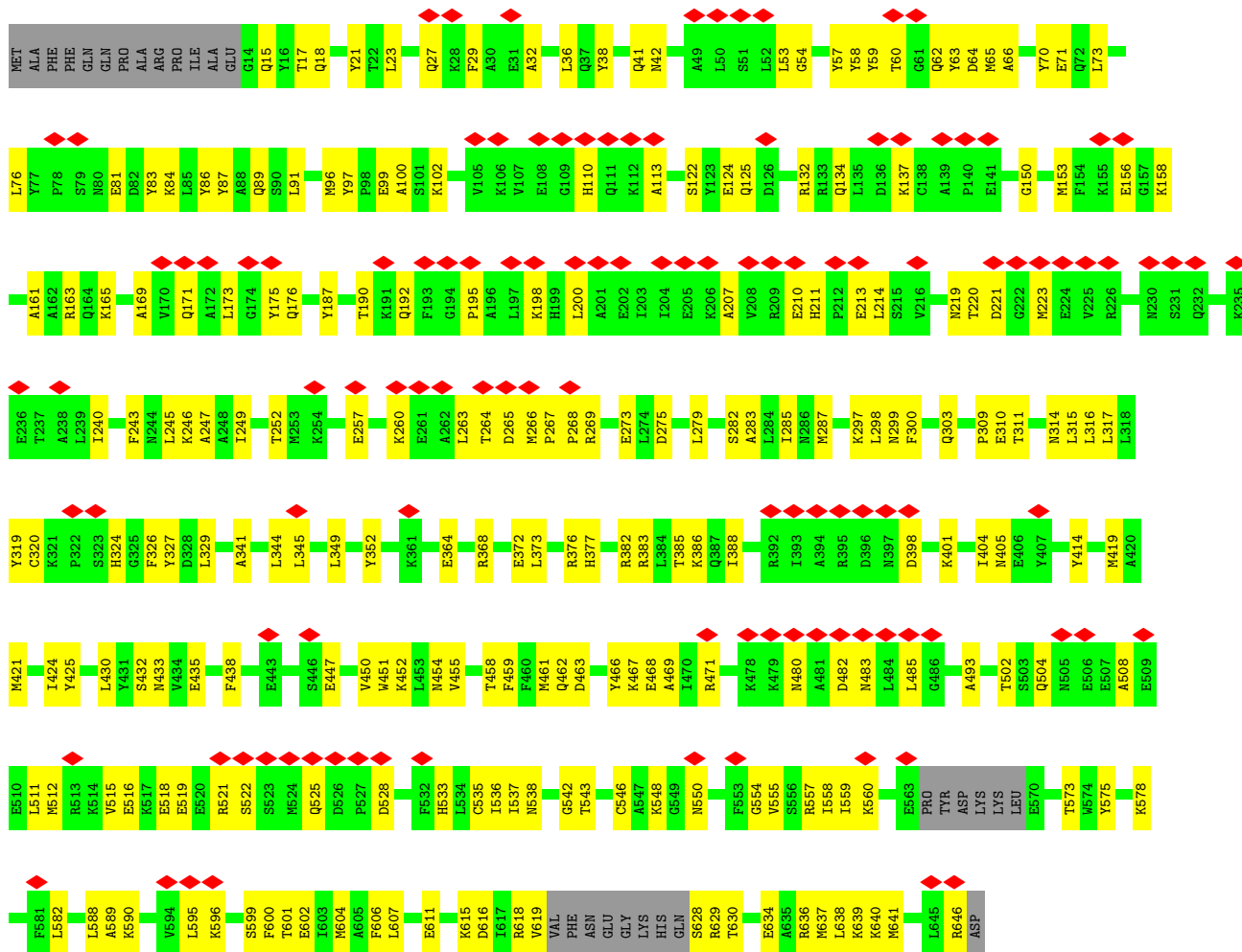




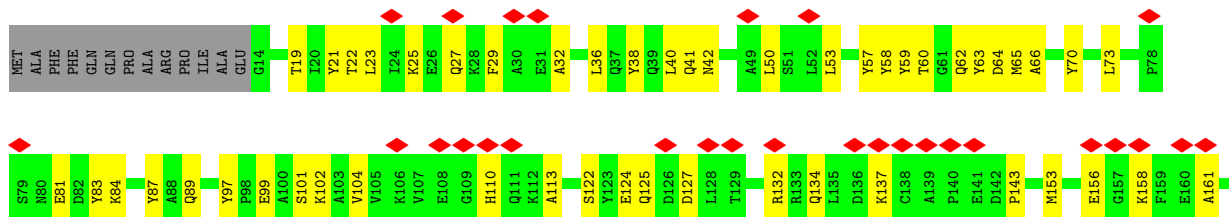


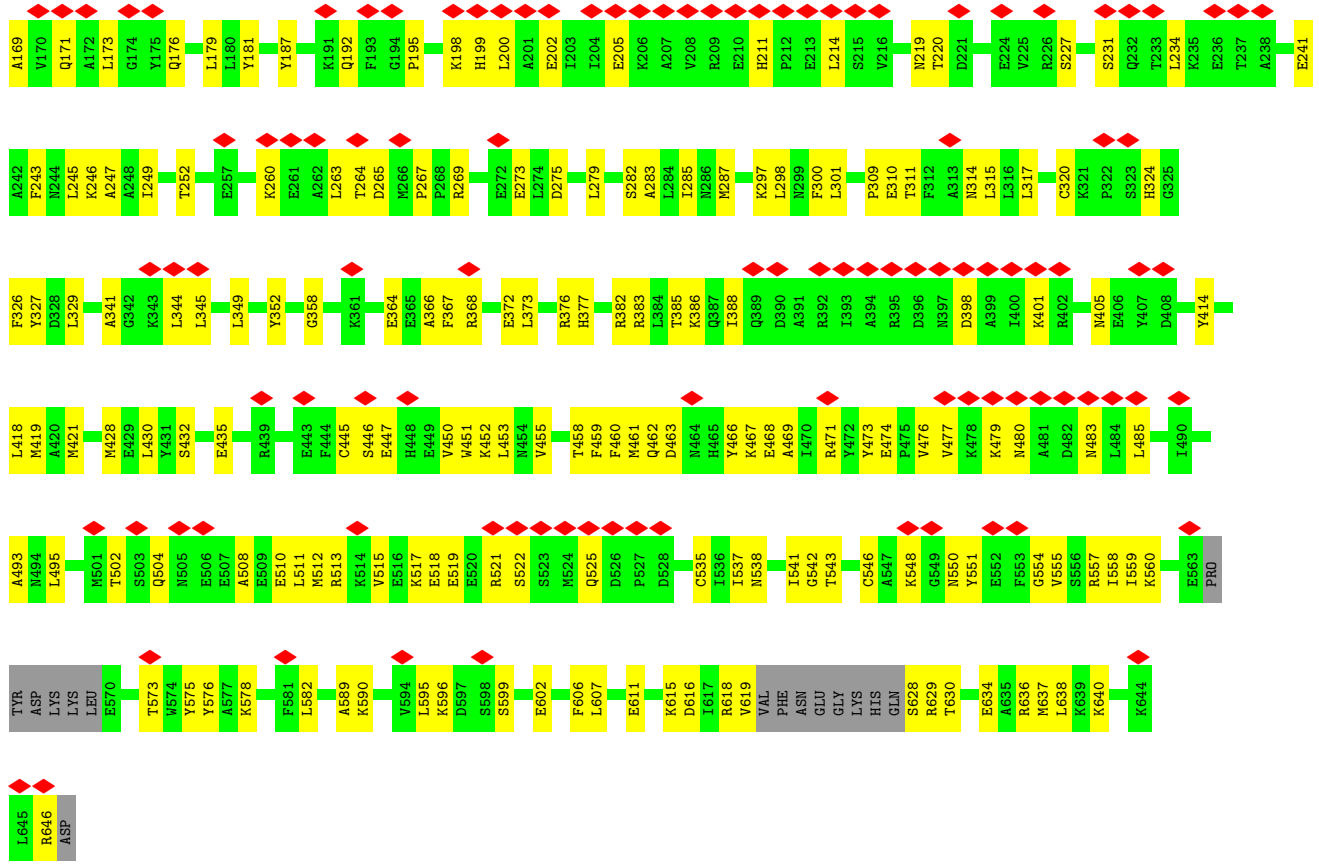


• Molecule 3: IFT70

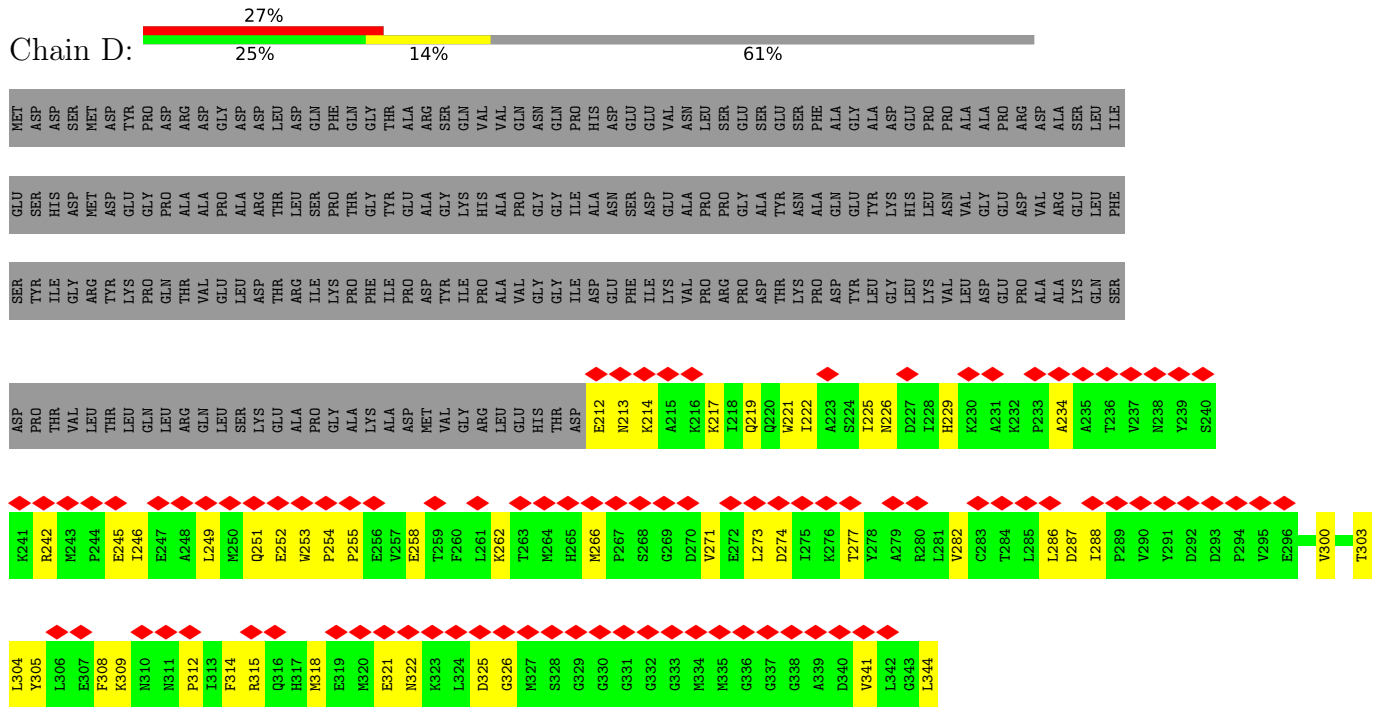


• Molecule 3: IFT70

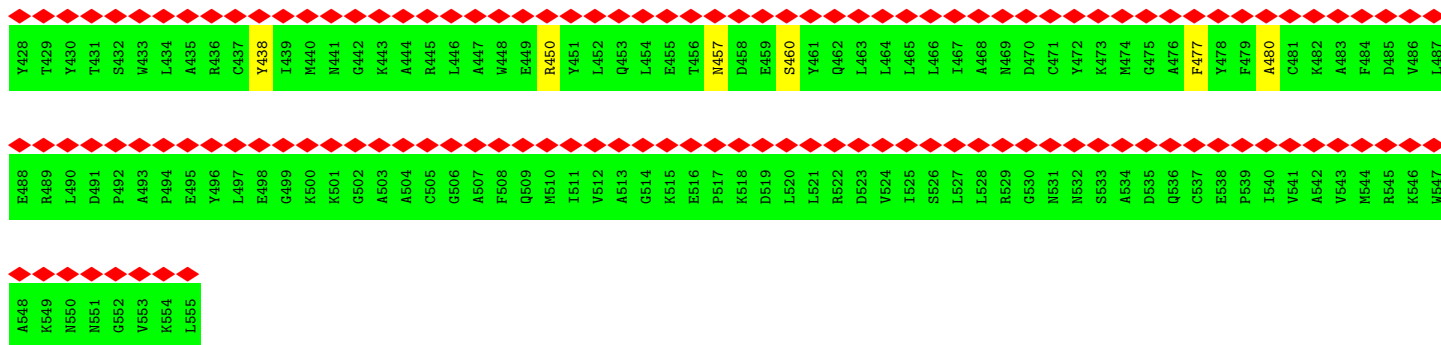




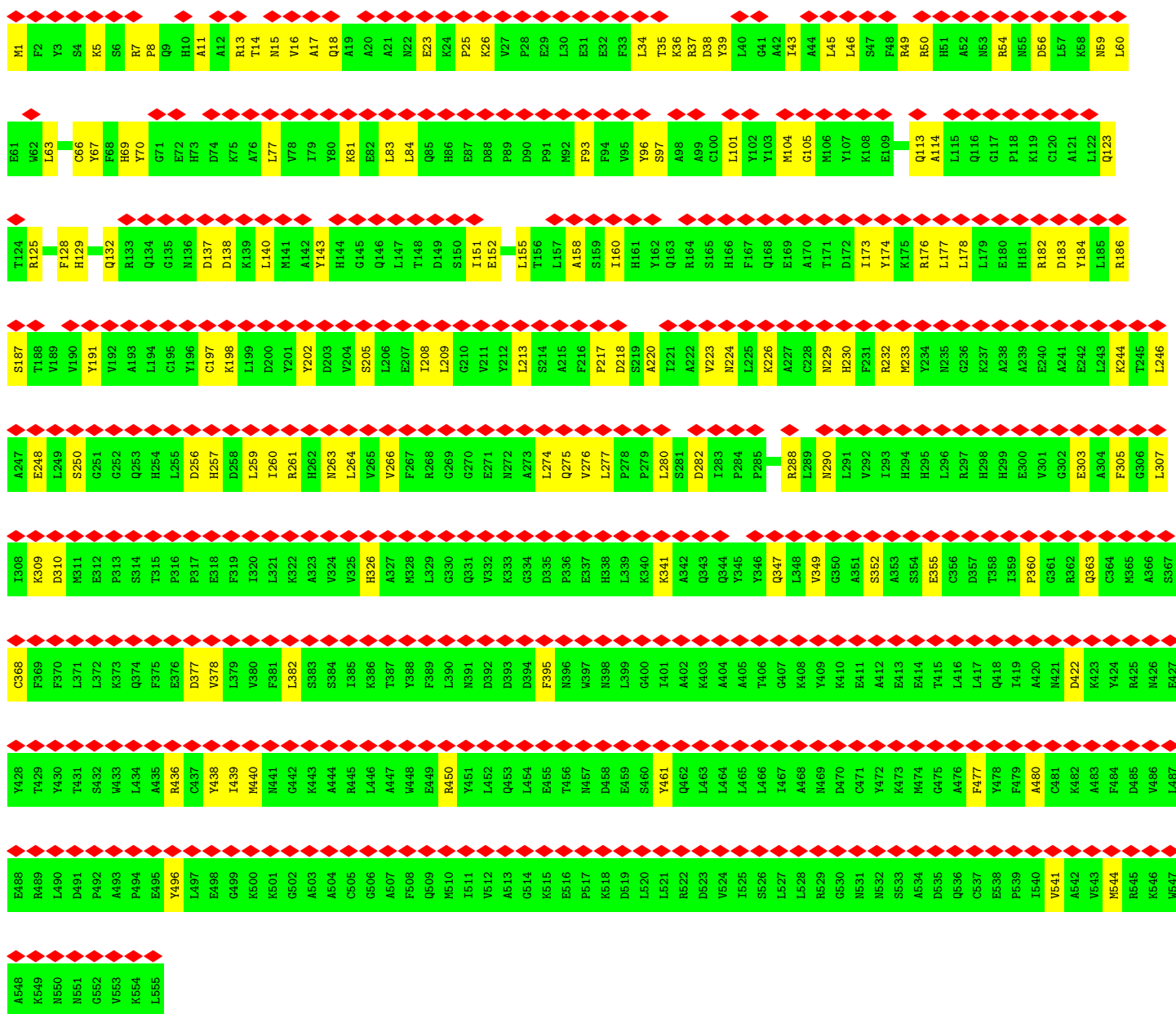
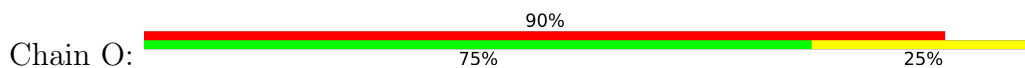
• Molecule 4: Intraflagellar transport protein 46







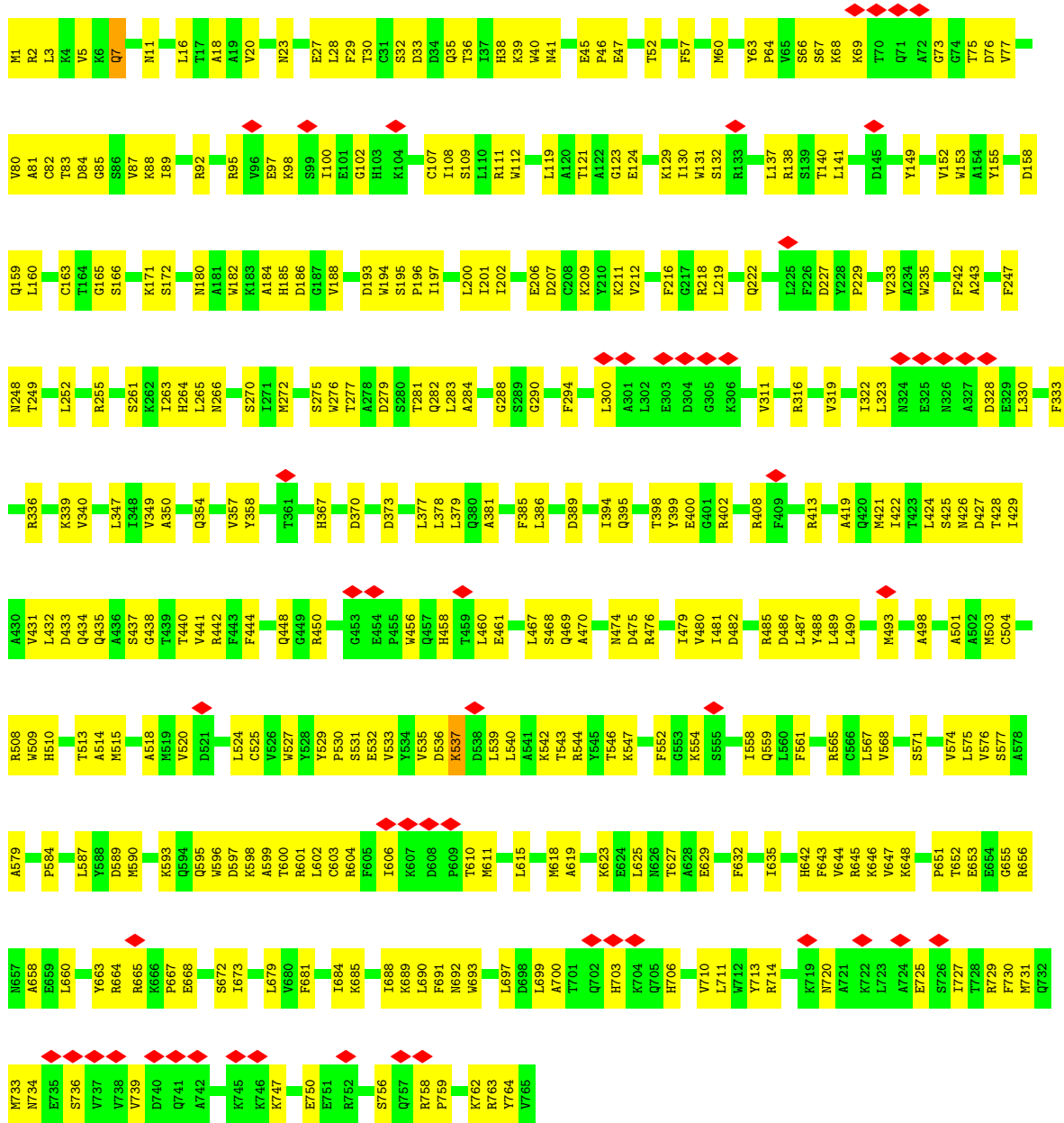
● Molecule 5: Intraflagellar transport protein 56



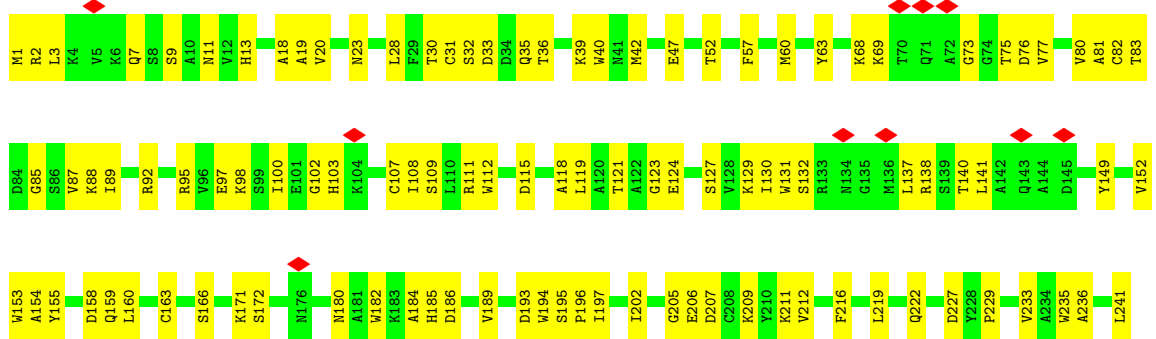






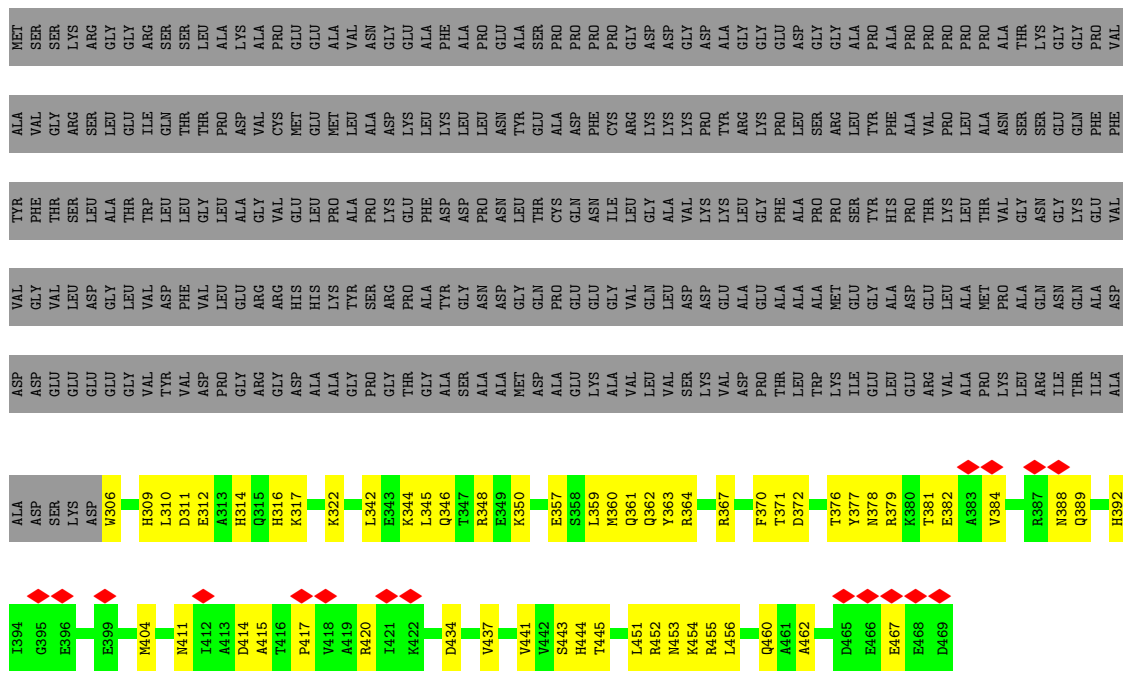


● Molecule 8: Intraflagellar transport protein 80

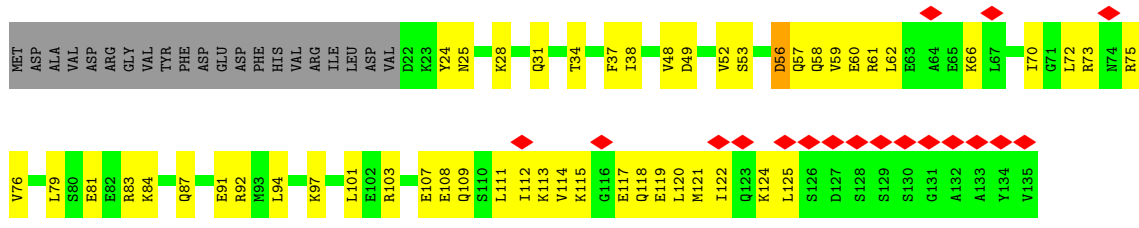




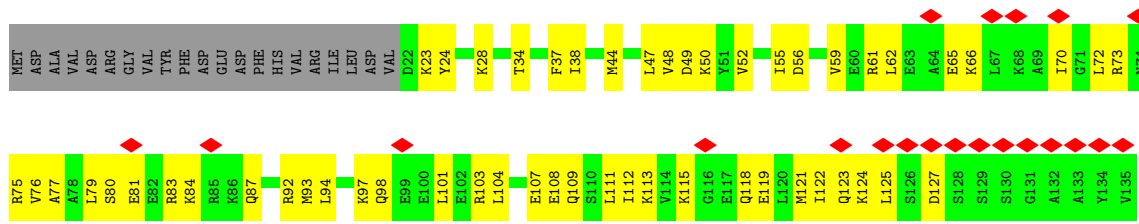




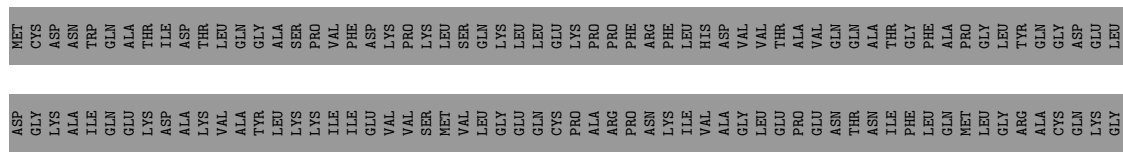
• Molecule 11: Intraflagellar transport particle protein IFT20



• Molecule 11: Intraflagellar transport particle protein IFT20



• Molecule 12: IFT54





A982	A983	E984	F985	E986	A987	A988	A989	K990	E993	A994	E995	K996	A997	G998	L999	A1000	A1001	G1002	G1003	D1004	D1005	V1006	A1007	D943	M944	A945	E946	D947	A948	E949	E950	E951	R954	A955	G956	K957	W958	M1022	L1023	A960	A961	L1024	L1025	V1026	T1027	Q1028	K1031	E1032	K1033	V1034	P1035	E1036	A1037	H1038	I1041	A1042	Q1043	Q1044	L1045	A982	A983	E984	F985	E986	A987	A988	A989	K990	E993	A994	E995	K996	A997	G998	L999	A1000	A1001	G1002	G1003	D1004	D1005	V1006	A1007	D943	M944	A945	E946	D947	A948	E949	E950	E951	R954	A955	G956	K957	W958	M1022	L1023	A960	A961	L1024	L1025	V1026	T1027	Q1028	K1031	E1032	K1033	V1034	P1035	E1036	A1037	H1038	I1041	A1042	Q1043	Q1044	L1045	F621	L624	T625	P626	E627	Q631	W632	L635	A636	E637	A638	A639	A640	T642	I643	Q644	L645	V646	L647	A648	E649	E650	R651	Y652	L655	L658	F663	L664	V667	E673	A676	E677	F678	G679	G680	D681	G682	T683	D684	A685	A690	M691	M692	A693	Q694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L716	L717	L718	L719	L720	L721	L722	L725	E726	D727	A728	L729	L730	L731	S734	T735	H736	H737	A738	L739	A740	A741	A742	L743	K744	Y747	W750	E758	A762	R766	E767	G768	D769	L770	L771	A772	A773	L774	L775	G776	L777	L778	L779	L780	L781	L782	R785	Q788	W789	M791	S792	L793	H794	L795	L796	L797	L798	D799	P800	A801	L802	L803	D804	L807	A808	S809	L810	A811	K812	A813	G814	L815	L816	E817	Y823	M826	S827	R828	S829	S830	M833	Q834	S835	Y836	R837	R838	G839	H840	A841	L842	R843	K844	L845	A846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	E861	E862	E863	W864	W867	L868	V869	T870	Q871	K872	Q873	M874	D875	E876	A877	L878	L879	M880	F881	L882	E883	S884	G885	A886	L887	L888	K889	K892	L895	D896	G897	R898	Q899	F900	A901	K902	A903	A904	G905	G906	Y907	E908	L909	T910	E911	L912	K913	L914	L915	L916	L917	L918	L919	P912	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	L181	W182	K183	F184	N185	F186	P187	A188	E189	E190	F191	G192	L193	P194	L195	S196	S197	Q198	L199	V200	V201	H202	S203	C204	V205	P206	Y207	S208	L209	G210	W211	G212	S213	C214	I215	A216	E217	A218	G219	N220	D221	N222	R223	V224	V225	F226	Y227	D228	L229	N230	Q231	R232	E233	L234	R235	S236	F237	D238	Y239	S240	N241	N242	D243	E244	R245	E247	F248	T249	T250	C251	A252	F253	N254	P255	S256	G257	D258	T259	V260	V261	F262	G263	T264	Y265	P266	R267	F268	Y269	M270	Y271	G272	F273	N274	I275	Q276	R277	N278	D279	W280	E281	E282	A283	G284	H285	K286	Q287	I288	D289	N290	F291	Y292	A293	V294	S295	A296	A297	S298	Y299	K300	P301	M306	V308	G309	S310	M311	T312	G313	A314	V315	D316	M317	Y318	D319	A320	S321	V322	K323	R324	H325	G329	E332	T334	Y335	V336	S337	K338	S339	A340	V341	I342	V343	K344	K347	T348	G349	M350	R351	I352	V353	L354	K355	S356	Y357	Y358	G359	Y360	E361	I362	E363	K364	R371	Y372	L373	I374	A375	R376	Y379	T380	L381	M382	G383	D385	L386	D387	T388	C389	K390	L391	S392	P395	M396	D397	S398	D399	G400	S401	E402	H405	F406	E407	M408	R410	V411	C412	M413	V414	H415	Y416	L420	H421	I422	Y423	G426	R427	M428	L431	R435	M440	P441	Y442	L443	L444	S445	Y448	E450	A451	R452	G453	L454	S458	D466	L467	Q468	T469	L470	R471	Q472	D473	L475	M476	A477	P478	T482	L483	A484	M487	H488	D489	T490	D493	W494	L495	M498	Q499	R500	G501	T502	H503	R507	D508	R511	H512	L513	H514	L515	S519	G520	R523	L527	C530	U531	V536	P537	V541	Q545	S546	R547	N548	M549	L550	V554	S555	M564	F565	P566	I567	K568	V571	R576	H577	N578	H579	R580	T581	E582	D586	E587	L588	L589	N590	T591	L596	D597	A598	L600	L601	Q610	Q611	Y612	E613	V616	D617	T618	L619	E620	F621	L624	T625	P626	E627	Q631	W632	L635	A636	E637	A638	A639	A640	T642	I643	Q644	L645	V646	L647	A648	E649	E650	R651	Y652	L655	L658	F663	L664	V667	E673	A676	E677	F678	G679	G680	D681	G682	T683	D684	A685	A690	M691	M692	A693	Q694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L716	L717	L718	L719	L720	L721	L722	L725	E726	D727	A728	L729	L730	L731	S734	T735	H736	H737	A738	L739	A740	A741	A742	L743	K744	Y747	W750	E758	A762	R766	E767	G768	D769	L770	L771	A772	A773	L774	L775	G776	L777	L778	L779	L780	L781	L782	R785	Q788	W789	M791	S792	L793	H794	L795	L796	L797	L798	D799	P800	A801	L802	L803	D804	L807	A808	S809	L810	A811	K812	A813	G814	L815	L816	E817	Y823	M826	S827	R828	S829	S830	M833	Q834	S835	Y836	R837	R838	G839	H840	A841	L842	R843	K844	L845	A846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	E861	E862	E863	W864	W867	L868	V869	T870	Q871	K872	Q873	M874	D875	E876	A877	L878	L879	M880	F881	L882	E883	S884	G885	A886	L887	L888	K889	K892	L895	D896	G897	R898	Q899	F900	A901	K902	A903	A904	G905	G906	Y907	E908	L909	T910	E911	L912	K913	L914	L915	L916	L917	L918	L919	P912	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020	L1021	L1022	L1023	L1024	L1025	L1026	L1027	L1028	L1029	L1030	L1031	L1032	L1033	L1034	L1035	L1036	L1037	L1038	L1039	L1040	L1041	L1042	L1043	L1044	L1045	W121	P122	K123	D124	R125	P126	M127	E128	V129	V130	F131	G132	L133	A134	D135	G136	K137	V138	R139	L140	G141	A142	L143	K144	N145	M146	K147	S148	Y149	T150	C151	Y152	A153	H154	P155	E156	N157	S158	Y159	V160	V161	A162	L163	A164	S165	S166	L167	M168	G169	Q170	N171	V172	L173	S174	G175	H176	M177	D178	G179	A180	W181	W182	K183	F184	N185	F186	P187	A188	E189	E190	F191	G192	L193	P194	L195	S196	S197	Q198	L199	V200	V201	H202	S203	C204	V205	P206	Y207	S208	L209	G210	W211	G212	S213	C214	I215	A216	E217	A218	G219	N220	D221	N222	R223	V224	V225	F226	Y227	D228	L229	N230	Q231	R232	E233	L234	R235	S236	F237	D238	Y239	S240	N241	N242	D243	E244	R245	E247	F248	T249	T250	C251	A252	F253	N254	P255	S256	G257	D258	T259	V260	V261	F262	G263	T264	Y265	P266	R267	F268	Y269	M270	Y271	G272	F273	N274	I275	Q276	R277	N278	D279	W280	E281	E282	A283	G284	H285	K286	Q287	I288	D289	N290	F291	Y292	A293	V294	S295	A296	A297	S298	Y299	K300	P301	M306	V308	G309	S310	M311	T312	G313	A314	V315	D316	M317	Y318	D319	A320	S321	V322	K323	R324	H325	G329	E332	T334	Y335	V336	S337	K338	S339	A340	V341	I342	V343	K344	K347	T348	G349	M350	R351	I352	V353	L354	K355	S356	Y357	Y358	G359	Y360	E361	I362	E363	K364	R371	Y372	L373	I374	A375	R376	Y379	T380	L381	M382	G383	D385	L386	D387	T388	C389	K390	L391	S392	P395	M396	D397	S398	D399	G400	S401	E402	H405	F406	E407	M408	R410	V411	C412	M413	V414	H415	Y416	L420	H421	I422	Y423	G426	R427	M428	L431	R435	M440	P441	Y442	L443	L444	S445	Y448	E450	A451	R452	G453	L454	S458	D466	L467	Q468	T469	L470	R471	Q472	D473	L475	M476	A477	P478	T482	L483	A484	M487	H488	D489	T490	D493	W494	L495	M498	Q499	R500	G501	T502	H503	R507	D508	R511	H512	L513	H514	L515	S519	G520	R523	L527	C530	U531	V536	P537	V541	Q545	S546	R547	N548	M549	L550	V554	S555	M564	F565	P566	I567	K568	V571	R576	H577	N578	H579	R580	T581	E582	D586	E587	L588	L589	N590	T591	L596	D597	A598	L
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GLU	N241	S304	R371	Y442	R523	I601	G682	L752	E821	K892	G956	L1025	G1069
VAL	N242	T307	Y372	L443	R683	E608	T683	E753	L822	A893	K957	V1026	V1090
HIS	D243	V308	I373	I444	D684	D609	D684	T754	Y823	A894	W958	T1027	M1091
LEU	E244	V309	I374	A446	A445	A685	A685	G755	E824	A895	W959	Q1028	M1092
TYR	E245	G309	A375	V447	A446	C530	C530	Q756	H825	I895	E959	R1029	A1092
ALA	R246	S310	E247	V448	A449	Q531	Q531	E757	R828	D896	A960	Y1029	S1093
MET	E247	M311	F248	V449	Q449	V536	V536	E758	S829	C897	A961	R1030	K1094
PHE	T249	T312	T250	E450	E450	A615	A615	Q759	M833	R898	R962	R1031	K1094
LEU	T250	G313	C251	D452	D540	V616	V616	V763	Q834	Q899	Q900	E1032	V1096
GLU	A252	A314	A252	G384	G384	Q617	Q617	R766	S835	F900	A901	K1033	A1097
ASP	F253	A315	F253	D385	D385	T618	T618	R766	S836	K902	K902	V1034	A1098
GLU	N254	D316	N254	D386	D386	L619	L619	E767	R837	A903	A903	P1035	A1099
ALA	P255	M317	P255	D387	D387	E620	E620	Q768	R838	A904	A904	G967	A1099
GLY	P256	Y318	P256	E455	E455	P621	P621	D769	G839	G905	G905	Y968	A1099
ARG	G257	D319	G257	S456	S456	L624	L624	Y770	S840	Y906	Y906	L969	W1100
PHE	G258	Y319	G258	E457	E457	E627	E627	A773	H840	Y907	Y907	T970	A1101
ALA	T259	A320	T259	S458	S458	L774	L774	A773	H841	E908	E908	E971	L1102
GLU	V260	K323	V260	K459	K459	G775	G775	A773	Y842	Y909	Y909	S972	L1103
GLY	V261	R324	V261	L467	L467	L776	L776	A773	Y843	Y910	Y910	Y978	L1104
ASP	F262	H325	F262	R471	R471	L777	L777	A773	R844	Y911	Y911	Y979	GLY
ASP	G263	K328	G263	I472	I472	L778	L778	A773	R845	Y912	Y912	A980	GLY
ASP	T264	G329	T264	Q631	Q631	L779	L779	A773	R846	Y913	Y913	A981	ASP
GLY	Y265	K330	Y265	M632	M632	G780	G780	A773	R847	Y914	Y914	A982	ASP
GLN	N266	F331	N266	L635	L635	G781	G781	A773	R848	Y915	Y915	A983	ALA
LEU	R267	F332	R267	Q638	Q638	L782	L782	A773	R849	Y916	Y916	A984	ALA
LEU	F268	F333	F268	D560	D560	P783	P783	A773	R850	Y917	Y917	A985	LEU
ASP	Y269	F334	Y269	M661	M661	A786	A786	A773	R851	Y918	Y918	A986	LEU
MET	M270	Y335	M270	L646	L646	A787	A787	A773	R852	Y919	Y919	A987	LEU
HIS	Y271	V336	Y271	L647	L647	Q788	Q788	A773	R853	Y920	Y920	A988	LEU
ASN	T272	V337	T272	A648	A648	W789	W789	A773	R854	Y921	Y921	A989	LEU
GLN	F273	K338	F273	V571	V571	V790	V790	A773	R855	Y922	Y922	K990	LEU
TRP	N274	M408	N274	V572	V572	W791	W791	A773	R856	Y923	Y923	K991	LEU
ALA	L275	E409	L275	A653	A653	R720	R720	A773	R857	Y924	Y924	E993	LEU
ALA	Q276	E409	Q276	A653	A653	D721	D721	A773	R858	Y925	Y925	A994	LEU
ARG	R277	E409	R277	A653	A653	A728	A728	A773	R859	Y926	Y926	A995	LEU
ALA	N278	V411	N278	A653	A653	I729	I729	A773	R860	Y927	Y927	A996	LEU
GLU	D279	C412	D279	A653	A653	R724	R724	A773	R861	Y928	Y928	A997	LEU
ARG	W280	M413	W280	A653	A653	W725	W725	A773	R862	Y929	Y929	A998	LEU
TYR	E281	M415	E281	A653	A653	A726	A726	A773	R863	Y930	Y930	A999	LEU
PRO	E282	L420	E282	A653	A653	D727	D727	A773	R864	Y931	Y931	A1000	LEU
THR	A283	L421	A283	A653	A653	A728	A728	A773	R865	Y932	Y932	A1001	LEU
MET	G284	L422	G284	A653	A653	I730	I730	A773	R866	Y933	Y933	A1002	LEU
VAL	H285	V423	H285	A653	A653	R731	R731	A773	R867	Y934	Y934	A1003	LEU
SER	K286	L431	K286	A653	A653	S734	S734	A773	R868	Y935	Y935	A1004	LEU
GLY	Q287	R435	Q287	A653	A653	H737	H737	A773	R869	Y936	Y936	A1005	LEU
ALA	I288	M428	I288	A653	A653	A738	A738	A773	R870	Y937	Y937	A1006	LEU
LEU	D289	L439	D289	A653	A653	S809	S809	A773	R871	Y938	Y938	A1007	LEU
PRO	N290	M440	N290	A653	A653	L810	L810	A773	R872	Y939	Y939	A1008	LEU
PRO	F291	P441	F291	A653	A653	A811	A811	A773	R873	Y940	Y940	A1009	LEU
ALA	A292	G520	A292	A653	A653	A812	A812	A773	R874	Y941	Y941	A1010	LEU
ALA	A293	G520	A293	A653	A653	A813	A813	A773	R875	Y942	Y942	A1011	LEU
ALA	S295	G520	S295	A653	A653	A814	A814	A773	R876	Y943	Y943	A1012	LEU
ALA	A296	G520	A296	A653	A653	A815	A815	A773	R877	Y944	Y944	A1013	LEU
ALA	A297	G520	A297	A653	A653	A816	A816	A773	R878	Y945	Y945	A1014	LEU
ALA	S298	G520	S298	A653	A653	A817	A817	A773	R879	Y946	Y946	A1015	LEU
ALA	P301	G520	P301	A653	A653	A818	A818	A773	R880	Y947	Y947	A1016	LEU
ALA				A653	A653	A819	A819	A773	R881	Y948	Y948	A1017	LEU
ALA				A653	A653	A820	A820	A773	R882	Y949	Y949	A1018	LEU
ALA				A653	A653	A821	A821	A773	R883	Y950	Y950	A1019	LEU
ALA				A653	A653	A822	A822	A773	R884	Y951	Y951	A1020	LEU
ALA				A653	A653	A823	A823	A773	R885	Y952	Y952	A1021	LEU
ALA				A653	A653	A824	A824	A773	R886	Y953	Y953	A1022	LEU
ALA				A653	A653	A825	A825	A773	R887	Y954	Y954	A1023	LEU
ALA				A653	A653	A826	A826	A773	R888	Y955	Y955	A1024	LEU
ALA				A653	A653	A827	A827	A773	R889	Y956	Y956	A1025	LEU
ALA				A653	A653	A828	A828	A773	R890	Y957	Y957	A1026	LEU
ALA				A653	A653	A829	A829	A773	R891	Y958	Y958	A1027	LEU
ALA				A653	A653	A830	A830	A773	R892	Y959	Y959	A1028	LEU
ALA				A653	A653	A831	A831	A773	R893	Y960	Y960	A1029	LEU
ALA				A653	A653	A832	A832	A773	R894	Y961	Y961	A1030	LEU
ALA				A653	A653	A833	A833	A773	R895	Y962	Y962	A1031	LEU
ALA				A653	A653	A834	A834	A773	R896	Y963	Y963	A1032	LEU
ALA				A653	A653	A835	A835	A773	R897	Y964	Y964	A1033	LEU
ALA				A653	A653	A836	A836	A773	R898	Y965	Y965	A1034	LEU
ALA				A653	A653	A837	A837	A773	R899	Y966	Y966	A1035	LEU
ALA				A653	A653	A838	A838	A773	R900	Y967	Y967	A1036	LEU
ALA				A653	A653	A839	A839	A773	R901	Y968	Y968	A1037	LEU
ALA				A653	A653	A840	A840	A773	R902	Y969	Y969	A1038	LEU
ALA				A653	A653	A841	A841	A773	R903	Y970	Y970	A1039	LEU
ALA				A653	A653	A842	A842	A773	R904	Y971	Y971	A1040	LEU
ALA				A653	A653	A843	A843	A773	R905	Y972	Y972	A1041	LEU
ALA				A653	A653	A844	A844	A773	R906	Y973	Y973	A1042	LEU
ALA				A653	A653	A845	A845	A773	R907	Y974	Y974	A1043	LEU
ALA				A653	A653	A846	A846	A773	R908	Y975	Y975	A1044	LEU
ALA				A653	A653	A847	A847	A773	R909	Y976	Y976	A1045	LEU
ALA				A653	A653	A848	A848	A773	R910	Y977	Y977	A1046	LEU
ALA				A653	A653	A849	A849	A773	R911	Y978	Y978	A1047	LEU
ALA				A653	A653	A850	A850	A773	R912	Y979	Y979	A1048	LEU
ALA				A653	A653	A851	A851	A773	R913	Y980	Y980	A1049	LEU
ALA				A653	A653	A852	A852	A773	R914	Y981	Y981	A1050	LEU
ALA				A653	A653	A853	A853	A773	R915	Y982	Y982	A1051	LEU
ALA				A653	A653	A854	A854	A773	R916	Y983	Y983	A1052	LEU
ALA				A653	A653	A855	A855	A773	R917	Y984	Y984	A1053	LEU
ALA				A653	A653	A856	A856	A773	R918	Y985	Y985	A1054	LEU
ALA				A653	A653	A857	A857	A773	R919	Y986	Y986	A1055	LEU
ALA													



## 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 ( $\text{\AA}$ )	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 ( $\text{\AA}$ )	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	0.23	0/4423	0.60	2/5956 (0.0%)
1	H	0.30	2/4423 (0.0%)	0.62	3/5956 (0.1%)
2	B	0.20	0/3635	0.47	0/4918
2	J	0.19	0/3635	0.49	0/4918
3	C	0.18	0/5080	0.49	0/6863
3	K	0.17	0/5080	0.48	0/6863
4	D	0.19	0/1068	0.53	0/1441
4	N	0.23	0/1068	0.55	0/1441
5	E	0.15	0/4570	0.41	0/6180
5	O	0.15	0/4570	0.40	0/6180
6	F	0.21	0/2740	0.53	0/3688
6	P	0.22	0/2740	0.56	0/3688
7	G	0.24	0/1687	0.59	0/2257
7	Q	0.31	1/1687 (0.1%)	0.62	1/2257 (0.0%)
8	I	0.18	0/6147	0.43	0/8333
8	R	0.17	0/6147	0.44	0/8333
9	L	0.21	0/2504	0.53	0/3356
9	T	0.39	3/2504 (0.1%)	0.58	2/3356 (0.1%)
10	M	0.19	0/1343	0.49	0/1804
10	U	0.23	0/1343	0.53	0/1804
11	W	0.56	1/922 (0.1%)	0.71	3/1226 (0.2%)
11	Y	0.27	0/922	0.64	0/1226
12	X	0.35	0/857	0.66	0/1144
12	Z	0.34	0/857	0.65	0/1144
13	S	0.19	2/8979 (0.0%)	0.43	0/12160
13	V	0.21	3/8979 (0.0%)	0.45	1/12160 (0.0%)
All	All	0.22	12/87910 (0.0%)	0.50	12/118652 (0.0%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	W	56	ASP	C-N	14.86	1.53	1.33
9	T	72	VAL	C-N	10.39	1.49	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	262	ILE	C-N	9.30	1.45	1.33
9	T	269	LEU	C-N	8.65	1.45	1.34
9	T	268	GLU	C-N	-8.11	1.22	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	658	ASN	CA-C-N	7.67	129.67	120.09
1	H	658	ASN	C-N-CA	7.67	129.67	120.09
1	A	658	ASN	CA-C-N	7.42	128.90	120.06
1	A	658	ASN	C-N-CA	7.42	128.90	120.06
11	W	56	ASP	CA-C-N	-7.23	110.48	120.38

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	4337	0	4306	196	0
1	H	4337	0	4306	207	0
2	B	3553	0	3523	158	0
2	J	3553	0	3523	150	0
3	C	4978	0	4912	171	0
3	K	4978	0	4912	161	0
4	D	1045	0	1039	48	0
4	N	1045	0	1039	48	0
5	E	4465	0	4396	110	0
5	O	4465	0	4396	98	0
6	F	2701	0	2731	81	0
6	P	2701	0	2731	80	0
7	G	1674	0	1673	49	0
7	Q	1674	0	1673	56	0
8	I	6025	0	5988	287	0
8	R	6025	0	5988	257	0
9	L	2472	0	2484	112	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	T	2472	0	2484	107	0
10	M	1328	0	1322	51	0
10	U	1328	0	1322	52	0
11	W	919	0	936	68	0
11	Y	919	0	936	56	0
12	X	849	0	863	51	0
12	Z	849	0	863	45	0
13	S	8788	0	8605	252	0
13	V	8788	0	8605	298	0
All	All	86268	0	85556	2893	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 17.

The worst 5 of 2893 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	1.50
9:L:136:ILE:CG2	12:X:410:GLU:CD	1.98	1.33
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 67
1	H	535/782 (68%)	474 (89%)	57 (11%)	4 (1%)	18 56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	452/454 (100%)	391 (86%)	60 (13%)	1 (0%)	43	78
2	J	452/454 (100%)	393 (87%)	58 (13%)	1 (0%)	43	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
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%)	49	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%)	456 (100%)	1 (0%)	87	87
1	H	457/627 (73%)	456 (100%)	1 (0%)	87	87
2	B	388/388 (100%)	388 (100%)	0	100	100
2	J	388/388 (100%)	388 (100%)	0	100	100
3	C	534/558 (96%)	534 (100%)	0	100	100
3	K	534/558 (96%)	534 (100%)	0	100	100
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%)	469 (100%)	0	100	100
5	O	469/469 (100%)	469 (100%)	0	100	100
6	F	296/581 (51%)	296 (100%)	0	100	100
6	P	296/581 (51%)	295 (100%)	1 (0%)	86	86
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%)	647 (100%)	1 (0%)	87	87
8	R	648/648 (100%)	648 (100%)	0	100	100
9	L	261/358 (73%)	261 (100%)	0	100	100
9	T	261/358 (73%)	261 (100%)	0	100	100
10	M	144/380 (38%)	144 (100%)	0	100	100
10	U	144/380 (38%)	144 (100%)	0	100	100
11	W	101/120 (84%)	101 (100%)	0	100	100
11	Y	101/120 (84%)	101 (100%)	0	100	100
12	X	90/401 (22%)	90 (100%)	0	100	100
12	Z	90/401 (22%)	90 (100%)	0	100	100
13	S	915/1431 (64%)	914 (100%)	1 (0%)	88	89
13	V	915/1431 (64%)	914 (100%)	1 (0%)	88	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9204/13550 (68%)	9198 (100%)	6 (0%)	87 89

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	449	TYR
6	P	86	GLN
13	V	495	LEU
8	I	7	GLN
1	A	449	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
10	U	378	ASN
13	V	274	ASN
9	L	277	GLN
9	L	274	GLN
13	V	408	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

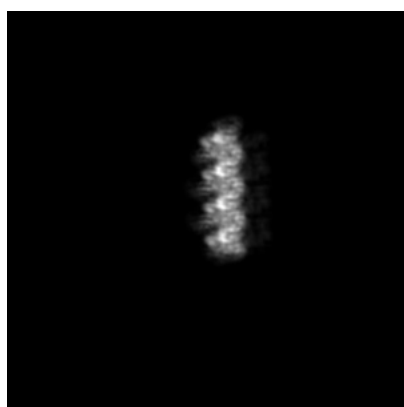
## 6 Map visualisation [i](#)

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

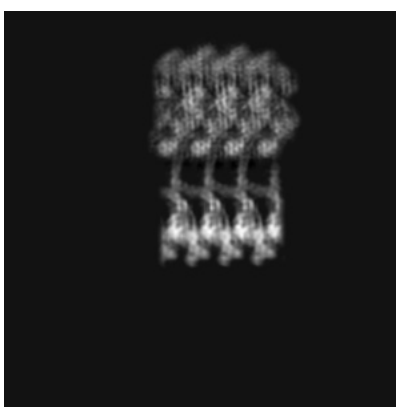
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

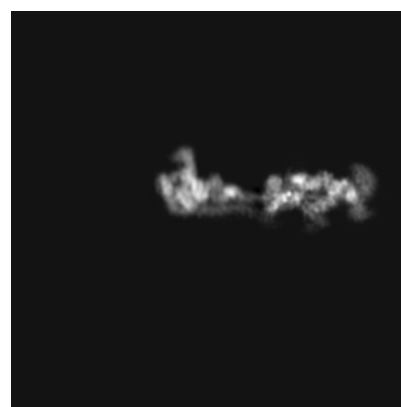
#### 6.1.1 Primary map



X



Y

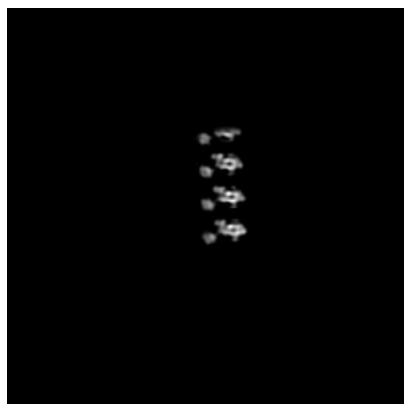


Z

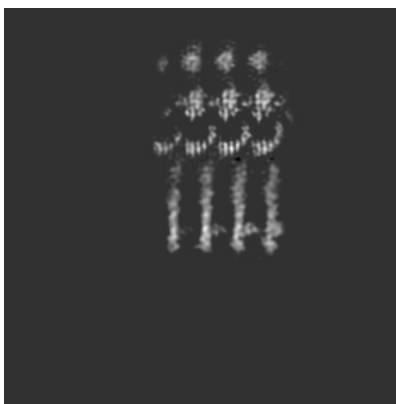
The images above show the map projected in three orthogonal directions.

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

#### 6.2.1 Primary map



X Index: 128



Y Index: 128

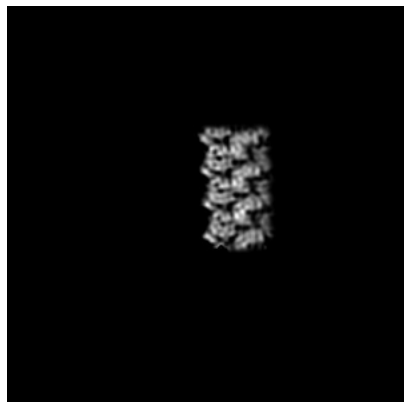


Z Index: 128

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

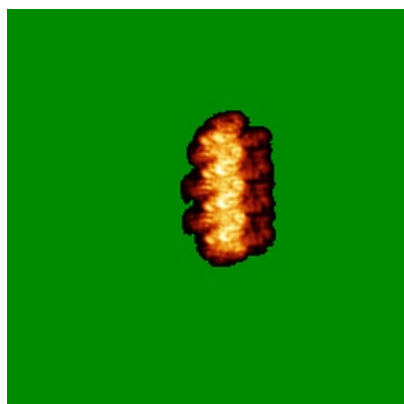


Z Index: 130

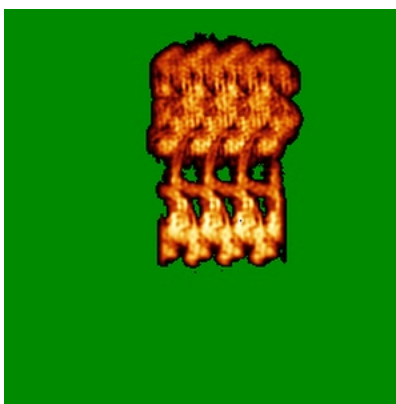
The images above show the largest variance slices of the map in three orthogonal directions.

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

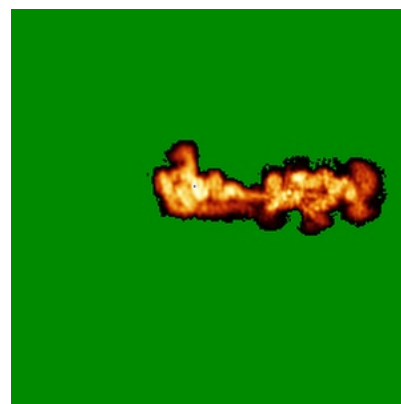
### 6.4.1 Primary map



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



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.

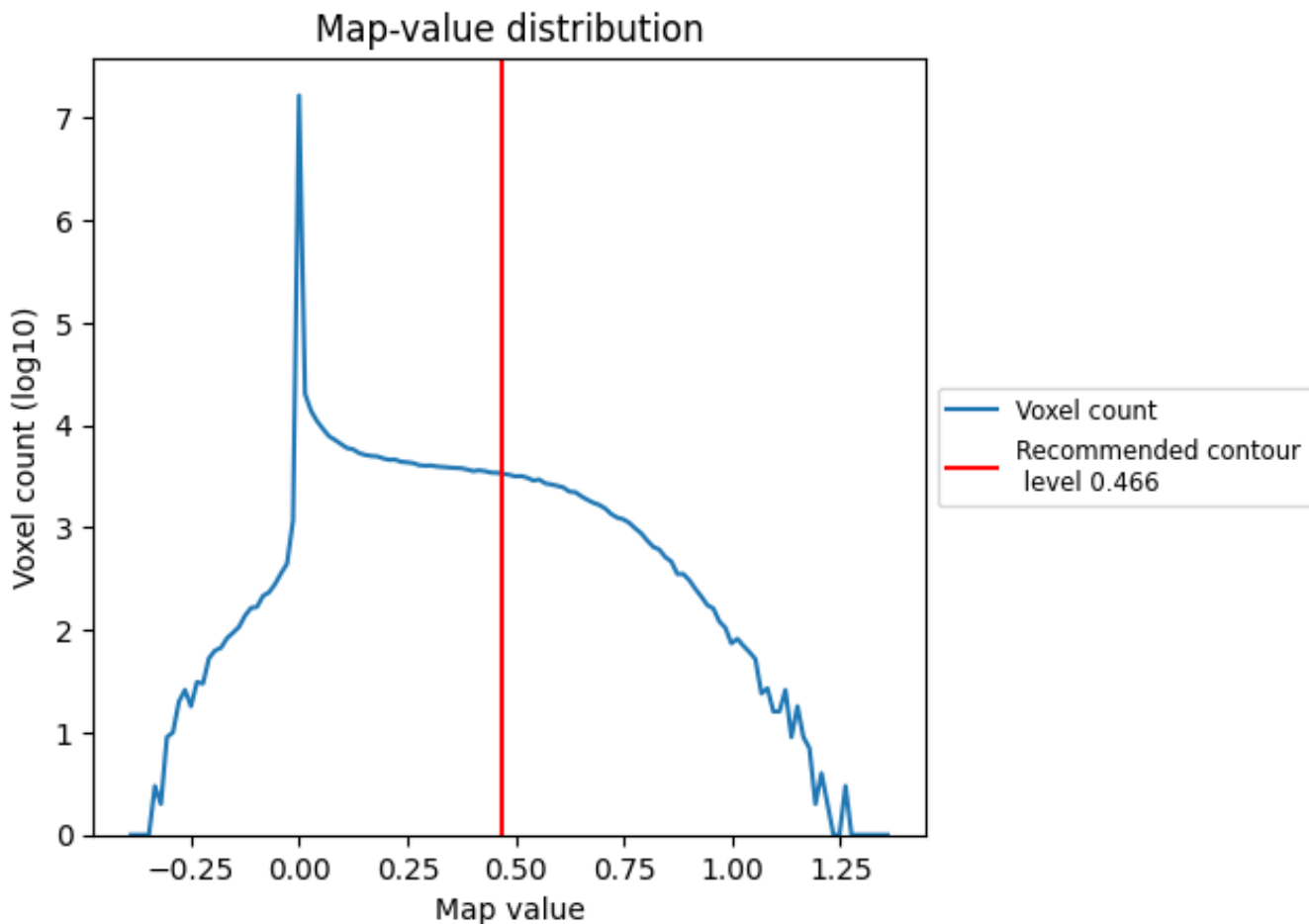
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

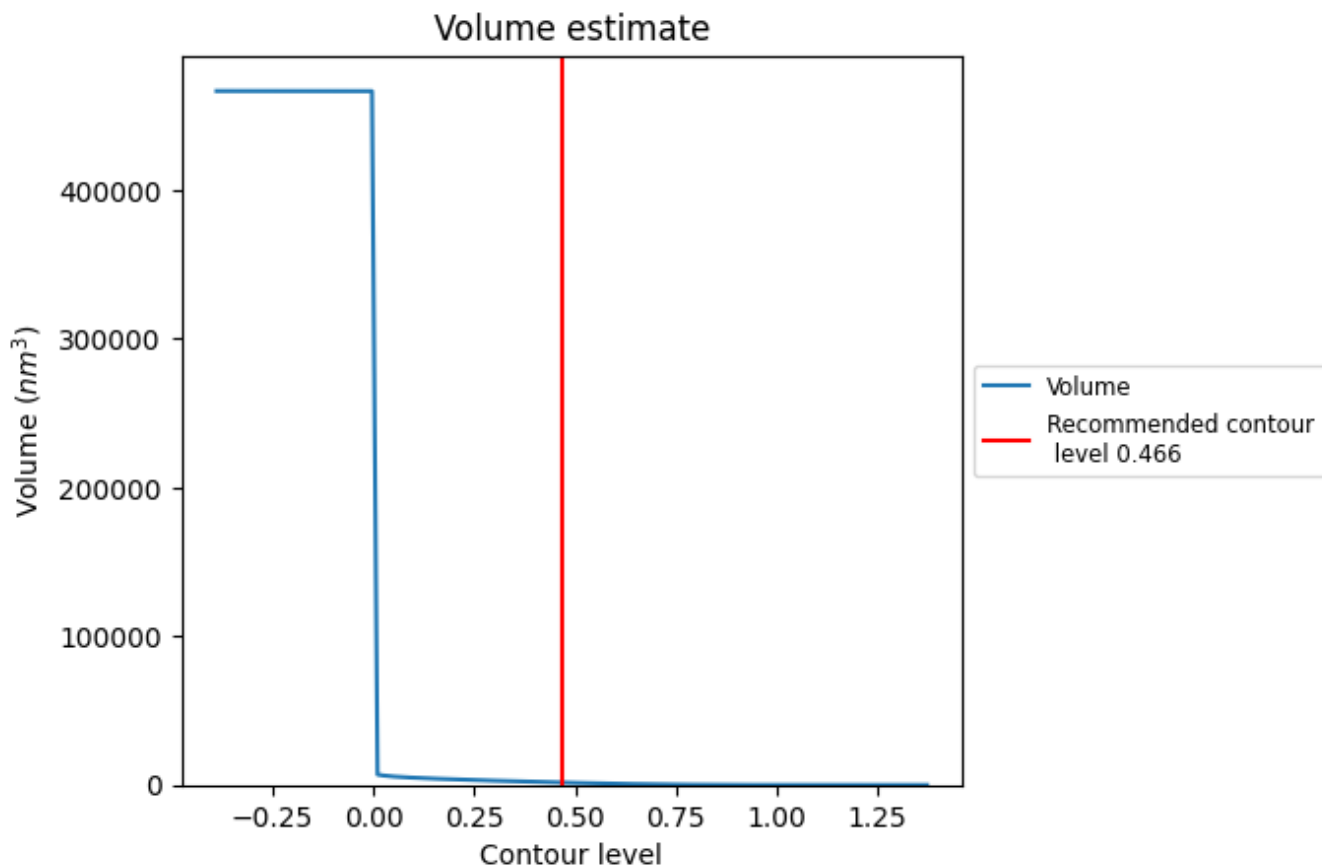
This section contains the results of statistical analysis of the map.

### 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.

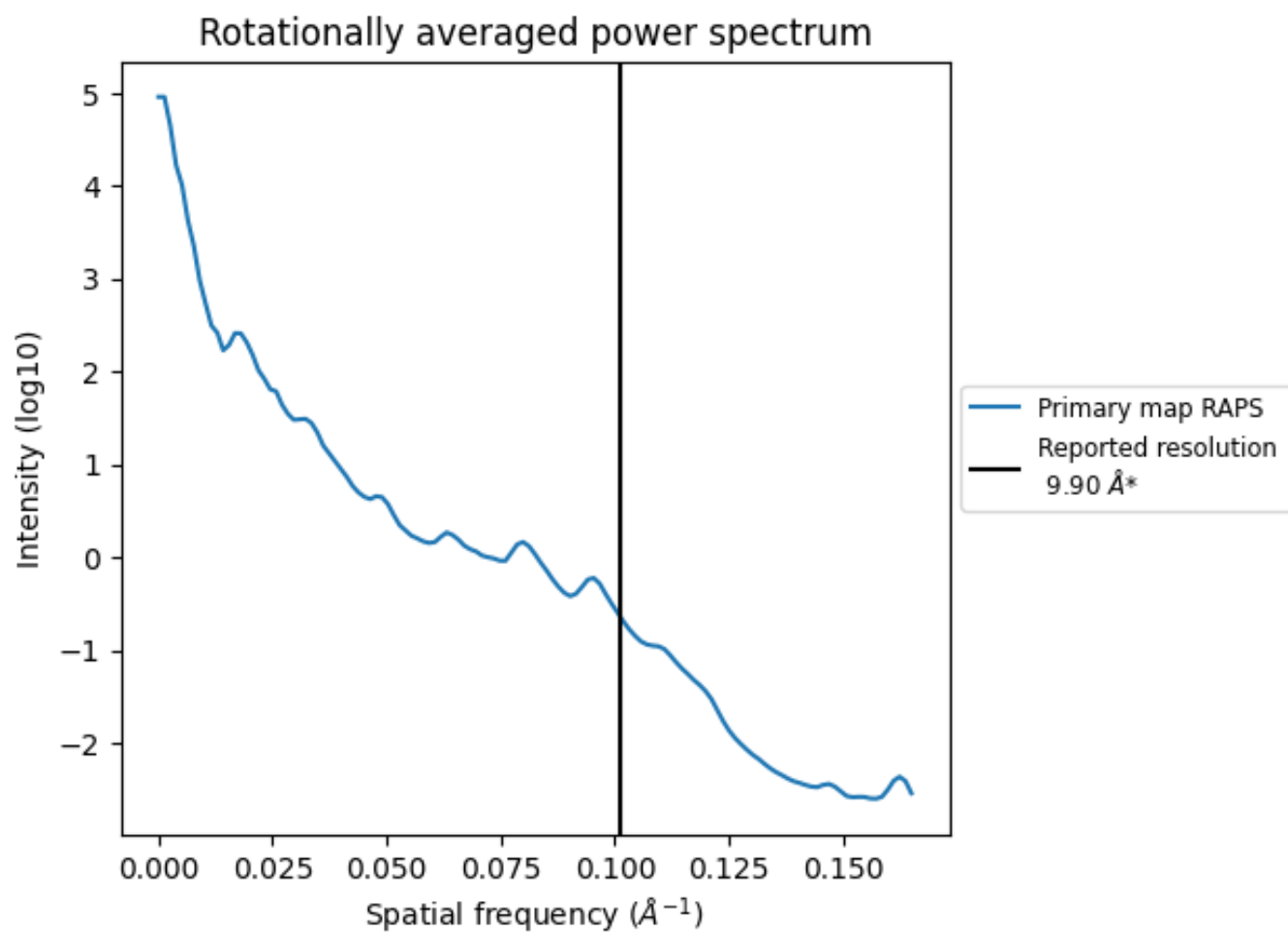
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1645 nm<sup>3</sup>; 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<sup>-1</sup>

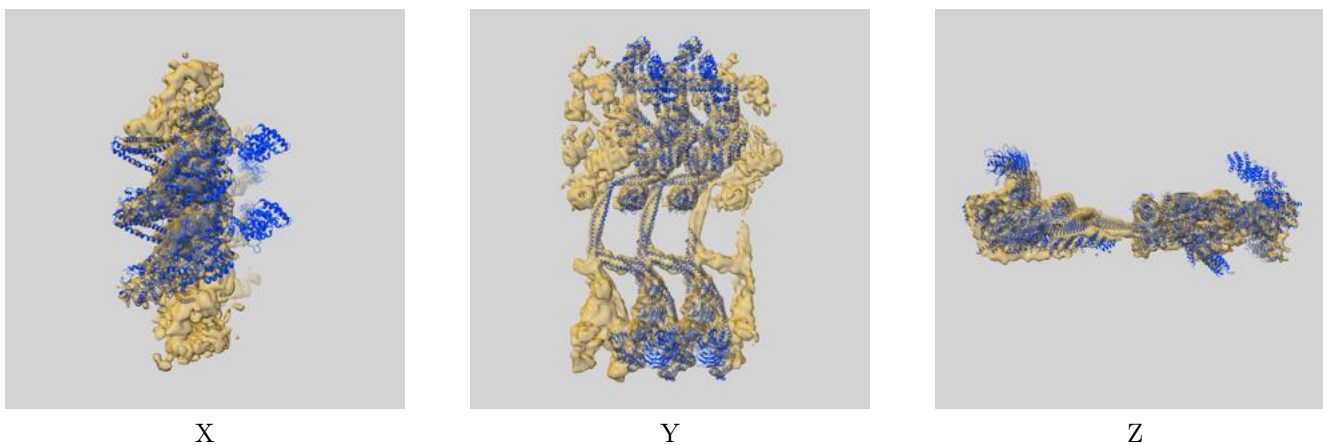
## 8 Fourier-Shell correlation

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

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

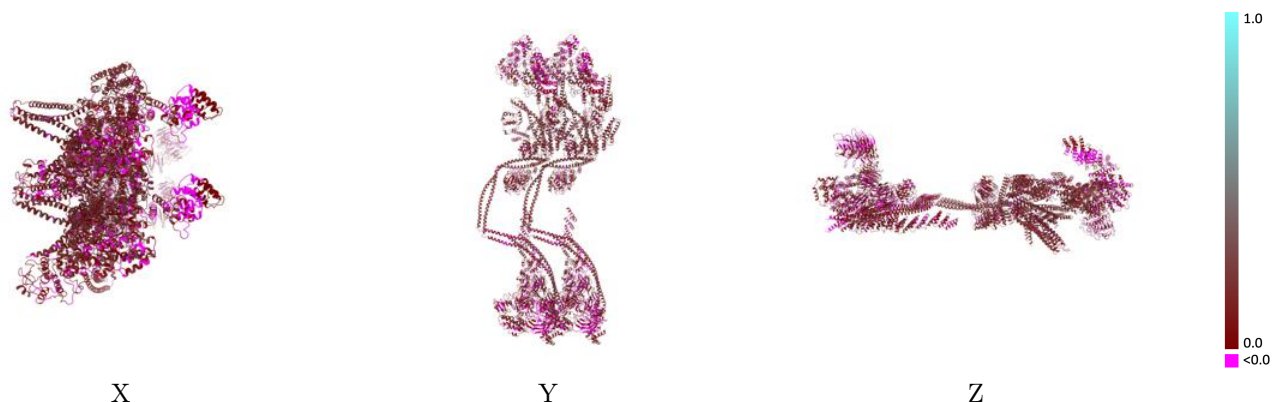
This section contains information regarding the fit between EMDB map EMD-15977 and PDB model 8BD7. Per-residue inclusion information can be found in section 3 on page 7.

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



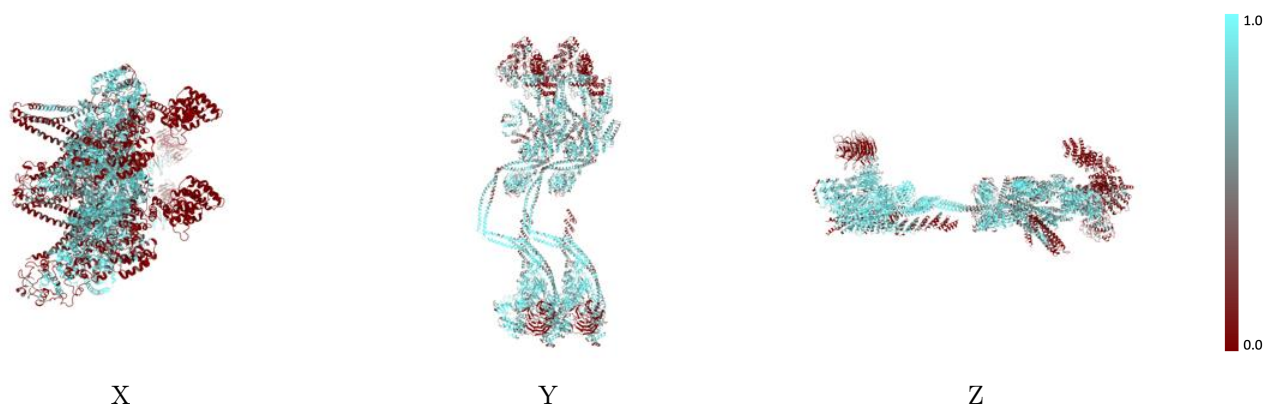
The images above show the 3D surface view of the map at the recommended contour level 0.466 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



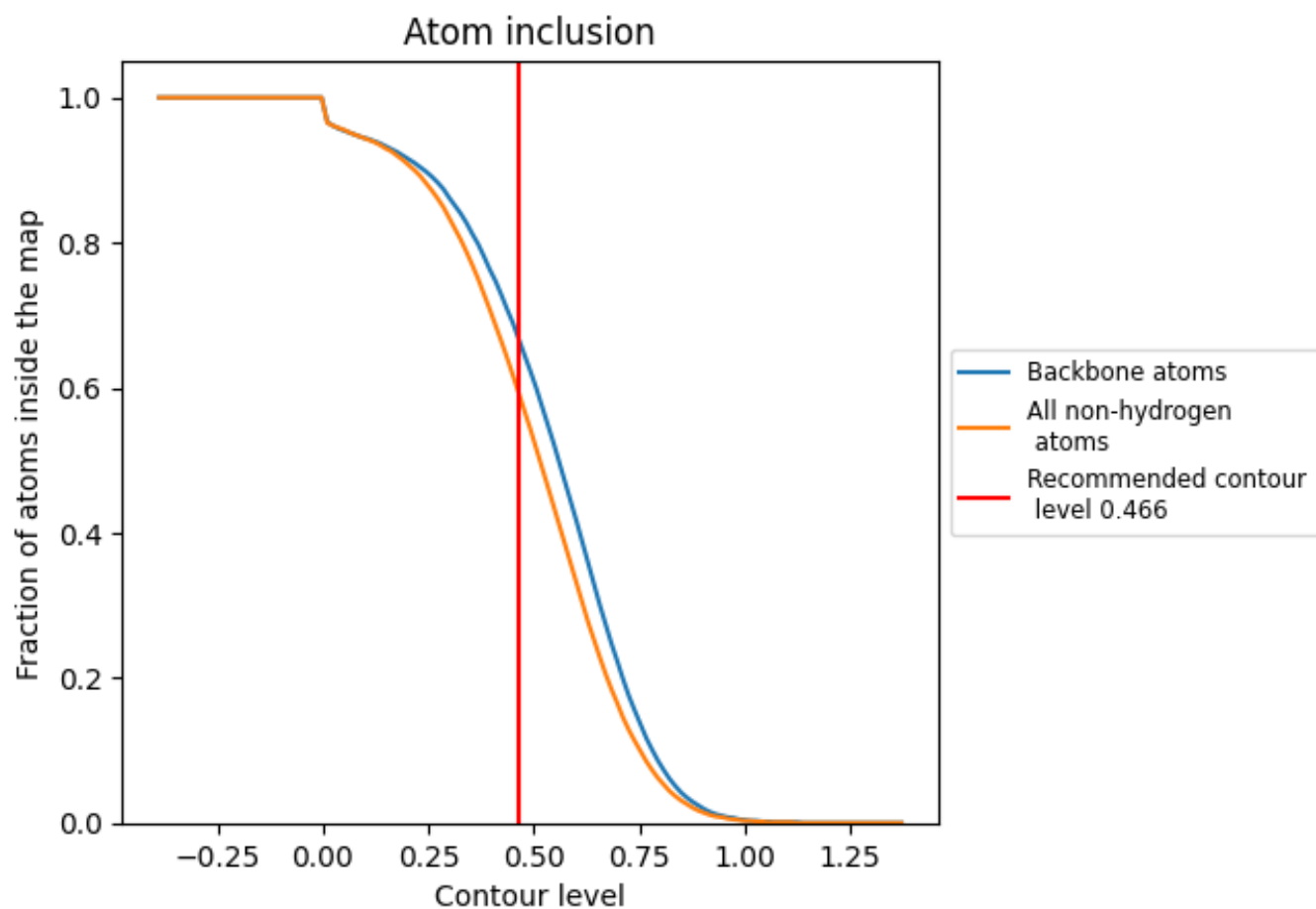
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.0400
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

