



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 02:50 AM UTC

PDB ID : 8Y6Q / pdb_00008y6q
EMDB ID : EMD-38995
Title : Structure of the Dark/Dronc complex
Authors : Tian, L.; Li, Y.; Shi, Y.
Deposited on : 2024-02-03
Resolution : 7.00 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:

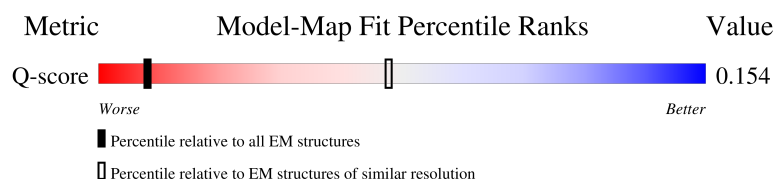
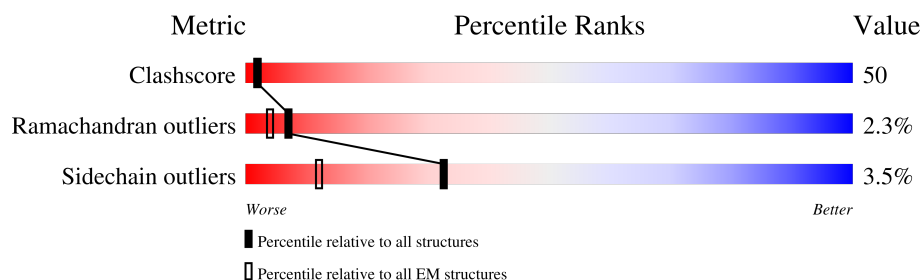
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 7.00 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	483 (6.50 - 7.50)

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	H	1237	
1	I	1237	
1	J	1237	
1	K	1237	

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Mol	Chain	Length	Quality of chain
1	L	1237	
1	M	1237	
1	O	1237	
1	Q	1237	
2	A	102	
2	B	102	
2	C	102	
2	D	102	
2	E	102	
2	F	102	
2	G	102	
2	N	102	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 75726 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 Apaf-1 related killer DARK.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	1068	Total	C	N	O	S	0	0
			8621	5529	1452	1593	47		
1	J	1074	Total	C	N	O	S	0	0
			8672	5562	1460	1603	47		
1	L	1072	Total	C	N	O	S	0	0
			8656	5553	1458	1598	47		
1	M	1066	Total	C	N	O	S	0	0
			8607	5522	1447	1591	47		
1	O	1064	Total	C	N	O	S	0	0
			8592	5511	1446	1588	47		
1	Q	1066	Total	C	N	O	S	0	0
			8608	5520	1450	1591	47		
1	I	1072	Total	C	N	O	S	0	0
			8658	5556	1457	1598	47		
1	K	1064	Total	C	N	O	S	0	0
			8592	5513	1445	1587	47		

- Molecule 2 is a protein called Caspase Dronc.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	102	Total	C	N	O	S	0	0
			840	522	160	152	6		
2	A	102	Total	C	N	O	S	0	0
			840	522	160	152	6		
2	B	102	Total	C	N	O	S	0	0
			840	522	160	152	6		
2	C	102	Total	C	N	O	S	0	0
			840	522	160	152	6		
2	D	102	Total	C	N	O	S	0	0
			840	522	160	152	6		
2	E	102	Total	C	N	O	S	0	0
			840	522	160	152	6		
2	F	102	Total	C	N	O	S	0	0
			840	522	160	152	6		

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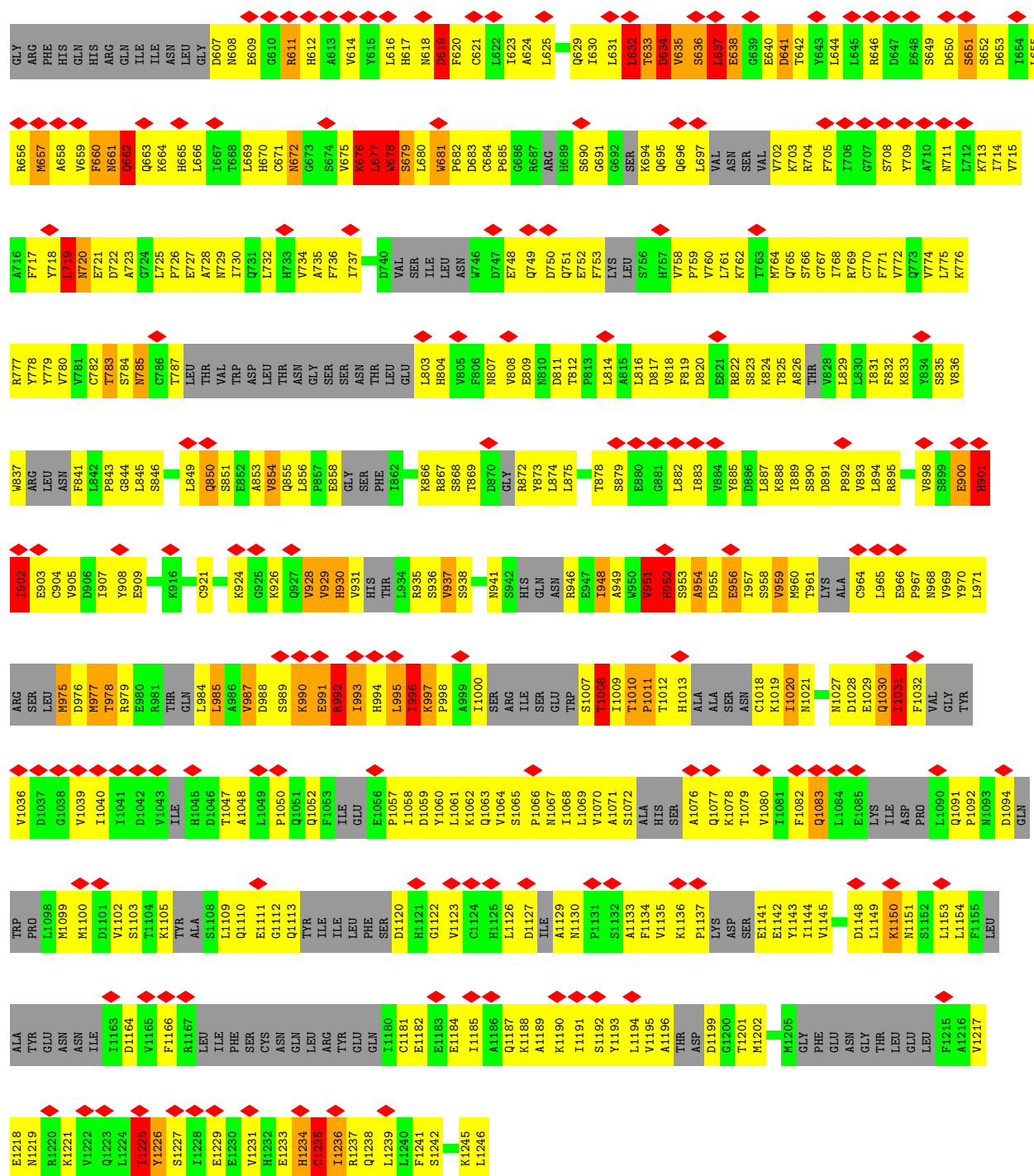
Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	102	Total	C	N	O	S	0	0
			840	522	160	152	6		

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: Apaf-1 related killer DARK

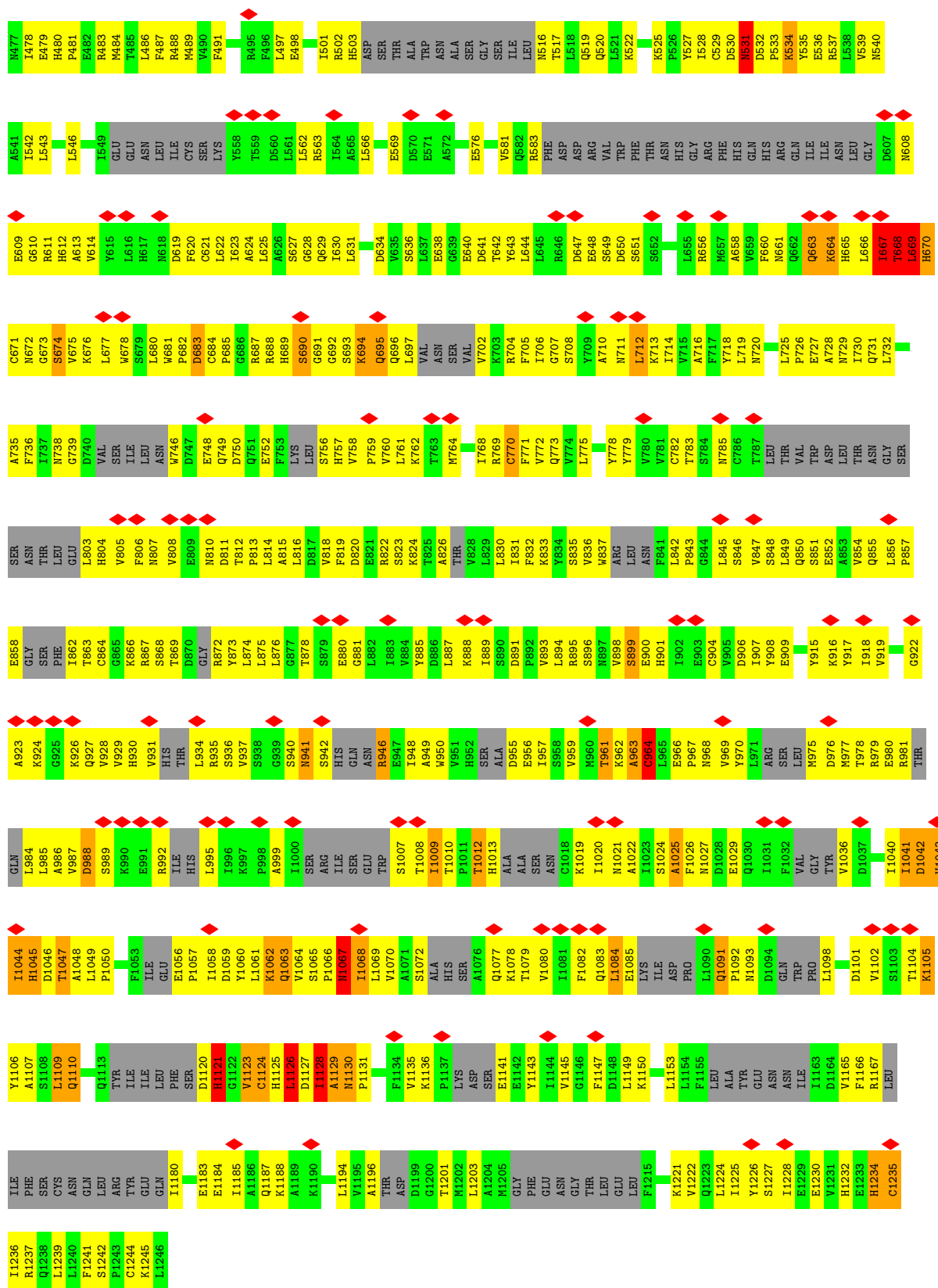




• Molecule 1: Apaf-1 related killer DARK

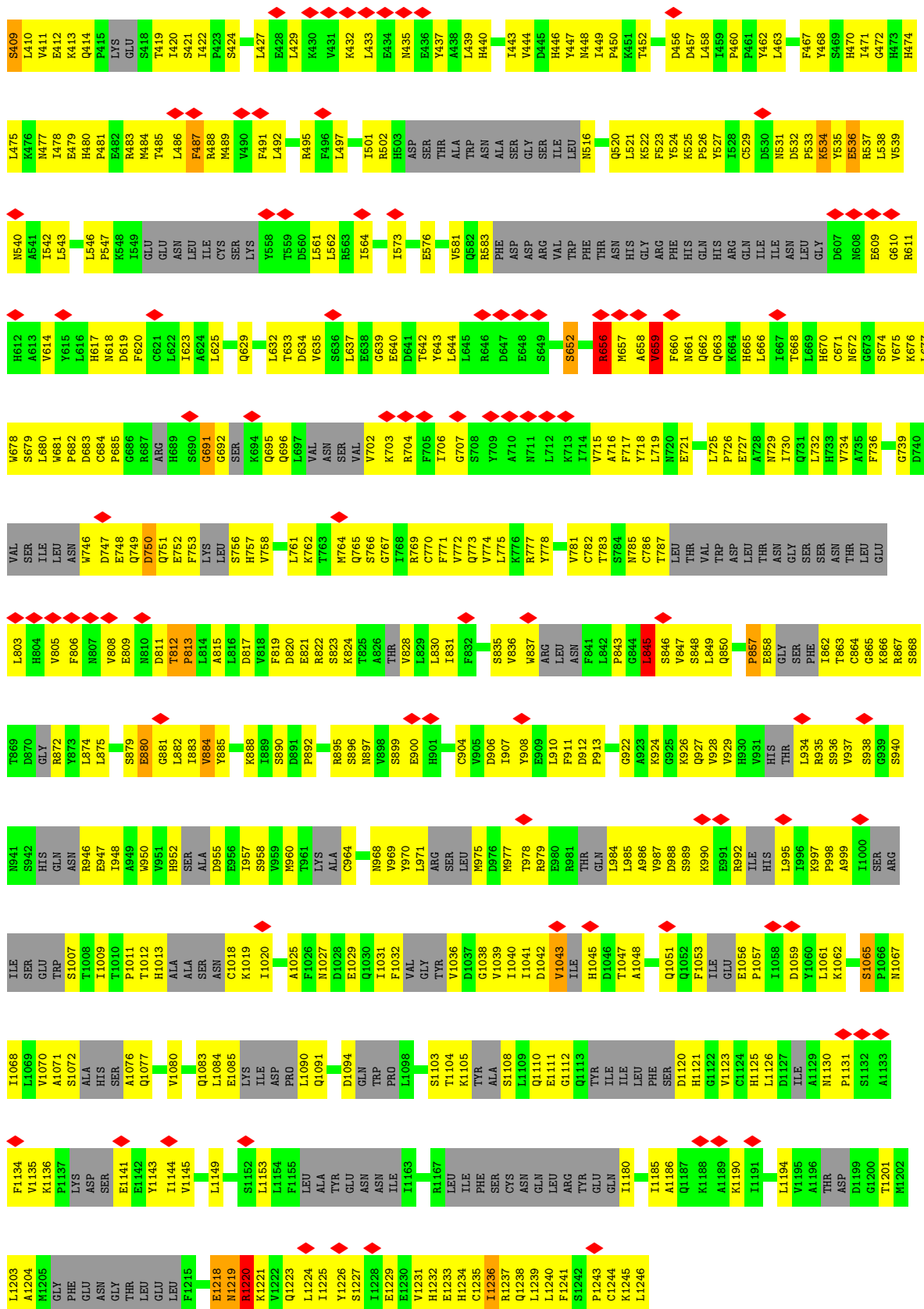


E909	L845	N785	G724	K664	G1N	I528	Q465	V401	V438	T266	L200	L138	V77
L910	S846	C786	L725	H665	I1E	C529	Y466	Y402	D339	R267	Y201	L139	E76
F911	V847	T787	F726	L666	ASN	D530	F467	N403	N340	R268	Q202	E140	E79
P913	S848	L787	E727	T667	LEU	N531	Y468	K404	W341	R269	I203	L141	V80
V914	L849	THR	A728	T668	GLY	D532	S469	L405	N345	Q270	D204	R142	R82
Y915	K850	VAL	N729	L669	P607	P533	H470	H406	C346	T271	I207	P143	I93
K916	S851	TRP	I730	H670	M608	K534	I471	K407	D347	T272	W207	A144	N84
Y917	S852	ASP	L732	C671	G612	E535	H474	S409	K348	T273	T208	K145	Y85
I918	A853	LEU	H733	N672	H612	R537	L475	L410	L349	S209	T209	K146	Y86
V919	V854	THR	V734	S674	A613	L538	K476	V411	T350	R210	S211	L147	K86
L920	K855	ASN	A735	V675	G614	I542	H477	E412	T351	T279	D212	L148	F87
C921	L856	GLY	F736	K676	V615	L543	L478	Q414	I352	T280	H213	L149	L88
A923	E858	SER	W737	W678	L616	I546	H480	P415	E354	T281	H214	V152	M89
	GLY	SER	N738	S679	H617	L549	H482	GLU	S356	L285	S215	G154	S90
K926	PHE	THR	G739	W681	N618	GLU	R483	T419	L357	D286	K218	G155	P91
Q927	T862	LEU	D740	W682	D619	GLU	R484	T420	L358	H287	L219	G156	K93
V929	T863	GLU	V741	P682	F620	ASN	L485	S421	V359	H288	L220	K157	T94
H930	C864	L803	S742	D683	C621	ILE	L486	I422	L360	Q290	H221	G157	E95
V931	G865	W805	I743	P685	L622	CYS	F487	P423	E361	M290	H222	G158	Q96
HIS	K866	W806	L744	G686	T623	SER	R488	S424	L362	T291	I221	T158	R97
THR	R867	N807	W745	R687	A624	ILE	F488	I425	L363	T292	H222	G159	Q98
L934	S868	W808	W746	P688	L625	GLY	R489	Y426	Y365	L293	I224	G160	P99
R935	T869	W809	D747	G688	A626	LYS	Y490	I426	Y366	T294	S223	G161	S100
S936	D870	SER	E748	S689	S627	Y558	F491	L427	Y367	D295	L224	G162	M101
V937	GLY	ASN	Q749	S690	G628	L562	R495	E428	K367	R229	L228	G163	R104
S938	R872	THR	D750	G691	Q629	R563	F496	L429	N368	R230	L229	G164	M105
	L873	SER	F752	G692	L630	R567	L497	K430	F369	L231	L232	G165	Y106
N941	L874	P813	I753	K694	L631	M567	L498	V431	D370	L232	K233	G166	I107
S942	L875	L814	L632	Q695	T633	D570	E498	K432	L372	L300	S234	G167	E108
HIS	L876	LEU	L633	Q696	D634	E571	Q499	K433	L373	L301	K235	G168	Q109
GLN	L877	L816	L634	Q697	V635	A572	R501	L433	L374	L302	P236	G169	D111
ASN	E880	D817	H757	L697	S636	I573	H503	E434	P375	L303	Y237	G170	R112
R946	G881	W818	W758	VAL	ASN	A573	ASP	N435	P376	K303	E238	G171	L113
E947	L882	F819	P759	SER	VAL	E576	THR	Y437	P377	K304	N239	G172	Y114
I948	G884	D820	W760	VAL	D641	E576	THR	Y438	S378	R309	C240	G173	N115
A949	Y885	E821	L761	K703	D642	V581	ALA	L439	A379	L317	L241	G174	D116
W950	D886	R822	T762	R704	T643	D582	TRP	H440	H380	T318	L242	G175	N117
V951	L887	S823	T763	W705	L644	R583	ALA	R441	P382	T319	V243	G176	Q118
H952	K888	T825	Q765	F706	L645	PHE	SER	S442	T383	N320	L244	G177	V119
ALA	I889	A826	S766	T706	R646	ASP	GLY	T443	I384	P321	L245	G178	F120
D955	S890	G707	G767	S708	D647	ASP	SER	V444	L385	R322	N246	G179	A121
E956	L894	K828	I768	S709	D648	ARG	SER	D445	L386	R323	Q247	G180	Y123
V959	R895	L829	R769	A710	S649	VAL	LEU	H446	S387	R324	Q248	G181	N124
M960	S896	I831	C770	M711	D650	TRP	THR	I449	L388	S325	N249	G182	V125
T961	N897	F832	F771	M712	D651	PHE	THR	P450	I389	L327	A250	G183	S126
LYS	W898	K833	W772	L713	S651	THR	THR	P451	T389	A328	W253	G184	R127
C964	E900	S835	L775	K714	S652	ASN	LEU	T452	PHE	E329	N254	G185	L128
L965	E966	W836	K776	V715	L655	HIS	GLY	T453	ASP	A255	A255	G186	Q129
V967	H901	W837	R777	A716	R656	GLY	ILE	F453	VAL	F256	F256	G187	P130
E903	E903	ARG	W779	F717	W657	ARG	K522	D456	LYS	N257	N257	G188	Y131
Q904	Q904	LEU	W780	Y718	A658	PHE	F523	D457	GLY	L258	L258	G189	L132
V905	V905	ASN	W781	L719	V659	HIS	Y524	L458	ASP	L259	L259	G190	L133
N968	N968	THR	T782	W782	F660	GLN	K525	Y462	THR	C260	C260	G191	L134
V970	V970	L842	T783	E721	N661	HIS	Y526	L463	M399	Q197	Q197	G192	R135
L971	L971	D722	W784	A723	Q663	ARG	Y527	D464	V400	L262	L262	G193	Q136
	Y908	G844								T265		G194	A137

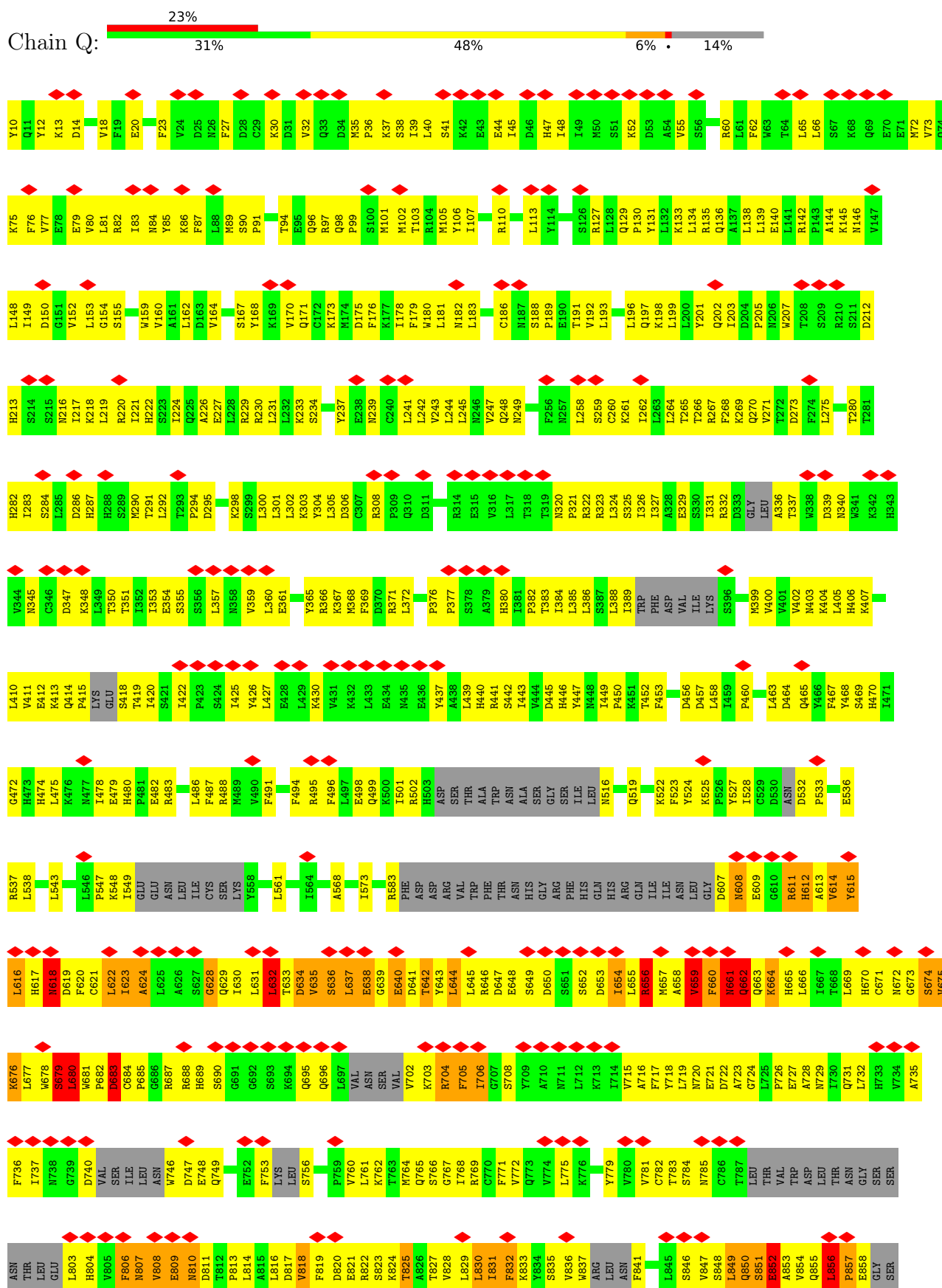


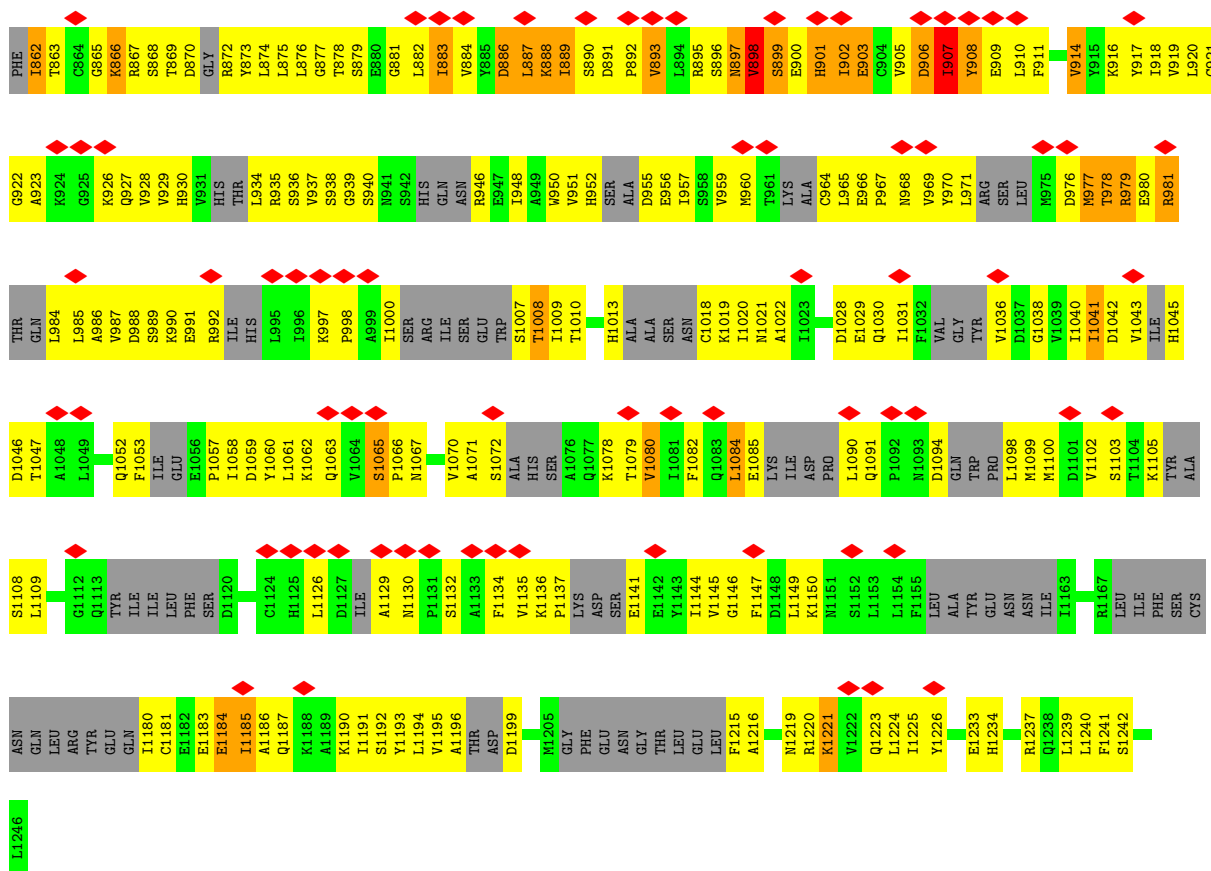
- Molecule 1: Apaf-1 related killer DARK



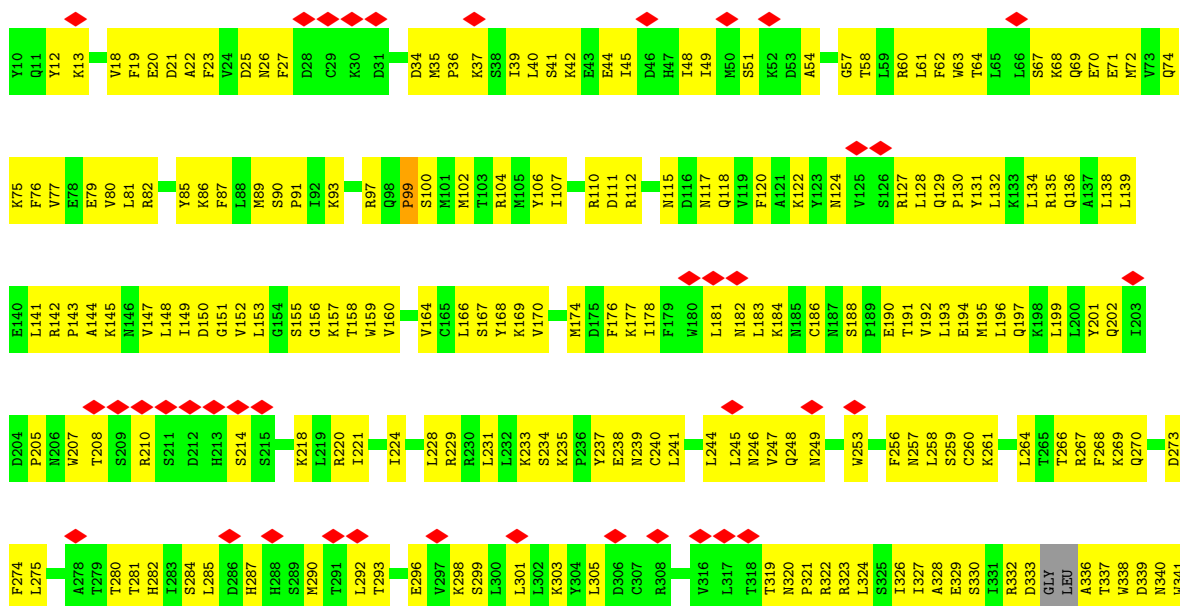


• Molecule 1: Apaf-1 related killer DARK

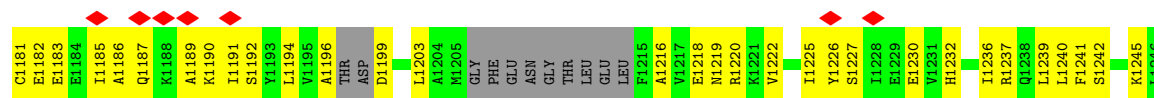




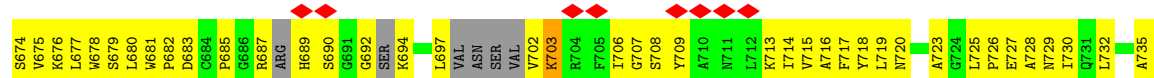
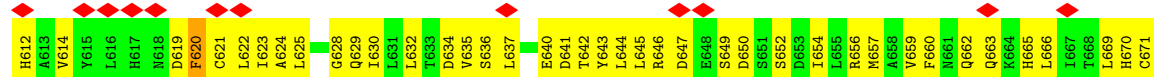
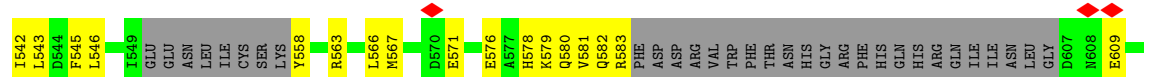
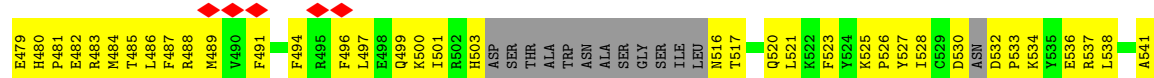
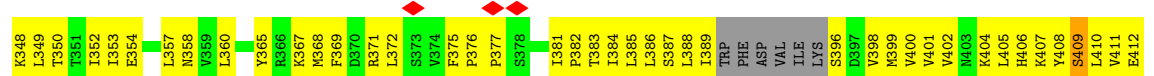
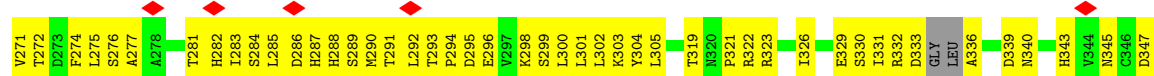
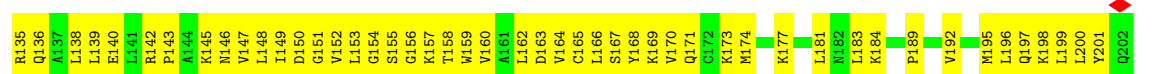
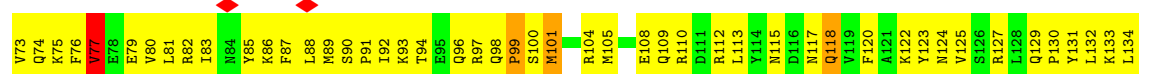
• Molecule 1: Apaf-1 related killer DARK

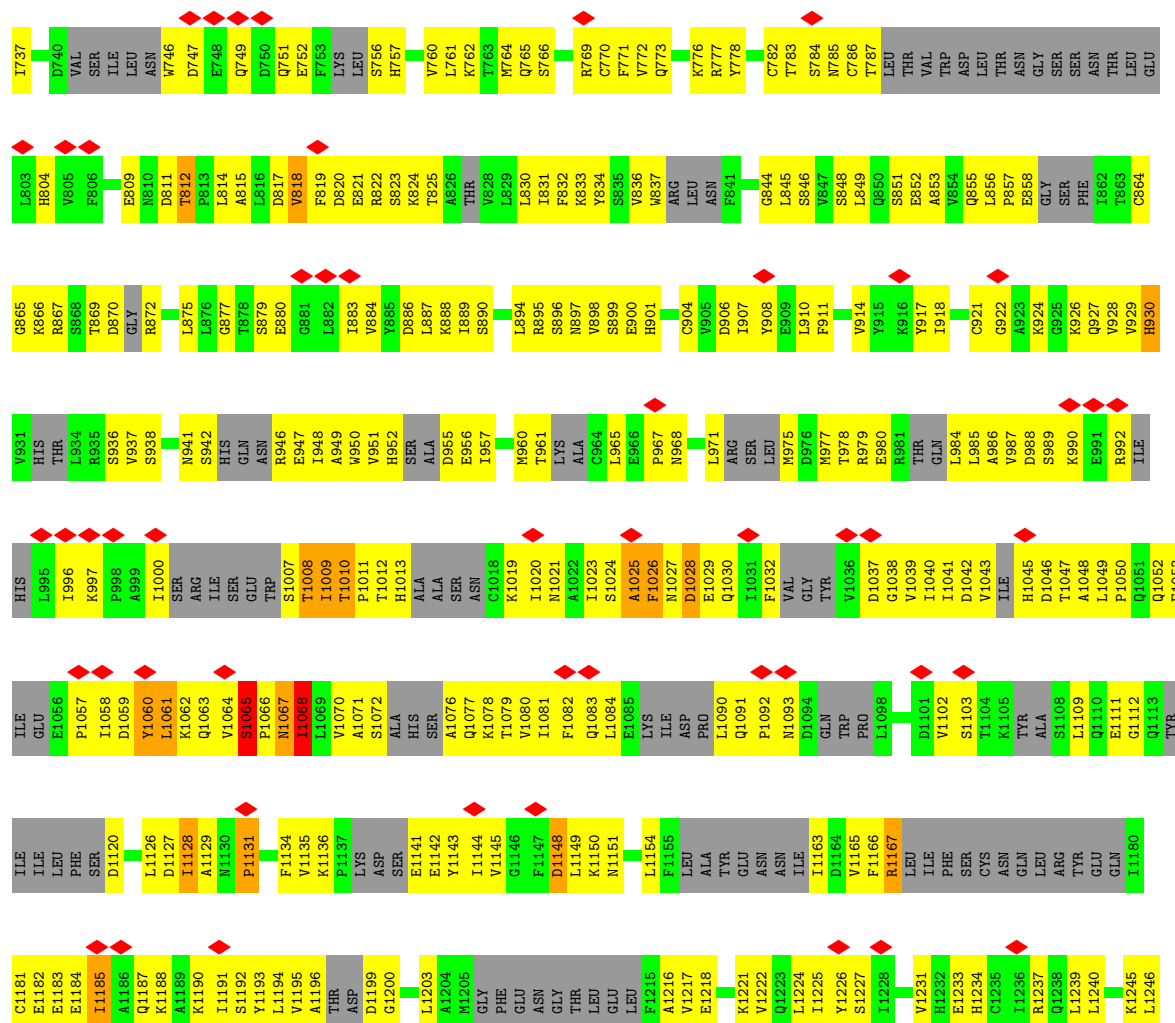




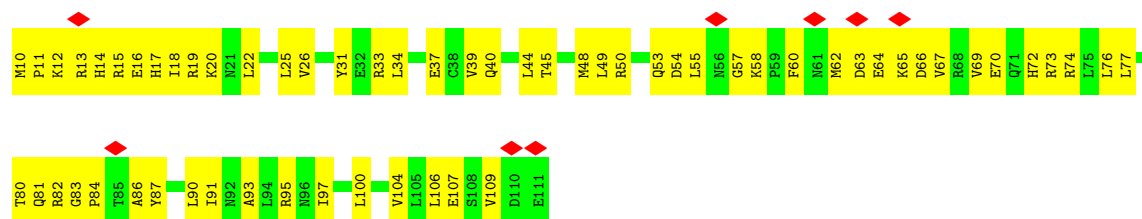
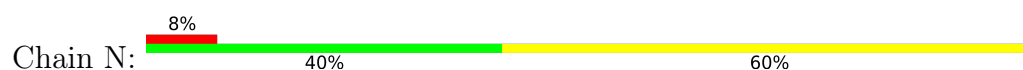


● Molecule 1: Apaf-1 related killer DARK



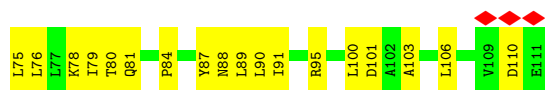


• Molecule 2: Caspase Dronc

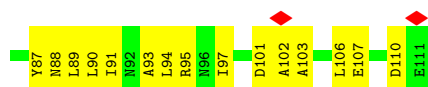
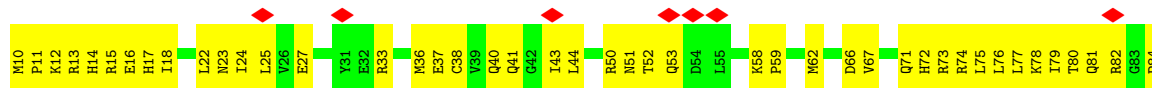
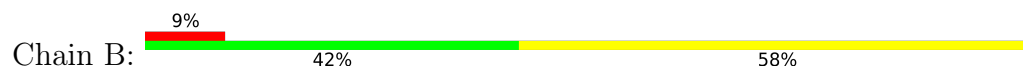


• Molecule 2: Caspase Dronc

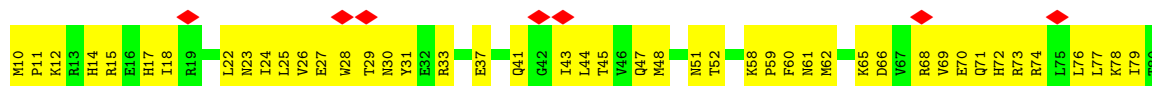




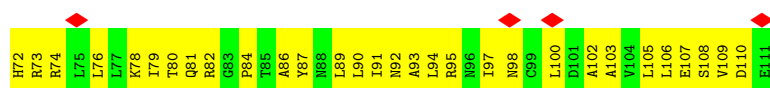
• Molecule 2: Caspase Dronc



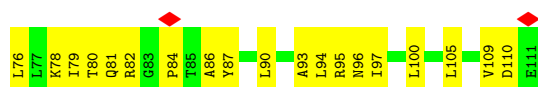
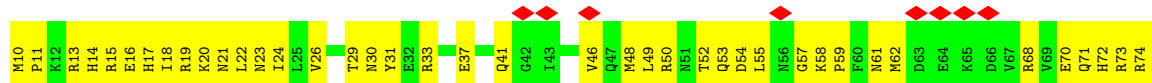
• Molecule 2: Caspase Dronc



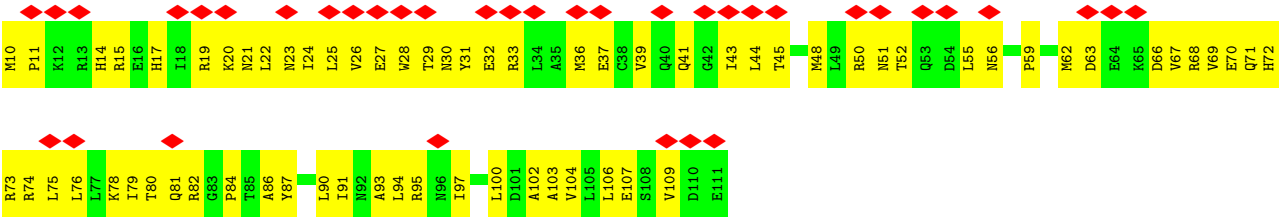
• Molecule 2: Caspase Dronc



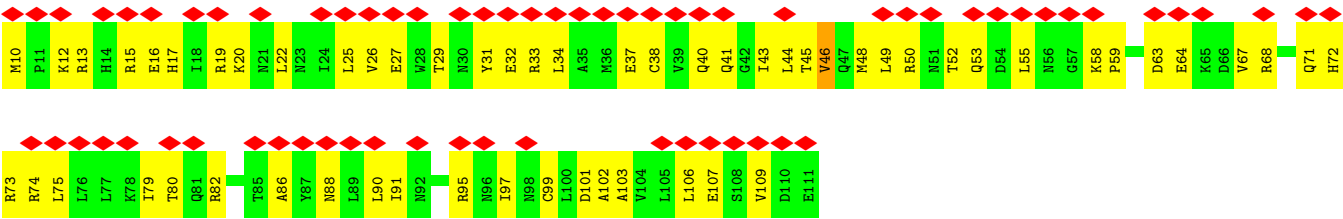
• Molecule 2: Caspase Dronc



• Molecule 2: Caspase Dronc



● Molecule 2: Caspase Dronc



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2710	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.530	Depositor
Minimum map value	-0.233	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	426.80002, 426.80002, 426.80002	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.97, 0.97, 0.97	Depositor

5 Model quality

5.1 Standard geometry

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	H	0.34	2/8768 (0.0%)	0.72	35/11830 (0.3%)
1	I	0.27	0/8809	0.66	21/11890 (0.2%)
1	J	0.35	3/8821 (0.0%)	0.78	34/11907 (0.3%)
1	K	0.31	2/8736 (0.0%)	0.61	13/11783 (0.1%)
1	L	0.29	0/8807	0.70	18/11888 (0.2%)
1	M	0.27	2/8753 (0.0%)	0.57	16/11808 (0.1%)
1	O	0.25	2/8736 (0.0%)	0.54	9/11783 (0.1%)
1	Q	0.31	1/8754 (0.0%)	0.75	42/11810 (0.4%)
2	A	0.25	0/850	0.47	0/1146
2	B	0.16	0/850	0.37	0/1146
2	C	0.16	0/850	0.35	0/1146
2	D	0.19	0/850	0.44	0/1146
2	E	0.18	0/850	0.49	0/1146
2	F	0.15	0/850	0.40	0/1146
2	G	0.20	0/850	0.49	0/1146
2	N	0.17	0/850	0.38	0/1146
All	All	0.29	12/76984 (0.0%)	0.65	188/103867 (0.2%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	661	ASN	C-N	15.61	1.55	1.33
1	K	77	VAL	C-O	-7.55	1.15	1.24
1	J	536	GLU	CA-C	-6.55	1.44	1.52
1	M	1103	SER	N-CA	6.38	1.54	1.46
1	Q	616	LEU	CA-C	6.26	1.56	1.52

The worst 5 of 188 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	1123	VAL	N-CA-C	14.89	123.38	111.62
1	I	773	GLN	N-CA-C	-12.37	97.83	111.07
1	M	1107	ALA	N-CA-C	-11.27	98.92	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	807	ASN	N-CA-C	11.05	117.84	108.78
1	J	977	MET	N-CA-C	10.93	124.18	108.00

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	H	8621	0	8600	1003	0
1	I	8658	0	8647	861	0
1	J	8672	0	8665	1191	0
1	K	8592	0	8575	777	0
1	L	8656	0	8648	915	0
1	M	8607	0	8584	740	0
1	O	8592	0	8570	742	0
1	Q	8608	0	8591	884	0
2	A	840	0	863	69	0
2	B	840	0	863	55	0
2	C	840	0	863	55	0
2	D	840	0	863	73	0
2	E	840	0	863	59	0
2	F	840	0	863	68	0
2	G	840	0	863	57	0
2	N	840	0	863	65	0
All	All	75726	0	75784	7534	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 50.

The worst 5 of 7534 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:977:MET:SD	1:I:989:SER:HB2	1.36	1.66
1:L:964:CYS:SG	1:L:980:GLU:HA	1.43	1.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:620:PHE:CE2	1:J:662:GLN:HB2	1.42	1.54
1:J:620:PHE:CE1	1:J:887:LEU:HD11	1.44	1.52
1:Q:866:LYS:CD	1:Q:876:LEU:HB2	1.38	1.52

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	H	992/1237 (80%)	793 (80%)	173 (17%)	26 (3%)	4	25
1	I	1002/1237 (81%)	843 (84%)	128 (13%)	31 (3%)	3	22
1	J	1004/1237 (81%)	823 (82%)	147 (15%)	34 (3%)	3	21
1	K	984/1237 (80%)	841 (86%)	129 (13%)	14 (1%)	9	40
1	L	1004/1237 (81%)	824 (82%)	156 (16%)	24 (2%)	4	27
1	M	988/1237 (80%)	839 (85%)	128 (13%)	21 (2%)	5	30
1	O	984/1237 (80%)	840 (85%)	127 (13%)	17 (2%)	7	36
1	Q	990/1237 (80%)	812 (82%)	145 (15%)	33 (3%)	3	21
2	A	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
2	B	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
2	C	100/102 (98%)	93 (93%)	7 (7%)	0	100	100
2	D	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
2	E	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
2	F	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
2	G	100/102 (98%)	87 (87%)	12 (12%)	1 (1%)	12	48
2	N	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
All	All	8748/10712 (82%)	7367 (84%)	1180 (14%)	201 (2%)	7	28

5 of 201 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	52	LYS
1	H	99	PRO
1	H	409	SER
1	H	662	GLN
1	H	783	THR

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	H	973/1140 (85%)	917 (94%)	56 (6%)	18	40
1	I	977/1140 (86%)	943 (96%)	34 (4%)	32	53
1	J	980/1140 (86%)	910 (93%)	70 (7%)	13	35
1	K	970/1140 (85%)	957 (99%)	13 (1%)	61	74
1	L	976/1140 (86%)	936 (96%)	40 (4%)	27	48
1	M	971/1140 (85%)	954 (98%)	17 (2%)	51	68
1	O	970/1140 (85%)	959 (99%)	11 (1%)	65	76
1	Q	972/1140 (85%)	918 (94%)	54 (6%)	19	40
2	A	94/94 (100%)	94 (100%)	0	100	100
2	B	94/94 (100%)	94 (100%)	0	100	100
2	C	94/94 (100%)	94 (100%)	0	100	100
2	D	94/94 (100%)	94 (100%)	0	100	100
2	E	94/94 (100%)	94 (100%)	0	100	100
2	F	94/94 (100%)	94 (100%)	0	100	100
2	G	94/94 (100%)	94 (100%)	0	100	100
2	N	94/94 (100%)	94 (100%)	0	100	100
All	All	8541/9872 (86%)	8246 (96%)	295 (4%)	32	53

5 of 295 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Q	862	ILE
1	K	1008	THR
1	Q	889	ILE
1	I	968	ASN
1	J	769	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 192 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	61	ASN
1	Q	850	GLN
2	D	47	GLN
1	Q	197	GLN
1	I	118	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.

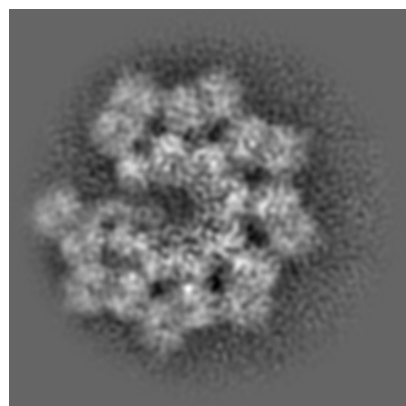
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38995. These allow visual inspection of the internal detail of the map and identification of artifacts.

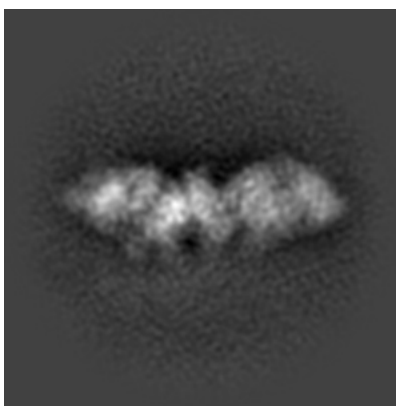
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

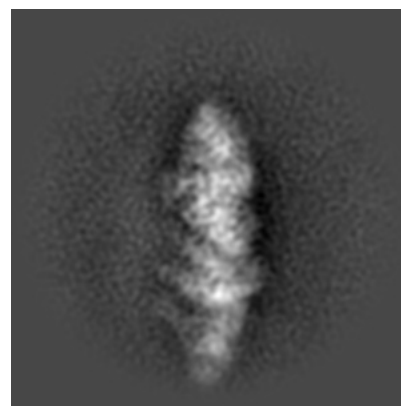
6.1.1 Primary map



X

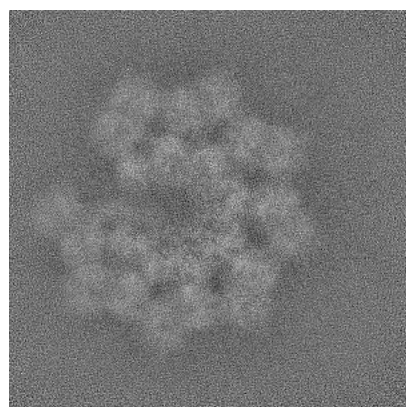


Y

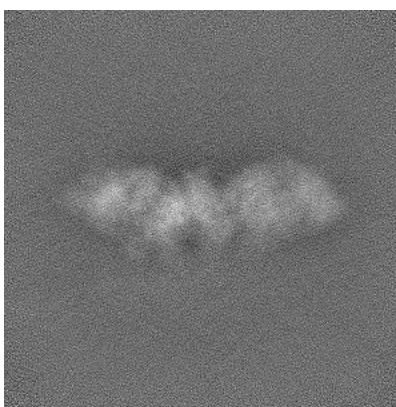


Z

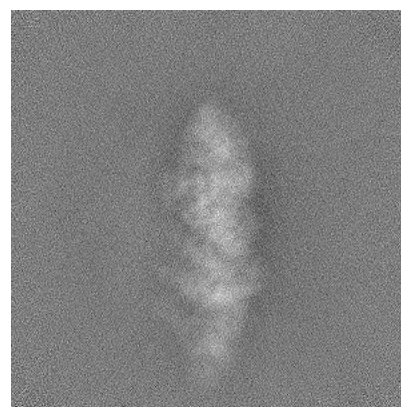
6.1.2 Raw map



X



Y

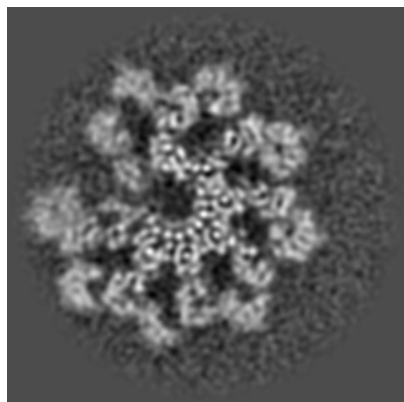


Z

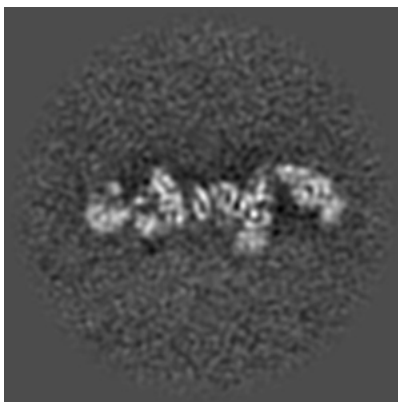
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

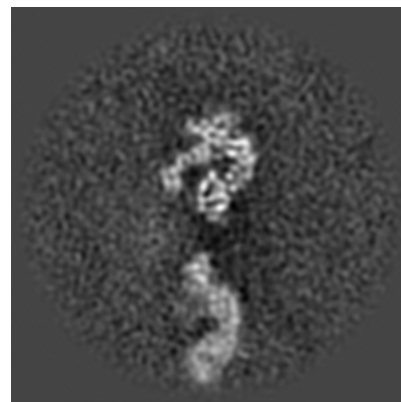
6.2.1 Primary map



X Index: 220

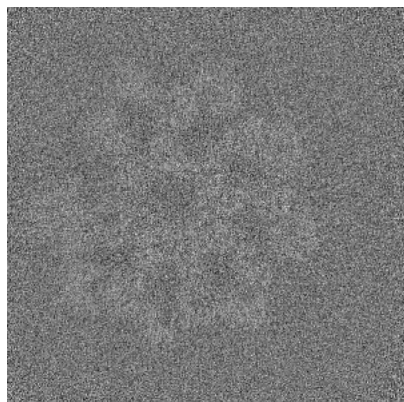


Y Index: 220

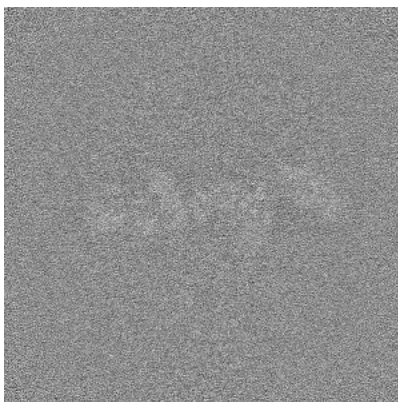


Z Index: 220

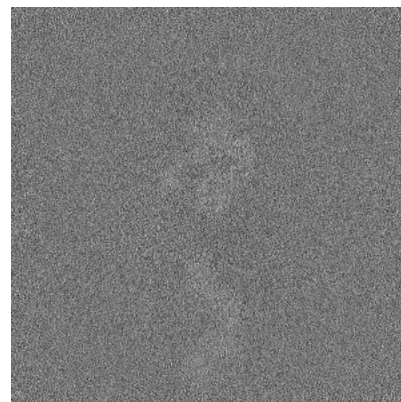
6.2.2 Raw map



X Index: 220



Y Index: 220

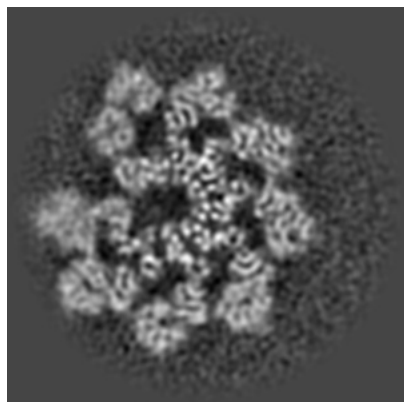


Z Index: 220

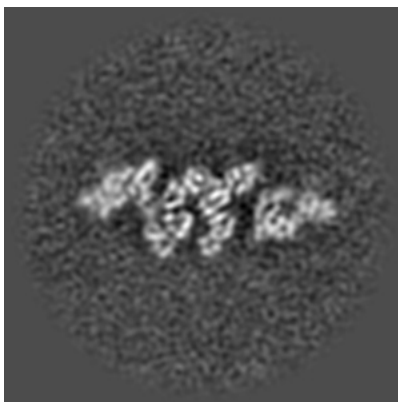
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

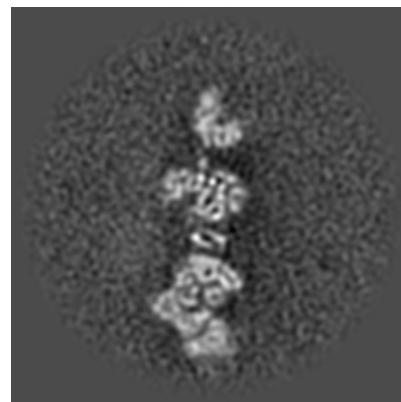
6.3.1 Primary map



X Index: 229

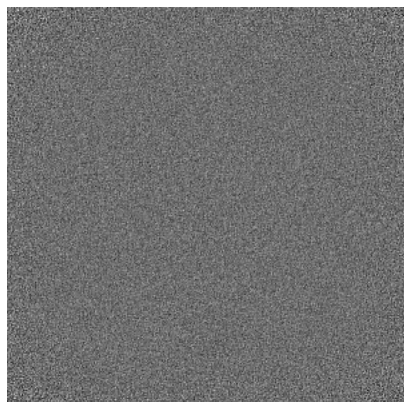


Y Index: 249

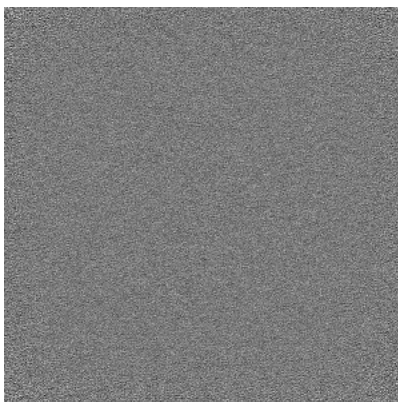


Z Index: 183

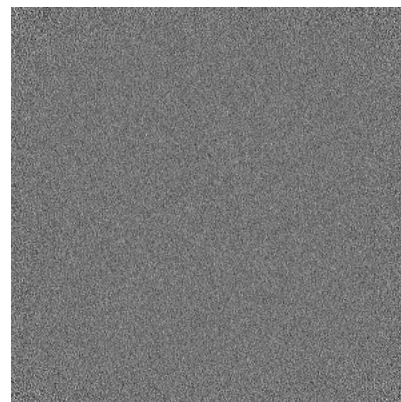
6.3.2 Raw map



X Index: 0



Y Index: 0

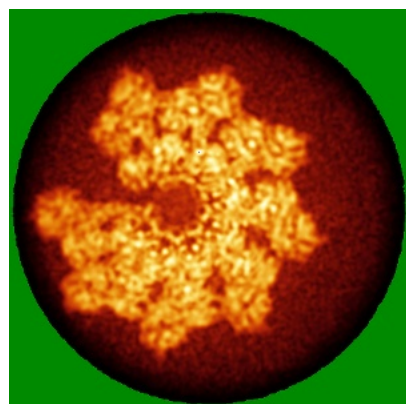


Z Index: 0

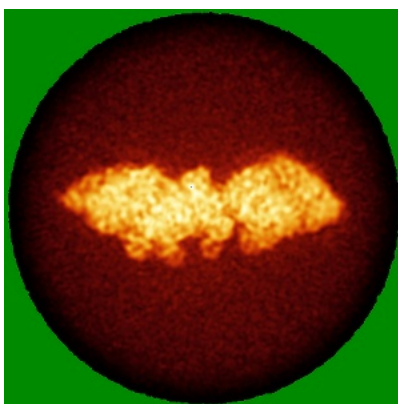
The images above show the largest variance slices of the map in three orthogonal directions.

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

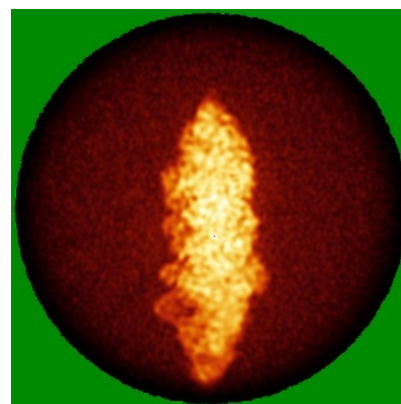
6.4.1 Primary map



X

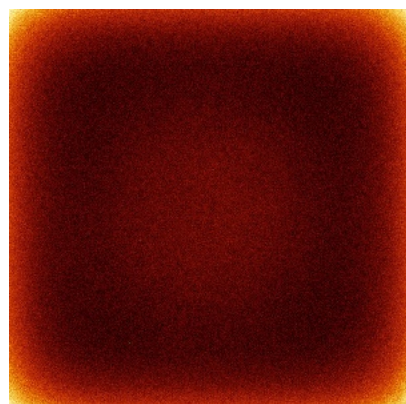


Y

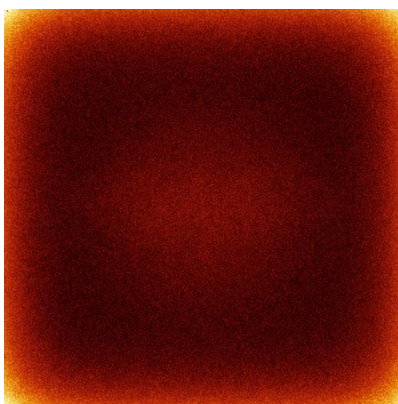


Z

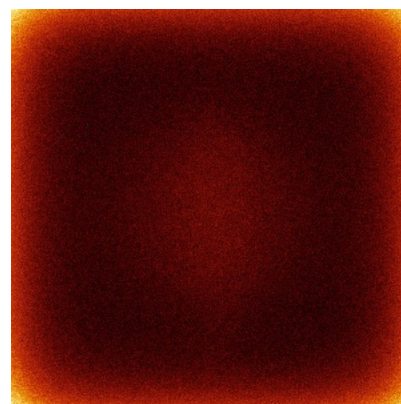
6.4.2 Raw map



X



Y

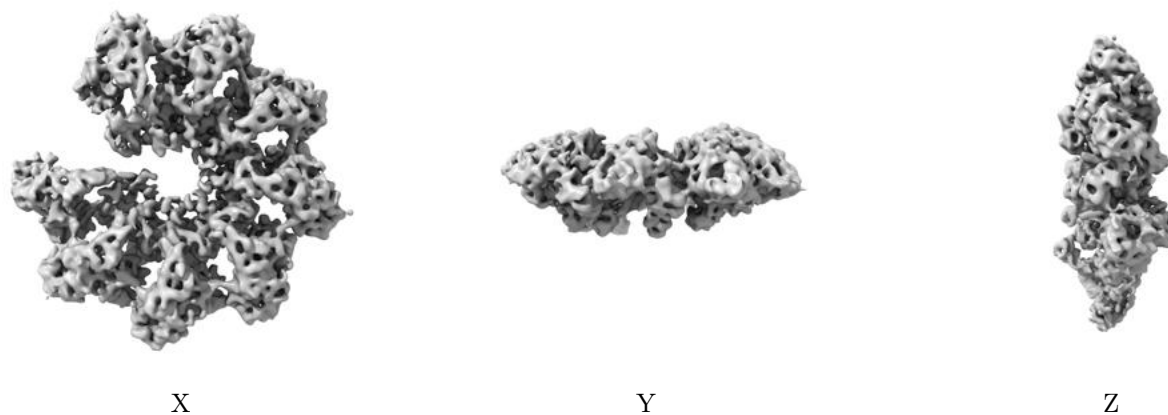


Z

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.

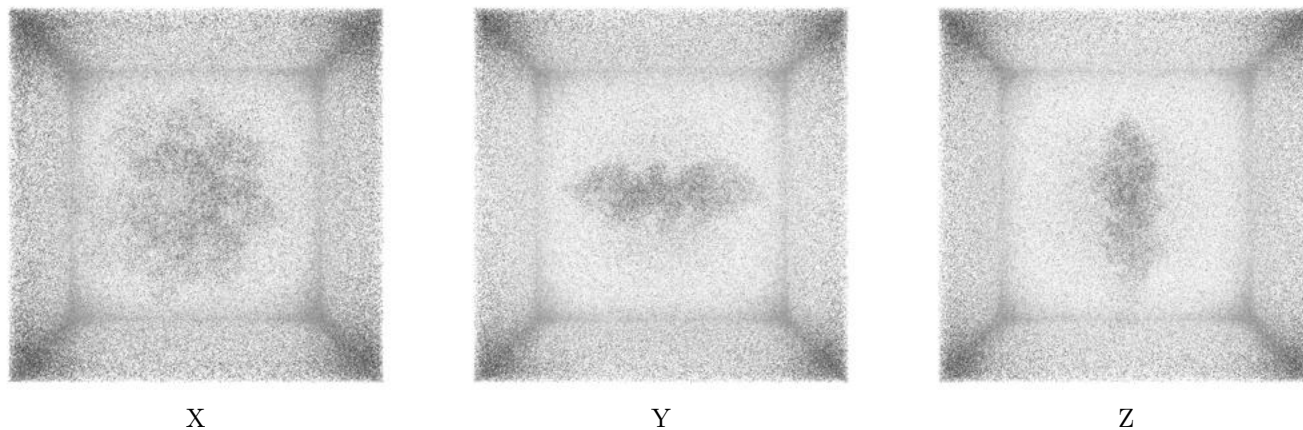
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

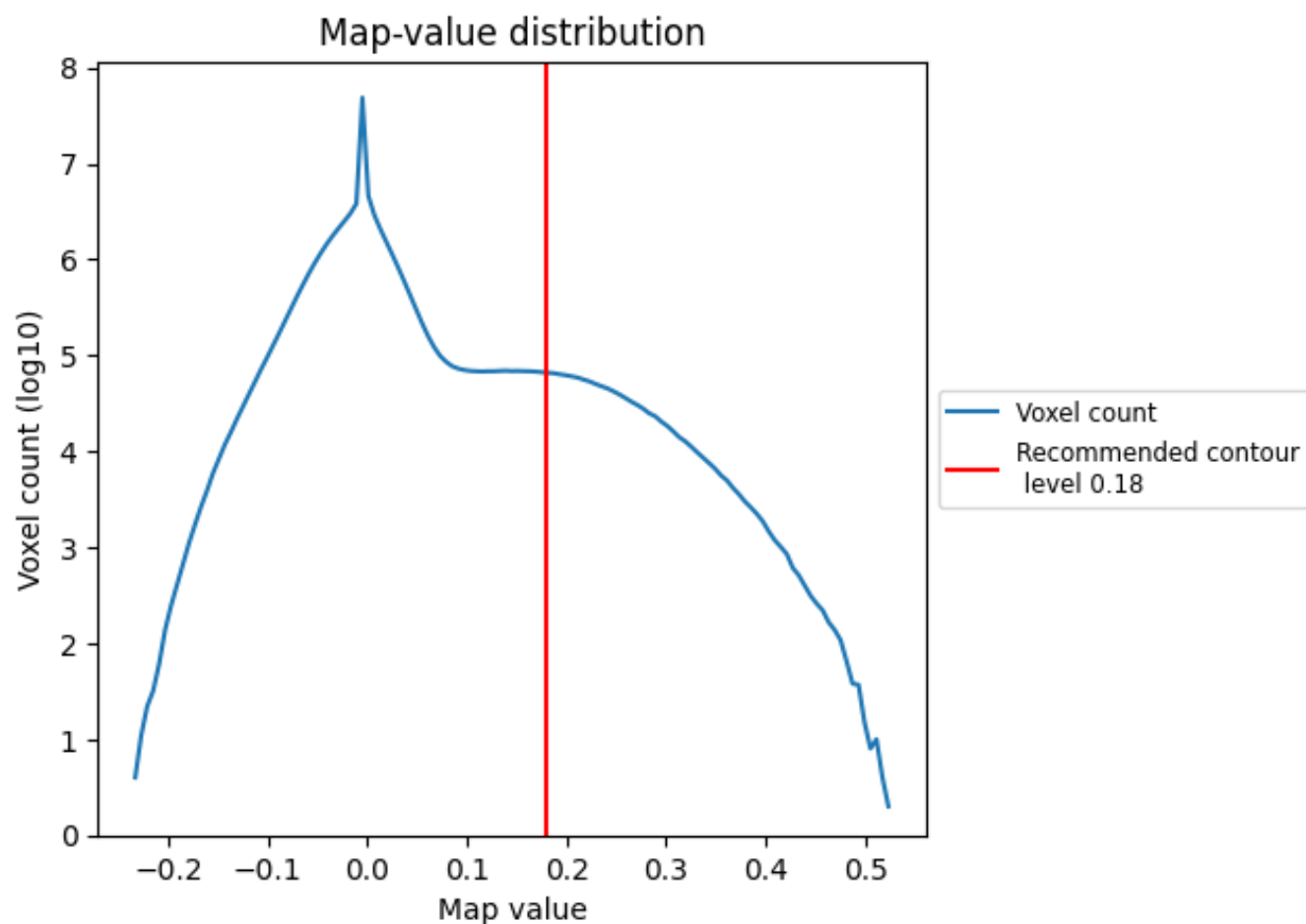
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

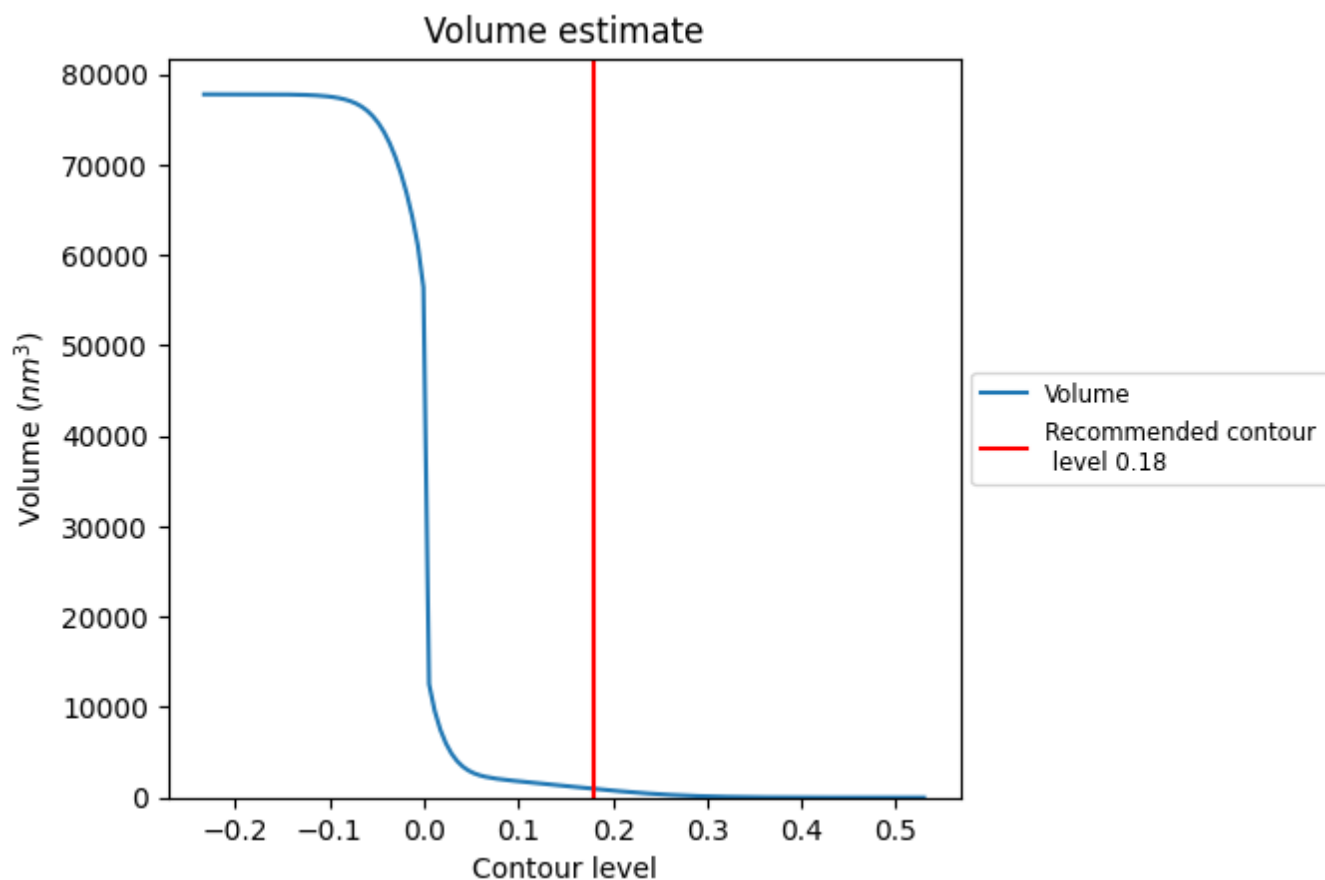
This section contains the results of statistical analysis of the map.

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.

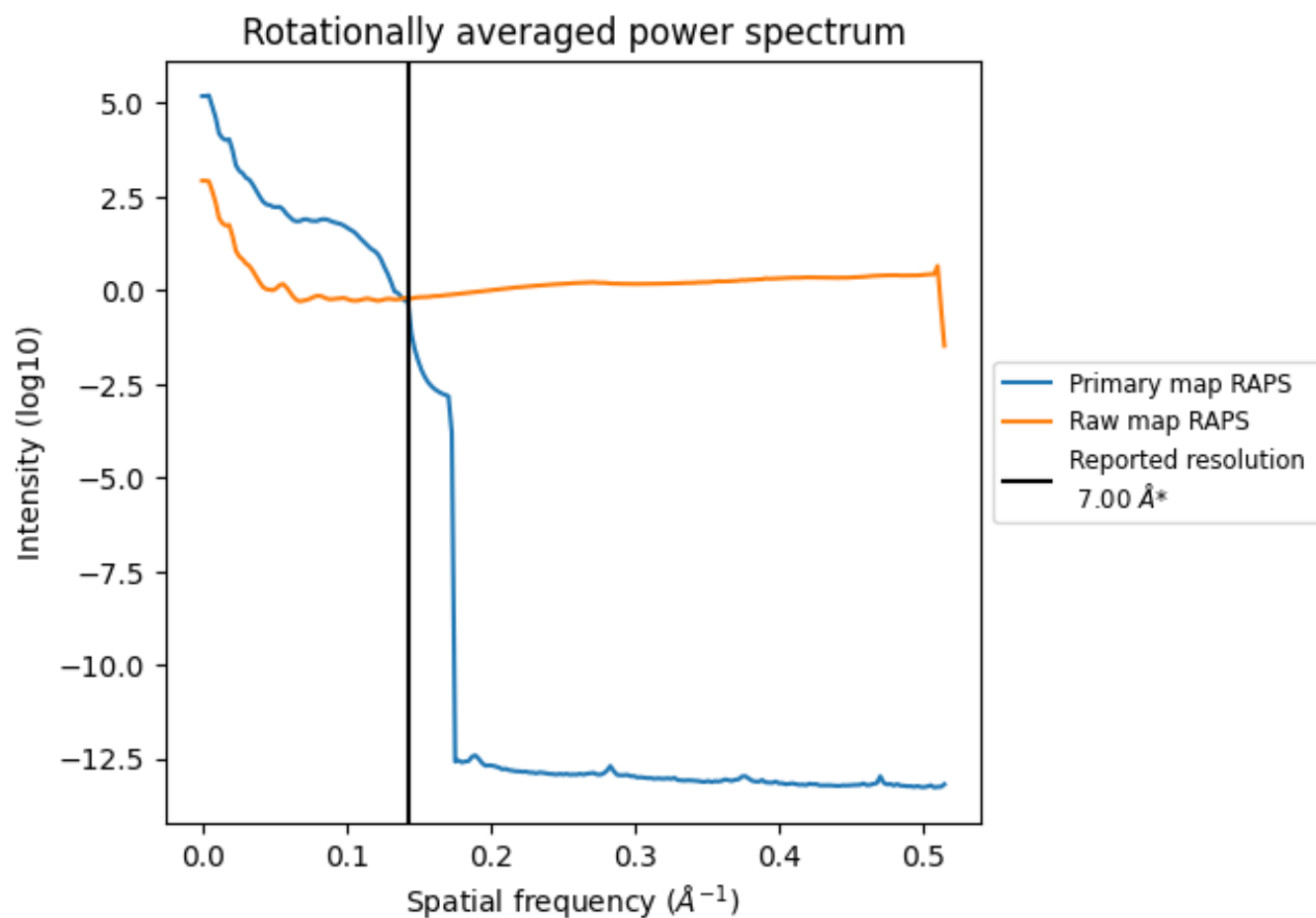
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 968 nm³; this corresponds to an approximate mass of 875 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 ⓘ

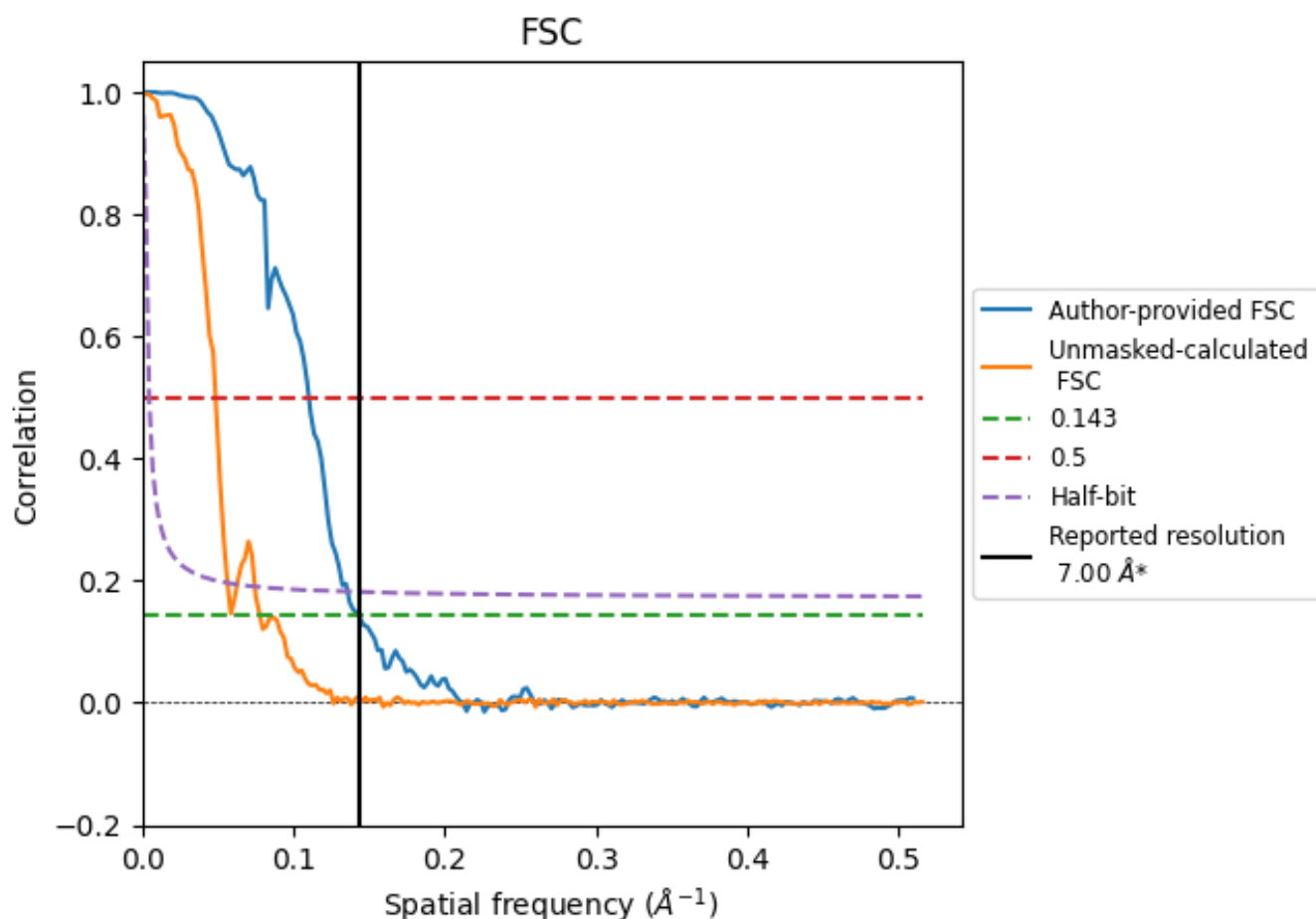


*Reported resolution corresponds to spatial frequency of 0.143 Å⁻¹

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 0.143 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

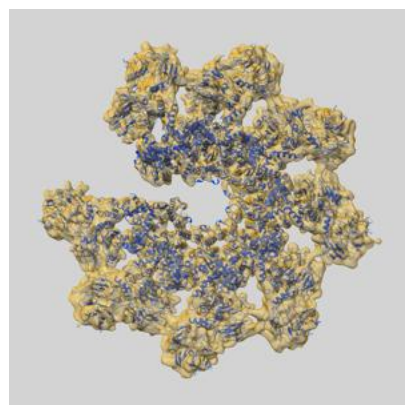
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.00	-	-
Author-provided FSC curve	7.01	9.08	7.37
Unmasked-calculated*	12.87	20.62	17.73

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 12.87 differs from the reported value 7.0 by more than 10 %

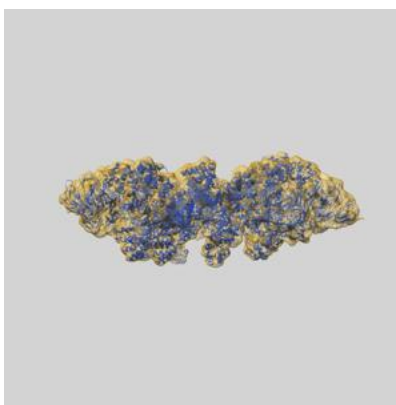
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38995 and PDB model 8Y6Q. Per-residue inclusion information can be found in section [3](#) on page [6](#).

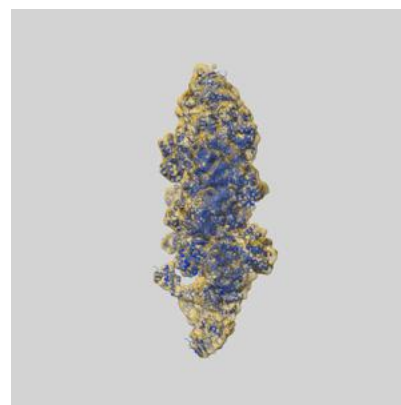
9.1 Map-model overlay [i](#)



X



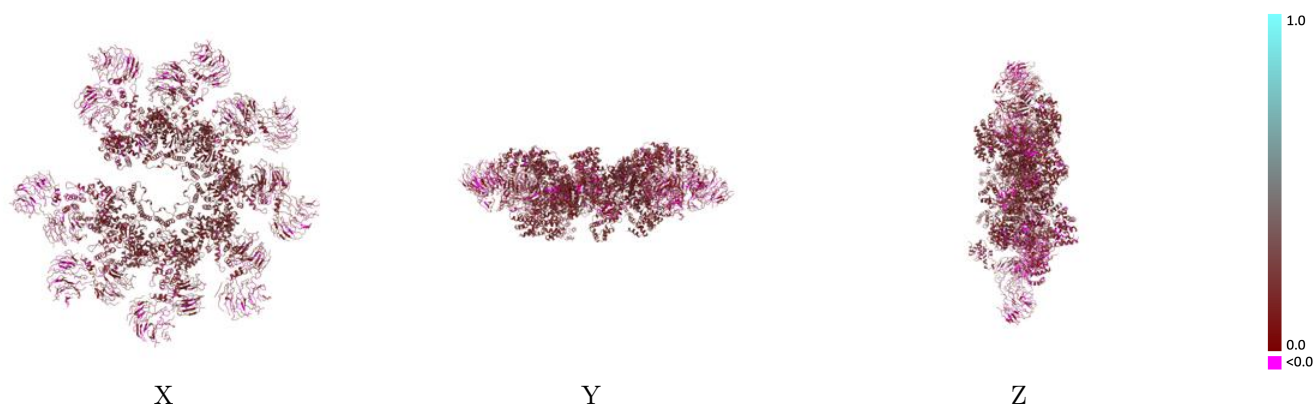
Y



Z

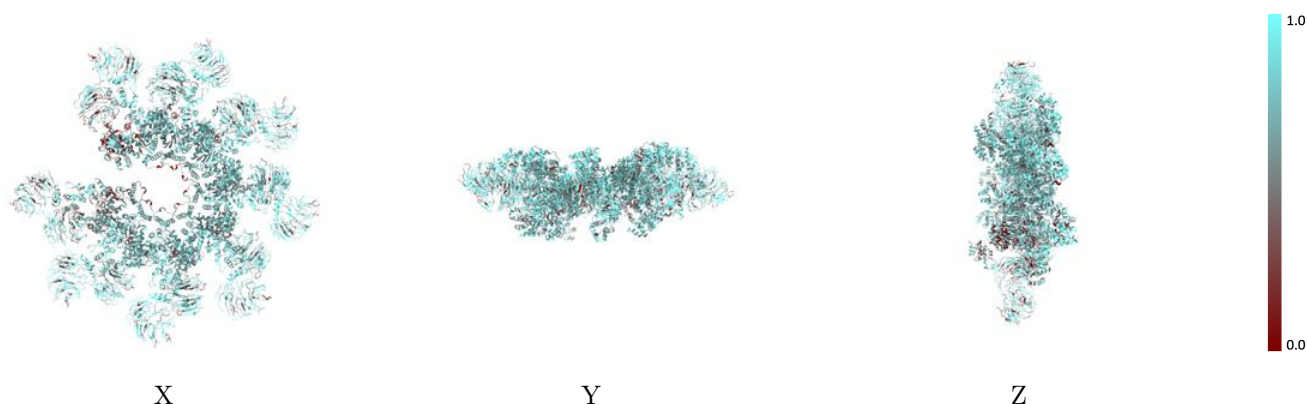
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



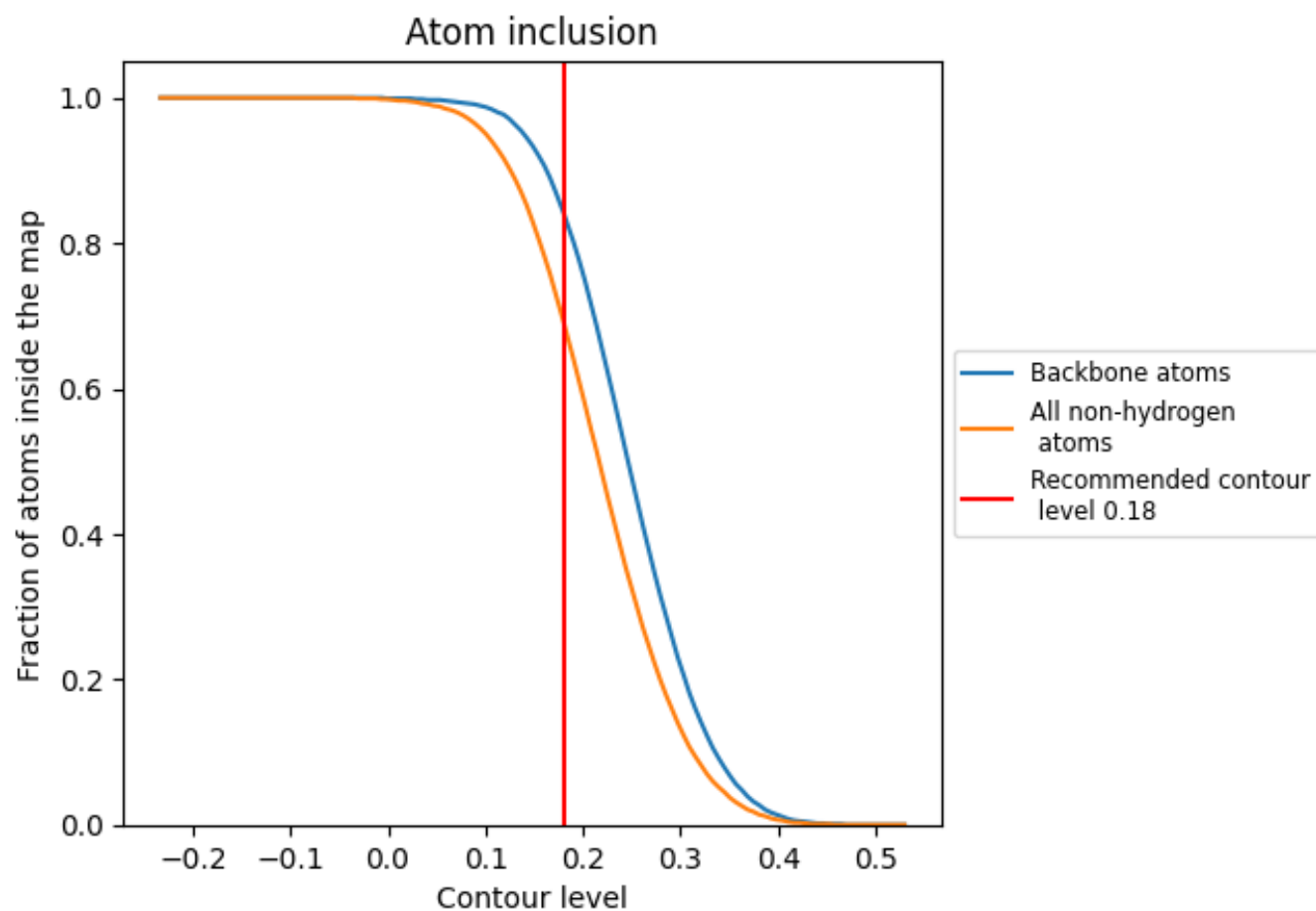
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 69% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6920	 0.1540
A	 0.6550	 0.1840
B	 0.6940	 0.1990
C	 0.7000	 0.1890
D	 0.7230	 0.1940
E	 0.7310	 0.1850
F	 0.5310	 0.1670
G	 0.3330	 0.1390
H	 0.5980	 0.1310
I	 0.7150	 0.1540
J	 0.7330	 0.1560
K	 0.7450	 0.1660
L	 0.7130	 0.1590
M	 0.7260	 0.1600
N	 0.7590	 0.1960
O	 0.7210	 0.1570
Q	 0.6240	 0.1260

