



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:09 AM UTC

PDB ID : 6R83 / pdb_00006r83
EMDB ID : EMD-4750
Title : CryoEM structure and molecular model of squid hemocyanin (Todarodes pacificus , TpH)
Authors : Tanaka, Y.; Kato, S.; Stabrin, M.; Raunser, S.; Matsui, T.; Gatsogiannis, C.
Deposited on : 2019-03-31
Resolution : 5.10 Å(reported)

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

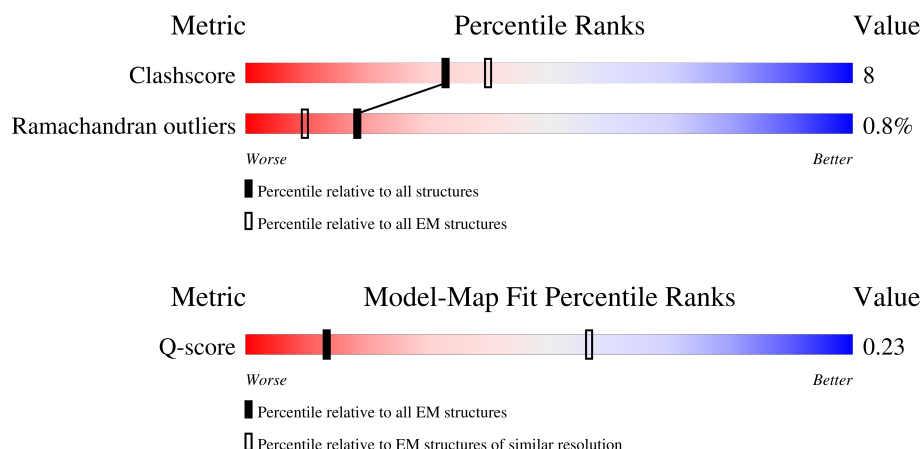
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 5.10 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.



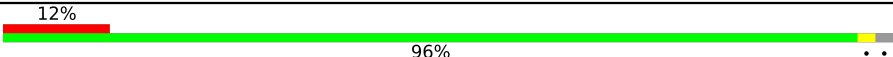
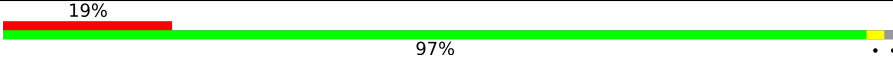
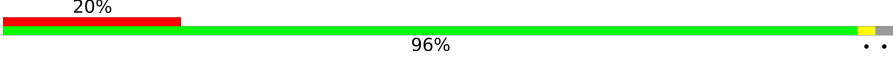
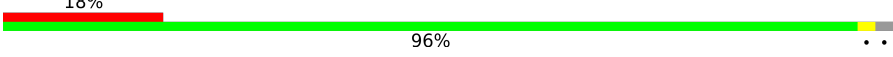
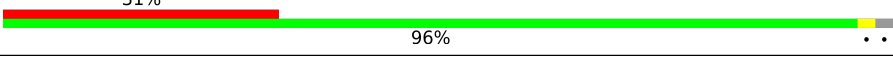
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	844 (4.60 - 5.60)

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	10a	3314	
1	1a	3314	
1	2a	3314	
1	3a	3314	
1	4a	3314	

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Mol	Chain	Length	Quality of chain
1	5a	3314	 12% 96% ..
1	6a	3314	 19% 97% ..
1	7a	3314	 20% 96% ..
1	8a	3314	 18% 96% ..
1	9a	3314	 31% 96% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 161300 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.

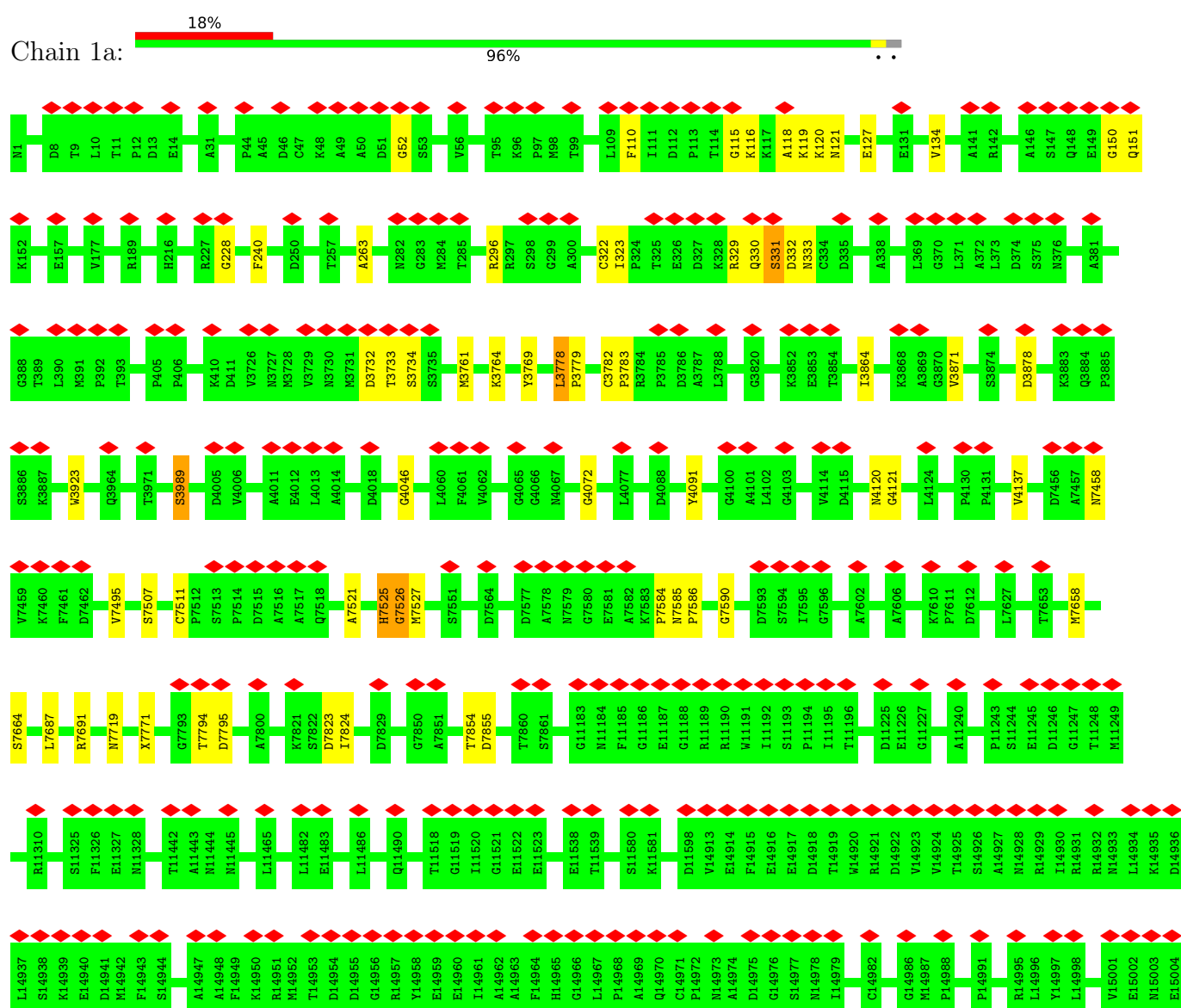
- Molecule 1 is a protein called Hemocyanin subunit 1.

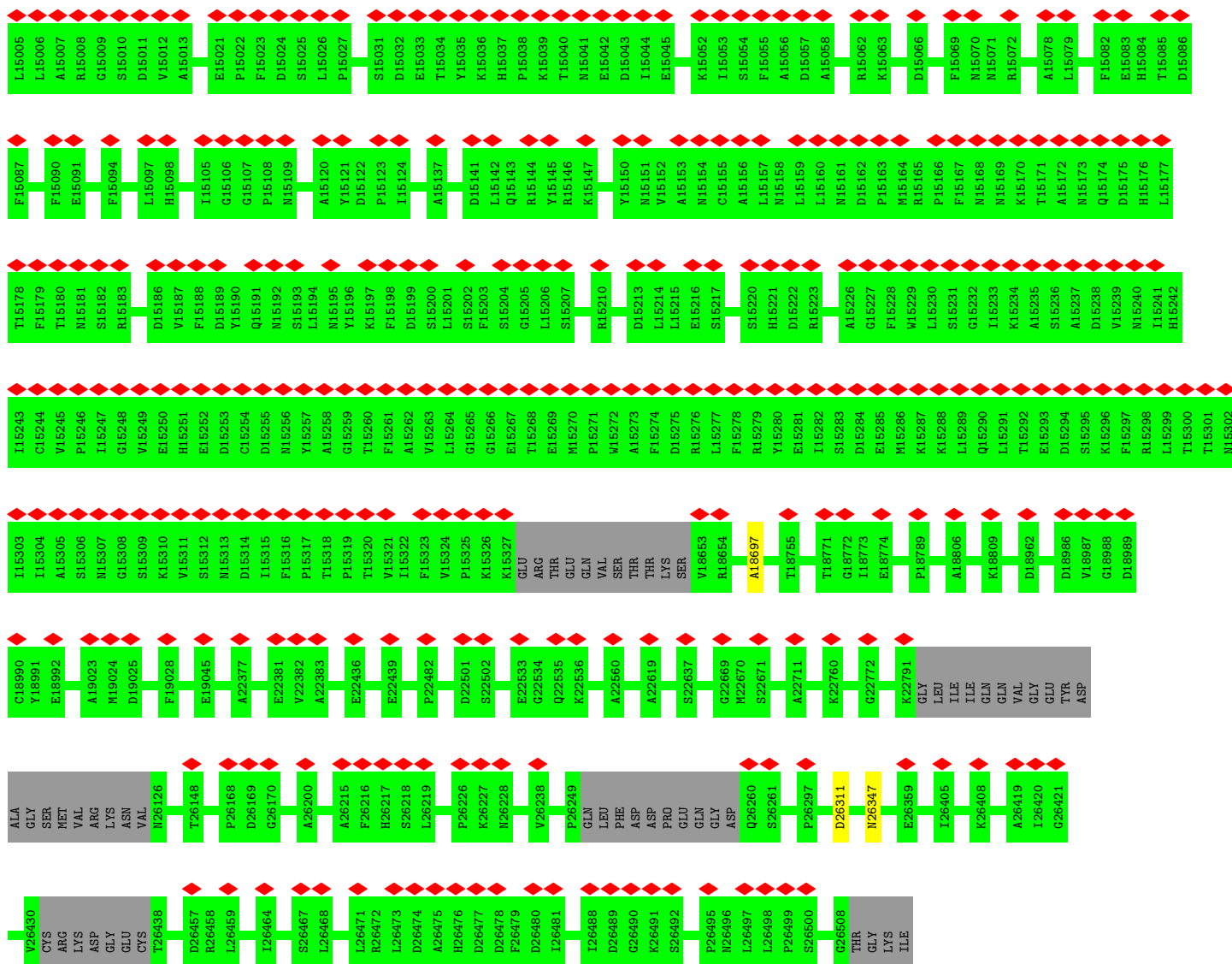
Mol	Chain	Residues	Atoms				AltConf	Trace
1	1a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	2a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	3a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	4a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	5a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	6a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	7a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	8a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	9a	3262	Total 16130	C 9606	N 3262	O 3262	0	0
1	10a	3262	Total 16130	C 9606	N 3262	O 3262	0	0

3 Residue-property plots [i](#)

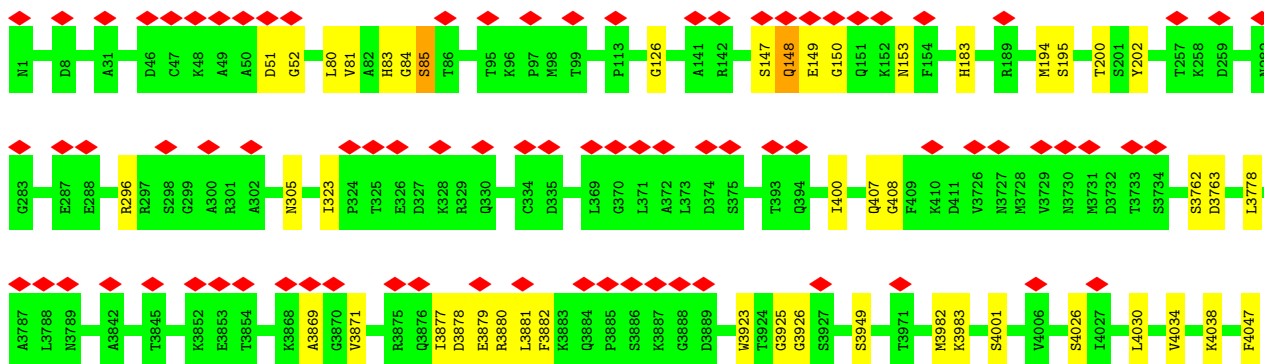
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Hemocyanin subunit 1

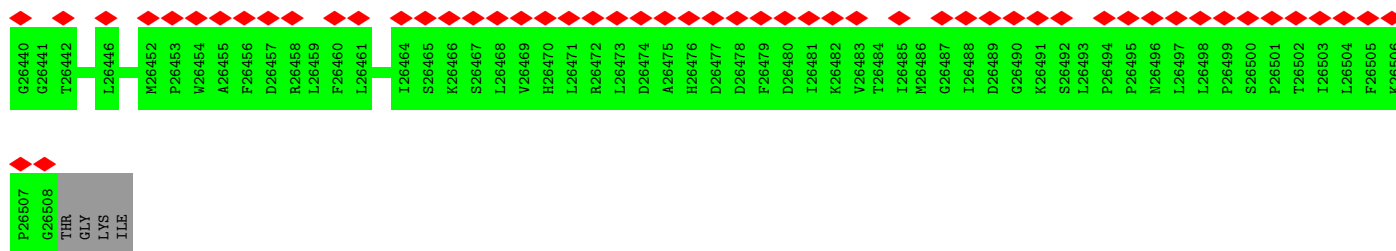




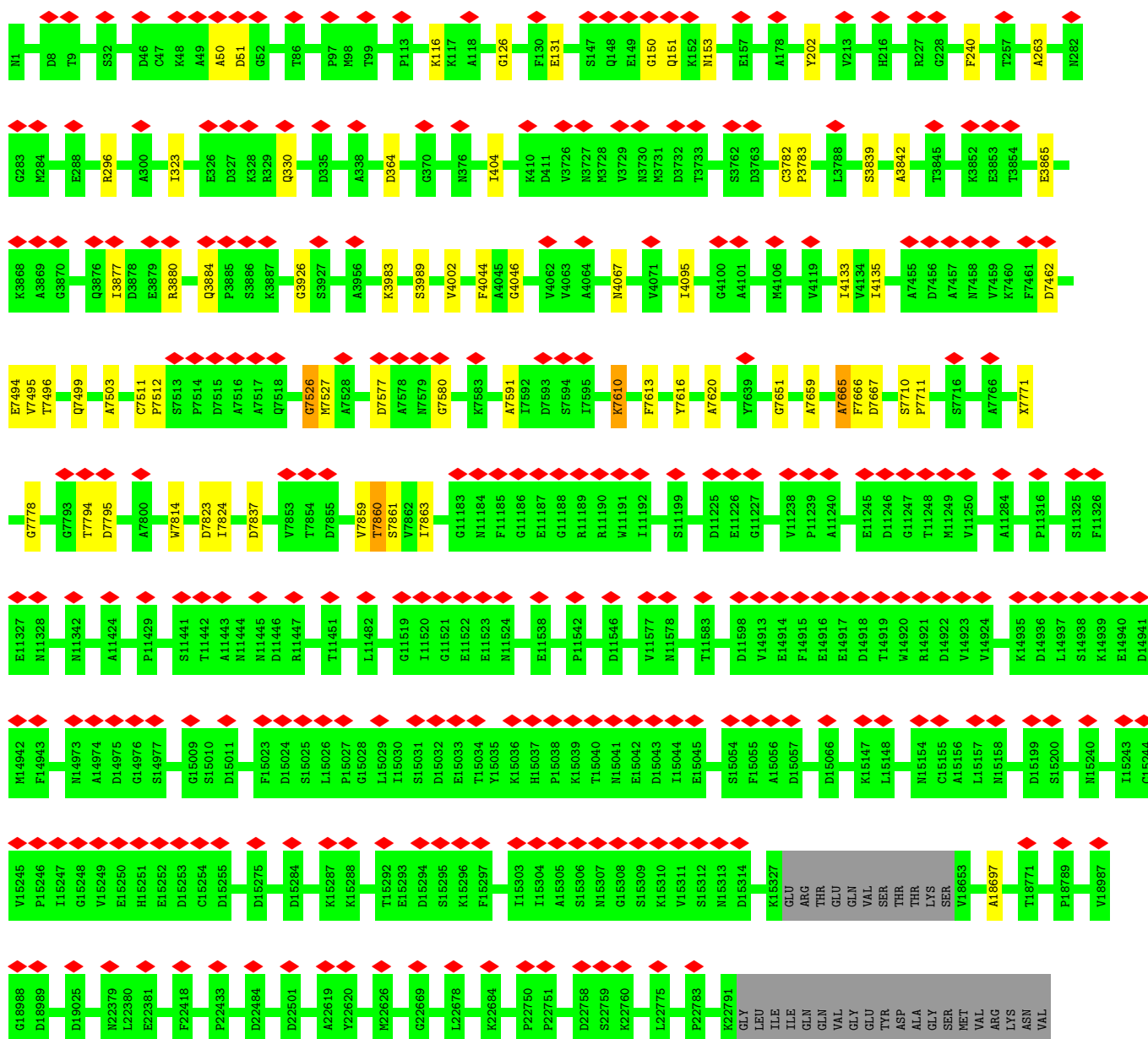
• Molecule 1: Hemocyanin subunit 1

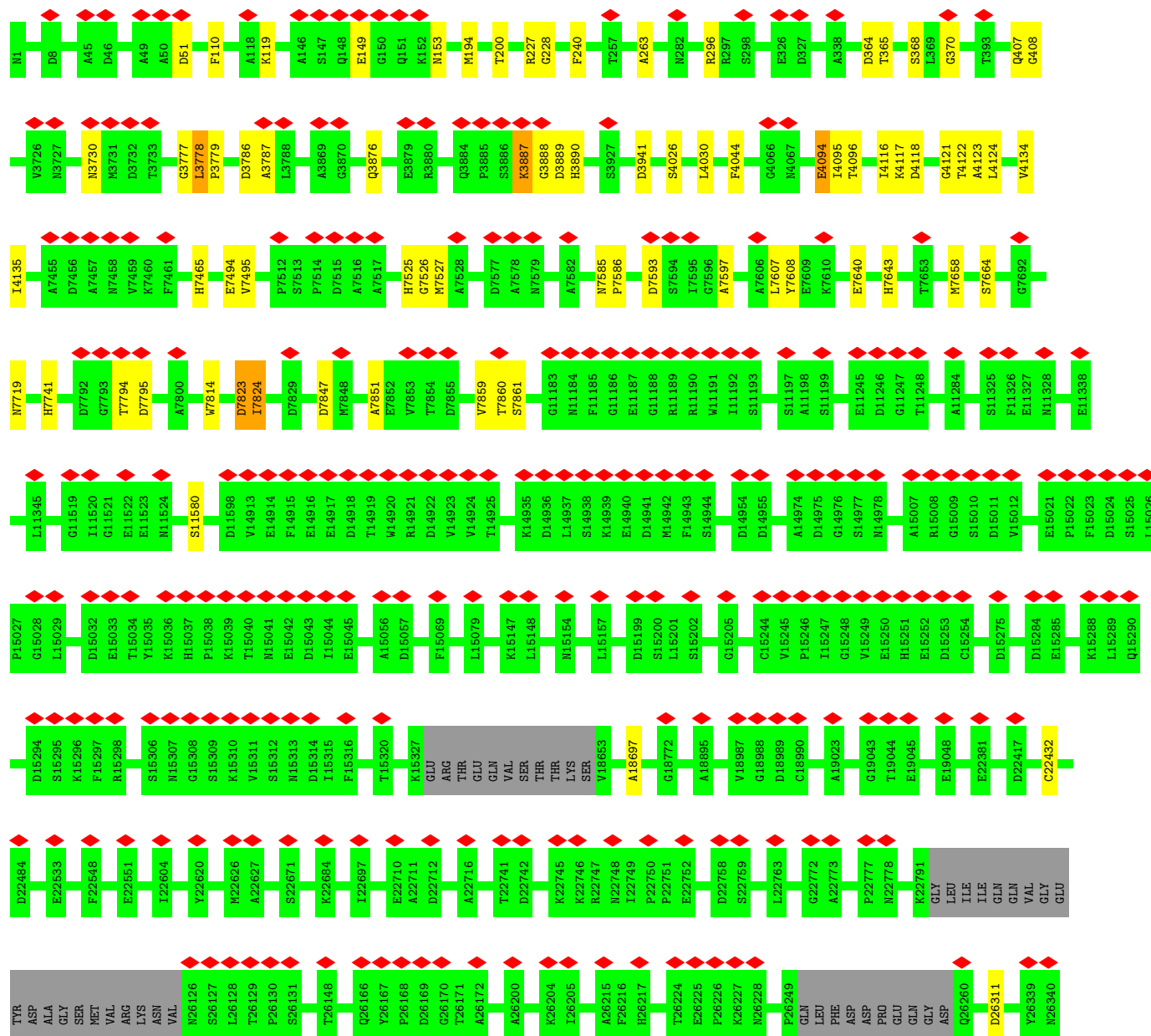


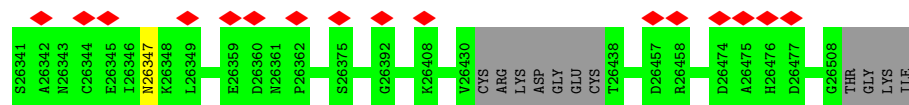
E26359	LEU	K19035	P15319	A15156	V15001	V14923	T7854	N7543	V4062
D26360	ILE	T19036	T15320	L15157	E15002	V14924	D7855	R7547	V4063
N26361	PHE	K19037	V15321	N15158	N15003	T14925	L7856	T7560	A4064
P26362	GLN	G19043	K15327	L15159	E15004	S14926	N11184	D7564	A4065
N26363	ASP	T19044	GLU	L15160	L15005	A14927	F11185	C4072	G4066
E26364	VAL	E19045	ARG	N15161	L15006	N14928	G11186	S4073	
K26367	GLY	T19046	THR	D15162	A15007	R14929	E11187	T4084	
A26368	GLU	A22377	GLN	F15167	R15008	I14930	G11188	A7568	
Q26369	ALA	A22377	VAL	N15168	G15009	L14934	R11189	D7577	
Q26370	SER	E22381	SER	F15261	S15010	K14935	R11190	A7578	
N26387	MET	V22382	THR	N15169	D15011	L14936	S11193	N7579	
R26388	VAL	A22383	THR	K15170	V15012	D14937	S11197	G7580	
Q26389	ARG	L22396	LYS	T15171	V15013	L14938	A11198	E7581	
F26390	LYS	S22395	SER	A15172	A15014	S14939	K7583	A4101	
H26391	ASN	V18653	V18653	N15173	V15014	K14940	S11199	L4102	
G26392	VAL	R18654	R18654	Q15174	D15024	E14941	S11225	G4103	
L26393	N26126	A18697	A18697	D15175	D15032	M14942	E11226	N7585	
M26394	S26127	K18708	K18708	T15176	E15033	M14943	G11227	P7586	
L26395	L26128	I18742	I18742	L15177	E15034	F14943	E11245	T4121	
L26396	T26129	P18755	P18755	T15178	V15035	S14944	D11246	T4122	
P26397	E26132	T18771	T18771	F15179	L15036	R14946	E11327	A4123	
L26398	E26132	T18772	T18772	N15180	K15037	A14947	N11328	P4126	
E26399	T26148	I18773	I18773	T15181	H15038	A14948	S11441	T4127	
H26400	D26149	R18774	R18774	S15182	P15039	F14949	T11442	V4137	
L26401	Q26166	E18774	E18774	R15183	T15040	K14950	A11278	L4140	
L26402	Y26167	P18789	P18789	D15186	N15041	R14951	A11284	A7455	
L26403	Y26167	E18790	E18790	V15187	E15042	M14952	F11326	D7456	
L26404	D26168	K18795	K18795	D15188	D15043	T14953	E11327	N7457	
L26405	D26169	E18796	E18796	N15192	I15044	D14954	N11328	N7458	
L26406	G26170	V18797	V18797	S15193	E15045	G14955	S11441	V7459	
E26407	K26199	A18806	A18806	L15194	N15046	R14957	T11442	K7460	
K26408	K26200	A18895	A18895	N15195	G15051	Y14958	A11443	F7461	
D26409	K26201	E18958	E18958	D15199	K15052	E14959	G11519	S7477	
K26410	K26204	D19966	D19966	S15204	S15053	I14961	T11520	A7487	
V26411	T26214	V19987	V19987	G15205	F15055	A14962	G11521	A7491	
F26412	A26215	D22717	D22717	F15228	D15057	A14963	G11561	T7508	
A26413	F26216	G22717	G22717	W15229	A15058	L14967	S11580	Q7509	
F26415	H26217	V22718	V22718	L15230	V15059	P14968	K11581	W7510	
L26416	S26218	T22741	T22741	S15231	T15060	A14969	D11598	C7511	
A26419	L26219	D22742	D22742	G15232	V15061	G14975	G14976	P7512	
L26420	P26220	K22745	K22745	K15233	R15062	S14977	T7824	S7513	
V26426	V26223	K22746	K22746	K15234	K15063	N14978	T7825	D7515	
N26427	E26224	S19002	S19002	A15235	D15066	I14979	F14913	D7516	
F26428	E26225	A19023	A19023	S15236	P15108	H14985	E14915	A7517	
L26429	K26227	M19024	M19024	D15238	N15109	G14986	F14916	M7848	
V26430	N26228	F19028	F19028	C15244	H15110	M14987	E14917	T7849	
CYS	D26237	D22758	D22758	V15245	H15111	G14988	T14919	E7852	
ARG	V26238	S22759	S22759	P15246	S15112	P14988	W14920	W7853	
LYS	K26350	A22790	A22790	I15247	Y15121	Y14997	R14921		
ASP	K26351	K22791	K22791	G15248	A15153	L14998	D14922		
GLY	P26352	GLY	GLY	F15249	N15154	S14999			
T26438	P26352			E15250	C15155				
F26439									



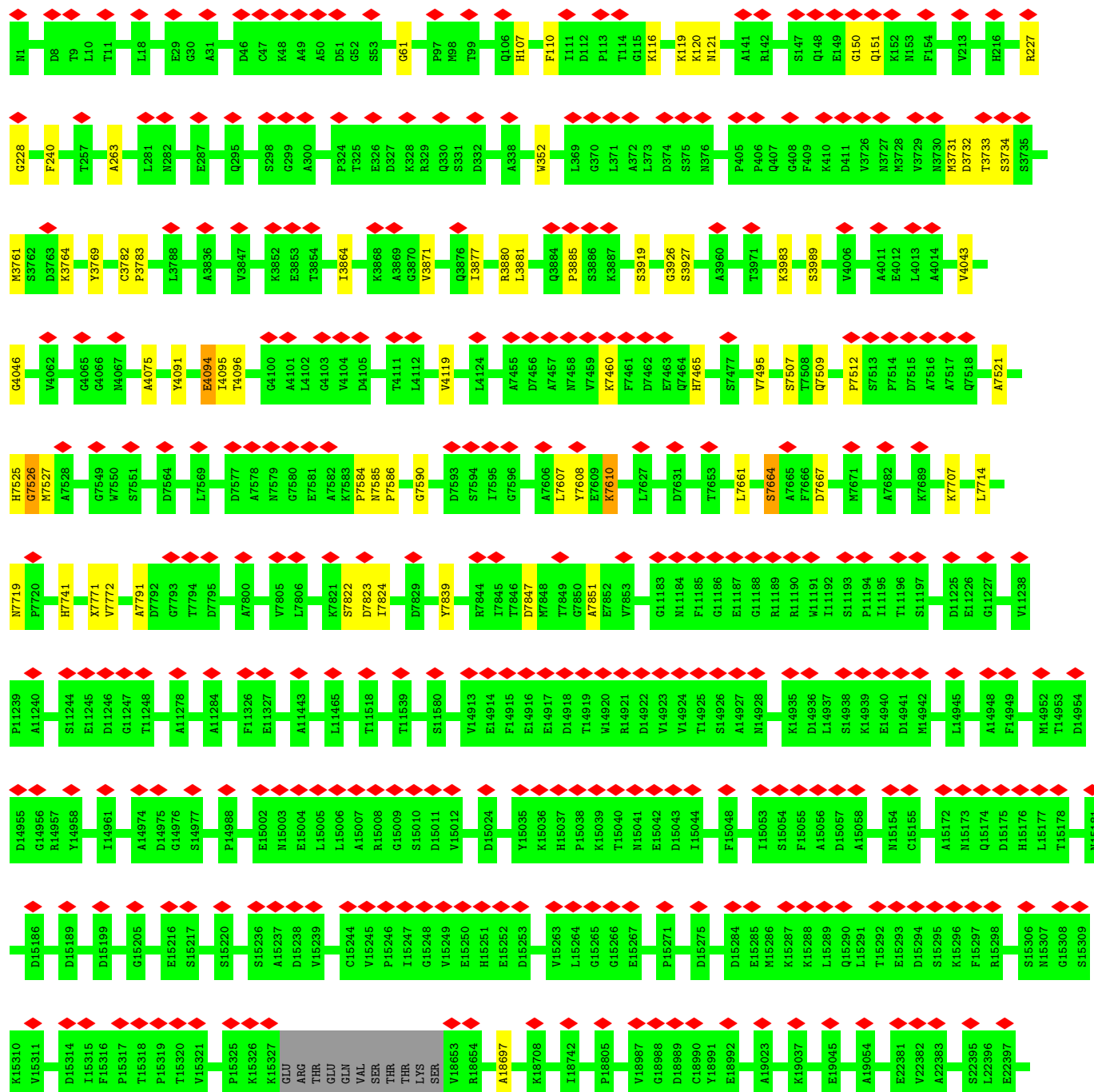
• Molecule 1: Hemocyanin subunit 1



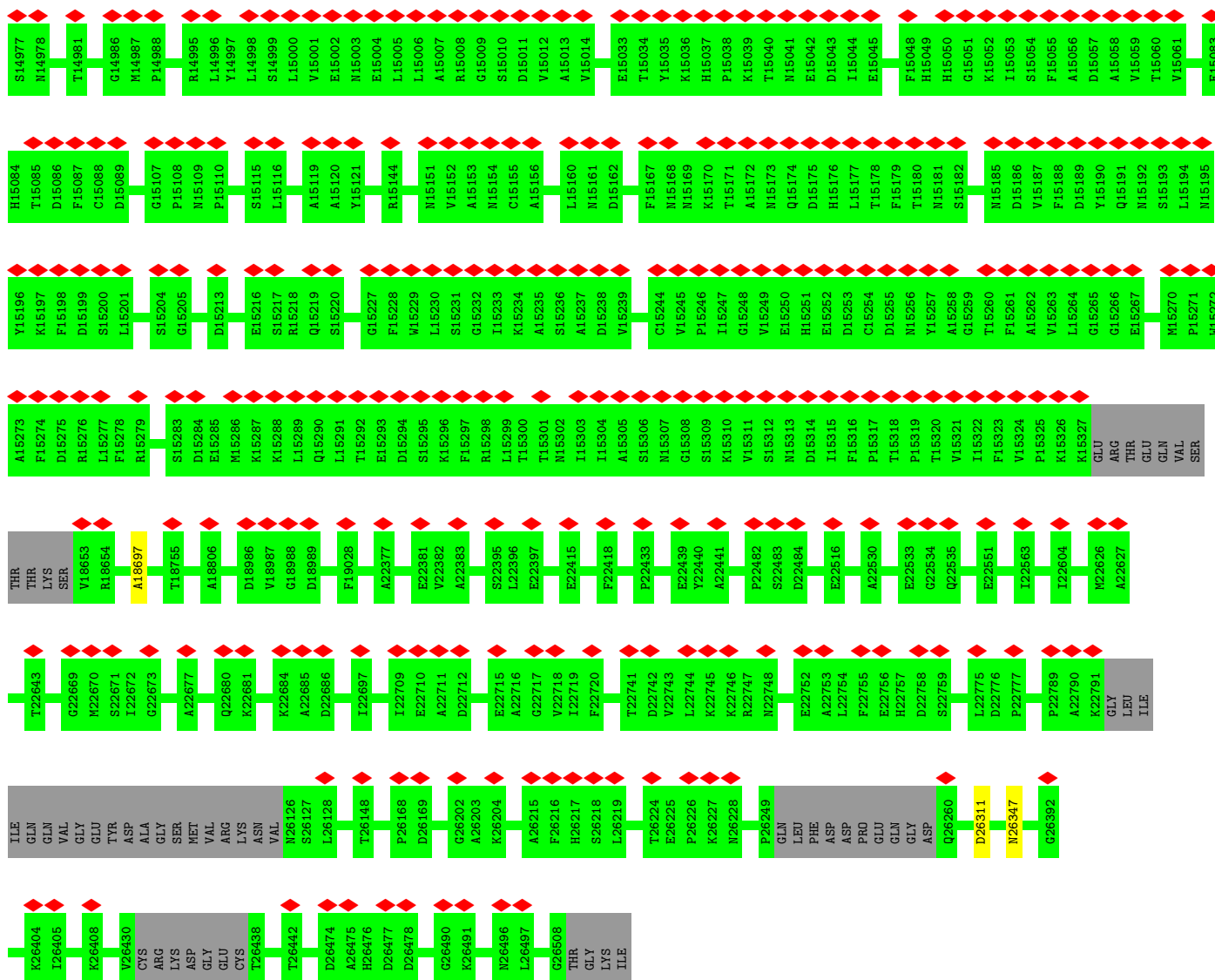




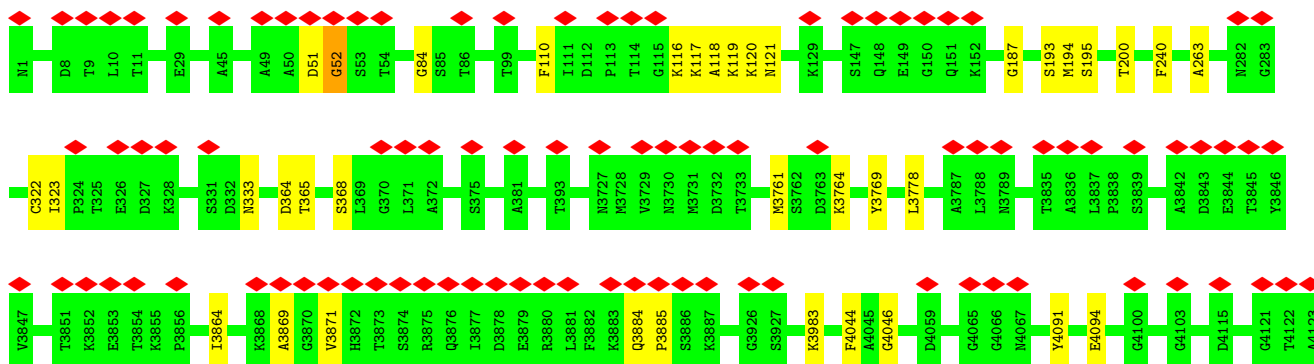
• Molecule 1: Hemocyanin subunit 1



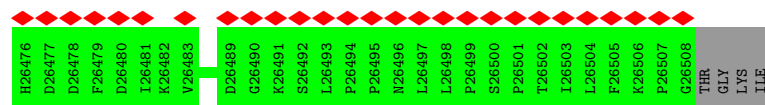
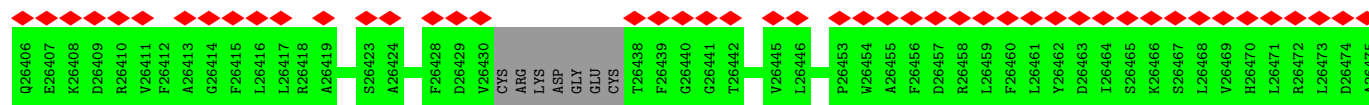




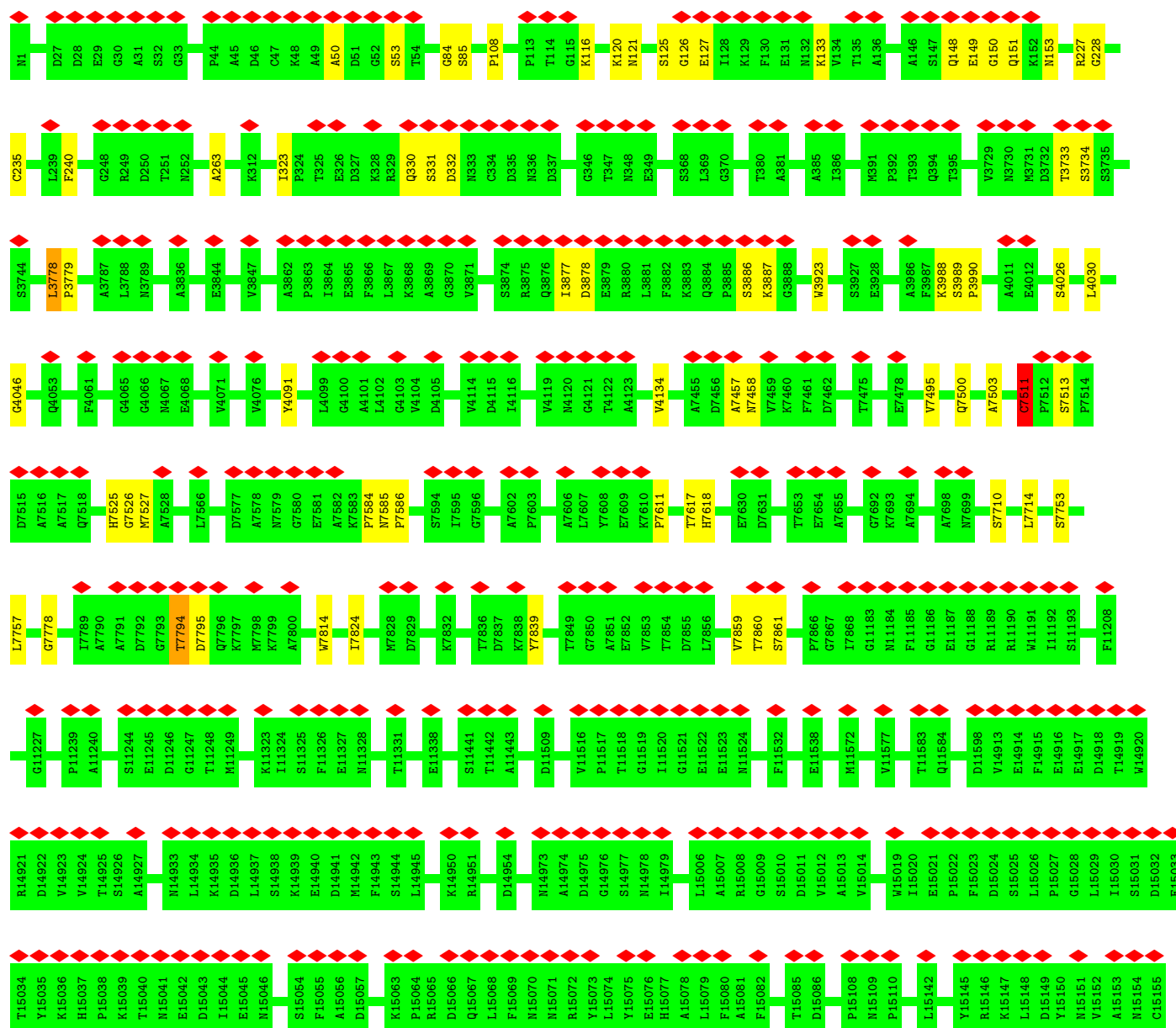
• Molecule 1: Hemocyanin subunit 1

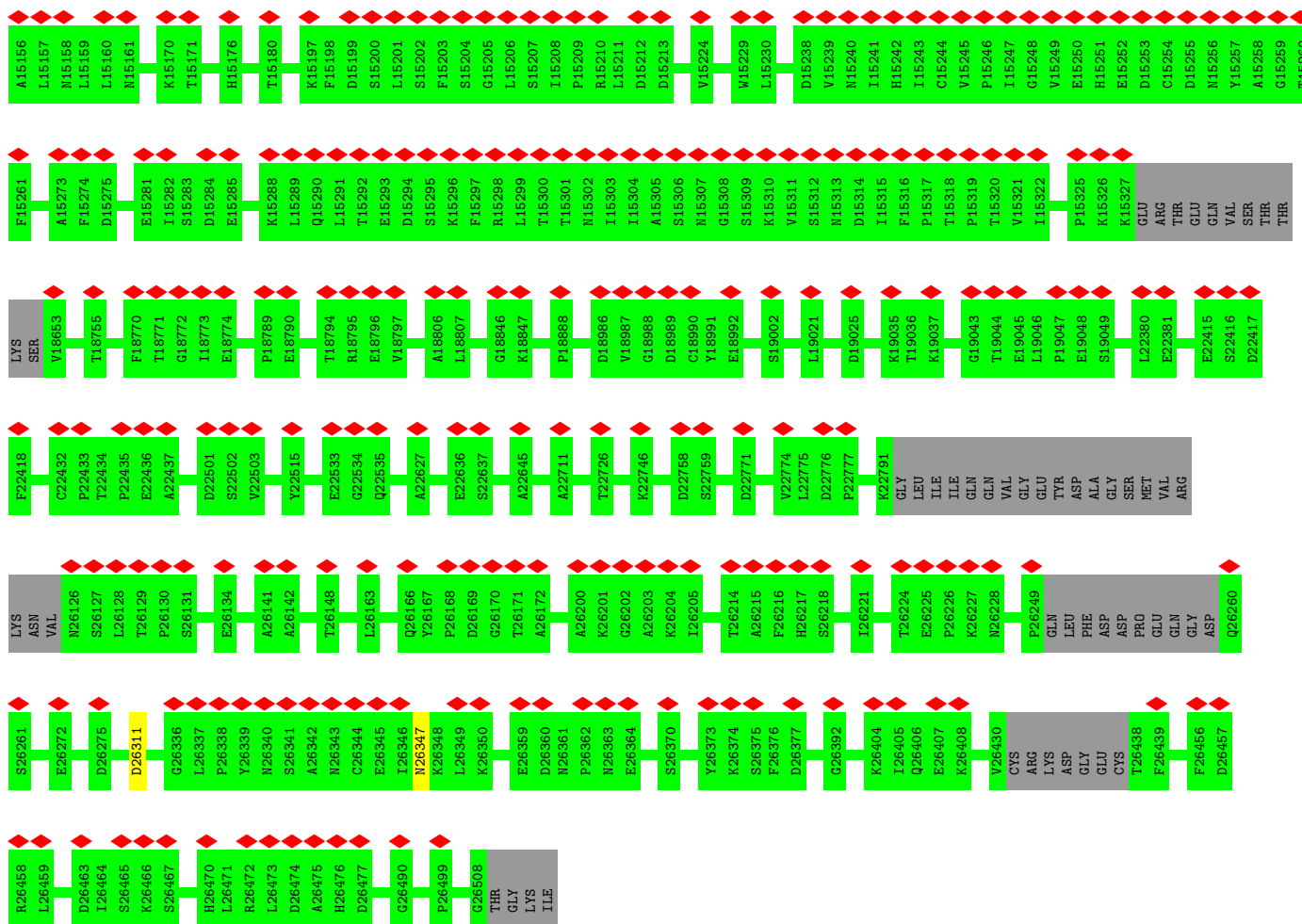




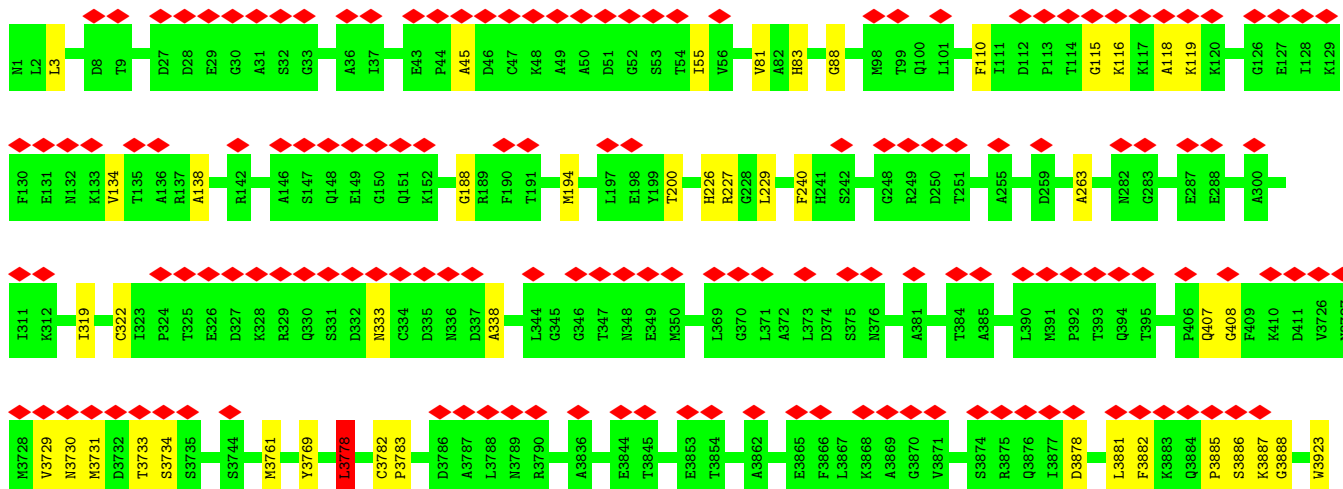


• Molecule 1: Hemocyanin subunit 1





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S15296	S15295	A15236	D15175	S15114	S15054	H14994	L14934	V11238	L7783	L7569	T4111	S3927
K15296	K15297	S15236	H15176	S15115	F15055	R14995	L14934	P11239	L7789	V7570	L4112	L4112
F15297	F15298	D15237	L15177	L15116	D15056	L14996	K14935	A11240		T7576	R4113	T3971
R15298	R15299	D15238	T15178	D15117	D15057	Y14997	D14936	P11243	D7792	D7577	D4115	K3983
L15299	L15300	D15239	F15179	F15118	A15058	L14998	S14937	S11244	T7793	A7578	V4119	S3989
T15301	T15302	N15240	A15119	A15120	V15059	S14999	K14938	E11245	T7794	N7579	N4120	P3990
M15303	M15304	I15241	M15181	Y15121	T15060	E15001	E14940	D11246	D7795	G7580	G4121	L3991
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A15305	A15305	I15124	M15185	I15124	P15064	E15004	F14943	M11249	G7801	K7583	L4124	A4011
S15306	S15306	F15125	D15186	F15125	R15065	L15005	S14944	F11326		P7584	P4125	E4012
M15307	M15307	F15126	Q15127	F15126	D15066	A15007	L14945	E11327		N7585	L4013	L4013
G15308	G15308	L15127	L15127		Q15067	R15008	R14946	N11328	L7806	P7586	T4127	A4014
S15309	S15309				L15068	G15009	A14947			F7587	A4128	
K15310	K15310	S15130	Y15190	S15130	F15069	S15010	A14948	G11341	W7814	G7590	I4129	L4020
V15311	V15311	T15131	Q15191	T15131	N15070	S15011	F14949				I4133	L4027
S15312	S15312	V15132	M15192	V15132	D15071	D15011	K14950	T11442	D7823	D7593	I4140	C4046
M15313	M15313	L15133	S15193	D15133	R15072	V15012	R14951	A11443	W7824	S7594	A7455	
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P15319	P15319	W15139	W15199	A15078	A15078	V15019	R14957	I11520		A7606	K7460	F4061
T15320	T15320	Q15140	L15079	L15079	L15079	I15020	Y14958	G11521		L7607	F7461	V4062
V15321	V15321	D15141	D15141	F15080	F15080	E15021	E14959	E11522		Y7608	D7462	V4063
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K15327	K15327	L15148	F15087	F15087	F15087	P15027	G14966	S11580		Y7616	F4070	G4072
GLU	GLU	L15149	C15088	C15088	C15088	G15028	L14967	T11583		L7627	E7494	V4071
ARG	ARG	D15149	C15089	C15089	C15089	L15029	P14968	Q11584			W7495	G4072
THR	THR	Y15150	D15089	D15089	D15089	I15030	A14969				C7511	S4073
GLN	GLN	N15151	F15090	F15090	F15090	I15031	Q14970	D11598			S7512	V4076
VAL	VAL	V15152	E15091	E15091	E15091	S15032	C14971	V14913			P7514	L4077
THR	THR	A15153	V15092	V15092	V15092	D15033	P14972	E14914			D7515	
THR	THR	L15154	H15093	H15093	H15093	E15033	P14973	F14915			A7516	
LYS	LYS	C15155	F15094	F15094	F15094	T15034	A14974	E14916			A7517	
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K13708	K13708	L15158	H15097	H15097	H15097	L15037	G14977	D14919				E4084
T13765	T13765	L15159	H15098	H15098	H15098	P15038	S14977	T14919				D4097
E13764	E13764	L15160	H15099	H15099	H15099	K15039	N14978	W14920				A4098
P13769	P13769	N15161	T15040	T15040	T15040	P15039	I14979	R14921				L4099
G13772	G13772	D15162	S15100	S15100	S15100	L15041	I14979	D14922				G4100
I13773	I13773	P15163	I15101	I15101	I15101	H14980	H14980	W11191				A4101
E13774	E13774	S15163	H15102	H15102	H15102	T14981	T14981	D14923				L4102
		M15164	S15103	S15103	S15103	D15043	C14982	V14924				G4103
		R15165	W15104	W15104	W15104	I15044	C14983	T14925				V4104
		P15166	I15105	I15105	I15105	E15045	L14984	S14926				D4105
		F15167	G15106	G15106	G15106	N15046	H14985	A14927				
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		K15170	N15109	N15109	N15109	F15049	P14988	I14930				
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		A15172	S15112	S15112	S15112	G15051	H14992					
		N15173	S15113	S15113	S15113	K15052	L14993					
		Q15174				I15053						



P26453	W26454	A26455	F26456	D26457	R26458	L26459	F26460	L26461	Y26462	D26463	L26464	S26465	K26466	S26467	L26468	V26469	H26470	L26471	R26472	L26473	D26474	A26475	H26476	D26477	D26478	F26479	D26480	I26481	K26482	V26483	T26484	I26485	N26486	G26487	I26488	D26489	G26490	K26491																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
N26389	F26390	H26391	G26392	M26393	T26394	I26395	P26396	Q26397	L26398	E26399	V26400	H26401	L26402	K26403	K26404	I26405	Q26406	E26407	K26408	D26409	R26410	V26411	F26412	A26413	G26414	F26415	L26416	L26417	R26418	A26419	I26420	G26421	Q26422	S26423	A26424	D26425	V26426	N26427	F26428	D26429	V26430	CYS	ARG	LYS	ASP	GLY	GLU	CYS	T26438	F26439	G26440	G26441	T26442	F26443	C26444	V26445	L26446	G26447																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
S26303	D26311	R26323	A26326	Q26329	A26330	K26333	Y26334	R26335	G26336	L26337	P26338	Y26339	N26340	S26341	A26342	N26343	C26344	E26345	I26346	N26347	K26348	L26349	K26350	K26351	P26352	S26357	S26358	E26359	P26362	N26363	E26364	V26365	A26368	Y26373	K26374	S26375	F26376	D26377	Y26378	Q26379	Q26380	L26381	N26382	Y26383	E26384	Y26385	D26386	N26387	L26388																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	196315	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 ($e^-/\text{\AA}^2$)	56	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	513.0, 513.0, 513.0	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.14, 1.14, 1.14	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	10a	0.45	0/6115	1.09	28/8514 (0.3%)
1	1a	0.44	0/6115	1.08	20/8514 (0.2%)
1	2a	0.43	0/6115	1.04	16/8514 (0.2%)
1	3a	0.45	0/6115	1.06	23/8514 (0.3%)
1	4a	0.44	0/6115	1.04	17/8514 (0.2%)
1	5a	0.44	0/6115	1.05	24/8514 (0.3%)
1	6a	0.44	0/6115	1.08	24/8514 (0.3%)
1	7a	0.46	0/6115	1.08	17/8514 (0.2%)
1	8a	0.46	0/6115	1.05	16/8514 (0.2%)
1	9a	0.46	0/6115	1.09	13/8514 (0.2%)
All	All	0.44	0/61150	1.07	198/85140 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	10a	0	5
1	1a	0	5
1	2a	0	5
1	3a	0	3
1	4a	0	7
1	5a	0	3
1	6a	0	4
1	7a	0	7
1	8a	0	3
1	9a	0	5
All	All	0	47

There are no bond length outliers.

The worst 5 of 198 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9a	3778	LEU	CA-C-N	-16.02	99.81	119.84
1	9a	3778	LEU	C-N-CA	-16.02	99.81	119.84
1	7a	7511	CYS	CA-C-N	-12.82	103.81	119.84
1	7a	7511	CYS	C-N-CA	-12.82	103.81	119.84
1	1a	3778	LEU	CA-C-N	-12.28	104.49	119.84

There are no chirality outliers.

5 of 47 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1a	127	GLU	Peptide
1	1a	18697	ALA	Peptide
1	1a	26311	ASP	Mainchain
1	1a	26347	ASN	Peptide
1	1a	3778	LEU	Peptide

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	10a	16130	0	2801	41	0
1	1a	16130	0	2801	26	0
1	2a	16130	0	2800	36	0
1	3a	16130	0	2801	27	0
1	4a	16130	0	2801	47	0
1	5a	16130	0	2801	27	0
1	6a	16130	0	2800	25	0
1	7a	16130	0	2801	45	0
1	8a	16130	0	2801	25	0
1	9a	16130	0	2801	33	0
All	All	161300	0	28008	332	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 8.

The worst 5 of 332 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)
1:5a:3864:ILE:N	1:5a:3871:VAL:O	2.07	0.87
1:10a:3864:ILE:N	1:10a:3871:VAL:O	2.15	0.78
1:6a:7838:LYS:HA	1:6a:7839:TYR:CB	2.15	0.76
1:2a:3881:LEU:N	1:2a:3882:PHE:HA	2.00	0.76
1:1a:118:ALA:HB1	1:1a:119:LYS:HA	1.69	0.75

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	10a	1237/3314 (37%)	1157 (94%)	69 (6%)	11 (1%)	14	50
1	1a	1237/3314 (37%)	1167 (94%)	62 (5%)	8 (1%)	21	58
1	2a	1237/3314 (37%)	1176 (95%)	53 (4%)	8 (1%)	21	58
1	3a	1237/3314 (37%)	1167 (94%)	57 (5%)	13 (1%)	11	45
1	4a	1237/3314 (37%)	1185 (96%)	46 (4%)	6 (0%)	24	63
1	5a	1237/3314 (37%)	1164 (94%)	62 (5%)	11 (1%)	14	50
1	6a	1237/3314 (37%)	1169 (94%)	57 (5%)	11 (1%)	14	50
1	7a	1237/3314 (37%)	1143 (92%)	84 (7%)	10 (1%)	16	53
1	8a	1237/3314 (37%)	1162 (94%)	59 (5%)	16 (1%)	9	40
1	9a	1237/3314 (37%)	1151 (93%)	76 (6%)	10 (1%)	16	53
All	All	12370/33140 (37%)	11641 (94%)	625 (5%)	104 (1%)	18	53

5 of 104 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1a	134	VAL
1	1a	331	SER
1	1a	3989	SER

Continued on next page...

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Mol	Chain	Res	Type
1	2a	148	GLN
1	3a	7495	VAL

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	3a	1
1	4a	1
1	7a	1
1	10a	1
1	8a	1

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
1	2a	1
1	1a	1
1	6a	1
1	5a	1
1	9a	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	3a	11598:ASP	C	14913:VAL	N	29.53
1	4a	11598:ASP	C	14913:VAL	N	27.35
1	7a	11598:ASP	C	14913:VAL	N	27.29
1	10a	11598:ASP	C	14913:VAL	N	25.41
1	8a	11598:ASP	C	14913:VAL	N	24.86

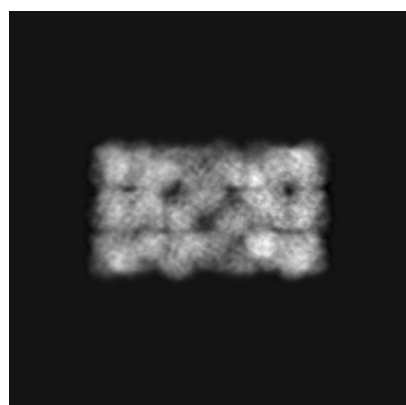
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4750. These allow visual inspection of the internal detail of the map and identification of artifacts.

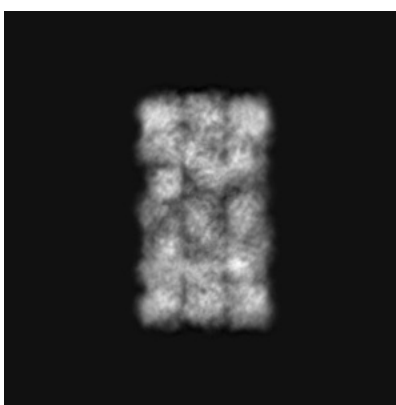
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

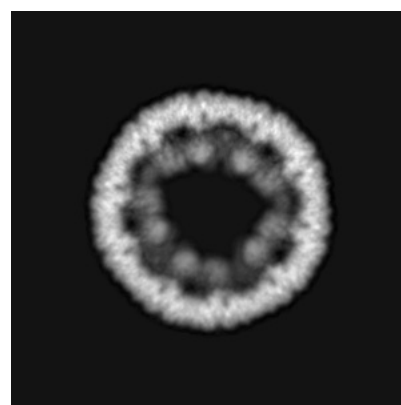
6.1.1 Primary map



X



Y

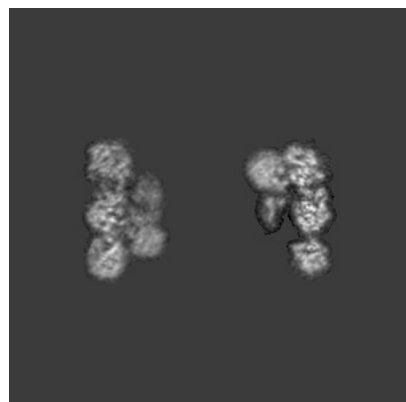


Z

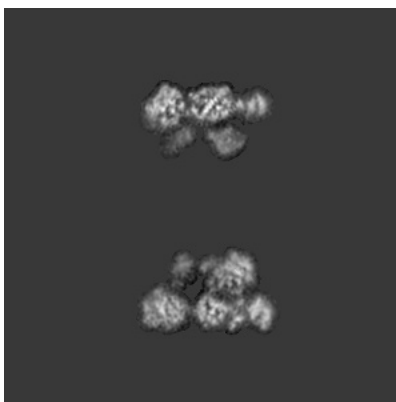
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 225



Y Index: 225

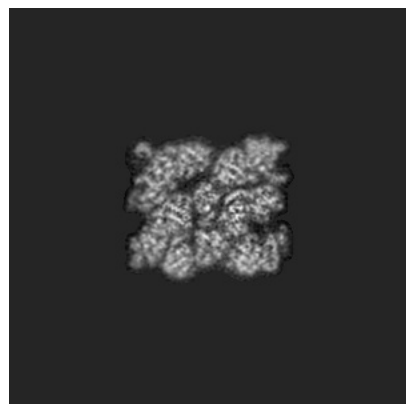


Z Index: 225

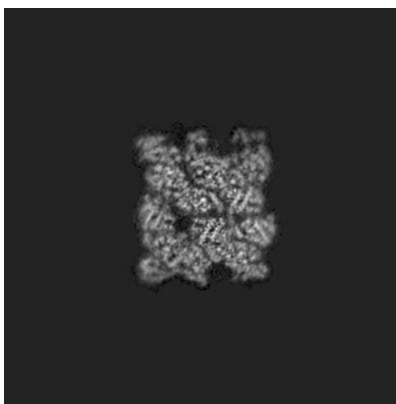
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

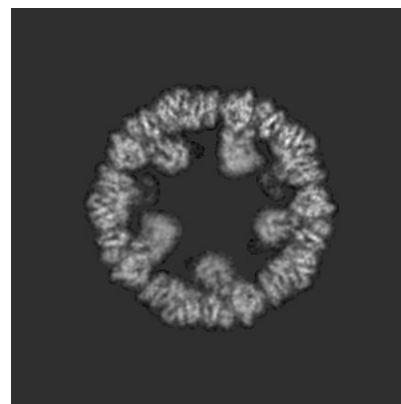
6.3.1 Primary map



X Index: 331



Y Index: 333

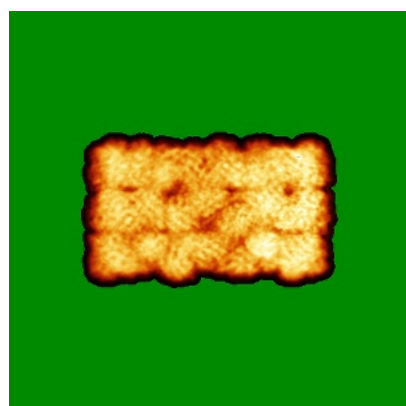


Z Index: 181

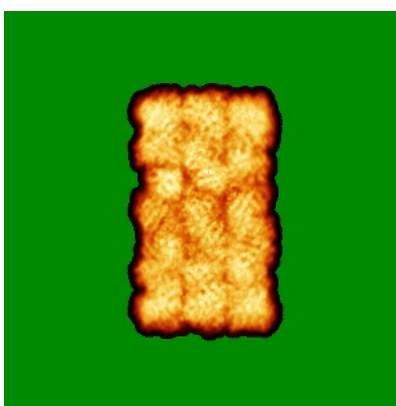
The images above show the largest variance slices of the map in three orthogonal directions.

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

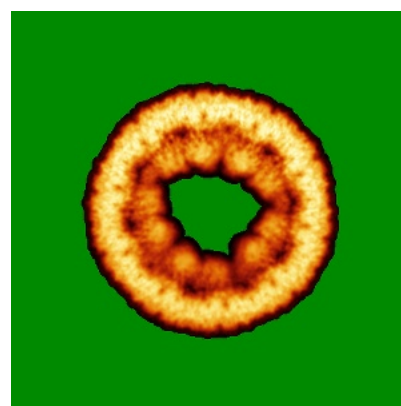
6.4.1 Primary map



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

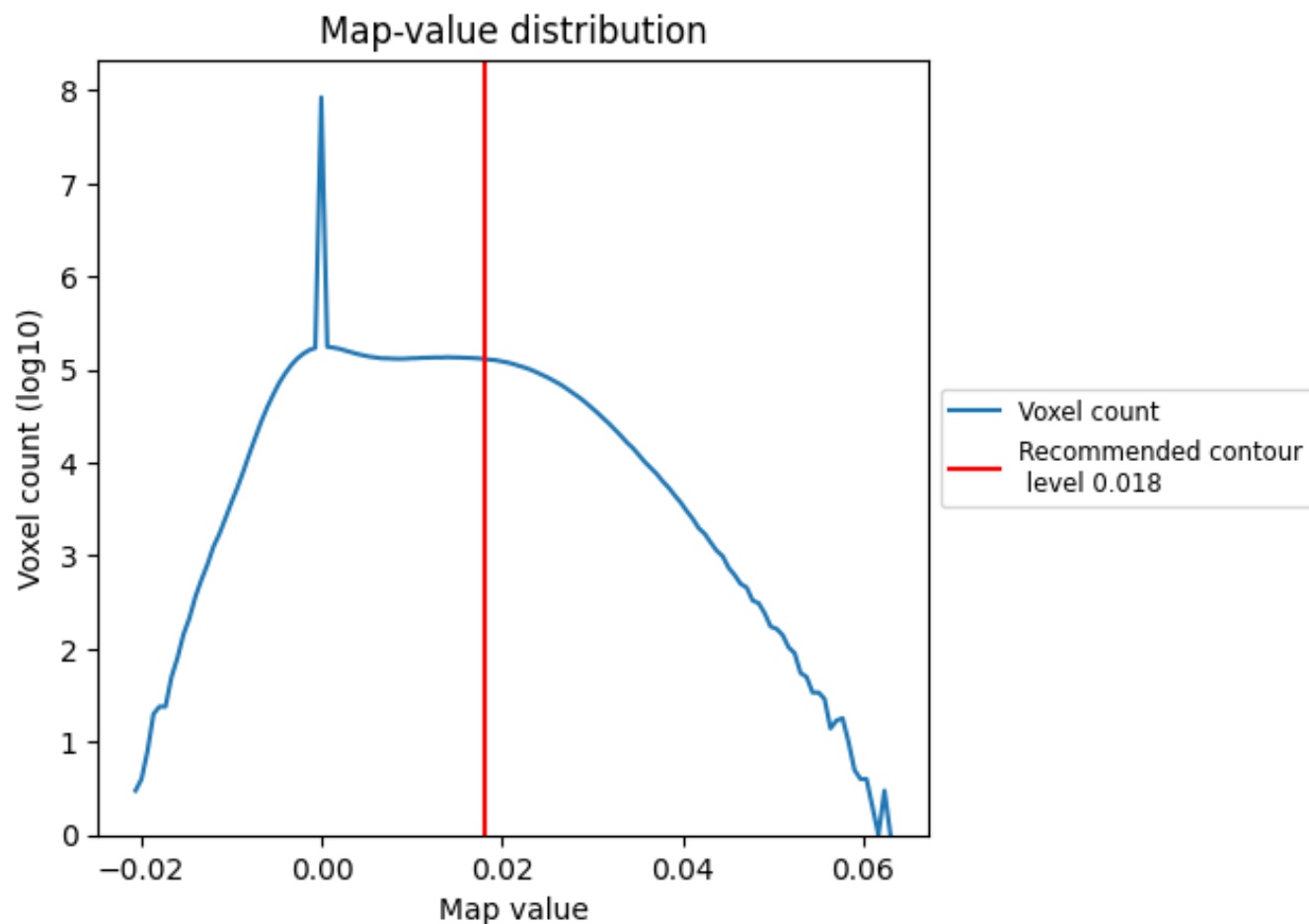
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

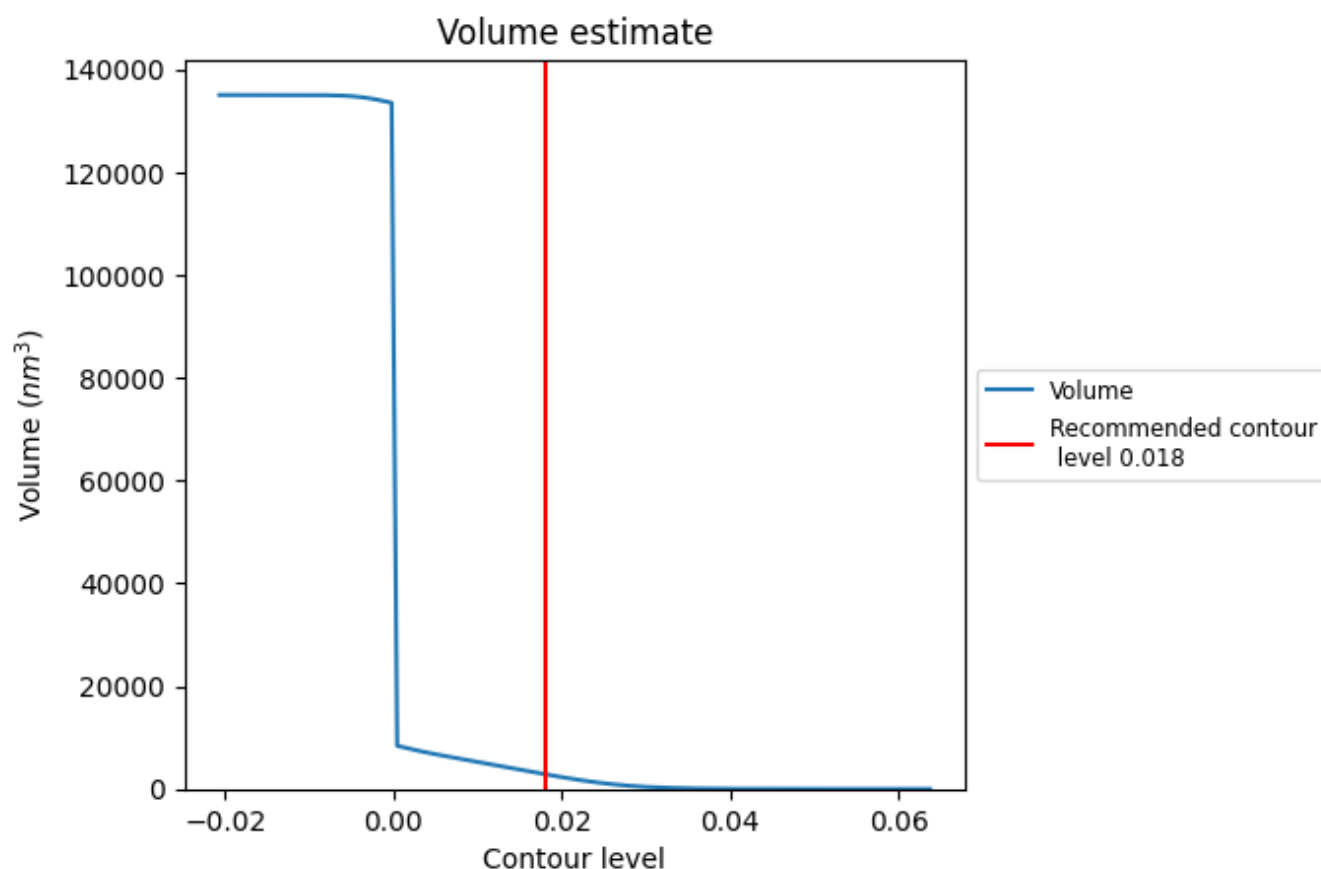
This section contains the results of statistical analysis of the map.

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.

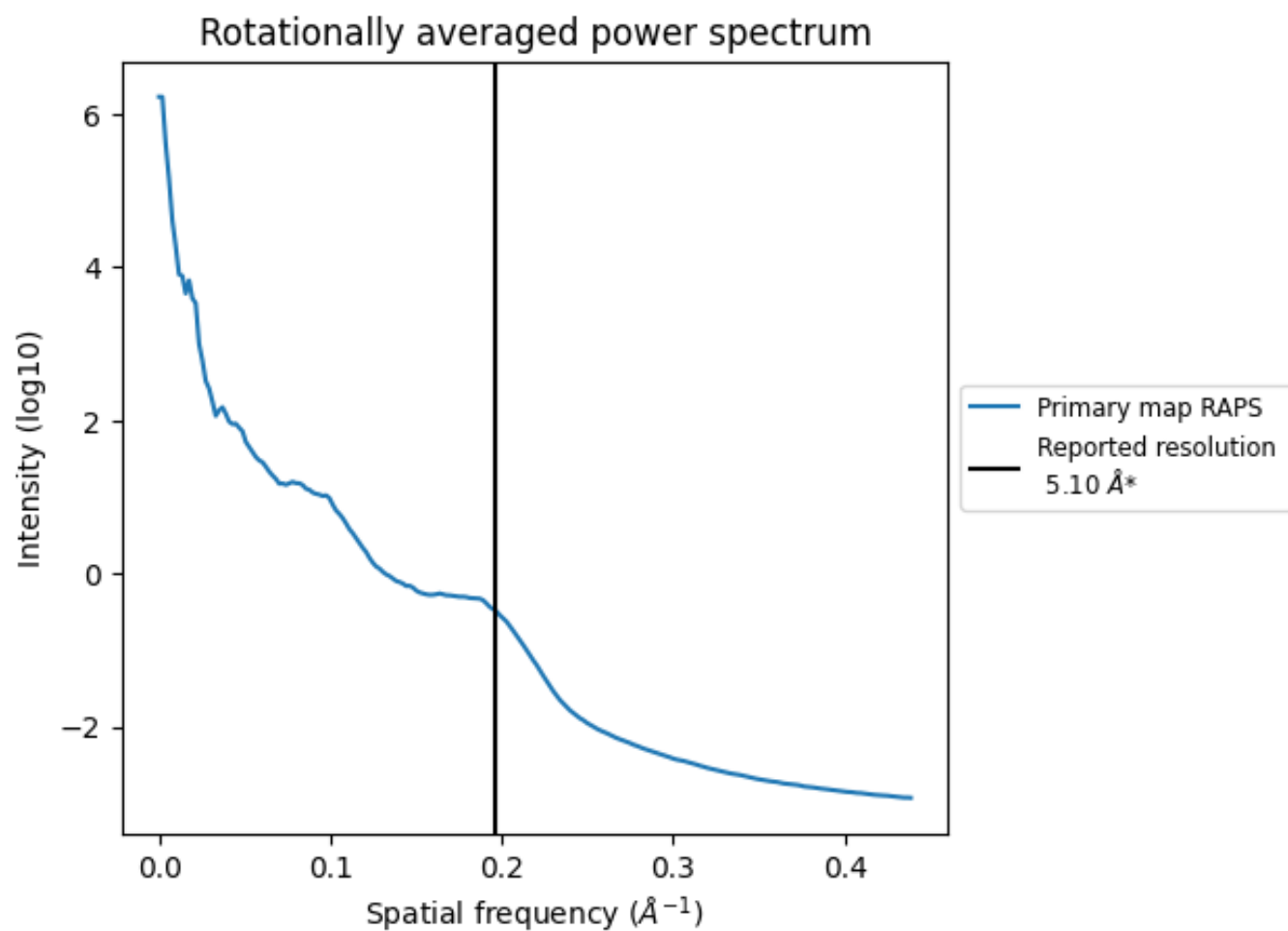
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2864 nm^3 ; this corresponds to an approximate mass of 2587 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 0.196 Å⁻¹

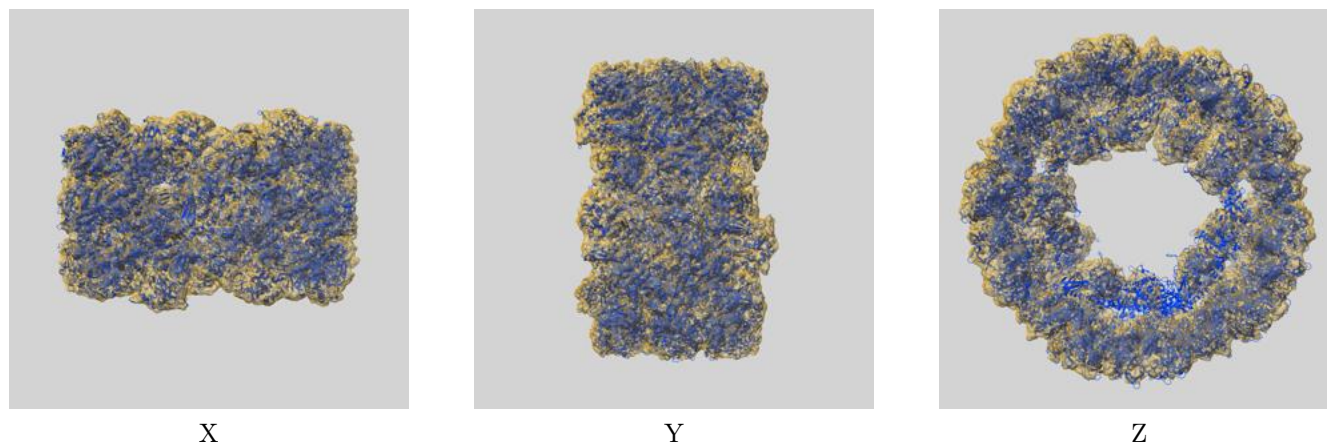
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

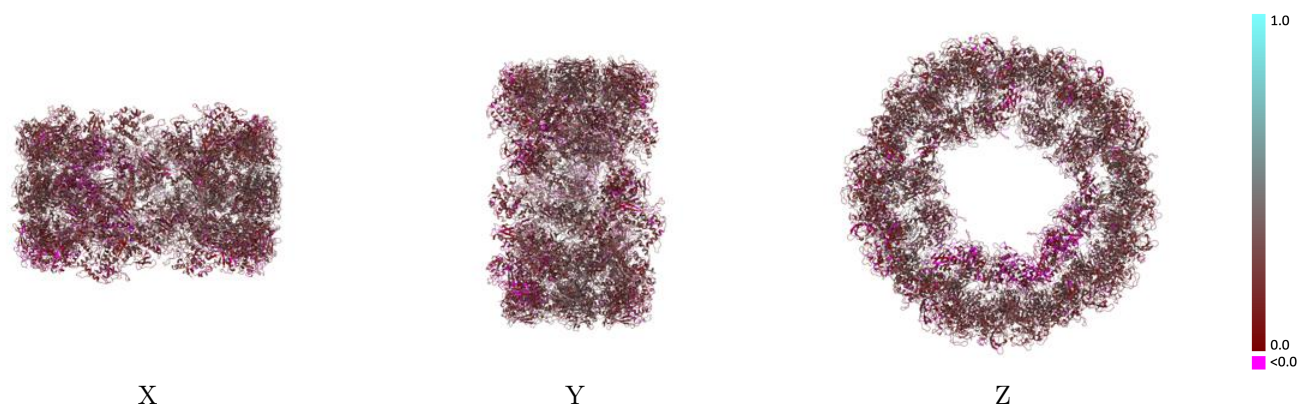
This section contains information regarding the fit between EMDB map EMD-4750 and PDB model 6R83. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



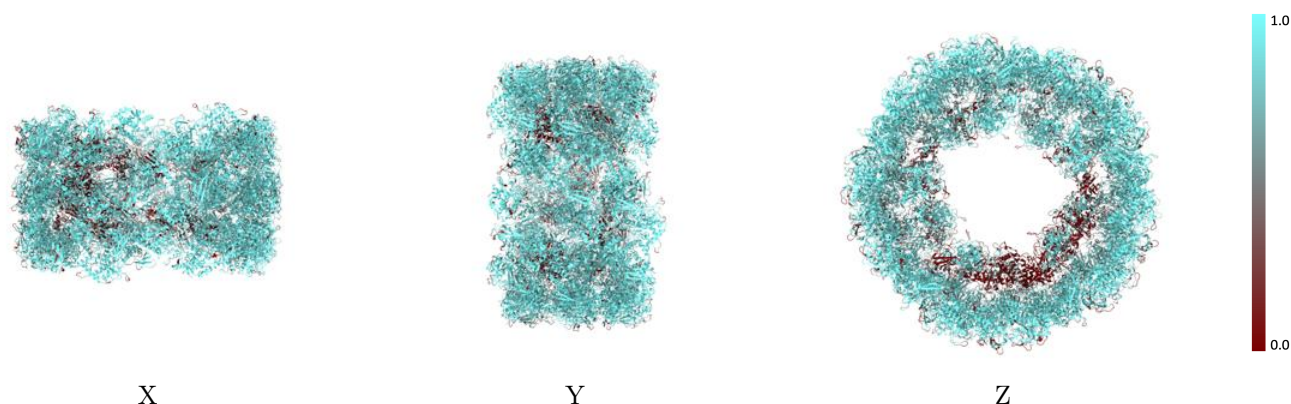
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



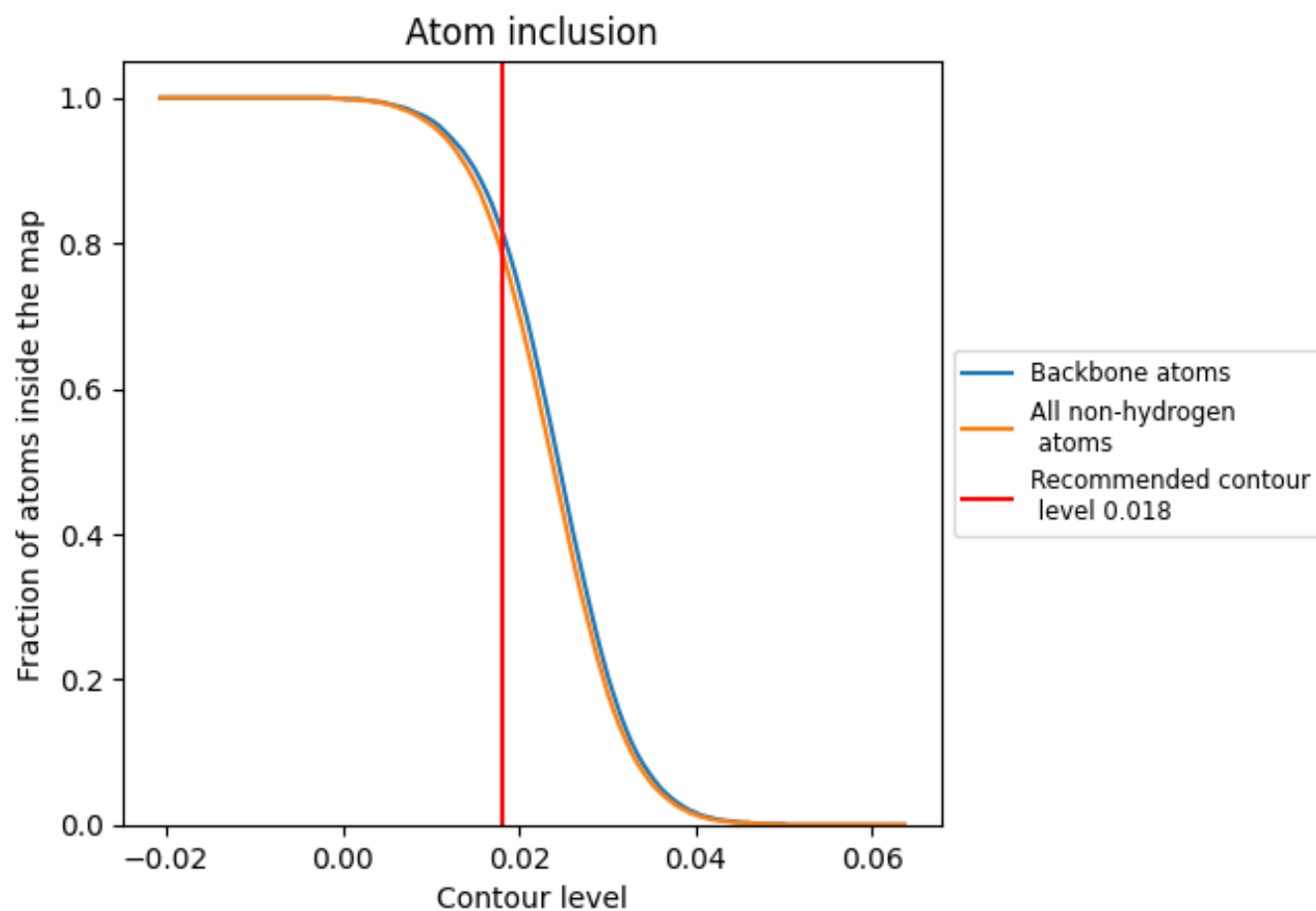
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 79% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7900	0.2300
10a	0.7430	0.2150
1a	0.7860	0.2310
2a	0.7830	0.2310
3a	0.8730	0.2430
4a	0.8780	0.2550
5a	0.8320	0.2410
6a	0.7810	0.2290
7a	0.7740	0.2260
8a	0.7840	0.2350
9a	0.6620	0.1930

1.0

0.0

<0.0