



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:58 PM UTC

PDB ID : 9GNI / pdb_00009gni
EMDB ID : EMD-51471
Title : NONO/SFPQ filament: composite structure
Authors : Rasmussen, T.; Bottcher, B.
Deposited on : 2024-09-03
Resolution : 3.90 Å (reported)
Based on initial models : 9GLC, 6WMZ, 9GLD

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

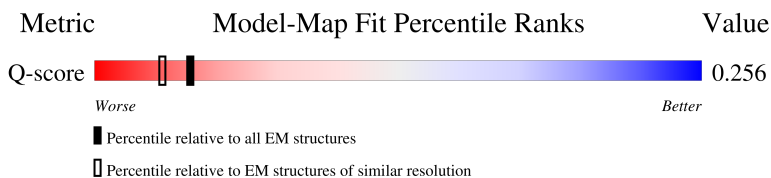
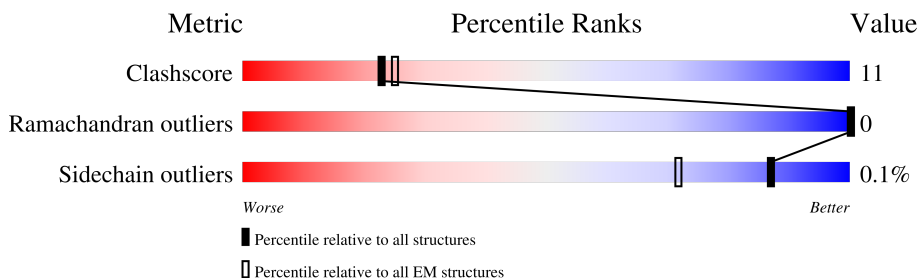
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.




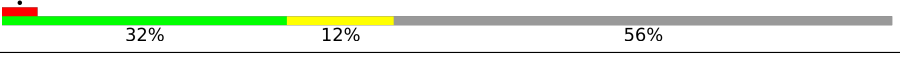



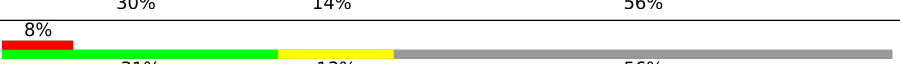
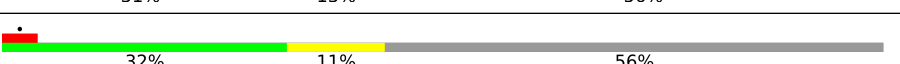



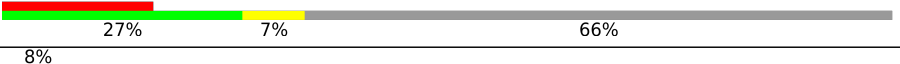
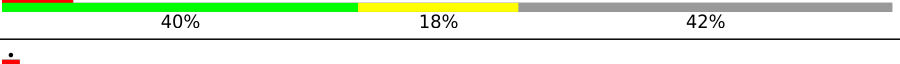
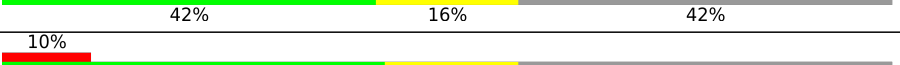
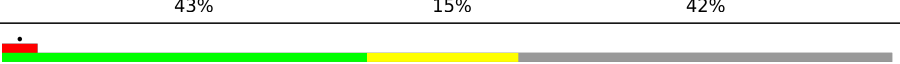
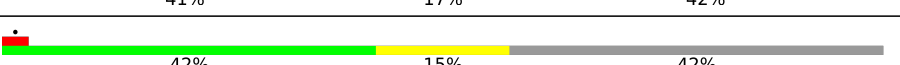
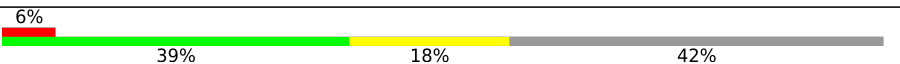
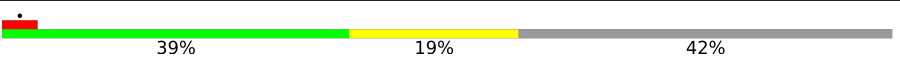
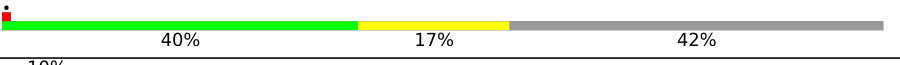
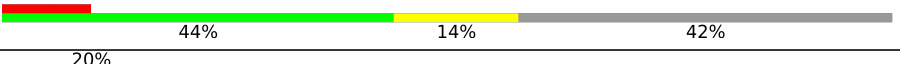

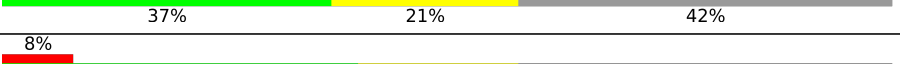
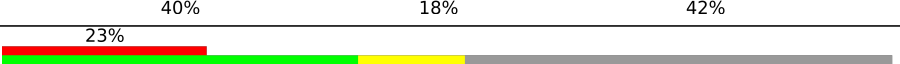
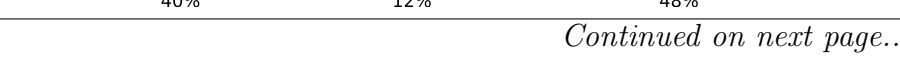


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	703	 32% 12% 56%
1	AC	703	 31% 12% 57%
1	AE	703	 6% 33% 11% 56%
1	AG	703	 7% 30% 14% 56%

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Mol	Chain	Length	Quality of chain
1	BA	703	
1	BC	703	
1	BE	703	
1	BG	703	
1	CA	703	
1	CC	703	
1	CE	703	
1	CG	703	
1	DA	703	
1	DC	703	
1	DE	703	
1	DG	703	
2	AB	472	
2	AD	472	
2	AF	472	
2	AH	472	
2	BB	472	
2	BD	472	
2	BF	472	
2	BH	472	
2	CB	472	
2	CD	472	
2	CF	472	
2	CH	472	
2	DB	472	

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Mol	Chain	Length	Quality of chain
2	DD	472	<div><div><div></div><div></div><div></div></div><div>7%37%21%42%</div></div>
2	DF	472	<div><div><div></div><div></div><div></div></div><div>34%44%14%42%</div></div>
2	DH	472	<div><div><div></div><div></div><div></div></div><div>20%41%17%42%</div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 74499 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 Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	AC	304	Total	C	N	O	S	0	0
			2527	1561	469	482	15		
1	AE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	AG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BC	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CA	275	Total	C	N	O	S	0	0
			2251	1405	406	429	11		
1	CC	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	DA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	DC	276	Total	C	N	O	S	0	0
			2262	1411	410	430	11		
1	DG	239	Total	C	N	O	S	0	0
			1932	1215	339	371	7		
1	DE	236	Total	C	N	O	S	0	0
			1901	1195	334	365	7		

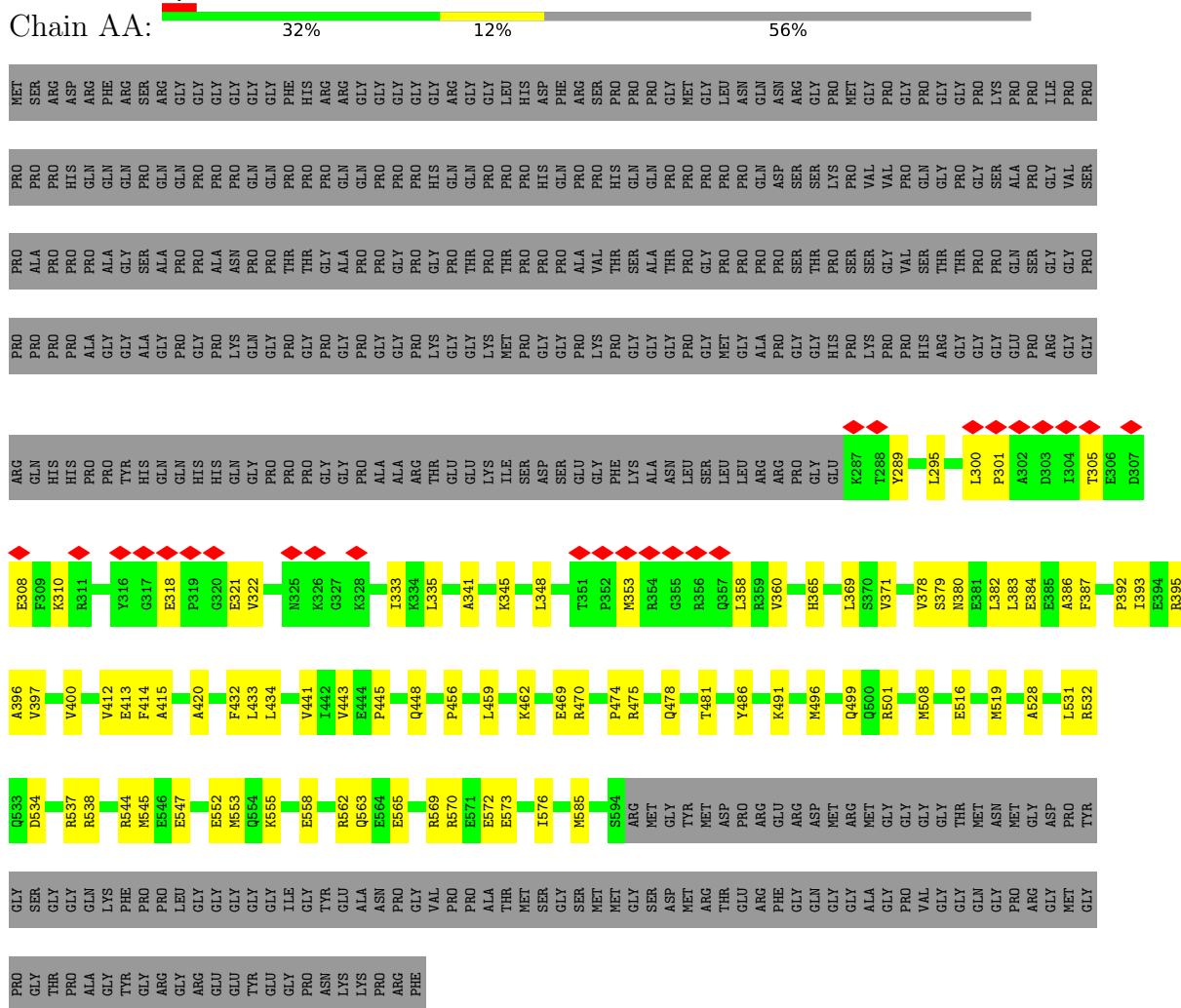
- Molecule 2 is a protein called Non-POU domain-containing octamer-binding protein isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CD	243	Total	C	N	O	S	0	0
			1979	1246	355	368	10		
2	CF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DB	244	Total	C	N	O	S	0	0
			1987	1252	356	369	10		
2	DD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		

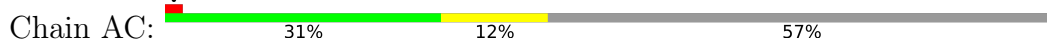
3 Residue-property plots

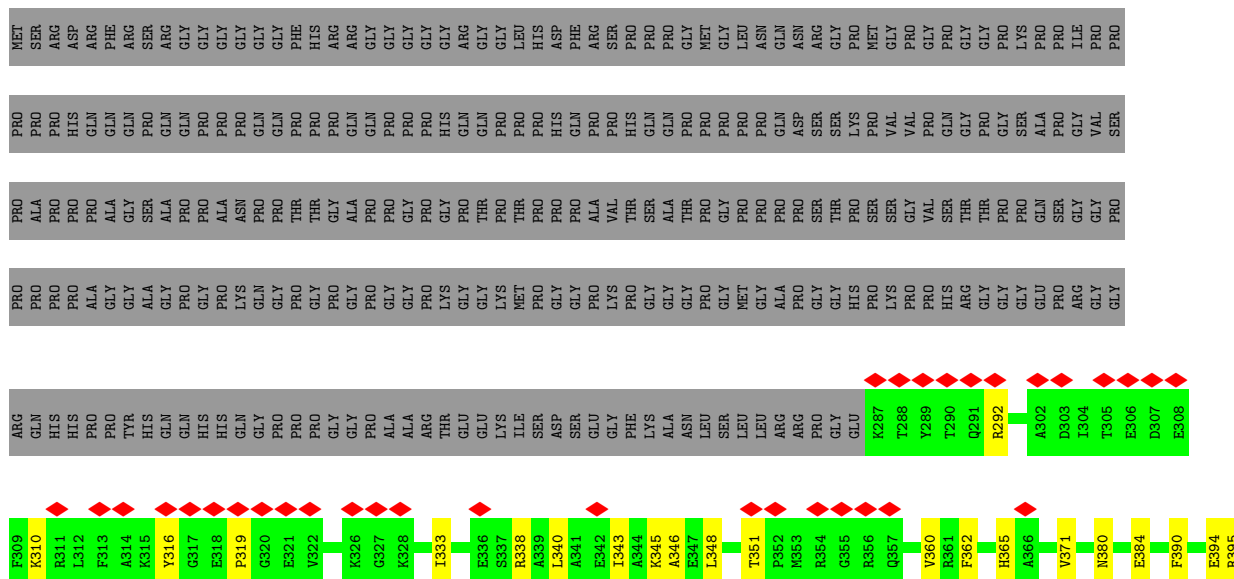
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

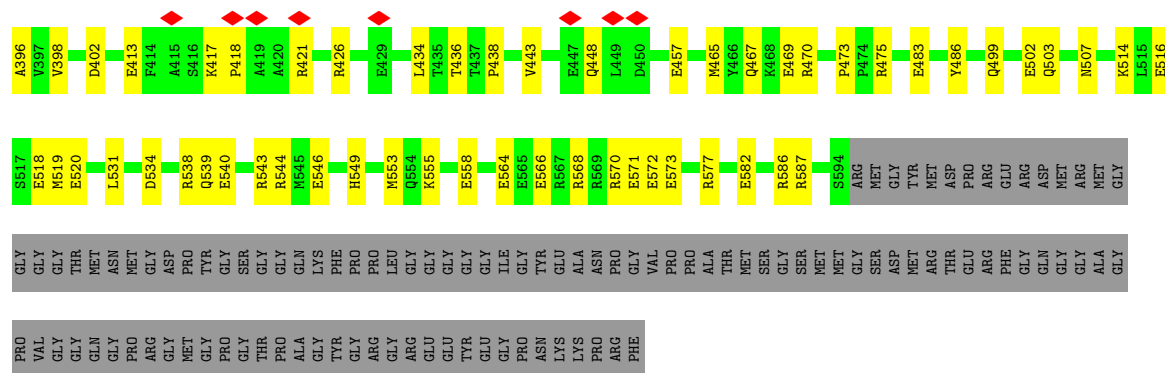
- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)



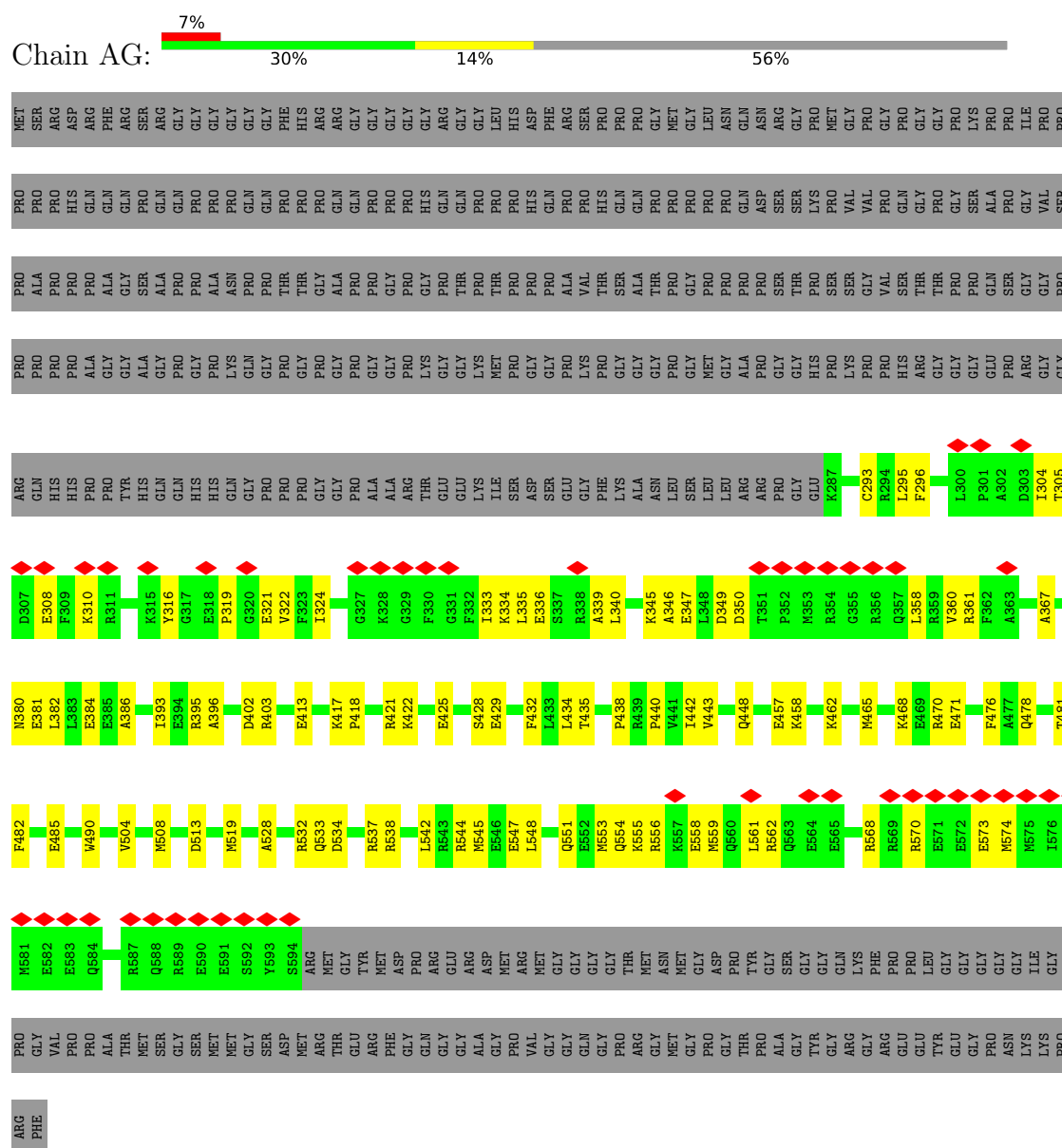
- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)



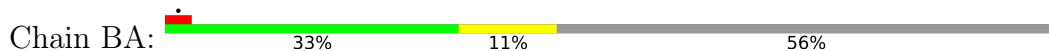




- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)



- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)



MET	ARG	ARG	ASP	ARG	PHE	ARG	SER	SER	GLY	GLY	GLY	GLY	PHE	HIS	ARG	ARG	GLY	GLY	GLY	GLY	GLY	GLY	LEU	LEU	ASP	PHE	ARG	SER	PRO	PRO	PRO	GLY	GLY	GLY	GLY	LEU	ASN	GLN	ASN	ARG	GLY	PRO	PRO	PRO	GLY	GLY	GLY	GLY	PRO	LYS	PRO	PRO	ILE	ILE	PRO	PRO	PRO
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PRO	PRO	PRO	HIS	GLN	GLN	GLN	PRO	GLN	GLN	PRO	PRO	PRO	PRO	PRO	HIS	GLN	GLN	GLN	GLN	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLN	ASP	SER	SER	LYS	PRO	VAL	VAL	GLN	GLN	GLN	GLY	PRO	PRO	GLY	GLY	SER	ALA	PRO	GLY	PRO	VAL	VAL	SER
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PRO	ALA	PRO	PRO	PRO	PRO	GLY	SER	ALA	PRO	PRO	ALA	ALA	ASN	PRO	PRO	THR	THR	GLY	ALA	PRO	PRO	GLY	GLY	PRO	PRO	PRO	PRO	VAL	ALA	ALA	SER	SER	THR	THR	GLY	VAL	SER	SER	THR	THR	PRO	PRO	GLN	SER	SER	GLY	GLY	PRO	PRO
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PRO	PRO	PRO	PRO	ALA	GLY	GLY	GLY	GLY	LYS	GLN	GLY	PRO	GLY	PRO	PRO	PRO	LYS	GLY	GLY	GLY	LYS	MET	GLY	GLY	PRO	PRO	PRO	PRO	ALA	GLY	GLY	GLY	GLY	GLY	HIS	PRO	PRO	PRO	GLY	GLY	GLY	GLU	ARG	GLY	GLY
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ARG	GLN	HIS	HIS	PRO	PRO	TYR	HIS	GLN	GLN	HIS	HIS	GLN	GLY	PRO	PRO	PRO	GLY	GLY	GLY	PRO	ALA	ALA	ARG	THR	GLU	GLU	LYS	ILE	SER	ASP	SER	SER	GLY	GLY	PHE	LYS	ALA	ASN	LEU	SER	SER	LEU	LEU	LEU	LEU	ARG	ARG	ARG	PRO	GLY	GLY	K287	T288	Y289	T290	C293	R294	L295	F296	V297	C298	N299	L300	P301	P302	P303	P304	P305	P306	P307	P308	P309	P310	P311	P312	P313	P314	P315	P316	P317	P318	P319	P320	P321	P322	P323	P324	P325	P326	P327	P328	P329	P330	P331	P332	P333	P334	P335	P336	P337	P338	P339	P340	P341	P342	P343	P344	P345	P346	P347	P348	P349	P350	P351	P352	P353	P354	P355	P356	P357	P358	P359	P360	P361	P362	P363	P364	P365	P366	P367	P368	P369	P370	P371	P372	P373	P374	P375	P376	P377	P378	P379	P380	P381	P382	P383	P384	P385	P386	P387	P388	P389	P390	P391	P392	P393	P394	P395	P396	P397	P398	P399	P400	P401	P402	P403	P404	P405	P406	P407	P408	P409	P410	P411	P412	P413	P414	P415	P416	P417	P418	P419	P420	P421	P422	P423	P424	P425	P426	P427	P428	P429	P430	P431	P432	P433	P434	P435	P436	P437	P438	P439	P440	P441	P442	P443	P444	P445	P446	P447	P448	P449	P450	P451	P452	P453	P454	P455	P456	P457	P458	P459	P460	P461	P462	P463	P464	P465	P466	P467	P468	P469	P470	P471	P472	P473	P474	P475	P476	P477	P478	P479	P480	P481	P482	P483	P484	P485	P486	P487	P488	P489	P490	P491	P492	P493	P494	P495	P496	P497	P498	P499	P500	P501	P502	P503	P504	P505	P506	P507	P508	P509	P510	P511	P512	P513	P514	P515	P516	P517	P518	P519	P520	P521	P522	P523	P524	P525	P526	P527	P528	P529	P530	P531	P532	P533	P534	P535	P536	P537	P538	P539	P540	P541	P542	P543	P544	P545	P546	P547	P548	P549	P550	P551	P552	P553	P554	P555	P556	P557	P558	P559	P560	P561	P562	P563	P564	P565	P566	P567	P568	P569	P570	P571	P572	P573	P574	P575	P576	P577	P578	P579	P580	P581	P582	P583	P584	P585	P586	P587	P588	P589	P590	P591	P592	P593	P594	P595	P596	P597	P598	P599	P600	P601	P602	P603	P604	P605	P606	P607	P608	P609	P610	P611	P612	P613	P614	P615	P616	P617	P618	P619	P620	P621	P622	P623	P624	P625	P626	P627	P628	P629	P630	P631	P632	P633	P634	P635	P636	P637	P638	P639	P640	P641	P642	P643	P644	P645	P646	P647	P648	P649	P650	P651	P652	P653	P654	P655	P656	P657	P658	P659	P660	P661	P662	P663	P664	P665	P666	P667	P668	P669	P670	P671	P672	P673	P674	P675	P676	P677	P678	P679	P680	P681	P682	P683	P684	P685	P686	P687	P688	P689	P690	P691	P692	P693	P694	P695	P696	P697	P698	P699	P700	P701	P702	P703	P704	P705	P706	P707	P708	P709	P710	P711	P712	P713	P714	P715	P716	P717	P718	P719	P720	P721	P722	P723	P724	P725	P726	P727	P728	P729	P730	P731	P732	P733	P734	P735	P736	P737	P738	P739	P740	P741	P742	P743	P744	P745	P746	P747	P748	P749	P750	P751	P752	P753	P754	P755	P756	P757	P758	P759
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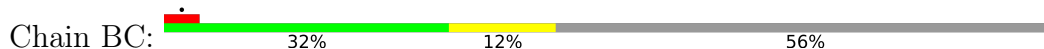
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Residue	Position	Frequency	Conservation	Structure
R562	562	0.00	0.00	Arginine
E565	565	0.00	0.00	Glutamic acid
R568	568	0.00	0.00	Arginine
M575	575	0.00	0.00	Methionine
R579	579	0.00	0.00	Arginine
R586	586	0.00	0.00	Arginine
R587	587	0.00	0.00	Arginine
E591	591	0.00	0.00	Glutamic acid
S592	592	0.00	0.00	Serine
Y593	593	0.00	0.00	Tyrosine
S594	594	0.00	0.00	Serine
ARG		0.00	0.00	Arginine
MET		0.00	0.00	Methionine
GLY		0.00	0.00	Glycine
TYR		0.00	0.00	Tyrosine
MET		0.00	0.00	Methionine
ASP		0.00	0.00	Aspartic acid
PRO		0.00	0.00	Proline
ARG		0.00	0.00	Arginine
GLU		0.00	0.00	Glutamic acid
ARG		0.00	0.00	Arginine
ASP		0.00	0.00	Aspartic acid
MET		0.00	0.00	Methionine
ARG		0.00	0.00	Arginine
MET		0.00	0.00	Methionine
GLY		0.00	0.00	Glycine
GLY		0.00	0.00	Glycine
GLY		0.00	0.00	Glycine
THR		0.00	0.00	Threonine
MET		0.00	0.00	Methionine
ASN		0.00	0.00	Asparagine
MET		0.00	0.00	Methionine
GLY		0.00	0.00	Glycine
ASP		0.00	0.00	Aspartic acid
PRO		0.00	0.00	Proline
TYR		0.00	0.00	Tyrosine
GLY		0.00	0.00	Glycine
SER		0.00	0.00	Serine
GLY		0.00	0.00	Glycine
GLY		0.00	0.00	Glycine
GLN		0.00	0.00	Glutamine
LYS		0.00	0.00	Lysine
PHE		0.00	0.00	Phenylalanine
PRO		0.00	0.00	Proline
PRO		0.00	0.00	Proline
LEU		0.00	0.00	Leucine
GLY		0.00	0.00	Glycine
GLY		0.00	0.00	Glycine
GLY		0.00	0.00	Glycine
GLY		0.00	0.00	Glycine

GLY	TYR	GLU	ALA	ASN	PRO	GLY	VAL	PRO	PRO	ALA	THR	MET	SER	GLY	SER	ASP	MET	MET	GLY	GLY	GLN	GLY	GLY	ALA	GLY	PRO	VAL	GLY	GLY	GLN	GLY	PRO	ARG	GLY	MET	GLY	GLY	TYR	ALA	ALA	PRO	THR	GLY	GLY	ARG	GLY	GLU	GLU	TYR	GLU	GLY	GLY
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PRO
ASN
LYS
LYS
PRO
ARG
PHE

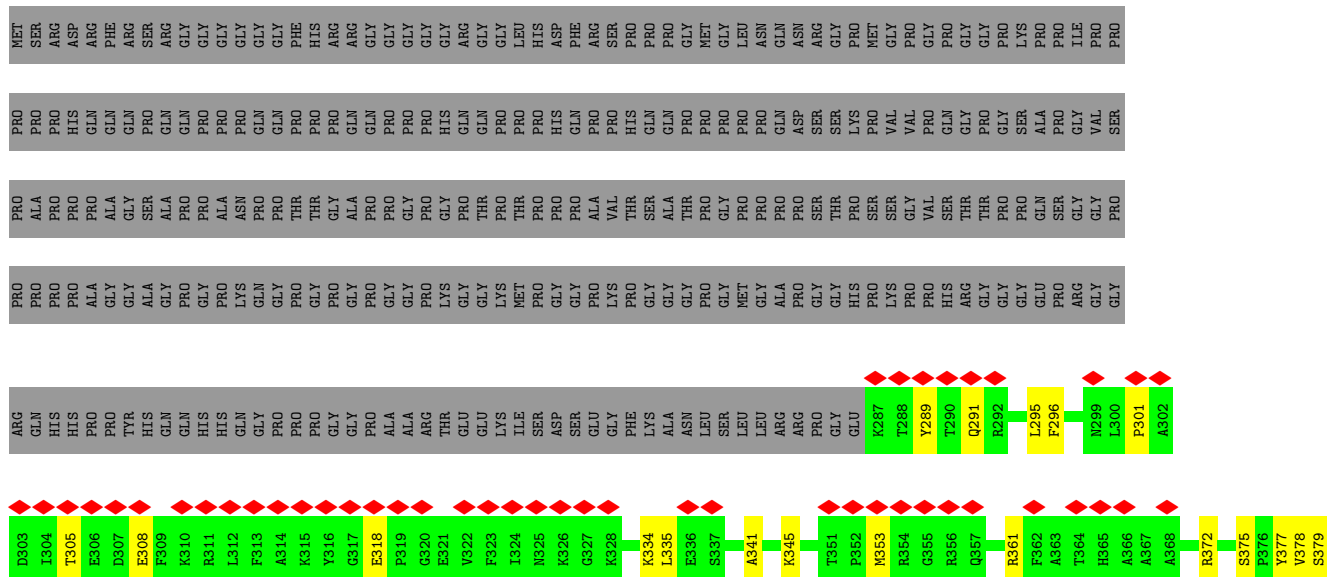
- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

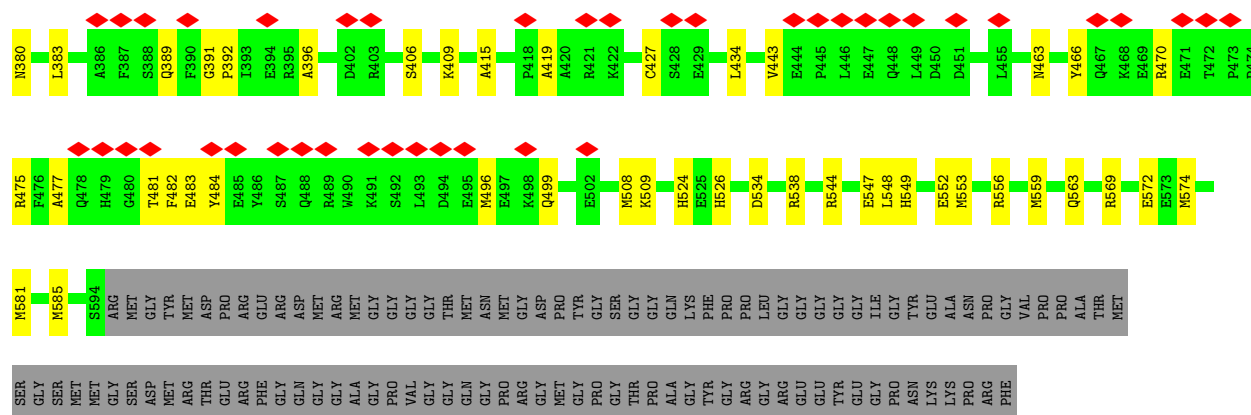
[illegible]

PRO	PRO	PRO	HIS	GLN	GLN	GLN	PRO	PRO	GLN	GLN	PRO	PRO	PRO	PRO	PRO	HIS	GLN	GLN	GLN	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLN	ASP	SER	SER	LYS	VAL	VAL	VAL	PRO	GLN	GLY	PRO	GLY	GLY	SER	ALA	PRO	GLY	GLY	VAL	VAL	SER
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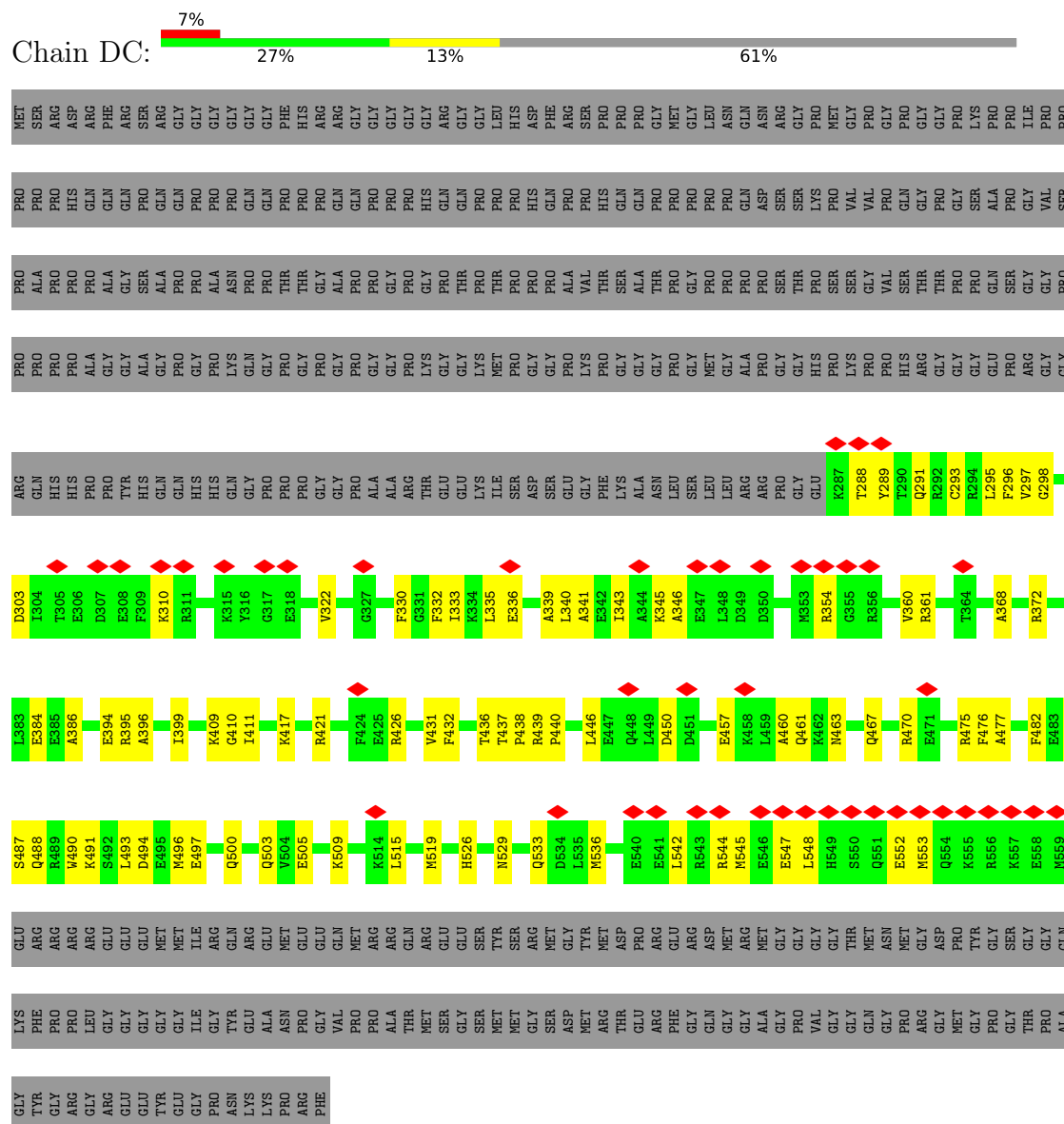
PRO	ALA	PRO	PRO	PRO	PRO	GLY	SER	ALA	PRO	ALA	ALA	ASN	PRO	PRO	THR	THR	GLY	ALA	PRO	PRO	GLY	GLY	PRO	GLY	THR	THR	THR	PRO	PRO	VAL	ALA	ALA	SER	SER	ALA	THR	THR	GLY	VAL	SER	SER	SER	THR	THR	PRO	PRO	Gln	SER	GLY	GLY	PRO
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[illegible]

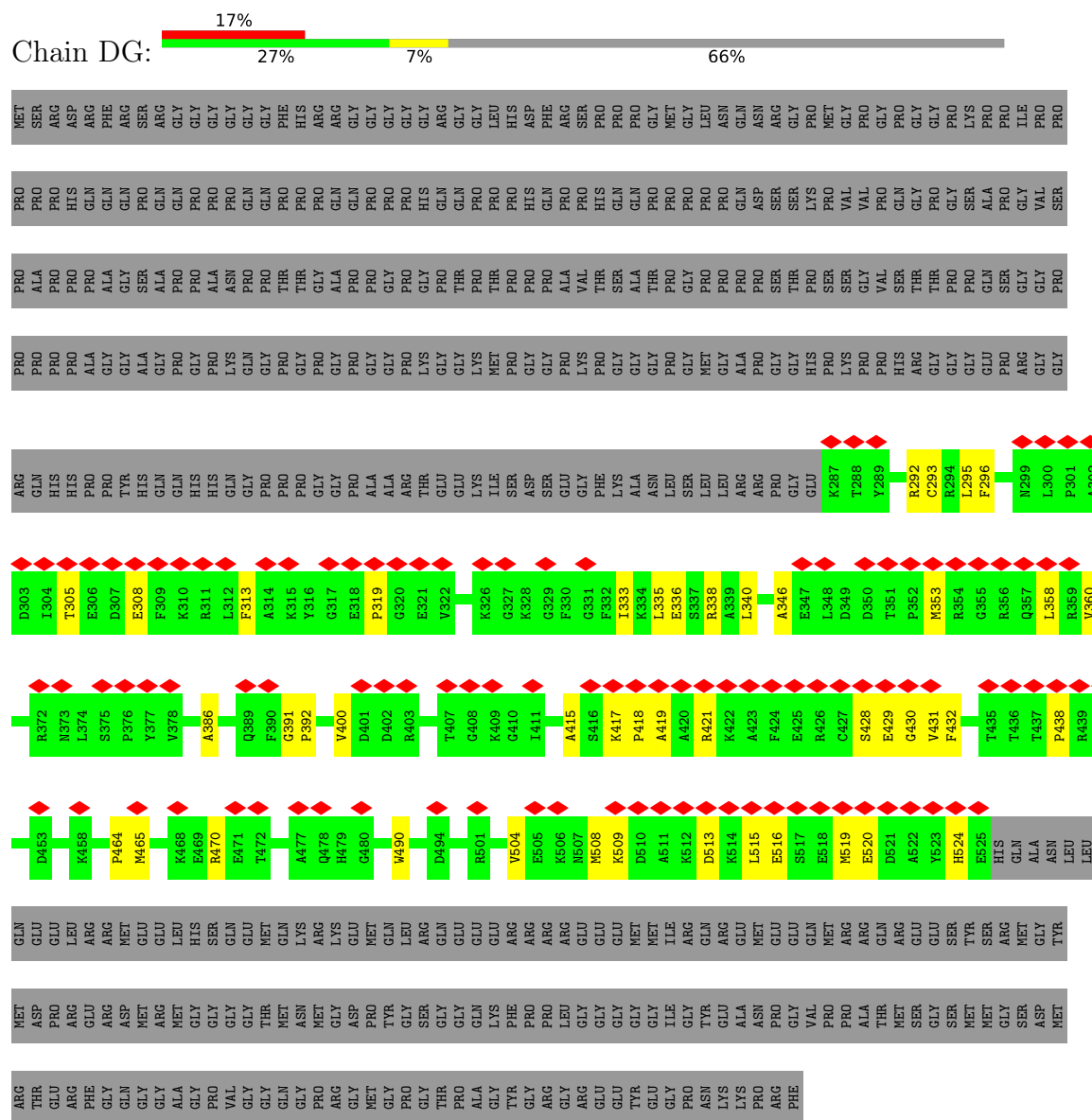




- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

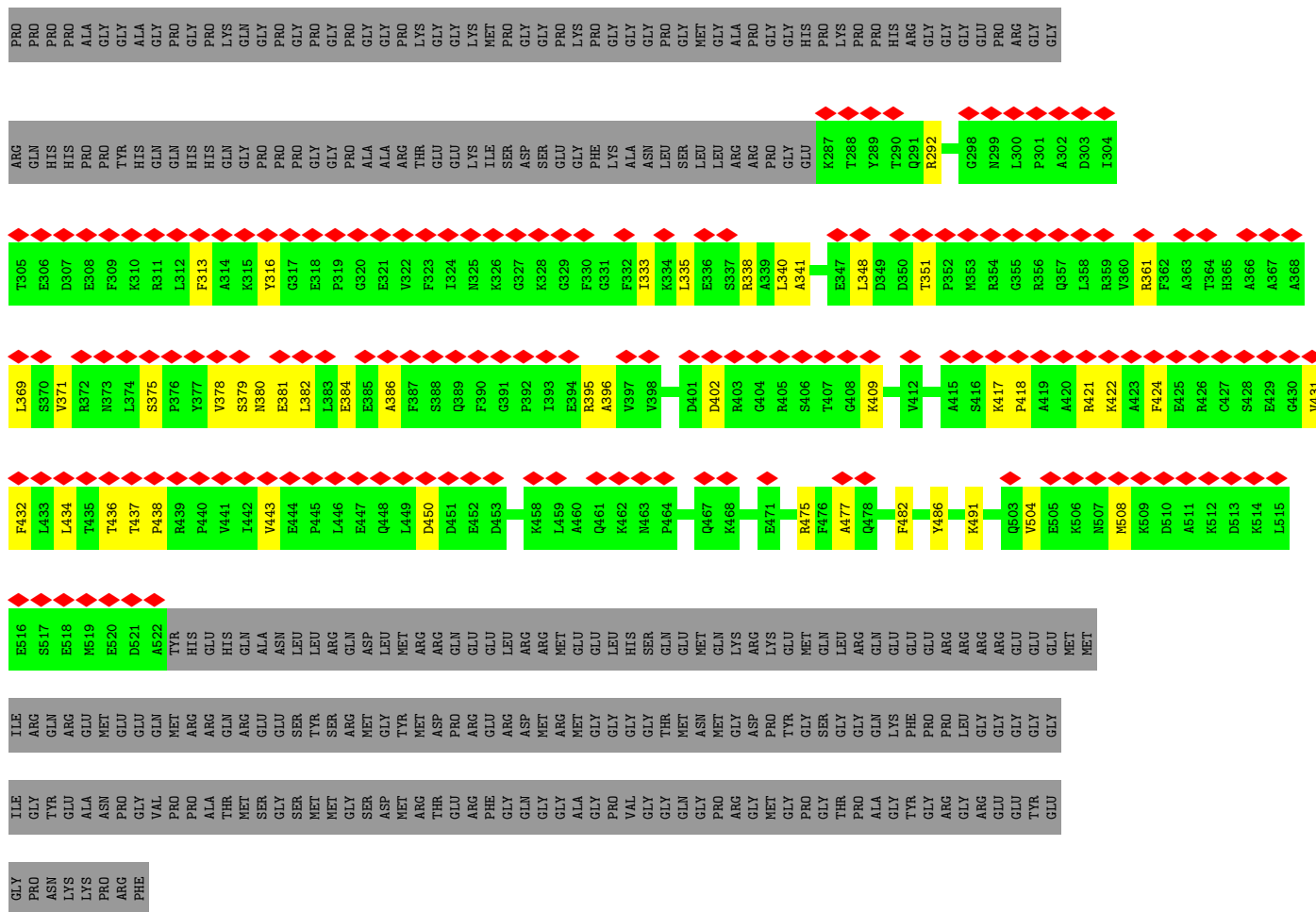


- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

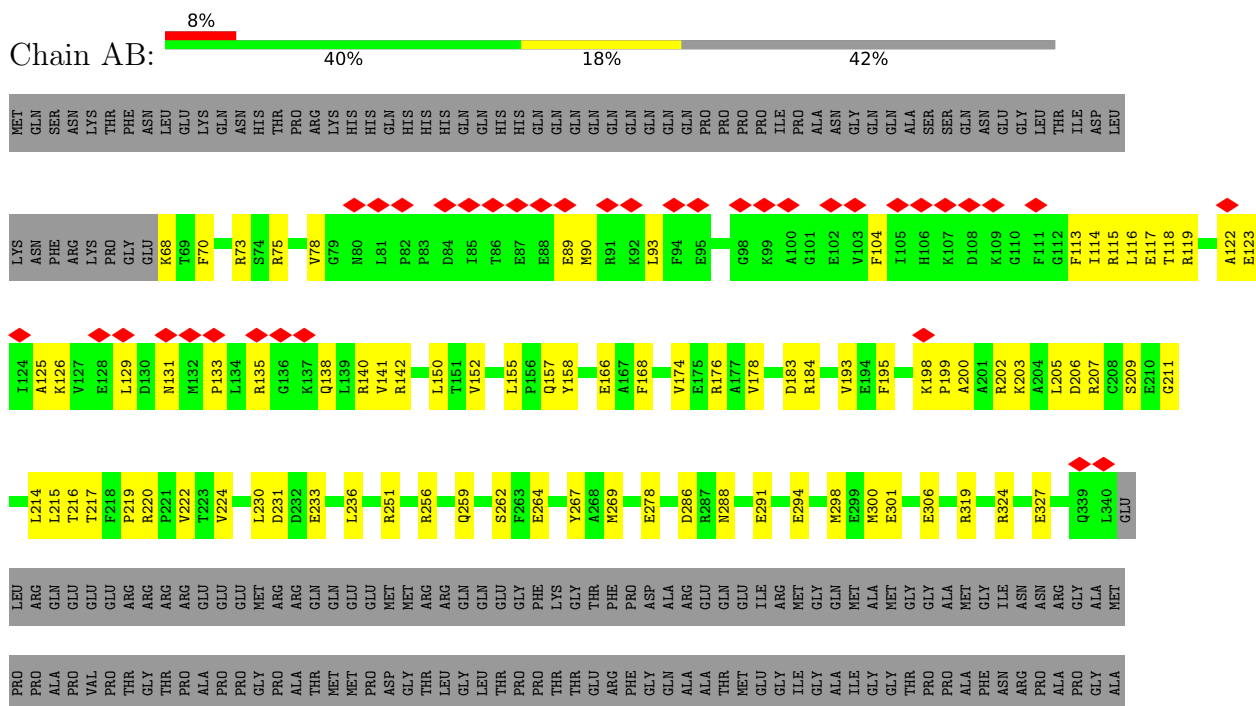


- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

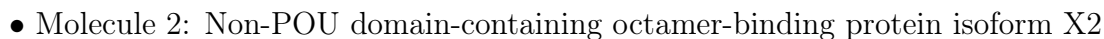




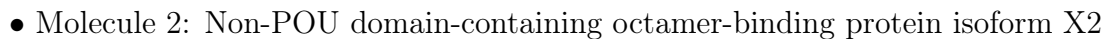
- Molecule 2: Non-POU domain-containing octamer-binding protein isoform X2



Frequency	Percentage
Daily	41%
Weekly	17%
Monthly	42%

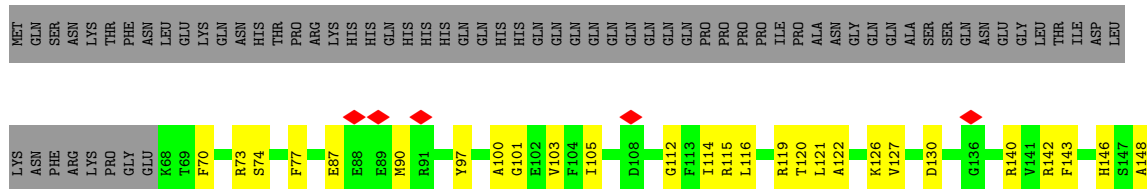


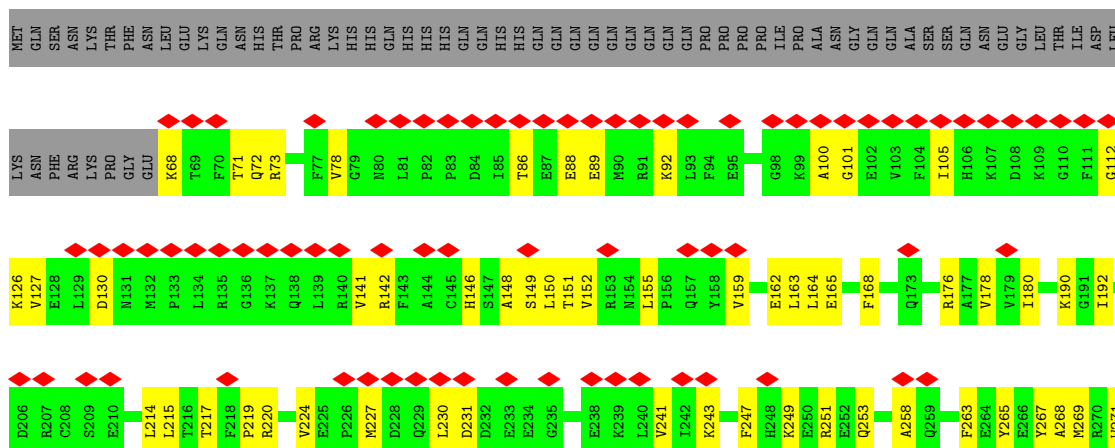
Frequency	Percentage
Daily	42%
Weekly	15%
Monthly	42%



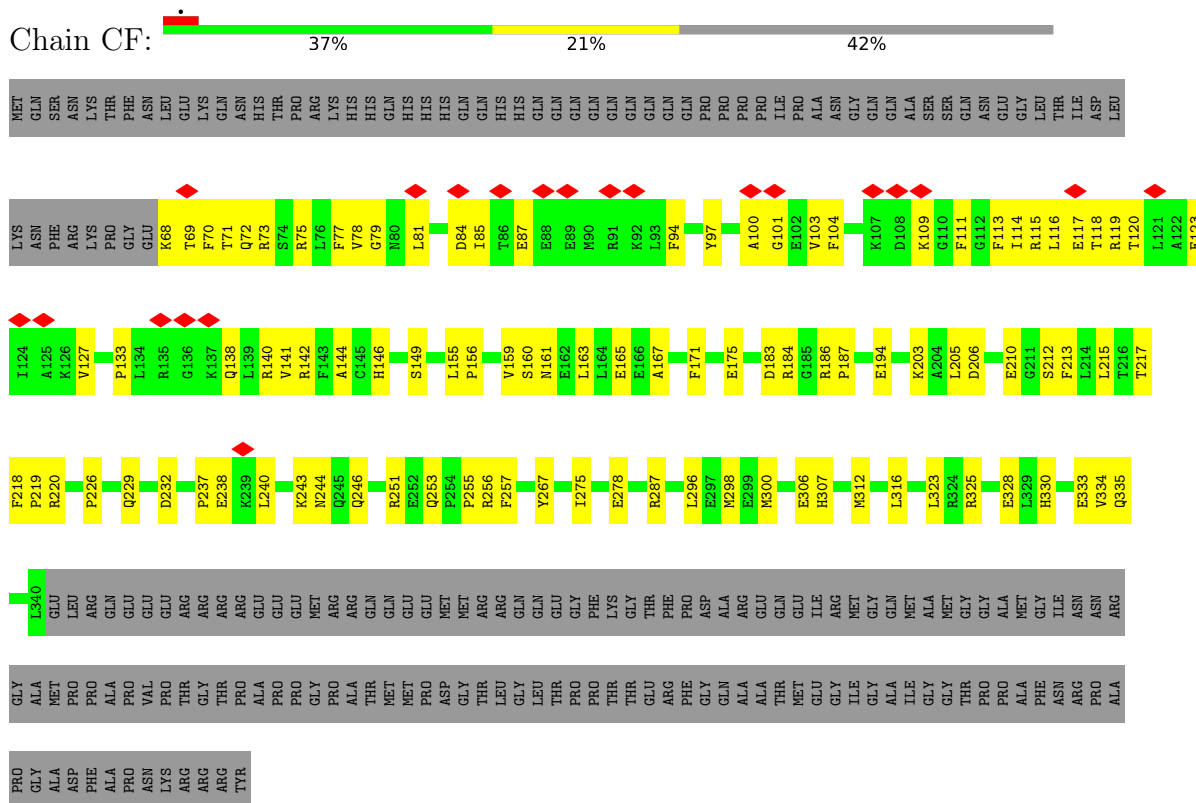
Frequency	Percentage
Very often	6%
Often	39%
Sometimes	18%
Never	42%



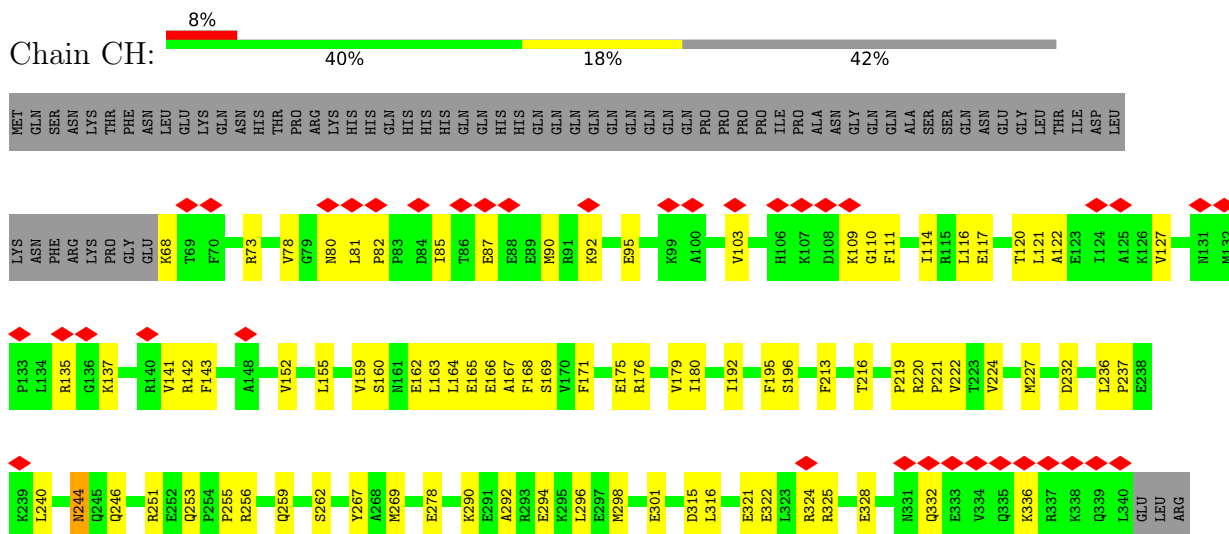




- Molecule 2: Non-POU domain-containing octamer-binding protein isoform X2



- Molecule 2: Non-POU domain-containing octamer-binding protein isoform X2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2974535	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	85.165	Depositor
Minimum map value	-51.683	Depositor
Average map value	-0.012	Depositor
Map value standard deviation	1.132	Depositor
Recommended contour level	5	Depositor
Map size (Å)	484.352, 484.352, 484.352	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.946, 0.946, 0.946	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	AA	0.16	0/2601	0.34	0/3476
1	AC	0.19	0/2567	0.38	0/3430
1	AE	0.13	0/2601	0.32	0/3476
1	AG	0.16	0/2601	0.37	0/3476
1	BA	0.17	0/2601	0.34	0/3476
1	BC	0.17	0/2601	0.34	0/3476
1	BE	0.17	0/2601	0.36	0/3476
1	BG	0.16	0/2601	0.35	0/3476
1	CA	0.13	0/2291	0.30	0/3071
1	CC	0.12	0/2601	0.30	0/3476
1	CE	0.16	0/2601	0.33	0/3476
1	CG	0.14	0/2601	0.32	0/3476
1	DA	0.11	0/2601	0.29	0/3476
1	DC	0.14	0/2302	0.30	0/3085
1	DE	0.11	0/1937	0.28	0/2603
1	DG	0.09	0/1970	0.25	0/2648
2	AB	0.15	0/2289	0.35	0/3065
2	AD	0.20	0/2289	0.39	0/3065
2	AF	0.11	0/2289	0.31	0/3065
2	AH	0.18	0/2289	0.35	0/3065
2	BB	0.16	0/2289	0.33	0/3065
2	BD	0.17	0/2289	0.34	0/3065
2	BF	0.21	0/2289	0.39	0/3065
2	BH	0.18	0/2289	0.33	0/3065
2	CB	0.11	0/2289	0.29	0/3065
2	CD	0.11	0/2017	0.30	0/2707
2	CF	0.17	0/2289	0.35	0/3065
2	CH	0.16	0/2289	0.31	0/3065
2	DB	0.15	0/2025	0.31	0/2718
2	DD	0.11	0/2289	0.34	0/3065
2	DF	0.11	0/2289	0.33	0/3065
2	DH	0.10	0/2289	0.29	0/3065
All	All	0.15	0/75766	0.33	0/101408

There are no bond length outliers.

There are no bond angle outliers.

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	AA	2560	0	2521	70	0
1	AC	2527	0	2496	70	0
1	AE	2560	0	2521	65	0
1	AG	2560	0	2521	86	0
1	BA	2560	0	2521	59	0
1	BC	2560	0	2521	69	0
1	BE	2560	0	2521	81	0
1	BG	2560	0	2521	80	0
1	CA	2251	0	2227	39	0
1	CC	2560	0	2521	80	0
1	CE	2560	0	2521	77	0
1	CG	2560	0	2521	58	0
1	DA	2560	0	2521	46	0
1	DC	2262	0	2240	67	0
1	DE	1901	0	1881	34	0
1	DG	1932	0	1903	37	0
2	AB	2250	0	2256	66	0
2	AD	2250	0	2256	65	0
2	AF	2250	0	2256	50	0
2	AH	2250	0	2256	65	0
2	BB	2250	0	2256	58	0
2	BD	2250	0	2256	76	0
2	BF	2250	0	2256	68	0
2	BH	2250	0	2256	67	0
2	CB	2250	0	2256	47	0
2	CD	1979	0	1974	55	0
2	CF	2250	0	2256	77	0
2	CH	2250	0	2256	63	0
2	DB	1987	0	1985	38	0
2	DD	2250	0	2256	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	DF	2250	0	2256	47	0
2	DH	2250	0	2256	64	0
All	All	74499	0	74021	1658	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 11.

The worst 5 of 1658 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)
2:DH:129:LEU:HA	2:DH:132:MET:HE3	1.58	0.86
1:BE:452:GLU:HA	2:BF:176:ARG:HH22	1.41	0.85
1:BE:292:ARG:HD2	1:BE:395:ARG:HD2	1.57	0.85
1:BC:339:ALA:HB1	2:BD:127:VAL:HG13	1.59	0.84
2:CF:186:ARG:HE	2:CF:187:PRO:HD2	1.42	0.82

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	AA	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	AC	302/703 (43%)	295 (98%)	7 (2%)	0	100	100
1	AE	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	AG	306/703 (44%)	297 (97%)	9 (3%)	0	100	100
1	BA	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	BC	306/703 (44%)	297 (97%)	9 (3%)	0	100	100
1	BE	306/703 (44%)	298 (97%)	8 (3%)	0	100	100
1	BG	306/703 (44%)	294 (96%)	12 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CA	273/703 (39%)	268 (98%)	5 (2%)	0	100	100
1	CC	306/703 (44%)	302 (99%)	4 (1%)	0	100	100
1	CE	306/703 (44%)	296 (97%)	10 (3%)	0	100	100
1	CG	306/703 (44%)	301 (98%)	5 (2%)	0	100	100
1	DA	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	DC	274/703 (39%)	270 (98%)	4 (2%)	0	100	100
1	DE	234/703 (33%)	229 (98%)	5 (2%)	0	100	100
1	DG	237/703 (34%)	231 (98%)	6 (2%)	0	100	100
2	AB	271/472 (57%)	264 (97%)	7 (3%)	0	100	100
2	AD	271/472 (57%)	266 (98%)	5 (2%)	0	100	100
2	AF	271/472 (57%)	265 (98%)	6 (2%)	0	100	100
2	AH	271/472 (57%)	268 (99%)	3 (1%)	0	100	100
2	BB	271/472 (57%)	263 (97%)	8 (3%)	0	100	100
2	BD	271/472 (57%)	265 (98%)	6 (2%)	0	100	100
2	BF	271/472 (57%)	260 (96%)	11 (4%)	0	100	100
2	BH	271/472 (57%)	267 (98%)	4 (2%)	0	100	100
2	CB	271/472 (57%)	266 (98%)	5 (2%)	0	100	100
2	CD	241/472 (51%)	236 (98%)	5 (2%)	0	100	100
2	CF	271/472 (57%)	267 (98%)	4 (2%)	0	100	100
2	CH	271/472 (57%)	260 (96%)	11 (4%)	0	100	100
2	DB	242/472 (51%)	237 (98%)	5 (2%)	0	100	100
2	DD	271/472 (57%)	268 (99%)	3 (1%)	0	100	100
2	DF	271/472 (57%)	266 (98%)	5 (2%)	0	100	100
2	DH	271/472 (57%)	266 (98%)	5 (2%)	0	100	100
All	All	8963/18800 (48%)	8762 (98%)	201 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	AA	273/557 (49%)	273 (100%)	0	100	100
1	AC	269/557 (48%)	269 (100%)	0	100	100
1	AE	273/557 (49%)	273 (100%)	0	100	100
1	AG	273/557 (49%)	273 (100%)	0	100	100
1	BA	273/557 (49%)	273 (100%)	0	100	100
1	BC	273/557 (49%)	273 (100%)	0	100	100
1	BE	273/557 (49%)	273 (100%)	0	100	100
1	BG	273/557 (49%)	273 (100%)	0	100	100
1	CA	240/557 (43%)	240 (100%)	0	100	100
1	CC	273/557 (49%)	273 (100%)	0	100	100
1	CE	273/557 (49%)	273 (100%)	0	100	100
1	CG	273/557 (49%)	273 (100%)	0	100	100
1	DA	273/557 (49%)	273 (100%)	0	100	100
1	DC	241/557 (43%)	241 (100%)	0	100	100
1	DE	202/557 (36%)	202 (100%)	0	100	100
1	DG	205/557 (37%)	205 (100%)	0	100	100
2	AB	243/406 (60%)	243 (100%)	0	100	100
2	AD	243/406 (60%)	243 (100%)	0	100	100
2	AF	243/406 (60%)	243 (100%)	0	100	100
2	AH	243/406 (60%)	243 (100%)	0	100	100
2	BB	243/406 (60%)	243 (100%)	0	100	100
2	BD	243/406 (60%)	242 (100%)	1 (0%)	84	83
2	BF	243/406 (60%)	243 (100%)	0	100	100
2	BH	243/406 (60%)	242 (100%)	1 (0%)	84	83
2	CB	243/406 (60%)	243 (100%)	0	100	100
2	CD	213/406 (52%)	213 (100%)	0	100	100
2	CF	243/406 (60%)	243 (100%)	0	100	100
2	CH	243/406 (60%)	242 (100%)	1 (0%)	84	83
2	DB	214/406 (53%)	214 (100%)	0	100	100
2	DD	243/406 (60%)	243 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	DF	243/406 (60%)	243 (100%)	0	100	100
2	DH	243/406 (60%)	242 (100%)	1 (0%)	84	83
All	All	7989/15408 (52%)	7985 (100%)	4 (0%)	87	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	BD	253	GLN
2	BH	244	ASN
2	CH	244	ASN
2	DH	244	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	DB	307	HIS
1	DC	365	HIS
1	DE	463	ASN
2	AF	332	GLN
2	BD	253	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.

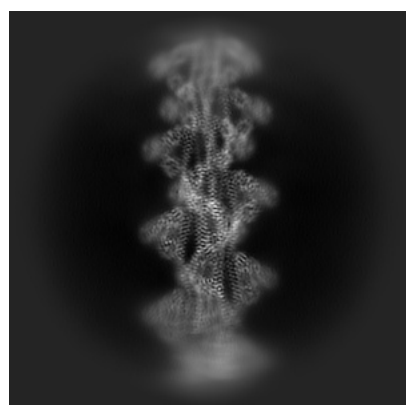
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51471. These allow visual inspection of the internal detail of the map and identification of artifacts.

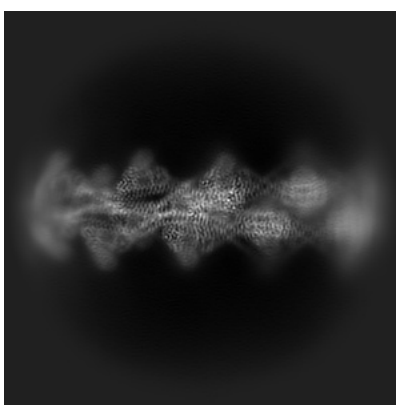
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

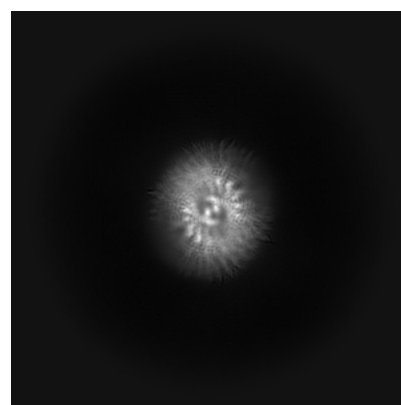
6.1.1 Primary map



X



Y

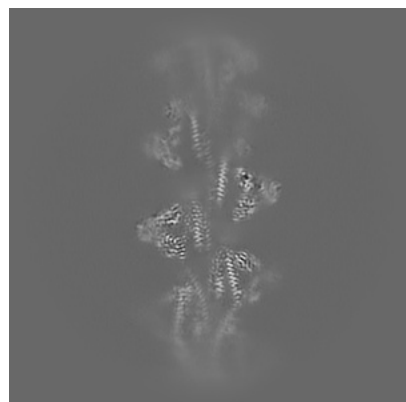


Z

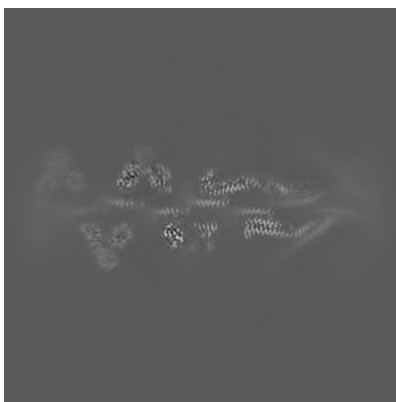
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

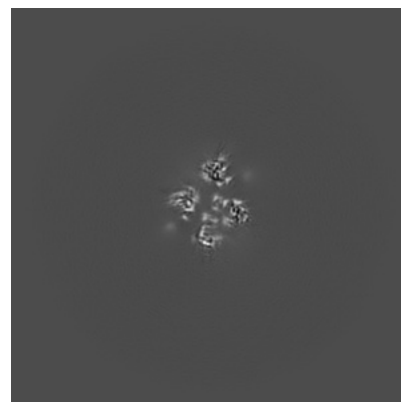
6.2.1 Primary map



X Index: 256



Y Index: 256

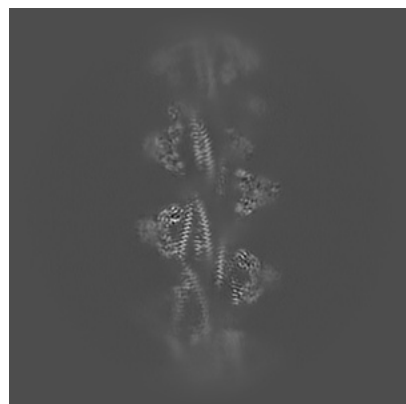


Z Index: 256

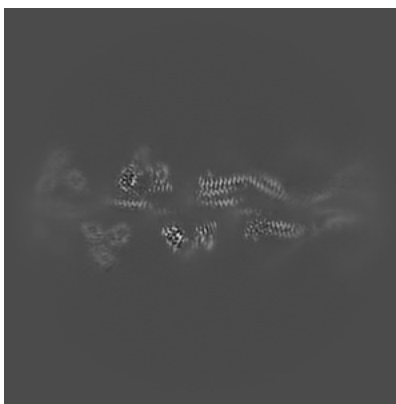
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

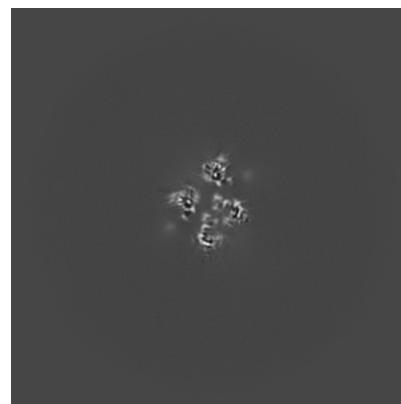
6.3.1 Primary map



X Index: 251



Y Index: 260

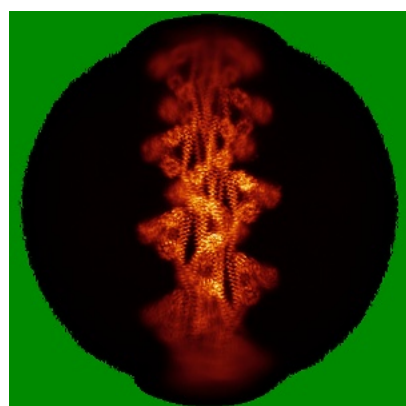


Z Index: 255

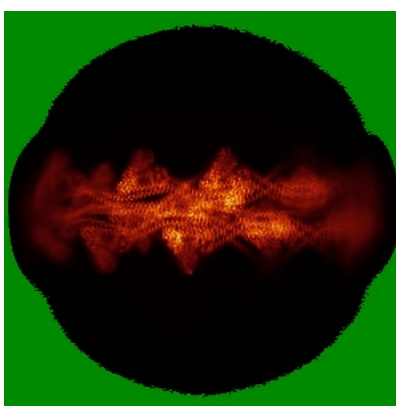
The images above show the largest variance slices of the map in three orthogonal directions.

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

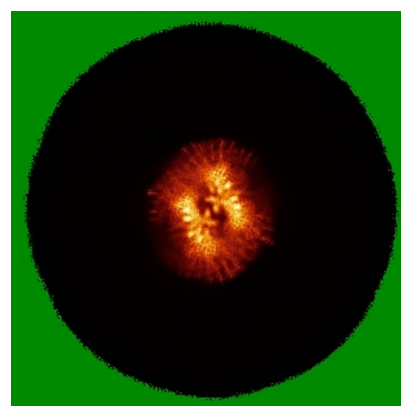
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

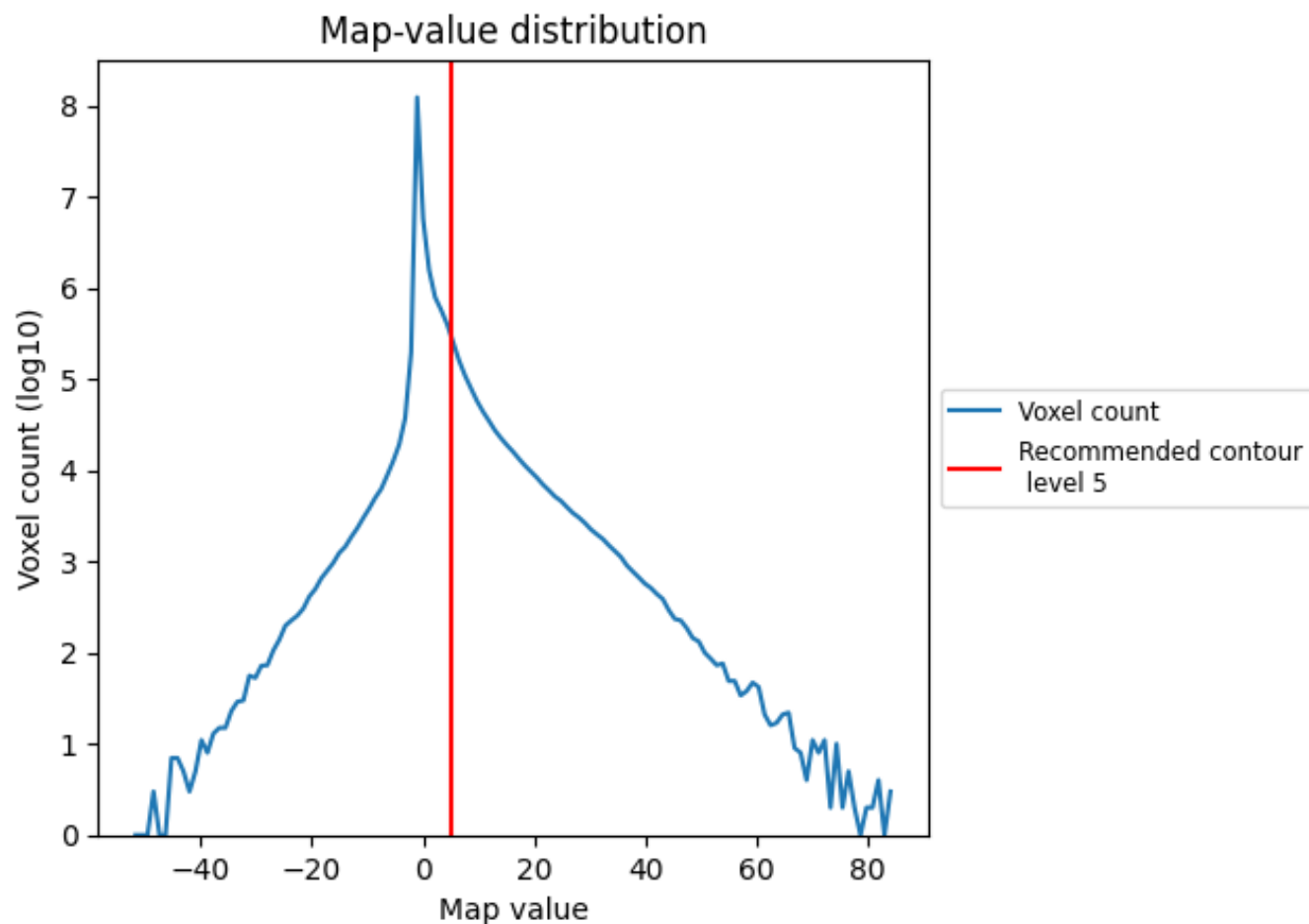
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

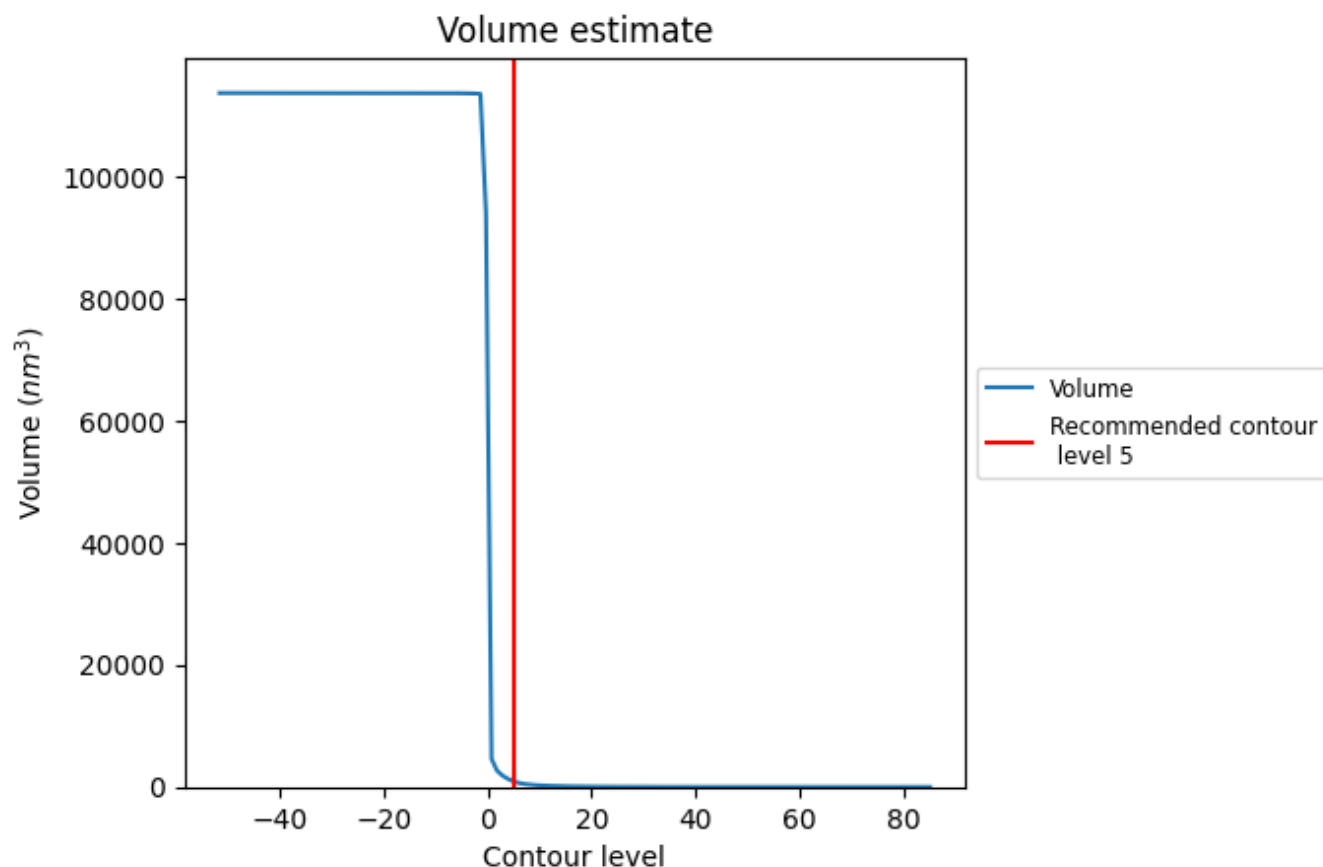
This section contains the results of statistical analysis of the map.

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.

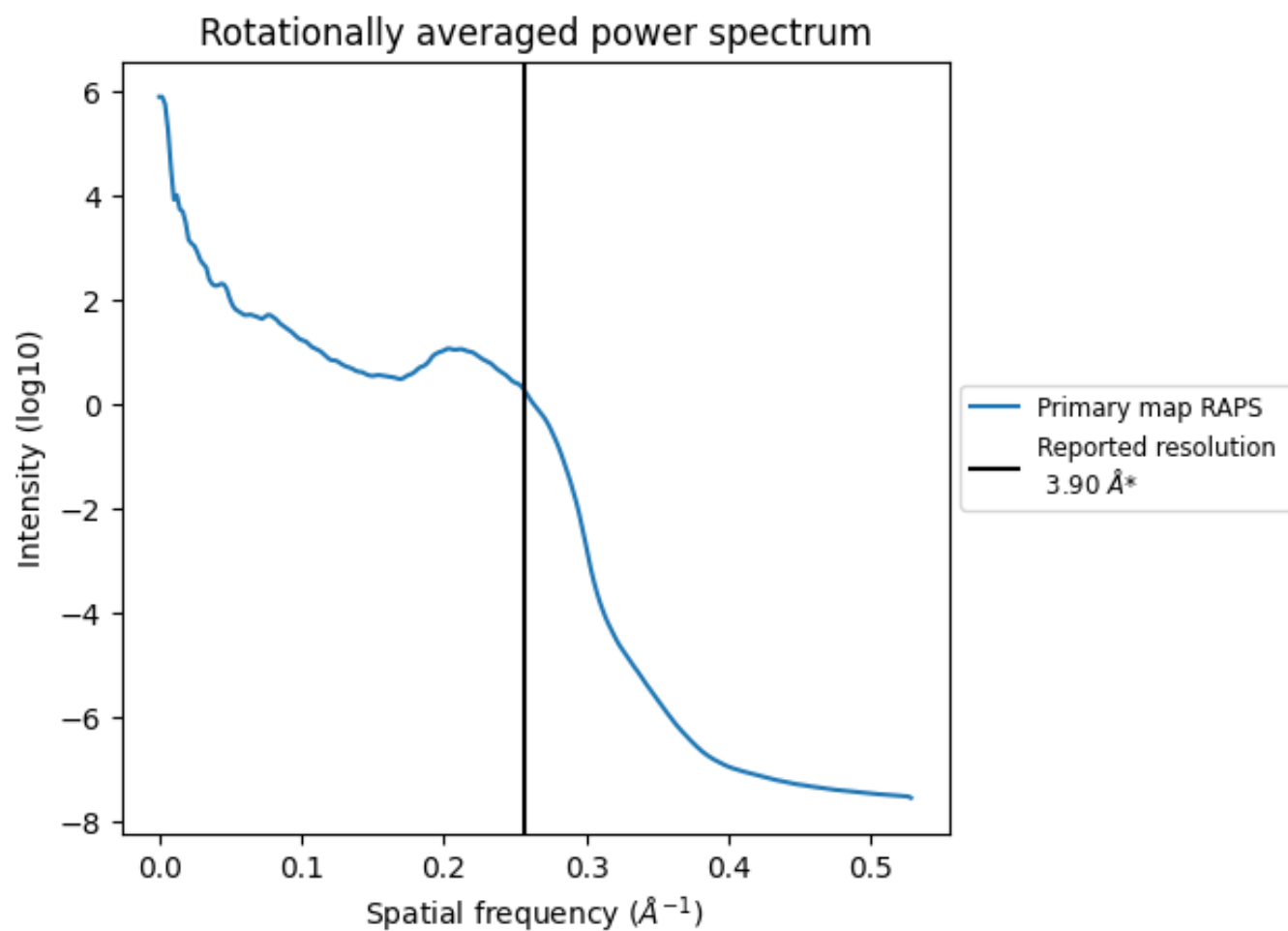
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 899 nm^3 ; this corresponds to an approximate mass of 812 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 0.256 \AA^{-1}

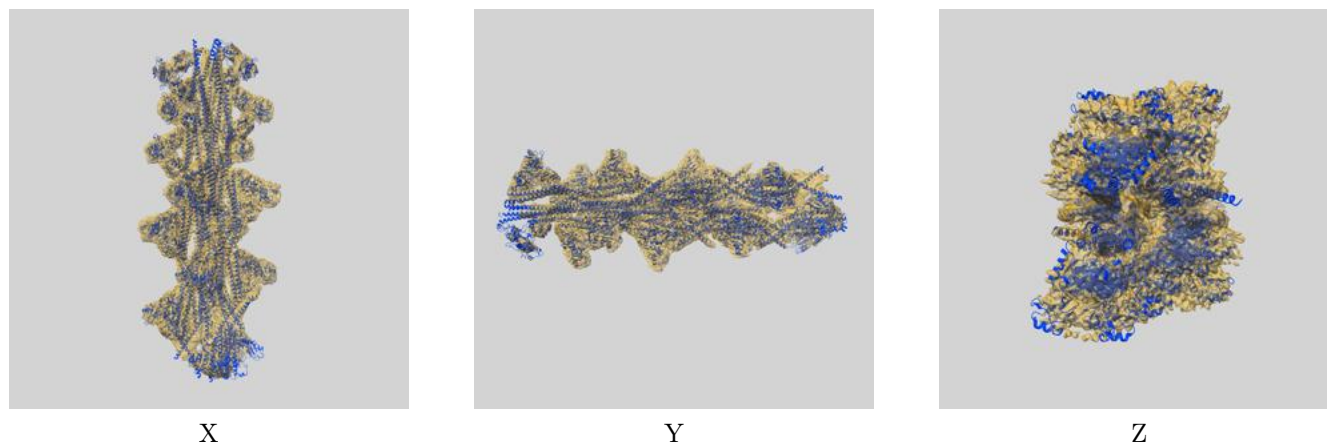
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

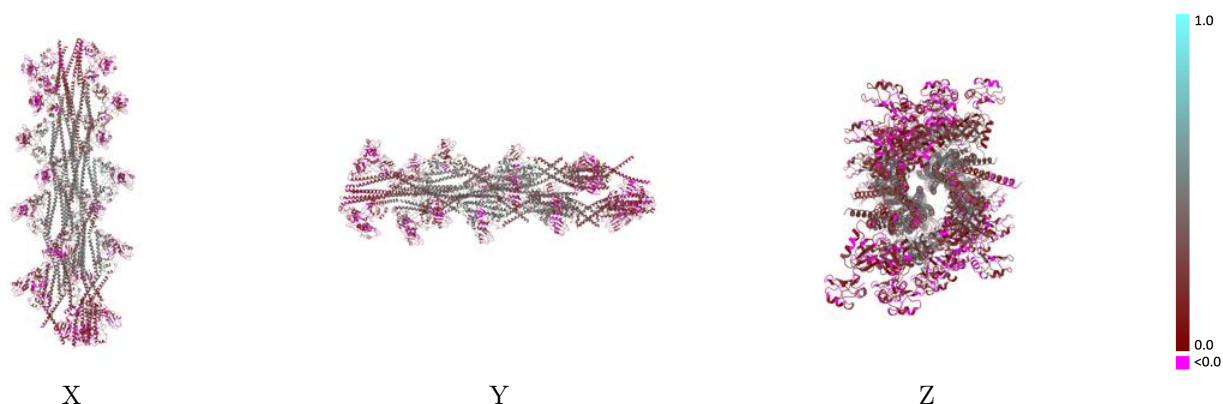
This section contains information regarding the fit between EMDB map EMD-51471 and PDB model 9GNI. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



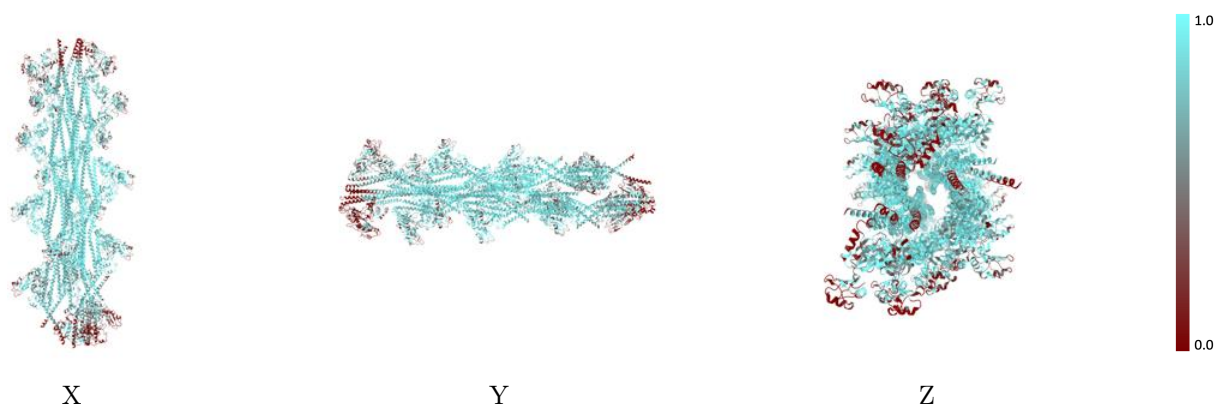
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



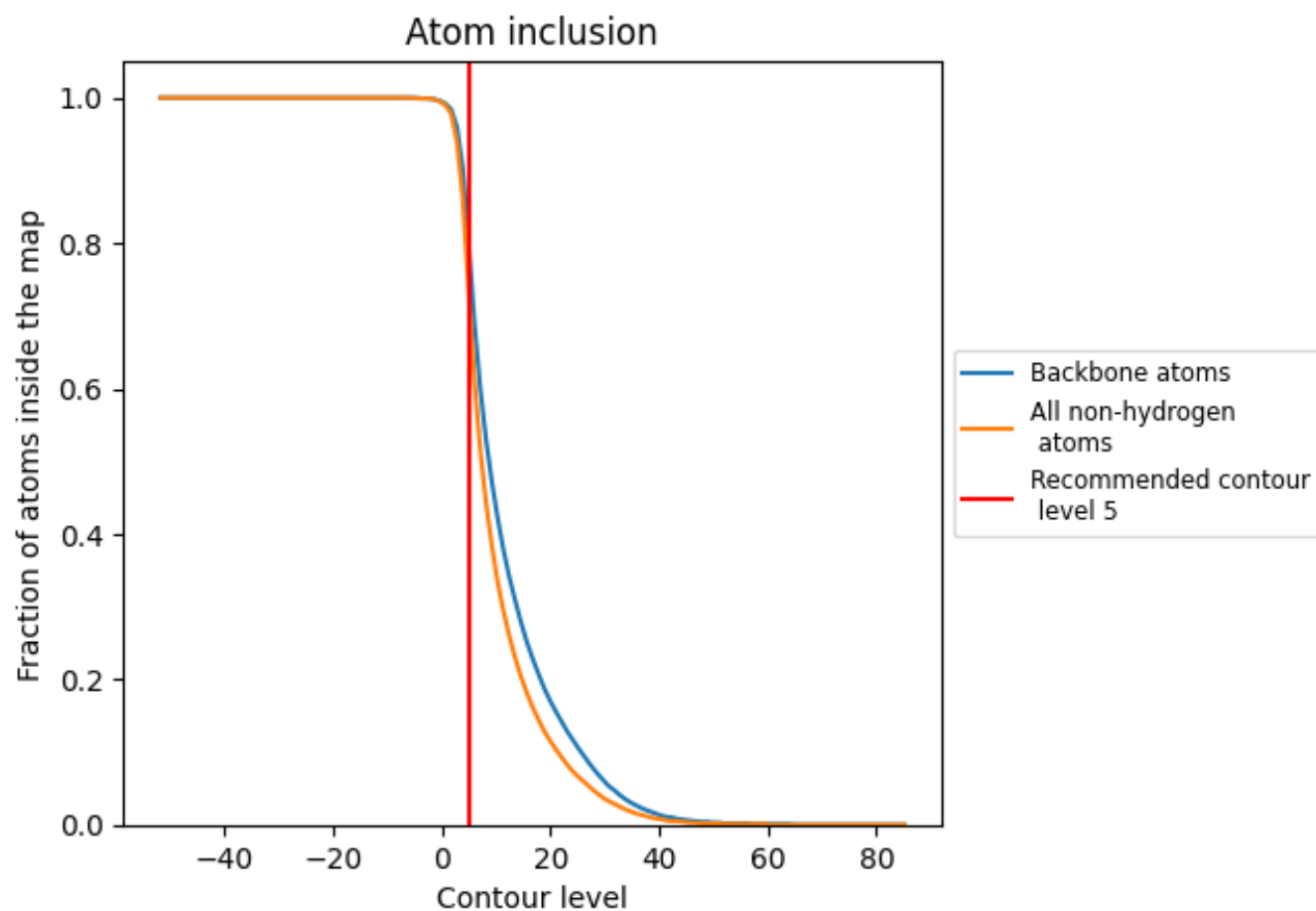
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 73% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7330	 0.2560
AA	 0.8540	 0.3370
AB	 0.8020	 0.3120
AC	 0.8610	 0.3170
AD	 0.8920	 0.3490
AE	 0.7600	 0.2560
AF	 0.6970	 0.2230
AG	 0.7340	 0.2710
AH	 0.8550	 0.3320
BA	 0.8620	 0.3240
BB	 0.8870	 0.3340
BC	 0.8490	 0.3390
BD	 0.8270	 0.3380
BE	 0.8890	 0.3660
BF	 0.8860	 0.3630
BG	 0.8840	 0.3350
BH	 0.9210	 0.3860
CA	 0.6580	 0.1700
CB	 0.7230	 0.2190
CC	 0.6340	 0.1850
CD	 0.5030	 0.1360
CE	 0.7270	 0.2620
CF	 0.8450	 0.3280
CG	 0.8080	 0.2670
CH	 0.7570	 0.2360
DA	 0.5990	 0.1850
DB	 0.4670	 0.1260
DC	 0.6580	 0.1500
DD	 0.7500	 0.2100
DE	 0.2690	 0.1010
DF	 0.3480	 0.0940
DG	 0.4390	 0.0860
DH	 0.5500	 0.1230

