



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:57 PM UTC

PDB ID : 7QXN / pdb_00007qxn
EMDB ID : EMD-14201
Title : Proteasome-ZFAND5 Complex Z+A state
Authors : Zhu, Y.; Lu, Y.
Deposited on : 2022-01-26
Resolution : 3.70 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:

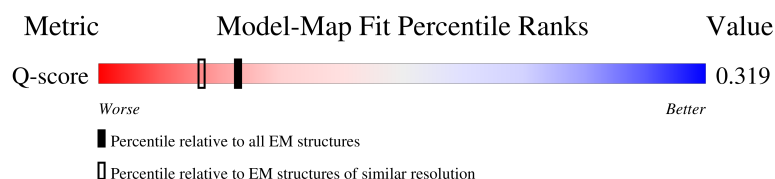
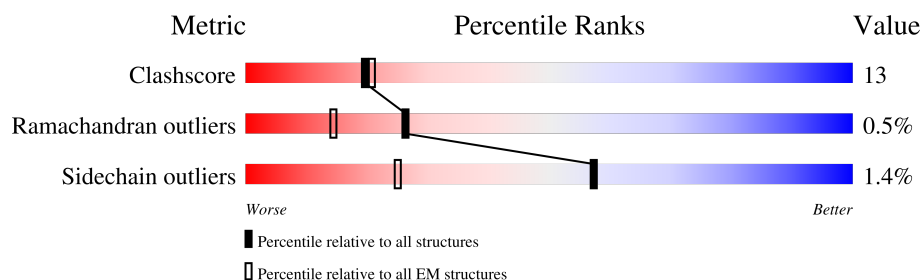
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	U	953	23% 59% 26% • 15%
2	V	533	35% 62% 31% • 5%
3	W	456	21% 66% 30% •
4	X	422	37% 73% 17% 10%

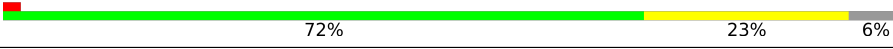
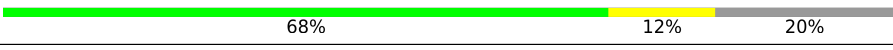
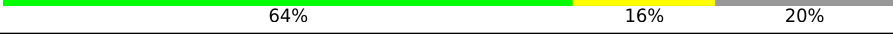
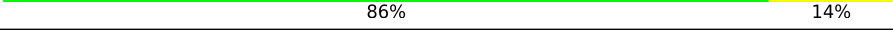
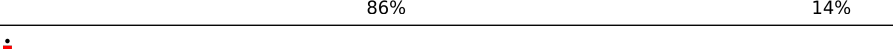
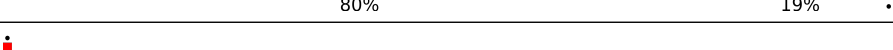
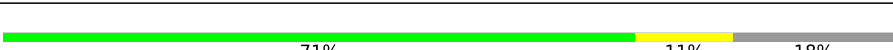
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Mol	Chain	Length	Quality of chain
5	Y	389	
6	Z	324	
7	a	376	
8	b	377	
9	c	309	
10	d	349	
11	e	70	
12	f	908	
13	A	433	
14	B	440	
15	C	398	
16	D	418	
17	E	403	
18	F	439	
19	G	245	
19	g	245	
20	H	233	
20	h	233	
21	I	260	
21	i	260	
22	J	247	
22	j	247	
23	K	240	
23	k	240	
24	L	268	

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Mol	Chain	Length	Quality of chain
24	l	268	
25	M	254	
25	m	254	
26	N	238	
26	n	238	
27	O	276	
27	o	276	
28	P	204	
28	p	204	
29	Q	201	
29	q	201	
30	R	262	
30	r	262	
31	S	240	
31	s	240	
32	T	263	
32	t	263	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 103713 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 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	812	Total	C	N	O	S	0	0
			6334	4023	1078	1189	44		

- Molecule 2 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V	508	Total	C	N	O	S	0	0
			3994	2530	712	738	14		

- Molecule 3 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	456	Total	C	N	O	S	0	0
			3693	2332	635	701	25		

- Molecule 4 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	380	Total	C	N	O	S	0	0
			3009	1918	509	570	12		

- Molecule 5 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Y	378	Total	C	N	O	S	0	0
			3115	1987	533	578	17		

- Molecule 6 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Z	286	Total	C	N	O	S	0	0
			2281	1457	392	427	5		

- Molecule 7 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	a	373	Total	C	N	O	S	0	0
			2995	1911	510	559	15		

- Molecule 8 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	b	191	Total	C	N	O	S	0	0
			1458	910	261	279	8		

- Molecule 9 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	c	287	Total	C	N	O	S	0	0
			2260	1430	389	422	19		

- Molecule 10 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	d	257	Total	C	N	O	S	0	0
			2116	1371	346	390	9		

- Molecule 11 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e	40	Total	C	N	O	S	0	0
			334	200	55	77	2		

- Molecule 12 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	f	889	Total	C	N	O	S	0	0
			6857	4306	1174	1331	46		

- Molecule 13 is a protein called 26S protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A	394	Total	C	N	O	S	0	0
			3096	1951	543	584	18		

- Molecule 14 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	B	384	Total	C	N	O	S	0	0
			3018	1901	515	587	15		

- Molecule 15 is a protein called Isoform 2 of 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	C	363	Total	C	N	O	S	0	0
			2864	1808	515	525	16		

- Molecule 16 is a protein called 26S protease regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	D	380	Total	C	N	O	S	0	0
			3039	1923	524	579	13		

- Molecule 17 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	E	375	Total	C	N	O	S	0	0
			2860	1796	512	536	16		

- Molecule 18 is a protein called 26S protease regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F	376	Total	C	N	O	S	0	0
			2858	1802	496	545	15		

- Molecule 19 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	G	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		
19	g	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		

- Molecule 20 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	H	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		
20	h	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		

- Molecule 21 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	I	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		
21	i	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		

- Molecule 22 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	J	239	Total	C	N	O	S	0	0
			1713	1062	311	335	5		
22	j	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		

- Molecule 23 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	228	Total	C	N	O	S	0	0
			1722	1080	284	348	10		
23	k	228	Total	C	N	O	S	0	0
			1722	1080	284	348	10		

- Molecule 24 is a protein called Isoform Long of Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		
24	l	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		

- Molecule 25 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	M	240	Total	C	N	O	S	0	0
			1856	1178	314	353	11		
25	m	240	Total	C	N	O	S	0	0
			1856	1178	314	353	11		

- Molecule 26 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	N	191	Total	C	N	O	S	0	0
			1430	893	245	280	12		
26	n	191	Total	C	N	O	S	0	0
			1430	893	245	280	12		

- Molecule 27 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	O	220	Total	C	N	O	S	0	0
			1643	1033	280	318	12		
27	o	220	Total	C	N	O	S	0	0
			1643	1033	280	318	12		

- Molecule 28 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	P	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		
28	p	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		

- Molecule 29 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		
29	q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		

- Molecule 30 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	R	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		
30	r	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		

- Molecule 31 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	S	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
31	s	213	Total	C	N	O	S	0	0
			1644	1039	282	313	10		

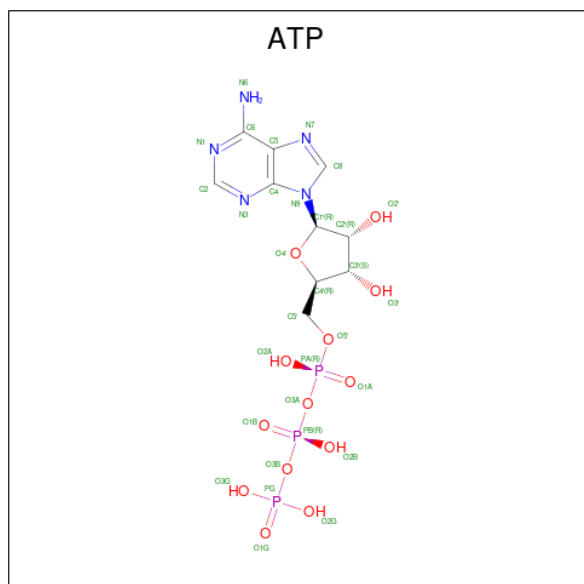
- Molecule 32 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	T	215	Total	C	N	O	S	0	0
			1667	1052	285	318	12		
32	t	215	Total	C	N	O	S	0	0
			1667	1052	285	318	12		

- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
33	c	1	Total	Zn	0
			1	1	

- Molecule 34 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



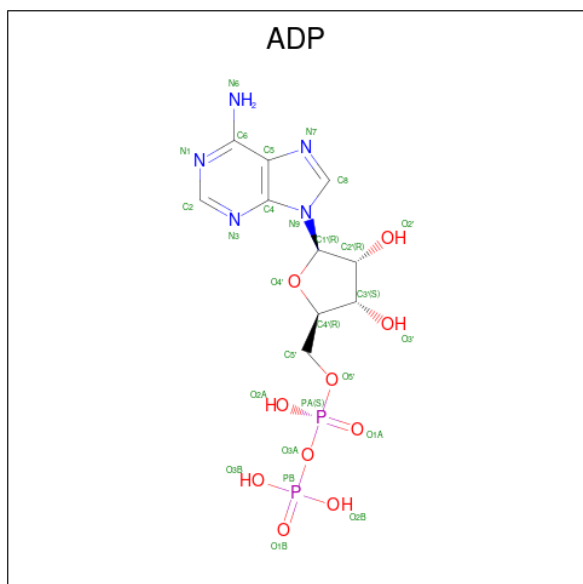
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Mol	Chain	Residues	Atoms					AltConf
34	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
34	E	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
35	A	1	Total	Mg	0
			1	1	
35	B	1	Total	Mg	0
			1	1	
35	D	1	Total	Mg	0
			1	1	
35	E	1	Total	Mg	0
			1	1	
35	F	1	Total	Mg	0
			1	1	

- Molecule 36 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
36	C	1	Total	C	N	O	P	0
			27	10	5	10	2	

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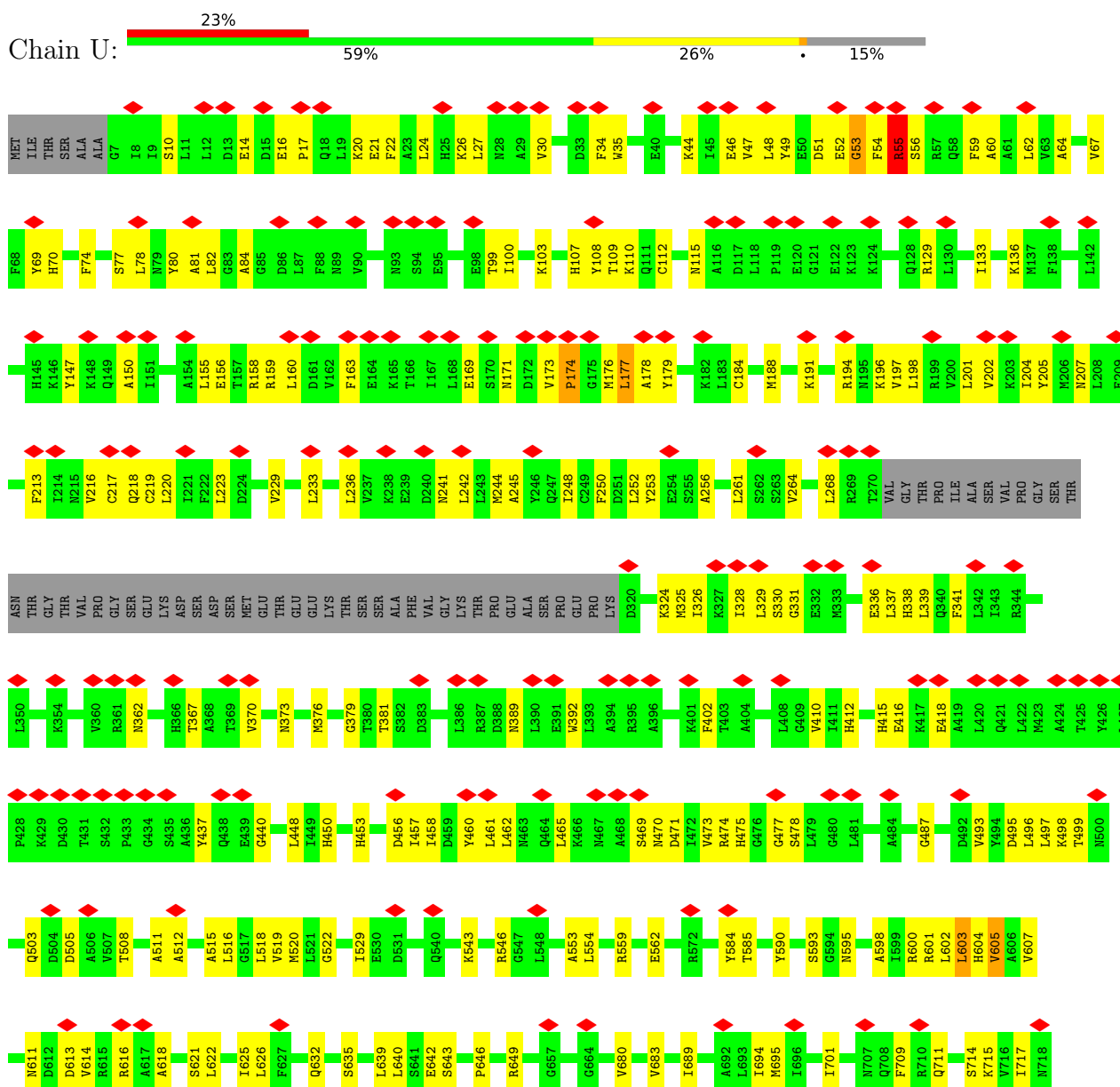
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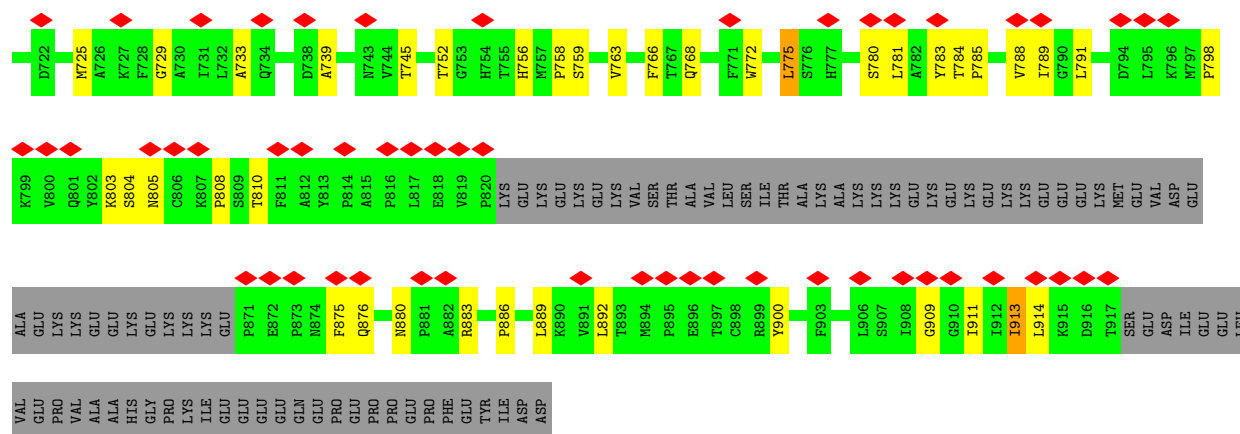
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	F	1	27	10	5	10	2	0

3 Residue-property plots [i](#)

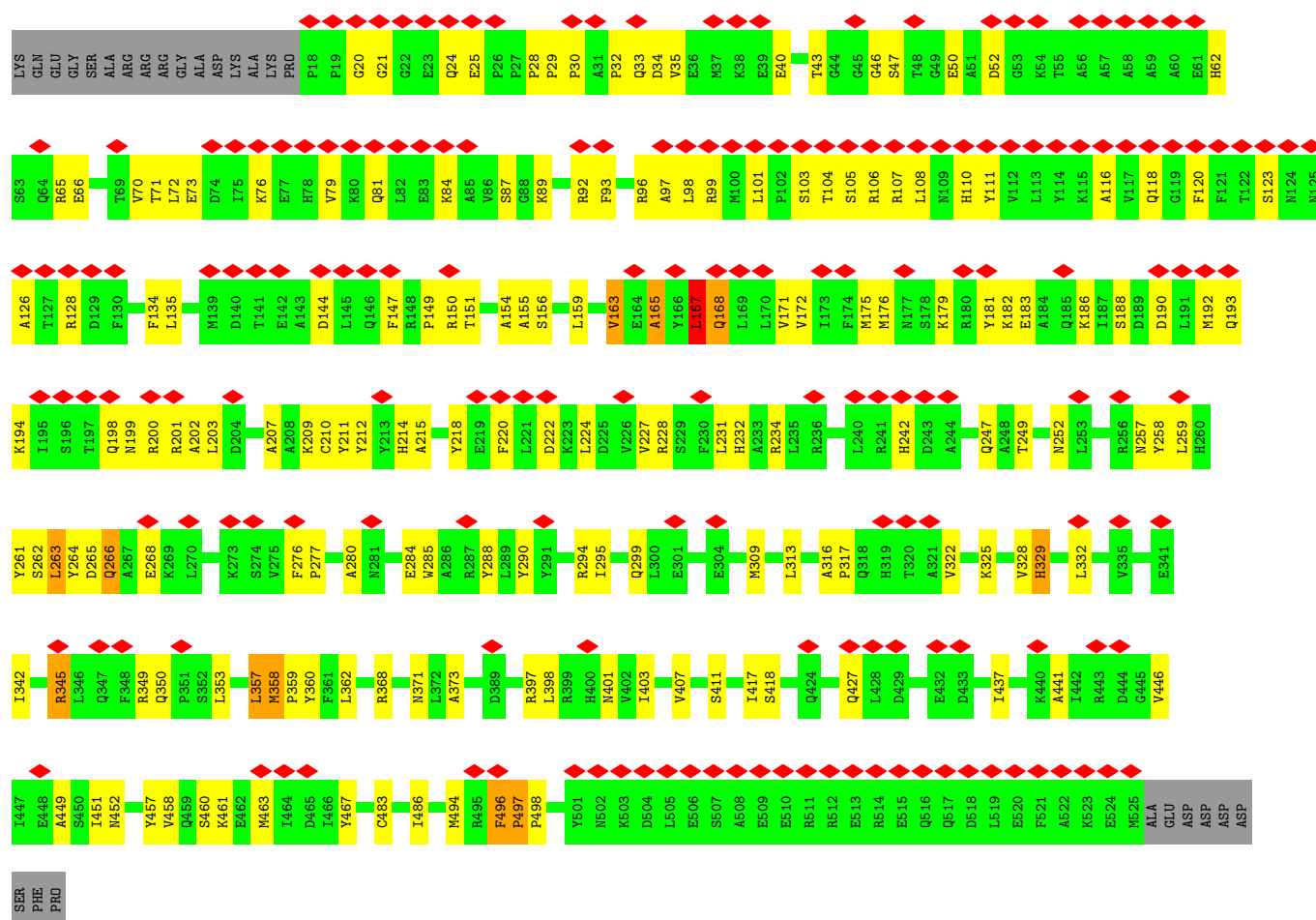
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 26S proteasome non-ATPase regulatory subunit 1



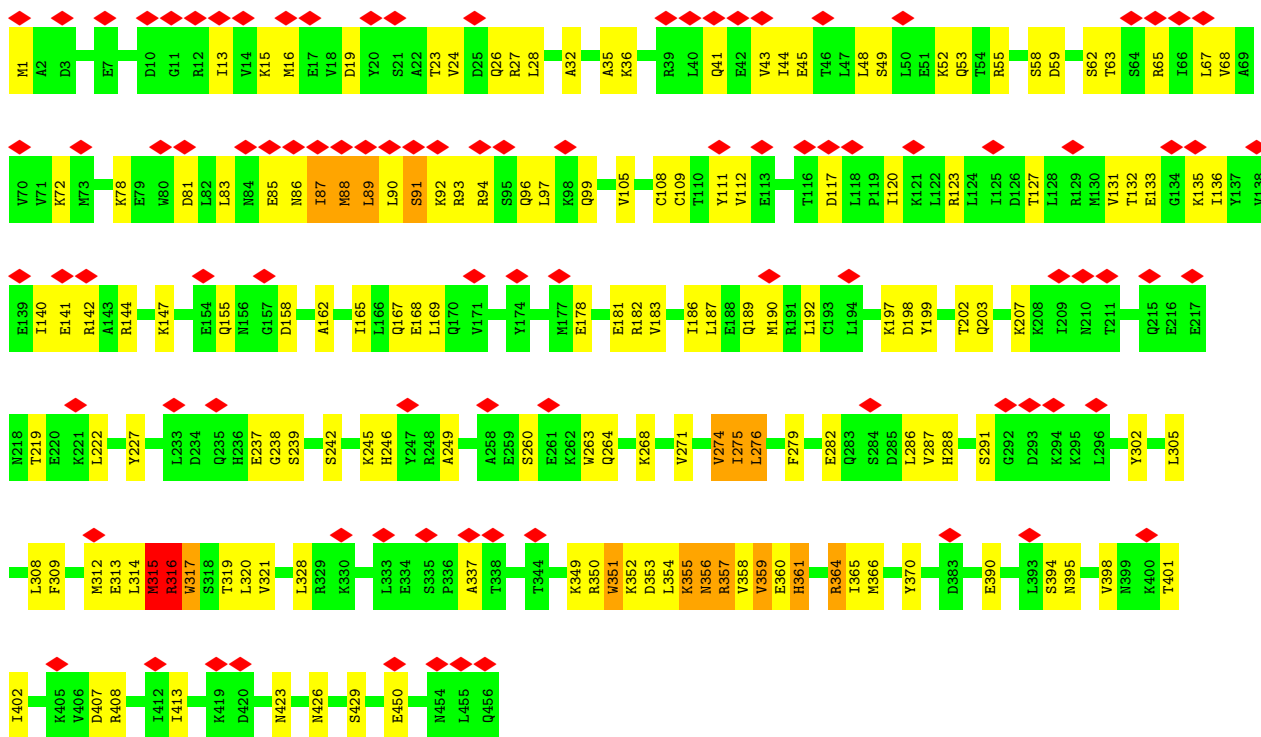


• Molecule 2: 26S proteasome non-ATPase regulatory subunit 3

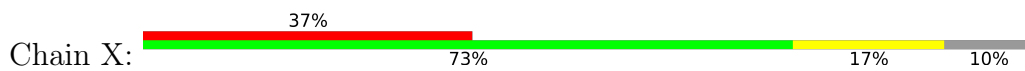


• Molecule 3: 26S proteasome non-ATPase regulatory subunit 12



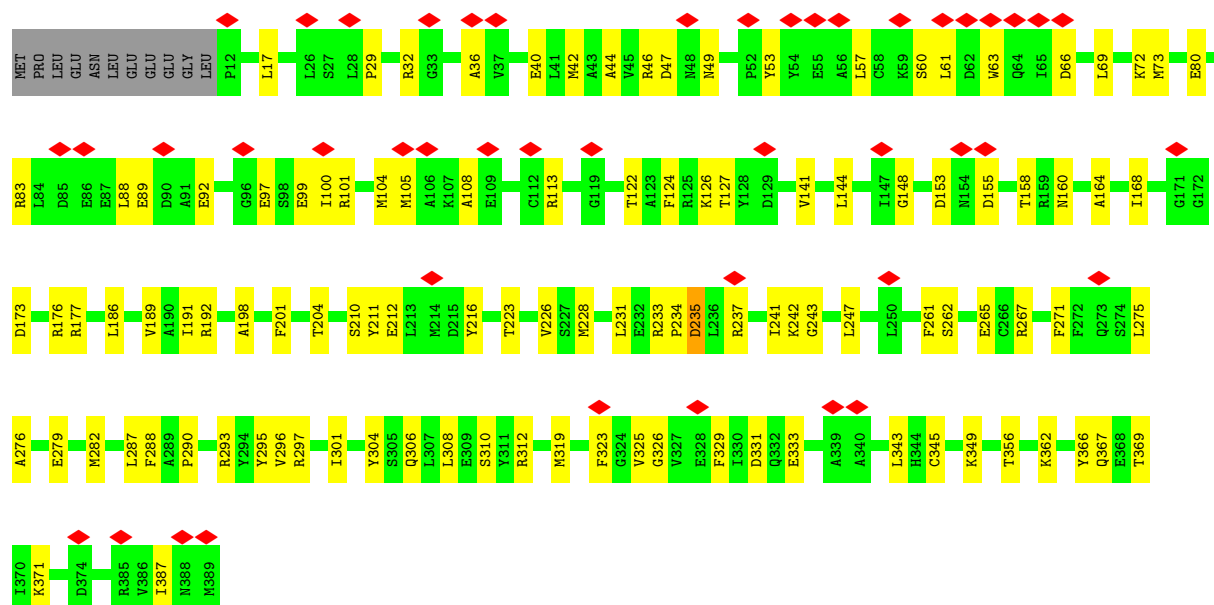


• Molecule 4: 26S proteasome non-ATPase regulatory subunit 11

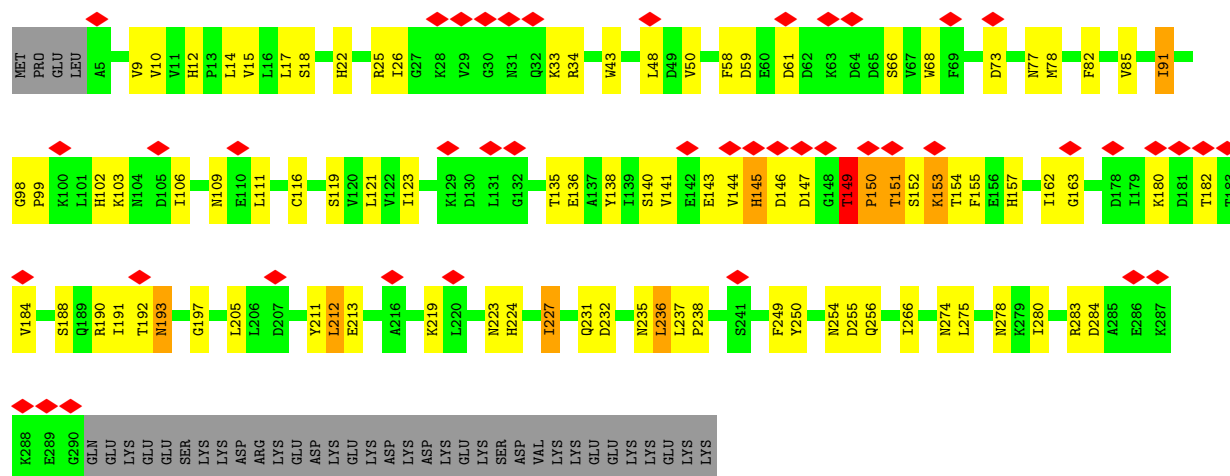


• Molecule 5: 26S proteasome non-ATPase regulatory subunit 6

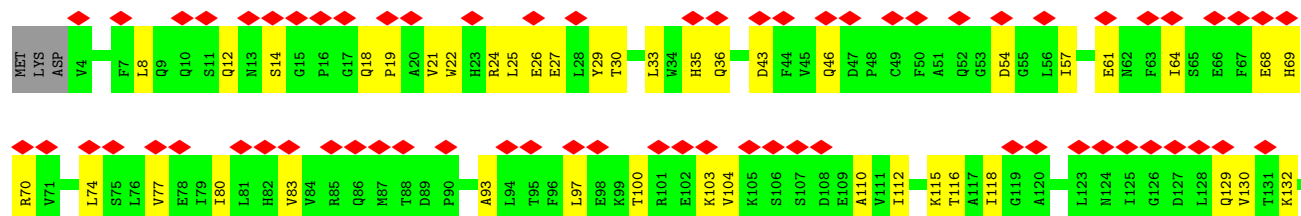


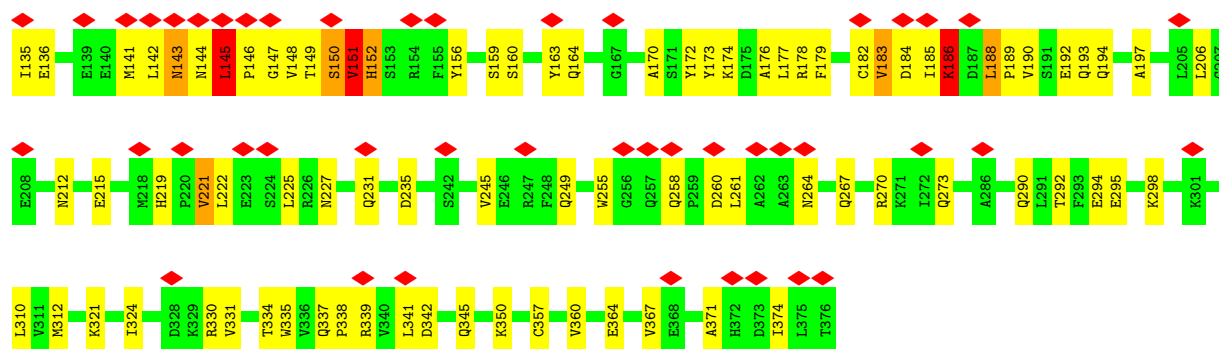


- Molecule 6: 26S proteasome non-ATPase regulatory subunit 7

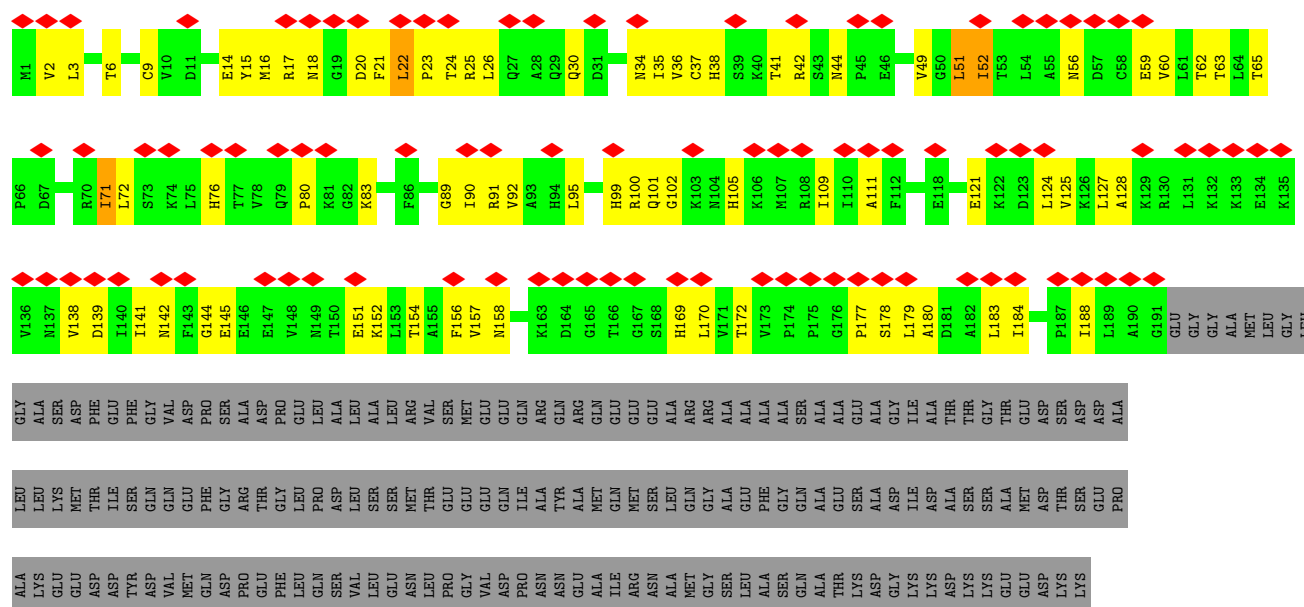


- Molecule 7: 26S proteasome non-ATPase regulatory subunit 13

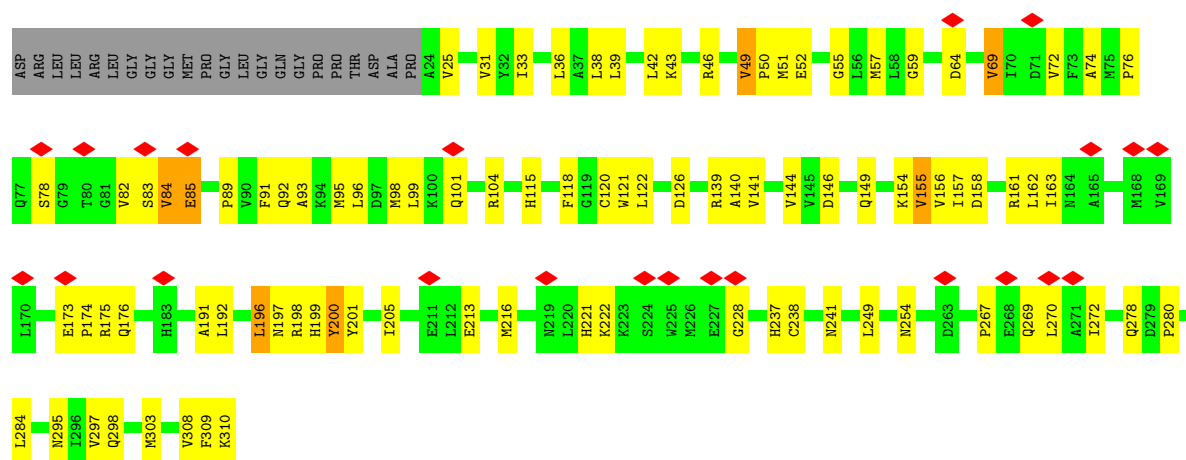




• Molecule 8: 26S proteasome non-ATPase regulatory subunit 4



• Molecule 9: 26S proteasome non-ATPase regulatory subunit 14

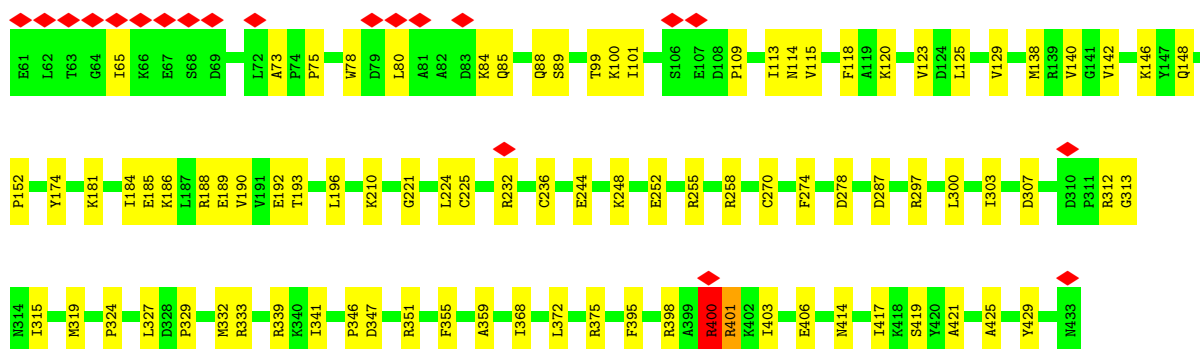


ARG	P841	Y781	V721	A661	A601	T541	S481	D421	S361	H301	P241
LYS	V842	H782	S722	M662	G602	I542	I482	V422	G362	G302	E242
ASN	S843	S783	Y723	G663	S603	M543	F483	G423	S363	P243	
ASN	V844	D784	N724	E664	G604	E544	G484	G424	Q364	F304	E244
TYR	R845	S785	N725	E665	M605	K545	L485	G425	V365	L305	N245
ASP	V846	Q786	I726	I666	V606	S546	L486	L426	D366	E306	S246
LEU	G847	L787	F727	G667	L607	E547	L487	T427	S367	L307	A247
	Q848	W788	A728	A668	K608	T548	A488	Q428	A368	S308	L248
	A849	S789	M729	E669	V609	E549	Y489	I429	R369	E309	L249
	V850	Q790	G730	M670	Q610	L550	A490	D430	K370	D310	R250
	D851	A791	M731	A671	Q611	K551	G491	K431	N371	V311	C251
	W852	Y792	V732	L672	L612	D552	S492	Y432	L372	E312	A252
	V853	G793	G733	R673	L613	T553	H493	L433	A373	E313	L253
	G854	A794	S734	T674	H614	Y554	R494	Y434	S374	Y314	G254
	Q855	G795	G735	F675	I615	A555	E495	S435	S375	E315	V255
	A856	L796	T736	G676	C616	R556	D496	S436	F376	D316	F256
	G857	L797	N737	H677	S617	W557	V497	E437	V377	L317	R257
	K858	T798	N738	L678	E618	L558	L498	D438	N378	T318	K258
	P859	V799	A739	L679	H619	P559	T499	Y439	G379	E319	F259
	K860	L800	R740	L679	F620	L560	L500	I440	F380	I320	S260
	T861	R801	L741	Y681	D621	G561	L501	K441	V381	M321	R261
	I862	S802	A742	G682	S622	L562	L502	S442	N382	S322	F262
	T863	F803	A743	E683	K623	G563	P503	G443	N383	N323	P263
	G864	L804	M744	P684	E624	L564	Y504	A444	A384	V324	E264
	F865	D805	L745	T685	K625	N665	M505	L445	F385	Q325	A265
	Q866	V806	R746	L686	E626	H566	G506	L446	G386	L326	L266
	T867	R807	Q747	R687	E627	L567	D507	A447	Q387	N327	R267
	H868	N808	L748	R688	D628	G568	K509	C448	D388	S328	L268
	T869	I809	A749	A689	K629	K569	G449	C449	K389	N329	A269
	T870	I810	Q750	V690	D630	G570	S510	I450	L390	F330	L270
	L871	P691	Y751	P691	K631	E571	S511	V451	L391	L331	M271
	V872	G812	H752	L692	K632	A572	M512	M452	T392	A332	L272
	L873	K813	A753	A693	E633	I573	E513	S453	D393	L333	N273
	L874	S814	K754	L694	K634	E574	V514	G454	D394	A334	D274
	A875	H815	D755	A695	K635	I575	A515	V455	G395	A334	M275
	H876	Y816	P756	L696	D636	A576	G516	R456	N396	E276	E276
	G877	V817	N757	I697	K637	L577	V517	M457	K397	L337	L277
	E878	L818	N758	S698	D638	A578	T518	E458	V398	D338	V278
	R879	Y819	L759	V699	K639	A579	A519	C459	L399	I339	E279
	A880	G820	F760	N701	K640	L580	L520	D460	Y400	M340	D280
	E881	L821	M761	I701	E641	E581	A521	P461	K401	E341	I281
	L882	V822	V762	P702	A642	V582	C522	A462	N402	P342	F282
	A883	A823	R763	R703	P643	V583	G523	L463	K403	K343	T283
	T884	L824	L764	A644	A644	S584	M524	A464	D404	V344	S284
	E885	M825	A765	N705	D645	E585	I525	L465	H405	P345	C285
	Q886	Q826	Q766	I706	M646	P586	A526	L466	G406	D346	K286
	F887	P827	G767	L707	G647	F587	V527	S467	M407	D347	D287
	L888	R828	L768	D708	A648	R588	G528	D468	L408	I348	V288
	P889	H829	T769	T709	H649	S589	S529	Y469	S409	Y349	V289
	VAL	L830	H770	L710	Q650	F590	N530	V470	A410	K350	V290
THR	V831	W831	L771	S711	G651	A591	G531	L471	A411	T351	Q291
PRO	T832	T832	G772	K712	V652	N592	G532	H472	A412	H352	K292
ILE	F833	F833	K773	F713	A653	T593	D533	M473	S413	L353	Q293
GLU	D834	D834	G774	S714	V654	L594	V534	S474	L414	E354	M294
GLY	E835	E835	T775	H715	L655	V595	T535	M475	G415	N355	A295
PHE	E836	E836	L776	D716	G656	D596	S536	T476	M416	N356	F296
VAL	L837	L837	T777	A717	G656	V597	T537	T477	N357	N356	F296
ILE	L837	L837	L778	A717	G658	V597	T538	M477	I417	F358	M297
LEU	L837	L837	C779	D718	A658	C598	L539	R478	L418	L298	L298
	P839	P839	P780	E720	T660	V600	G540	L479	L419	G359	R300

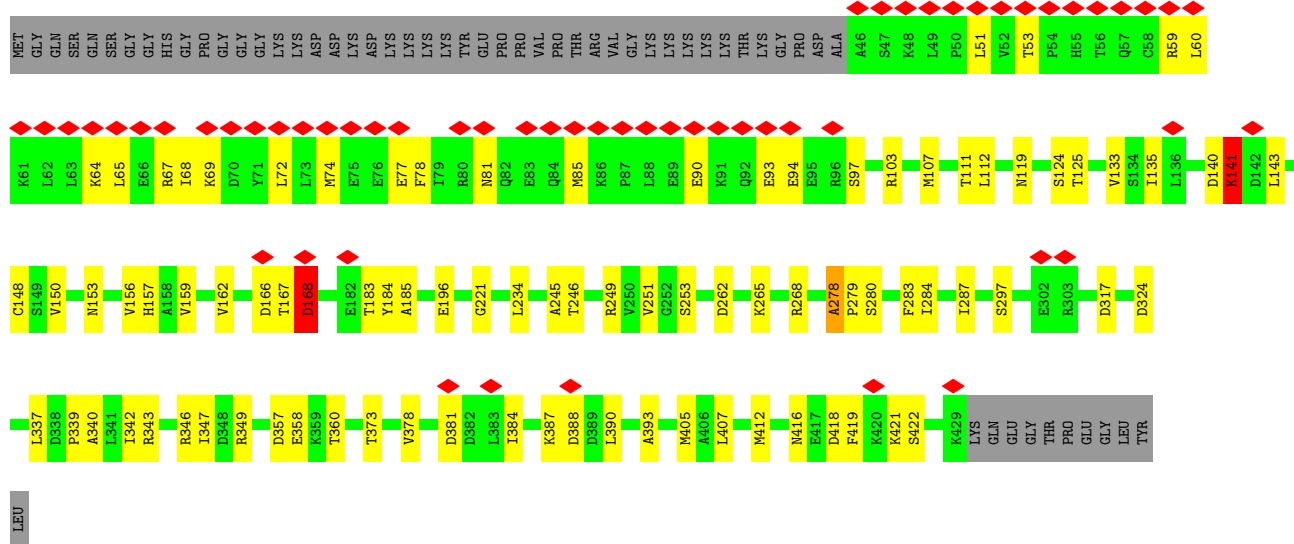
• Molecule 13: 26S protease regulatory subunit 7



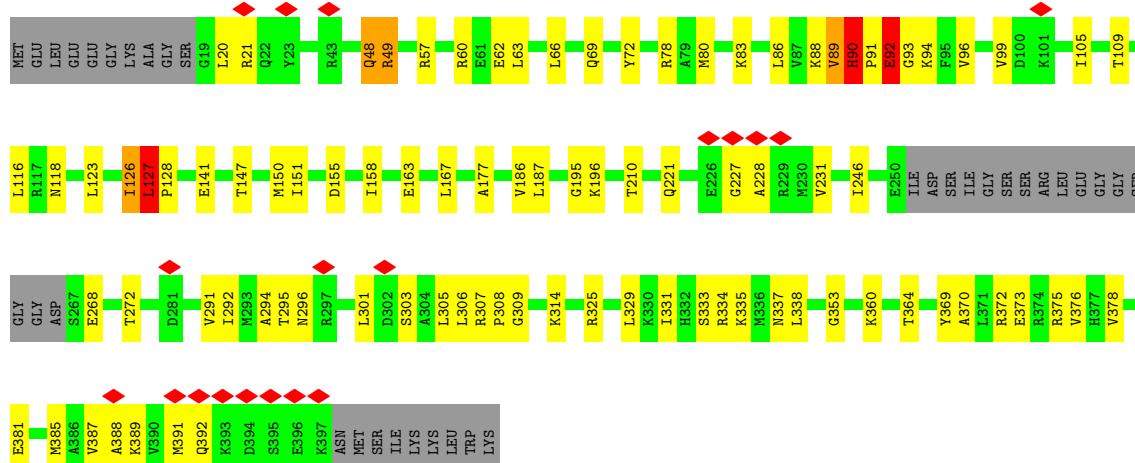
MET	PRO	ASP	TYR	LEU	GLY	ALA	ASP	GLN	LYS	THR	LYS	GLU	ASP	ASP	LYS	PRO	ARG	ALA	LEU	ASP	GLU	GLY	THR	TYR	GLN	SER	T40	Y41	S42	R43	Q44	I45	K46	Q47	V48	E49	D50	D51	I52	Q53	Q54	L55	L56	K57	K58	I59	N60
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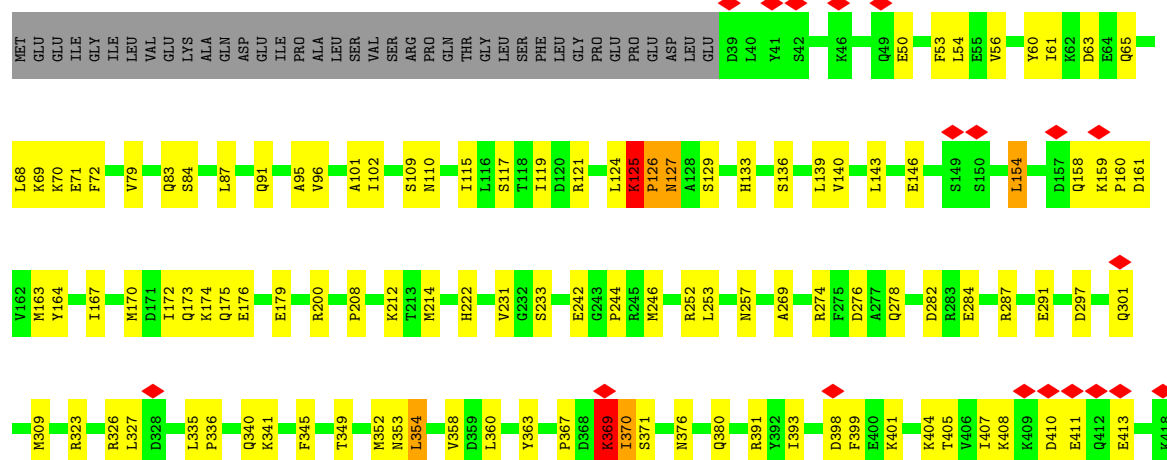
• Molecule 14: 26S protease regulatory subunit 4



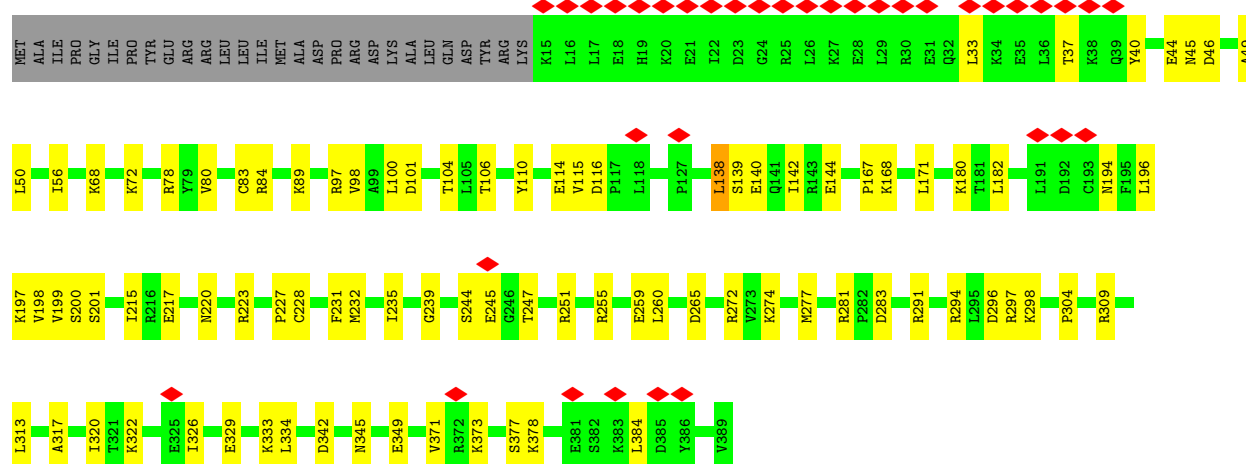
• Molecule 15: Isoform 2 of 26S proteasome regulatory subunit 8



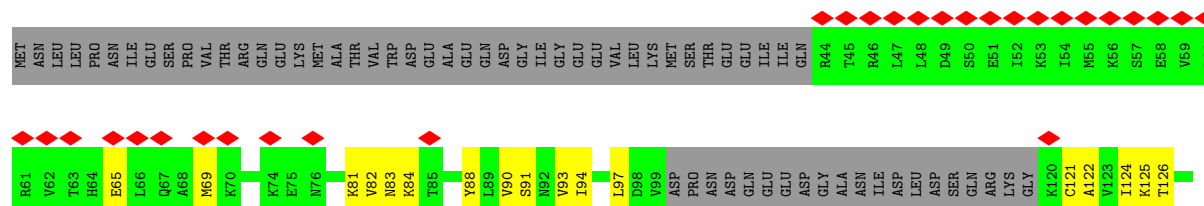
Chain D:

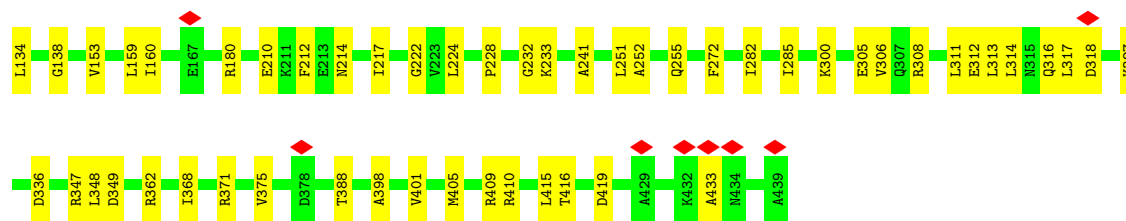


Chain E:

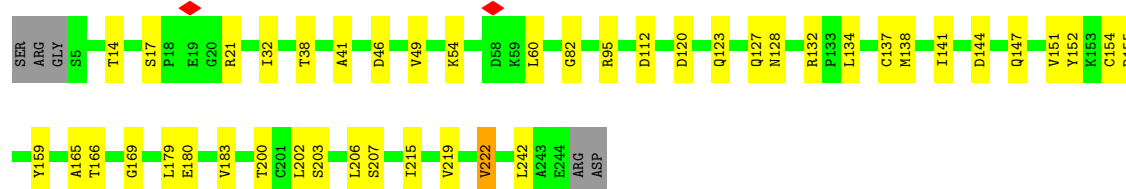
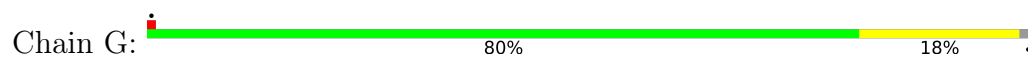


Chain F:

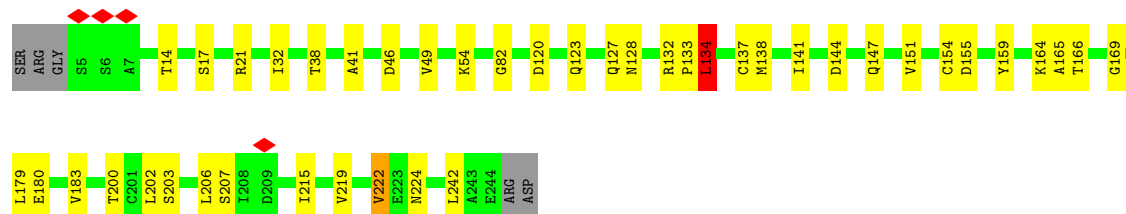
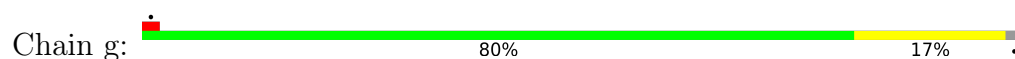




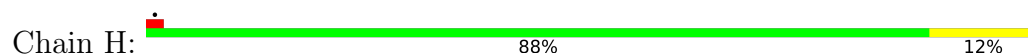
• Molecule 19: Proteasome subunit alpha type-6



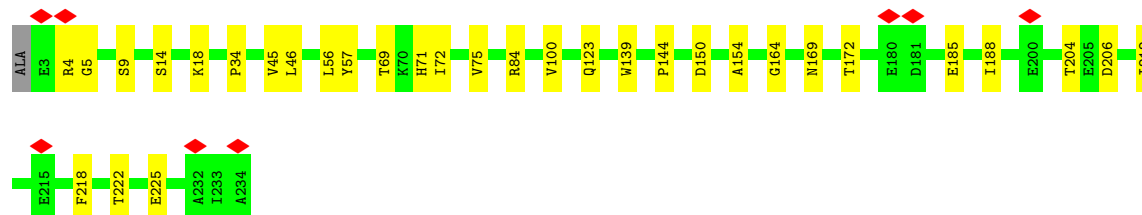
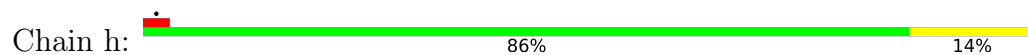
• Molecule 19: Proteasome subunit alpha type-6



• Molecule 20: Proteasome subunit alpha type-2

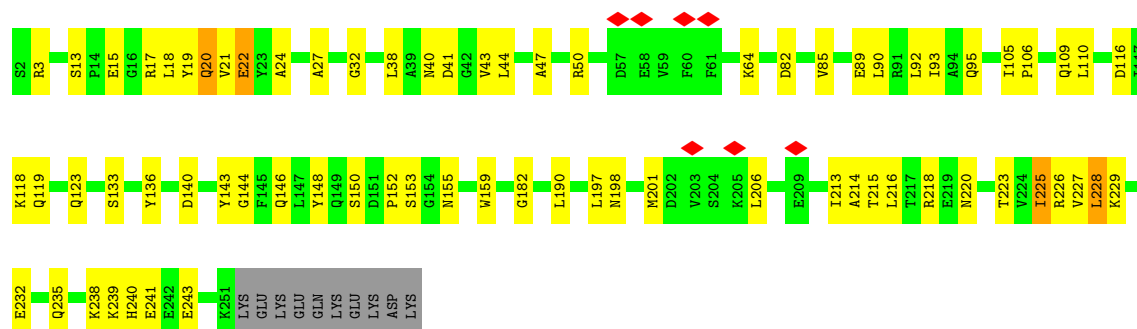


• Molecule 20: Proteasome subunit alpha type-2



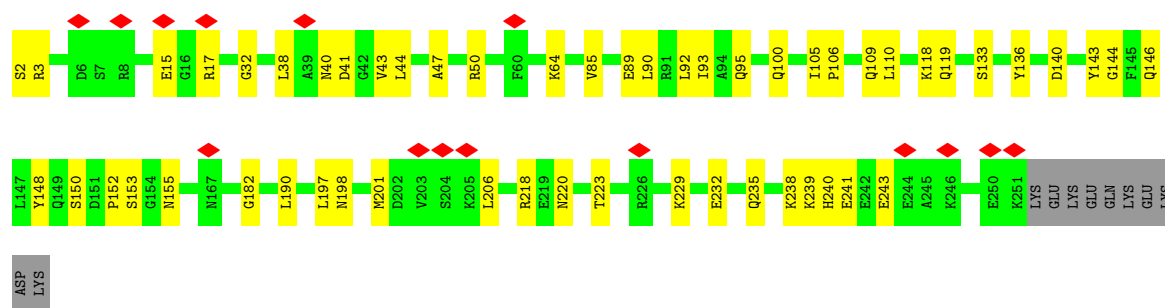
• Molecule 21: Proteasome subunit alpha type-4

Chain I:  68% 26%



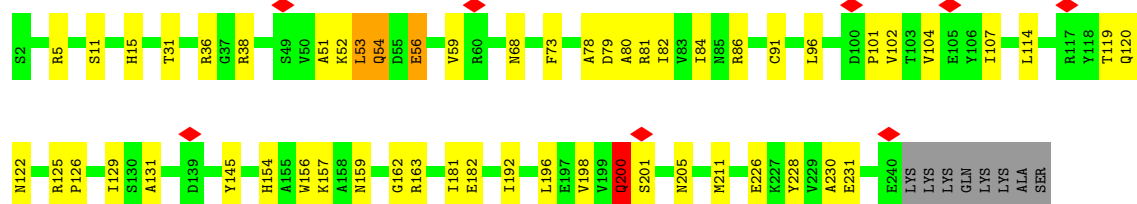
• Molecule 21: Proteasome subunit alpha type-4

Chain i:  6% 75% 21%



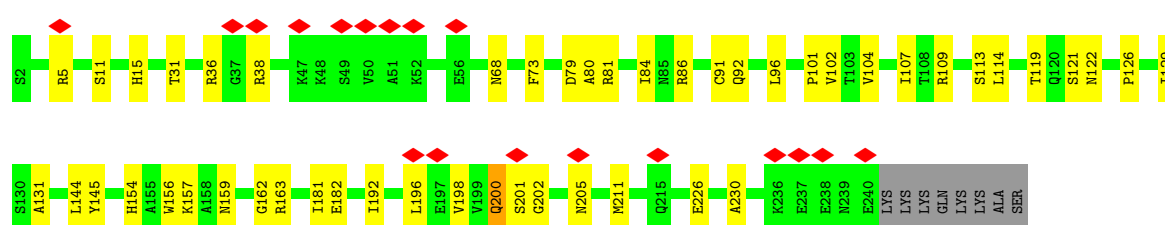
• Molecule 22: Proteasome subunit alpha type-7

Chain J:  74% 21%



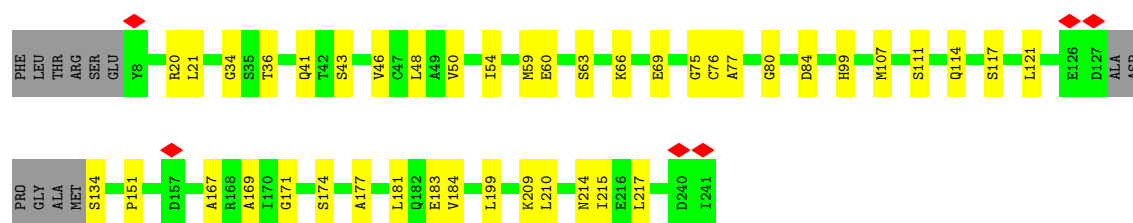
• Molecule 22: Proteasome subunit alpha type-7

Chain j:  7% 77% 19%



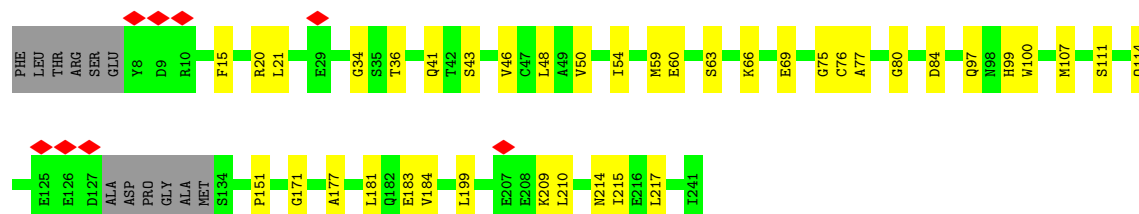
• Molecule 23: Proteasome subunit alpha type-5

Chain K: 



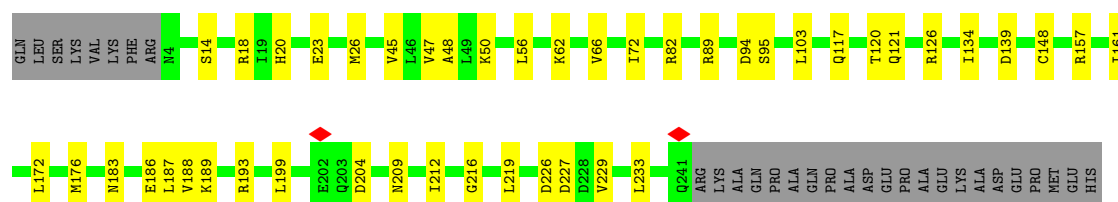
• Molecule 23: Proteasome subunit alpha type-5

Chain k: 



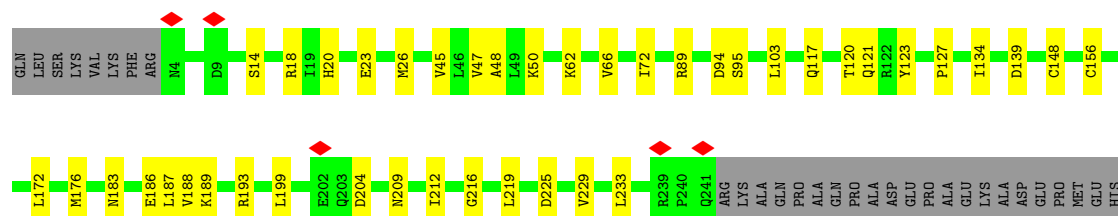
• Molecule 24: Isoform Long of Proteasome subunit alpha type-1

Chain L: 



• Molecule 24: Isoform Long of Proteasome subunit alpha type-1

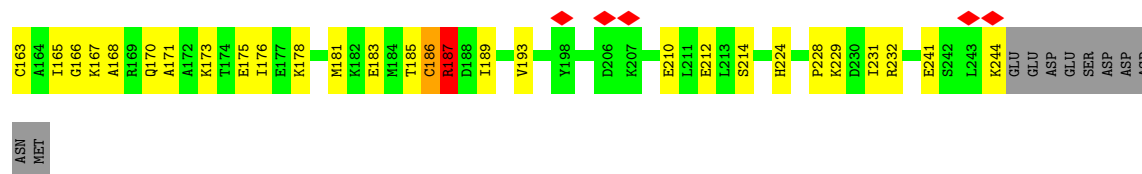
Chain l: 



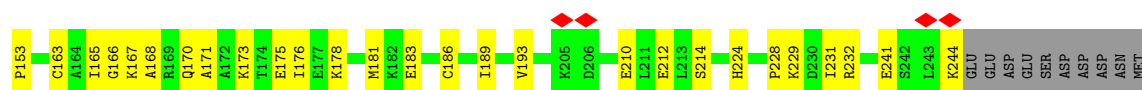
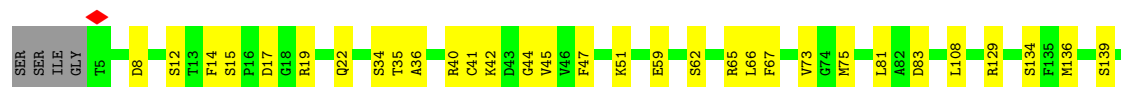
• Molecule 25: Proteasome subunit alpha type-3

Chain M: 

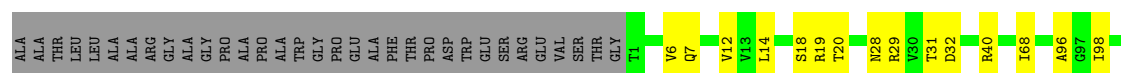




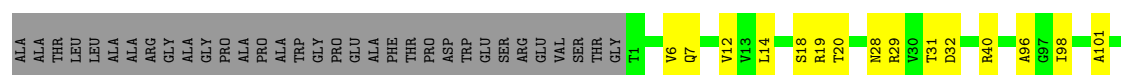
• Molecule 25: Proteasome subunit alpha type-3



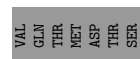
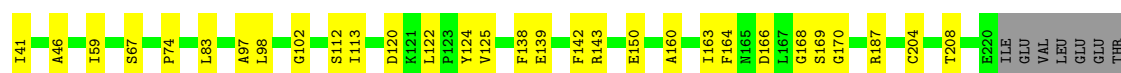
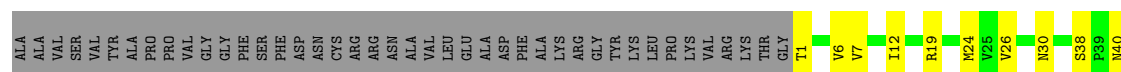
• Molecule 26: Proteasome subunit beta type-6



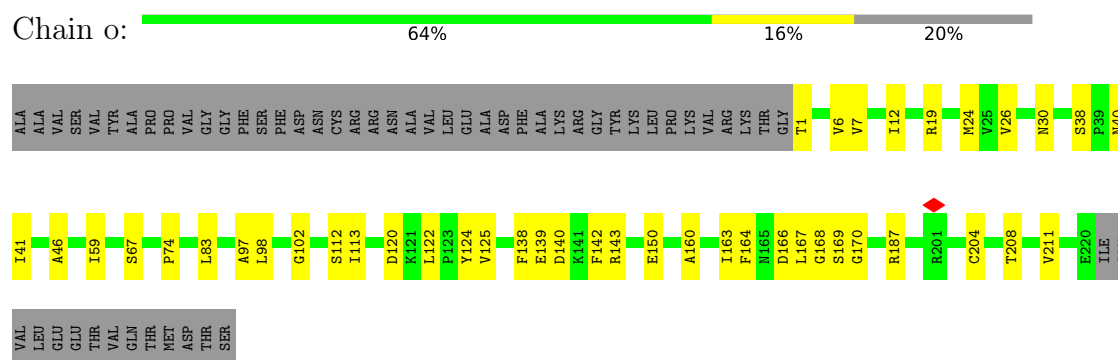
• Molecule 26: Proteasome subunit beta type-6



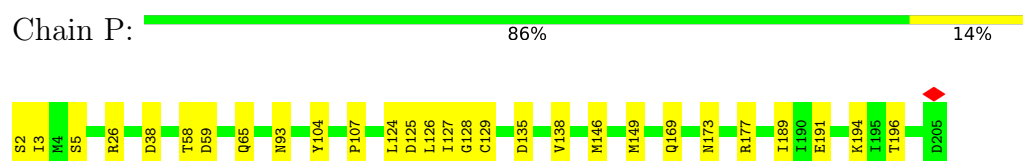
• Molecule 27: Proteasome subunit beta type-7



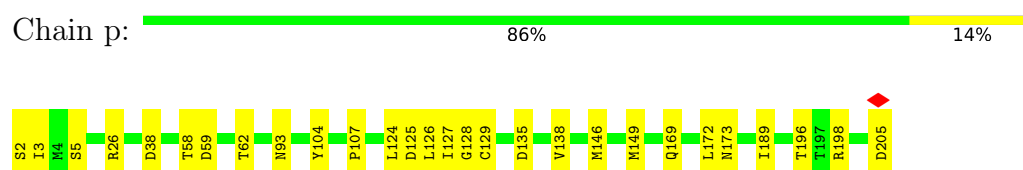
- Molecule 27: Proteasome subunit beta type-7



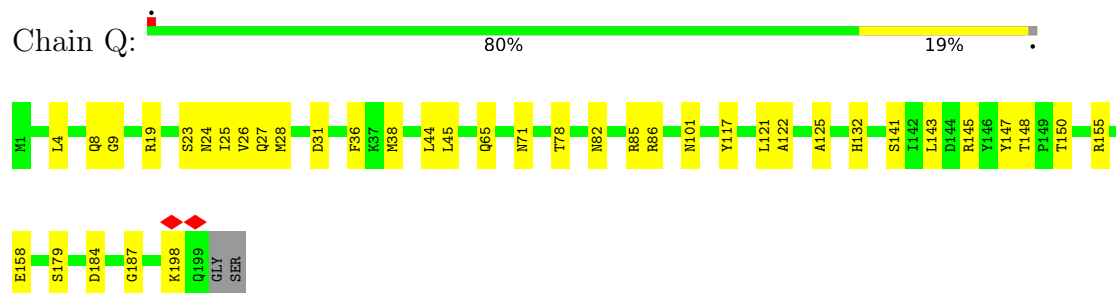
- Molecule 28: Proteasome subunit beta type-3



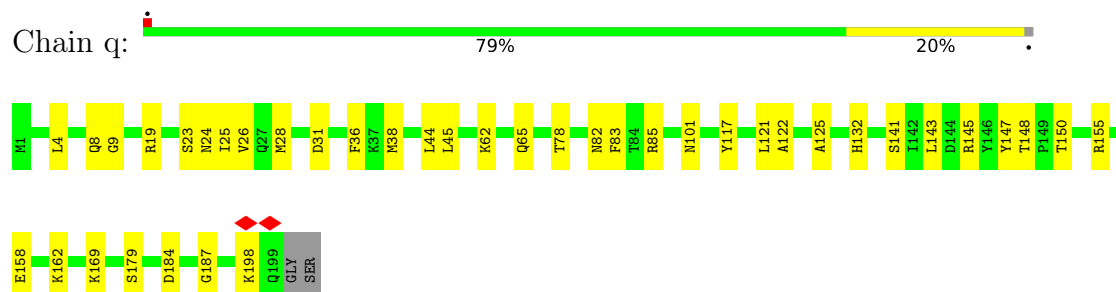
- Molecule 28: Proteasome subunit beta type-3



- Molecule 29: Proteasome subunit beta type-2

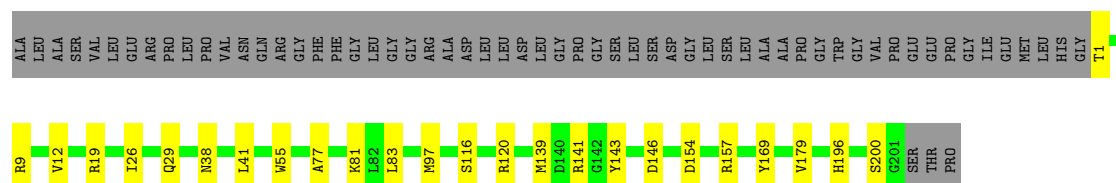


- Molecule 29: Proteasome subunit beta type-2



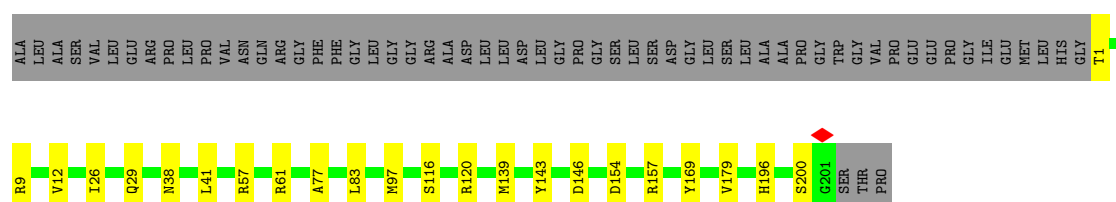
- Molecule 30: Proteasome subunit beta type-5

Chain R:  67% 10% 23%



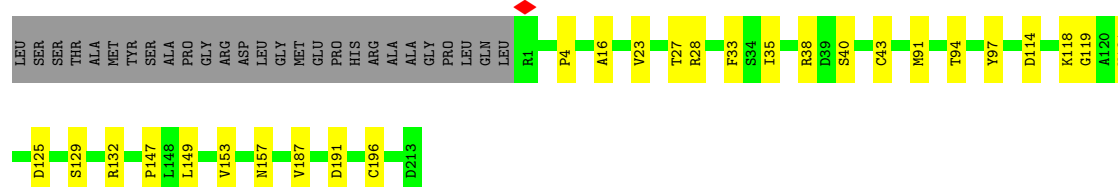
- Molecule 30: Proteasome subunit beta type-5

Chain r:  68% 9% 23%



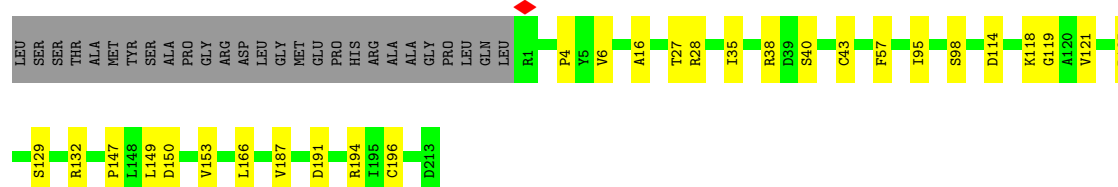
- Molecule 31: Proteasome subunit beta type-1

Chain S:  78% 11% 11%



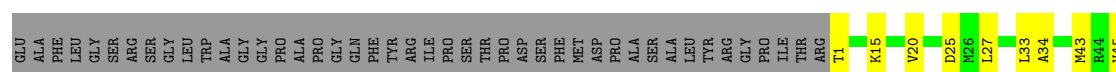
- Molecule 31: Proteasome subunit beta type-1

Chain s:  77% 12% 11%



- Molecule 32: Proteasome subunit beta type-4

Chain T:  71% 11% 18%





● Molecule 32: Proteasome subunit beta type-4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	80224	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.6	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.172	Depositor
Minimum map value	-0.077	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0394	Depositor
Map size ($\text{\AA}$)	438.4, 438.4, 438.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.37, 1.37, 1.37	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, ATP, ADP

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	U	0.26	0/6449	0.61	4/8729 (0.0%)
2	V	0.31	0/4072	0.72	3/5510 (0.1%)
3	W	0.30	0/3740	0.70	4/5027 (0.1%)
4	X	0.24	0/3053	0.56	0/4115
5	Y	0.30	0/3173	0.64	0/4273
6	Z	0.27	0/2324	0.64	1/3150 (0.0%)
7	a	0.27	0/3053	0.64	1/4133 (0.0%)
8	b	0.23	0/1478	0.65	0/2001
9	c	0.29	0/2302	0.65	0/3110
10	d	0.28	0/2162	0.71	0/2919
11	e	0.24	0/338	0.64	0/450
12	f	0.26	0/6970	0.74	8/9420 (0.1%)
13	A	0.29	0/3148	0.62	1/4250 (0.0%)
14	B	0.30	1/3061 (0.0%)	0.61	1/4129 (0.0%)
15	C	0.28	0/2902	0.60	2/3904 (0.1%)
16	D	0.31	0/3089	0.68	2/4168 (0.0%)
17	E	0.28	0/2904	0.59	2/3924 (0.1%)
18	F	0.28	0/2896	0.54	0/3912
19	G	0.26	0/1859	0.48	0/2523
19	g	0.25	0/1859	0.47	0/2523
20	H	0.26	0/1743	0.47	0/2372
20	h	0.26	0/1743	0.47	0/2372
21	I	0.28	0/1942	0.55	0/2628
21	i	0.27	0/1942	0.53	0/2628
22	J	0.27	0/1737	0.55	0/2369
22	j	0.26	0/1728	0.54	0/2358
23	K	0.27	0/1747	0.47	0/2364
23	k	0.27	0/1747	0.47	0/2364
24	L	0.27	0/1885	0.55	0/2552
24	l	0.27	0/1885	0.57	2/2552 (0.1%)
25	M	0.27	0/1891	0.54	2/2552 (0.1%)
25	m	0.27	0/1891	0.51	0/2552

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	N	0.27	0/1454	0.44	0/1967
26	n	0.27	0/1454	0.44	0/1967
27	O	0.28	0/1670	0.46	0/2265
27	o	0.28	0/1670	0.46	0/2265
28	P	0.28	0/1620	0.46	0/2184
28	p	0.28	0/1620	0.46	0/2184
29	Q	0.30	0/1603	0.52	0/2174
29	q	0.30	0/1603	0.52	0/2174
30	R	0.30	0/1579	0.45	0/2134
30	r	0.30	0/1579	0.44	0/2134
31	S	0.29	0/1671	0.46	0/2253
31	s	0.29	0/1674	0.46	0/2257
32	T	0.29	0/1700	0.49	0/2305
32	t	0.29	0/1700	0.49	0/2305
All	All	0.28	1/105310 (0.0%)	0.58	33/142401 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	B	53	THR	C-N	5.05	1.40	1.34

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Z	106	ILE	N-CA-C	-10.48	103.75	113.71
13	A	65	ILE	N-CA-C	-8.82	104.73	113.20
3	W	356	ASN	O-C-N	7.94	130.60	122.03
3	W	351	TRP	N-CA-C	-7.58	102.99	111.71
12	f	713	PHE	N-CA-C	-7.56	102.98	111.07

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	U	6334	0	6366	194	0
2	V	3994	0	3960	177	0
3	W	3693	0	3813	203	0
4	X	3009	0	3113	48	0
5	Y	3115	0	3120	85	0
6	Z	2281	0	2312	94	0
7	a	2995	0	3012	154	0
8	b	1458	0	1505	79	0
9	c	2260	0	2276	81	0
10	d	2116	0	2146	130	0
11	e	334	0	294	16	0
12	f	6857	0	6850	310	0
13	A	3096	0	3140	80	0
14	B	3018	0	3082	90	0
15	C	2864	0	2971	98	0
16	D	3039	0	3075	113	0
17	E	2860	0	2827	59	0
18	F	2858	0	2853	46	0
19	G	1826	0	1796	34	0
19	g	1826	0	1796	32	0
20	H	1708	0	1594	18	0
20	h	1708	0	1594	19	0
21	I	1912	0	1851	62	0
21	i	1912	0	1851	33	0
22	J	1713	0	1537	47	0
22	j	1704	0	1517	29	0
23	K	1722	0	1673	26	0
23	k	1722	0	1673	23	0
24	L	1850	0	1822	29	0
24	l	1850	0	1822	27	0
25	M	1856	0	1816	53	0
25	m	1856	0	1816	38	0
26	N	1430	0	1398	19	0
26	n	1430	0	1398	17	0
27	O	1643	0	1644	26	0
27	o	1643	0	1644	29	0
28	P	1591	0	1609	20	0
28	p	1591	0	1609	20	0
29	Q	1570	0	1547	27	0
29	q	1570	0	1547	29	0
30	R	1548	0	1499	17	0
30	r	1548	0	1499	14	0
31	S	1641	0	1618	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	s	1644	0	1627	19	0
32	T	1667	0	1628	21	0
32	t	1667	0	1628	18	0
33	c	1	0	0	0	0
34	A	31	0	12	1	0
34	B	31	0	12	1	0
34	D	31	0	12	1	0
34	E	31	0	12	3	0
35	A	1	0	0	0	0
35	B	1	0	0	0	0
35	D	1	0	0	0	0
35	E	1	0	0	0	0
35	F	1	0	0	0	0
36	C	27	0	12	1	0
36	F	27	0	12	1	0
All	All	103713	0	102840	2588	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 13.

The worst 5 of 2588 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)
13:A:49:GLU:HA	14:B:65:LEU:CD1	1.31	1.59
13:A:49:GLU:CA	14:B:65:LEU:HD13	1.29	1.57
3:W:89:LEU:CD1	3:W:93:ARG:HG2	1.41	1.48
15:C:127:LEU:HD21	16:D:96:VAL:CG2	1.44	1.46
25:M:41:CYS:SG	25:M:186:CYS:HB3	1.53	1.46

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	U	806/953 (85%)	731 (91%)	72 (9%)	3 (0%)	30	60
2	V	506/533 (95%)	445 (88%)	55 (11%)	6 (1%)	10	40
3	W	454/456 (100%)	401 (88%)	49 (11%)	4 (1%)	14	45
4	X	378/422 (90%)	352 (93%)	25 (7%)	1 (0%)	36	65
5	Y	376/389 (97%)	336 (89%)	40 (11%)	0	100	100
6	Z	284/324 (88%)	240 (84%)	38 (13%)	6 (2%)	5	31
7	a	371/376 (99%)	324 (87%)	42 (11%)	5 (1%)	9	38
8	b	189/377 (50%)	170 (90%)	18 (10%)	1 (0%)	24	56
9	c	285/309 (92%)	244 (86%)	39 (14%)	2 (1%)	18	50
10	d	255/349 (73%)	208 (82%)	46 (18%)	1 (0%)	30	60
11	e	36/70 (51%)	27 (75%)	9 (25%)	0	100	100
12	f	887/908 (98%)	698 (79%)	176 (20%)	13 (2%)	8	36
13	A	392/433 (90%)	340 (87%)	50 (13%)	2 (0%)	24	56
14	B	382/440 (87%)	338 (88%)	41 (11%)	3 (1%)	16	48
15	C	359/398 (90%)	332 (92%)	25 (7%)	2 (1%)	21	52
16	D	378/418 (90%)	327 (86%)	46 (12%)	5 (1%)	9	38
17	E	373/403 (93%)	338 (91%)	35 (9%)	0	100	100
18	F	372/439 (85%)	339 (91%)	33 (9%)	0	100	100
19	G	238/245 (97%)	230 (97%)	8 (3%)	0	100	100
19	g	238/245 (97%)	228 (96%)	9 (4%)	1 (0%)	30	60
20	H	230/233 (99%)	218 (95%)	12 (5%)	0	100	100
20	h	230/233 (99%)	218 (95%)	12 (5%)	0	100	100
21	I	248/260 (95%)	228 (92%)	20 (8%)	0	100	100
21	i	248/260 (95%)	228 (92%)	20 (8%)	0	100	100
22	J	237/247 (96%)	216 (91%)	19 (8%)	2 (1%)	16	48
22	j	237/247 (96%)	217 (92%)	18 (8%)	2 (1%)	16	48
23	K	224/240 (93%)	213 (95%)	11 (5%)	0	100	100
23	k	224/240 (93%)	213 (95%)	11 (5%)	0	100	100
24	L	236/268 (88%)	218 (92%)	17 (7%)	1 (0%)	30	60
24	l	236/268 (88%)	217 (92%)	19 (8%)	0	100	100
25	M	238/254 (94%)	221 (93%)	16 (7%)	1 (0%)	30	60
25	m	238/254 (94%)	221 (93%)	17 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	N	189/238 (79%)	181 (96%)	8 (4%)	0	100	100
26	n	189/238 (79%)	181 (96%)	8 (4%)	0	100	100
27	O	218/276 (79%)	210 (96%)	8 (4%)	0	100	100
27	o	218/276 (79%)	210 (96%)	8 (4%)	0	100	100
28	P	202/204 (99%)	191 (95%)	11 (5%)	0	100	100
28	p	202/204 (99%)	191 (95%)	11 (5%)	0	100	100
29	Q	197/201 (98%)	183 (93%)	14 (7%)	0	100	100
29	q	197/201 (98%)	183 (93%)	14 (7%)	0	100	100
30	R	199/262 (76%)	190 (96%)	9 (4%)	0	100	100
30	r	199/262 (76%)	190 (96%)	9 (4%)	0	100	100
31	S	211/240 (88%)	203 (96%)	8 (4%)	0	100	100
31	s	211/240 (88%)	203 (96%)	8 (4%)	0	100	100
32	T	213/263 (81%)	201 (94%)	12 (6%)	0	100	100
32	t	213/263 (81%)	201 (94%)	12 (6%)	0	100	100
All	All	13243/14859 (89%)	11994 (91%)	1188 (9%)	61 (0%)	26	56

5 of 61 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	U	55	ARG
2	V	167	LEU
2	V	168	GLN
6	Z	149	THR
6	Z	150	PRO

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	U	692/816 (85%)	683 (99%)	9 (1%)	61	71
2	V	415/459 (90%)	406 (98%)	9 (2%)	45	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	W	414/416 (100%)	400 (97%)	14 (3%)	32	55
4	X	327/362 (90%)	326 (100%)	1 (0%)	86	83
5	Y	334/344 (97%)	332 (99%)	2 (1%)	78	79
6	Z	257/295 (87%)	242 (94%)	15 (6%)	18	45
7	a	333/336 (99%)	324 (97%)	9 (3%)	39	59
8	b	167/312 (54%)	164 (98%)	3 (2%)	51	67
9	c	252/267 (94%)	243 (96%)	9 (4%)	31	54
10	d	231/293 (79%)	223 (96%)	8 (4%)	32	54
11	e	38/63 (60%)	38 (100%)	0	100	100
12	f	743/763 (97%)	717 (96%)	26 (4%)	32	54
13	A	337/372 (91%)	334 (99%)	3 (1%)	70	75
14	B	339/385 (88%)	334 (98%)	5 (2%)	57	68
15	C	314/346 (91%)	305 (97%)	9 (3%)	37	57
16	D	333/366 (91%)	327 (98%)	6 (2%)	51	67
17	E	298/353 (84%)	295 (99%)	3 (1%)	68	74
18	F	296/379 (78%)	296 (100%)	0	100	100
19	G	193/209 (92%)	192 (100%)	1 (0%)	81	80
19	g	193/209 (92%)	190 (98%)	3 (2%)	55	68
20	H	164/190 (86%)	164 (100%)	0	100	100
20	h	164/190 (86%)	164 (100%)	0	100	100
21	I	193/220 (88%)	188 (97%)	5 (3%)	40	60
21	i	193/220 (88%)	193 (100%)	0	100	100
22	J	154/210 (73%)	149 (97%)	5 (3%)	34	56
22	j	152/210 (72%)	151 (99%)	1 (1%)	76	77
23	K	186/202 (92%)	186 (100%)	0	100	100
23	k	186/202 (92%)	186 (100%)	0	100	100
24	L	198/229 (86%)	195 (98%)	3 (2%)	57	68
24	l	198/229 (86%)	196 (99%)	2 (1%)	68	74
25	M	192/211 (91%)	191 (100%)	1 (0%)	81	80
25	m	192/211 (91%)	192 (100%)	0	100	100
26	N	148/180 (82%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	n	148/180 (82%)	148 (100%)	0	100	100
27	O	177/227 (78%)	177 (100%)	0	100	100
27	o	177/227 (78%)	177 (100%)	0	100	100
28	P	173/173 (100%)	173 (100%)	0	100	100
28	p	173/173 (100%)	173 (100%)	0	100	100
29	Q	164/171 (96%)	164 (100%)	0	100	100
29	q	164/171 (96%)	164 (100%)	0	100	100
30	R	153/201 (76%)	153 (100%)	0	100	100
30	r	153/201 (76%)	153 (100%)	0	100	100
31	S	174/198 (88%)	174 (100%)	0	100	100
31	s	175/198 (88%)	175 (100%)	0	100	100
32	T	175/214 (82%)	175 (100%)	0	100	100
32	t	175/214 (82%)	175 (100%)	0	100	100
All	All	11007/12597 (87%)	10855 (99%)	152 (1%)	57	70

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	C	89	VAL
24	L	161	ILE
15	C	126	ILE
17	E	384	LEU
24	l	103	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 217 such sidechains are listed below:

Mol	Chain	Res	Type
14	B	241	ASN
19	G	12	HIS
23	k	98	ASN
15	C	48	GLN
16	D	257	ASN

5.3.3 RNA ⓘ

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](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
34	ATP	B	501	35	32,33,33	1.30	5 (15%)	48,52,52	1.76	11 (22%)
36	ADP	F	501	35	28,29,29	1.38	5 (17%)	43,45,45	1.79	10 (23%)
36	ADP	C	501	-	28,29,29	1.37	3 (10%)	43,45,45	2.02	9 (20%)
34	ATP	A	501	35	32,33,33	1.31	5 (15%)	48,52,52	1.78	10 (20%)
34	ATP	E	401	35	32,33,33	1.30	4 (12%)	48,52,52	1.82	8 (16%)
34	ATP	D	501	35	32,33,33	1.30	5 (15%)	48,52,52	1.77	10 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	ATP	B	501	35	-	0/22/38/38	0/3/3/3
36	ADP	F	501	35	-	6/16/32/32	0/3/3/3
36	ADP	C	501	-	-	3/16/32/32	0/3/3/3
34	ATP	A	501	35	-	1/22/38/38	0/3/3/3
34	ATP	E	401	35	-	6/22/38/38	0/3/3/3
34	ATP	D	501	35	-	6/22/38/38	0/3/3/3

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	C	501	ADP	C5-C4	4.55	1.47	1.39
34	E	401	ATP	C5-C4	4.51	1.47	1.39
36	F	501	ADP	C5-C4	4.44	1.47	1.39
34	D	501	ATP	C5-C4	4.39	1.46	1.39
34	A	501	ATP	C5-C4	4.34	1.46	1.39

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	C	501	ADP	C5-C4-N3	-6.73	117.45	126.72
34	E	401	ATP	C5-C4-N3	-6.12	118.29	126.72
34	A	501	ATP	C5-C4-N3	-5.76	118.79	126.72
36	C	501	ADP	N3-C4-N9	5.67	136.82	127.17
34	D	501	ATP	C5-C4-N3	-5.65	118.93	126.72

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	E	401	ATP	PB-O3B-PG-O2G
34	E	401	ATP	C5'-O5'-PA-O2A
34	E	401	ATP	C5'-O5'-PA-O3A
34	E	401	ATP	O4'-C4'-C5'-O5'
36	C	501	ADP	C5'-O5'-PA-O1A

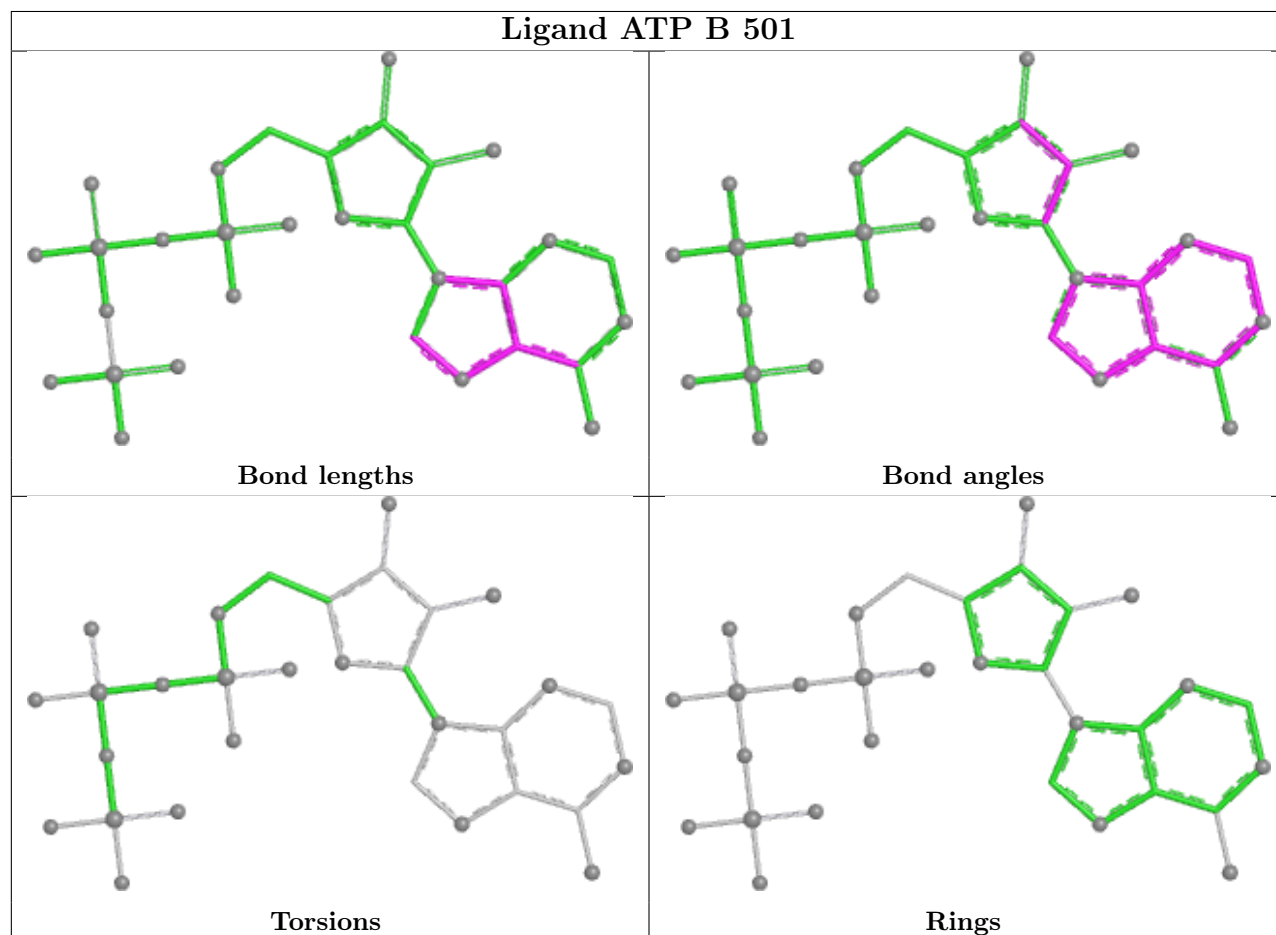
There are no ring outliers.

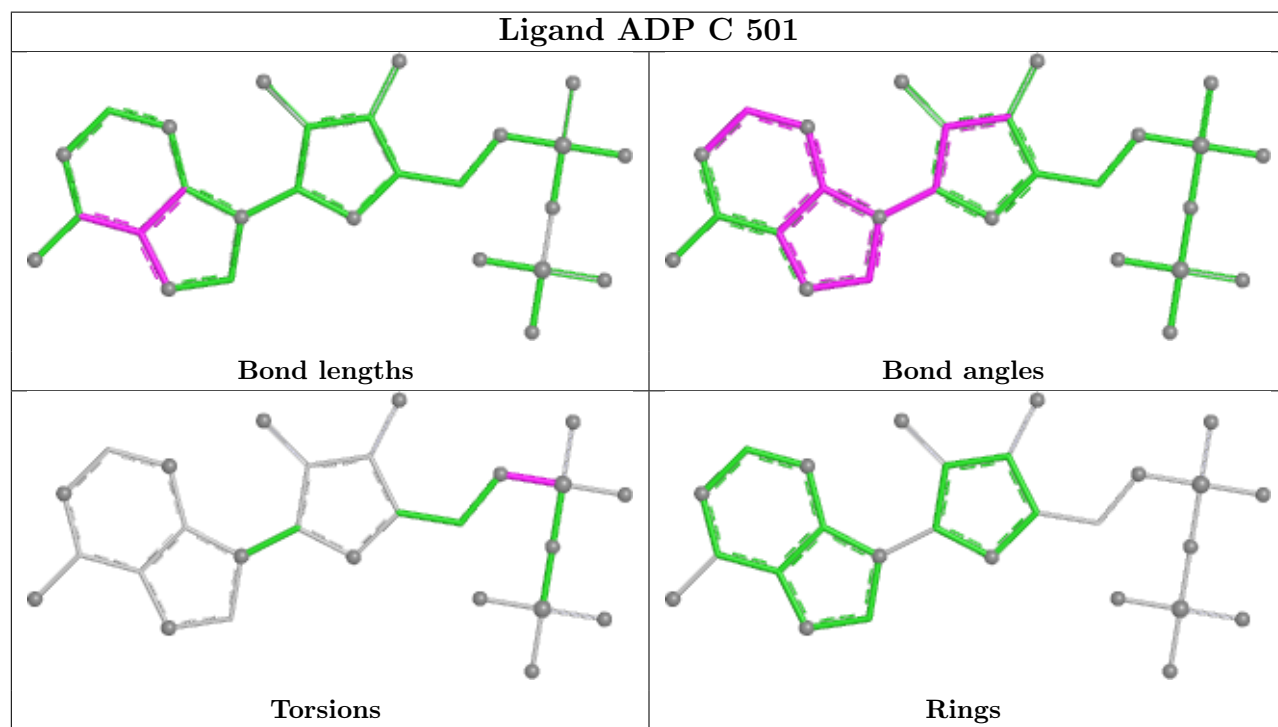
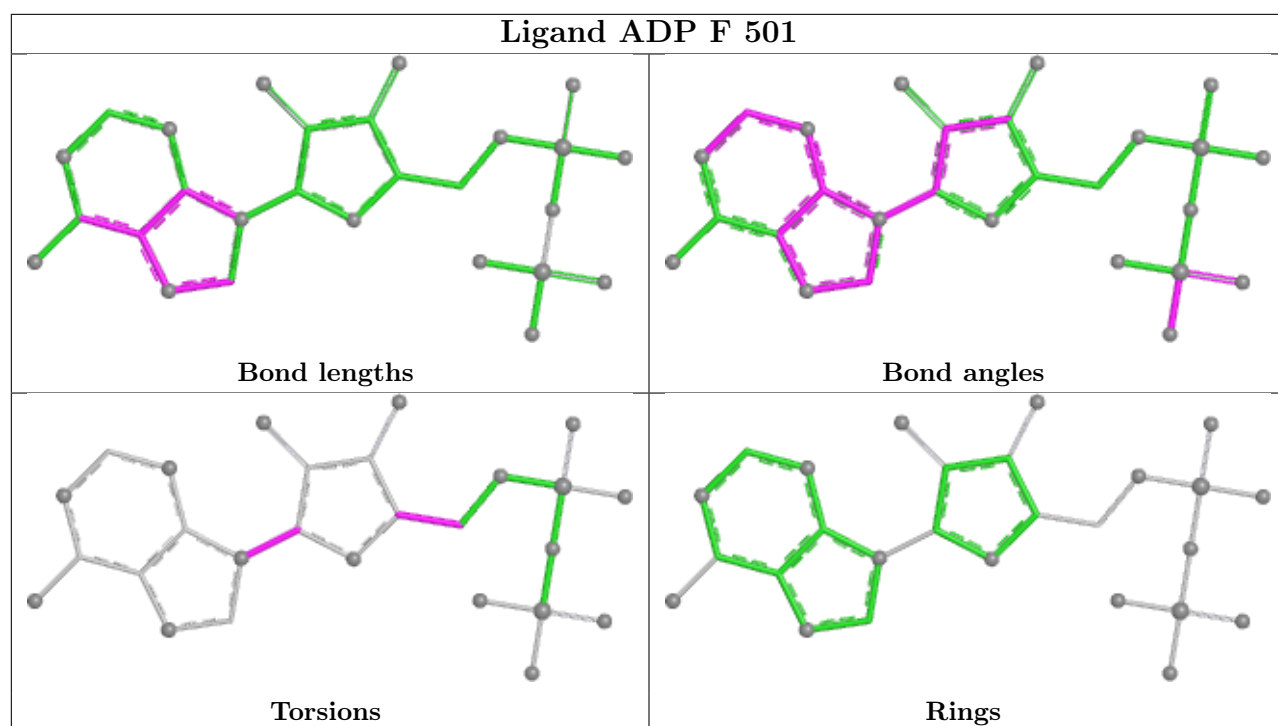
6 monomers are involved in 8 short contacts:

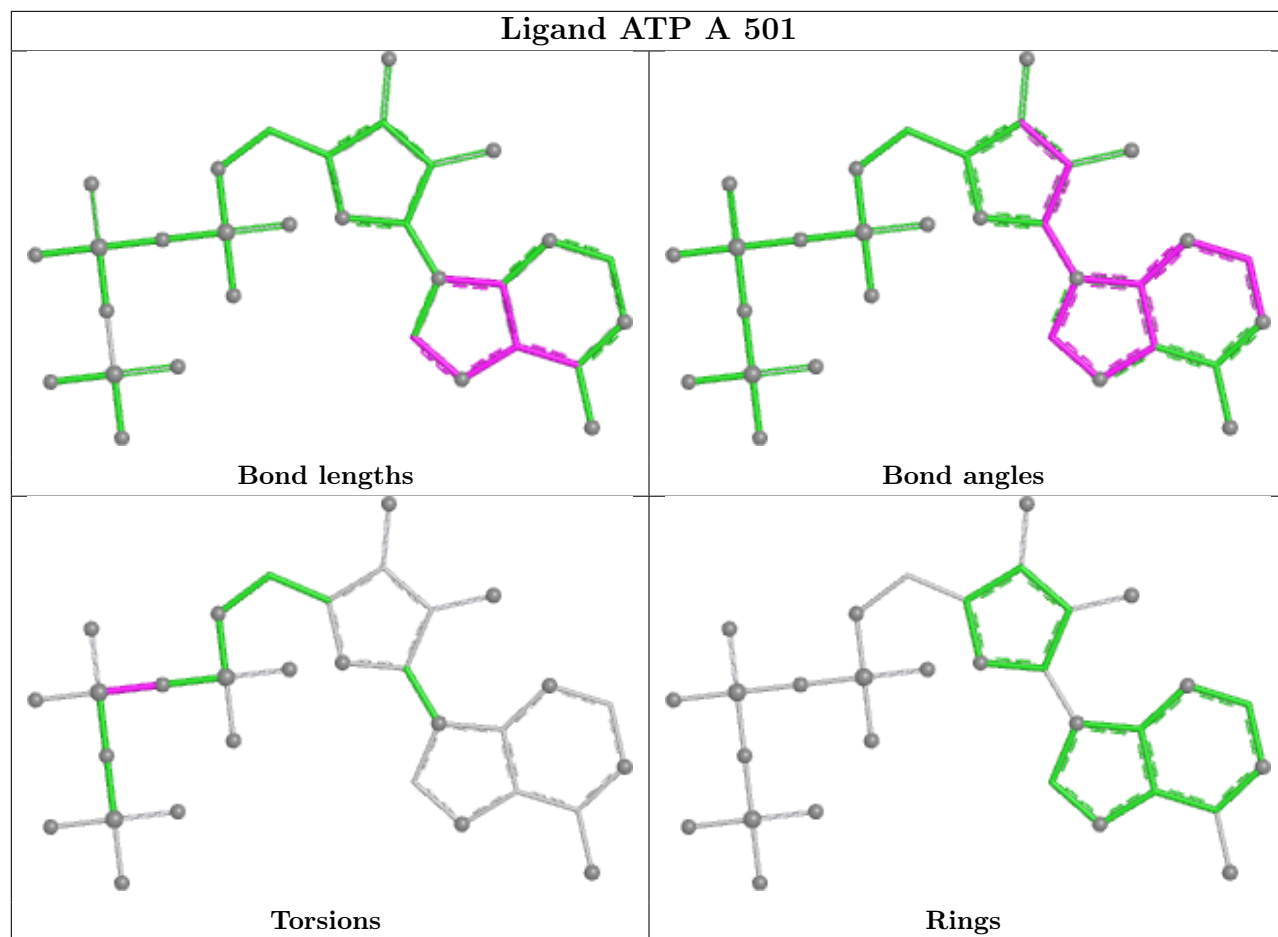
Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	B	501	ATP	1	0
36	F	501	ADP	1	0
36	C	501	ADP	1	0
34	A	501	ATP	1	0
34	E	401	ATP	3	0
34	D	501	ATP	1	0

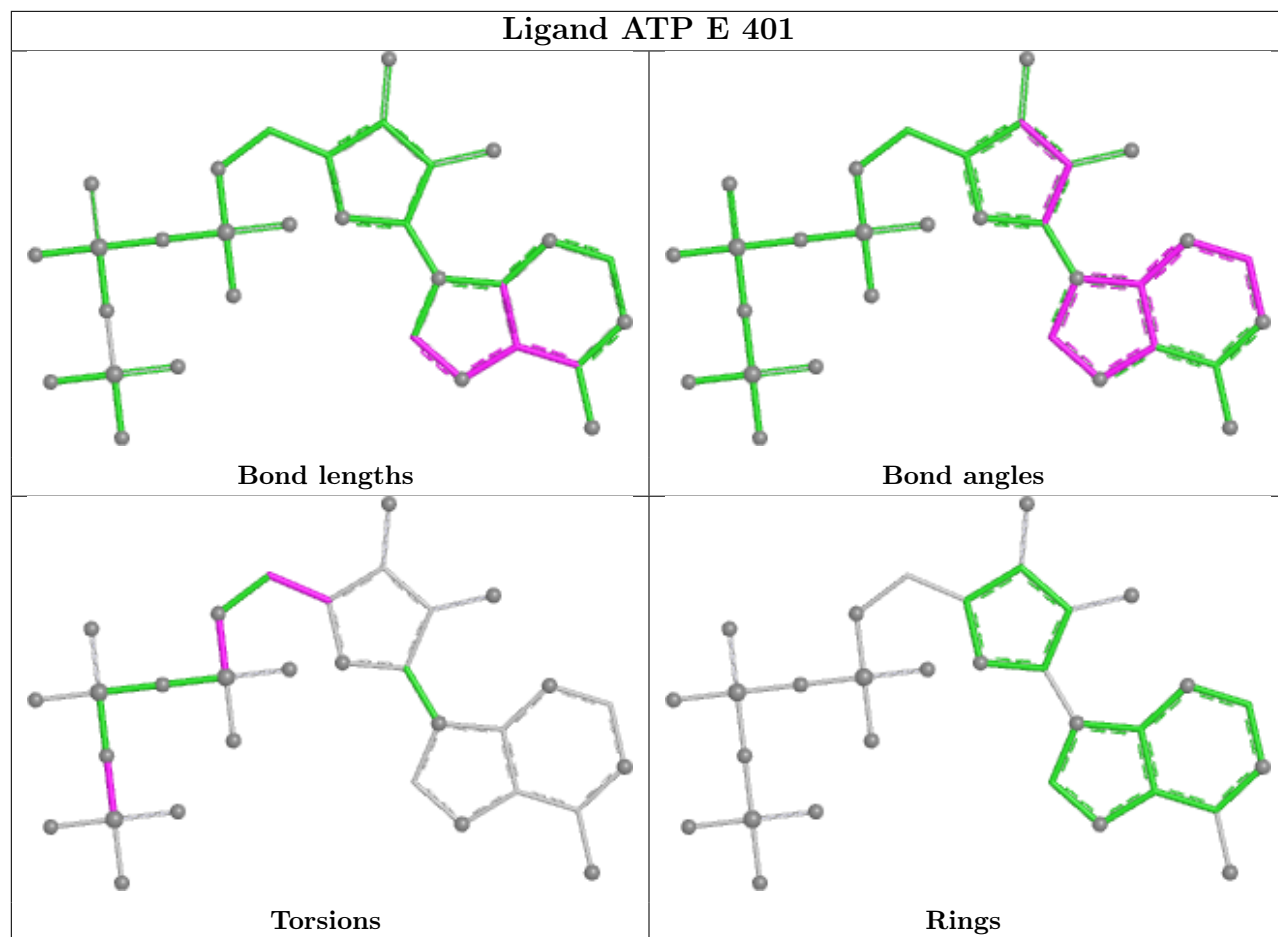
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

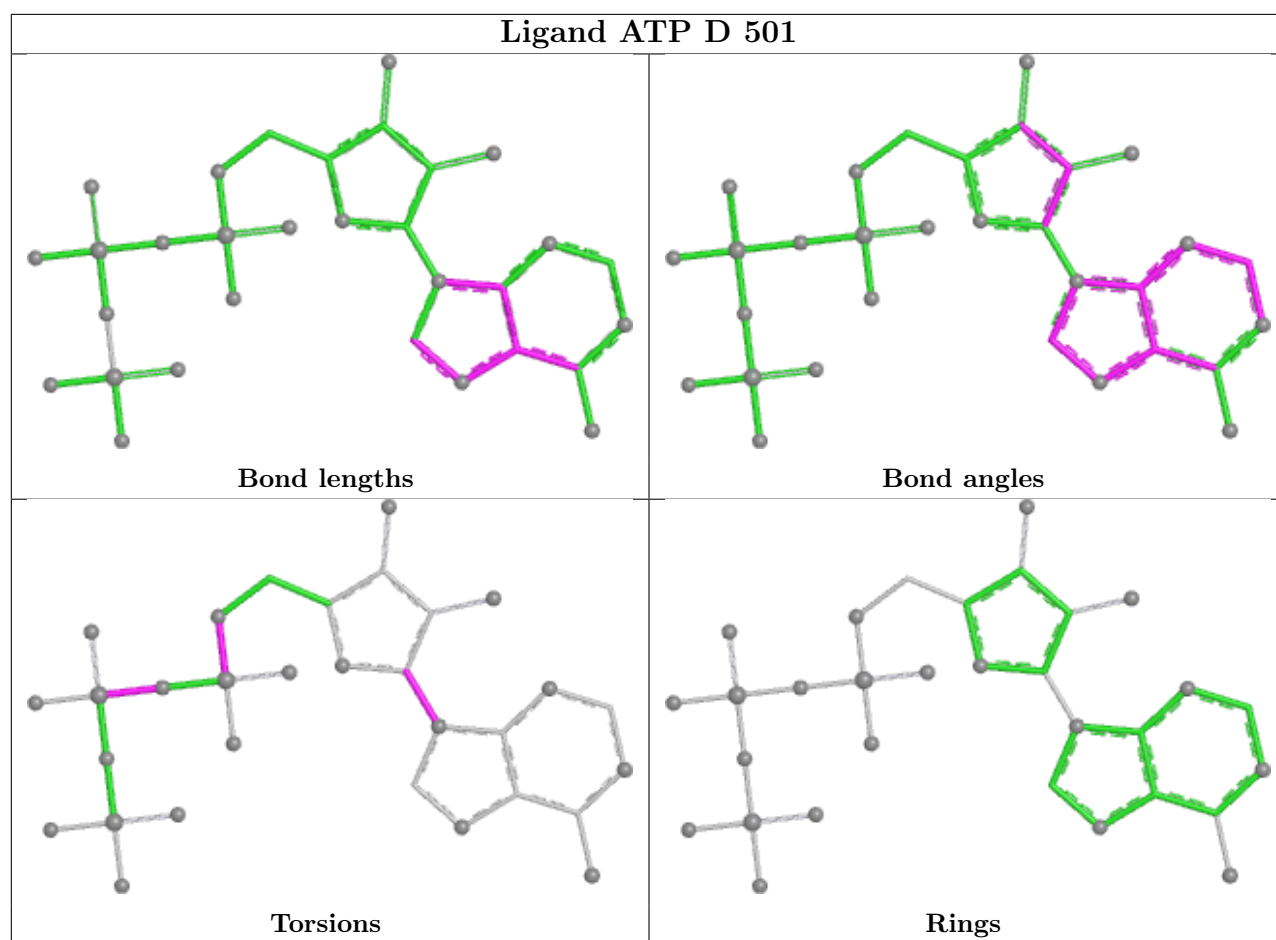
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











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.

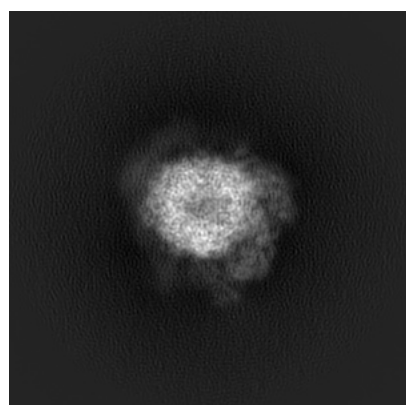
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14201. These allow visual inspection of the internal detail of the map and identification of artifacts.

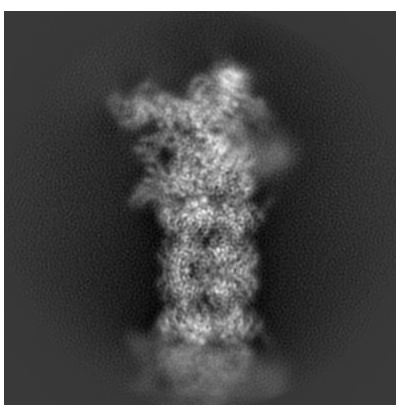
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

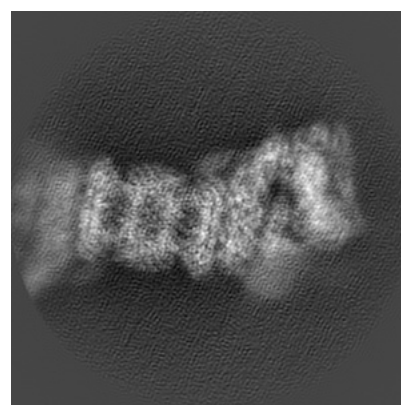
6.1.1 Primary map



X



Y

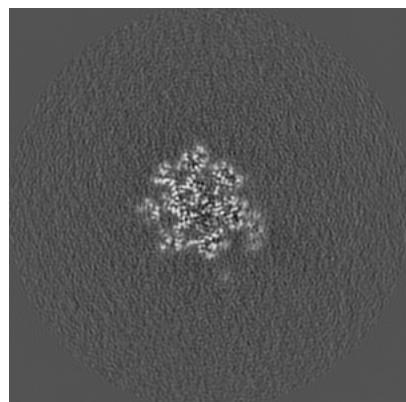


Z

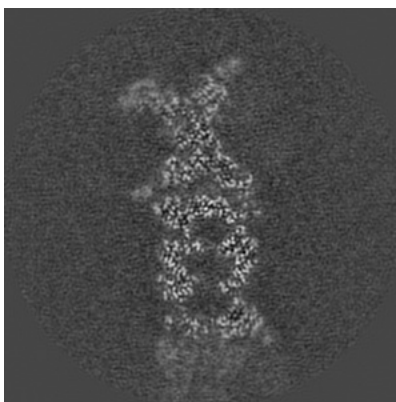
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

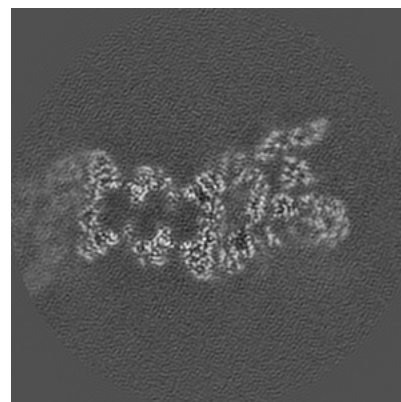
6.2.1 Primary map



X Index: 160



Y Index: 160

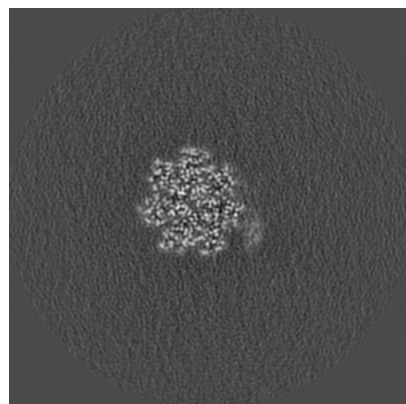


Z Index: 160

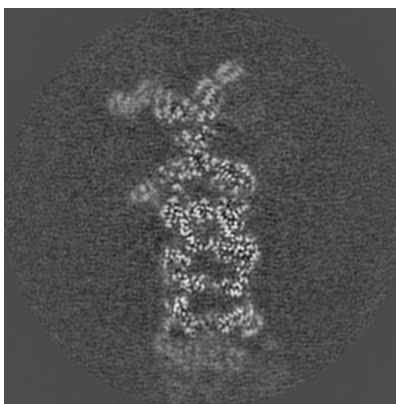
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

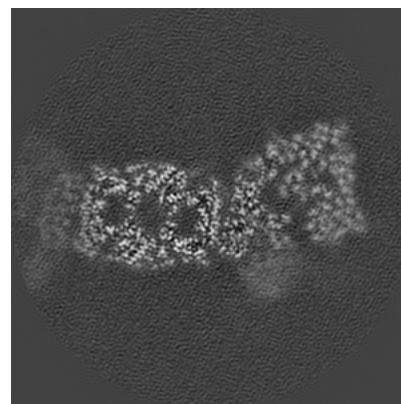
6.3.1 Primary map



X Index: 154



Y Index: 165

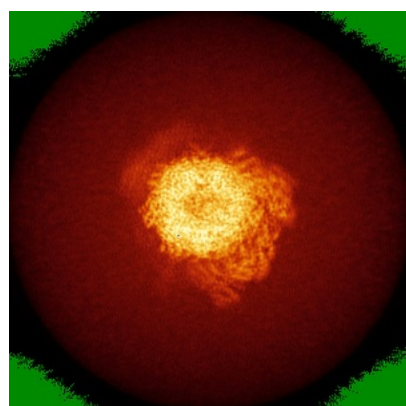


Z Index: 176

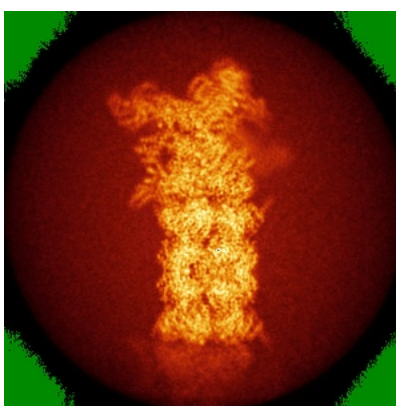
The images above show the largest variance slices of the map in three orthogonal directions.

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

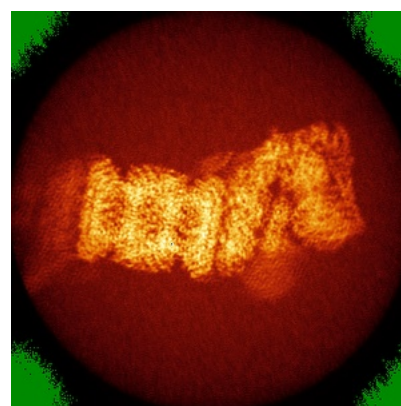
6.4.1 Primary map



X



Y

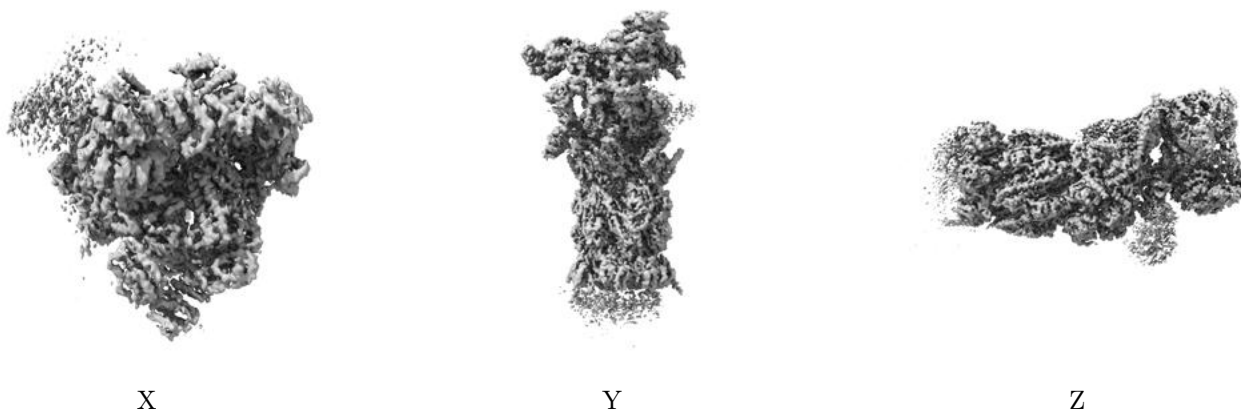


Z

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 0.0394. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

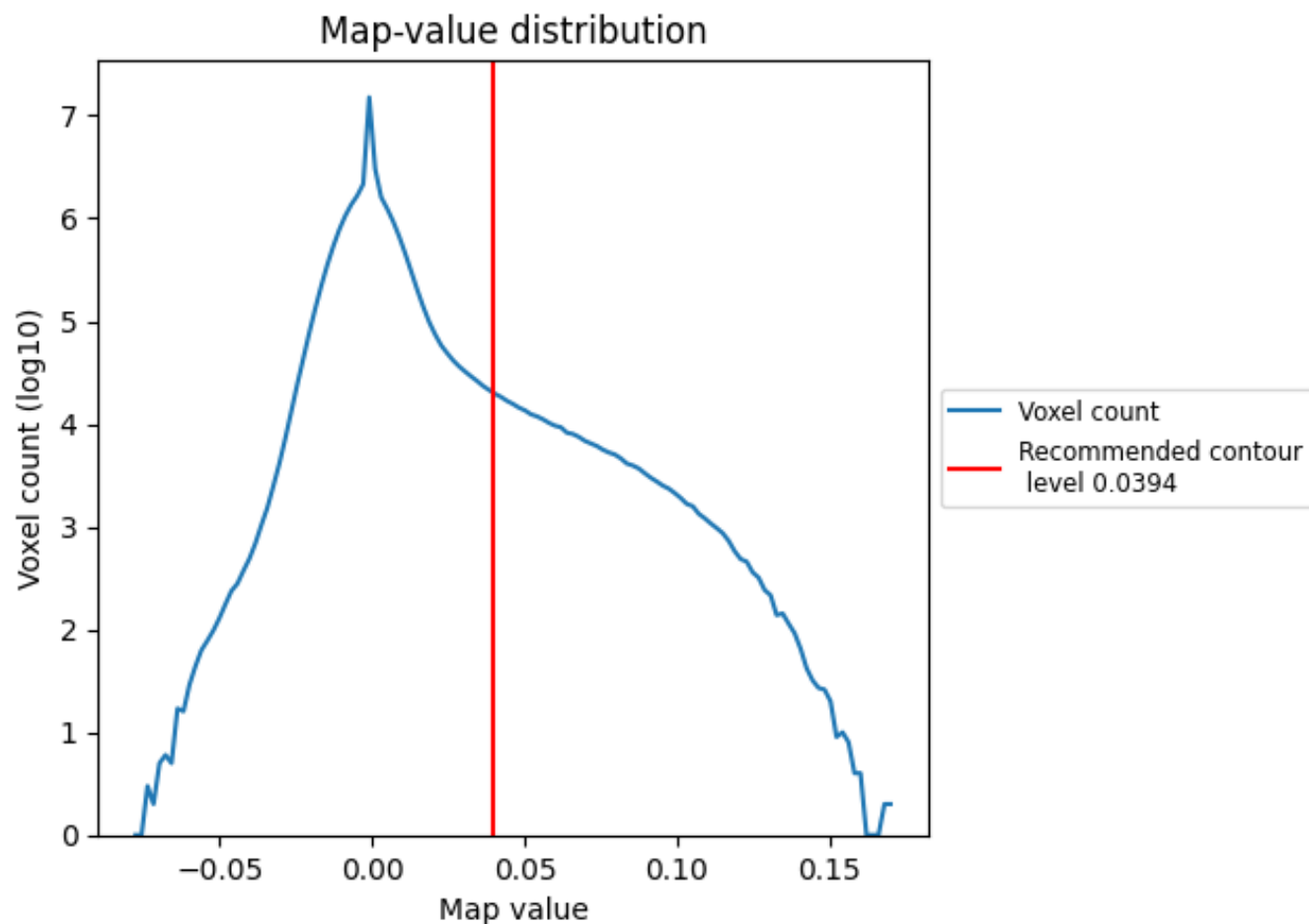
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

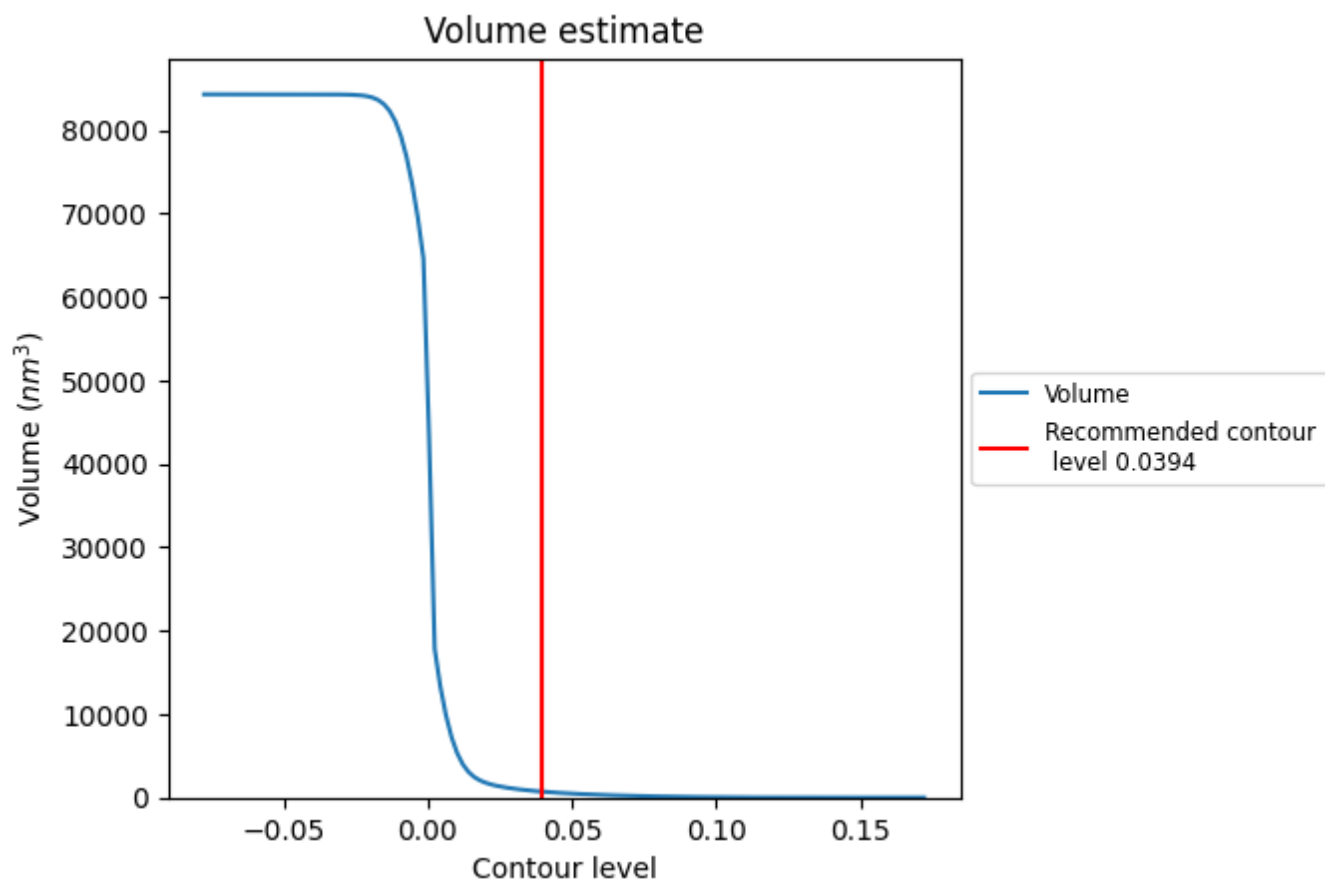
This section contains the results of statistical analysis of the map.

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.

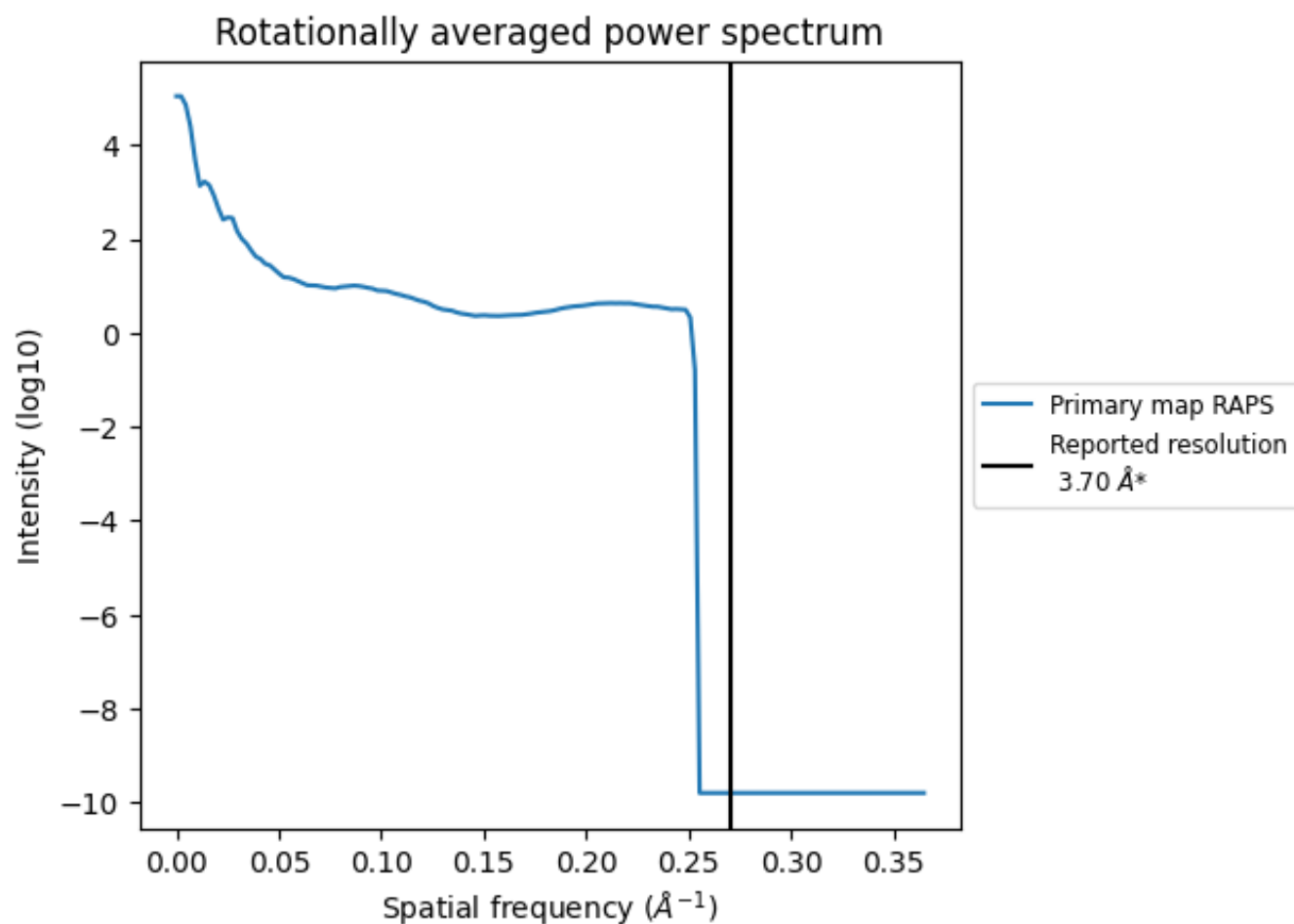
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 717 nm³; this corresponds to an approximate mass of 648 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 0.270 Å⁻¹

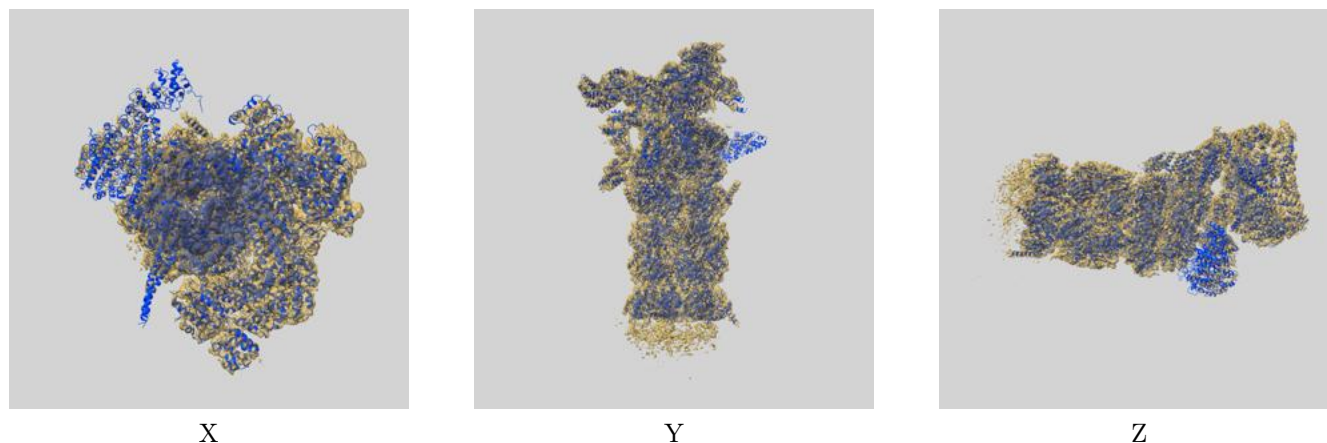
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

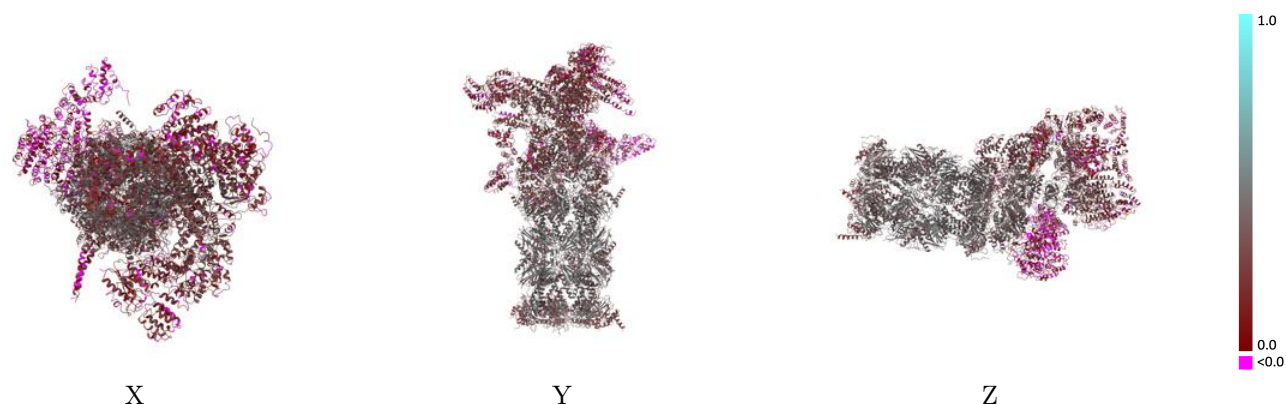
This section contains information regarding the fit between EMDB map EMD-14201 and PDB model 7QXN. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



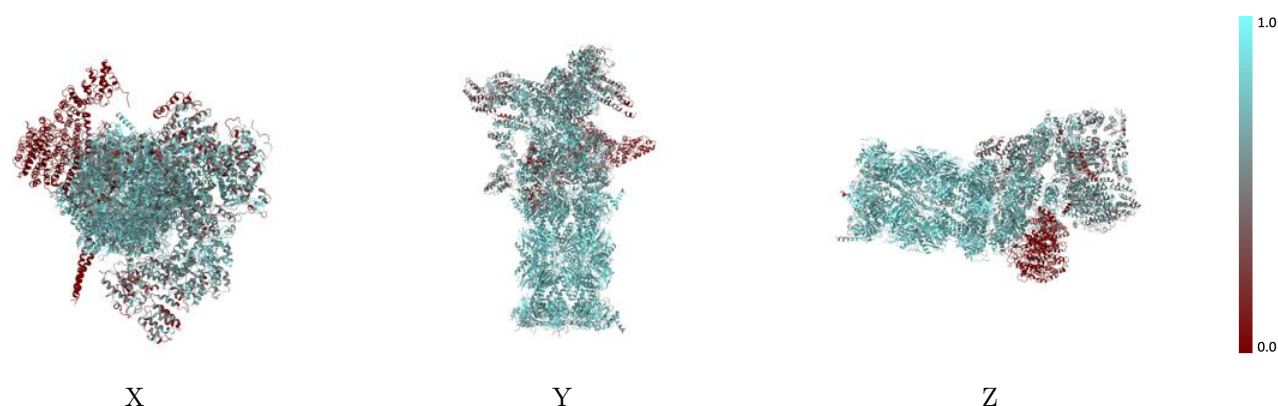
The images above show the 3D surface view of the map at the recommended contour level 0.0394 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



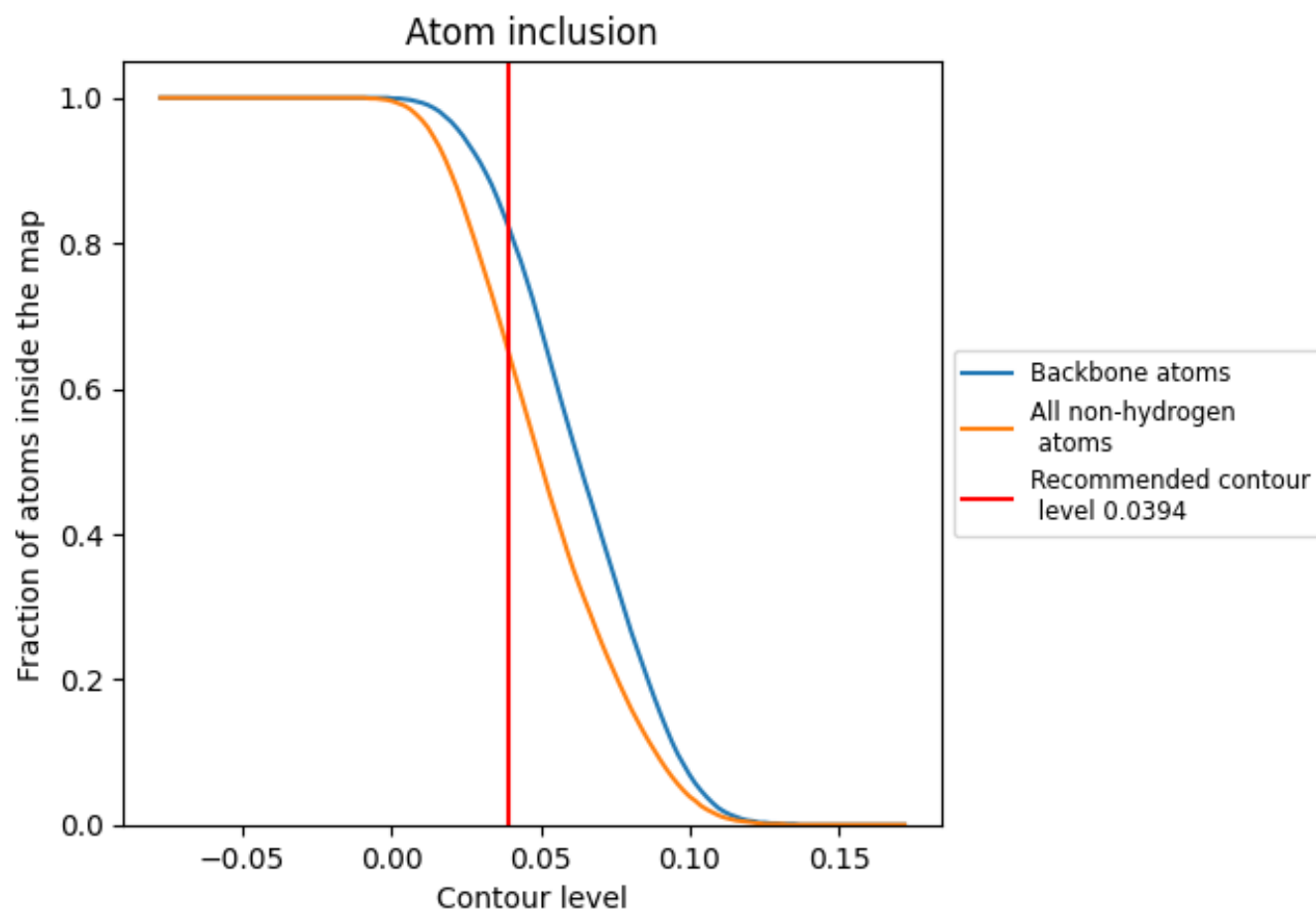
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0394).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 65% 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 (0.0394) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6470	 0.3190
A	 0.6810	 0.3510
B	 0.6280	 0.3260
C	 0.7050	 0.3540
D	 0.6960	 0.3530
E	 0.6960	 0.3440
F	 0.7030	 0.3630
G	 0.8000	 0.4100
H	 0.7980	 0.4130
I	 0.7730	 0.3880
J	 0.7850	 0.3870
K	 0.7830	 0.4010
L	 0.8060	 0.4150
M	 0.7880	 0.4030
N	 0.8280	 0.4300
O	 0.8250	 0.4290
P	 0.8200	 0.4350
Q	 0.8240	 0.4210
R	 0.8490	 0.4440
S	 0.8290	 0.4380
T	 0.8390	 0.4360
U	 0.5540	 0.2170
V	 0.4750	 0.1770
W	 0.5700	 0.2100
X	 0.4650	 0.2630
Y	 0.6530	 0.2480
Z	 0.6040	 0.2940
a	 0.5190	 0.2120
b	 0.3910	 0.1780
c	 0.6570	 0.3130
d	 0.4880	 0.1680
e	 0.4490	 0.1280
f	 0.0360	 0.0660
g	 0.7360	 0.3870
h	 0.7530	 0.3930



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Chain	Atom inclusion	Q-score
i	 0.7100	 0.3650
j	 0.7280	 0.3530
k	 0.7290	 0.3820
l	 0.7540	 0.3880
m	 0.7390	 0.3780
n	 0.8190	 0.4240
o	 0.8150	 0.4260
p	 0.8160	 0.4340
q	 0.8090	 0.4180
r	 0.8250	 0.4230
s	 0.8130	 0.4180
t	 0.8370	 0.4280