



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:10 PM UTC

PDB ID : 7QXU / pdb_00007qxu
EMDB ID : EMD-14203
Title : Proteasome-ZFAND5 Complex Z+C state
Authors : Zhu, Y.; Lu, Y.
Deposited on : 2022-01-27
Resolution : 4.30 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:

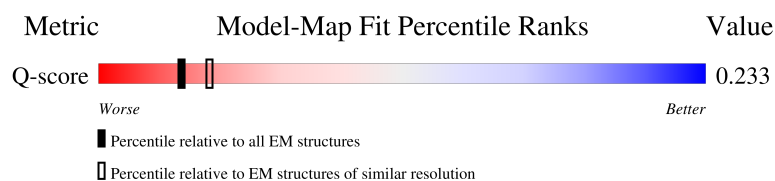
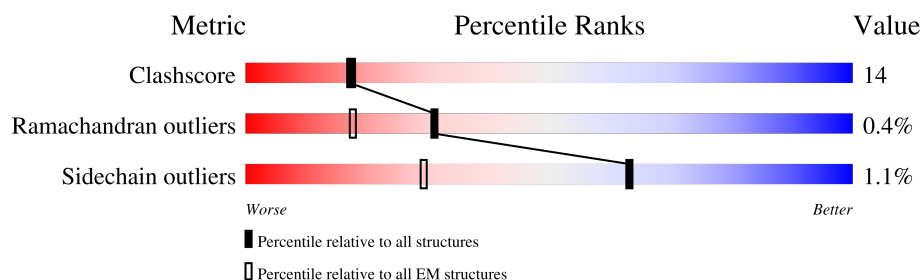
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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	50% 61% 24% 15%
2	V	533	56% 67% 27% 5%
3	W	456	15% 61% 36% ..
4	X	422	14% 76% 14% 10%

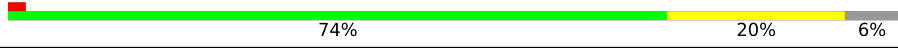
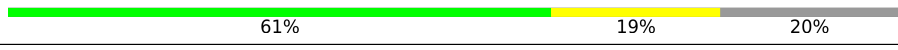
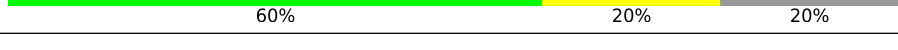
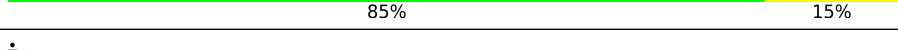
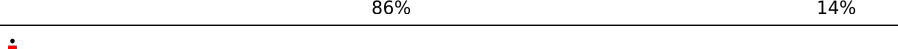
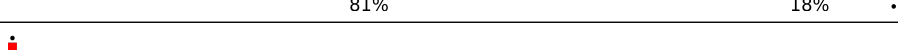
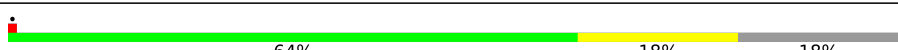
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Mol	Chain	Length	Quality of chain
5	Y	389	
6	Z	324	
7	a	376	
8	b	377	
9	c	309	
10	d	349	
11	e	70	
12	f	908	
13	A	433	
14	B	429	
15	C	389	
16	D	418	
17	E	403	
18	F	439	
19	G	245	
19	g	245	
20	H	233	
20	h	233	
21	I	260	
21	i	260	
22	J	247	
22	j	247	
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	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	ATP	E	401	-	-	X	-
36	ADP	C	501	-	-	X	-

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 103719 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
			3703	2339	635	704	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
			6860	4309	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 proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	B	384	Total	C	N	O	S	0	0
			3011	1895	515	586	15		

- Molecule 15 is a protein called 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		

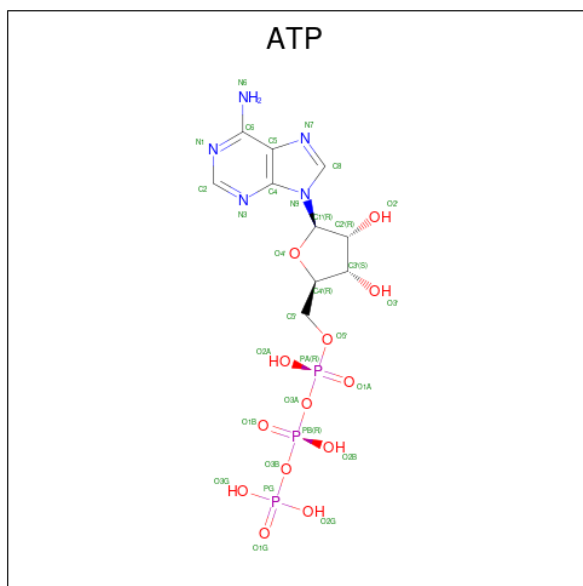
- Molecule 32 is a protein called Proteasome subunit beta type-4.

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).



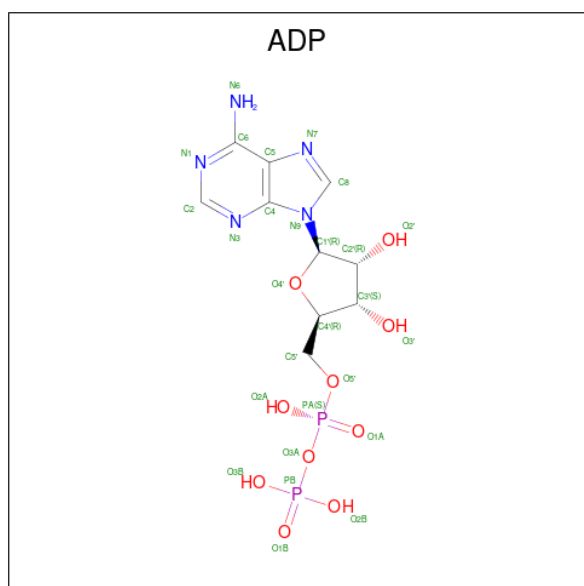
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Mol	Chain	Residues	Atoms					AltConf
34	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
34	E	1	Total	C	N	O	P	0
			31	10	5	13	3	

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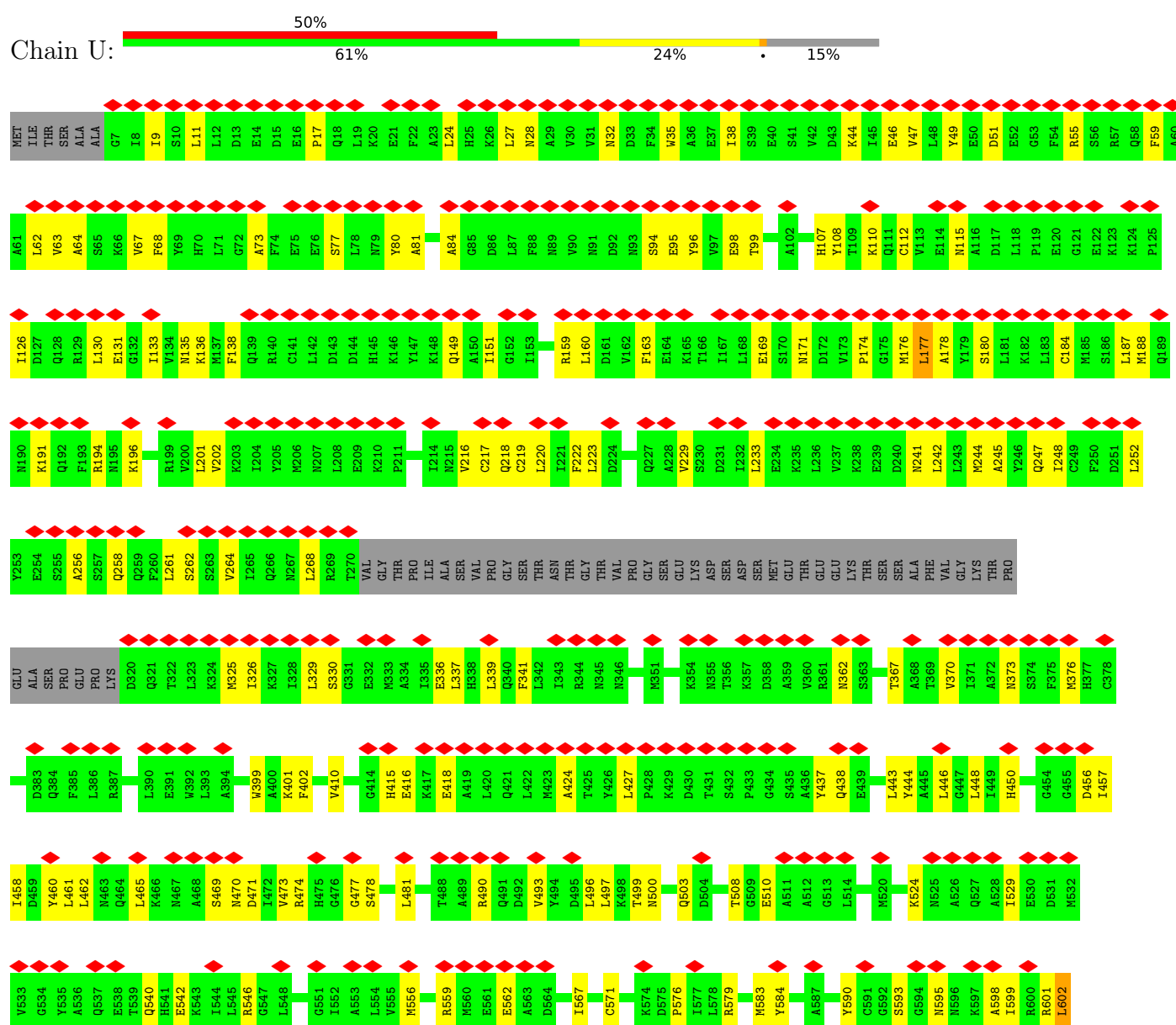
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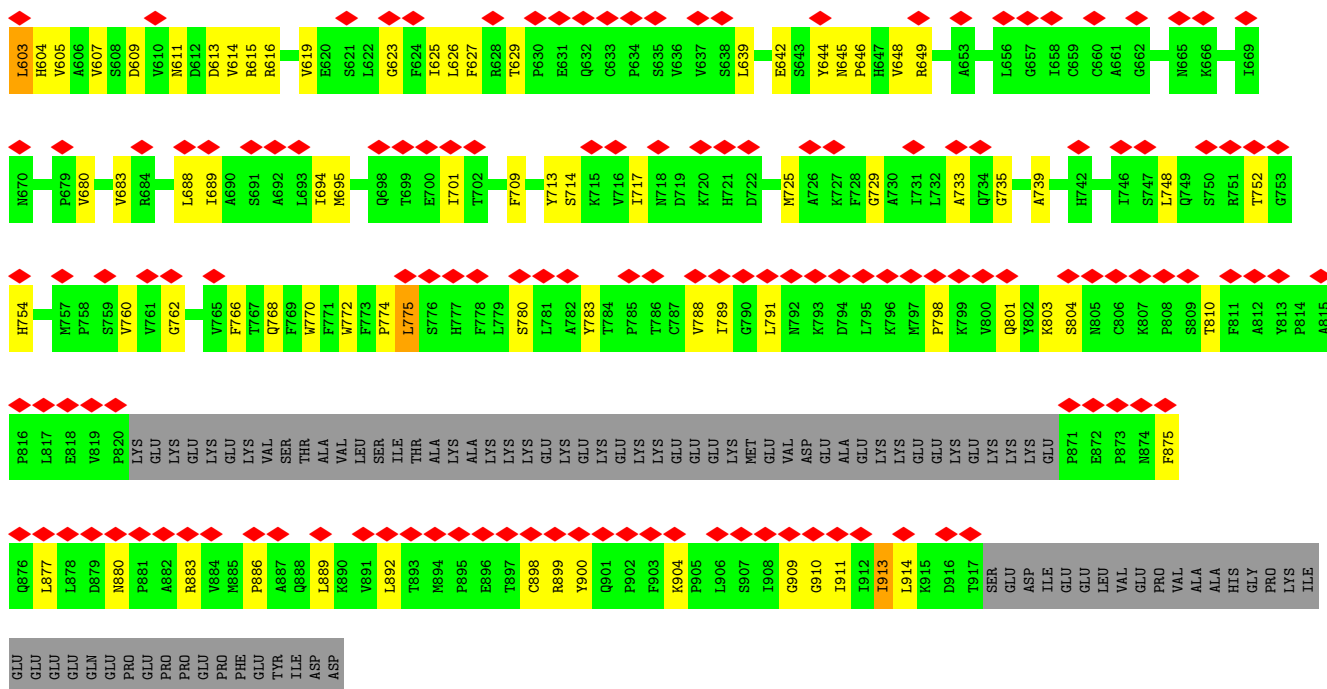
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	F	1	27	10	5	10	2	0

3 Residue-property plots

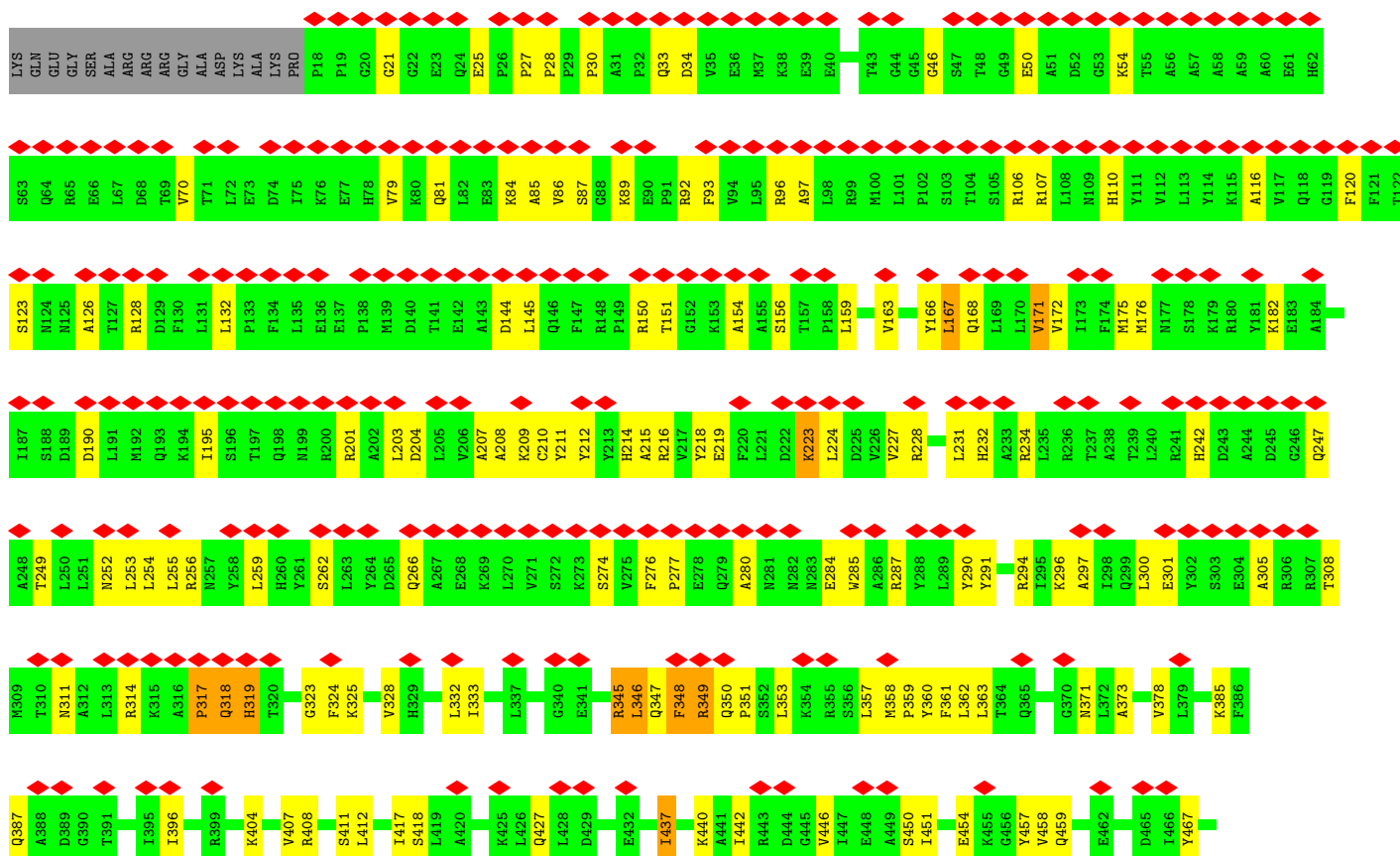
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

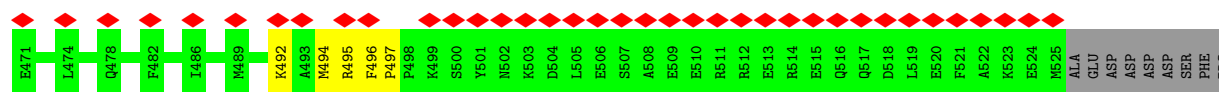
- Molecule 1: 26S proteasome non-ATPase regulatory subunit 1



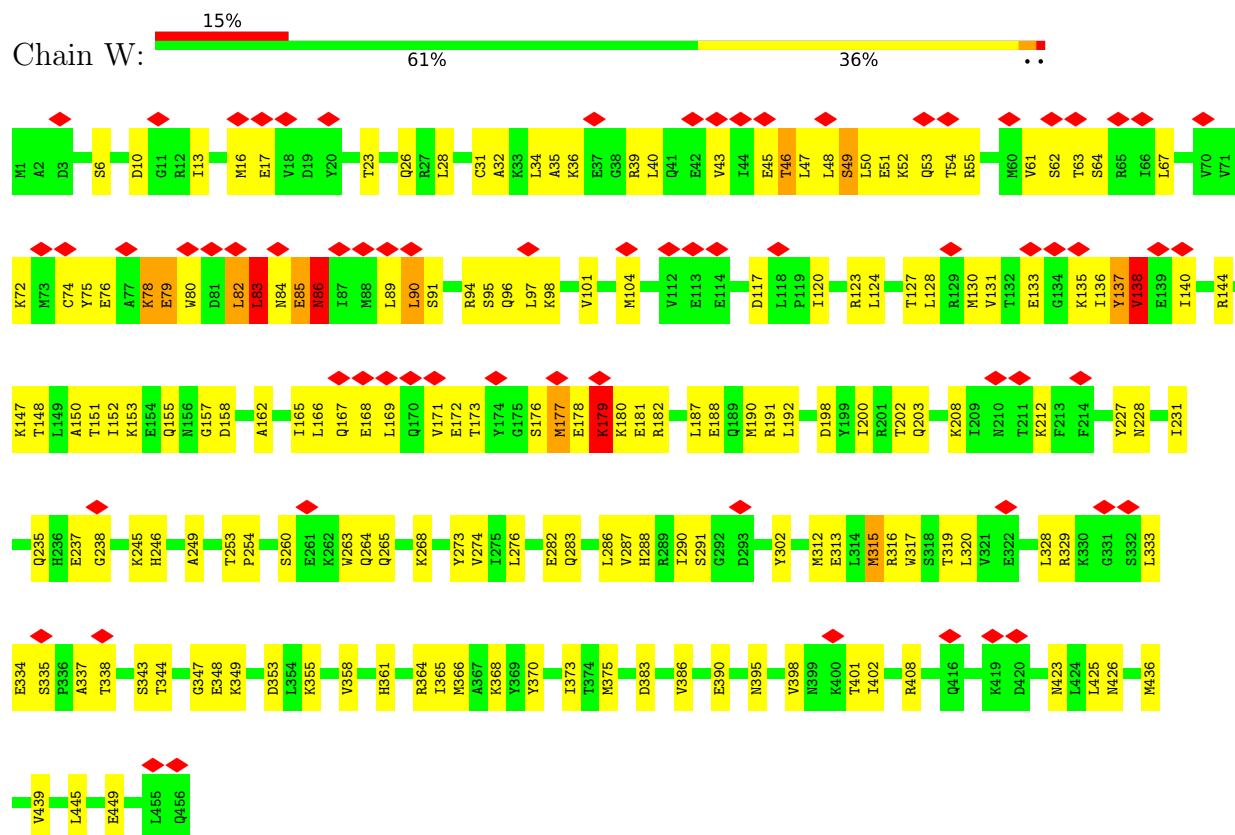


- Molecule 2: 26S proteasome non-ATPase regulatory subunit 3

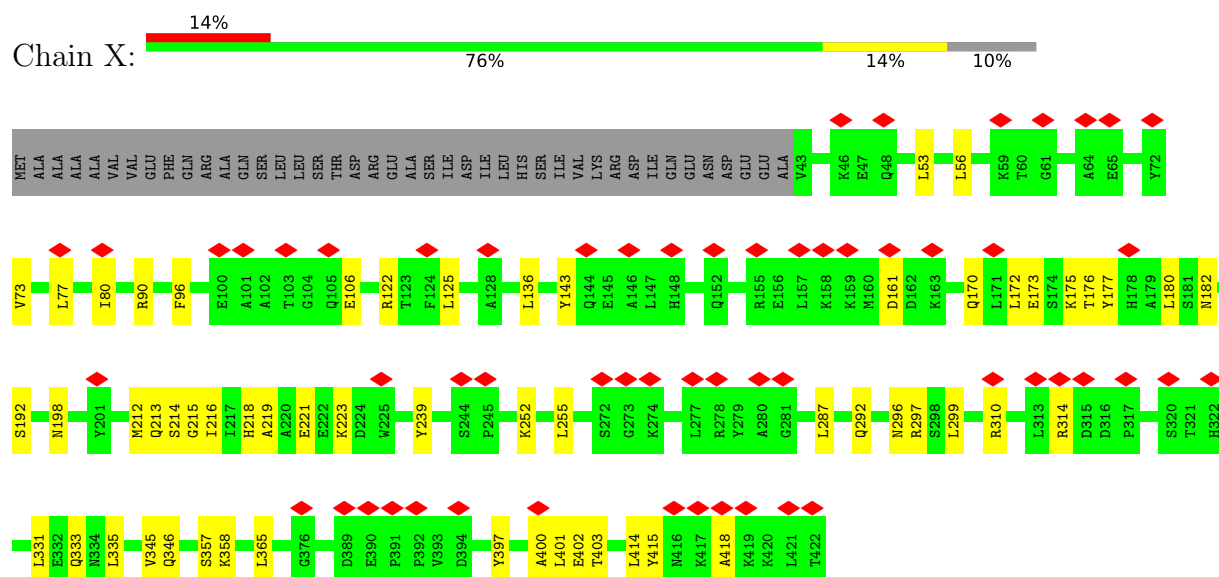




- Molecule 3: 26S proteasome non-ATPase regulatory subunit 12



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



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

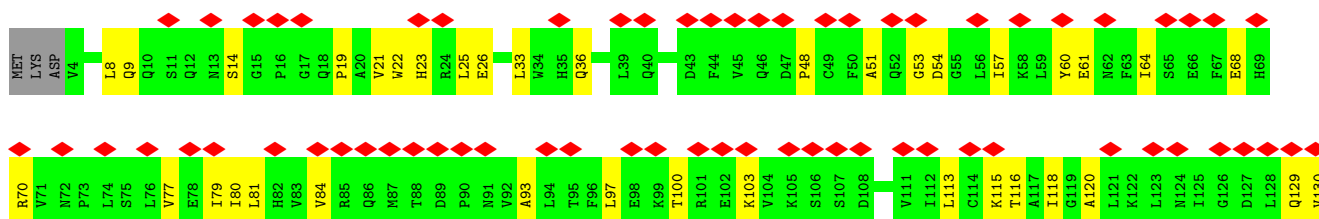
Chain Y:

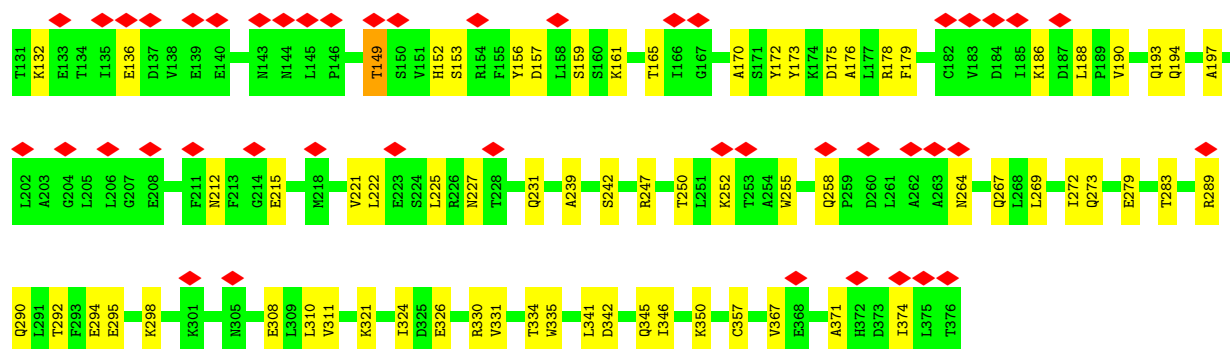
- Molecule 6: 26S proteasome non-ATPase regulatory subunit 7

Chain Z:

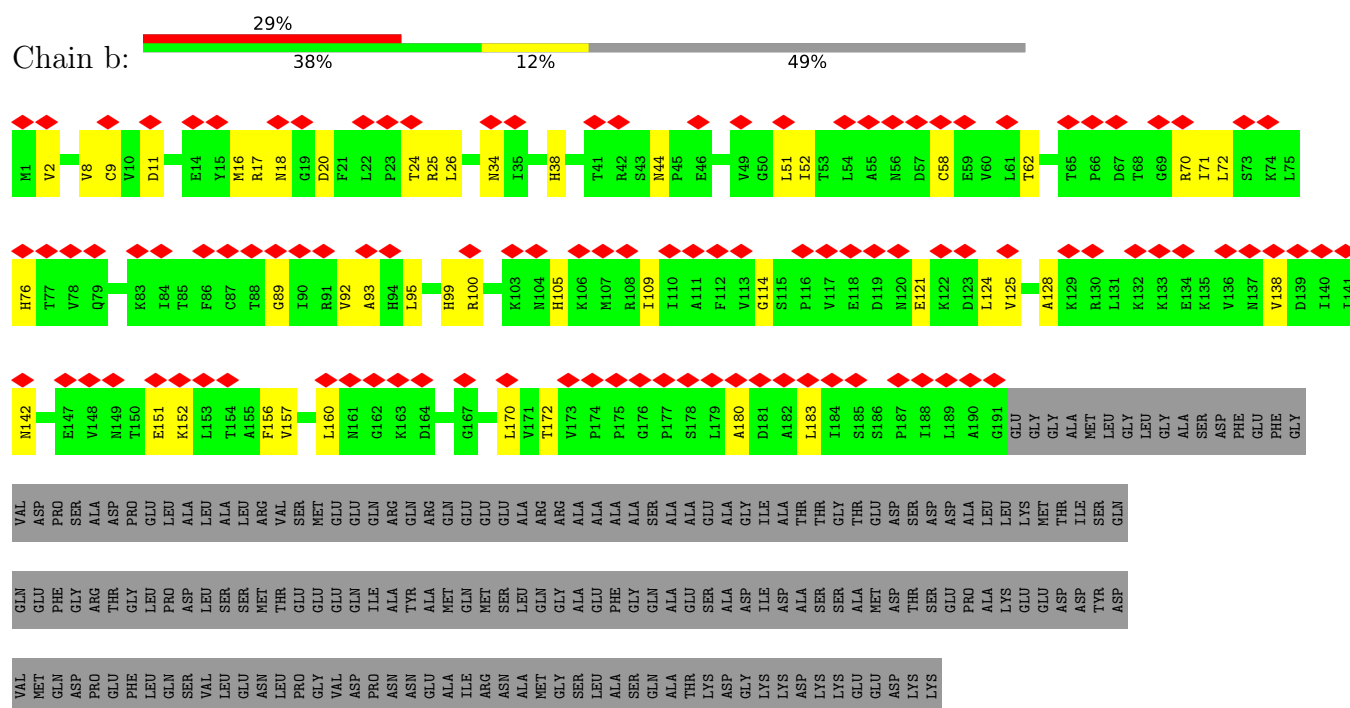
- Molecule 7: 26S proteasome non-ATPase regulatory subunit 13

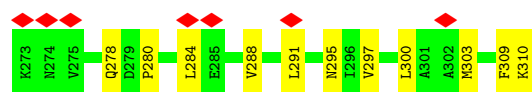
Chain a:



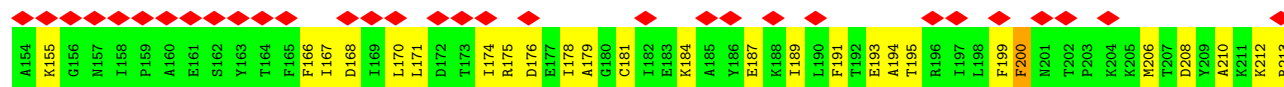
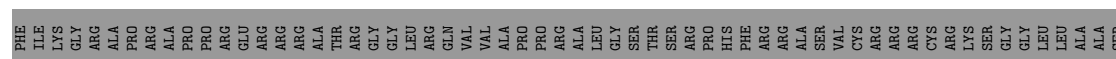


• Molecule 8: 26S proteasome non-ATPase regulatory subunit 4

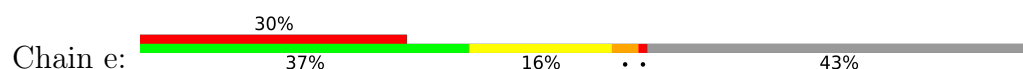




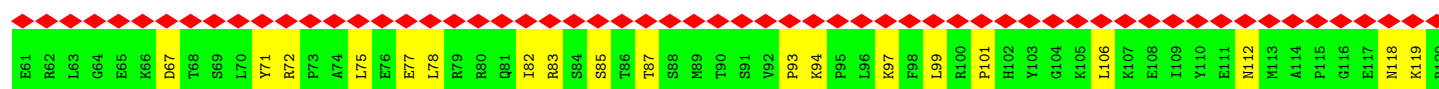
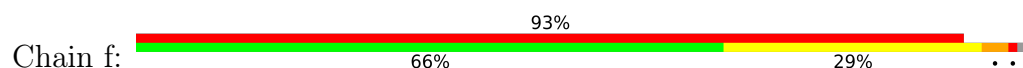
• Molecule 10: 26S proteasome non-ATPase regulatory subunit 8



• Molecule 11: 26S proteasome complex subunit SEM1

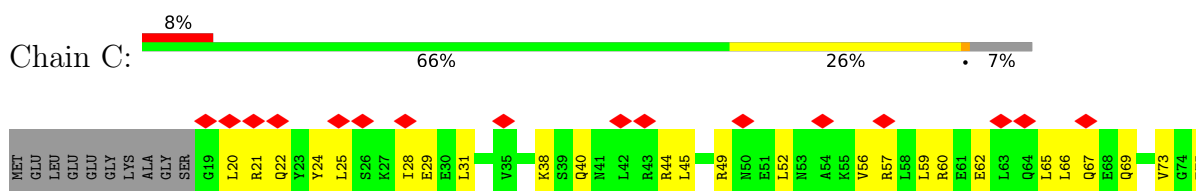


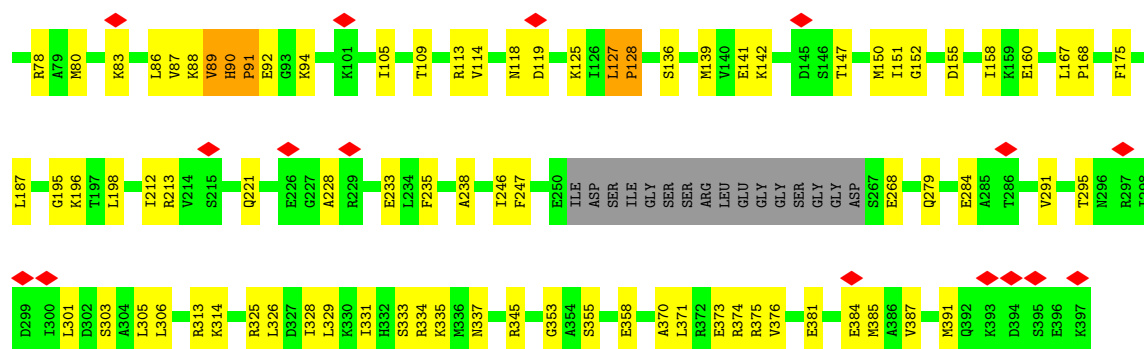
• Molecule 12: 26S proteasome non-ATPase regulatory subunit 2



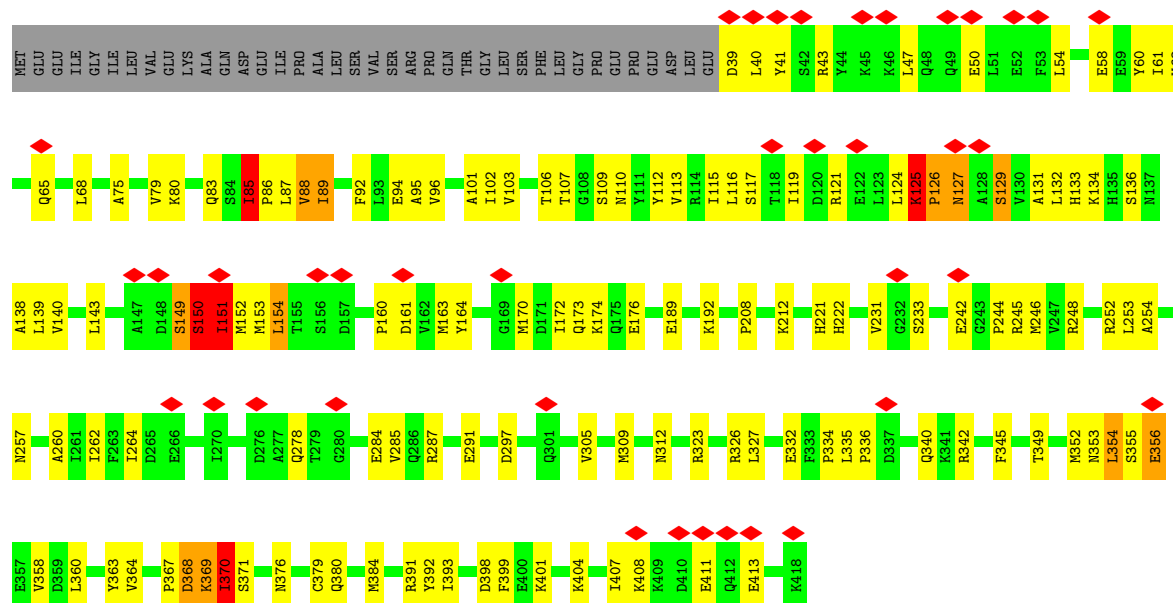
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TTR	V846	Q786	T726	T666	H605	K545	G484	V422	G362	G302	E242	E182	A122
ASP	G847	L787	F727	G667	V606	S546	L485	D423	S363	V303	P243	P183	A123
LEU	Q848	K788	A728	A668	L607	E547	G486	G424	Q364	F304	E244	L184	D124
	A849	S789	M729	E669	K608	T548	L487	G425	V365	L305	N245	L185	I125
	V850	Q790	G730	H670	V609	E549	A488	L426	D366	E306	S246	T186	I126
	V851	V791	M731	A671	Q610	L550	Y489	T427	S367	L307	A247	L187	S127
	V852	A792	V732	L673	Q611	K551	S492	Q428	A368	S308	L248	V188	V128
	V853	V793	G733	R673		D552	N493	L429	R369	E309	L249	K189	L129
	G854	A794	S734	T674	H614	T553	N494	D430	M370	D310	R250	E190	A130
	Q855	G795	G735	F675	L615	Y554	R494	K431	N371	V311	C251	I191	M131
	A856	L796	T736	G676	C616	A555	E495	Y432	L372	E312	A252	V192	T132
	G857	L797	T737	H677	S617	R556	D496	L433	A373	E313	L253	P193	M133
	K858	T798	M738	L678	E618	N557	V497	Y434	S374	Y314	G254	P194	S134
	P859	V799	A739	R679	H619	L558	L498	S435	S375	E315	V255	N195	G135
	K860	L800	R740	R680	F620	P559	T499	S436	F376	D316	F256	M196	E136
	T861	V801	L741	Y681	D621	L560	L500	E437	V377	L317	R257	A197	R137
	I862	S802	A742	G682	S622	G561	L501	D438	N378	T318	K258	H198	E138
	T863	F803	A743	E683	K623	L562	L502	Y439	G379	E319	F259	N199	C139
	L864	L804	M744	P684	E624	G563	P503	L440	F380	I320	S260	A200	L140
	P865	D805	L745	T685	K625	L564	V504	K441	N381	M321	R261	E201	K141
	V866	V806	R746	L686	E626	H566	M505	S442	V382	S322	F262	H202	Y142
	R867	R807	Q747	R687	F627	L567	G506	G443	A383	N323	P263	E203	R143
	H868	L808	L748	A689	D628	G568	D507	A444	A384	V324	E264	A204	L144
	T869	I809	A749	V690	K629	K569	S808	L445	F385	Q255	A265	C205	V145
	T870	L810	Q750	P691	G631	G570	K509	L446	G386	L266	D206	G206	G146
	P871	L811	Y751	L692	K632	E571	S510	A447	Q387	R267	L207	L207	S147
	V872	G812	H752	A693	E633	A572	M512	C448	D388	S328	L268	L208	Q148
	L873	K813	A753	L694	K634	I573	E513	G449	K389	N329	A269	E149	E149
	L874	S814	K754	L695	K635	E574	V514	I450	L390	F330	L270	E210	E150
	A875	H815	D755	A695	D636	A575	A515	V451	L391	L331	M271	I211	L151
	H876	Y816	P756	L697	D638	I576	G516	G455	T392	A332	L272	E212	A152
	G877	V817	N757	S698	K639	L577	V517	K456	D393	L333	N273	Q213	S153
	E878	L818	N758	V699	K640	A578	T518	M457	D394	A334	D274	V214	W154
	R879	Y819	L759	S700	F641	A579	A519	E458	G395	R335	M275	D215	G155
	A880	G820	F760	N701	A642	L580	L520	C459	N396	E336	E276	M216	H156
	E881	L821	M761	P643	A643	E581	A521	D460	K397	L337	L277	E217	E157
	L882	V822	V762	R702	A644	G582	C522	P461	K398	D338	L278	E218	Y158
	A883	R763	L764	R703	D645	V583	G523	A462	L399	I339	E279	K219	V159
	T884	L764	N705	L704	D646	S584	M524	L463	Y400	M340	D280	D220	R160
	S885	M825	A765	T706	G647	E585	I525	A464	K401	I221	I281	I221	H161
	P886	Q826	Q766	L707	A648	P586	A526	L465	M402	P342	F282	D222	L162
	F887	P827	G767	D708	K649	F587	G528	L466	K403	K343	T283	E223	A163
	L888	R828	L768	T709	Q650	H588	S529	L466	D404	V344	S284	N224	G164
	P889	H829	T769	T709	Y652	S589	C530	D468	H405	P345	C285	A225	E165
	VAL	L830	H770	L710	V653	F590	N531	Y469	G406	D347	K286	Y226	V166
THR	V831	F831	L771	S711	A653	G532	G532	V470	M407	D347	D287	A227	A167
PRO	T832	K712	G772	K712	V654	A591	G532	L471	L408	I348	V288	K228	K168
LEU	F833	F713	G773	F713	L655	N592	D533	L471	S409	V349	V289	V229	E169
GLU	D834	S714	G774	T593	T593	L594	V534	H472	A410	K350	V290	G230	W170
GLY	E835	H715	T775	L657	L594	T535	F535	M473	A410	T351	Q291	L231	Q171
PHE	E836	D716	L776	A658	V595	S536	T537	S474	A412	H352	Q292	Y232	E172
VAL	L837	L659	T777	L659	D596	T537	T537	M475	A412	L353	Q293	L233	L173
ILE	L837	L660	T777	L660	V597	I538	I538	T476	S413	H353	Q294	T234	D174
LEU	R838	A661	L778	A661	V597	I539	I539	M477	L414	E354	M294	T234	D174
ARG	P839	L662	G779	L662	V599	Q540	Q540	R478	G415	N355	A295	S235	D175
LYS	L840	E663	E720	E663	A599	T541	T541	M416	M416	N356	F296	C236	A176
ASN	P841	V721	V781	E664	V600	I542	I542	L479	I417	R357	M297	V237	E177
PRO	V842	S723	H782	E664	G602	I543	I543	G480	L418	F358	N298	N238	K178
	S843	S723	S783	E664	S603			S481	L419	G359	G299	Y239	V179
	V844		D784					I482	W420	G360	R300	V240	Q180

- Molecule 13: 26S protease regulatory subunit 7

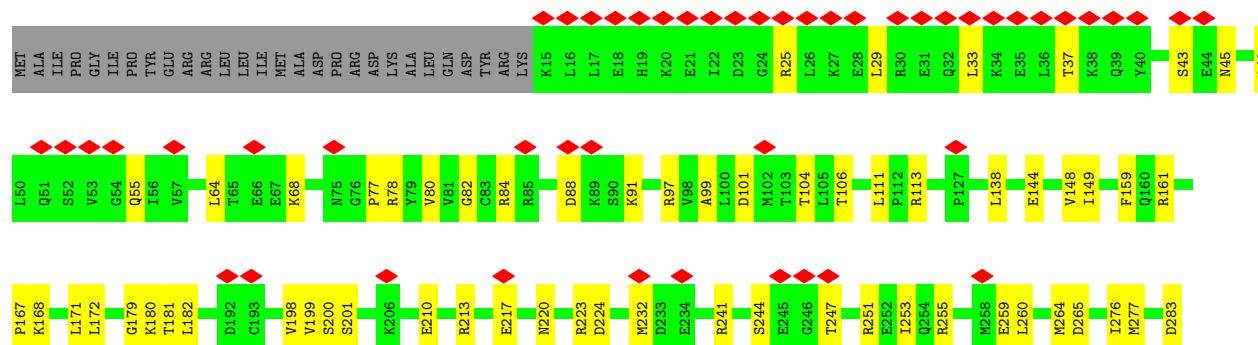




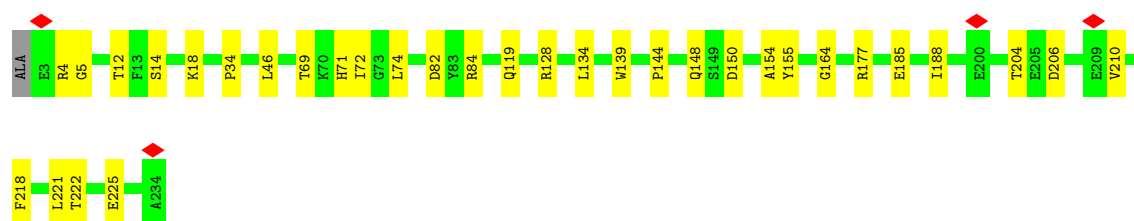
• Molecule 16: 26S protease regulatory subunit 6B



• Molecule 17: 26S proteasome regulatory subunit 10B

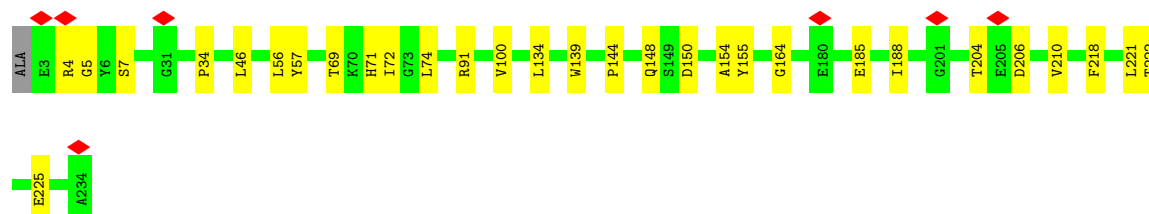


Chain H:  85% 14%



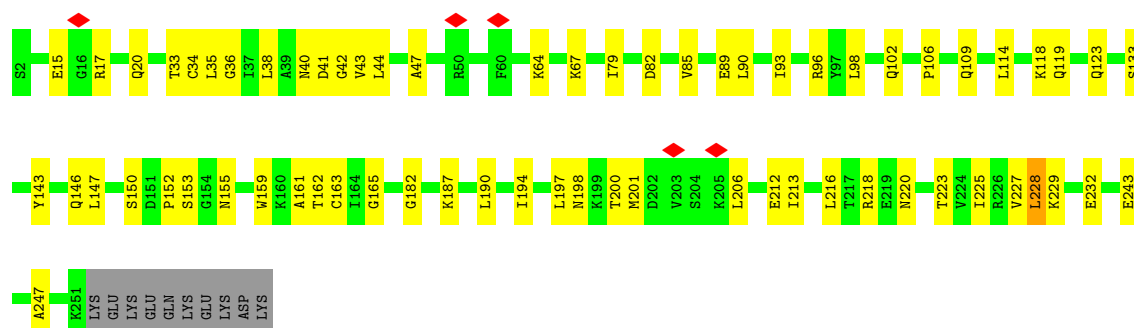
- Molecule 20: Proteasome subunit alpha type-2

Chain h:  87% 13%



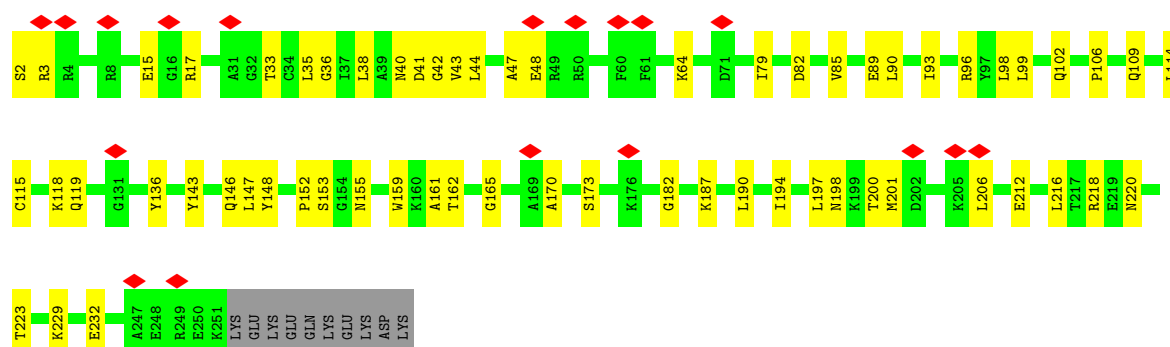
- Molecule 21: Proteasome subunit alpha type-4

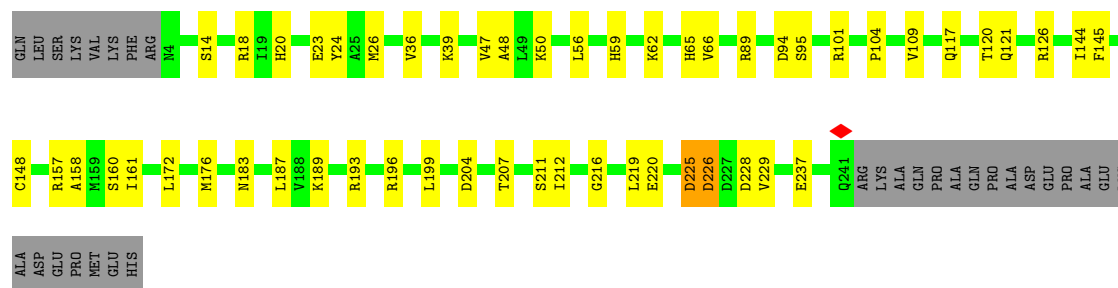
Chain I:  71% 25%



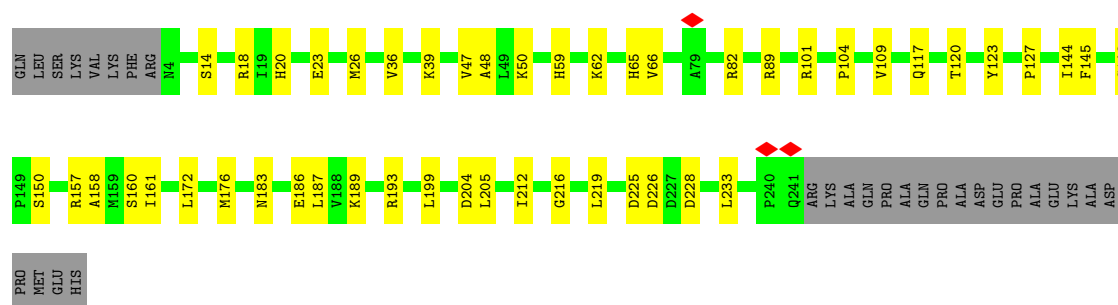
- Molecule 21: Proteasome subunit alpha type-4

Chain i:  7% 72% 24%

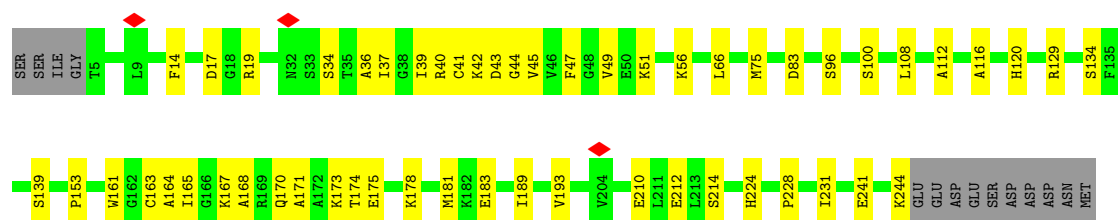




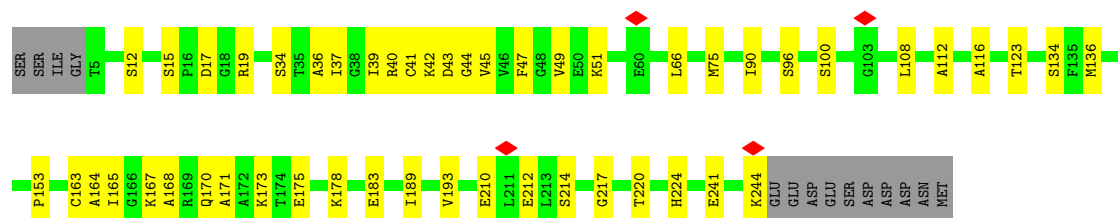
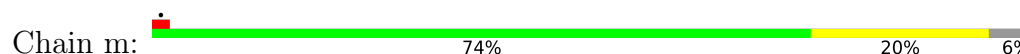
- Molecule 24: Isoform Long of Proteasome subunit alpha type-1



- Molecule 25: Proteasome subunit alpha type-3

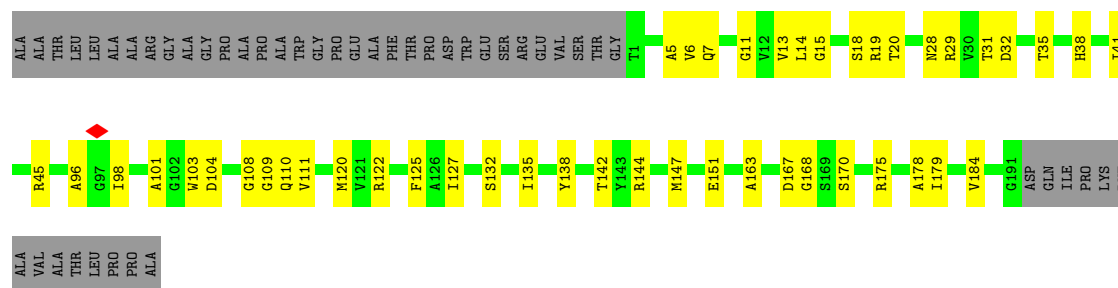


- Molecule 25: Proteasome subunit alpha type-3



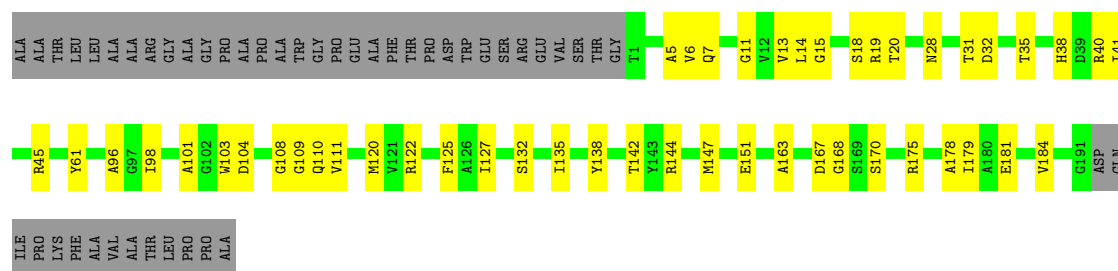
- Molecule 26: Proteasome subunit beta type-6





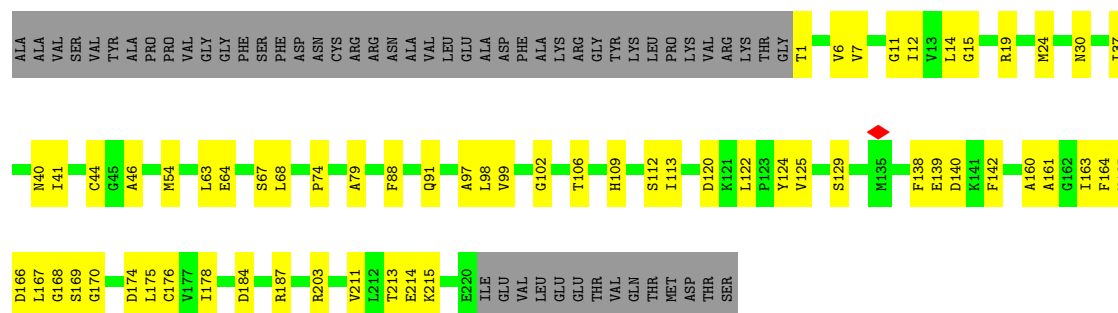
- Molecule 26: Proteasome subunit beta type-6

Chain n: 60% 20% 20%



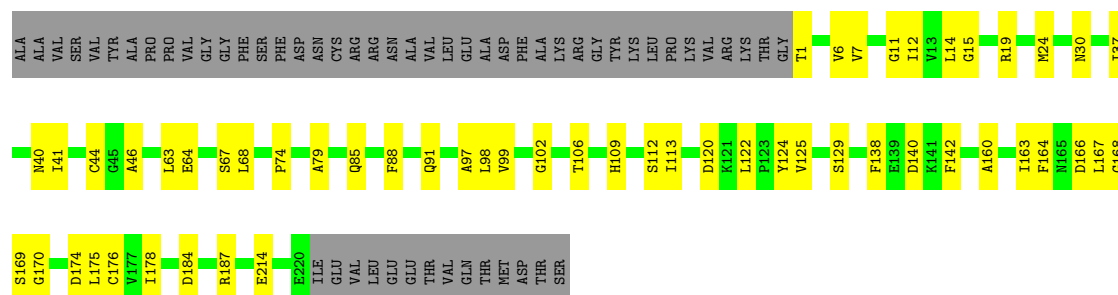
- Molecule 27: Proteasome subunit beta type-7

Chain O: 57% 22% 20%



- Molecule 27: Proteasome subunit beta type-7

Chain o: 60% 20% 20%



- Molecule 28: Proteasome subunit beta type-3

Chain P:  85% 15%



- Molecule 28: Proteasome subunit beta type-3

Chain p:  86% 14%



- Molecule 29: Proteasome subunit beta type-2

Chain Q:  81% 18%



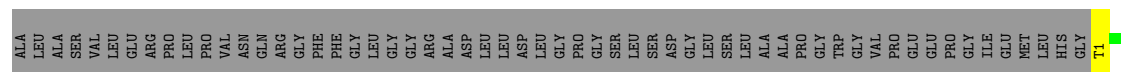
- Molecule 29: Proteasome subunit beta type-2

Chain q:  79% 20%



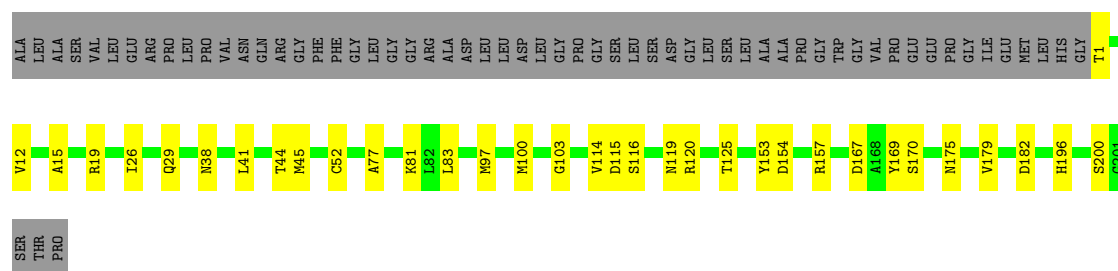
- Molecule 30: Proteasome subunit beta type-5

Chain R:  61% 16% 23%



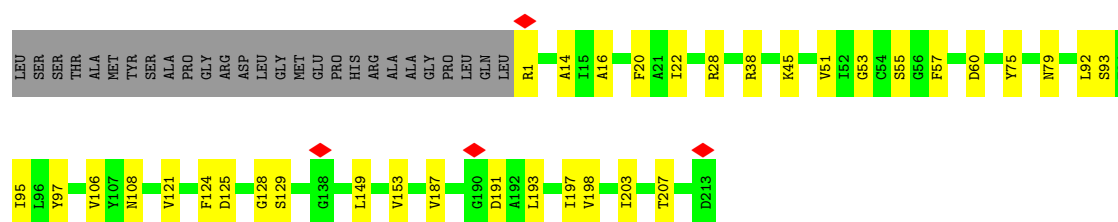
- Molecule 30: Proteasome subunit beta type-5

Chain r:  64% 13% 23%



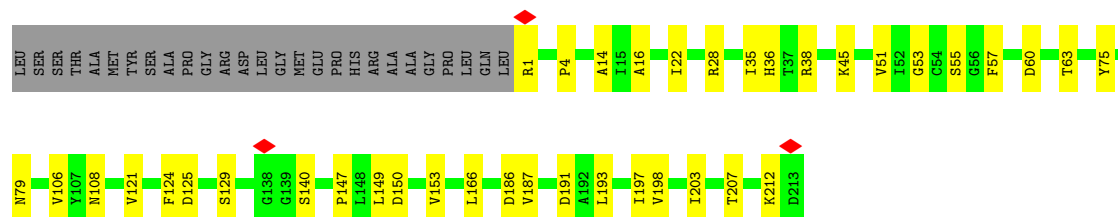
• Molecule 31: Proteasome subunit beta type-1

Chain S:  74% 15% 11%



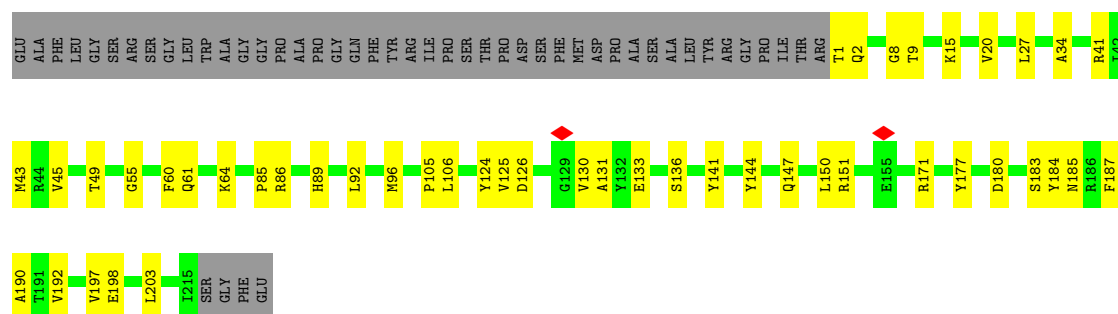
• Molecule 31: Proteasome subunit beta type-1

Chain s:  72% 16% 11%



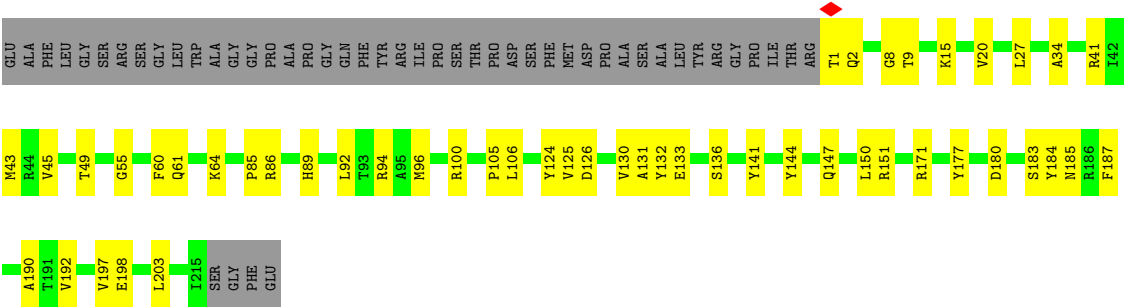
• Molecule 32: Proteasome subunit beta type-4

Chain T:  64% 18% 18%



• Molecule 32: Proteasome subunit beta type-4

Chain t:  63% 19% 18%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29419	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	0.119	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0332	Depositor
Map size (Å)	438.4, 438.4, 438.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: ATP, ZN, ADP, MG

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	0.24	0/6449	0.63	2/8729 (0.0%)
2	V	0.33	1/4072 (0.0%)	0.78	5/5510 (0.1%)
3	W	0.30	0/3751	0.77	2/5042 (0.0%)
4	X	0.24	0/3053	0.56	0/4115
5	Y	0.26	0/3173	0.63	0/4273
6	Z	0.25	0/2324	0.67	2/3150 (0.1%)
7	a	0.23	0/3053	0.63	2/4133 (0.0%)
8	b	0.22	0/1478	0.63	0/2001
9	c	0.27	0/2302	0.70	2/3110 (0.1%)
10	d	0.26	0/2162	0.69	2/2919 (0.1%)
11	e	0.28	0/338	0.79	0/450
12	f	0.30	0/6973	0.83	16/9424 (0.2%)
13	A	0.27	0/3148	0.68	2/4250 (0.0%)
14	B	0.28	0/3053	0.74	6/4118 (0.1%)
15	C	0.25	0/2902	0.66	2/3904 (0.1%)
16	D	0.28	0/3089	0.67	4/4168 (0.1%)
17	E	0.26	0/2904	0.62	0/3924
18	F	0.25	0/2896	0.57	0/3912
19	G	0.24	0/1859	0.53	0/2523
19	g	0.24	0/1859	0.53	0/2523
20	H	0.24	0/1743	0.50	0/2372
20	h	0.24	0/1743	0.50	0/2372
21	I	0.24	0/1942	0.57	0/2628
21	i	0.24	0/1942	0.56	0/2628
22	J	0.23	0/1737	0.56	0/2369
22	j	0.23	0/1728	0.56	0/2358
23	K	0.24	0/1747	0.51	0/2364
23	k	0.24	0/1747	0.51	0/2364
24	L	0.26	0/1885	0.59	1/2552 (0.0%)
24	l	0.25	0/1885	0.60	2/2552 (0.1%)
25	M	0.24	0/1891	0.52	0/2552
25	m	0.24	0/1891	0.52	0/2552

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	N	0.22	0/1454	0.50	0/1967
26	n	0.22	0/1454	0.50	0/1967
27	O	0.23	0/1670	0.49	0/2265
27	o	0.23	0/1670	0.49	0/2265
28	P	0.24	0/1620	0.48	0/2184
28	p	0.24	0/1620	0.48	0/2184
29	Q	0.26	0/1603	0.52	0/2174
29	q	0.26	0/1603	0.53	0/2174
30	R	0.25	0/1579	0.46	0/2134
30	r	0.25	0/1579	0.46	0/2134
31	S	0.24	0/1671	0.49	0/2253
31	s	0.24	0/1674	0.49	0/2257
32	T	0.24	0/1700	0.51	0/2305
32	t	0.24	0/1700	0.51	0/2305
All	All	0.26	1/105316 (0.0%)	0.62	50/142409 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	V	132	LEU	C-N	5.32	1.38	1.33

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	B	53	THR	CA-C-N	13.59	136.82	119.84
14	B	53	THR	C-N-CA	13.59	136.82	119.84
12	f	651	GLY	N-CA-C	-10.85	99.36	112.49
6	Z	245	PHE	N-CA-C	-10.61	99.72	111.28
12	f	755	ASP	CA-C-N	10.47	132.93	119.84

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	6365	203	0
2	V	3994	0	3960	203	0
3	W	3703	0	3822	227	0
4	X	3009	0	3113	37	0
5	Y	3115	0	3120	75	0
6	Z	2281	0	2310	74	0
7	a	2995	0	3011	67	0
8	b	1458	0	1505	33	0
9	c	2260	0	2275	107	0
10	d	2116	0	2146	71	0
11	e	334	0	294	47	0
12	f	6860	0	6859	372	0
13	A	3096	0	3138	76	0
14	B	3011	0	3075	143	0
15	C	2864	0	2969	228	0
16	D	3039	0	3075	234	0
17	E	2860	0	2826	98	0
18	F	2858	0	2852	61	0
19	G	1826	0	1796	41	0
19	g	1826	0	1796	47	0
20	H	1708	0	1594	22	0
20	h	1708	0	1594	18	0
21	I	1912	0	1851	53	0
21	i	1912	0	1851	44	0
22	J	1713	0	1537	30	0
22	j	1704	0	1517	27	0
23	K	1722	0	1673	35	0
23	k	1722	0	1673	33	0
24	L	1850	0	1822	39	0
24	l	1850	0	1822	30	0
25	M	1856	0	1814	35	0
25	m	1856	0	1814	32	0
26	N	1430	0	1398	28	0
26	n	1430	0	1398	29	0
27	O	1643	0	1644	43	0
27	o	1643	0	1644	38	0
28	P	1591	0	1609	24	0
28	p	1591	0	1609	21	0
29	Q	1570	0	1547	26	0
29	q	1570	0	1547	30	0
30	R	1548	0	1499	30	0
30	r	1548	0	1499	23	0
31	S	1641	0	1616	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	s	1644	0	1625	30	0
32	T	1667	0	1628	30	0
32	t	1667	0	1628	36	0
33	c	1	0	0	0	0
34	A	31	0	12	0	0
34	B	31	0	12	8	0
34	D	31	0	12	2	0
34	E	31	0	10	35	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	13	0
36	F	27	0	12	8	0
All	All	103719	0	102830	2825	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 14.

The worst 5 of 2825 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)
3:W:137:TYR:CE1	16:D:392:TYR:CD1	1.78	1.68
3:W:137:TYR:CZ	16:D:392:TYR:CD1	1.79	1.62
12:f:222:ASP:CB	14:B:60:LEU:CD2	1.76	1.62
15:C:90:HIS:HE1	16:D:109:SER:CB	1.03	1.61
3:W:97:LEU:HD21	3:W:138:VAL:CG2	1.23	1.60

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%)	732 (91%)	73 (9%)	1 (0%)	48	83
2	V	506/533 (95%)	434 (86%)	67 (13%)	5 (1%)	12	47
3	W	454/456 (100%)	389 (86%)	61 (13%)	4 (1%)	14	49
4	X	378/422 (90%)	360 (95%)	18 (5%)	0	100	100
5	Y	376/389 (97%)	346 (92%)	30 (8%)	0	100	100
6	Z	284/324 (88%)	252 (89%)	30 (11%)	2 (1%)	18	55
7	a	371/376 (99%)	331 (89%)	39 (10%)	1 (0%)	36	71
8	b	189/377 (50%)	171 (90%)	18 (10%)	0	100	100
9	c	285/309 (92%)	243 (85%)	40 (14%)	2 (1%)	18	55
10	d	255/349 (73%)	213 (84%)	41 (16%)	1 (0%)	30	66
11	e	36/70 (51%)	25 (69%)	10 (28%)	1 (3%)	4	24
12	f	887/908 (98%)	705 (80%)	170 (19%)	12 (1%)	9	39
13	A	392/433 (90%)	339 (86%)	50 (13%)	3 (1%)	16	52
14	B	382/429 (89%)	339 (89%)	35 (9%)	8 (2%)	5	30
15	C	359/389 (92%)	330 (92%)	27 (8%)	2 (1%)	21	58
16	D	378/418 (90%)	331 (88%)	38 (10%)	9 (2%)	4	27
17	E	373/403 (93%)	337 (90%)	36 (10%)	0	100	100
18	F	372/439 (85%)	339 (91%)	33 (9%)	0	100	100
19	G	238/245 (97%)	229 (96%)	9 (4%)	0	100	100
19	g	238/245 (97%)	229 (96%)	9 (4%)	0	100	100
20	H	230/233 (99%)	221 (96%)	9 (4%)	0	100	100
20	h	230/233 (99%)	221 (96%)	9 (4%)	0	100	100
21	I	248/260 (95%)	223 (90%)	25 (10%)	0	100	100
21	i	248/260 (95%)	226 (91%)	22 (9%)	0	100	100
22	J	237/247 (96%)	214 (90%)	19 (8%)	4 (2%)	7	35
22	j	237/247 (96%)	219 (92%)	16 (7%)	2 (1%)	16	52
23	K	224/240 (93%)	215 (96%)	9 (4%)	0	100	100
23	k	224/240 (93%)	215 (96%)	9 (4%)	0	100	100
24	L	236/268 (88%)	219 (93%)	16 (7%)	1 (0%)	30	66
24	l	236/268 (88%)	219 (93%)	16 (7%)	1 (0%)	30	66
25	M	238/254 (94%)	223 (94%)	15 (6%)	0	100	100
25	m	238/254 (94%)	223 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	N	189/238 (79%)	183 (97%)	6 (3%)	0	100	100
26	n	189/238 (79%)	183 (97%)	6 (3%)	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%)	189 (94%)	13 (6%)	0	100	100
28	p	202/204 (99%)	190 (94%)	12 (6%)	0	100	100
29	Q	197/201 (98%)	187 (95%)	10 (5%)	0	100	100
29	q	197/201 (98%)	187 (95%)	10 (5%)	0	100	100
30	R	199/262 (76%)	193 (97%)	6 (3%)	0	100	100
30	r	199/262 (76%)	193 (97%)	6 (3%)	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%)	203 (95%)	10 (5%)	0	100	100
32	t	213/263 (81%)	203 (95%)	10 (5%)	0	100	100
All	All	13243/14839 (89%)	12049 (91%)	1135 (9%)	59 (0%)	31	66

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	V	168	GLN
2	V	349	ARG
2	V	446	VAL
3	W	83	LEU
12	f	756	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	72
2	V	415/459 (90%)	404 (97%)	11 (3%)	39	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	W	416/416 (100%)	402 (97%)	14 (3%)	32	54
4	X	327/362 (90%)	326 (100%)	1 (0%)	86	84
5	Y	334/344 (97%)	332 (99%)	2 (1%)	78	80
6	Z	257/295 (87%)	251 (98%)	6 (2%)	44	64
7	a	333/336 (99%)	333 (100%)	0	100	100
8	b	167/312 (54%)	167 (100%)	0	100	100
9	c	252/267 (94%)	246 (98%)	6 (2%)	43	63
10	d	231/293 (79%)	228 (99%)	3 (1%)	61	72
11	e	38/63 (60%)	35 (92%)	3 (8%)	11	32
12	f	744/763 (98%)	721 (97%)	23 (3%)	35	56
13	A	337/372 (91%)	333 (99%)	4 (1%)	63	73
14	B	338/376 (90%)	330 (98%)	8 (2%)	43	63
15	C	314/337 (93%)	311 (99%)	3 (1%)	68	76
16	D	333/366 (91%)	319 (96%)	14 (4%)	26	48
17	E	298/353 (84%)	297 (100%)	1 (0%)	86	84
18	F	296/379 (78%)	295 (100%)	1 (0%)	86	84
19	G	193/209 (92%)	192 (100%)	1 (0%)	81	81
19	g	193/209 (92%)	191 (99%)	2 (1%)	68	76
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%)	192 (100%)	1 (0%)	81	81
21	i	193/220 (88%)	193 (100%)	0	100	100
22	J	154/210 (73%)	151 (98%)	3 (2%)	50	66
22	j	152/210 (72%)	151 (99%)	1 (1%)	76	79
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%)	197 (100%)	1 (0%)	81	81
24	l	198/229 (86%)	197 (100%)	1 (0%)	81	81
25	M	192/211 (91%)	192 (100%)	0	100	100
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	11009/12579 (88%)	10890 (99%)	119 (1%)	63	74

5 of 119 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	f	615	ILE
21	I	228	LEU
12	f	809	ILE
19	G	222	VAL
24	l	161	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 208 such sidechains are listed below:

Mol	Chain	Res	Type
16	D	237	GLN
22	J	159	ASN
29	q	8	GLN
16	D	353	ASN
19	G	33	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	A	501	35	32,33,33	1.37	5 (15%)	48,52,52	1.86	9 (18%)
36	ADP	F	501	35	28,29,29	1.41	4 (14%)	43,45,45	1.85	9 (20%)
36	ADP	C	501	-	28,29,29	1.42	4 (14%)	43,45,45	1.85	9 (20%)
34	ATP	B	501	35	32,33,33	1.41	4 (12%)	48,52,52	1.77	9 (18%)
34	ATP	D	501	35	32,33,33	1.32	4 (12%)	48,52,52	1.85	8 (16%)
34	ATP	E	401	35	32,33,33	1.42	4 (12%)	48,52,52	1.77	9 (18%)

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	A	501	35	-	6/22/38/38	0/3/3/3
36	ADP	F	501	35	-	11/16/32/32	0/3/3/3
36	ADP	C	501	-	-	4/16/32/32	0/3/3/3
34	ATP	B	501	35	-	3/22/38/38	0/3/3/3
34	ATP	D	501	35	-	4/22/38/38	0/3/3/3
34	ATP	E	401	35	-	5/22/38/38	0/3/3/3

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	E	401	ATP	C5-C4	4.76	1.47	1.39
36	C	501	ADP	C5-C4	4.75	1.47	1.39
34	B	501	ATP	C5-C4	4.73	1.47	1.39
36	F	501	ADP	C5-C4	4.71	1.47	1.39
34	D	501	ATP	C5-C4	4.57	1.47	1.39

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	A	501	ATP	C5-C4-N3	-6.35	117.98	126.72
34	D	501	ATP	C5-C4-N3	-6.24	118.12	126.72
36	F	501	ADP	C5-C4-N3	-5.84	118.67	126.72
36	C	501	ADP	C5-C4-N3	-5.84	118.68	126.72
34	B	501	ATP	C5-C4-N3	-5.84	118.68	126.72

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	A	501	ATP	C5'-O5'-PA-O2A
34	B	501	ATP	PB-O3B-PG-O3G
34	E	401	ATP	PB-O3B-PG-O2G
36	C	501	ADP	C5'-O5'-PA-O2A
36	C	501	ADP	C5'-O5'-PA-O3A

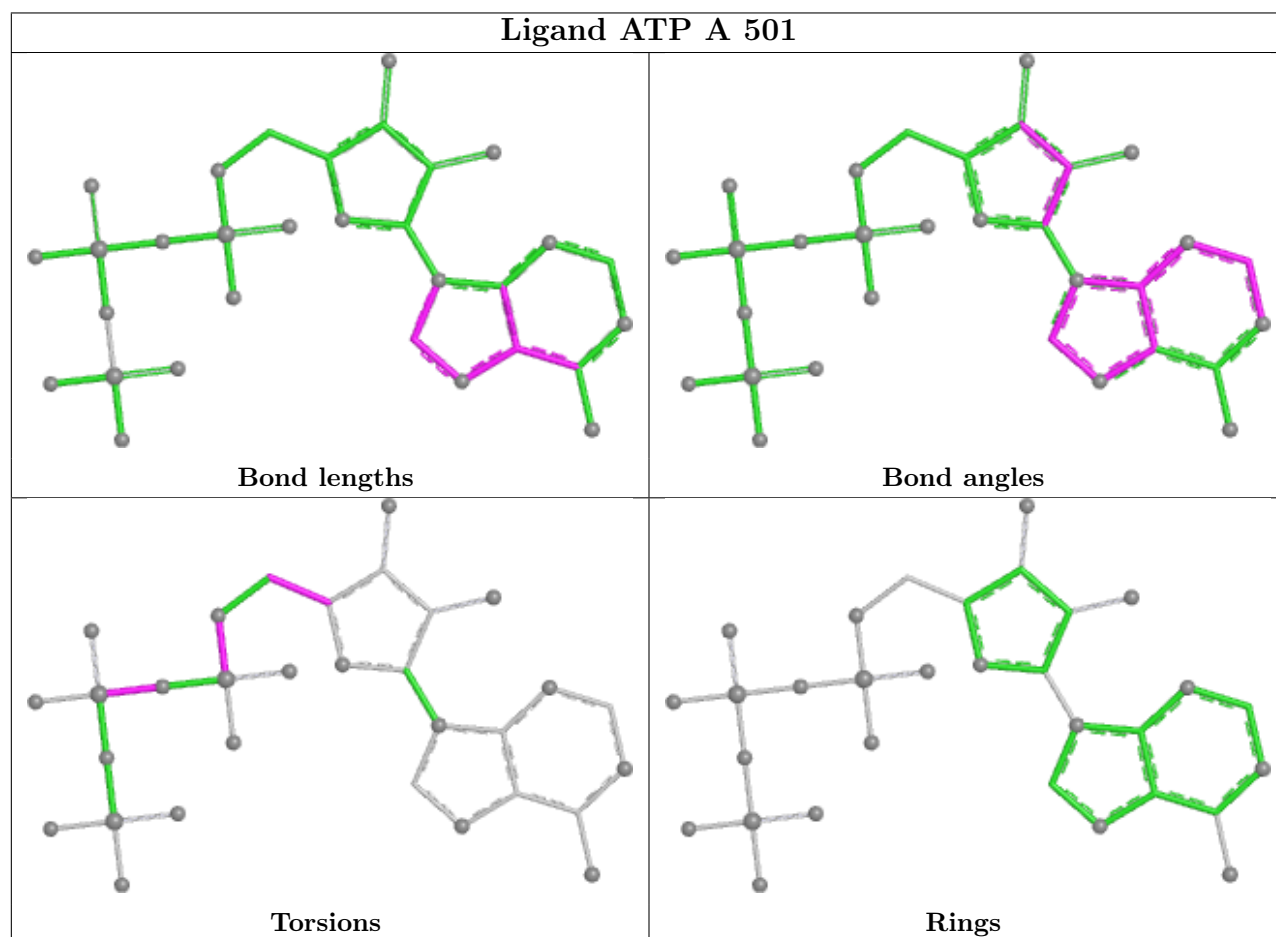
There are no ring outliers.

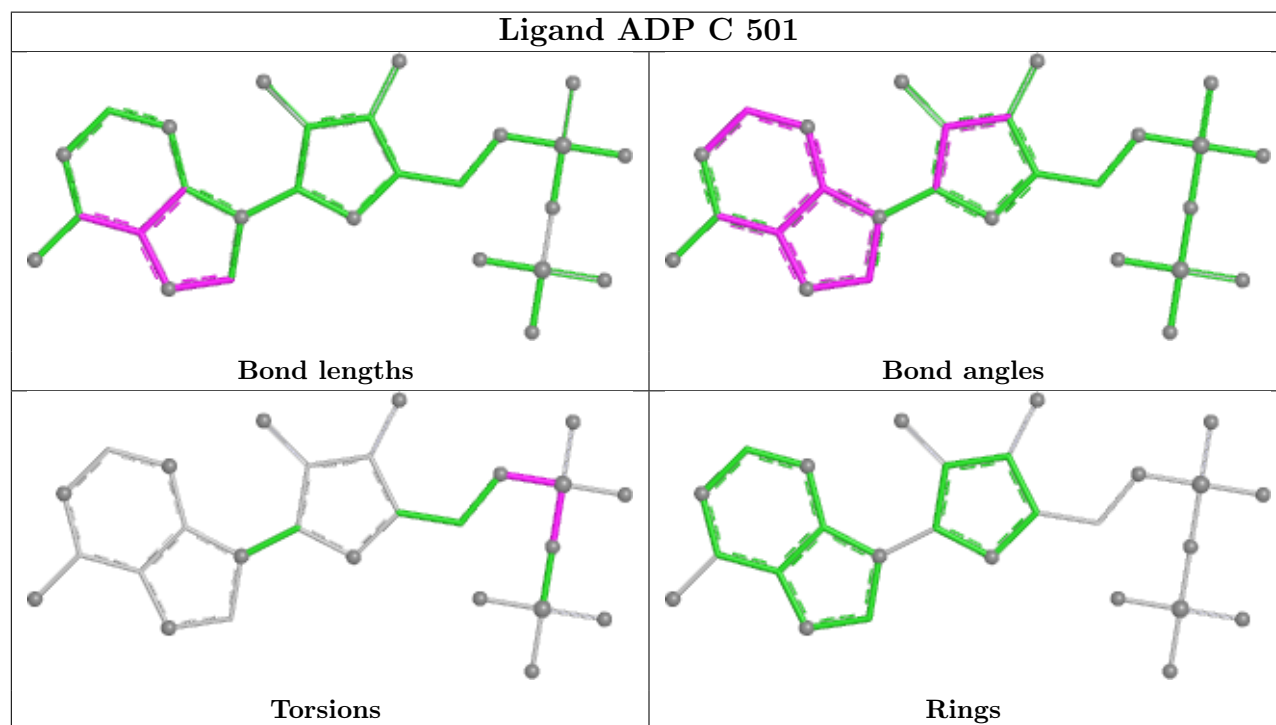
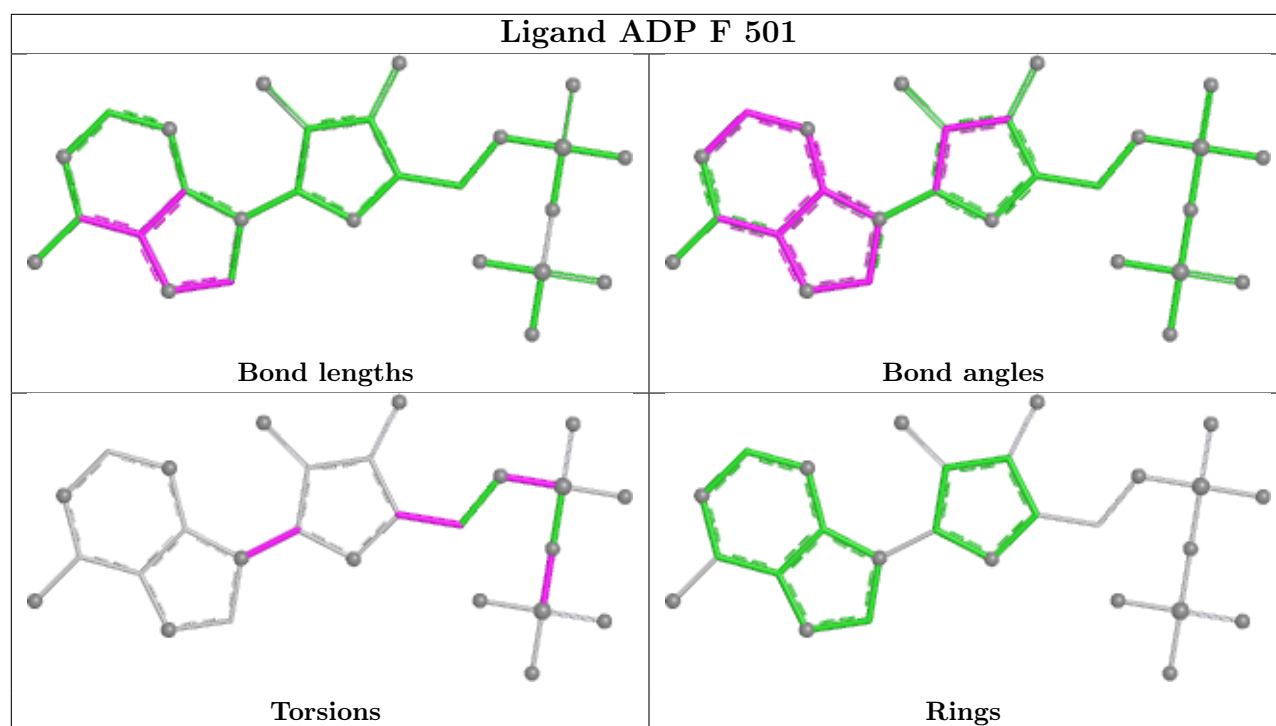
5 monomers are involved in 66 short contacts:

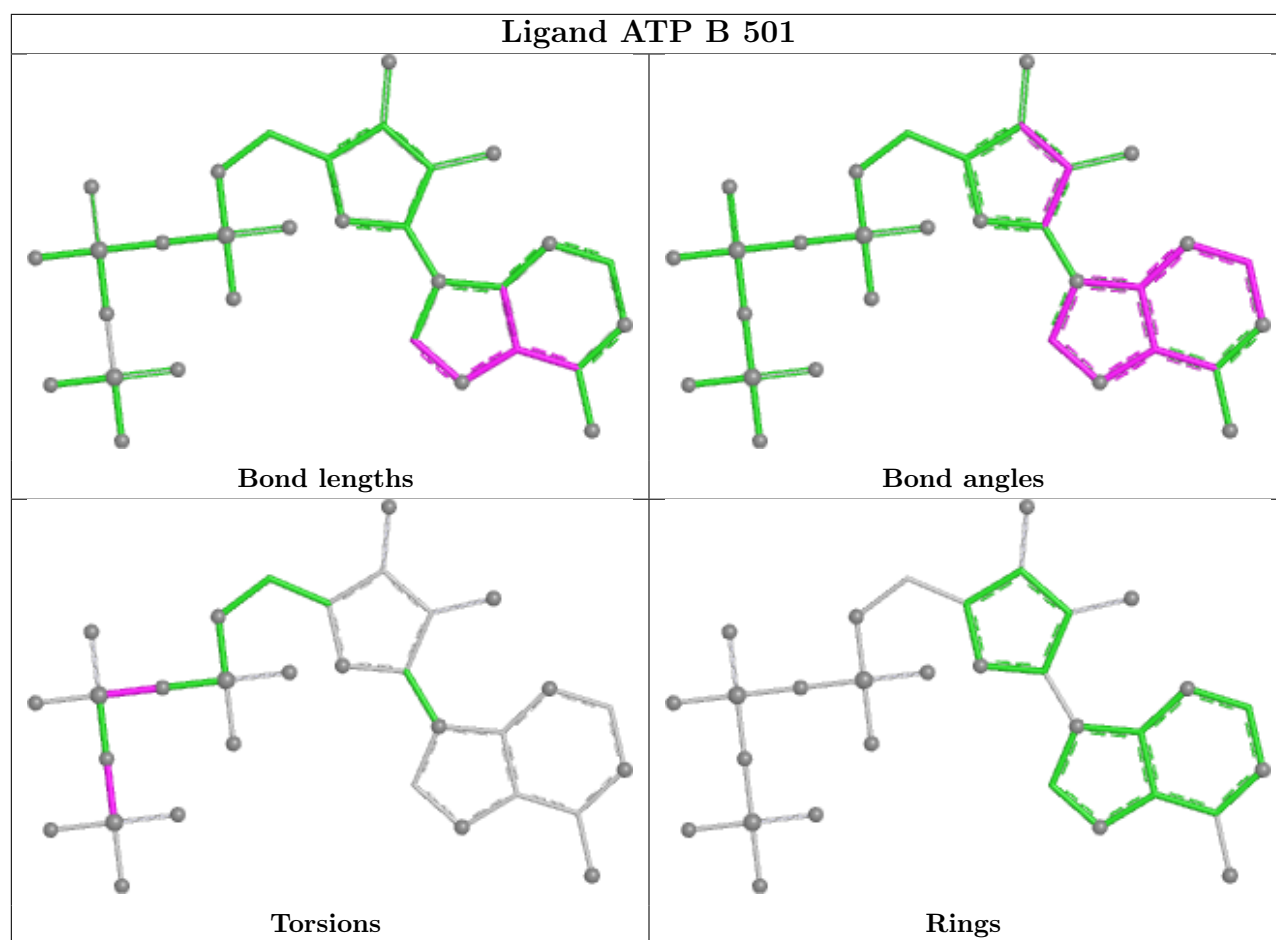
Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	F	501	ADP	8	0
36	C	501	ADP	13	0
34	B	501	ATP	8	0
34	D	501	ATP	2	0
34	E	401	ATP	35	0

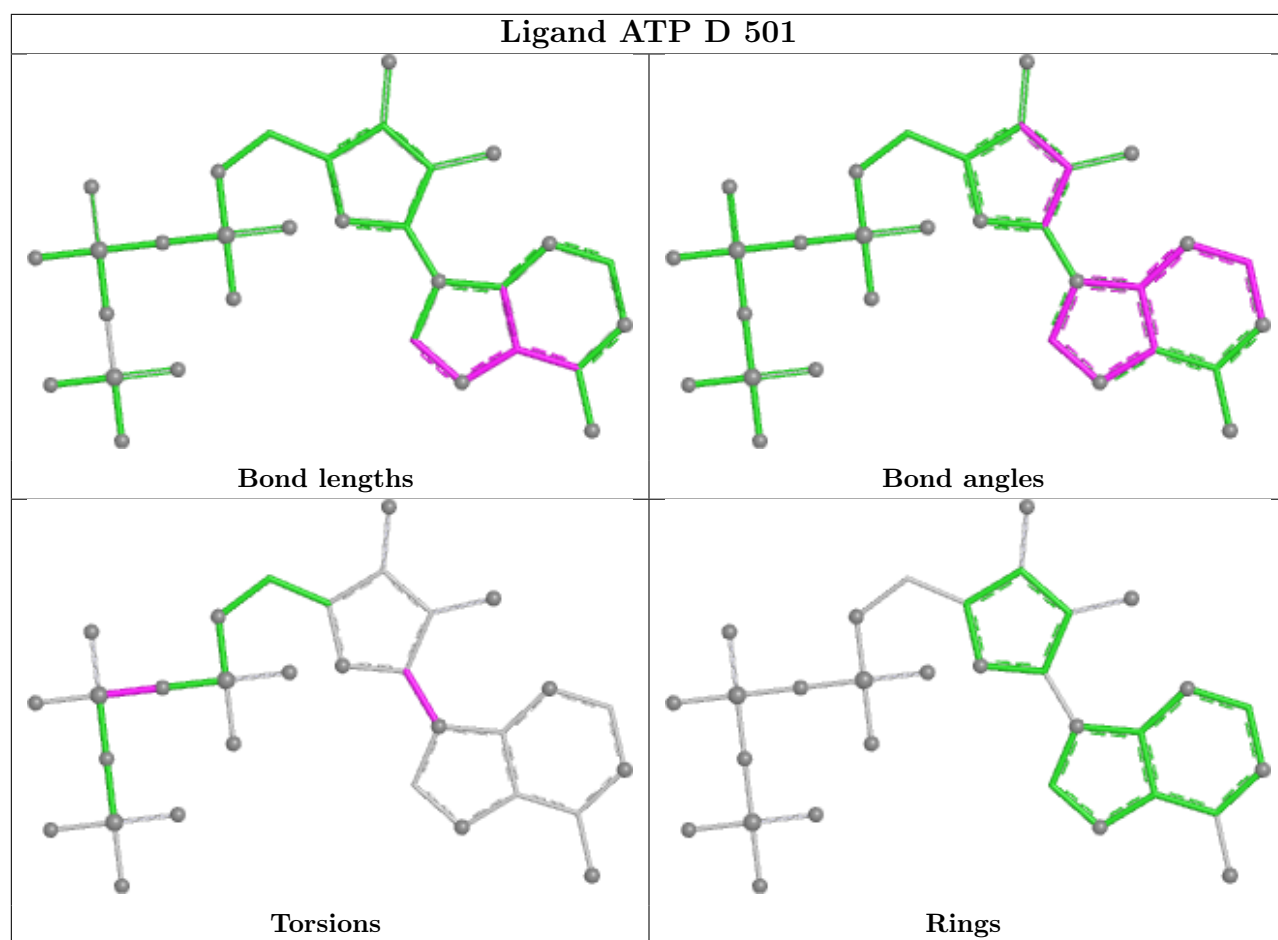
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

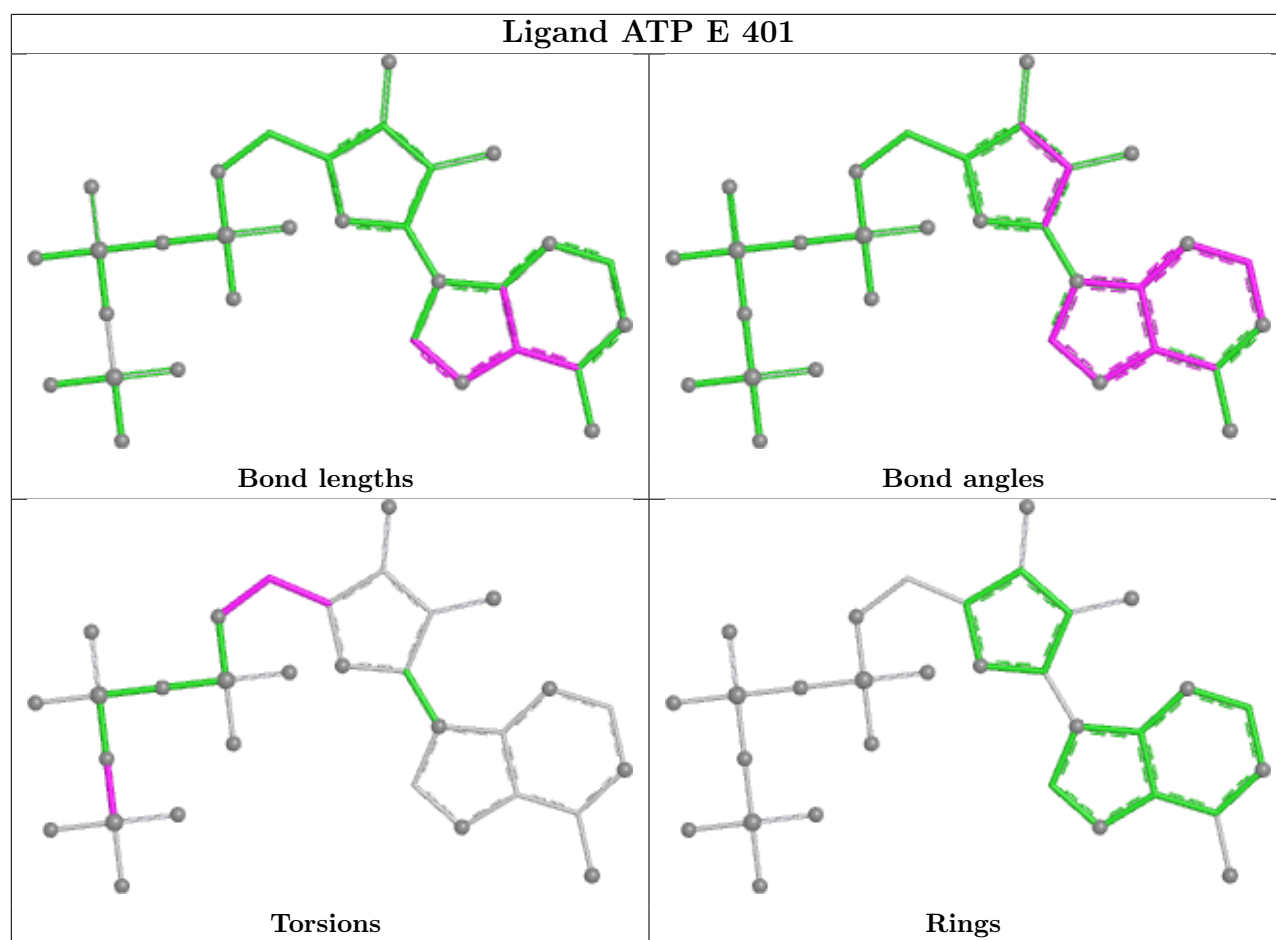
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

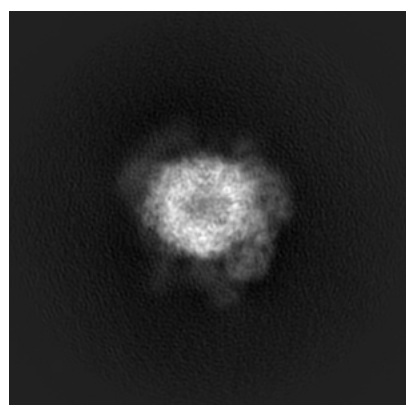
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14203. These allow visual inspection of the internal detail of the map and identification of artifacts.

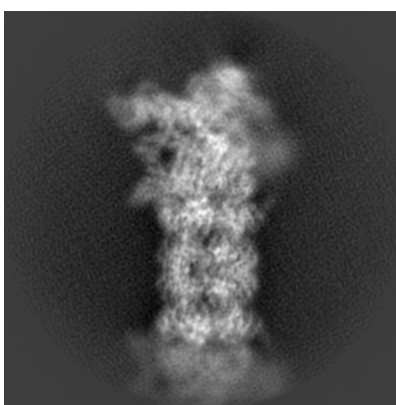
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

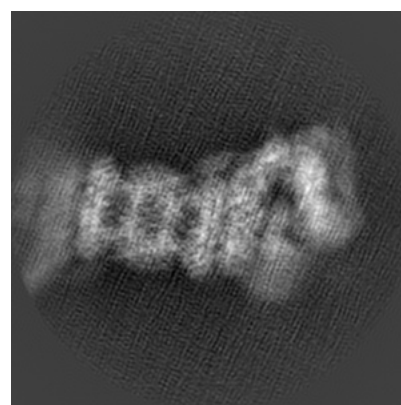
6.1.1 Primary map



X



Y

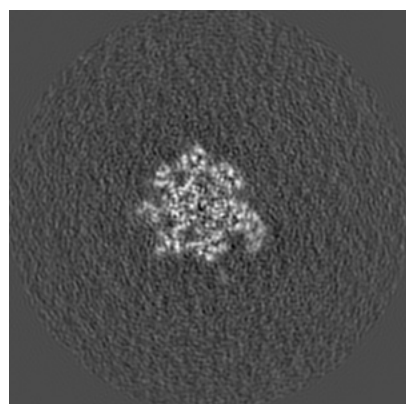


Z

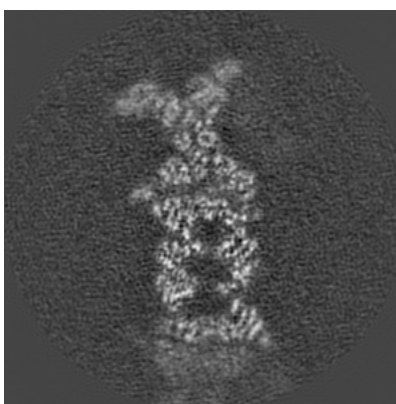
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

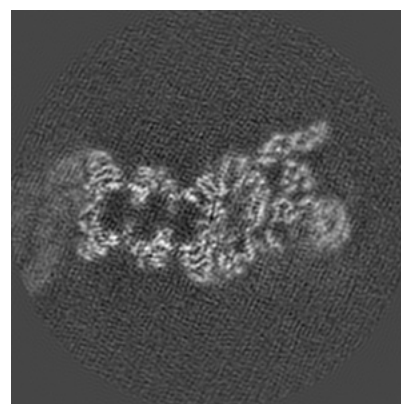
6.2.1 Primary map



X Index: 160



Y Index: 160

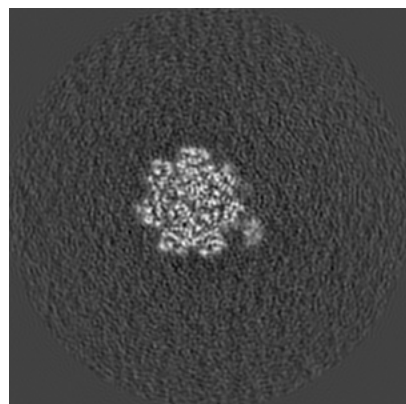


Z Index: 160

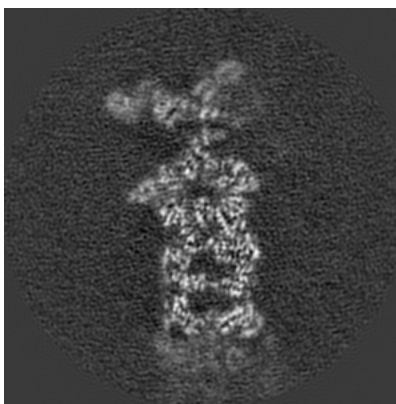
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

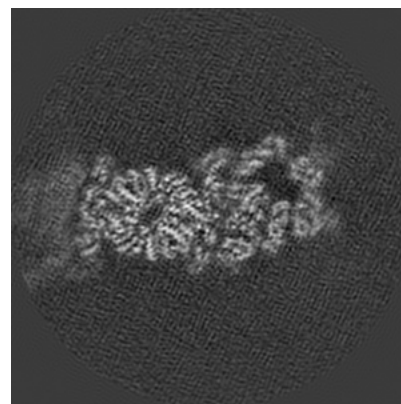
6.3.1 Primary map



X Index: 154



Y Index: 166

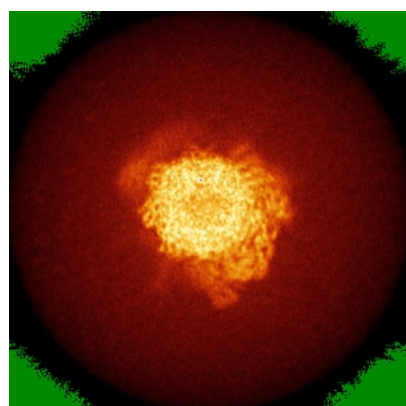


Z Index: 145

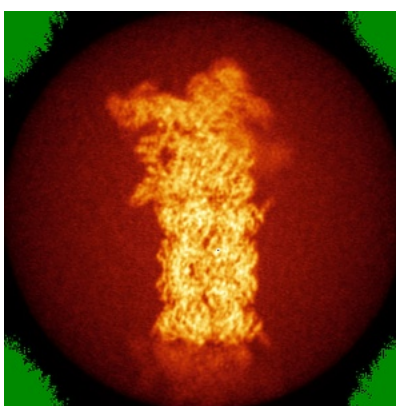
The images above show the largest variance slices of the map in three orthogonal directions.

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

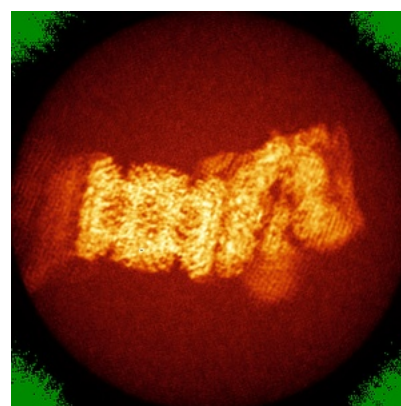
6.4.1 Primary map



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

This section was not generated.

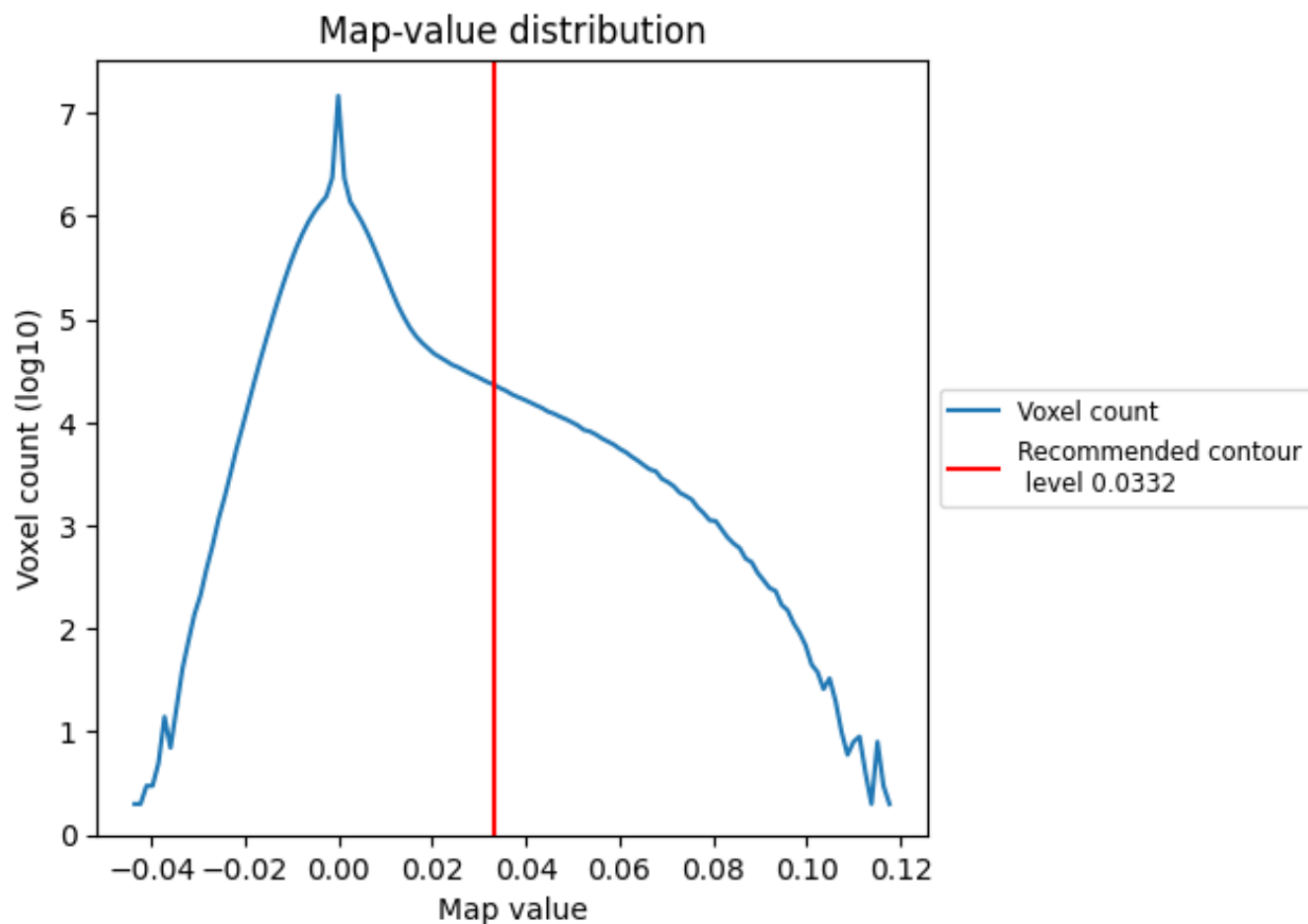
6.6 Mask visualisation

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

7 Map analysis [i](#)

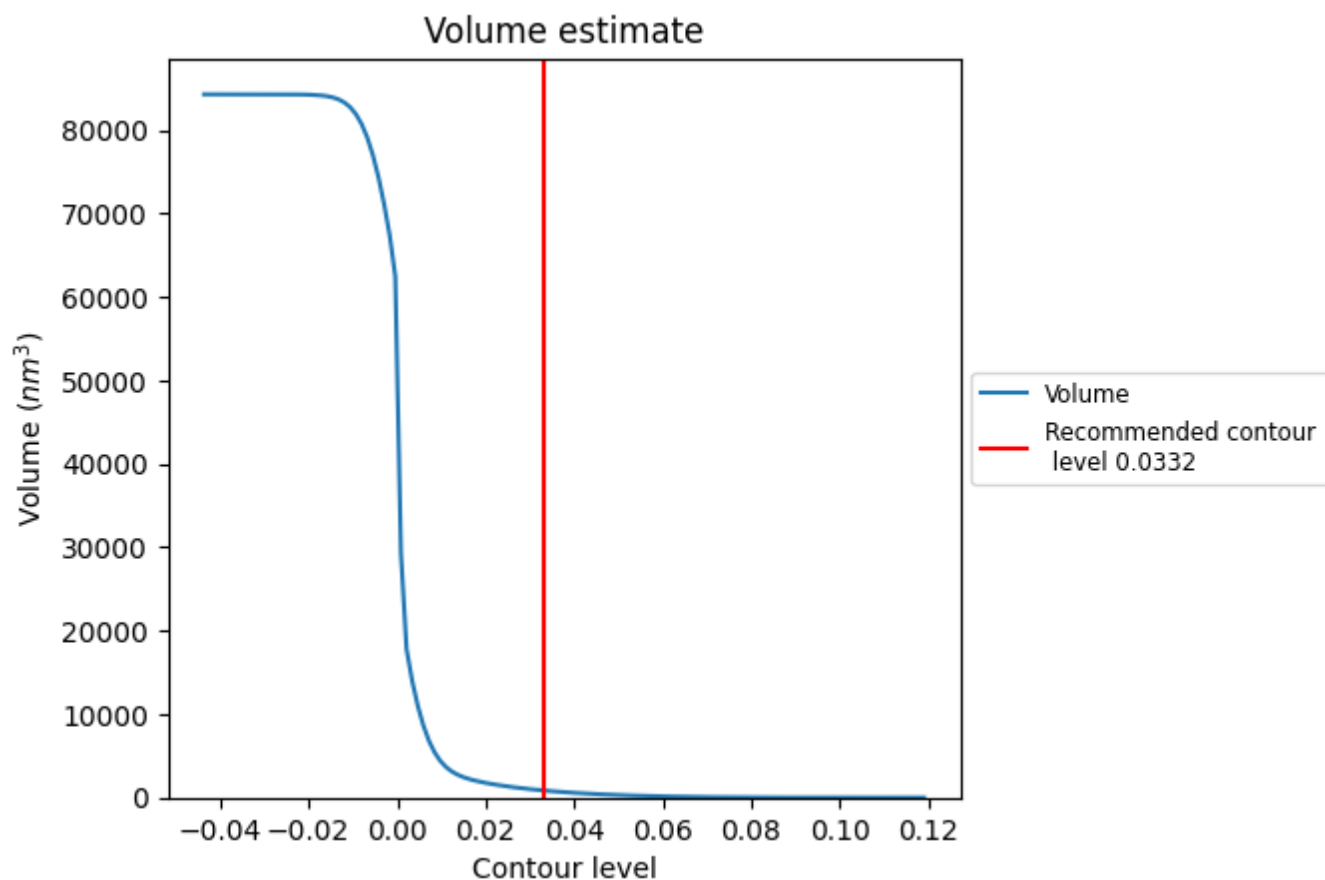
This section contains the results of statistical analysis of the map.

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.

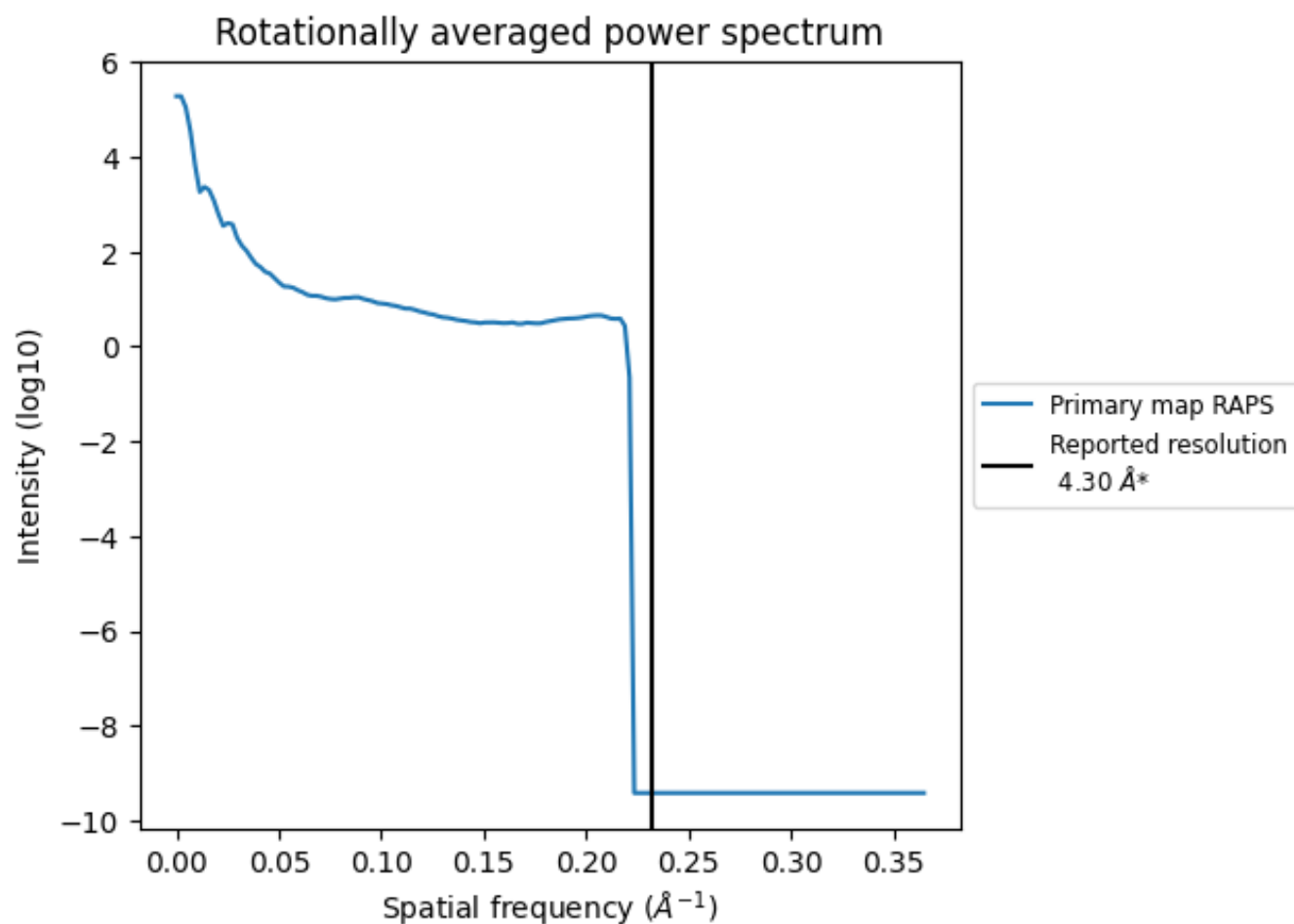
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 842 nm³; this corresponds to an approximate mass of 760 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 0.233 Å⁻¹

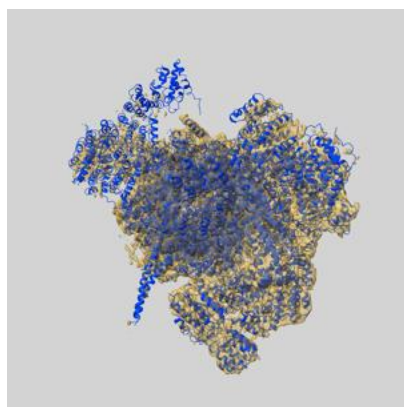
8 Fourier-Shell correlation

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

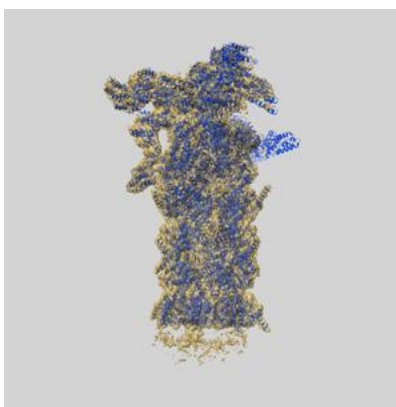
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14203 and PDB model 7QXU. Per-residue inclusion information can be found in section [3](#) on page [13](#).

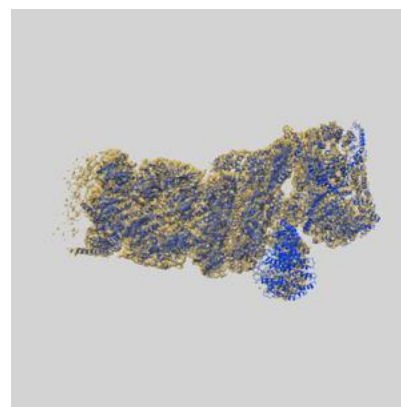
9.1 Map-model overlay [i](#)



X



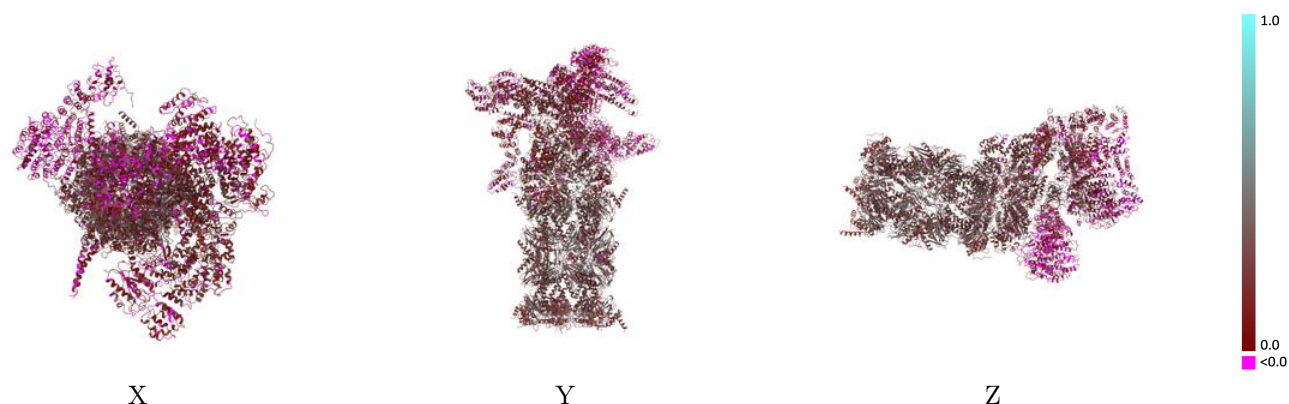
Y



Z

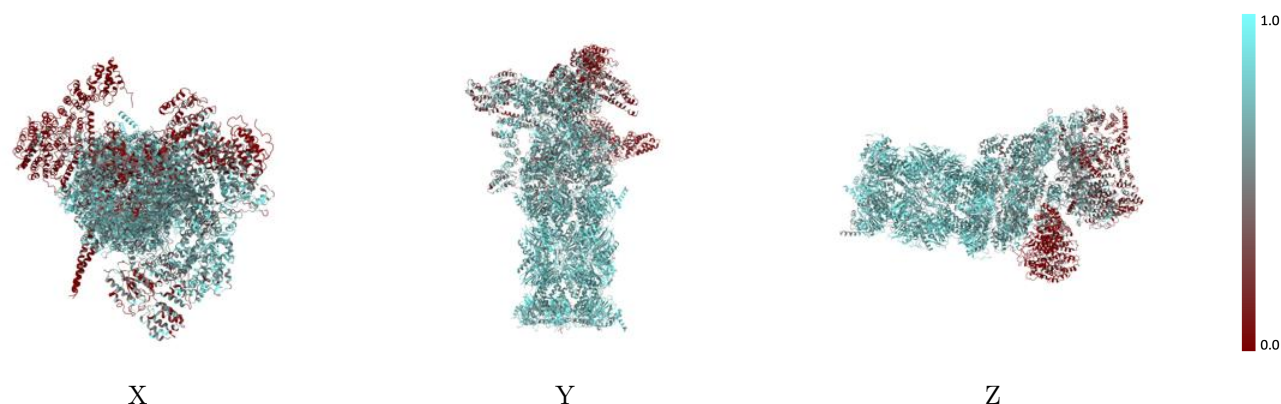
The images above show the 3D surface view of the map at the recommended contour level 0.0332 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



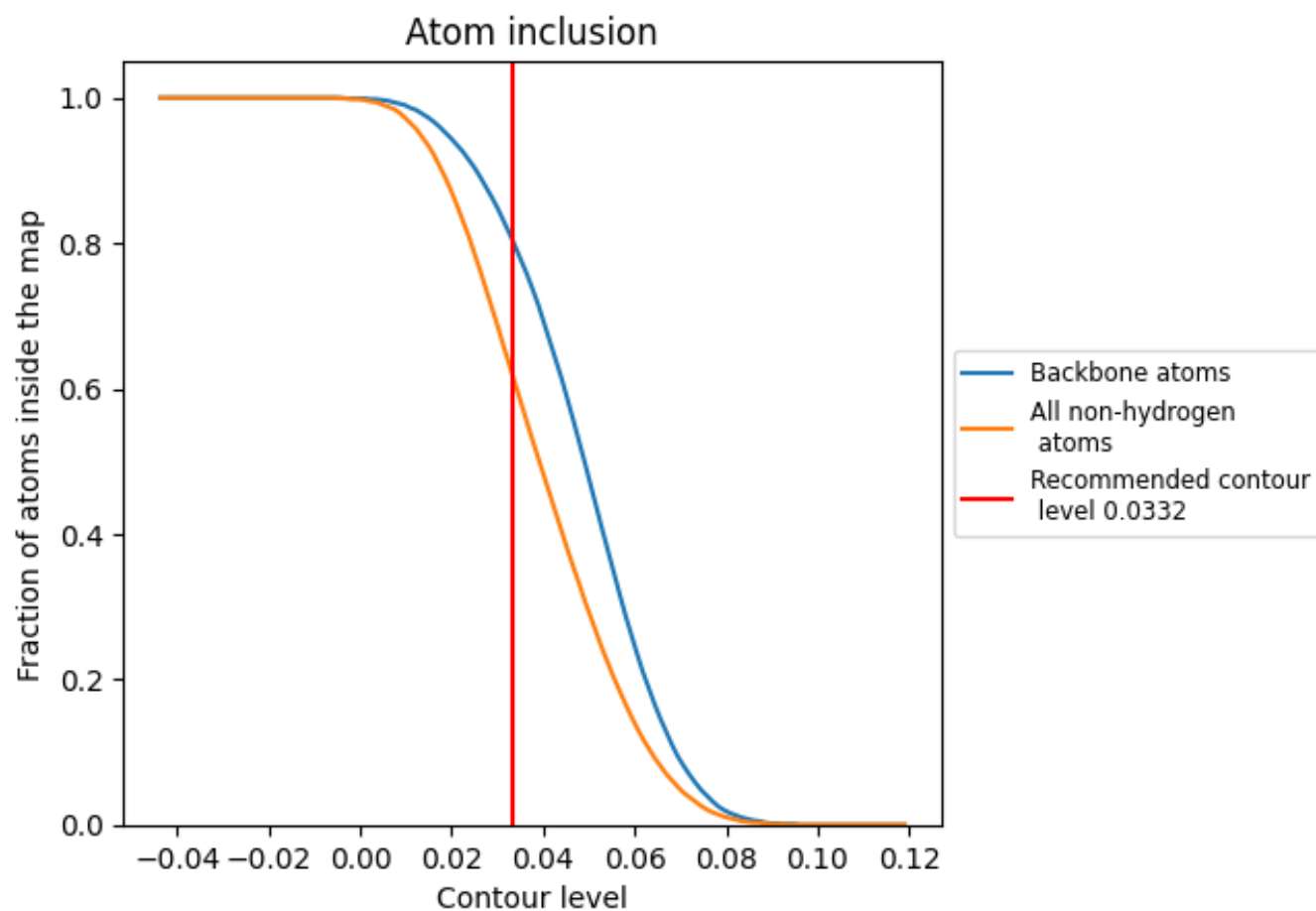
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0332).

9.4 Atom inclusion ⓘ



At the recommended contour level, 81% of all backbone atoms, 62% 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 (0.0332) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6210	 0.2330
A	 0.6320	 0.2630
B	 0.6190	 0.2390
C	 0.6810	 0.2610
D	 0.6450	 0.2480
E	 0.6690	 0.2490
F	 0.6630	 0.2680
G	 0.7730	 0.3080
H	 0.7870	 0.3120
I	 0.7810	 0.2920
J	 0.7960	 0.3020
K	 0.7800	 0.3080
L	 0.7890	 0.3080
M	 0.7630	 0.2980
N	 0.8200	 0.3230
O	 0.8000	 0.3180
P	 0.7850	 0.3160
Q	 0.7860	 0.3160
R	 0.8260	 0.3150
S	 0.7940	 0.3240
T	 0.8190	 0.3160
U	 0.3590	 0.0960
V	 0.3570	 0.1260
W	 0.6170	 0.1690
X	 0.5990	 0.2000
Y	 0.6810	 0.1890
Z	 0.5870	 0.1780
a	 0.5480	 0.1560
b	 0.3500	 0.1190
c	 0.6020	 0.2000
d	 0.2660	 0.1130
e	 0.3910	 0.0830
f	 0.0550	 0.0500
g	 0.7310	 0.2930
h	 0.7490	 0.2960



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Chain	Atom inclusion	Q-score
i	 0.7180	 0.2790
j	 0.7560	 0.2870
k	 0.7370	 0.2920
l	 0.7620	 0.2830
m	 0.7410	 0.3000
n	 0.7950	 0.3110
o	 0.8170	 0.3300
p	 0.7900	 0.3260
q	 0.7990	 0.3210
r	 0.8230	 0.3220
s	 0.7980	 0.3160
t	 0.8070	 0.3200