wwPDB EM Validation Summary Report (i)

Oct 26, 2024 – 09:33 AM EDT

PDB ID	:	5T0I
EMDB ID	:	EMD-8336
Title	:	Structural basis for dynamic regulation of the human 26S proteasome
Authors	:	Chen, S.; Wu, J.; Lu, Y.; Ma, Y.B.; Lee, B.H.; Yu, Z.; Ouyang, Q.; Finley, D.; Kirschner, M.W.; Mao, Y.
Deposited on	:	2016-08-16
Resolution	:	8.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

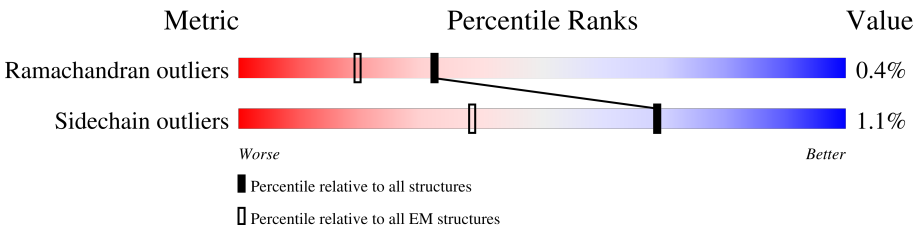
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 8.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=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	A	433	24% 81% • 17%
2	B	440	33% 77% • 21%
3	C	398	35% 93% • •
4	D	418	30% 90% • 9%
5	E	403	32% 87% • 12%
6	F	439	26% 82% • 17%
7	G	245	27% 96% • •
8	H	233	18% 100%
9	I	260	24% 95% • •

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Mol	Chain	Length	Quality of chain
10	J	247	33% 95%
11	K	240	20% 93% 5%
12	L	268	15% 88% 11%
13	M	254	26% 94% 6%
14	N	238	26% 80% 20%
15	O	276	16% 79% 20%
16	P	204	21% 100%
17	Q	201	33% 99%
18	R	262	25% 77% 23%
19	S	240	12% 88% 11%
20	T	263	15% 82% 18%
21	U	953	11% 84% 15%
22	V	533	27% 88% 10%
23	W	456	77% 98%
24	X	422	44% 57% 43%
25	Y	389	30% 96%
26	Z	324	34% 86% 12%
27	a	376	66% 98%
28	b	377	45% 50% 49%
29	c	309	34% 87% 10%
30	d	349	30% 72% 26%
31	e	70	17% 56% 43%
32	f	749	49% 90% 7%

2 Entry composition (i)

There are 34 unique types of molecules in this entry. The entry contains 76616 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 protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	361	2835	1788	501	528	18	0	0

- Molecule 2 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	348	2717	1708	460	537	12	0	0

- Molecule 3 is a protein called 26S protease regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	384	3015	1894	540	564	17	0	0

- Molecule 4 is a protein called 26S protease regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	380	3040	1923	524	580	13	0	0

- Molecule 5 is a protein called 26S protease regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	353	2790	1755	494	525	16	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	366	2863	1802	496	549	16	0	0

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

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

- Molecule 8 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	233	1713	1084	290	334	5	0	0

- Molecule 9 is a protein called Proteasome subunit alpha type-4.

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

- Molecule 10 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	239	1704	1056	308	335	5	0	0

- Molecule 11 is a protein called Proteasome subunit alpha type-5.

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

- Molecule 12 is a protein called Proteasome subunit alpha type-1.

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

- Molecule 13 is a protein called Proteasome subunit alpha type-3.

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

- Molecule 14 is a protein called Proteasome subunit beta type-6.

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

- Molecule 15 is a protein called Proteasome subunit beta type-7.

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

- Molecule 16 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	204	1585	1010	262	294	19	0	0

- Molecule 17 is a protein called Proteasome subunit beta type-2.

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

- Molecule 18 is a protein called Proteasome subunit beta type-5.

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

- Molecule 19 is a protein called Proteasome subunit beta type-1.

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

- Molecule 20 is a protein called Proteasome subunit beta type-4.

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

- Molecule 21 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	U	806	6287	3990	1075	1178	44	0	0

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	V	480	3852	2444	684	710	14	0	0

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	W	456	3703	2339	635	704	25	0	0

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	X	241	1905	1212	320	365	8	0	0

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

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

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

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

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

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

- Molecule 28 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

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

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	c	278	2187	1389	374	406	18	0	0

- Molecule 30 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

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

- Molecule 31 is a protein called 26S proteasome complex subunit DSS1.

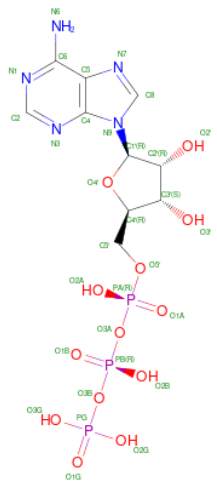
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	e	40	334	200	55	77	2	0	0

- Molecule 32 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	f	694	5331	3364	899	1027	41	0	0

- Molecule 33 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

ATP



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

- Molecule 34 is ZINC ION (three-letter code: ZN) (formula: Zn).

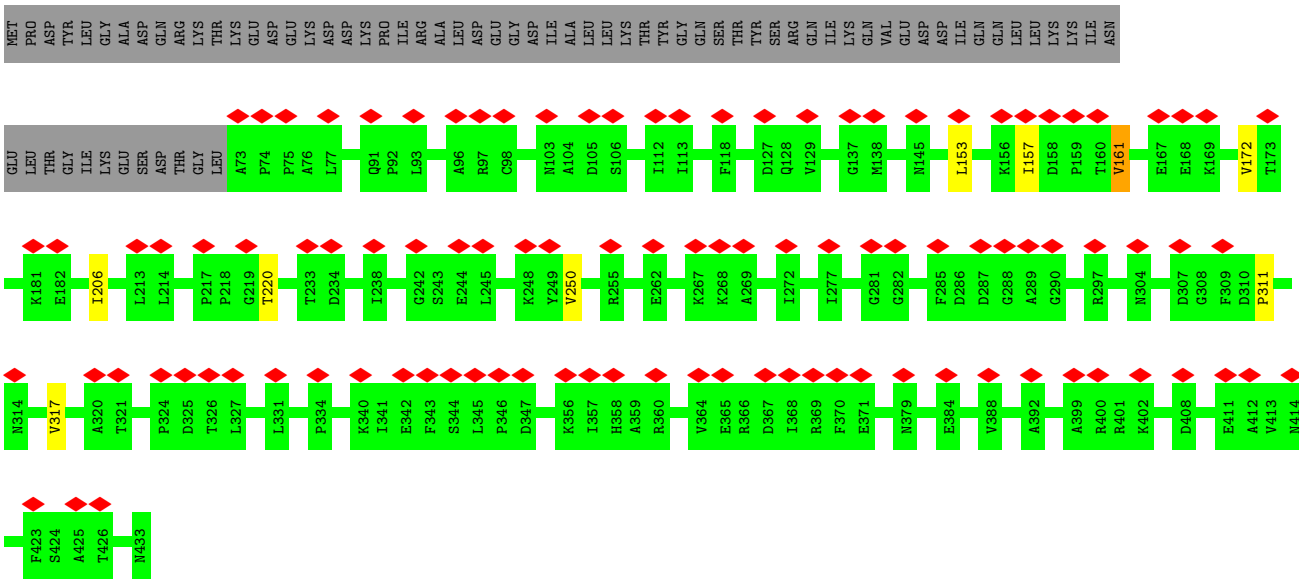
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
34	c	1	1	1	0

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.

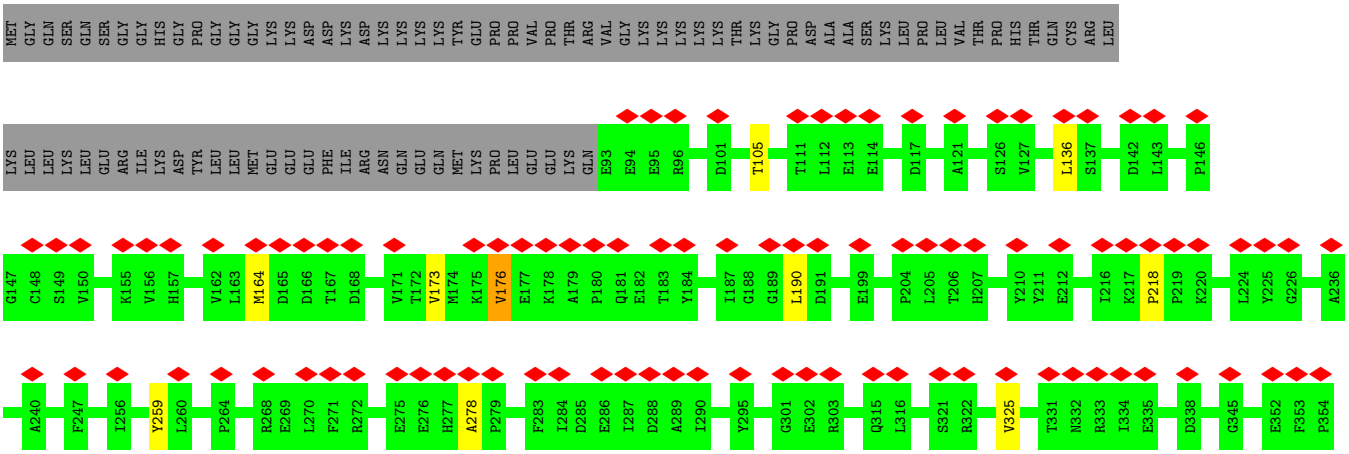
- Molecule 1: 26S protease regulatory subunit 7

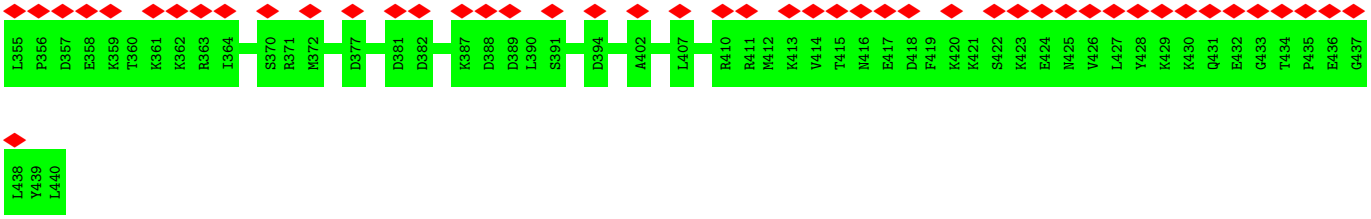
Chain A:



- Molecule 2: 26S protease regulatory subunit 4

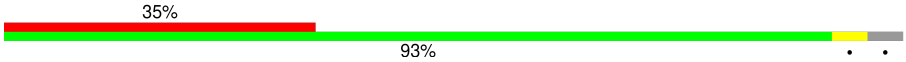
Chain B:

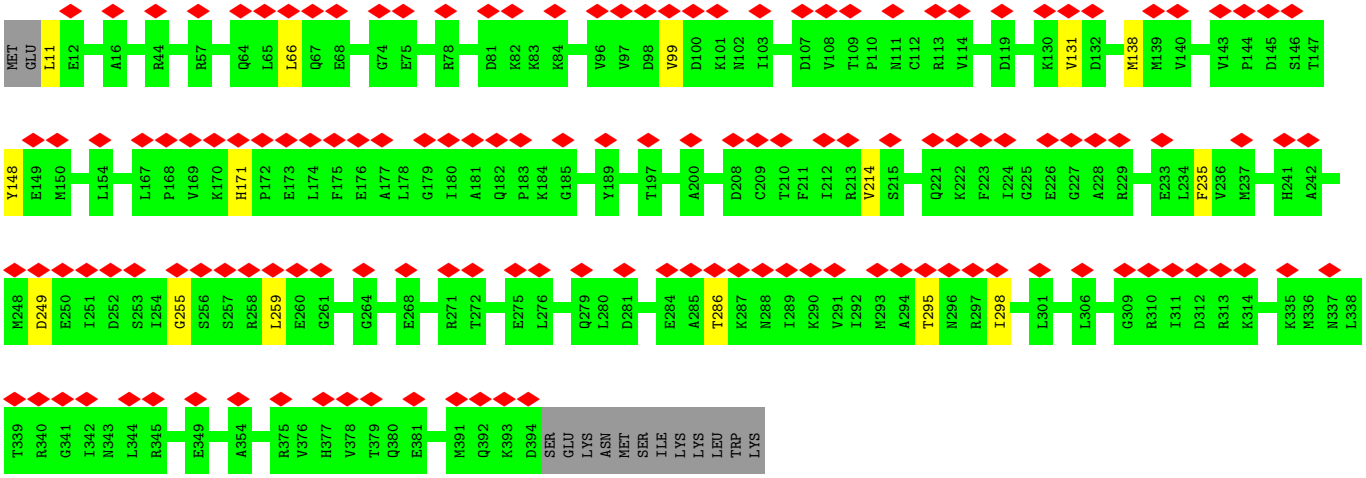




- Molecule 3: 26S protease regulatory subunit 8

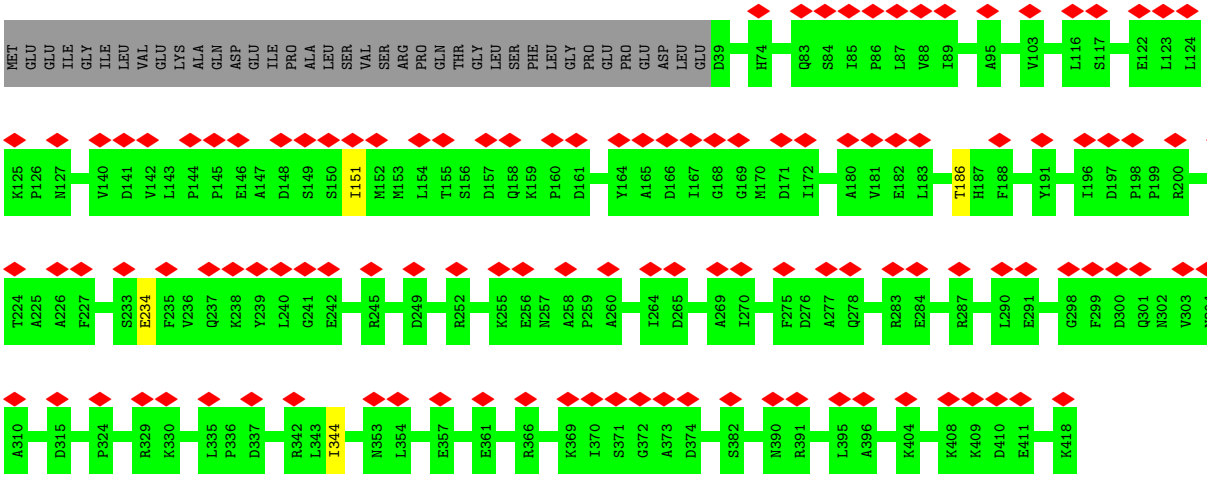
Chain C:





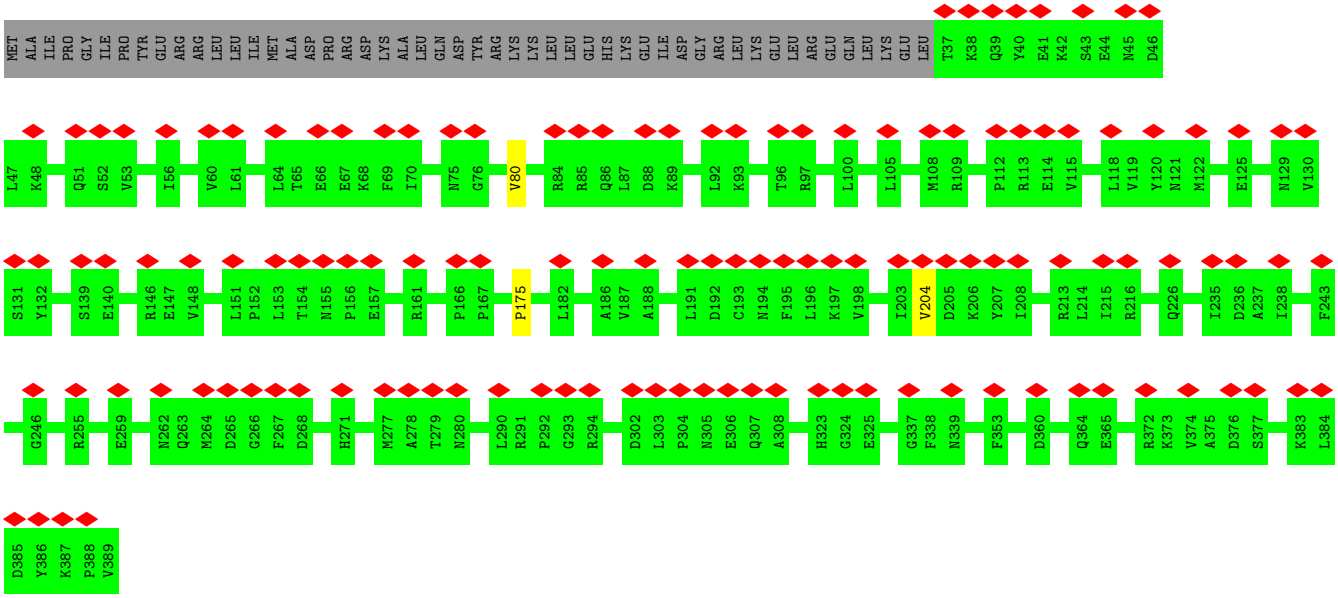
- Molecule 4: 26S protease regulatory subunit 6B

Chain D:



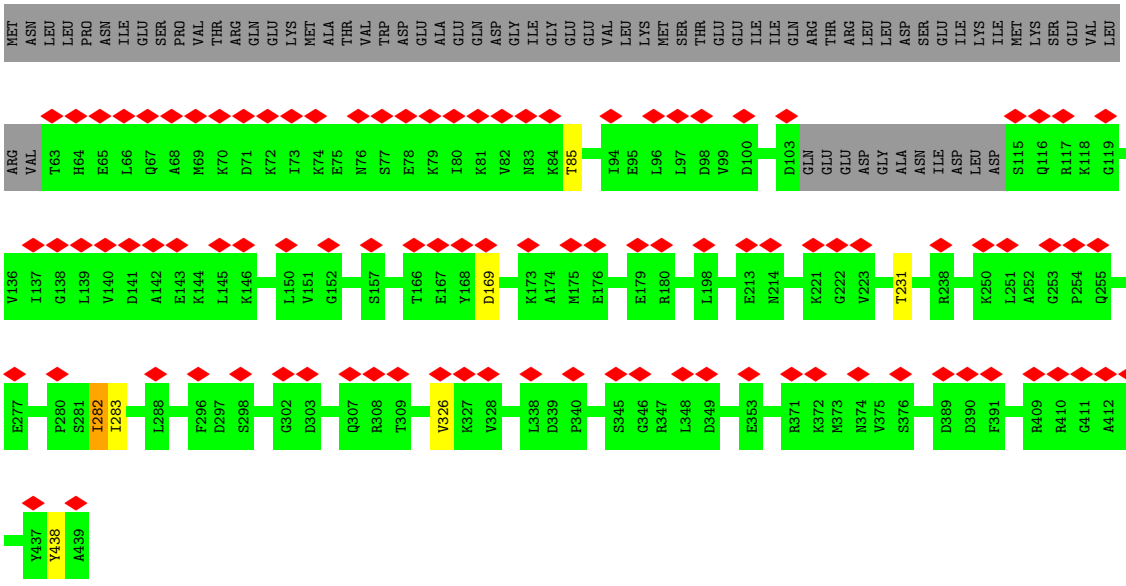
- Molecule 5: 26S protease regulatory subunit 10B

Chain E:



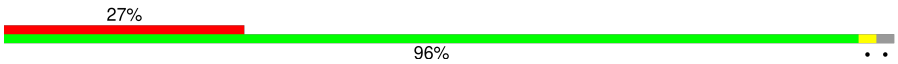
- Molecule 6: 26S protease regulatory subunit 6A

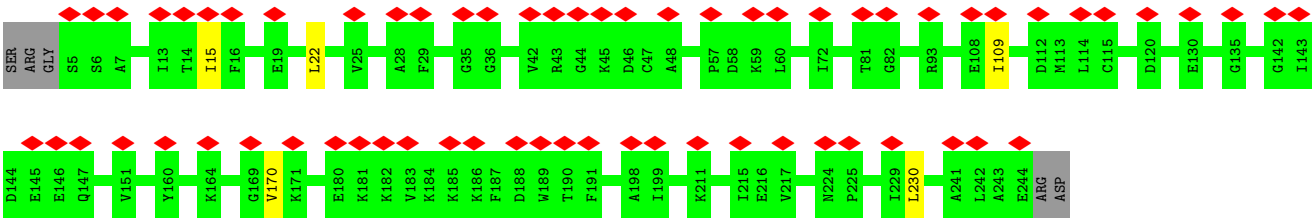
Chain F:



- Molecule 7: Proteasome subunit alpha type-6

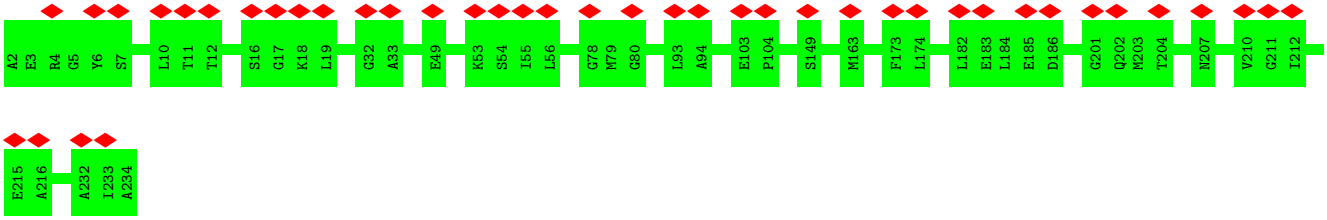
Chain G:





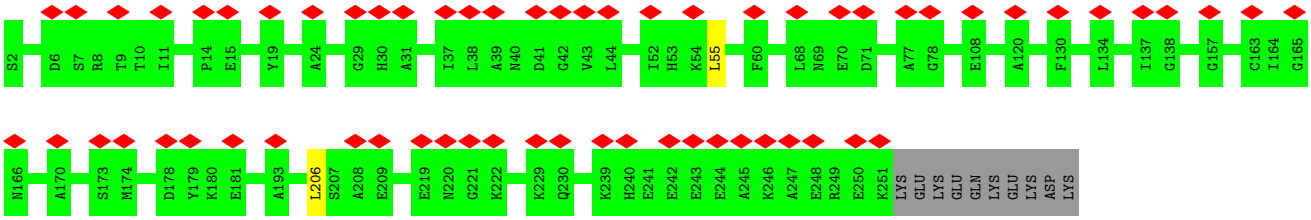
• Molecule 8: Proteasome subunit alpha type-2

Chain H: 18% 100%



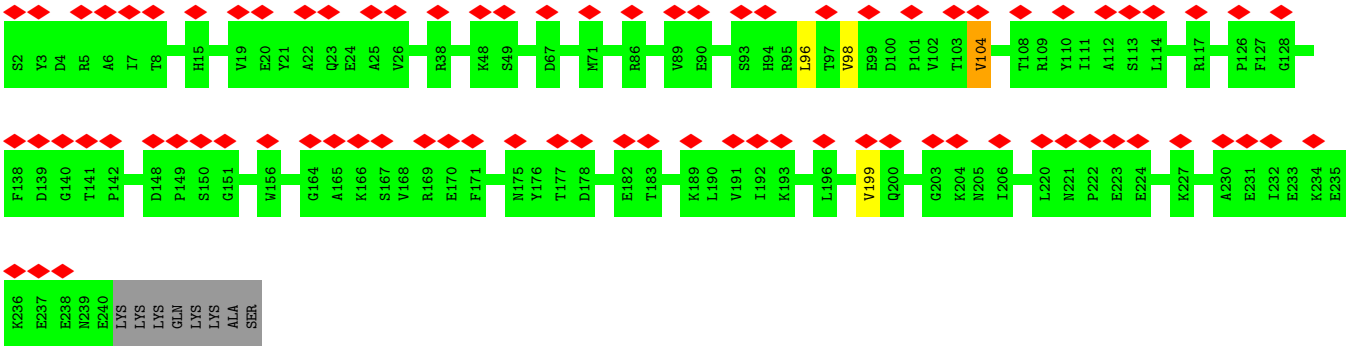
• Molecule 9: Proteasome subunit alpha type-4

Chain I: 24% 95%



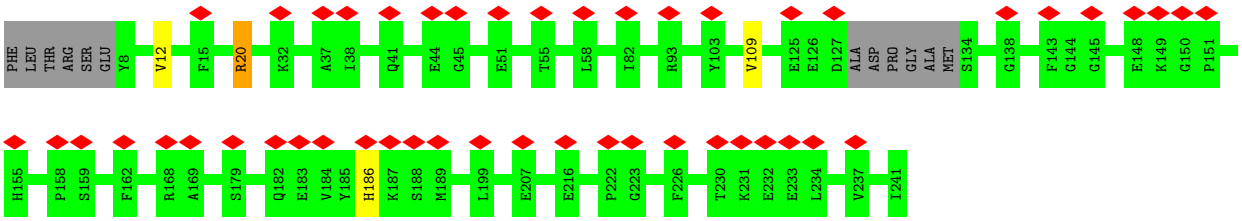
• Molecule 10: Proteasome subunit alpha type-7

Chain J: 33% 95%



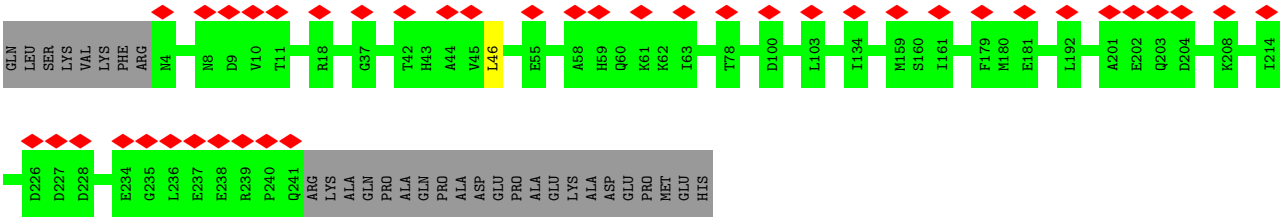
• Molecule 11: Proteasome subunit alpha type-5

Chain K: 20% 93% 5%



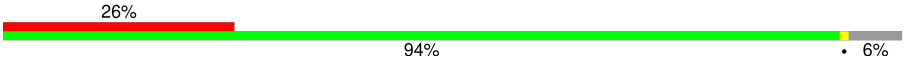
• Molecule 12: Proteasome subunit alpha type-1

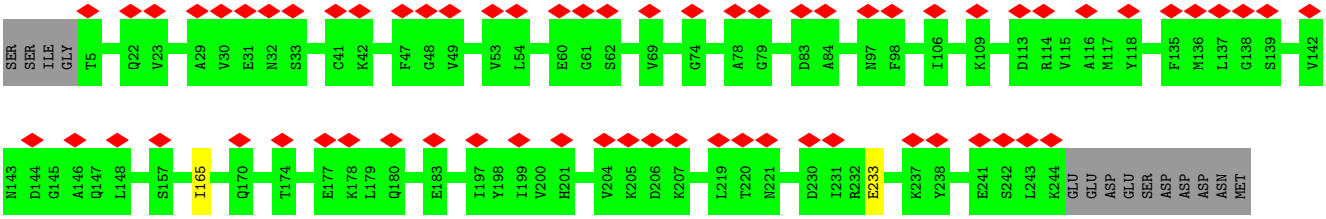
Chain L:



- Molecule 13: Proteasome subunit alpha type-3

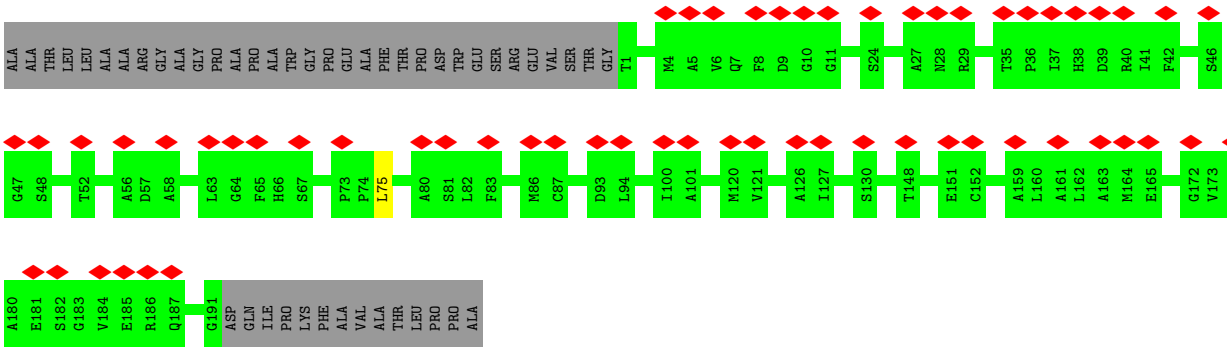
Chain M:





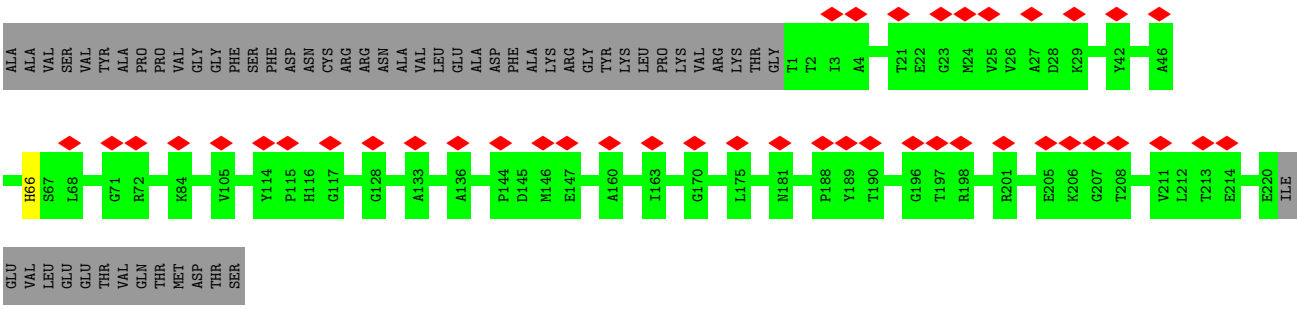
- Molecule 14: Proteasome subunit beta type-6

Chain N:



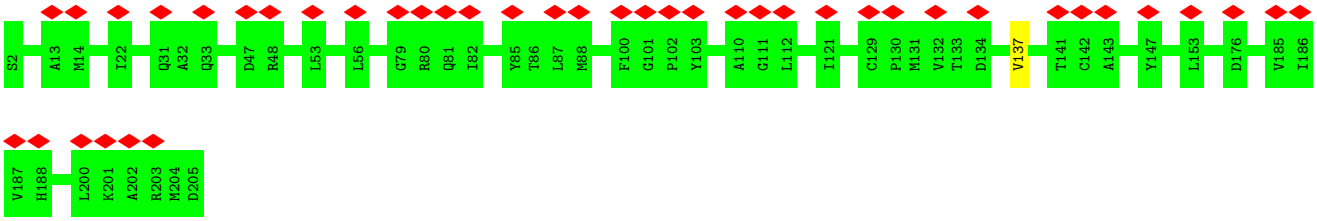
- Molecule 15: Proteasome subunit beta type-7

Chain O:



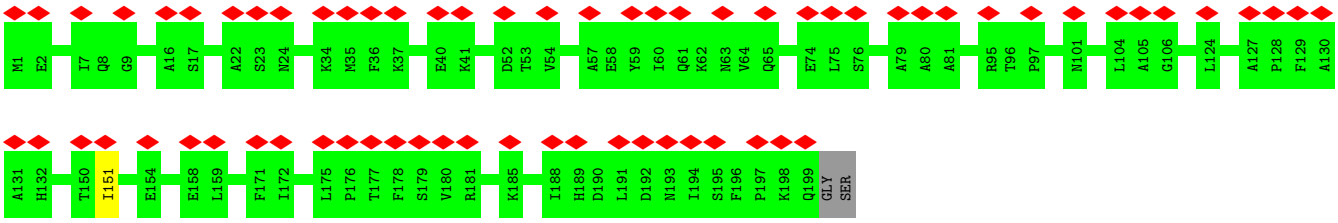
- Molecule 16: Proteasome subunit beta type-3

Chain P: 21% 100%



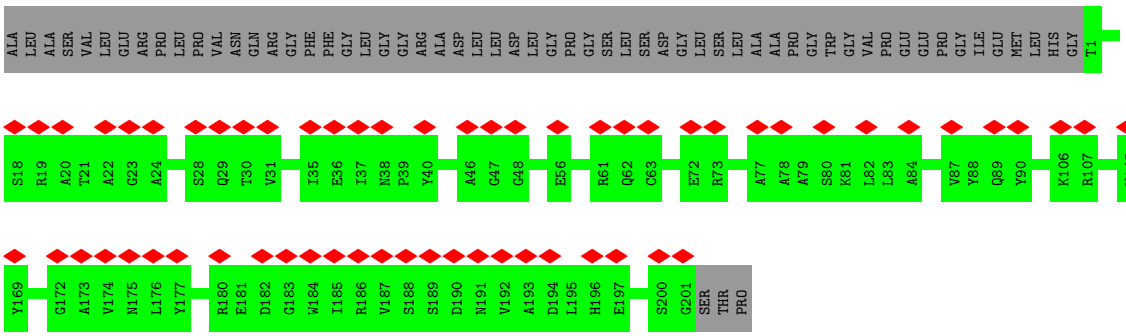
- Molecule 17: Proteasome subunit beta type-2

Chain Q: 33% 99%



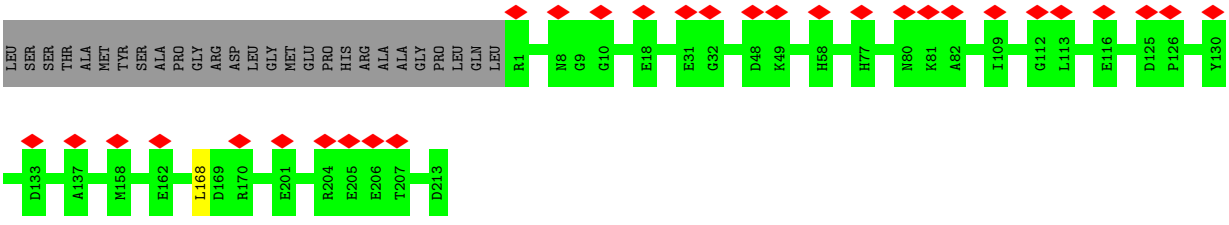
- Molecule 18: Proteasome subunit beta type-5

Chain R: 25% 77% 23%



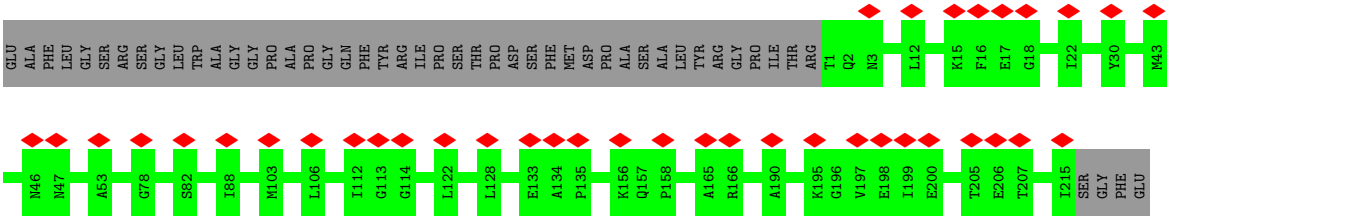
- Molecule 19: Proteasome subunit beta type-1

Chain S: 12% 88% 11%



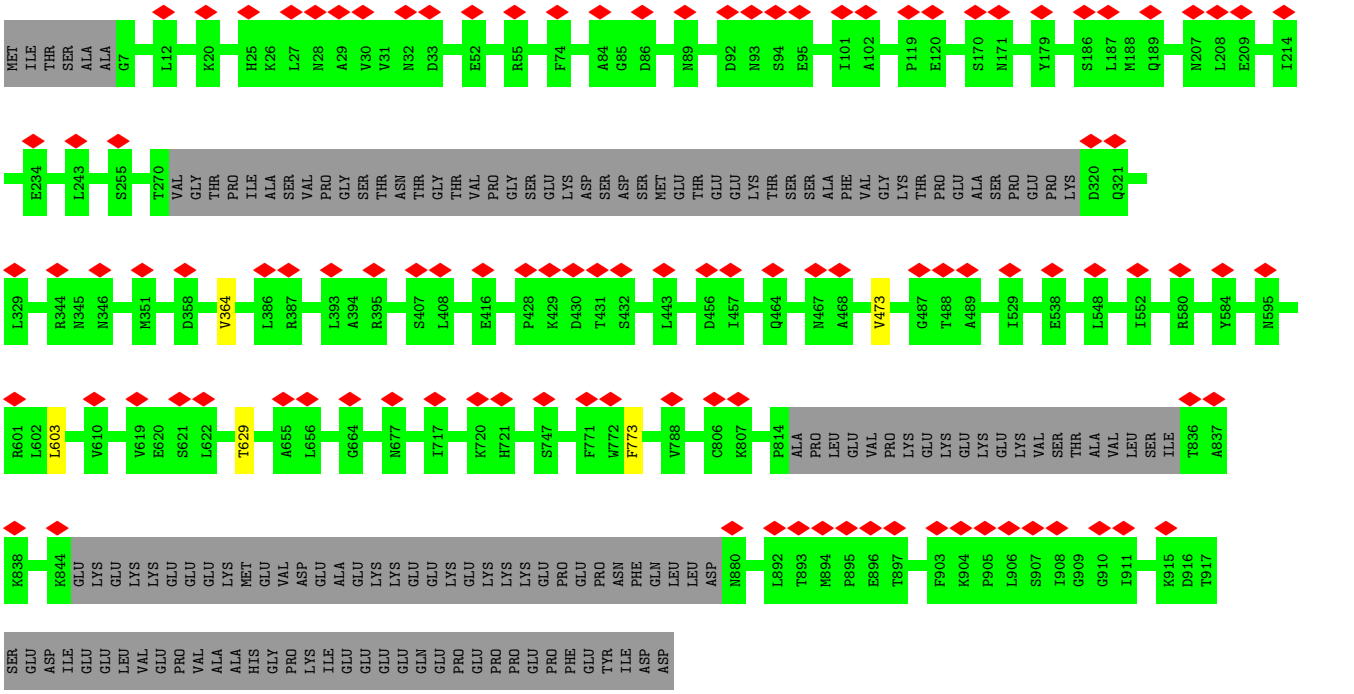
- Molecule 20: Proteasome subunit beta type-4

Chain T: 15% 82% 18%



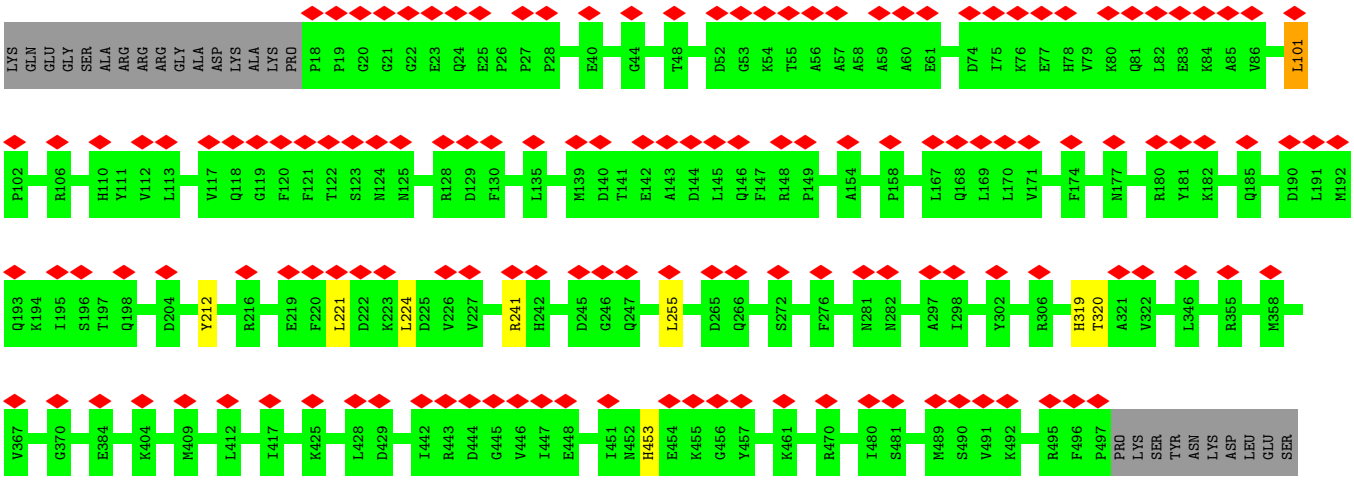
• Molecule 21: 26S proteasome non-ATPase regulatory subunit 1

Chain U:



• Molecule 22: 26S proteasome non-ATPase regulatory subunit 3

Chain V:



ALA GLU GLU ARG ARG GLU ARG GLU GLN GLN GLN ASP LEU GLU PHE ALA LYS GLU MET ALA GLU ASP ASP ASP SER PHE PRO

- Molecule 23: 26S proteasome non-ATPase regulatory subunit 12

Chain W: 77% 98%

M1 A2 D3 G4 G5 S6 E7 R8 A9 D10 G11 R12 I13 V14 K15 M16 E17 V18 D19 Y20 S21 A22 T23 V24 D25 Q26 R27 L28 P29 E30 C31 A32 K33 K36 E37 G38 R39 L40 Q41 E42 V43 I44 E45 T46 L47 L48 S49 L50 E51 K52 Q53 T54 R55 T56 A57 S58 D59 M60 V61

S62 T63 S64 R65 I66 L67 V68 A69 V70 V71 K72 M73 C74 Y75 E76 A77 K78 E79 W80 D81 L82 L83 N84 E85 N86 I87 M88 L89 L90 S91 K92 R93 R94 S95 Q96 L97 K98 Q99 A100 V101 A102 K103 M104 V105 Q106 Q107 C108 C109 T110 Y111 V112 E113 E114 I115 T116 D117 L118 P119 I120 K121

L122 R123 L124 I125 D126 T127 L128 R129 M130 V131 T132 E133 G134 K135 I136 Y137 V138 E139 I140 E141 R142 A143 R144 L145 T146 K147 T148 L149 A150 T151 I152 K153 E154 Q155 N156 G157 D158 V159 K160 E161 A162 A163 S164 I165 L166 Q167 E168 L169 Q170 V171 E172 T173 Y174 M177 E178 K179 K180 E181 R182

V183 E184 F185 I186 L187 E188 Q189 M190 R191 L192 C193 L194 A195 V196 K197 D198 Y199 I200 R201 T202 K207 K208 I209 N210 T211 K212 F213 F214 Q215 E216 E217 N218 T219 E220 K221 L222 K223 L224 K225 Y226 Y227 N228 L229 M230 I231 Q232 Q235 H236 E237 G238 S239 Y240 L241 S242 I243 C244 K245 H246

I250 Y251 D252 T253 P254 C255 I256 Q257 A258 E259 S260 E261 K262 W263 A266 L267 K268 V271 L272 Y273 V274 I275 P278 F279 D280 N281 E282 Q283 S284 D285 L286 V287 H288 R289 I290 S291 G292 D293 K294 K295 L296 E297 E298 I299 Y302 K303 K307 L308 F309 T310 T311 M312 M315

R316 W317 S318 T319 L320 V321 E322 G325 M326 E327 L328 R329 K330 G331 S332 S335 P336 F341 G342 S343 T344 E345 E346 G347 E348 K349 R350 W351 K352 K355 M356 H361 N362 I363 R364 I365 M366 A367 K368 Y369 Y370 T371 R372 M375 K376 R377 Q380 L381 L382 D383 L384 S385 V386

D387 E388 S389 E390 A391 F392 N395 L396 V397 V398 N399 K400 T401 I402 F403 A404 K405 G411 N414 F415 Q416 R417 P418 K419 D420 P421 N422 N423 L424 L425 W428 S429 N433 S437 L438 V439 H444 L445 M451 I452 H453 N454 L455 Q456

- Molecule 24: 26S proteasome non-ATPase regulatory subunit 11

Chain X: 44% 57% 43%

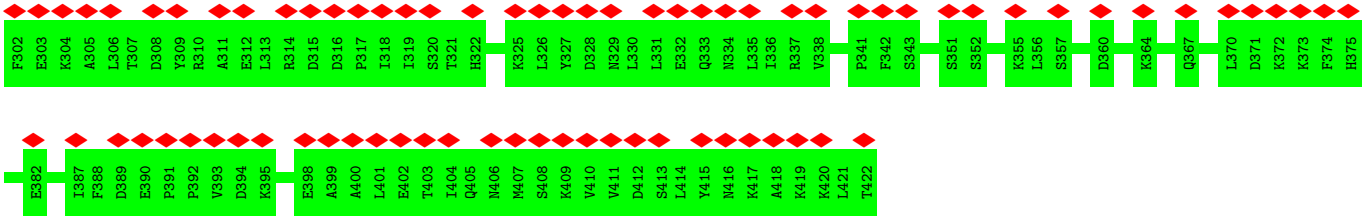
MET ALA ALA ALA ALA VAL VAL GLU PHE GLN ARG ALA GLN SER LEU LEU SER THR ASP ARG GLU ALA SER ILE ASP ILE LEU HIS SER ILE VAL LYS ARG ASP ILE GLN GLU ASN ASP GLU GLU ALA VAL GLN VAL LYS GLU GLN SER ILE LEU GLU LEU GLY SER LEU LEU ALA LYS THR

GLY GLN ALA ALA GLU LEU GLY GLY LEU LEU LYS TYR VAL ARG PRO PHE LEU ASN SER ILE SER LYS ALA LYS ALA ARG LEU VAL ARG SER LEU LEU ASP LEU PHE LEU ASP MET GLU ALA ALA THR GLY GLN GLU VAL GLU LEU CYS LEU GLU CYS ILE GLU TRP ALA LYS SER GLU

LYS ARG THR PHE LEU ARG GLN ALA LEU GLU ALA ARG LEU VAL SER LEU TYR PHE ASP THR LYS ARG TYR GLN GLU ALA LEU HIS LEU GLY SER GLN LEU LEU ARG GLU LEU LYS LYS MET ASP ASP LYS ALA LEU LEU VAL GLU VAL GLN LEU LEU GLU SER LYS THR TYR HIS ALA LEU

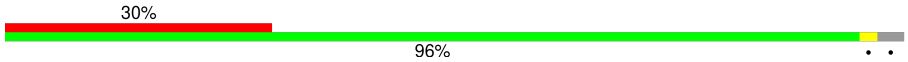
SER N182 L183 P184 K185 A186 R187 A188 A189 L190 T191 S192 A193 R194 T195 T196 A197 N198 A199 I200 Y201 C202 P203 P204 K205 L206 Q207 A208 T209 L210 D211 M212 Q213 S214 G215 I216 I217 H218 A219 A220 E221 E222 K223 D224 W225 K226 T227 A228 Y229 S230 Y231 F232 Y233 E234 A235 F236 E237 G238 Y239 D240

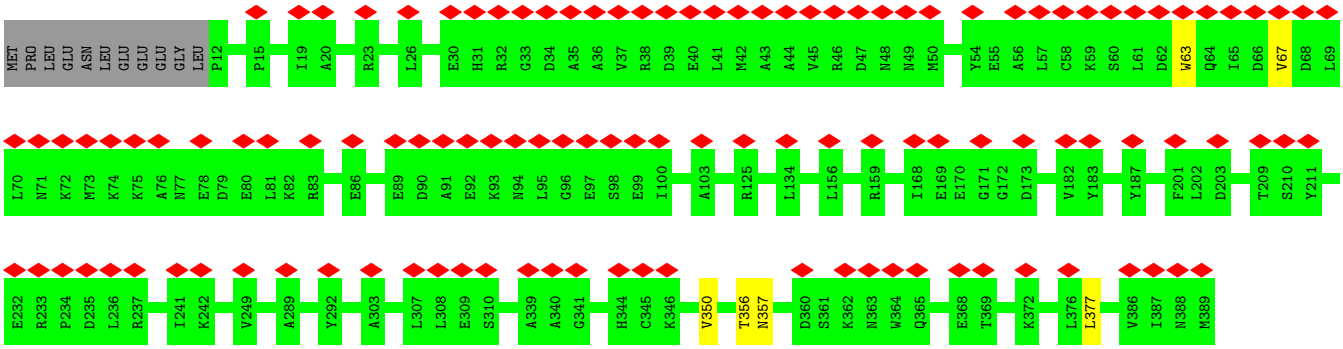
S241 I242 D243 S244 P245 K246 A247 I248 T249 S250 L251 K252 Y253 L256 C257 K258 I259 M260 L261 N262 T263 P264 E265 D266 V267 Q268 A269 L270 V271 S272 G273 K274 L275 A276 L277 R278 Y279 A280 G281 R282 Q283 T284 E285 A286 L287 K288 C289 V290 A291 Q292 A293 S294 K295 N296 R297 S298 L299 A300 D301



• Molecule 25: 26S proteasome non-ATPase regulatory subunit 6

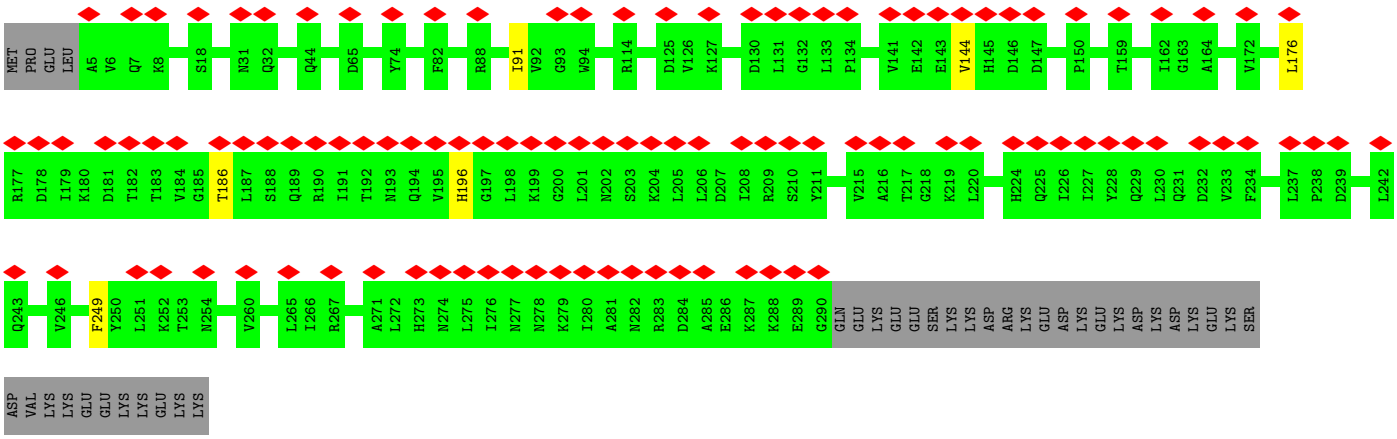
Chain Y:





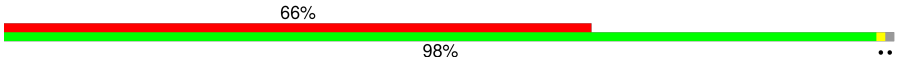
• Molecule 26: 26S proteasome non-ATPase regulatory subunit 7

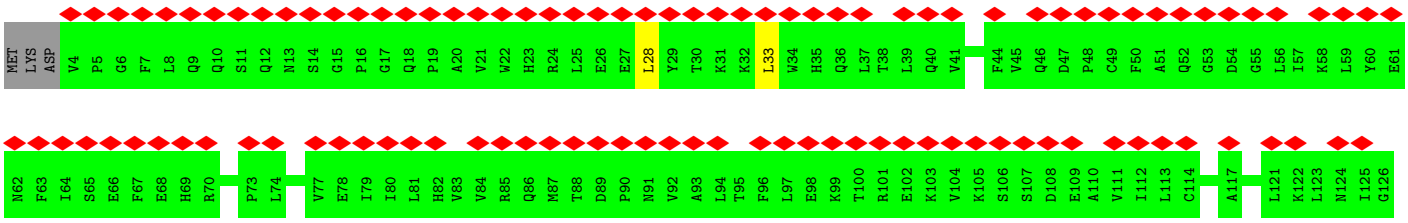
Chain Z:



• Molecule 27: 26S proteasome non-ATPase regulatory subunit 13

Chain a:





D127 L128 Q129 V130 T131 K132 E133 T134 I135 E136 D137 V138 E139 E140 M141 L142 N143 N144 L145 P146 G147 S150 V151 H152 F155 Y156 D157 L158 S159 S160 K161 Y162 I166 G167 N168 H169 A170 S171 R178 F179 L180 G181 D184 I185 K186 D187 V190 S191 Q194 E195 R196 A197

L200 G204 L205 L206 V210 F211 N212 F213 G214 E215 L216 L217 M218 H219 P220 V221 L222 E223 S224 L225 R226 N227 T228 Q231 W232 L233 I234 D235 N241 S242 G243 F248 Q249 T250 L251 K252 W255 G256 Q257 Q258 P259 D260 L261 A262 A263 N264 E265 A266 Q267 L268 L269 R270 Q273

L274 M280 A286 N287 H288 R289 Q290 I296 S299 A314 L315 S316 V317 G318 L319 V320 K321 G322 S323 I324 D328 K329 T334 W335 V336 Q337 P338 R339 V340 L341 D342 L343 Q344 Q345 I346 K347 G348 M349 K350 D351 D359 V360 K361 S362 M363 E364 M365 L366 V367 E368 H369

H372 D373 I374 L375 T376

- Molecule 28: 26S proteasome non-ATPase regulatory subunit 4

Chain b:

M1 V2 L3 E4 S5 T6 M7 V8 C9 V10 D11 N12 S13 E14 Y15 M16 R17 N18 F21 L22 P23 T24 R25 L26 Q27 A28 Q29 Q30 D31 A32 V33 N34 I35 V36 C37 H38 S39 K40 T41 R42 S43 N44 P45 E46 N47 N48 V49 G50 L51 I52 T53 L54 A55 N56 D57 C58 E59 V60 L61

T62 T63 L64 T65 P66 D67 T68 G69 R70 I71 L72 S73 K74 L75 H76 T77 V78 Q79 P80 K81 G82 K83 I84 T85 F86 C87 T88 G89 I90 R91 V92 A93 H94 L95 A96 L97 K98 H99 R100 Q101 G102 K103 N104 H105 K106 M107 R108 I109 I110 A111 F112 V113 G114 S115 P116 V117 E118 D119 N120 E121

K122 D123 L124 V125 A128 K129 R130 L131 K132 K133 E134 K135 V136 N137 V138 D139 T140 I141 N142 F143 G144 E145 E146 E147 V148 N149 T150 E151 K152 L153 T154 A155 F156 V157 N158 T159 L160 N161 G162 K163 D164 G167 S168 H169 L170 V171 T172 V173 P174 P175 G176 P177 S178 L179 A180 D181 A182 L183

I184 S185 S186 P187 I188 L189 A190 G191 GLU GLY GLY ALA MET LEU GLY LEU GLY ALA SER ASP PHE GLU PHE GLY VAL ASP PRO SER ALA ASP PRO GLU LEU ALA LEU ALA LEU ARG VAL SER MET GLU GLU GLN ARG GLN ARG GLN GLU GLU GLU ALA ARG ARG ALA ALA ALA ALA SER ALA

ALA GLU ALA GLY ILE ALA THR THR GLY THR GLU ASP SER ASP ASP ALA LEU LEU LYS MET THR ILE SER GLN GLN GLU PHE GLY ARG THR GLY LEU PRO ASP LEU SER SER MET THR GLU GLU GLU GLN ILE ALA TYR ALA MET GLN MET SER LEU GLN GLY ALA GLU PHE GLY GLN ALA

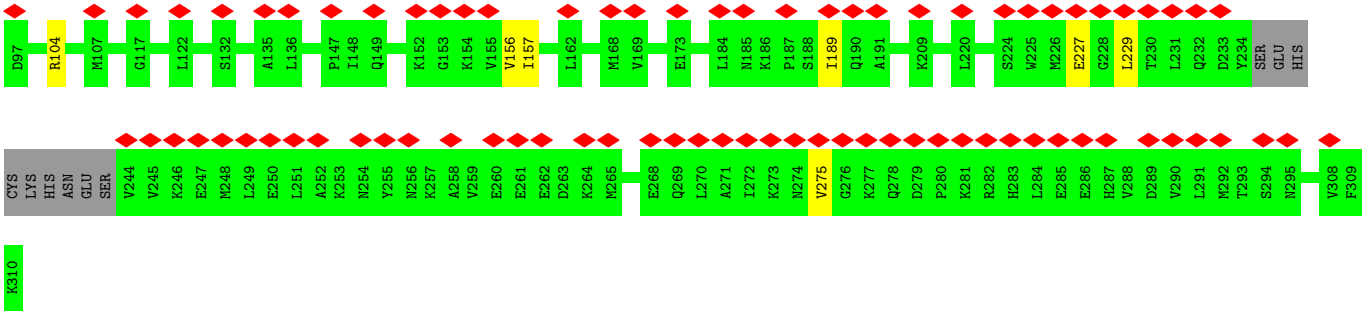
GLU SER ALA ASP ILE ASP ALA SER SER ALA MET ASP THR SER GLU PRO ALA LYS GLU GLU ASP ASP TYR ASP VAL MET GLN ASP PRO GLU PHE LEU GLN SER VAL LEU GLU ASN LEU PRO GLY VAL ASP PRO ASN ASN GLU ALA ILE ARG ASN ALA MET GLY SER LEU ALA SER GLN ALA

THR LYS ASP GLY LYS LYS ASP LYS LYS GLU GLU ASP LYS LYS

- Molecule 29: 26S proteasome non-ATPase regulatory subunit 14

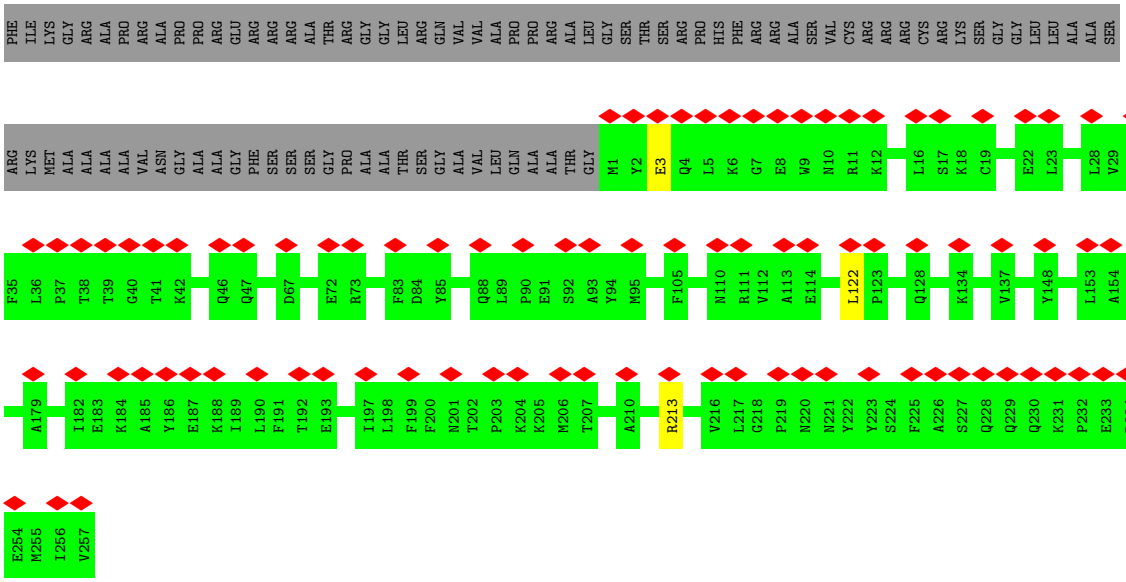
Chain c:

ASP ARG LEU LEU ARG LEU GLY GLY GLY MET PRO GLY LEU GLY GLN GLY PRO PRO THR ASP ALA PRO A24 S35 L36 A47 M51 E60 F61 V62 V69 I70 A74 Q77 S78 G79 T80 G81 V82 S83 V84 E85 A86 V87 D88 P89 V90 F91 Q92 A93 K94 M95 L96



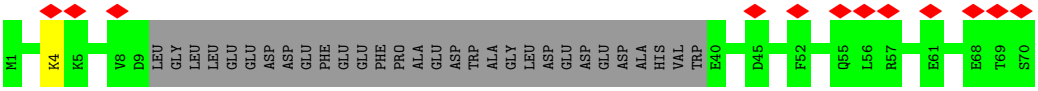
- Molecule 30: 26S proteasome non-ATPase regulatory subunit 8

Chain d:



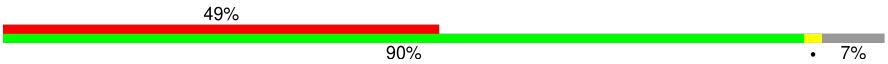
- Molecule 31: 26S proteasome complex subunit DSS1

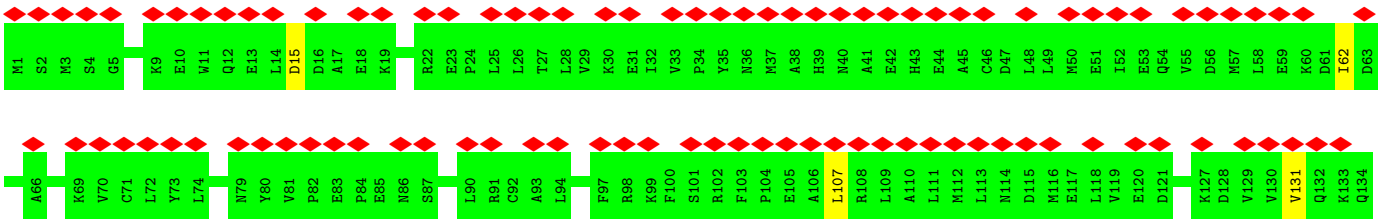
Chain e:

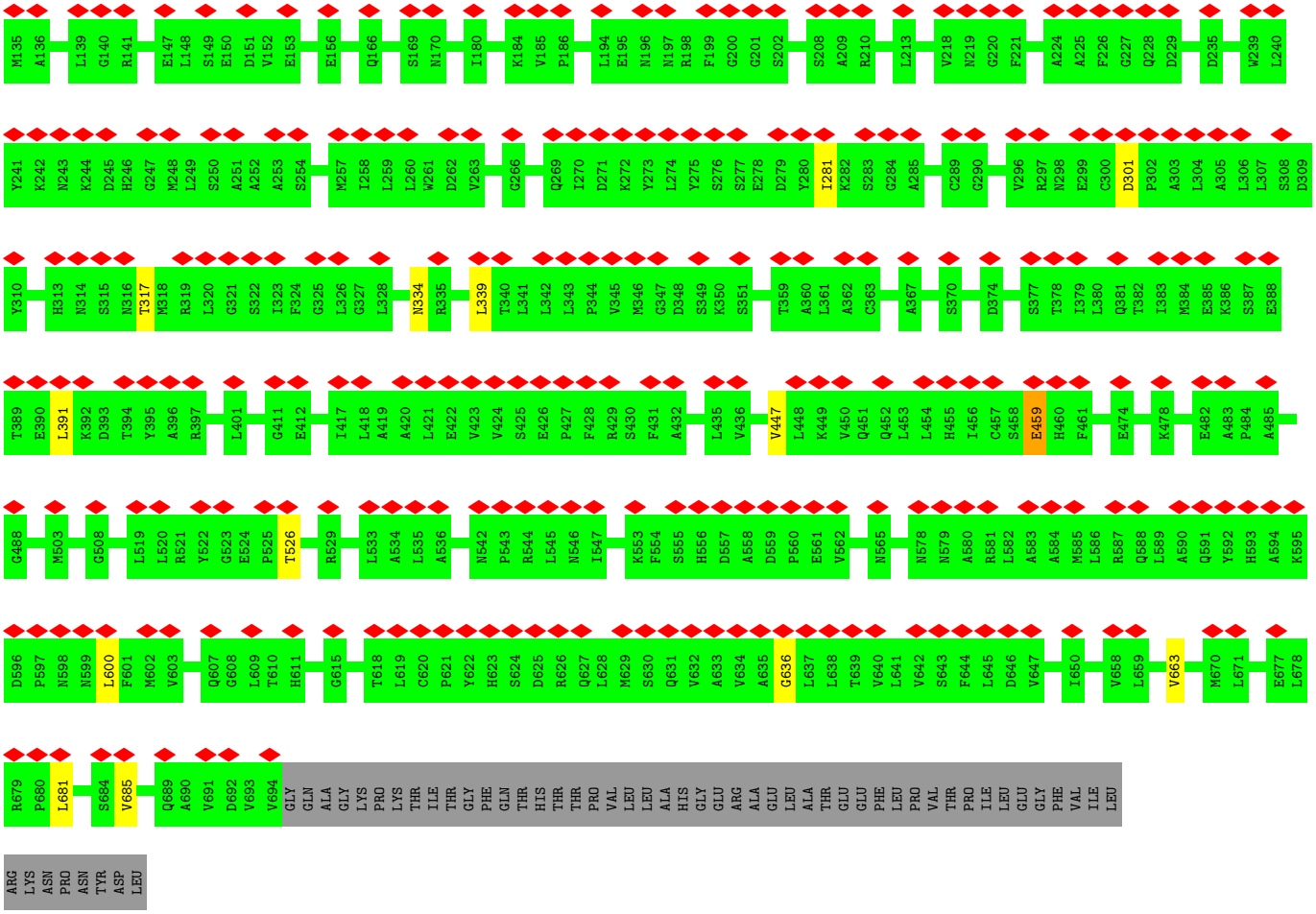


- Molecule 32: 26S proteasome non-ATPase regulatory subunit 2

Chain f:






M135 A136 L139 G140 R141 E147 L148 S149 E150 D151 V152 E153 E156 Q166 S169 N170 I180 K184 V185 P186 L194 E195 N196 N197 R198 F199 G200 G201 S202 S208 A209 R210 L213 V218 N219 G220 F221 A224 A225 F226 G227 Q228 D229 D235 W239 L240
Y241 K242 N243 K244 D245 H246 G247 M248 L249 S250 A251 A252 A253 S254 M257 I258 L259 L260 W261 D262 V263 G266 Q269 I270 D271 K272 Y273 L274 Y275 S276 S277 E278 D279 Y280 T281 K282 S283 G284 A285 C289 G290 V296 R297 N298 E299 C300 D301 P302 A303 L304 A305 L306 L307 S308 D309
Y310 H313 N314 S315 N316 T317 M318 R319 L320 G321 S322 I323 F324 G325 L326 G327 L328 N334 R335 L339 T340 L341 L342 L343 P344 V345 M346 G347 D348 S349 K350 S351 T359 A360 L361 A362 C363 A367 S370 D374 S377 T378 I379 L380 Q381 T382 I383 M384 E385 K386 S387 E388
T389 E390 L391 K392 D393 T394 Y395 A396 R397 L401 G411 E412 I417 L418 A419 A420 L421 E422 V423 V424 S425 E426 P427 F428 R429 S430 F431 A432 L435 V436 V447 L448 K449 V450 Q451 Q452 L453 L454 H455 I456 C457 S458 E459 H460 F461 E474 K478 E482 A483 P484 A485
G488 M503 G508 L519 L520 R521 Y522 G523 E524 P525 T526 R529 L533 A534 L535 A536 N542 P543 R544 L545 N546 I547 K553 F554 S555 H556 D557 A558 D559 P560 E561 V562 N565 N578 N579 A580 R581 L582 A583 A584 M585 L586 R587 Q588 L589 A590 Q591 Y592 H593 A594 K595
D596 P597 N598 N599 L600 F601 M602 V603 Q607 G608 L609 T610 H611 G615 T618 L619 C620 P621 Y622 H623 S624 D625 R626 Q627 L628 M629 S630 Q631 V632 A633 V634 A635 G636 L637 L638 T639 V640 L641 V642 S643 F644 L645 D646 V647 I650 V658 L659 V663 M670 L671 E677 L678
R679 P680 L681 S684 V685 Q689 A690 V691 D692 V693 V694 GLY GLN ALA GLY LYS PRO LYS THR ILE THR GLY PHE GLN THR HIS THR THR PRO VAL LEU LEU ALA HIS GLY GLU ARG ALA GLU LEU ALA THR GLU GLU PHE LEU PRO VAL THR PRO ILE LEU GLU GLY PHE VAL ILE LEU
ARG LYS ASN PRO ASN TYR ASP LEU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10622	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.005	Depositor
Minimum map value	-0.002	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0015	Depositor
Map size (Å)	309.6, 309.6, 309.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	A	0.25	0/2886	0.48	0/3899
2	B	0.26	0/2757	0.57	0/3724
3	C	0.26	0/3054	0.48	0/4107
4	D	0.24	0/3090	0.46	0/4168
5	E	0.24	0/2835	0.44	0/3821
6	F	1.42	6/2903 (0.2%)	0.49	0/3912
7	G	0.24	0/1859	0.44	0/2523
8	H	0.24	0/1747	0.44	0/2376
9	I	0.24	0/1942	0.45	0/2628
10	J	0.25	0/1728	0.45	0/2358
11	K	1.56	1/1747 (0.1%)	0.53	2/2364 (0.1%)
12	L	0.24	0/1885	0.44	0/2552
13	M	0.25	0/1891	0.44	0/2552
14	N	0.24	0/1454	0.41	0/1967
15	O	0.24	0/1669	0.46	0/2262
16	P	0.24	0/1613	0.41	0/2174
17	Q	0.24	0/1603	0.42	0/2174
18	R	0.23	0/1579	0.39	0/2134
19	S	0.24	0/1671	0.41	0/2253
20	T	0.23	0/1700	0.41	0/2305
21	U	0.23	0/6396	0.41	0/8646
22	V	1.26	6/3929 (0.2%)	0.51	0/5309
23	W	0.24	0/3751	0.48	3/5042 (0.1%)
24	X	0.23	0/1936	0.43	0/2614
25	Y	0.24	0/3173	0.49	1/4273 (0.0%)
26	Z	0.24	0/2324	0.49	0/3150
27	a	0.23	0/3053	0.43	0/4133
28	b	0.25	0/1478	0.44	0/2001
29	c	0.27	1/2226 (0.0%)	0.48	0/3007
30	d	0.25	0/2162	0.50	0/2919
31	e	3.67	1/338 (0.3%)	0.74	2/450 (0.4%)
32	f	0.35	1/5413 (0.0%)	0.52	2/7317 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
All	All	0.57	16/77792 (0.0%)	0.47	10/105114 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	2
3	C	0	2
22	V	0	2
23	W	0	1
25	Y	0	1
27	a	0	1
30	d	0	1
32	f	0	1
All	All	0	12

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	e	4	LYS	CD-CE	67.35	3.19	1.51
11	K	20	ARG	CB-CG	64.16	3.25	1.52
22	V	212	TYR	CD2-CE2	40.36	1.99	1.39
22	V	212	TYR	CD1-CE1	40.15	1.99	1.39
6	F	438	TYR	CD2-CE2	39.43	1.98	1.39

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	K	20	ARG	CA-CB-CG	10.22	135.88	113.40
11	K	20	ARG	CB-CG-CD	8.29	133.16	111.60
31	e	4	LYS	CD-CE-NZ	8.20	130.57	111.70
31	e	4	LYS	CG-CD-CE	7.33	133.88	111.90
32	f	459	GLU	N-CA-C	6.21	127.77	111.00

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	311	PRO	Peptide
2	B	176	VAL	Peptide
2	B	278	ALA	Peptide
3	C	171	HIS	Peptide
3	C	255	GLY	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	A	359/433 (83%)	311 (87%)	44 (12%)	4 (1%)	12	47
2	B	346/440 (79%)	297 (86%)	46 (13%)	3 (1%)	14	52
3	C	382/398 (96%)	339 (89%)	41 (11%)	2 (0%)	25	64
4	D	378/418 (90%)	333 (88%)	44 (12%)	1 (0%)	37	73
5	E	351/403 (87%)	322 (92%)	28 (8%)	1 (0%)	37	73
6	F	362/439 (82%)	322 (89%)	38 (10%)	2 (1%)	22	60
7	G	238/245 (97%)	213 (90%)	23 (10%)	2 (1%)	16	55
8	H	229/233 (98%)	211 (92%)	18 (8%)	0	100	100
9	I	248/260 (95%)	220 (89%)	28 (11%)	0	100	100
10	J	237/247 (96%)	214 (90%)	20 (8%)	3 (1%)	10	43
11	K	224/240 (93%)	204 (91%)	18 (8%)	2 (1%)	14	52
12	L	236/268 (88%)	222 (94%)	14 (6%)	0	100	100
13	M	238/254 (94%)	216 (91%)	22 (9%)	0	100	100
14	N	189/238 (79%)	180 (95%)	9 (5%)	0	100	100
15	O	216/276 (78%)	197 (91%)	19 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	P	200/204 (98%)	185 (92%)	15 (8%)	0	100	100
17	Q	197/201 (98%)	180 (91%)	17 (9%)	0	100	100
18	R	199/262 (76%)	184 (92%)	15 (8%)	0	100	100
19	S	211/240 (88%)	200 (95%)	11 (5%)	0	100	100
20	T	213/263 (81%)	208 (98%)	5 (2%)	0	100	100
21	U	798/953 (84%)	735 (92%)	62 (8%)	1 (0%)	48	83
22	V	478/533 (90%)	413 (86%)	63 (13%)	2 (0%)	30	68
23	W	454/456 (100%)	407 (90%)	44 (10%)	3 (1%)	19	57
24	X	239/422 (57%)	213 (89%)	26 (11%)	0	100	100
25	Y	376/389 (97%)	335 (89%)	39 (10%)	2 (0%)	25	64
26	Z	284/324 (88%)	253 (89%)	30 (11%)	1 (0%)	30	68
27	a	371/376 (99%)	331 (89%)	38 (10%)	2 (0%)	25	64
28	b	189/377 (50%)	174 (92%)	15 (8%)	0	100	100
29	c	274/309 (89%)	242 (88%)	28 (10%)	4 (2%)	8	40
30	d	255/349 (73%)	227 (89%)	27 (11%)	1 (0%)	30	68
31	e	36/70 (51%)	31 (86%)	5 (14%)	0	100	100
32	f	686/749 (92%)	573 (84%)	109 (16%)	4 (1%)	22	60
All	All	9693/11269 (86%)	8692 (90%)	961 (10%)	40 (0%)	32	68

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	VAL
10	J	104	VAL
11	K	12	VAL
11	K	109	VAL
21	U	364	VAL

5.3.2 Protein sidechains (i)

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	A	308/372 (83%)	303 (98%)	5 (2%)	58	73
2	B	304/385 (79%)	298 (98%)	6 (2%)	50	68
3	C	332/346 (96%)	321 (97%)	11 (3%)	33	52
4	D	333/366 (91%)	330 (99%)	3 (1%)	75	83
5	E	308/353 (87%)	306 (99%)	2 (1%)	84	88
6	F	312/379 (82%)	306 (98%)	6 (2%)	52	69
7	G	193/209 (92%)	190 (98%)	3 (2%)	58	73
8	H	164/190 (86%)	164 (100%)	0	100	100
9	I	193/220 (88%)	191 (99%)	2 (1%)	73	82
10	J	152/210 (72%)	150 (99%)	2 (1%)	65	77
11	K	186/202 (92%)	184 (99%)	2 (1%)	70	80
12	L	198/229 (86%)	197 (100%)	1 (0%)	86	89
13	M	192/211 (91%)	190 (99%)	2 (1%)	73	82
14	N	148/180 (82%)	147 (99%)	1 (1%)	81	87
15	O	177/227 (78%)	176 (99%)	1 (1%)	84	88
16	P	172/173 (99%)	171 (99%)	1 (1%)	84	88
17	Q	164/171 (96%)	163 (99%)	1 (1%)	84	88
18	R	153/201 (76%)	153 (100%)	0	100	100
19	S	174/198 (88%)	173 (99%)	1 (1%)	84	88
20	T	175/214 (82%)	175 (100%)	0	100	100
21	U	685/816 (84%)	681 (99%)	4 (1%)	84	88
22	V	414/459 (90%)	409 (99%)	5 (1%)	67	78
23	W	416/416 (100%)	412 (99%)	4 (1%)	73	82
24	X	208/362 (58%)	207 (100%)	1 (0%)	86	89
25	Y	334/344 (97%)	332 (99%)	2 (1%)	84	88
26	Z	257/295 (87%)	252 (98%)	5 (2%)	52	69
27	a	333/336 (99%)	331 (99%)	2 (1%)	84	88
28	b	167/312 (54%)	165 (99%)	2 (1%)	67	78
29	c	243/267 (91%)	240 (99%)	3 (1%)	67	78
30	d	231/293 (79%)	229 (99%)	2 (1%)	75	83
31	e	38/63 (60%)	38 (100%)	0	100	100
32	f	582/628 (93%)	571 (98%)	11 (2%)	52	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	8246/9627 (86%)	8155 (99%)	91 (1%)	69 80

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	V	320	THR
27	a	28	LEU
23	W	250	ILE
25	Y	377	LEU
29	c	69	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
22	V	281	ASN
25	Y	365	GLN
22	V	459	GLN
23	W	444	HIS
26	Z	224	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\#\|Z\| > 2$
33	ATP	D	501	-	28,33,33	1.01	2 (7%)	34,52,52	1.46	4 (11%)
33	ATP	A	501	-	28,33,33	0.98	0	34,52,52	1.24	3 (8%)
33	ATP	F	501	-	28,33,33	0.95	0	34,52,52	1.15	2 (5%)
33	ATP	E	401	-	28,33,33	0.98	0	34,52,52	1.16	2 (5%)

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
33	ATP	D	501	-	-	4/18/38/38	0/3/3/3
33	ATP	A	501	-	-	3/18/38/38	0/3/3/3
33	ATP	F	501	-	-	4/18/38/38	0/3/3/3
33	ATP	E	401	-	-	3/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	D	501	ATP	PA-O3A	2.05	1.61	1.59
33	D	501	ATP	O4'-C1'	2.04	1.43	1.40

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	D	501	ATP	O4'-C1'-N9	4.49	114.69	108.75
33	A	501	ATP	N3-C2-N1	-3.82	123.49	128.67
33	E	401	ATP	N3-C2-N1	-3.71	123.64	128.67
33	D	501	ATP	N3-C2-N1	-3.55	123.85	128.67
33	D	501	ATP	C4'-O4'-C1'	-3.53	106.69	109.92

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

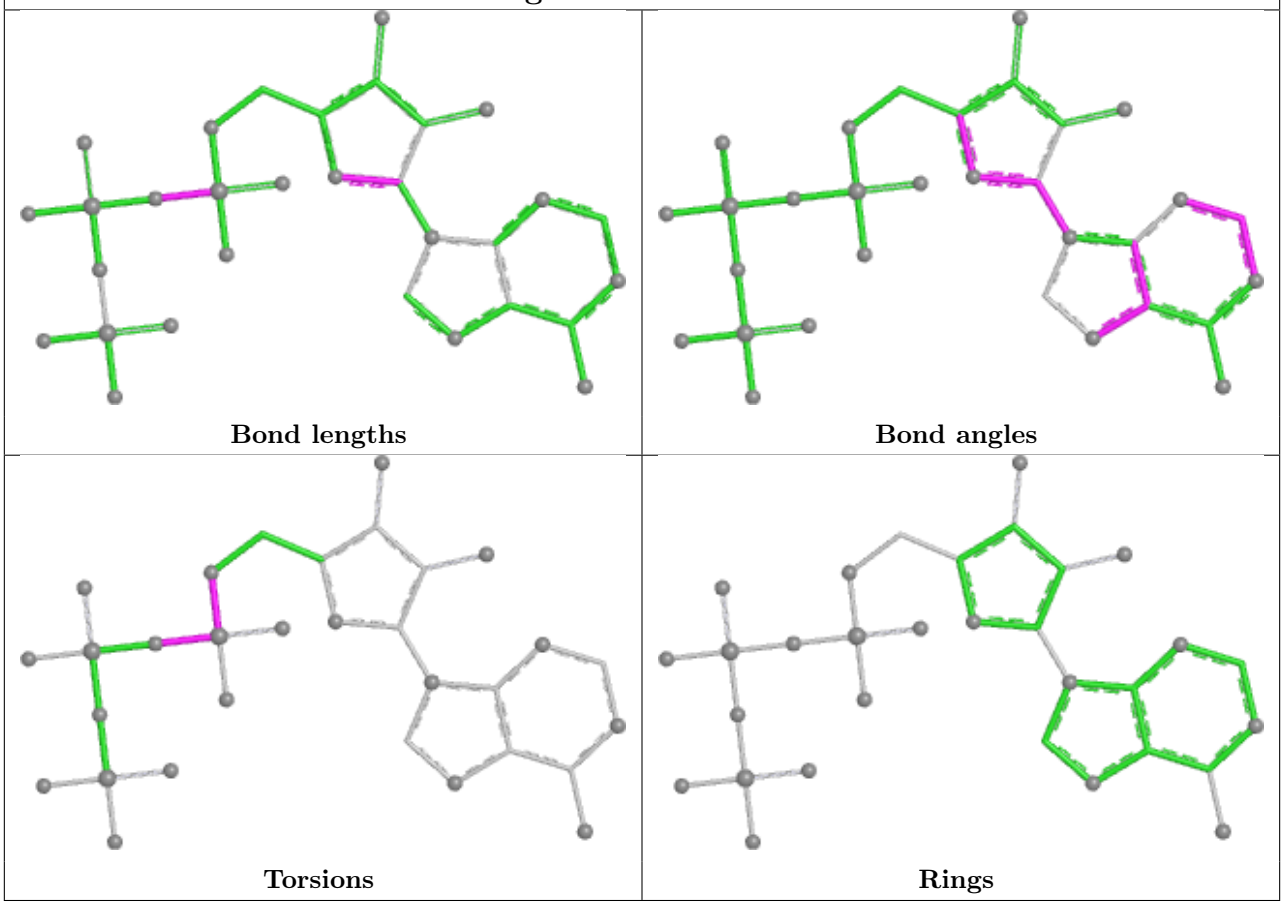
Mol	Chain	Res	Type	Atoms
33	D	501	ATP	C5'-O5'-PA-O1A
33	F	501	ATP	C5'-O5'-PA-O3A
33	F	501	ATP	O4'-C4'-C5'-O5'
33	F	501	ATP	C3'-C4'-C5'-O5'
33	D	501	ATP	PB-O3A-PA-O5'

There are no ring outliers.

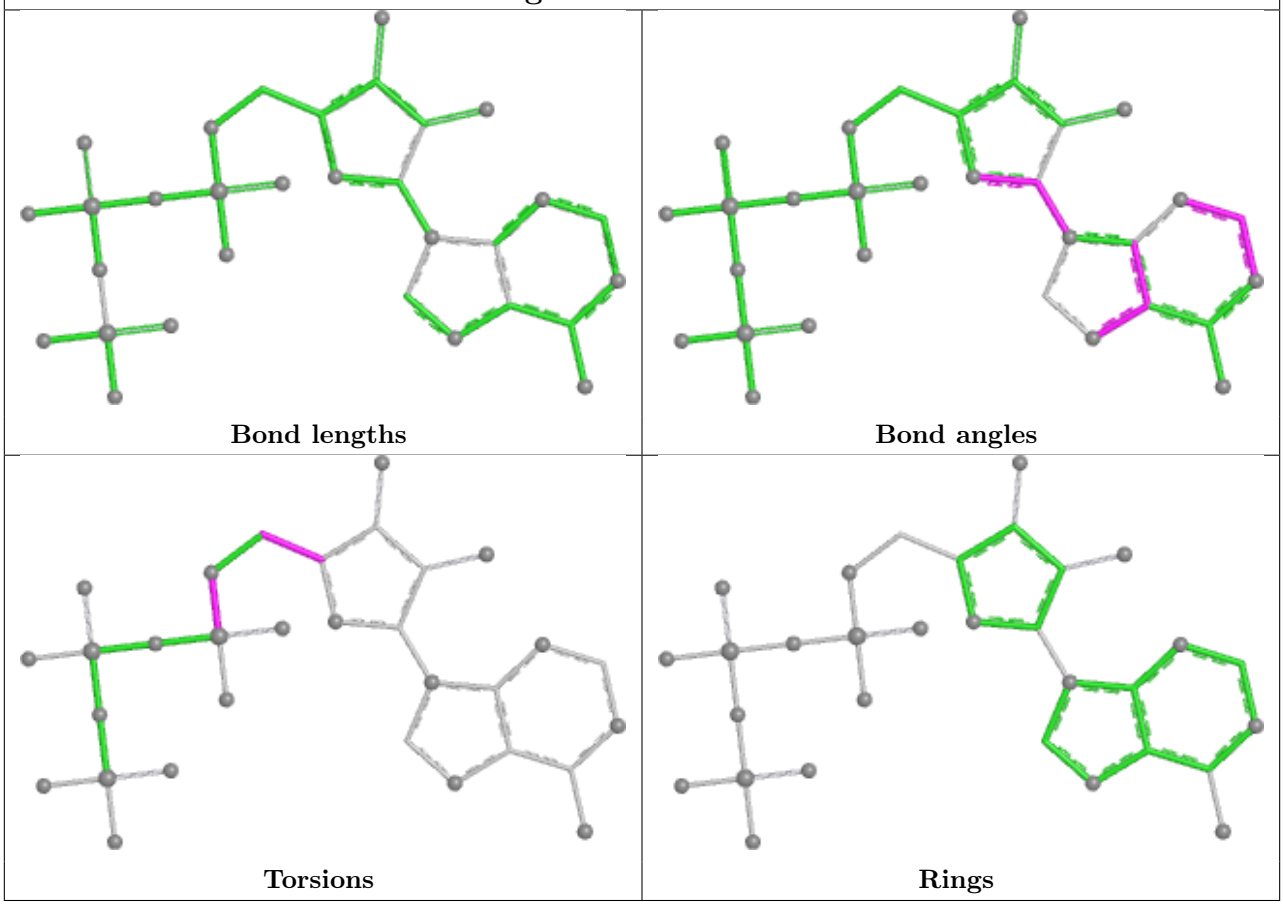
No monomer is involved in short contacts.

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 then 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.

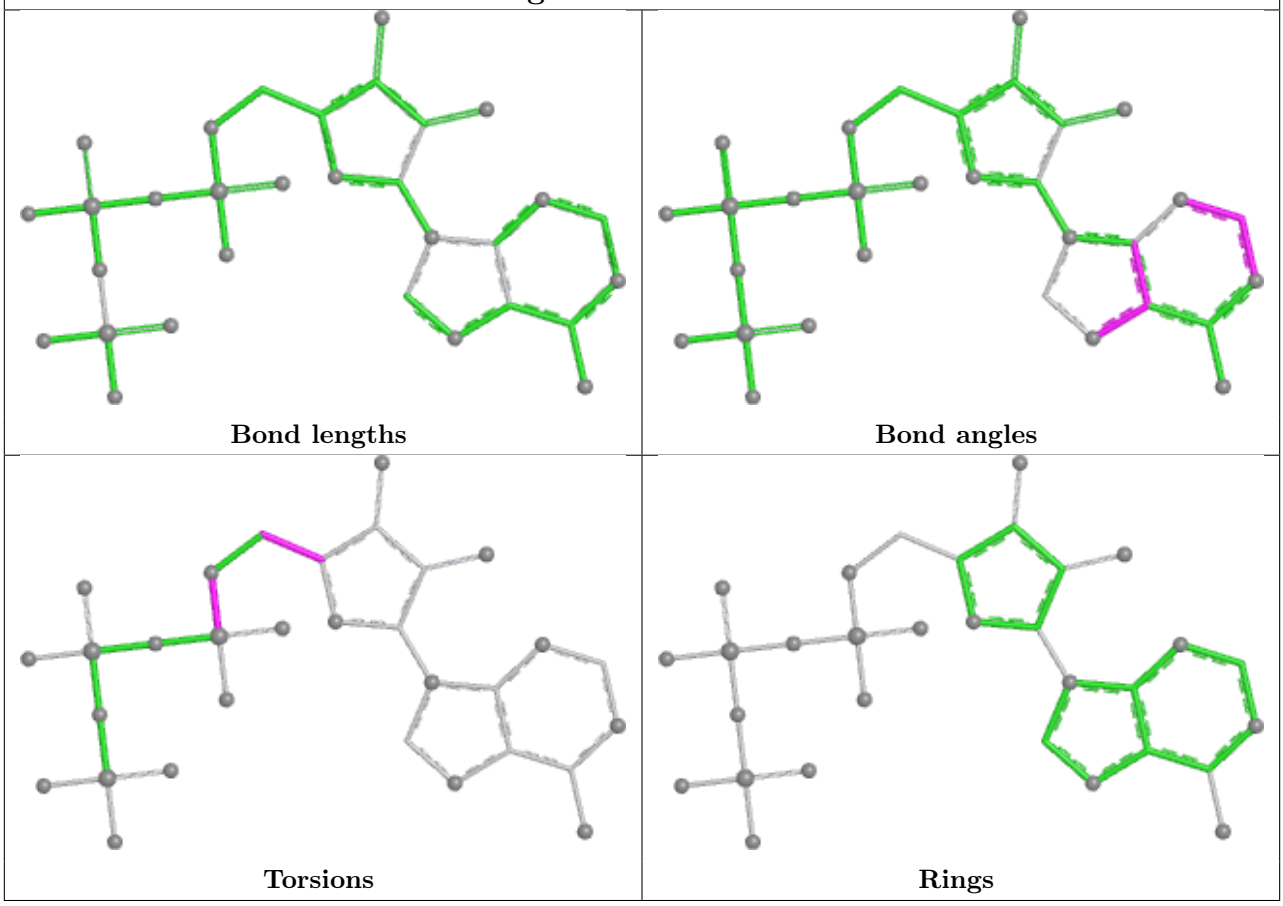
Ligand ATP D 501



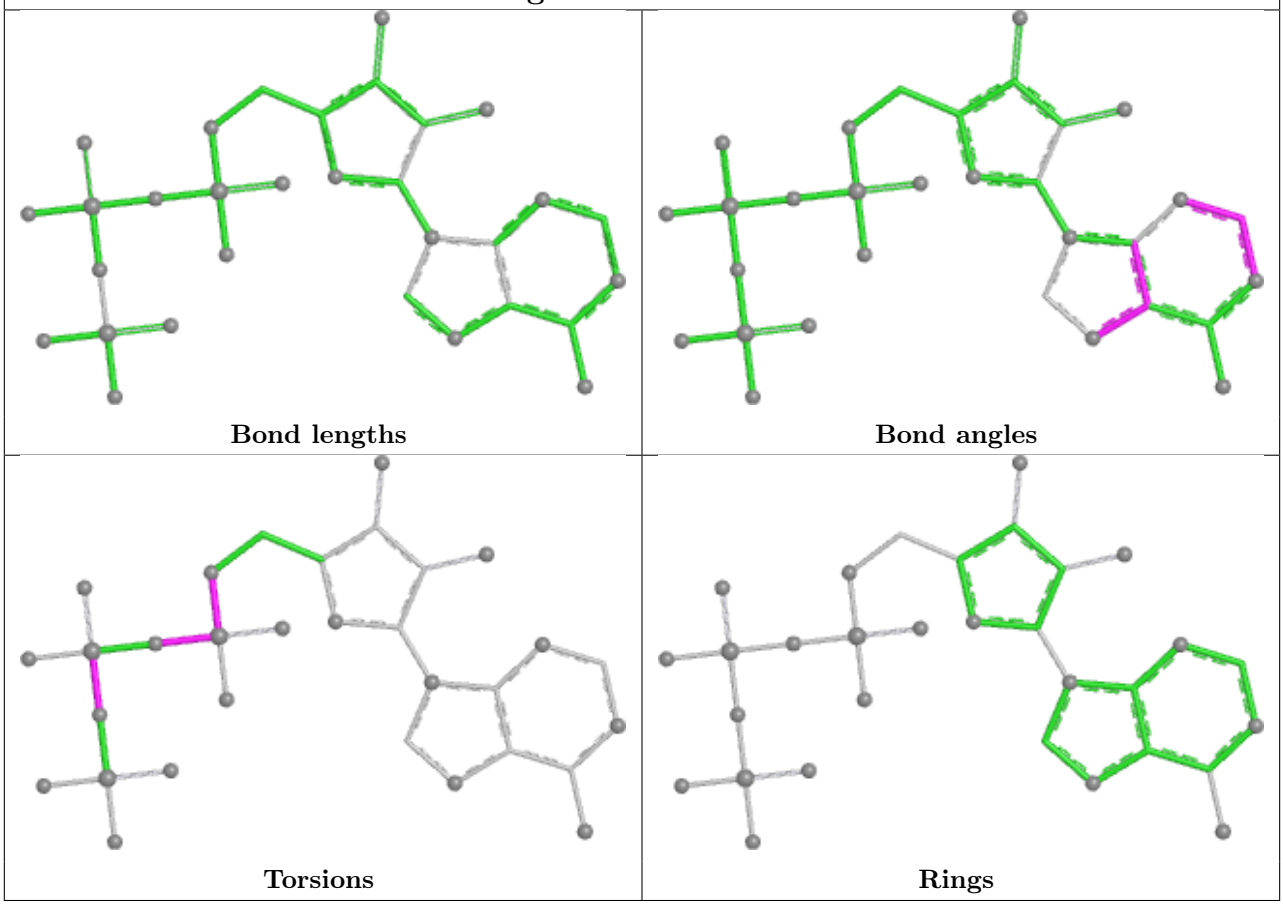
Ligand ATP A 501



Ligand ATP F 501



Ligand ATP E 401



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	f	4
16	P	1
15	O	1
8	H	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	f	110:ALA	C	111:LEU	N	9.37
1	f	79:ASN	C	80:TYR	N	8.13

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	f	348:ASP	C	349:SER	N	6.07
1	P	81:GLN	C	82:ILE	N	4.19
1	O	74:PRO	C	75:ARG	N	3.14

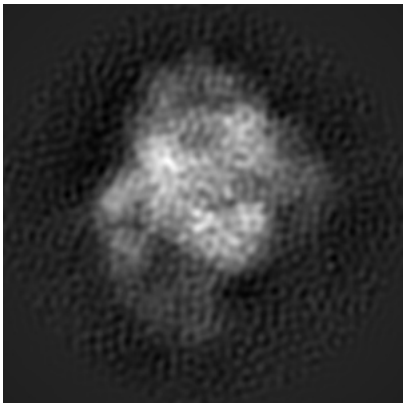
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8336. These allow visual inspection of the internal detail of the map and identification of artifacts.

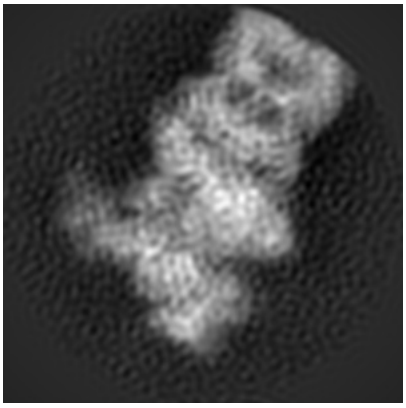
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

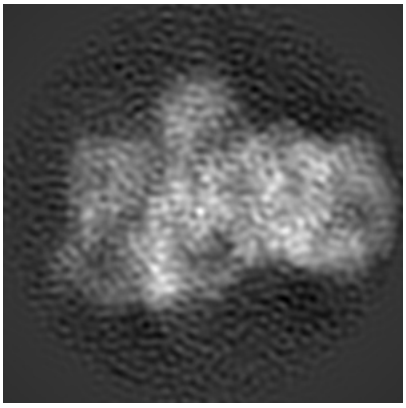
6.1.1 Primary map



X



Y

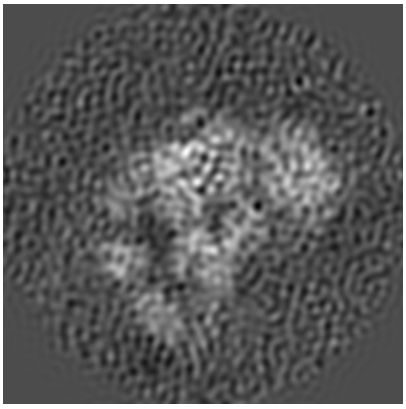


Z

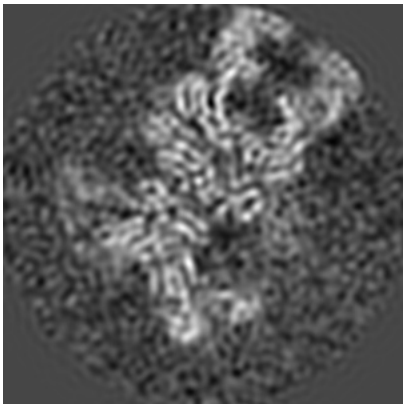
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

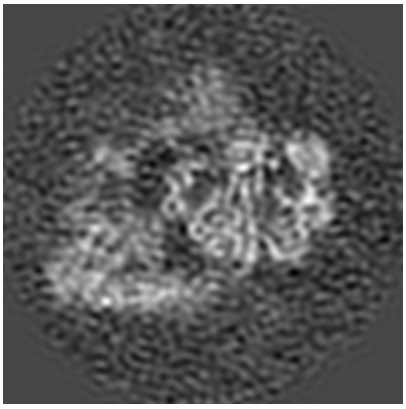
6.2.1 Primary map



X Index: 180



Y Index: 180

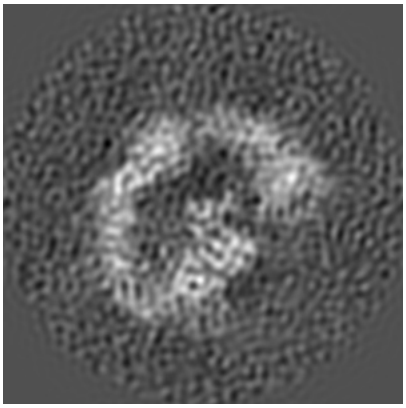


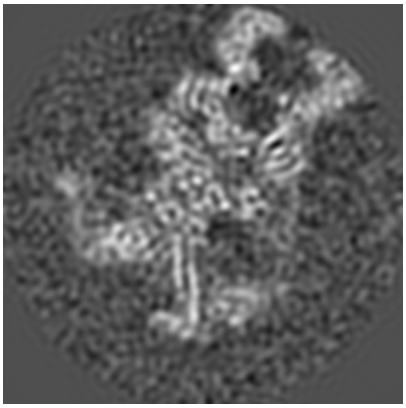
Z Index: 180

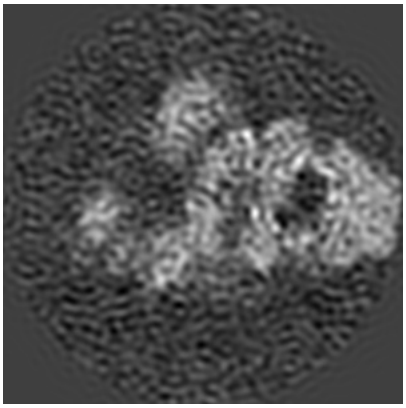
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 150

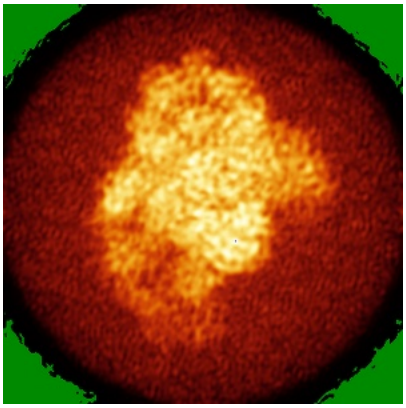

Y Index: 174

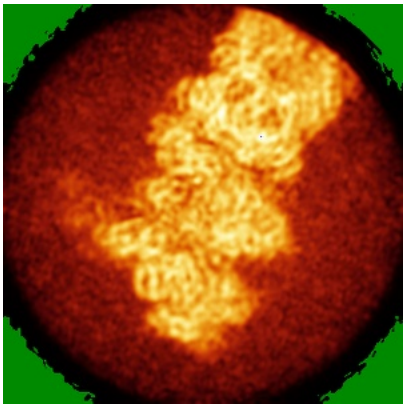

Z Index: 216

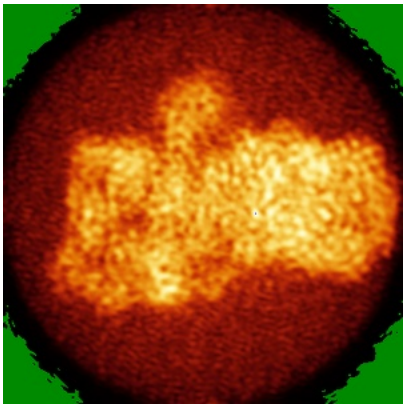
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map


X

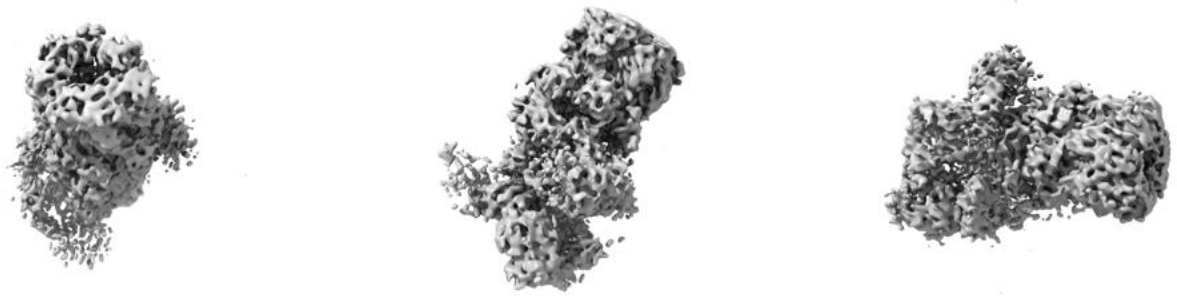

Y


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

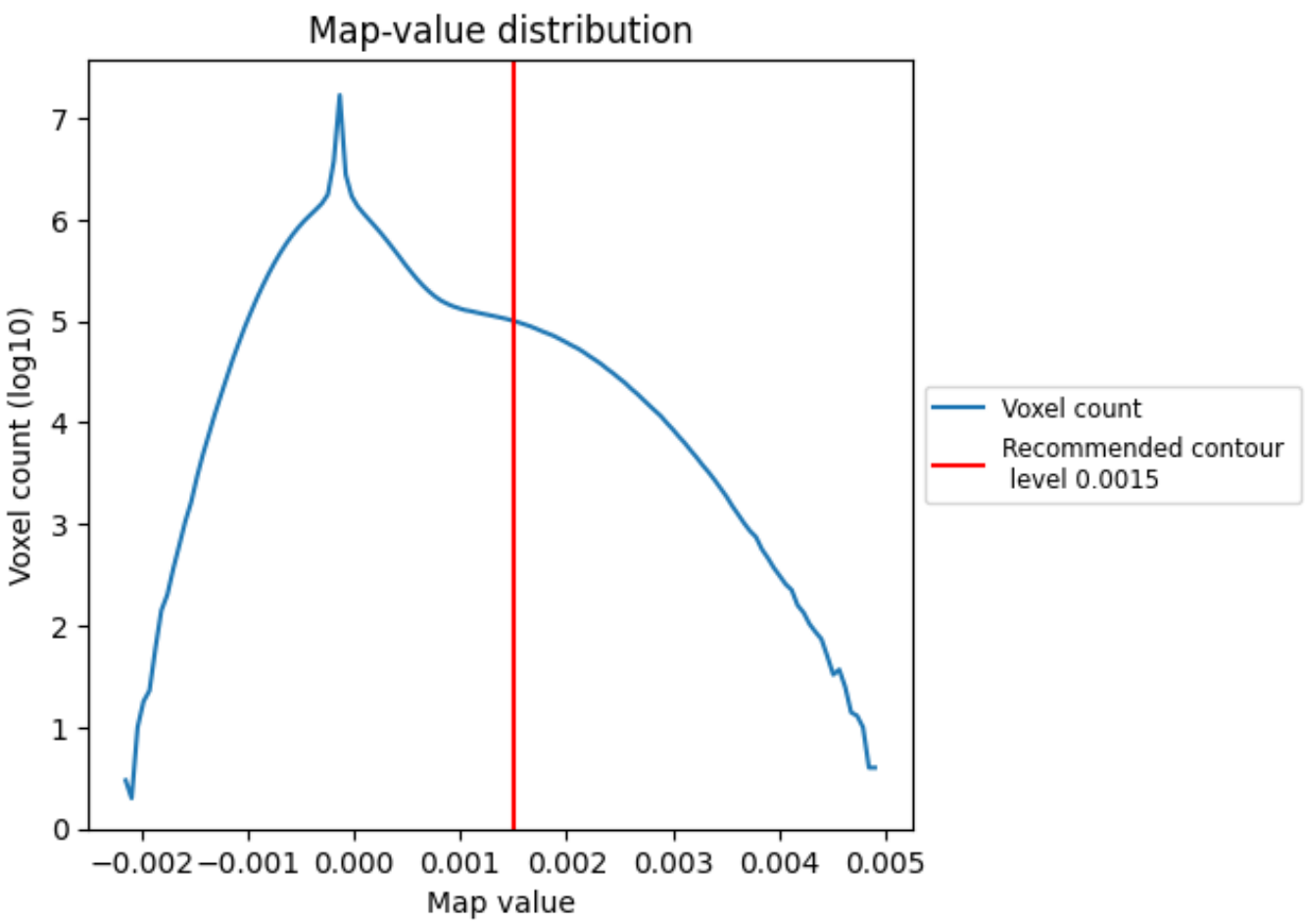
6.6 Mask visualisation (i)

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

7 Map analysis (i)

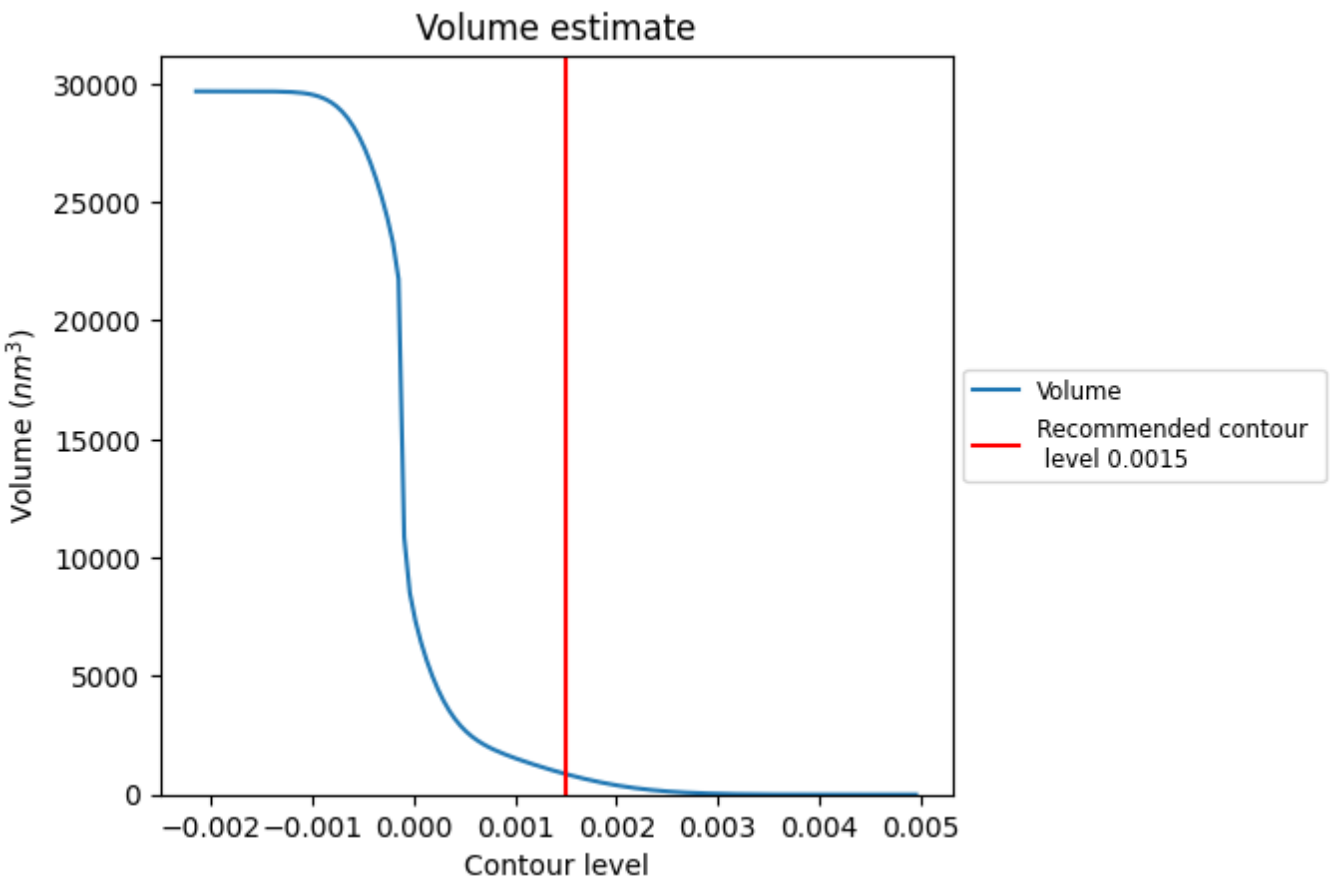
This section contains the results of statistical analysis of the map.

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.

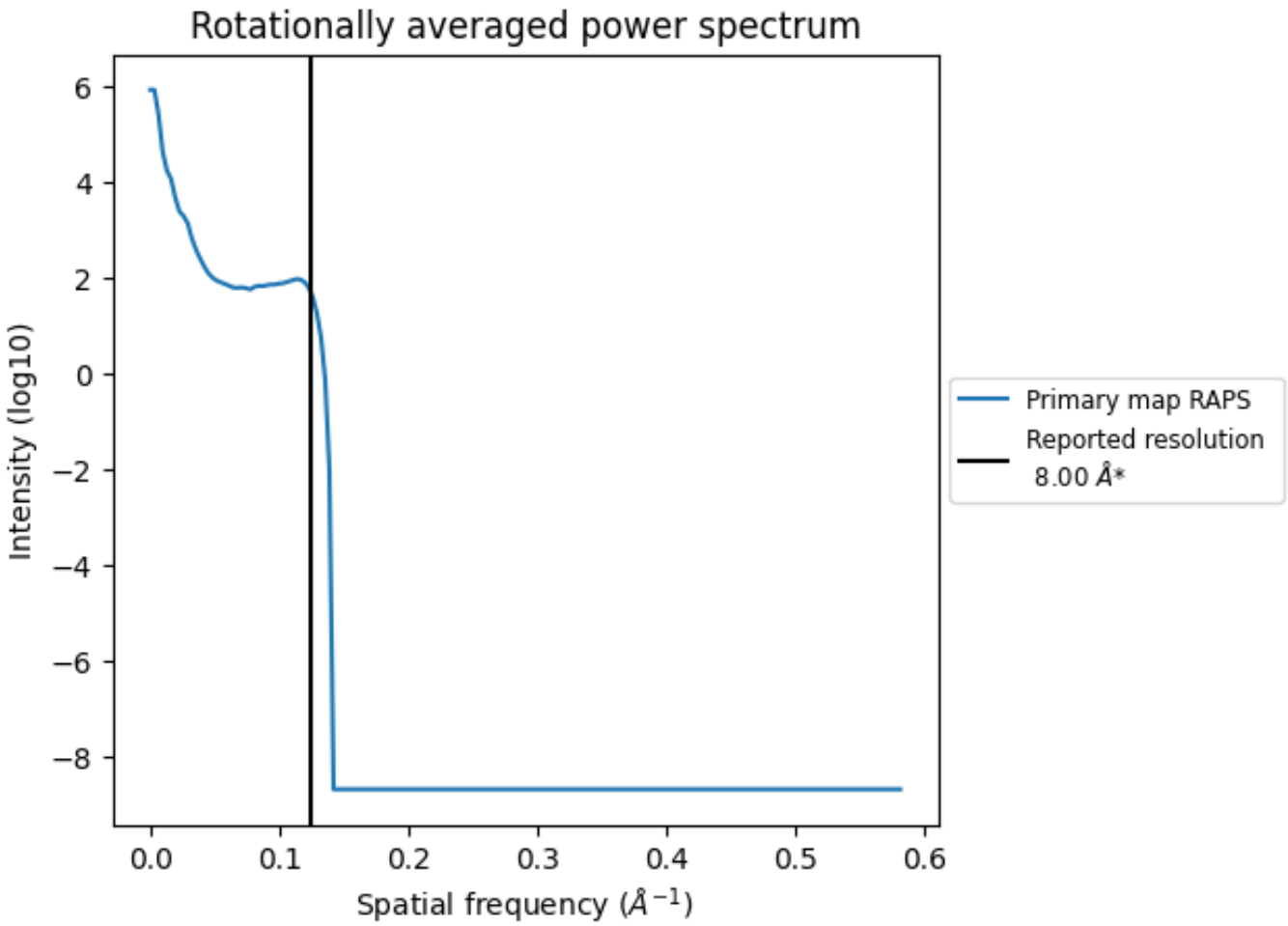
7.2 Volume estimate (i)



The volume at the recommended contour level is 868 nm^3; this corresponds to an approximate mass of 784 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 (i)



*Reported resolution corresponds to spatial frequency of 0.125 Å^{-1}

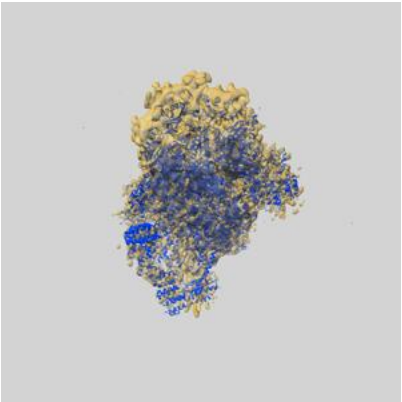
8 Fourier-Shell correlation (i)

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

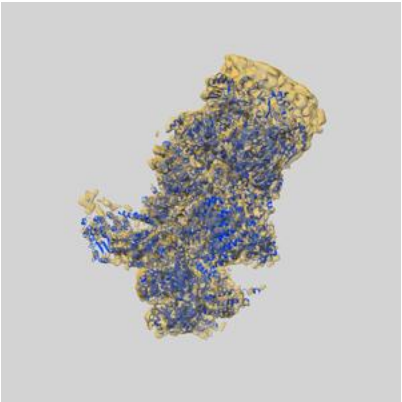
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8336 and PDB model 5T0I. Per-residue inclusion information can be found in section 3 on page 10.

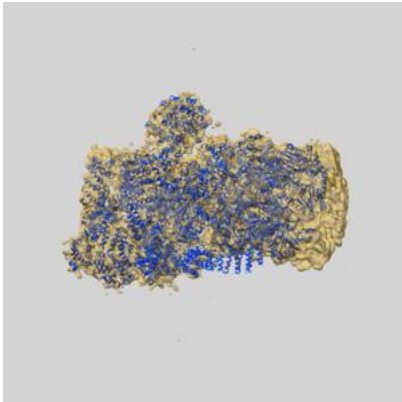
9.1 Map-model overlay (i)



X



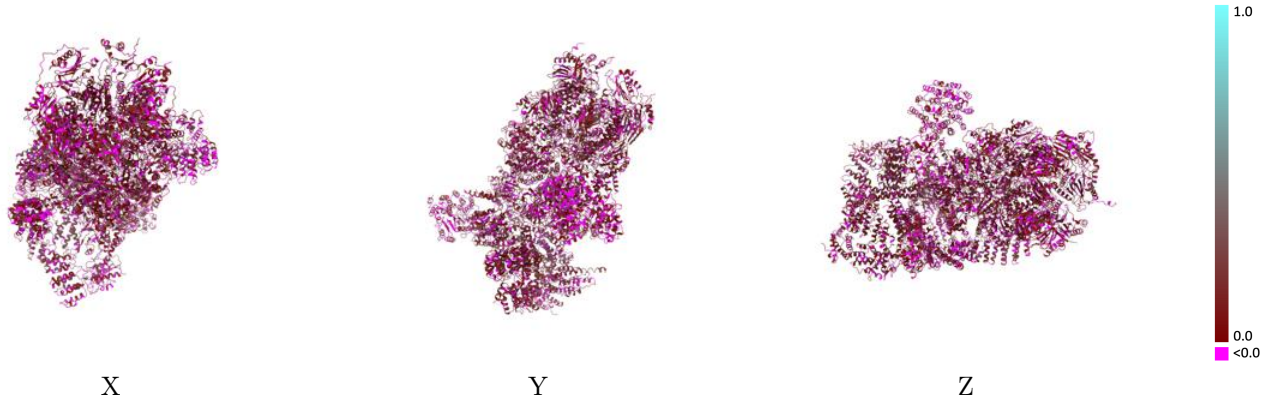
Y



Z

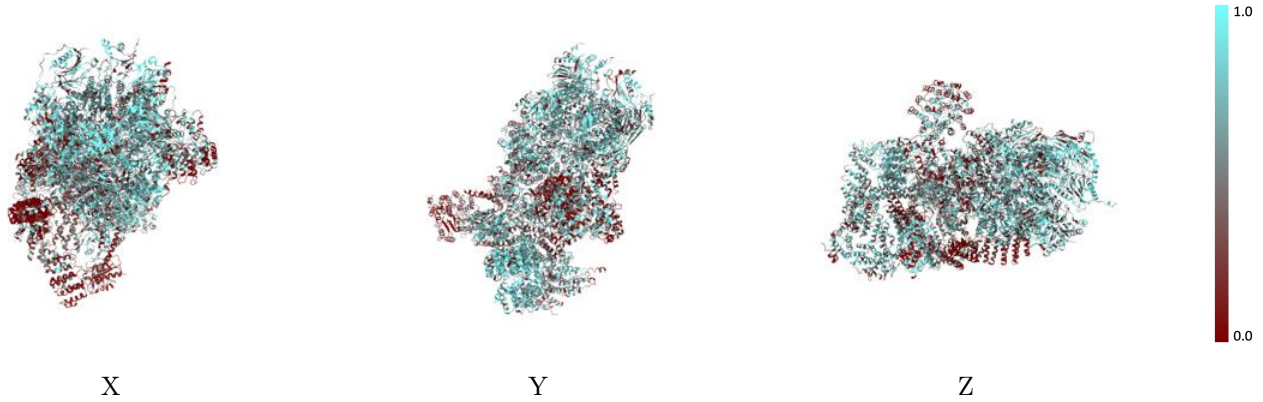
The images above show the 3D surface view of the map at the recommended contour level 0.0015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



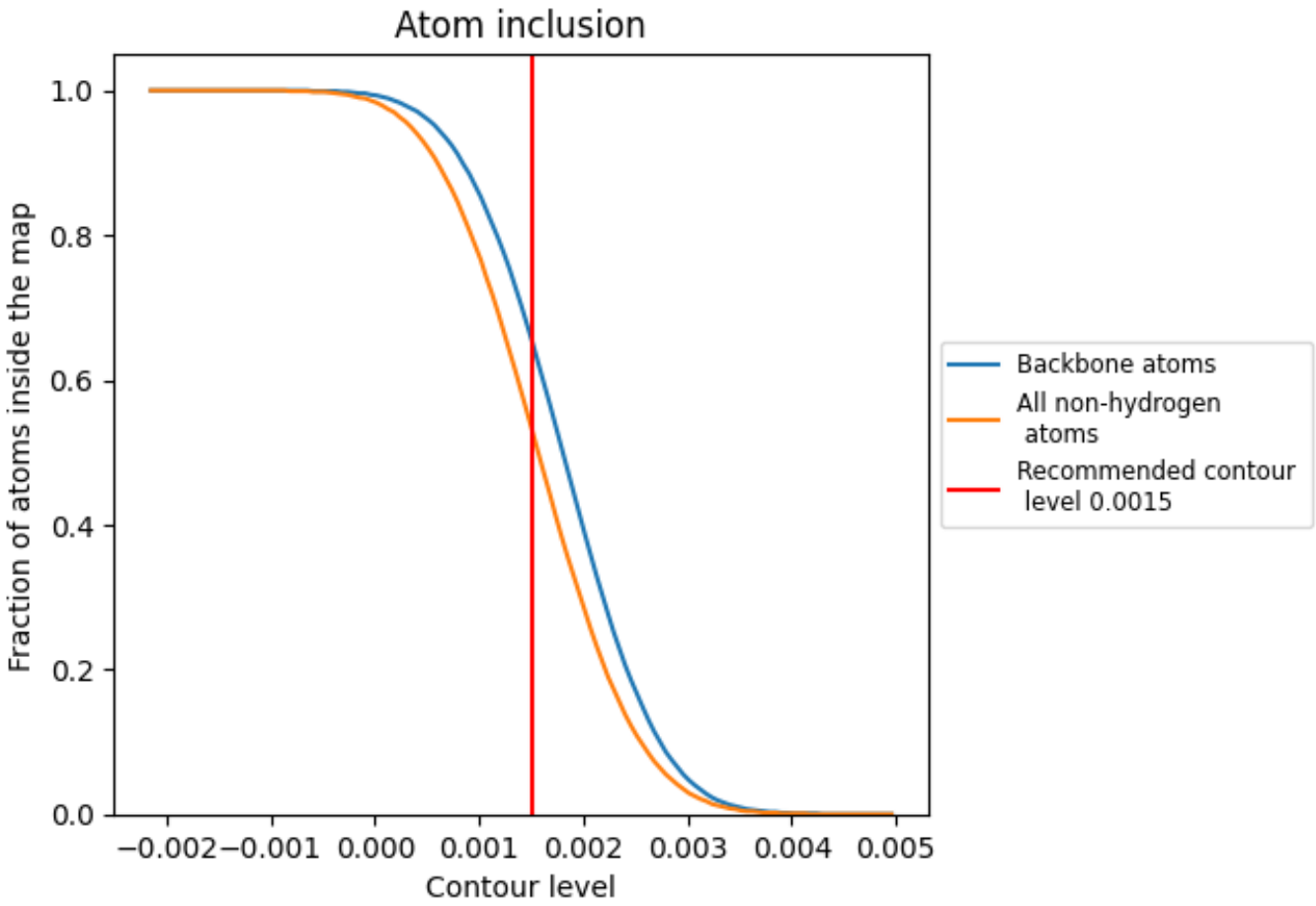
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0015).

9.4 Atom inclusion (i)



At the recommended contour level, 66% of all backbone atoms, 54% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5360	0.0930
A	0.5950	0.1120
B	0.4740	0.1100
C	0.5090	0.1010
D	0.5380	0.1100
E	0.5180	0.1120
F	0.5610	0.1080
G	0.6320	0.1080
H	0.6790	0.1010
I	0.6170	0.1140
J	0.5880	0.1120
K	0.6520	0.0980
L	0.7030	0.1200
M	0.5990	0.1010
N	0.5820	0.0900
O	0.6750	0.1000
P	0.6570	0.0950
Q	0.5970	0.0910
R	0.6080	0.0760
S	0.6940	0.1000
T	0.7150	0.1020
U	0.7090	0.1140
V	0.5630	0.1080
W	0.2230	0.0720
X	0.2170	0.0470
Y	0.6030	0.0880
Z	0.5070	0.0810
a	0.2840	0.0690
b	0.1120	0.0440
c	0.5220	0.1080
d	0.5140	0.0820
e	0.6000	0.0890
f	0.4160	0.0390