



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 02:21 PM UTC

PDB ID : 7ZYJ / pdb_00007zyj
EMDB ID : EMD-15025
Title : Leishmania tarentolae proteasome 20S subunit in complex with compound 2
Authors : Srinivas, H.
Deposited on : 2022-05-24
Resolution : 2.70 Å(reported)

This is a Full wwPDB EM Validation 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:

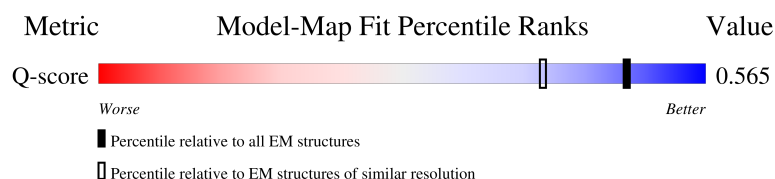
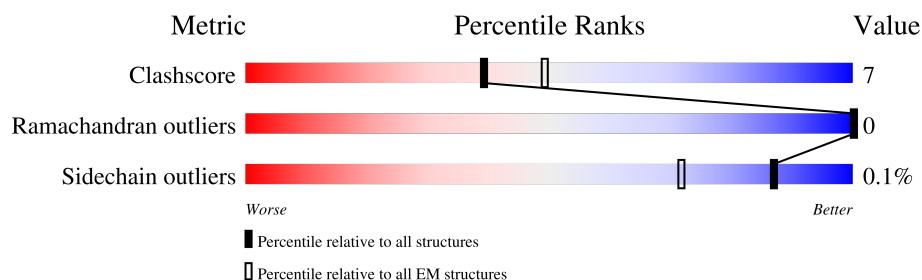
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10327 (2.20 - 3.20)

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

Mol	Chain	Length	Quality of chain
1	A	250	60% 85% 13% .
1	a	250	61% 85% 13% .
2	B	231	61% 88% 11% .
2	b	231	61% 87% 12% .

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Mol	Chain	Length	Quality of chain
3	C	285	
3	c	285	
4	D	248	
4	d	248	
5	E	344	
5	e	344	
6	F	428	
6	f	428	
7	G	238	
7	g	238	
8	H	229	
8	h	229	
9	I	225	
9	i	225	
10	J	205	
10	j	205	
11	K	206	
11	k	206	
12	L	203	
12	l	203	
13	M	339	
13	m	339	
14	N	219	
14	n	219	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 49234 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 Proteasome subunit alpha type.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	245	Total	C	N	O	S	0	0
			1861	1171	324	354	12		
1	a	245	Total	C	N	O	S	0	0
			1861	1171	324	354	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	229	Total	C	N	O	S	0	0
			1753	1112	292	341	8		
2	b	229	Total	C	N	O	S	0	0
			1753	1112	292	341	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	272	Total	C	N	O	S	0	0
			2155	1357	371	415	12		
3	c	272	Total	C	N	O	S	0	0
			2155	1357	371	415	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	240	Total	C	N	O	S	0	0
			1882	1186	324	364	8		
4	d	240	Total	C	N	O	S	0	0
			1882	1186	324	364	8		

- Molecule 5 is a protein called Proteasome alpha 5 subunit, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	235	Total	C	N	O	S	0	0
			1802	1119	315	356	12		
5	e	235	Total	C	N	O	S	0	0
			1802	1119	315	356	12		

- Molecule 6 is a protein called Proteasome alpha 1 subunit, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	238	Total	C	N	O	S	0	0
			1869	1173	325	359	12		
6	f	238	Total	C	N	O	S	0	0
			1869	1173	325	359	12		

- Molecule 7 is a protein called Proteasome alpha 7 subunit, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	230	Total	C	N	O	S	0	0
			1741	1085	308	338	10		
7	g	230	Total	C	N	O	S	0	0
			1741	1085	308	338	10		

- Molecule 8 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	229	Total	C	N	O	S	0	0
			1709	1062	295	340	12		
8	h	229	Total	C	N	O	S	0	0
			1709	1062	295	340	12		

- Molecule 9 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	219	Total	C	N	O	S	0	0
			1659	1037	292	318	12		
9	i	219	Total	C	N	O	S	0	0
			1659	1037	292	318	12		

- Molecule 10 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	204	Total	C	N	O	S	0	0
			1557	980	259	302	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	204	Total	C	N	O	S	0	0
			1557	980	259	302	16		

- Molecule 11 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	206	Total	C	N	O	S	0	0
			1612	1012	280	304	16		
11	k	206	Total	C	N	O	S	0	0
			1612	1012	280	304	16		

- Molecule 12 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	202	Total	C	N	O	S	0	0
			1577	997	277	296	7		
12	l	202	Total	C	N	O	S	0	0
			1577	997	277	296	7		

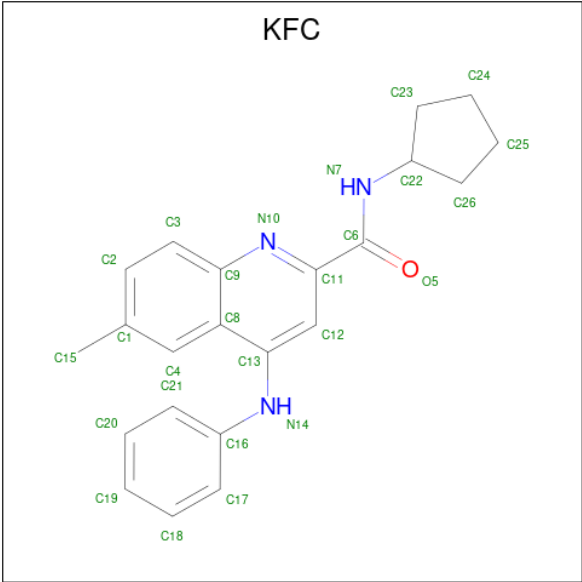
- Molecule 13 is a protein called Proteasome beta 6 subunit, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	214	Total	C	N	O	S	0	0
			1702	1079	287	324	12		
13	m	214	Total	C	N	O	S	0	0
			1702	1079	287	324	12		

- Molecule 14 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	218	Total	C	N	O	S	0	0
			1712	1083	292	323	14		
14	n	218	Total	C	N	O	S	0	0
			1712	1083	292	323	14		

- Molecule 15 is {N}-cyclopentyl-6-methyl-4-phenylazanyl-quinoline-2-carboxamide (CCD ID: KFC) (formula: C₂₂H₂₃N₃O) (labeled as "Ligand of Interest" by depositor).

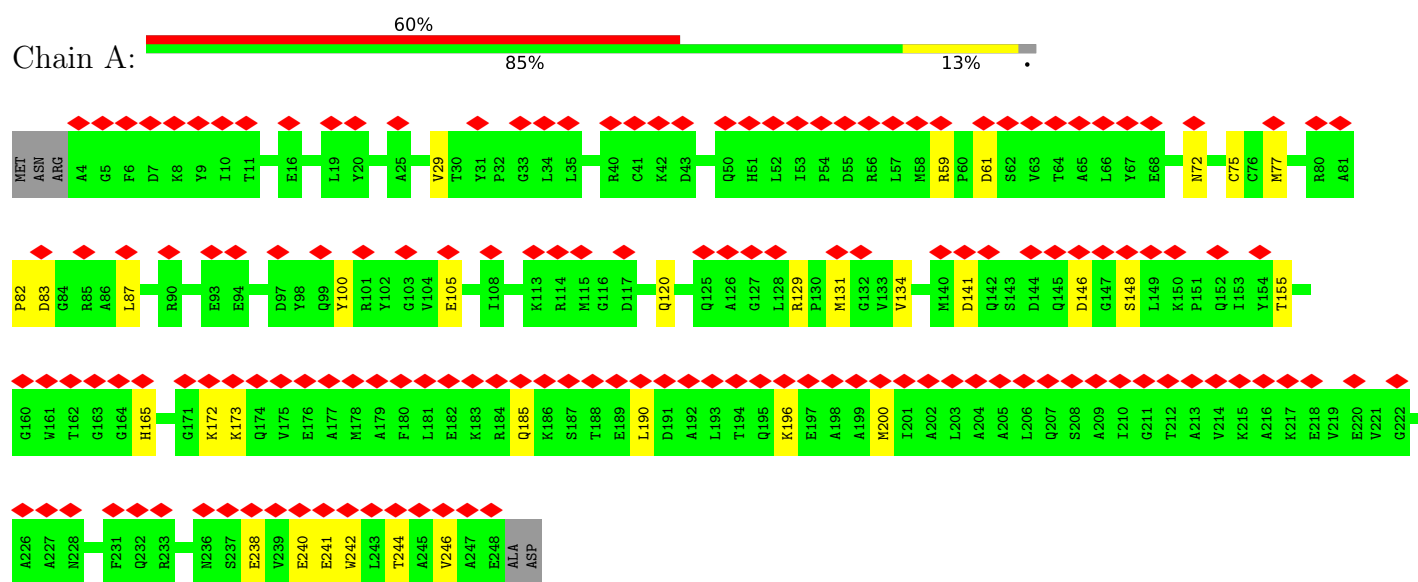


Mol	Chain	Residues	Atoms				AltConf
15	L	1	Total	C	N	O	0
			26	22	3	1	
15	1	1	Total	C	N	O	0
			26	22	3	1	

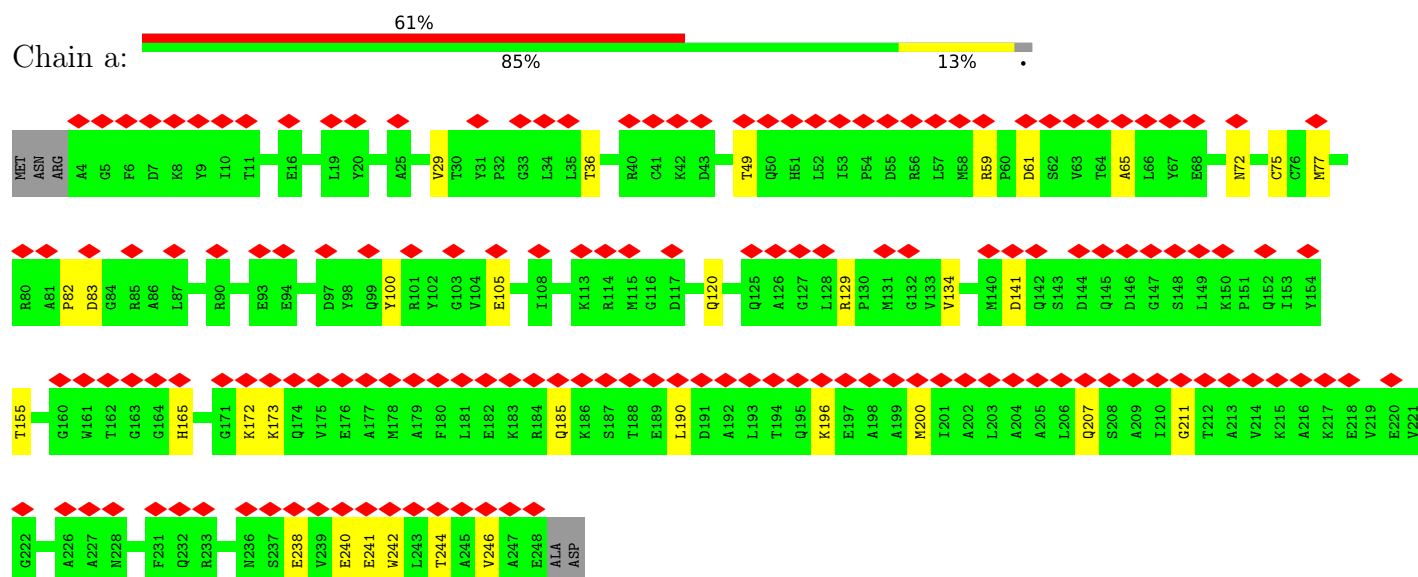
3 Residue-property plots

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.

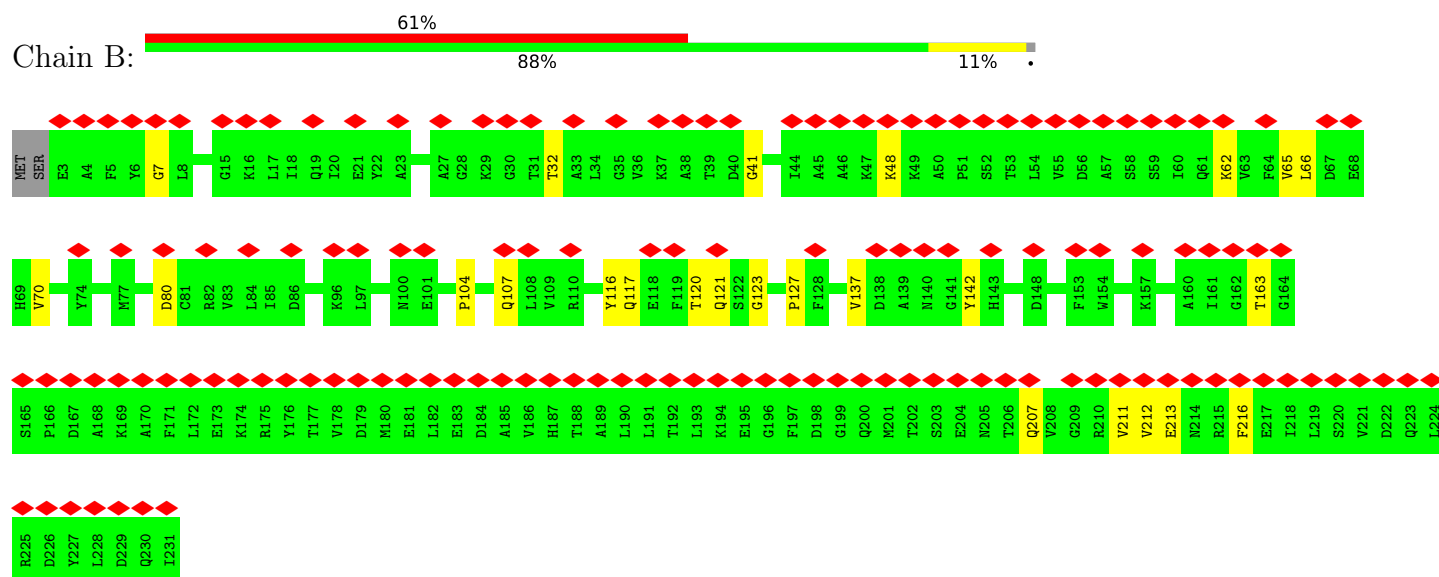
• Molecule 1: Proteasome subunit alpha type



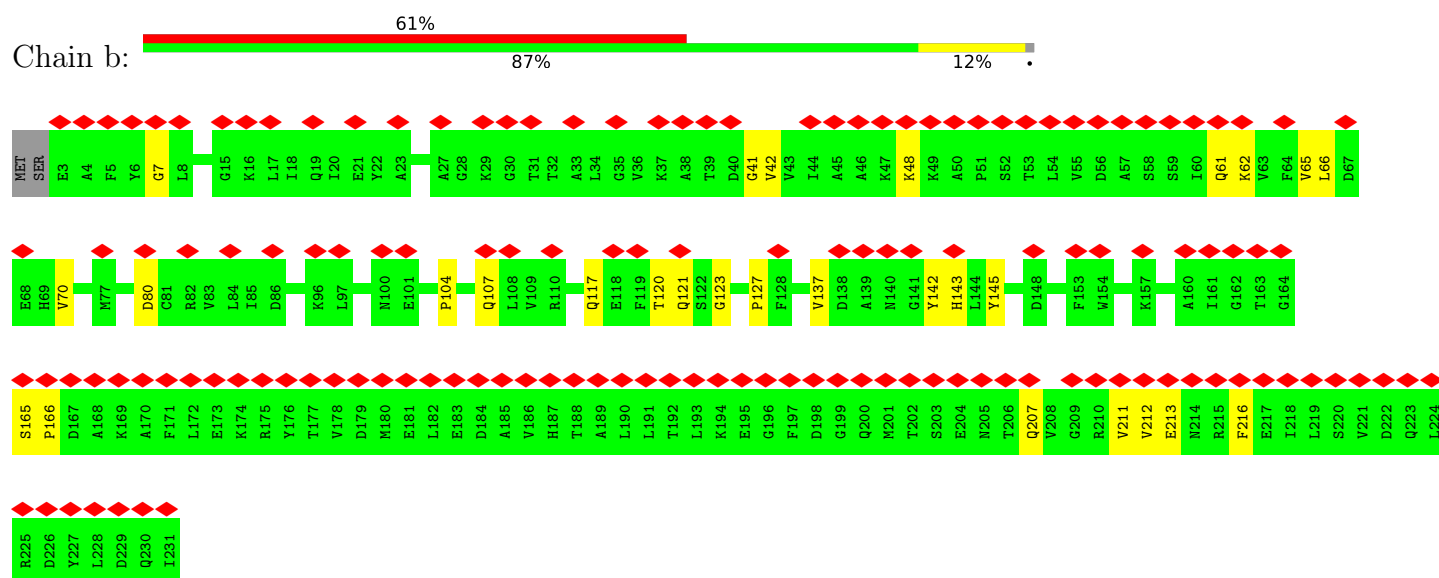
• Molecule 1: Proteasome subunit alpha type



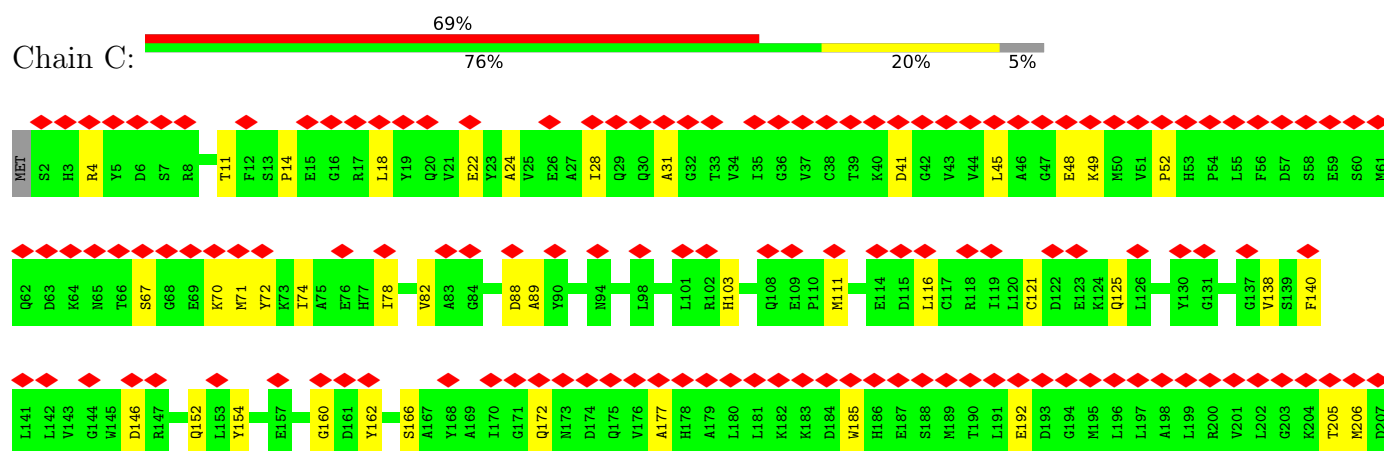
• Molecule 2: Proteasome subunit alpha type



• Molecule 2: Proteasome subunit alpha type

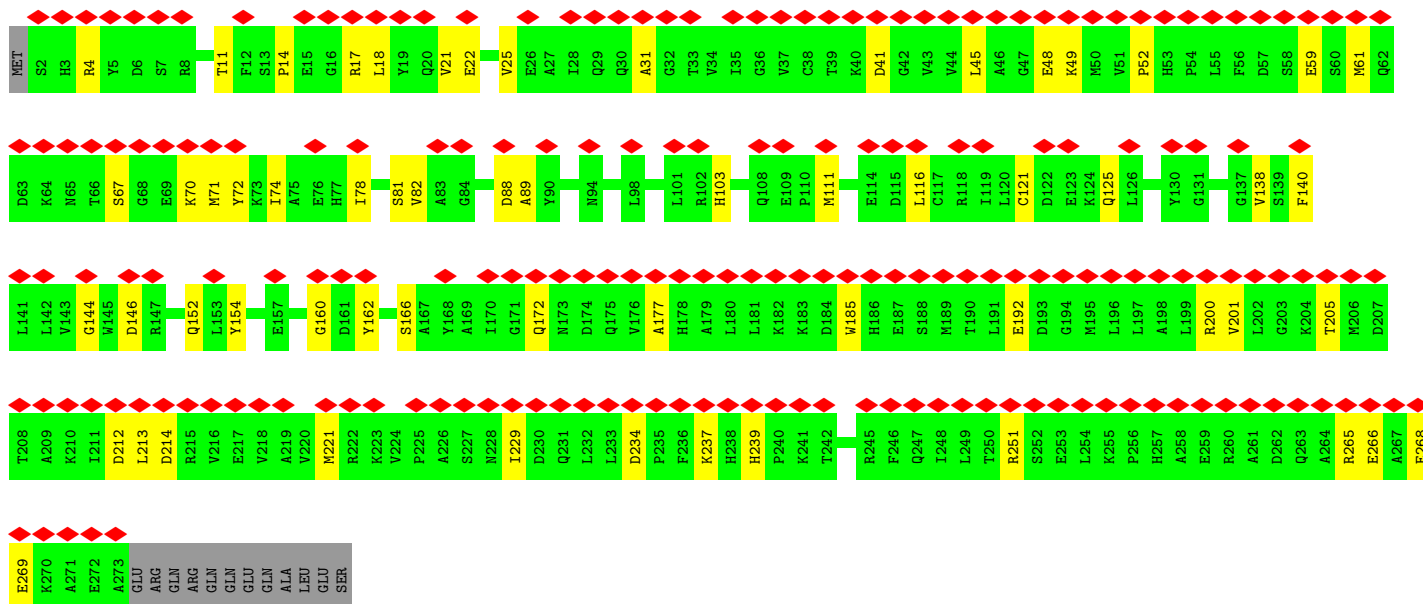
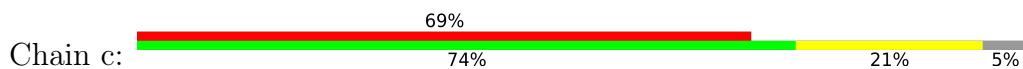


• Molecule 3: Proteasome subunit alpha type

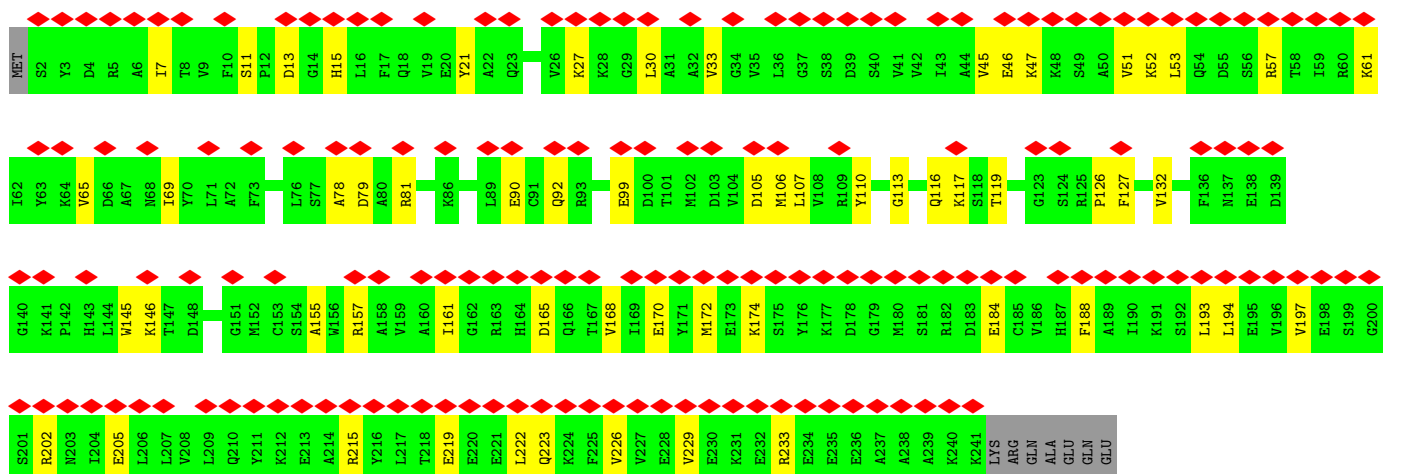
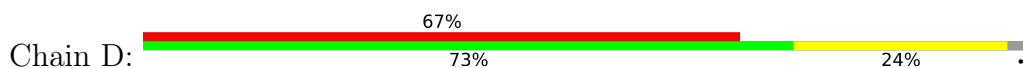




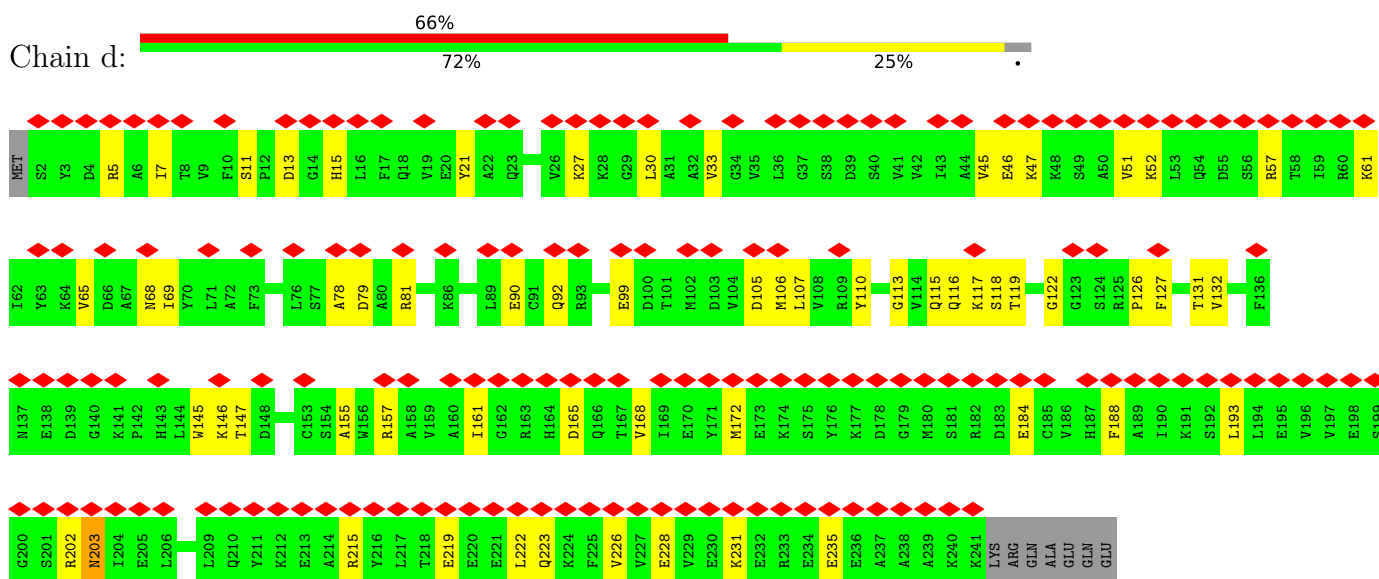
• Molecule 3: Proteasome subunit alpha type



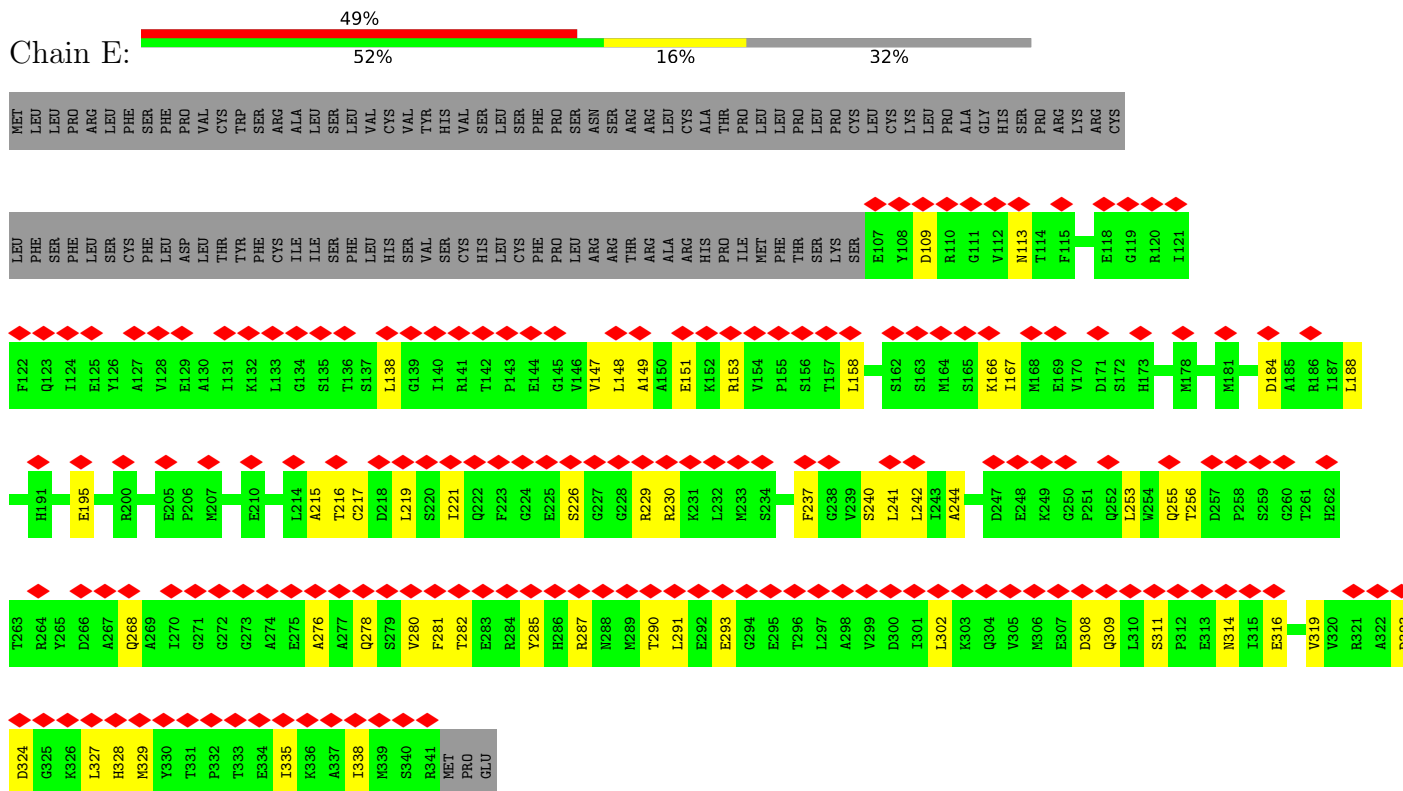
• Molecule 4: Proteasome subunit alpha type



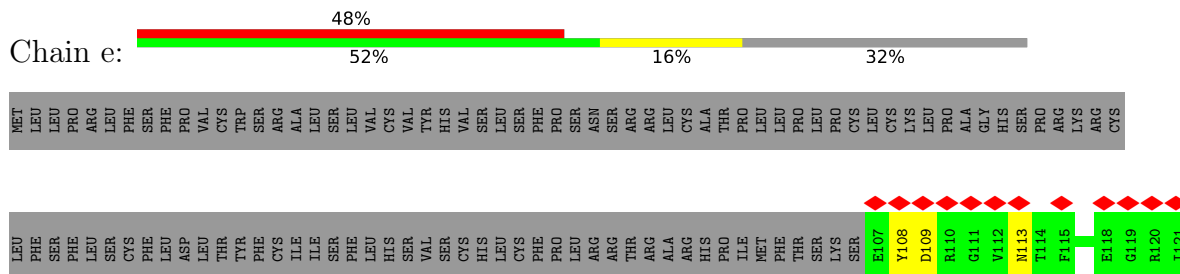
• Molecule 4: Proteasome subunit alpha type

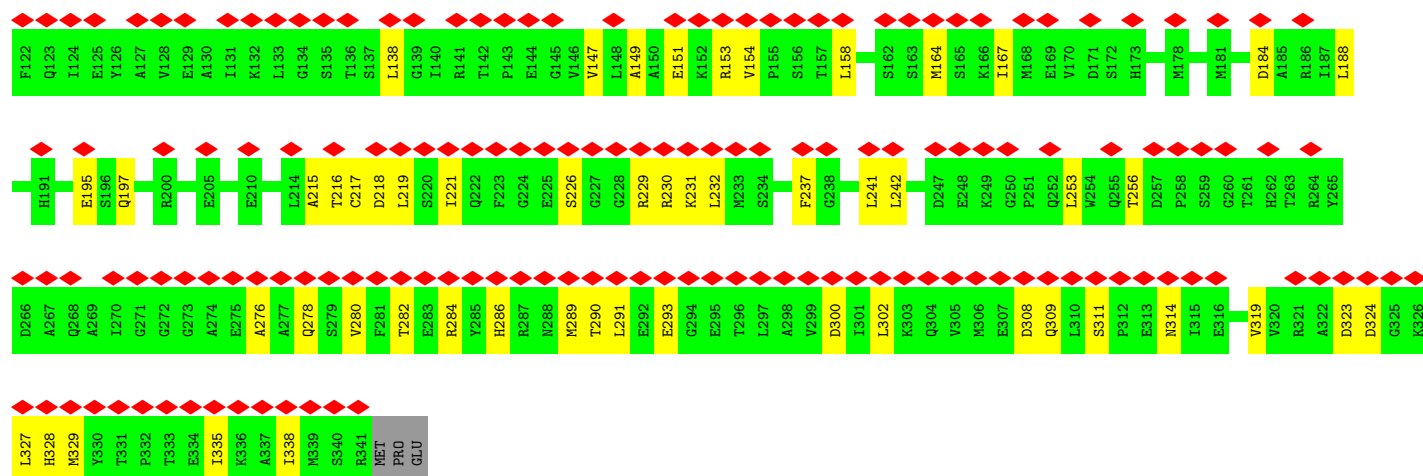


- Molecule 5: Proteasome alpha 5 subunit, putative

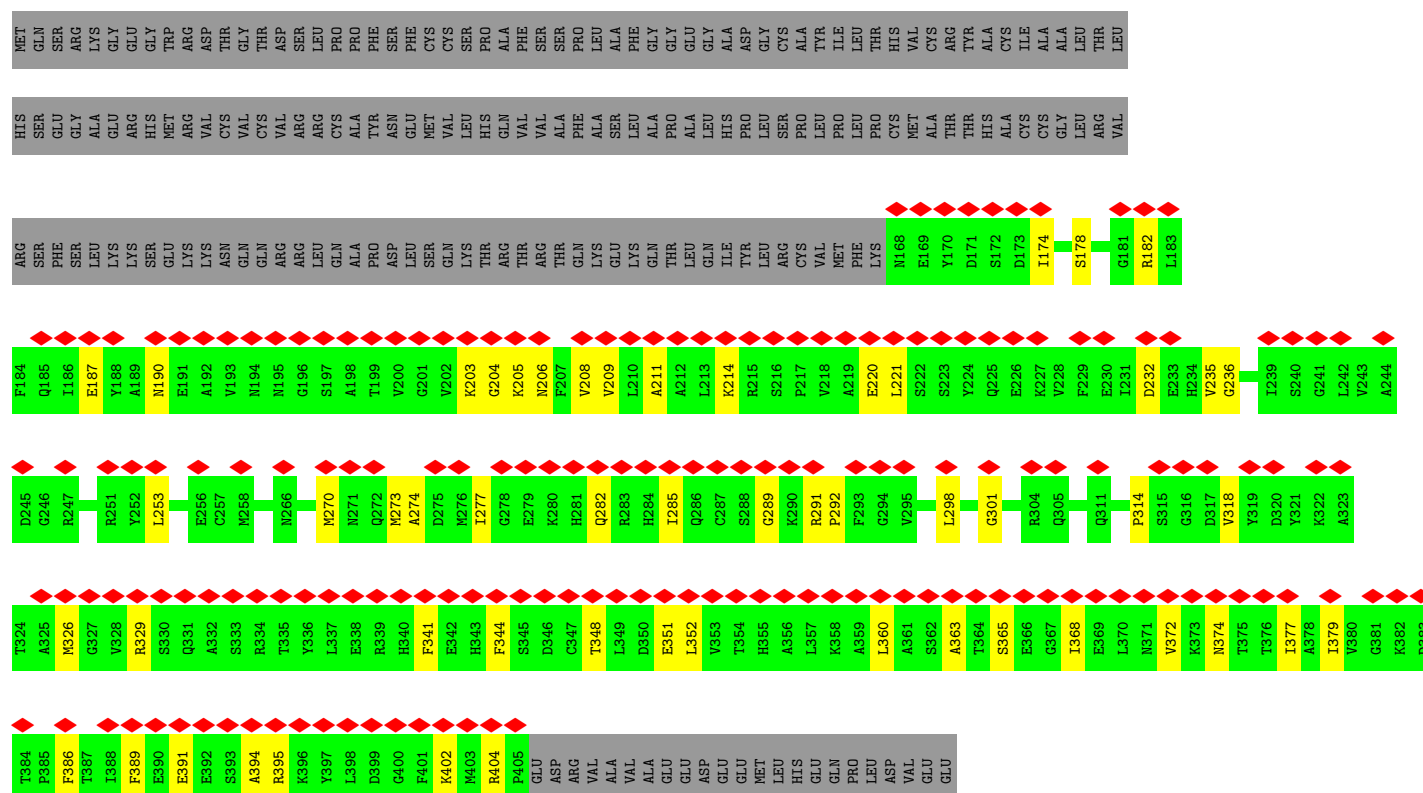


- Molecule 5: Proteasome alpha 5 subunit, putative

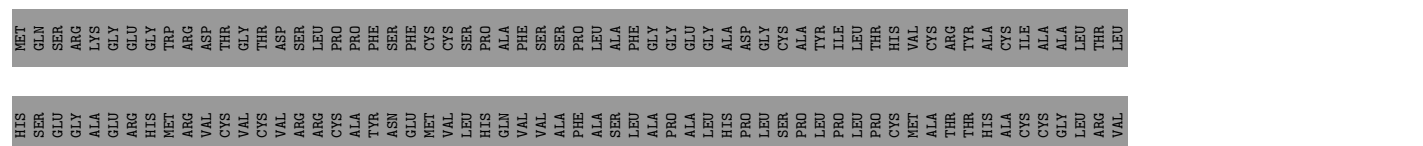
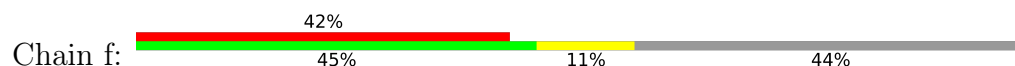


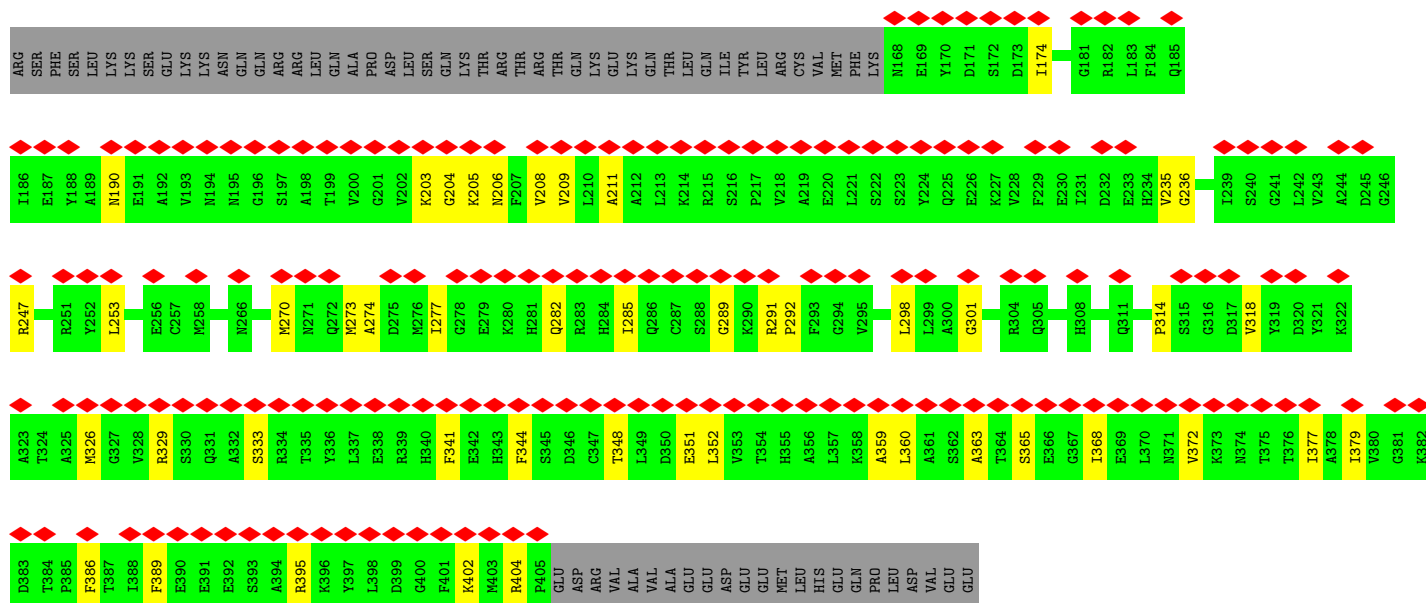


• Molecule 6: Proteasome alpha 1 subunit, putative

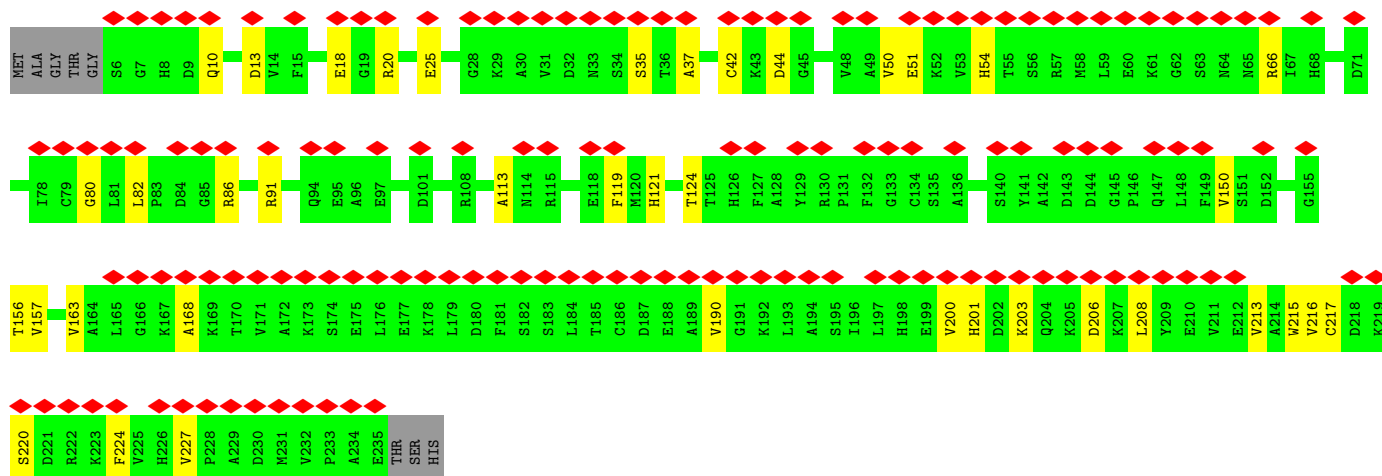
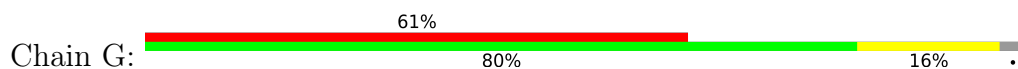


• Molecule 6: Proteasome alpha 1 subunit, putative

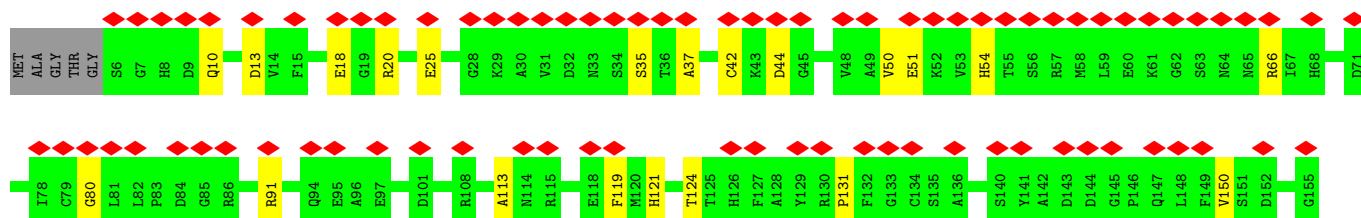
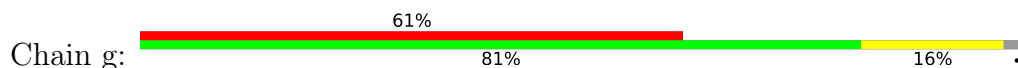


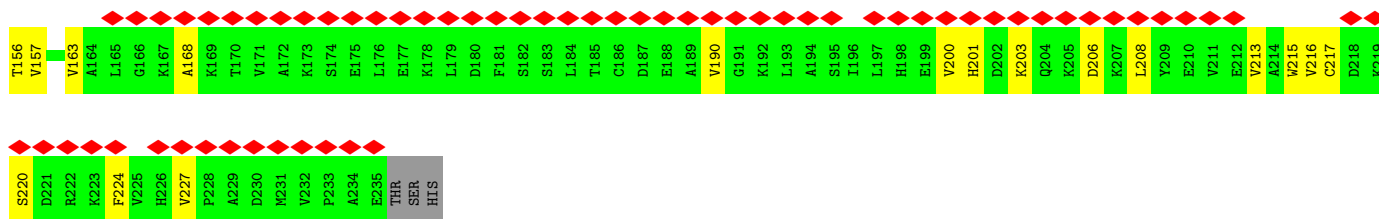


- Molecule 7: Proteasome alpha 7 subunit, putative

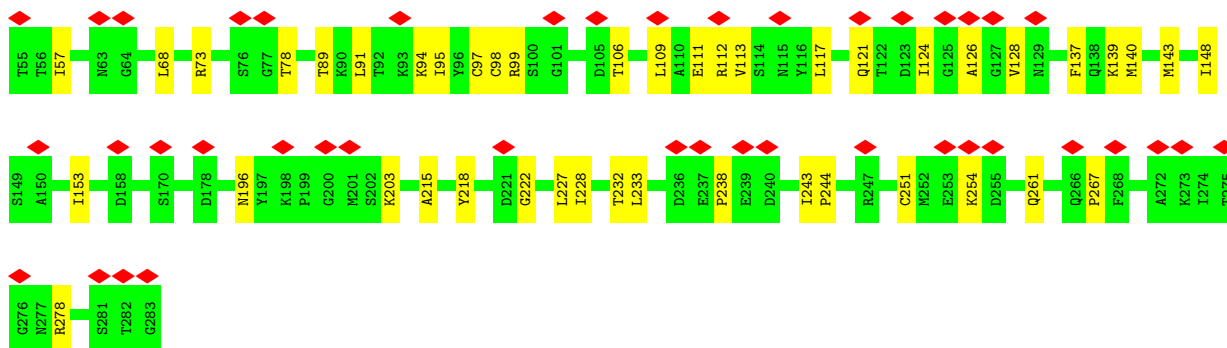
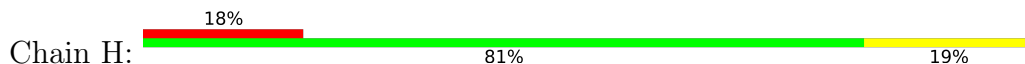


- Molecule 7: Proteasome alpha 7 subunit, putative

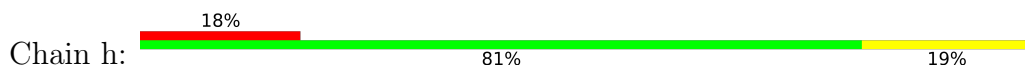




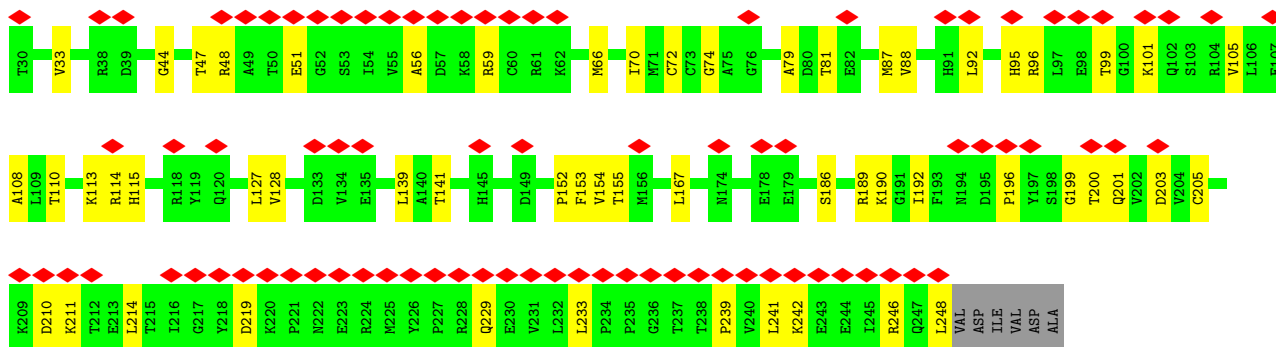
• Molecule 8: Proteasome subunit beta



• Molecule 8: Proteasome subunit beta

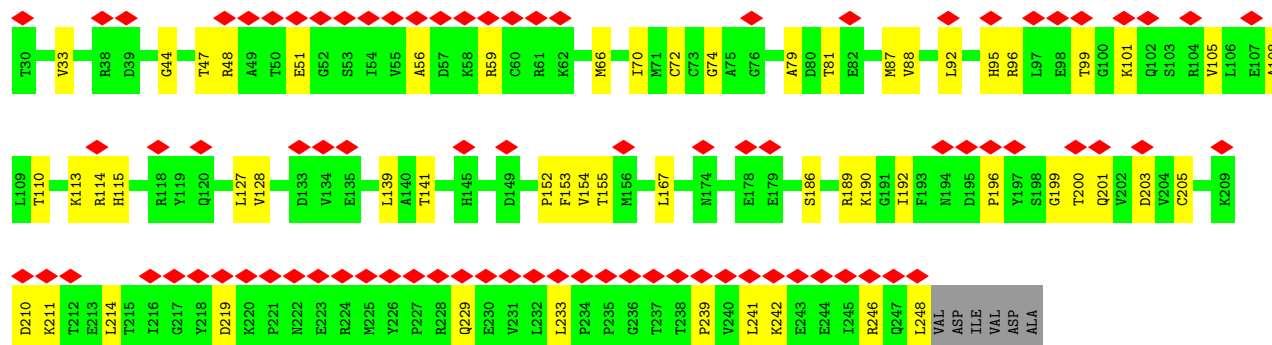


• Molecule 9: Proteasome subunit beta



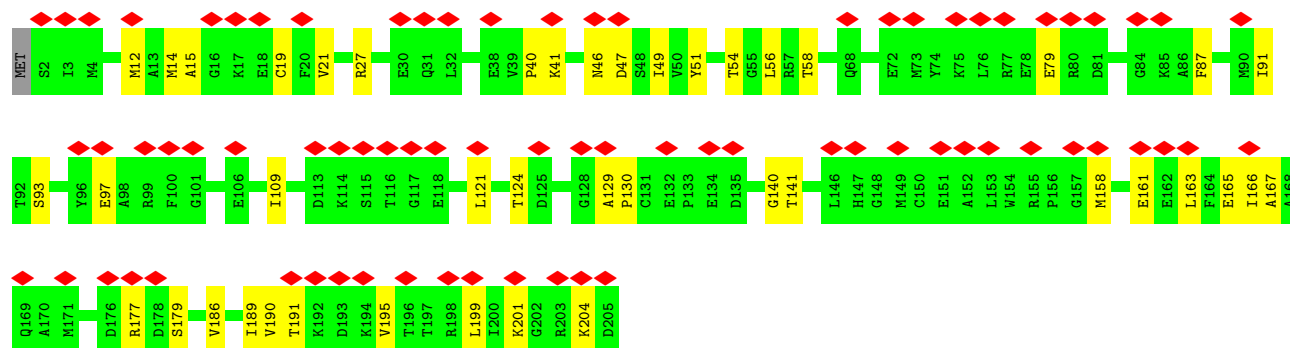
- Molecule 9: Proteasome subunit beta

Chain i: 



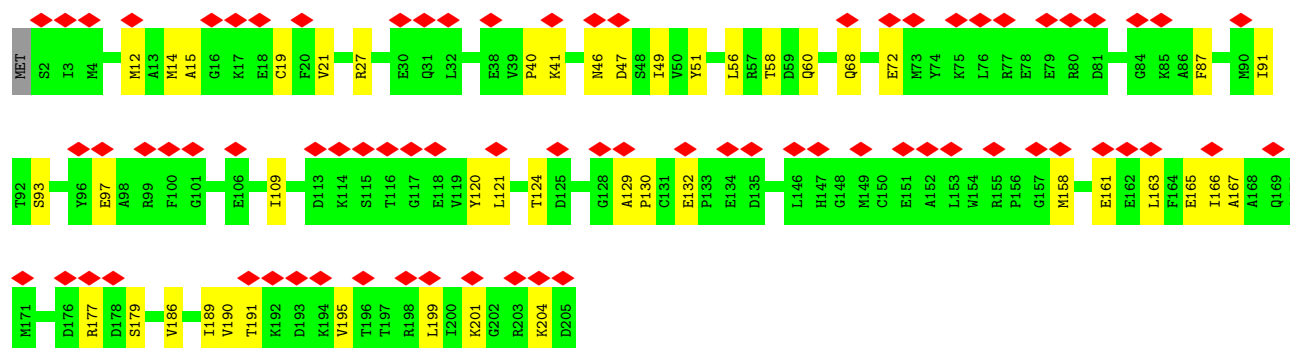
- Molecule 10: Proteasome subunit beta

Chain J: 



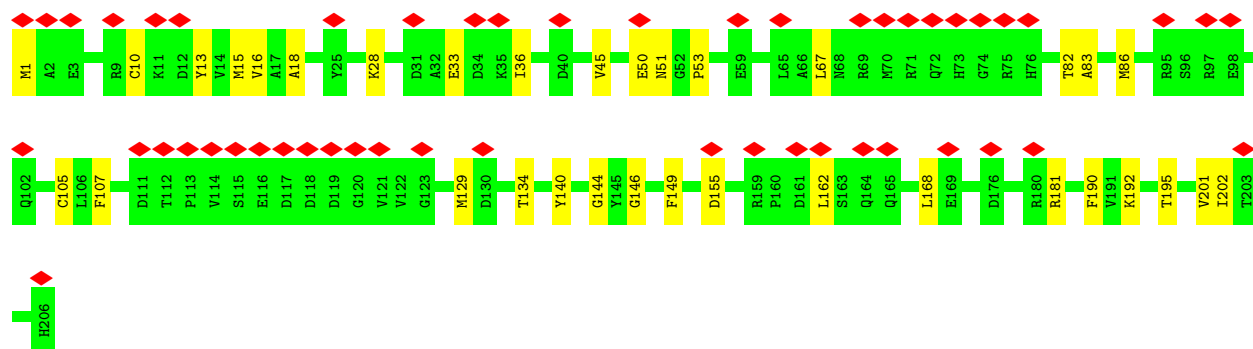
- Molecule 10: Proteasome subunit beta

Chain j: 

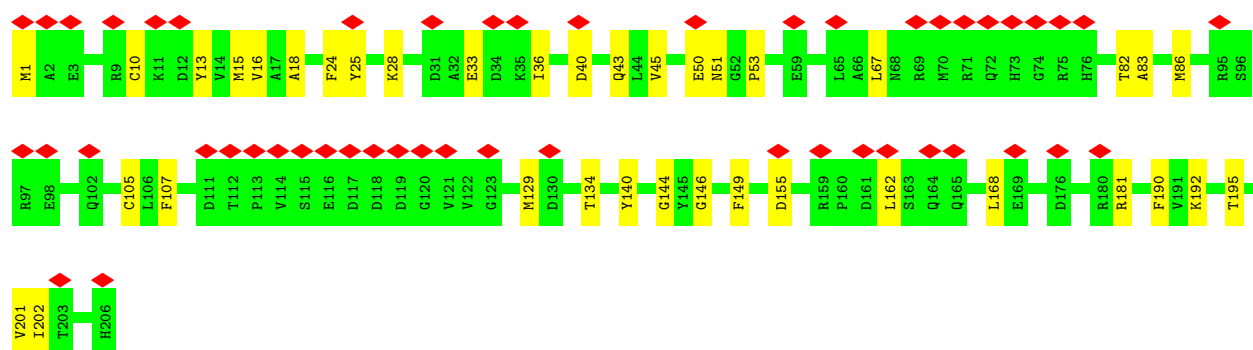
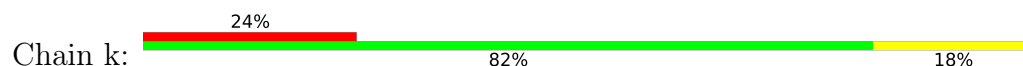


- Molecule 11: Proteasome subunit beta

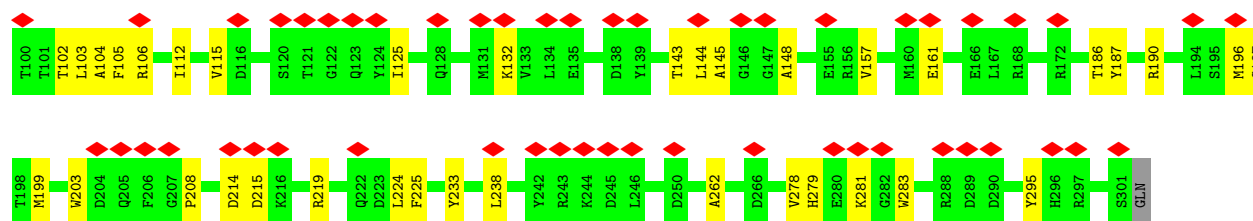
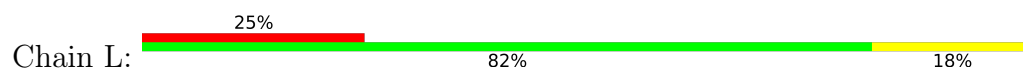
Chain K: 



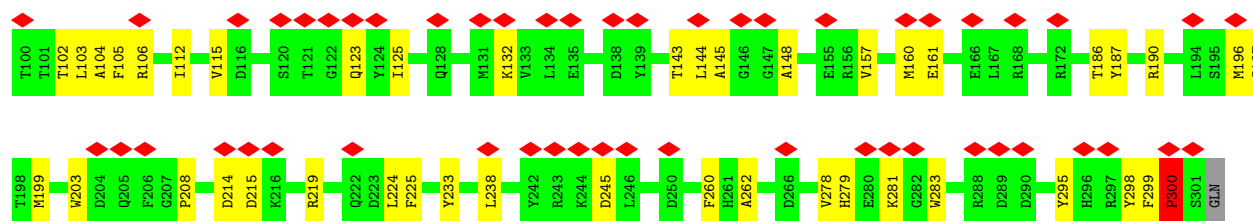
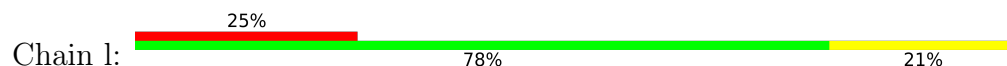
- Molecule 11: Proteasome subunit beta



- Molecule 12: Proteasome subunit beta



- Molecule 12: Proteasome subunit beta



- Molecule 13: Proteasome beta 6 subunit, putative

Chain M: 

MET ALA SER SER SER PRO PRO LEU LEU PHE HIS PRO PRO PHE SER SER PHE VAL VAL VAL VAL VAL ALA ALA HIS LEU SER PHE ARG VAL PHE CYS VAL GLY ALA GLN SER LEU CYS LYS CYS CYS SER CYS VAL ASN TYR PRO ALA CYS CYS LEU PRO LEU CYS PHE SER SER SER PRO VAL SER ALA GLU

ASP VAL ALA LEU LEU PHE HIS PRO LYS VAL SER THR HIS ARG PRO THR ALA ARG TYR SER PRO ILE SER LEU SER LEU LEU LEU LEU LEU ASP HIS ALA TYR PRO GLN LYS LEU ALA SER THR LEU PRO GLN GLY

ALA LYS GLN GLN W126 S127 P128 Y129 Q130 D131 N132 G133 G134 T135 G141 K142 D143 F144 Y145 D150 T151 R152 G155 G156 F157 C158 L159 R162 H163 D164 Q165 Y174 M182 D185 Q188 L189 M192 L193 K194 Y195 Y197 K198 K201 Y202 N203 Q204 G205 G206 K207 K212 K221 L222 Y223 H224 R225 K226 F227 F228 P229 Y230 T231 T232 F233 V237 D240 E241 E242 G243 H244 D251 A252 V253 G254 E257 P258 F259 L260 Y261 G262 T263 R264 G265 S266 A267 A268 S269 F270 V271 E272 P273 L274 L275 D276 C277 L278 I279 N280 R281 Q282 H283 M284 T285 S286 Q287 A288 P289 E291 M292 T293 K294 E295 E296 M300 L301 K302 N303 A304 F305 T306 G307 A308 A309 E310 R311 D312 I313 Y314 T315 G316 D317 S318 F321 F322 K326 D327 G328 V329 Q330 Q331 E332 S333 F334 E335 L336 R337 K338 D339

• Molecule 13: Proteasome beta 6 subunit, putative

Chain m: 

MET ALA SER SER SER PRO PRO LEU LEU PHE HIS PRO PRO PHE SER SER PHE VAL VAL VAL VAL VAL ALA ALA HIS LEU SER PHE ARG VAL PHE CYS VAL GLY ALA GLN SER LEU CYS LYS CYS CYS SER CYS VAL ASN TYR PRO ALA CYS CYS LEU PRO LEU CYS PHE SER SER SER PRO VAL SER ALA GLU

ASP VAL ALA LEU LEU PHE HIS PRO LYS VAL SER THR HIS ARG PRO THR ALA ARG TYR SER PRO ILE SER LEU SER LEU LEU LEU LEU ASP HIS ALA TYR PRO GLN LYS LEU ALA SER THR LEU PRO GLN GLY

ALA LYS GLN GLN W126 S127 P128 Y129 Q130 D131 N132 G133 G134 T135 G141 K142 D143 F144 Y145 D150 T151 R152 G155 G156 F157 C158 L159 R162 H163 D164 Q165 Y174 M182 D185 Q188 L189 M192 L193 K194 Y195 Y197 K198 K201 Y202 N203 Q204 G205 G206 K207 K212 K221 L222 Y223 H224 R225 K226 F227 F228 P229 Y230 T231 T232 F233 V237 D240 E241 E242 G243 H244 D251 A252 V253 G254 E257 P258 F259 L260 Y261 G262 T263 R264 G265 S266 A267 A268 S269 F270 V271 E272 P273 L274 L275 D276 C277 L278 I279 N280 R281 Q282 H283 M284 T285 S286 Q287 A288 P289 E291 M292 T293 K294 E295 E296 M300 L301 K302 N303 A304 F305 T306 G307 A308 A309 E310 R311 D312 I313 Y314 T315 G316 D317 S318 F321 F322 K326 D327 G328 V329 Q330 Q331 E332 S333 F334 E335 L336 R337 K338 D339

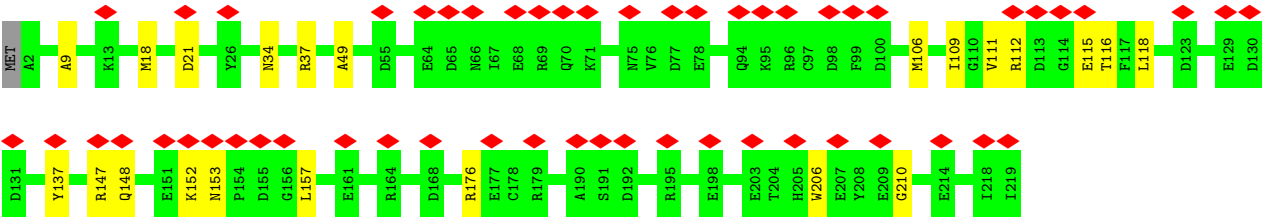
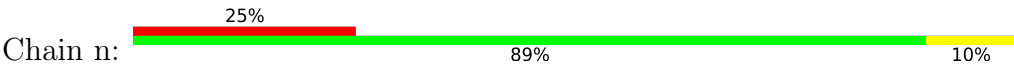
• Molecule 14: Proteasome subunit beta

Chain N: 

MET A2 A9 K13 M18 D21 Y26 N34 R37 A49 D55 E64 D65 N66 I67 E68 R69 Q70 K71 W75 V76 D77 E78 Q94 K95 R96 C97 F99 D100 M106 I109 V110 G111 R112 D113 G114 E115 T116 F117 L118 D123 E129 D130

D131 Y137 R147 Q148 E151 K152 M153 P154 D155 G156 L157 E161 R164 D168 E177 C178 R179 A190 S191 D192 R195 E198 E203 D204 H205 W206 Y208 G210 E214 I218 I219

• Molecule 14: Proteasome subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	260000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	20000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	9.886	Depositor
Minimum map value	-3.379	Depositor
Average map value	0.069	Depositor
Map value standard deviation	0.611	Depositor
Recommended contour level	4.8	Depositor
Map size ($\text{\AA}$)	258.0, 258.0, 258.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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: KFC

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	0.12	0/1893	0.33	0/2567
1	a	0.12	0/1893	0.35	0/2567
2	B	0.11	0/1786	0.36	0/2421
2	b	0.12	0/1786	0.37	0/2421
3	C	0.12	0/2202	0.32	0/2982
3	c	0.12	0/2202	0.33	0/2982
4	D	0.11	0/1911	0.33	0/2573
4	d	0.12	0/1911	0.34	0/2573
5	E	0.11	0/1831	0.31	0/2476
5	e	0.11	0/1831	0.30	0/2476
6	F	0.10	0/1907	0.30	0/2575
6	f	0.10	0/1907	0.30	0/2575
7	G	0.11	0/1773	0.31	0/2398
7	g	0.11	0/1773	0.31	0/2398
8	H	0.11	0/1741	0.31	0/2359
8	h	0.11	0/1741	0.31	0/2359
9	I	0.12	0/1685	0.33	0/2284
9	i	0.12	0/1685	0.33	0/2284
10	J	0.11	0/1583	0.33	0/2135
10	j	0.12	0/1583	0.33	0/2135
11	K	0.12	0/1643	0.34	0/2222
11	k	0.17	0/1643	0.38	0/2222
12	L	0.12	0/1611	0.30	0/2180
12	l	0.31	1/1611 (0.1%)	0.42	1/2180 (0.0%)
13	M	0.12	0/1743	0.32	0/2354
13	m	0.12	0/1743	0.32	0/2354
14	N	0.12	0/1748	0.31	0/2363
14	n	0.12	0/1748	0.31	0/2363
All	All	0.13	1/50114 (0.0%)	0.33	1/67778 (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
12	l	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	l	300	PRO	C-O	-10.43	1.13	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	l	300	PRO	O-C-N	-10.43	108.18	122.78

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	l	300	PRO	Mainchain

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	A	1861	0	1874	21	0
1	a	1861	0	1874	23	0
2	B	1753	0	1741	17	0
2	b	1753	0	1741	18	0
3	C	2155	0	2102	38	0
3	c	2155	0	2102	39	0
4	D	1882	0	1881	40	0
4	d	1882	0	1881	43	0
5	E	1802	0	1784	35	0
5	e	1802	0	1784	35	0
6	F	1869	0	1823	33	0
6	f	1869	0	1823	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1741	0	1702	27	0
7	g	1741	0	1702	28	0
8	H	1709	0	1665	30	0
8	h	1709	0	1665	28	0
9	I	1659	0	1684	43	0
9	i	1659	0	1684	40	0
10	J	1557	0	1552	29	0
10	j	1557	0	1552	29	0
11	K	1612	0	1571	23	0
11	k	1612	0	1571	25	0
12	L	1577	0	1534	22	0
12	l	1577	0	1534	29	0
13	M	1702	0	1638	21	0
13	m	1702	0	1638	20	0
14	N	1712	0	1668	15	0
14	n	1712	0	1668	17	0
15	L	26	0	0	0	0
15	l	26	0	0	0	0
All	All	49234	0	48438	698	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 7.

All (698) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:100:TYR:O	9:i:114:ARG:NH1	2.19	0.76
5:E:287:ARG:NH1	6:F:220:GLU:O	2.18	0.76
3:C:259:GLU:O	3:C:263:GLN:NE2	2.18	0.76
13:m:335:GLU:OE2	13:m:338:LYS:NZ	2.21	0.74
12:L:106:ARG:HD2	12:L:208:PRO:HB2	1.69	0.73
1:A:100:TYR:O	9:I:114:ARG:NH1	2.21	0.73
4:d:131:THR:HG1	4:d:147:THR:HG1	1.34	0.73
13:M:335:GLU:OE2	13:M:338:LYS:NZ	2.21	0.73
11:K:82:THR:HG22	11:K:86:MET:HE2	1.71	0.72
11:k:82:THR:HG22	11:k:86:MET:HE2	1.71	0.72
12:l:106:ARG:HD2	12:l:208:PRO:HB2	1.72	0.71
4:d:92:GLN:HG3	11:k:67:LEU:HB2	1.73	0.70
6:F:298:LEU:HG	6:F:326:MET:HE2	1.74	0.69
3:c:160:GLY:O	4:d:81:ARG:NH2	2.23	0.69
5:E:229:ARG:HG2	5:E:230:ARG:HG3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:92:GLN:HG3	11:K:67:LEU:HB2	1.74	0.68
6:f:298:LEU:HG	6:f:326:MET:HE2	1.75	0.68
11:K:50:GLU:HG2	11:K:53:PRO:HD2	1.75	0.68
6:F:235:VAL:HG21	6:F:273:MET:HE1	1.76	0.68
2:b:117:GLN:NE2	2:b:121:GLN:OE1	2.27	0.67
11:k:50:GLU:HG2	11:k:53:PRO:HD2	1.75	0.67
6:F:205:LYS:NZ	6:F:206:ASN:OD1	2.26	0.67
1:A:129:ARG:NH1	7:G:124:THR:O	2.27	0.67
5:e:229:ARG:HG2	5:e:230:ARG:HG3	1.75	0.67
13:M:337:ARG:HH22	9:i:200:THR:HG22	1.59	0.67
6:f:235:VAL:HG21	6:f:273:MET:HE1	1.77	0.67
3:C:160:GLY:O	4:D:81:ARG:NH2	2.23	0.67
8:H:196:ASN:HD21	8:h:196:ASN:HD21	1.43	0.66
7:G:113:ALA:HB1	7:G:157:VAL:HG11	1.77	0.66
9:I:152:PRO:HG3	14:n:210:GLY:HA3	1.77	0.66
1:a:129:ARG:NH1	7:g:124:THR:O	2.28	0.66
4:D:116:GLN:NE2	5:E:184:ASP:OD1	2.25	0.66
7:G:18:GLU:HG2	7:G:20:ARG:HG3	1.77	0.66
9:I:200:THR:HG22	13:m:337:ARG:HH22	1.60	0.66
7:g:18:GLU:HG2	7:g:20:ARG:HG3	1.77	0.66
4:d:116:GLN:NE2	5:e:184:ASP:OD1	2.25	0.65
9:I:51:GLU:HB2	9:I:56:ALA:HB2	1.77	0.65
6:f:174:ILE:HD12	6:f:292:PRO:HD3	1.77	0.65
5:E:113:ASN:HB3	6:F:291:ARG:HB3	1.79	0.65
5:e:323:ASP:OD1	5:e:324:ASP:N	2.30	0.65
5:e:327:LEU:HD21	5:e:329:MET:HE2	1.78	0.65
7:g:215:TRP:CD1	7:g:227:VAL:HG12	2.32	0.65
5:E:327:LEU:HD21	5:E:329:MET:HE2	1.78	0.65
9:i:189:ARG:NH1	9:i:219:ASP:OD2	2.30	0.65
12:l:196:MET:H	12:l:215:ASP:HB3	1.61	0.65
14:N:210:GLY:HA3	9:i:152:PRO:HG3	1.77	0.65
6:F:174:ILE:HD12	6:F:292:PRO:HD3	1.78	0.64
1:a:120:GLN:NE2	2:b:80:ASP:OD1	2.30	0.64
2:B:117:GLN:NE2	2:B:121:GLN:OE1	2.27	0.64
7:G:215:TRP:CD1	7:G:227:VAL:HG12	2.32	0.64
6:f:402:LYS:O	6:f:404:ARG:NH1	2.30	0.64
9:i:51:GLU:HB2	9:i:56:ALA:HB2	1.77	0.64
13:M:182:MET:HB3	13:M:185:ASP:HB2	1.79	0.64
5:e:113:ASN:HB3	6:f:291:ARG:HB3	1.80	0.64
7:g:113:ALA:HB1	7:g:157:VAL:HG11	1.78	0.64
7:g:150:VAL:HG21	7:g:163:VAL:HG21	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:48:LYS:HG2	2:b:62:LYS:HG3	1.80	0.64
1:A:196:LYS:HG2	1:A:200:MET:HE2	1.80	0.64
5:E:149:ALA:HB1	5:E:302:LEU:HD11	1.79	0.64
12:L:196:MET:H	12:L:215:ASP:HB3	1.61	0.63
2:B:48:LYS:HG2	2:B:62:LYS:HG3	1.78	0.63
13:m:159:LEU:O	14:n:147:ARG:NH2	2.26	0.63
13:M:159:LEU:O	14:N:147:ARG:NH2	2.26	0.63
6:f:329:ARG:NH1	6:f:363:ALA:O	2.32	0.63
2:b:66:LEU:HB2	2:b:70:VAL:HG13	1.80	0.63
9:I:189:ARG:NH1	9:I:219:ASP:OD2	2.31	0.63
1:a:196:LYS:HG2	1:a:200:MET:HE2	1.81	0.63
5:e:188:LEU:HD23	5:e:219:LEU:HD23	1.81	0.63
10:J:54:THR:HG21	10:J:140:GLY:HA2	1.80	0.63
5:e:149:ALA:HB1	5:e:302:LEU:HD11	1.81	0.62
9:I:92:LEU:HD11	9:I:108:ALA:HB2	1.81	0.62
3:c:229:ILE:HD12	3:c:239:HIS:HB3	1.81	0.62
12:l:260:PHE:HE2	12:l:299:PHE:HE2	1.44	0.62
6:F:273:MET:O	6:F:277:ILE:HG13	2.00	0.62
3:c:125:GLN:NE2	4:d:79:ASP:OD1	2.31	0.62
4:D:11:SER:OG	4:D:13:ASP:OD1	2.16	0.62
5:E:184:ASP:HB3	5:E:237:PHE:HD1	1.65	0.62
14:N:206:TRP:HB2	8:h:244:PRO:HB3	1.81	0.62
9:i:192:ILE:HG12	9:i:199:GLY:HA2	1.81	0.62
5:e:147:VAL:HG22	5:e:319:VAL:HG22	1.82	0.62
6:f:273:MET:O	6:f:277:ILE:HG13	2.00	0.61
6:F:329:ARG:NH1	6:F:363:ALA:O	2.33	0.61
8:H:244:PRO:HB3	14:n:206:TRP:HB2	1.81	0.61
8:h:117:LEU:HD22	8:h:128:VAL:HG11	1.82	0.61
5:E:188:LEU:HD23	5:E:219:LEU:HD23	1.82	0.61
6:F:253:LEU:HD21	6:F:277:ILE:HG12	1.83	0.61
7:G:150:VAL:HG21	7:G:163:VAL:HG21	1.82	0.61
5:E:323:ASP:OD1	5:E:324:ASP:N	2.34	0.61
8:H:117:LEU:HD22	8:H:128:VAL:HG11	1.82	0.61
5:e:184:ASP:HB3	5:e:237:PHE:HD1	1.65	0.61
2:B:66:LEU:HB2	2:B:70:VAL:HG13	1.81	0.61
9:I:192:ILE:HG12	9:I:199:GLY:HA2	1.81	0.61
1:A:120:GLN:NE2	2:B:80:ASP:OD1	2.30	0.60
1:A:172:LYS:HG3	1:A:173:LYS:HG3	1.83	0.60
2:B:117:GLN:NE2	3:C:88:ASP:OD1	2.34	0.60
6:f:253:LEU:HD21	6:f:277:ILE:HG12	1.82	0.60
5:E:147:VAL:HG22	5:E:319:VAL:HG22	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:172:LYS:HG3	1:a:173:LYS:HG3	1.83	0.60
9:i:92:LEU:HD11	9:i:108:ALA:HB2	1.82	0.60
10:J:40:PRO:HB3	10:J:186:VAL:HG11	1.83	0.60
6:F:365:SER:HB2	6:F:368:ILE:HD13	1.84	0.60
6:F:402:LYS:O	6:F:404:ARG:NH1	2.35	0.60
3:c:78:ILE:HD13	3:c:116:LEU:HD22	1.83	0.60
11:k:105:CYS:HB2	11:k:129:MET:HB2	1.84	0.60
4:d:11:SER:OG	4:d:13:ASP:OD1	2.16	0.60
3:C:78:ILE:HD13	3:C:116:LEU:HD22	1.83	0.59
3:C:229:ILE:HG13	9:I:246:ARG:HH22	1.68	0.59
4:d:65:VAL:HG11	4:d:107:LEU:HD21	1.84	0.59
11:K:105:CYS:HB2	11:K:129:MET:HB2	1.84	0.59
7:g:215:TRP:HD1	7:g:227:VAL:HG12	1.68	0.59
4:D:65:VAL:HG11	4:D:107:LEU:HD21	1.85	0.59
7:G:215:TRP:HD1	7:G:227:VAL:HG12	1.68	0.59
9:i:233:LEU:HD12	10:j:166:ILE:HD13	1.85	0.59
10:j:40:PRO:HB3	10:j:186:VAL:HG11	1.84	0.58
5:E:226:SER:HB2	6:F:289:GLY:HA3	1.84	0.58
13:M:145:VAL:HG11	13:M:237:VAL:HB	1.86	0.58
13:m:145:VAL:HG11	13:m:237:VAL:HB	1.85	0.58
1:A:82:PRO:HD3	7:G:156:THR:HB	1.85	0.58
9:I:33:VAL:HG22	9:I:155:THR:HG22	1.85	0.58
1:a:82:PRO:HD3	7:g:156:THR:HB	1.86	0.58
9:I:233:LEU:HD12	10:J:166:ILE:HD13	1.85	0.58
14:N:109:ILE:HG22	14:N:118:LEU:HD13	1.86	0.58
9:i:92:LEU:O	9:i:96:ARG:HG3	2.04	0.58
11:k:168:LEU:HD21	11:k:202:ILE:HD13	1.86	0.58
4:d:203:ASN:O	4:d:203:ASN:ND2	2.34	0.58
9:i:33:VAL:HG22	9:i:155:THR:HG22	1.85	0.58
2:B:65:VAL:HG22	2:B:216:PHE:HD2	1.68	0.58
9:i:87:MET:HE1	9:i:115:HIS:CD2	2.39	0.58
6:f:365:SER:HB2	6:f:368:ILE:HD13	1.85	0.58
12:L:132:LYS:HD3	12:L:144:LEU:HD23	1.86	0.57
3:c:52:PRO:HG3	3:c:214:ASP:HB3	1.86	0.57
6:f:203:LYS:HG3	6:f:208:VAL:HG22	1.86	0.57
10:J:179:SER:HB3	12:l:125:ILE:HD11	1.87	0.57
3:C:125:GLN:NE2	4:D:79:ASP:OD1	2.31	0.57
5:E:281:PHE:HB3	6:F:221:LEU:HD21	1.85	0.57
12:L:125:ILE:HD11	10:j:179:SER:HB3	1.85	0.57
12:L:143:THR:HG21	12:L:199:MET:HE3	1.87	0.57
4:d:27:LYS:NZ	4:d:165:ASP:OD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:119:THR:HG22	4:d:126:PRO:HB3	1.87	0.57
8:h:109:LEU:HD11	8:h:148:ILE:HD12	1.86	0.57
3:C:48:GLU:O	3:C:70:LYS:NZ	2.37	0.57
11:K:168:LEU:HD21	11:K:202:ILE:HG21	1.87	0.57
1:a:36:THR:HG22	1:a:49:THR:HG23	1.85	0.57
2:b:117:GLN:NE2	3:c:88:ASP:OD1	2.34	0.57
11:k:168:LEU:HD21	11:k:202:ILE:HG21	1.87	0.57
5:E:268:GLN:OE1	5:E:278:GLN:NE2	2.37	0.57
7:G:35:SER:HB2	7:G:51:GLU:HG3	1.86	0.57
11:K:168:LEU:HD21	11:K:202:ILE:HD13	1.86	0.57
8:h:124:ILE:HG13	8:h:126:ALA:H	1.70	0.57
1:a:49:THR:HG21	1:a:65:ALA:HB3	1.85	0.57
12:l:143:THR:HG21	12:l:199:MET:HE3	1.87	0.57
2:B:48:LYS:HD3	2:B:207:GLN:HB2	1.87	0.57
3:c:48:GLU:O	3:c:70:LYS:NZ	2.37	0.57
4:d:30:LEU:HB3	4:d:46:GLU:HB3	1.86	0.57
4:D:30:LEU:HB3	4:D:46:GLU:HB3	1.85	0.56
6:F:203:LYS:HG3	6:F:208:VAL:HG22	1.87	0.56
12:l:132:LYS:HD3	12:l:144:LEU:HD23	1.87	0.56
4:D:119:THR:HG22	4:D:126:PRO:HB3	1.87	0.56
6:f:209:VAL:HG22	6:f:379:ILE:HG12	1.86	0.56
8:H:78:THR:HG1	14:n:137:TYR:HH	1.51	0.56
2:b:120:THR:HG22	2:b:127:PRO:HB3	1.88	0.56
7:g:35:SER:HB2	7:g:51:GLU:HG3	1.86	0.56
4:D:223:GLN:HA	4:D:226:VAL:HG22	1.87	0.56
7:g:168:ALA:HB1	7:g:200:VAL:HG22	1.87	0.56
14:n:109:ILE:HG22	14:n:118:LEU:HD13	1.86	0.56
8:H:124:ILE:HG13	8:H:126:ALA:H	1.70	0.56
3:c:234:ASP:OD2	3:c:237:LYS:HB2	2.06	0.56
12:l:278:VAL:HG22	12:l:283:TRP:HB3	1.88	0.56
4:d:168:VAL:O	4:d:172:MET:HG2	2.06	0.56
5:e:216:THR:HG21	5:e:241:LEU:HD12	1.88	0.56
2:B:120:THR:HG22	2:B:127:PRO:HB3	1.88	0.56
7:G:168:ALA:HB1	7:G:200:VAL:HG22	1.88	0.56
9:I:44:GLY:HA2	9:I:203:ASP:O	2.07	0.55
4:d:157:ARG:HH21	5:e:158:LEU:HA	1.71	0.55
12:L:144:LEU:HD11	12:L:148:ALA:HA	1.88	0.55
12:L:278:VAL:HG22	12:L:283:TRP:HB3	1.88	0.55
8:H:109:LEU:HD11	8:H:148:ILE:HD12	1.86	0.55
1:A:129:ARG:HB2	7:G:13:ASP:HA	1.87	0.55
9:i:210:ASP:OD1	9:i:211:LYS:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:226:SER:HB2	6:f:289:GLY:HA3	1.89	0.55
9:i:44:GLY:HA2	9:i:203:ASP:O	2.06	0.55
3:C:52:PRO:HG3	3:C:214:ASP:HB3	1.89	0.55
11:K:181:ARG:NH1	11:k:28:LYS:O	2.38	0.55
1:a:129:ARG:HB2	7:g:13:ASP:HA	1.87	0.55
2:b:104:PRO:HG2	2:b:107:GLN:HG2	1.88	0.55
10:j:124:THR:HG22	10:j:130:PRO:HA	1.89	0.55
13:m:182:MET:HG2	13:m:185:ASP:H	1.72	0.54
12:L:103:LEU:HD22	12:L:238:LEU:HD22	1.89	0.54
12:l:144:LEU:HD11	12:l:148:ALA:HA	1.88	0.54
11:K:28:LYS:O	11:k:181:ARG:NH1	2.38	0.54
8:h:111:GLU:OE1	9:i:114:ARG:NH2	2.30	0.54
12:l:103:LEU:HD22	12:l:238:LEU:HD22	1.88	0.54
2:B:104:PRO:HG2	2:B:107:GLN:HG2	1.89	0.54
9:I:210:ASP:OD1	9:I:211:LYS:N	2.40	0.54
10:J:190:VAL:HG13	10:J:195:VAL:HG22	1.88	0.54
4:d:99:GLU:OE1	12:l:219:ARG:NH2	2.39	0.54
5:e:231:LYS:NZ	5:e:232:LEU:O	2.40	0.54
2:b:48:LYS:HD3	2:b:207:GLN:HB2	1.89	0.54
5:e:242:LEU:HG	5:e:253:LEU:HD11	1.89	0.54
4:D:157:ARG:HH21	5:E:158:LEU:HA	1.72	0.54
10:J:27:ARG:O	10:J:41:LYS:NZ	2.33	0.54
10:j:190:VAL:HG13	10:j:195:VAL:HG22	1.89	0.53
4:D:226:VAL:HA	4:D:229:VAL:HG22	1.88	0.53
5:E:216:THR:HG21	5:E:241:LEU:HD12	1.90	0.53
5:E:290:THR:HG23	5:E:293:GLU:H	1.73	0.53
10:J:124:THR:HG22	10:J:130:PRO:HA	1.89	0.53
10:J:177:ARG:HG3	13:m:273:PRO:HG3	1.91	0.53
1:a:155:THR:OG1	1:a:165:HIS:NE2	2.42	0.53
9:i:48:ARG:NH1	9:i:196:PRO:O	2.38	0.53
11:k:16:VAL:HG23	11:k:36:ILE:HD13	1.91	0.53
6:F:274:ALA:HB1	6:F:318:VAL:HG11	1.90	0.53
9:I:196:PRO:HB2	13:m:313:ILE:HD12	1.91	0.53
2:b:65:VAL:HG22	2:b:216:PHE:HD2	1.74	0.53
6:f:274:ALA:HB1	6:f:318:VAL:HG11	1.90	0.53
10:j:27:ARG:O	10:j:41:LYS:NZ	2.34	0.53
14:n:153:ASN:HD21	14:n:157:LEU:HD23	1.73	0.53
4:D:194:LEU:HA	4:D:197:VAL:HG22	1.91	0.52
7:G:91:ARG:HG2	7:G:119:PHE:CG	2.44	0.52
11:K:16:VAL:HG23	11:K:36:ILE:HD13	1.91	0.52
3:c:49:LYS:NZ	3:c:214:ASP:O	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:337:ARG:NH2	13:M:339:ASP:OD2	2.42	0.52
7:g:91:ARG:HG2	7:g:119:PHE:CG	2.44	0.52
1:A:83:ASP:OD1	7:G:121:HIS:NE2	2.32	0.52
9:I:48:ARG:NH1	9:I:196:PRO:O	2.39	0.52
4:d:223:GLN:HA	4:d:226:VAL:HG22	1.92	0.52
9:i:205:CYS:HB2	9:i:214:LEU:HD13	1.91	0.52
13:m:337:ARG:NH2	13:m:339:ASP:OD2	2.43	0.52
1:A:155:THR:OG1	1:A:165:HIS:NE2	2.43	0.52
8:H:111:GLU:OE1	9:I:114:ARG:NH2	2.31	0.52
13:M:313:ILE:HD12	9:i:196:PRO:HB2	1.90	0.52
10:J:15:ALA:HB2	10:J:121:LEU:HD11	1.92	0.52
13:M:273:PRO:HG3	10:j:177:ARG:HG3	1.91	0.52
4:D:27:LYS:NZ	4:D:165:ASP:OD1	2.35	0.51
4:D:99:GLU:OE1	12:L:219:ARG:NH2	2.38	0.51
10:J:141:THR:O	12:l:123:GLN:NE2	2.43	0.51
6:f:205:LYS:NZ	6:f:206:ASN:OD1	2.43	0.51
9:I:205:CYS:HB2	9:I:214:LEU:HD13	1.91	0.51
6:F:209:VAL:HG22	6:F:379:ILE:HG12	1.92	0.51
5:e:241:LEU:HB2	5:e:256:THR:HB	1.93	0.51
8:h:233:LEU:HD23	8:h:238:PRO:HB3	1.93	0.51
10:j:14:MET:HG2	10:j:163:LEU:HD11	1.93	0.51
10:J:14:MET:HG2	10:J:163:LEU:HD11	1.93	0.51
12:L:279:HIS:CE1	12:L:281:LYS:HB2	2.46	0.51
1:a:83:ASP:OD1	7:g:121:HIS:NE2	2.31	0.51
9:i:139:LEU:HD21	9:i:154:VAL:HG22	1.93	0.51
10:j:15:ALA:HB2	10:j:121:LEU:HD11	1.92	0.51
13:M:263:THR:HG21	13:M:271:VAL:HG23	1.93	0.51
4:d:47:LYS:NZ	4:d:202:ARG:O	2.42	0.51
5:e:290:THR:HG23	5:e:293:GLU:H	1.75	0.51
8:H:94:LYS:HE2	8:H:238:PRO:HD3	1.92	0.51
12:L:102:THR:HG23	12:L:115:VAL:HG12	1.93	0.51
12:l:102:THR:HG23	12:l:115:VAL:HG12	1.93	0.51
8:h:94:LYS:HE2	8:h:238:PRO:HD3	1.92	0.51
8:h:112:ARG:HB3	8:h:140:MET:HE1	1.92	0.51
13:m:201:LYS:HG3	13:m:206:GLY:HA2	1.93	0.51
14:N:153:ASN:HD21	14:N:157:LEU:HD23	1.74	0.50
2:B:7:GLY:HA2	2:B:123:GLY:HA2	1.93	0.50
9:I:87:MET:HE1	9:I:115:HIS:ND1	2.26	0.50
9:I:139:LEU:HD21	9:I:154:VAL:HG22	1.93	0.50
2:b:7:GLY:HA2	2:b:123:GLY:HA2	1.94	0.50
5:E:242:LEU:HG	5:E:253:LEU:HD11	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:151:GLU:HG2	5:e:153:ARG:HG3	1.93	0.50
12:l:279:HIS:CE1	12:l:281:LYS:HB2	2.46	0.50
9:I:248:LEU:HD13	10:J:47:ASP:HB3	1.94	0.50
11:K:45:VAL:HG22	11:K:107:PHE:HD1	1.77	0.50
5:e:109:ASP:N	5:e:109:ASP:OD1	2.42	0.50
9:i:248:LEU:HD13	10:j:47:ASP:HB3	1.94	0.50
6:F:372:VAL:HG13	6:F:394:ALA:HB3	1.92	0.50
9:I:186:SER:O	9:I:190:LYS:HG2	2.12	0.50
11:k:45:VAL:HG22	11:k:107:PHE:HD1	1.77	0.50
13:m:263:THR:HG21	13:m:271:VAL:HG23	1.93	0.50
4:D:45:VAL:HG21	4:D:61:LYS:HB2	1.94	0.50
5:E:151:GLU:HG2	5:E:153:ARG:HG3	1.94	0.50
13:M:201:LYS:HG3	13:M:206:GLY:HA2	1.93	0.50
3:C:266:GLU:HA	3:C:269:GLU:HG3	1.94	0.50
3:c:266:GLU:HA	3:c:269:GLU:HG3	1.94	0.50
8:H:233:LEU:HD23	8:H:238:PRO:HB3	1.93	0.49
4:d:45:VAL:HG21	4:d:61:LYS:HB2	1.93	0.49
14:n:21:ASP:OD1	14:n:37:ARG:NH1	2.45	0.49
14:N:21:ASP:OD1	14:N:37:ARG:NH1	2.45	0.49
11:K:18:ALA:O	11:K:190:PHE:HB2	2.13	0.49
12:l:157:VAL:O	12:l:161:GLU:HG2	2.13	0.49
9:i:74:GLY:HA3	9:i:81:THR:HG21	1.94	0.49
3:C:14:PRO:HA	4:D:21:TYR:CE1	2.47	0.49
3:C:45:LEU:HB3	3:C:71:MET:HE2	1.95	0.49
4:D:13:ASP:OD2	4:D:15:HIS:ND1	2.46	0.49
9:I:74:GLY:HA3	9:I:81:THR:HG21	1.94	0.49
9:I:239:PRO:HG2	10:J:201:LYS:HB2	1.94	0.49
9:i:239:PRO:HG2	10:j:201:LYS:HB2	1.94	0.49
5:E:241:LEU:HB2	5:E:256:THR:HB	1.93	0.49
8:H:112:ARG:HB3	8:H:140:MET:HE1	1.94	0.49
10:j:21:VAL:HG23	10:j:163:LEU:HD23	1.95	0.49
12:l:260:PHE:CE2	12:l:299:PHE:HE2	2.29	0.49
4:D:47:LYS:NZ	4:D:202:ARG:O	2.46	0.49
12:L:157:VAL:O	12:L:161:GLU:HG2	2.13	0.49
8:h:68:LEU:HD23	8:h:98:CYS:SG	2.53	0.49
8:H:68:LEU:HD23	8:H:98:CYS:SG	2.53	0.49
3:c:14:PRO:HA	4:d:21:TYR:CE1	2.48	0.49
9:i:186:SER:O	9:i:190:LYS:HG2	2.12	0.49
1:A:75:CYS:SG	1:A:77:MET:HE2	2.53	0.49
10:J:21:VAL:HG23	10:J:163:LEU:HD23	1.95	0.49
7:g:66:ARG:NH2	7:g:80:GLY:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:13:ASP:OD2	4:d:15:HIS:ND1	2.46	0.48
8:h:113:VAL:HG11	8:h:137:PHE:CE2	2.48	0.48
11:k:18:ALA:O	11:k:190:PHE:HB2	2.13	0.48
2:b:212:VAL:O	2:b:213:GLU:HG2	2.12	0.48
3:c:45:LEU:HB3	3:c:71:MET:HE2	1.95	0.48
6:f:211:ALA:HB1	6:f:360:LEU:HD22	1.95	0.48
4:d:5:ARG:HH22	5:e:108:TYR:HB3	1.77	0.48
6:F:391:GLU:O	6:F:395:ARG:NH1	2.46	0.48
3:c:74:ILE:HG21	3:c:116:LEU:HD21	1.95	0.48
6:f:372:VAL:HG21	6:f:395:ARG:HD3	1.96	0.48
8:h:215:ALA:HA	8:h:218:TYR:CE2	2.49	0.48
10:j:19:CYS:HB3	10:j:191:THR:HG22	1.95	0.48
7:G:54:HIS:HB2	7:G:208:LEU:HB3	1.96	0.48
8:H:113:VAL:HG11	8:H:137:PHE:CE2	2.49	0.48
9:i:128:VAL:HG22	9:i:141:THR:HG22	1.95	0.48
13:m:143:ASP:OD1	13:m:143:ASP:N	2.45	0.48
6:F:211:ALA:HB1	6:F:360:LEU:HD22	1.95	0.48
14:n:49:ALA:HB2	14:n:106:MET:HG2	1.95	0.48
8:H:215:ALA:HA	8:H:218:TYR:CE2	2.49	0.48
14:N:49:ALA:HB2	14:N:106:MET:HG2	1.95	0.48
10:J:19:CYS:HB3	10:J:191:THR:HG22	1.95	0.48
11:k:146:GLY:HA2	11:k:149:PHE:HD2	1.79	0.48
12:l:199:MET:SD	12:l:225:PHE:HB2	2.54	0.48
7:G:66:ARG:NH2	7:G:80:GLY:O	2.46	0.48
13:M:143:ASP:OD1	13:M:143:ASP:N	2.45	0.48
8:H:227:LEU:HD21	14:n:206:TRP:HB3	1.96	0.48
9:I:128:VAL:HG22	9:I:141:THR:HG22	1.95	0.48
11:K:140:TYR:OH	11:K:155:ASP:OD1	2.21	0.48
2:b:212:VAL:O	2:b:212:VAL:HG13	2.14	0.48
3:C:67:SER:HB2	3:C:72:TYR:HD1	1.79	0.47
1:a:83:ASP:OD2	1:a:129:ARG:NH2	2.47	0.47
5:e:167:ILE:HG22	5:e:329:MET:HE1	1.96	0.47
3:C:177:ALA:HB2	3:C:205:THR:HG21	1.95	0.47
4:D:90:GLU:HG2	4:D:110:TYR:CG	2.49	0.47
4:d:215:ARG:HG2	4:d:215:ARG:HH11	1.79	0.47
1:A:146:ASP:OD1	1:A:148:SER:OG	2.19	0.47
4:D:51:VAL:O	4:D:52:LYS:HB3	2.14	0.47
4:d:90:GLU:HG2	4:d:110:TYR:CG	2.49	0.47
3:C:74:ILE:HG21	3:C:116:LEU:HD21	1.95	0.47
4:D:69:ILE:HG21	4:D:107:LEU:HD23	1.97	0.47
5:E:167:ILE:HG22	5:E:329:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:125:GLN:HG3	4:d:78:ALA:HB1	1.97	0.47
7:g:54:HIS:HB2	7:g:208:LEU:HB3	1.95	0.47
9:i:200:THR:O	9:i:201:GLN:HG3	2.15	0.47
12:L:199:MET:SD	12:L:225:PHE:HB2	2.54	0.47
1:A:83:ASP:OD2	1:A:129:ARG:NH2	2.48	0.47
3:C:49:LYS:NZ	3:C:214:ASP:O	2.33	0.47
4:D:215:ARG:HG2	4:D:215:ARG:HH11	1.80	0.47
4:d:51:VAL:O	4:d:52:LYS:HB3	2.14	0.47
7:g:66:ARG:HH21	7:g:80:GLY:H	1.62	0.47
1:A:238:GLU:O	1:A:241:GLU:HG2	2.15	0.47
9:I:92:LEU:O	9:I:96:ARG:HG3	2.14	0.47
3:C:212:ASP:OD1	3:C:212:ASP:N	2.48	0.47
3:C:265:ARG:O	3:C:268:GLU:HG3	2.15	0.47
4:D:79:ASP:HB3	4:D:127:PHE:HD1	1.80	0.47
8:H:78:THR:OG1	14:n:137:TYR:OH	2.30	0.47
9:I:241:LEU:HD23	9:I:242:LYS:HD2	1.96	0.47
13:M:339:ASP:OD1	13:M:339:ASP:N	2.43	0.47
3:c:89:ALA:HB2	3:c:138:VAL:HG21	1.96	0.47
3:c:154:TYR:OH	4:d:57:ARG:NH2	2.48	0.47
11:k:192:LYS:HE2	11:k:201:VAL:HG22	1.97	0.47
11:K:146:GLY:HA2	11:K:149:PHE:HD2	1.79	0.47
4:d:79:ASP:HB3	4:d:127:PHE:HD1	1.80	0.47
9:i:241:LEU:HD23	9:i:242:LYS:HD2	1.96	0.47
14:N:206:TRP:HB3	8:h:227:LEU:HD21	1.96	0.46
3:C:11:THR:HG22	4:D:7:ILE:HG23	1.98	0.46
5:E:195:GLU:HG3	5:E:215:ALA:HB1	1.97	0.46
4:d:146:LYS:HE3	4:d:161:ILE:HG22	1.97	0.46
9:i:33:VAL:HG13	9:i:167:LEU:HD11	1.97	0.46
7:G:66:ARG:HH21	7:G:80:GLY:H	1.62	0.46
11:k:86:MET:HE1	11:k:107:PHE:CD1	2.51	0.46
12:l:187:TYR:O	12:l:190:ARG:NH1	2.45	0.46
3:C:125:GLN:HG3	4:D:78:ALA:HB1	1.97	0.46
3:C:166:SER:HB3	3:C:185:TRP:CZ2	2.50	0.46
4:d:69:ILE:HG21	4:d:107:LEU:HD23	1.97	0.46
7:g:37:ALA:HB2	7:g:50:VAL:HG23	1.98	0.46
10:j:161:GLU:O	10:j:165:GLU:HG2	2.16	0.46
3:C:89:ALA:HB2	3:C:138:VAL:HG21	1.96	0.46
5:E:291:LEU:HD21	5:E:319:VAL:HG11	1.97	0.46
12:L:233:TYR:HB2	12:L:262:ALA:HA	1.97	0.46
14:N:148:GLN:O	14:N:152:LYS:HG2	2.16	0.46
1:a:238:GLU:O	1:a:241:GLU:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:l:233:TYR:HB2	12:l:262:ALA:HA	1.97	0.46
8:H:73:ARG:NH1	8:H:222:GLY:O	2.49	0.46
9:I:200:THR:O	9:I:201:GLN:HG3	2.15	0.46
11:K:86:MET:HE1	11:K:107:PHE:CD1	2.51	0.46
1:A:240:GLU:O	1:A:244:THR:HG23	2.15	0.46
3:c:11:THR:HG22	4:d:7:ILE:HG23	1.98	0.46
14:n:148:GLN:O	14:n:152:LYS:HG2	2.16	0.46
4:D:113:GLY:O	4:D:117:LYS:HG3	2.16	0.46
4:D:229:VAL:O	4:D:233:ARG:HG3	2.16	0.46
7:G:37:ALA:HB2	7:G:50:VAL:HG23	1.98	0.46
9:i:66:MET:HE1	9:i:88:VAL:HG12	1.98	0.46
9:I:33:VAL:HG13	9:I:167:LEU:HD11	1.97	0.46
11:K:192:LYS:HE2	11:K:201:VAL:HG22	1.97	0.46
3:c:166:SER:HB3	3:c:185:TRP:CZ2	2.50	0.46
4:d:113:GLY:O	4:d:117:LYS:HG3	2.16	0.46
10:j:158:MET:HE1	10:j:166:ILE:HG13	1.98	0.46
12:l:203:TRP:CZ3	12:l:208:PRO:HG3	2.51	0.46
8:H:203:LYS:HE3	8:H:232:THR:HG21	1.98	0.45
1:a:240:GLU:O	1:a:244:THR:HG23	2.16	0.45
4:d:33:VAL:HG22	4:d:193:LEU:HD13	1.97	0.45
4:d:131:THR:OG1	4:d:147:THR:OG1	2.22	0.45
4:D:222:LEU:O	4:D:226:VAL:HG13	2.16	0.45
3:c:177:ALA:HB2	3:c:205:THR:HG21	1.97	0.45
5:e:291:LEU:HD21	5:e:319:VAL:HG11	1.98	0.45
3:C:206:MET:HG3	3:C:208:THR:HG22	1.97	0.45
4:D:146:LYS:HE3	4:D:161:ILE:HG22	1.98	0.45
10:J:161:GLU:O	10:J:165:GLU:HG2	2.16	0.45
8:h:73:ARG:NH1	8:h:222:GLY:O	2.48	0.45
2:B:212:VAL:O	2:B:212:VAL:HG13	2.16	0.45
11:K:181:ARG:HA	11:K:181:ARG:HD3	1.71	0.45
10:j:51:TYR:HB2	10:j:109:ILE:HG13	1.98	0.45
5:E:335:ILE:HA	5:E:338:ILE:HD12	1.99	0.45
12:L:203:TRP:CZ3	12:L:208:PRO:HG3	2.51	0.45
11:k:40:ASP:HB3	11:k:43:GLN:HB2	1.98	0.45
3:C:262:ASP:OD1	3:C:263:GLN:N	2.50	0.45
9:I:66:MET:HE1	9:I:88:VAL:HG12	1.98	0.45
3:c:67:SER:HB2	3:c:72:TYR:HD1	1.79	0.45
7:g:20:ARG:HD2	7:g:25:GLU:OE2	2.17	0.45
8:h:203:LYS:HE3	8:h:232:THR:HG21	1.99	0.45
12:L:186:THR:HG21	12:L:214:ASP:O	2.17	0.45
14:N:112:ARG:O	14:N:115:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:75:CYS:SG	1:a:77:MET:HE2	2.57	0.45
10:j:93:SER:O	10:j:97:GLU:HG3	2.17	0.45
12:l:105:PHE:HB3	12:l:224:LEU:HD13	1.99	0.45
12:l:186:THR:HG21	12:l:214:ASP:O	2.17	0.45
13:m:196:ARG:HG3	13:m:221:MET:SD	2.57	0.45
8:H:267:PRO:HG3	8:H:278:ARG:HB2	1.98	0.45
11:K:33:GLU:OE2	11:K:51:ASN:ND2	2.50	0.45
1:a:207:GLN:O	1:a:211:GLY:N	2.39	0.45
4:d:122:GLY:H	5:e:231:LYS:NZ	2.15	0.45
4:d:184:GLU:O	4:d:188:PHE:N	2.47	0.45
9:i:70:ILE:HG12	9:i:105:VAL:HG22	1.98	0.45
11:k:24:PHE:CE2	11:k:25:TYR:HD2	2.34	0.45
5:E:285:TYR:O	6:F:220:GLU:HG2	2.17	0.45
10:J:51:TYR:HB2	10:J:109:ILE:HG13	1.98	0.45
10:J:158:MET:HE1	10:J:166:ILE:HG13	1.98	0.45
2:B:211:VAL:HG22	2:B:216:PHE:HD1	1.82	0.45
7:G:215:TRP:CH2	7:G:220:SER:HB3	2.52	0.45
12:L:105:PHE:HB3	12:L:224:LEU:HD13	1.99	0.45
4:d:231:LYS:O	4:d:235:GLU:OE1	2.34	0.45
12:l:102:THR:HG21	12:l:143:THR:HB	1.99	0.45
8:H:57:ILE:HB	8:H:98:CYS:HB3	1.99	0.44
10:J:93:SER:O	10:J:97:GLU:HG3	2.17	0.44
3:c:103:HIS:CG	3:c:111:MET:HG3	2.52	0.44
14:n:9:ALA:HB2	14:n:18:MET:HG3	2.00	0.44
4:D:132:VAL:HG23	4:D:161:ILE:HD13	1.99	0.44
10:J:46:ASN:HD21	10:J:49:ILE:HD12	1.83	0.44
4:d:132:VAL:HG23	4:d:161:ILE:HD13	1.98	0.44
6:f:270:MET:SD	6:f:301:GLY:HA3	2.57	0.44
7:g:215:TRP:CH2	7:g:220:SER:HB3	2.52	0.44
5:E:276:ALA:O	5:E:280:VAL:HG23	2.18	0.44
6:F:190:ASN:ND2	6:F:314:PRO:HD2	2.33	0.44
12:L:102:THR:HG21	12:L:143:THR:HB	1.99	0.44
5:e:276:ALA:O	5:e:280:VAL:HG23	2.18	0.44
4:D:184:GLU:O	4:D:188:PHE:N	2.47	0.44
5:E:309:GLN:O	5:E:314:ASN:ND2	2.51	0.44
11:K:1:MET:HA	11:K:144:GLY:HA2	1.99	0.44
3:c:31:ALA:O	3:c:172:GLN:HG3	2.18	0.44
9:i:241:LEU:HD23	9:i:242:LYS:CD	2.48	0.44
11:k:1:MET:HA	11:k:144:GLY:HA2	2.00	0.44
2:b:61:GLN:HG3	2:b:207:GLN:HE22	1.82	0.44
12:l:245:ASP:OD1	12:l:245:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:195:GLU:HG3	5:e:215:ALA:HB1	1.99	0.44
8:h:91:LEU:HD12	8:h:95:ILE:HG22	1.98	0.44
11:k:140:TYR:OH	11:k:155:ASP:OD1	2.21	0.44
4:D:105:ASP:OD1	4:D:106:MET:N	2.51	0.44
10:J:56:LEU:HG	10:J:58:THR:HG22	2.00	0.44
13:m:135:THR:N	13:m:150:ASP:OD1	2.41	0.44
3:C:31:ALA:O	3:C:172:GLN:HG3	2.18	0.44
6:F:282:GLN:HG2	6:F:285:ILE:HD11	2.00	0.44
7:G:20:ARG:HD2	7:G:25:GLU:OE2	2.17	0.44
8:H:99:ARG:HD2	8:H:106:THR:HB	1.99	0.44
4:d:228:GLU:O	4:d:231:LYS:HG3	2.18	0.44
14:n:112:ARG:O	14:n:115:GLU:HG2	2.17	0.44
5:E:148:LEU:HD21	5:E:244:ALA:HB2	1.99	0.44
9:I:246:ARG:HD3	9:I:246:ARG:HA	1.79	0.44
14:N:9:ALA:HB2	14:N:18:MET:HG3	2.00	0.44
3:c:121:CYS:SG	3:c:162:TYR:HB3	2.58	0.44
3:c:200:ARG:HH21	3:c:268:GLU:HG2	1.83	0.44
11:k:33:GLU:OE2	11:k:51:ASN:ND2	2.50	0.44
13:M:196:ARG:HG3	13:M:221:MET:SD	2.58	0.43
1:a:29:VAL:HG21	1:a:134:VAL:HG23	1.99	0.43
5:e:308:ASP:OD1	5:e:309:GLN:N	2.47	0.43
7:G:190:VAL:HG13	7:G:213:VAL:HG11	2.00	0.43
8:H:139:LYS:O	8:H:143:MET:HG2	2.18	0.43
4:d:219:GLU:O	4:d:223:GLN:HG2	2.19	0.43
1:A:87:LEU:HD21	1:A:131:MET:HG3	2.01	0.43
2:B:212:VAL:O	2:B:213:GLU:HG2	2.17	0.43
8:H:91:LEU:HD12	8:H:95:ILE:HG22	1.98	0.43
8:H:97:CYS:HA	8:H:153:ILE:O	2.18	0.43
12:L:104:ALA:HA	12:L:112:ILE:O	2.18	0.43
6:f:282:GLN:HG2	6:f:285:ILE:HD11	2.00	0.43
6:f:333:SER:OG	6:f:359:ALA:O	2.32	0.43
9:i:95:HIS:O	9:i:99:THR:HG23	2.17	0.43
12:L:295:TYR:CZ	10:j:204:LYS:HE2	2.54	0.43
6:f:190:ASN:ND2	6:f:314:PRO:HD2	2.33	0.43
8:h:97:CYS:HA	8:h:153:ILE:O	2.18	0.43
8:h:267:PRO:HG3	8:h:278:ARG:HB2	2.01	0.43
9:I:110:THR:HA	9:I:113:LYS:HG2	2.01	0.43
9:I:248:LEU:HD11	10:J:195:VAL:HG23	2.00	0.43
4:d:68:ASN:OD1	4:d:68:ASN:N	2.52	0.43
9:i:248:LEU:HD11	10:j:195:VAL:HG23	2.01	0.43
10:j:46:ASN:HD21	10:j:49:ILE:HD12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:l:104:ALA:HA	12:l:112:ILE:O	2.19	0.43
13:m:251:ASP:OD1	13:m:254:GLY:N	2.52	0.43
3:C:103:HIS:CG	3:C:111:MET:HG3	2.52	0.43
5:E:217:CYS:O	5:E:221:ILE:HG23	2.19	0.43
5:E:311:SER:OG	5:E:314:ASN:HB2	2.18	0.43
4:d:105:ASP:OD1	4:d:106:MET:N	2.51	0.43
6:f:341:PHE:HA	6:f:344:PHE:CD2	2.53	0.43
8:h:99:ARG:HD2	8:h:106:THR:HB	1.99	0.43
8:h:139:LYS:O	8:h:143:MET:HG2	2.18	0.43
13:m:223:TYR:O	13:m:226:ARG:HB2	2.18	0.43
3:C:121:CYS:SG	3:C:162:TYR:HB3	2.58	0.43
9:I:47:THR:HB	9:I:59:ARG:HA	2.00	0.43
9:I:241:LEU:HD23	9:I:242:LYS:CD	2.48	0.43
14:N:137:TYR:OH	8:h:78:THR:OG1	2.29	0.43
3:c:212:ASP:OD1	3:c:212:ASP:N	2.49	0.43
5:e:218:ASP:OD1	6:f:247:ARG:NH2	2.51	0.43
7:g:216:VAL:HB	7:g:224:PHE:HA	1.99	0.43
9:i:47:THR:HB	9:i:59:ARG:HA	1.99	0.43
9:I:95:HIS:O	9:I:99:THR:HG23	2.18	0.43
13:M:223:TYR:O	13:M:226:ARG:HB2	2.18	0.43
5:e:154:VAL:HA	5:e:164:MET:HE1	2.01	0.43
8:h:57:ILE:HB	8:h:98:CYS:HB3	1.99	0.43
4:D:33:VAL:HG22	4:D:193:LEU:HD13	2.01	0.43
4:D:219:GLU:O	4:D:223:GLN:HG2	2.18	0.43
6:F:270:MET:SD	6:F:301:GLY:HA3	2.59	0.43
7:G:216:VAL:HB	7:G:224:PHE:HA	1.99	0.43
8:H:261:GLN:HA	14:n:34:ASN:HB2	2.01	0.43
14:N:34:ASN:HB2	8:h:261:GLN:HA	2.01	0.43
10:j:56:LEU:HG	10:j:58:THR:HG22	2.00	0.43
13:M:261:TYR:OH	13:M:280:ASN:OD1	2.36	0.43
3:c:265:ARG:O	3:c:268:GLU:HG3	2.19	0.43
5:e:286:HIS:CE1	5:e:289:MET:HG2	2.54	0.43
3:C:234:ASP:OD2	3:C:237:LYS:HB2	2.19	0.42
5:E:278:GLN:O	5:E:282:THR:HG23	2.19	0.42
9:I:87:MET:HE1	9:I:115:HIS:CE1	2.54	0.42
7:g:190:VAL:HG13	7:g:213:VAL:HG11	2.00	0.42
8:h:251:CYS:SG	8:h:254:LYS:HG2	2.59	0.42
10:j:12:MET:HE1	10:j:167:ALA:HA	2.00	0.42
1:A:29:VAL:HG21	1:A:134:VAL:HG23	2.00	0.42
3:C:146:ASP:OD1	3:C:152:GLN:NE2	2.51	0.42
10:J:204:LYS:HE2	12:l:295:TYR:CZ	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:18:LEU:O	3:C:22:GLU:HG3	2.19	0.42
6:F:341:PHE:HA	6:F:344:PHE:CD2	2.54	0.42
7:G:18:GLU:OE1	7:G:18:GLU:N	2.52	0.42
3:c:18:LEU:O	3:c:22:GLU:HG3	2.19	0.42
3:c:146:ASP:OD1	3:c:152:GLN:NE2	2.50	0.42
7:g:18:GLU:OE1	7:g:18:GLU:N	2.52	0.42
3:C:154:TYR:OH	4:D:57:ARG:NH2	2.51	0.42
8:H:251:CYS:SG	8:H:254:LYS:HG2	2.59	0.42
9:i:110:THR:HA	9:i:113:LYS:HG2	2.01	0.42
13:m:188:GLN:OE1	13:m:192:MET:HE3	2.19	0.42
2:B:137:VAL:HG22	2:B:142:TYR:CD1	2.54	0.42
8:H:227:LEU:HD23	8:H:244:PRO:HA	2.02	0.42
14:N:21:ASP:O	14:N:37:ARG:HD3	2.19	0.42
5:e:138:LEU:HB2	5:e:149:ALA:HB3	2.01	0.42
5:e:197:GLN:HB3	12:l:160:MET:HG3	2.01	0.42
6:f:236:GLY:HA3	6:f:386:PHE:CZ	2.54	0.42
11:k:129:MET:HA	11:k:134:THR:O	2.20	0.42
6:F:232:ASP:OD1	13:M:198:LYS:NZ	2.51	0.42
12:L:187:TYR:O	12:L:190:ARG:NH1	2.45	0.42
13:M:251:ASP:OD1	13:M:254:GLY:N	2.52	0.42
2:b:165:SER:OG	2:b:166:PRO:HD3	2.20	0.42
5:e:217:CYS:O	5:e:221:ILE:HG23	2.19	0.42
1:A:242:TRP:O	1:A:246:VAL:HG23	2.20	0.42
6:F:178:SER:HB3	6:F:182:ARG:H	1.84	0.42
12:L:145:ALA:HB3	12:L:197:GLY:O	2.20	0.42
8:h:227:LEU:HD23	8:h:244:PRO:HA	2.02	0.42
9:i:246:ARG:HD3	9:i:246:ARG:HA	1.81	0.42
14:n:21:ASP:O	14:n:37:ARG:HD3	2.19	0.42
2:B:41:GLY:HA2	2:B:142:TYR:CD1	2.55	0.42
7:G:42:CYS:C	7:G:44:ASP:H	2.28	0.42
8:H:89:THR:HB	8:H:97:CYS:SG	2.60	0.42
9:I:241:LEU:HB3	10:J:199:LEU:HD22	2.02	0.42
5:e:278:GLN:O	5:e:282:THR:HG23	2.19	0.42
5:e:311:SER:OG	5:e:314:ASN:HB2	2.19	0.42
9:i:79:ALA:HB2	10:j:129:ALA:HB2	2.02	0.42
13:m:339:ASP:OD1	13:m:339:ASP:N	2.43	0.42
3:C:4:ARG:NH1	7:G:10:GLN:HG3	2.35	0.42
3:C:41:ASP:OD1	3:C:41:ASP:N	2.53	0.42
5:E:308:ASP:OD1	5:E:309:GLN:N	2.47	0.42
3:c:192:GLU:CD	3:c:192:GLU:H	2.28	0.42
4:d:115:GLN:O	4:d:118:SER:OG	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:201:HIS:NE2	7:g:206:ASP:HB2	2.35	0.42
9:i:241:LEU:HB3	10:j:199:LEU:HD22	2.02	0.42
6:F:236:GLY:HA3	6:F:386:PHE:CZ	2.55	0.41
9:I:72:CYS:SG	9:I:127:LEU:HB3	2.60	0.41
1:a:72:ASN:HB2	1:a:105:GLU:OE2	2.20	0.41
7:g:201:HIS:CE1	7:g:203:LYS:HD3	2.55	0.41
12:l:298:TYR:C	12:l:300:PRO:HD3	2.45	0.41
6:F:182:ARG:NH2	6:F:187:GLU:OE1	2.53	0.41
7:G:201:HIS:CE1	7:G:203:LYS:HD3	2.55	0.41
11:K:83:ALA:HA	11:K:86:MET:HE3	2.02	0.41
1:a:242:TRP:O	1:a:246:VAL:HG23	2.20	0.41
3:c:41:ASP:OD1	3:c:41:ASP:N	2.53	0.41
9:i:72:CYS:SG	9:i:127:LEU:HB3	2.60	0.41
9:i:153:PHE:HB2	9:i:167:LEU:HD13	2.02	0.41
12:l:145:ALA:HB3	12:l:197:GLY:O	2.20	0.41
3:C:82:VAL:HG12	3:C:140:PHE:CE1	2.56	0.41
5:E:240:SER:OG	5:E:255:GLN:NE2	2.53	0.41
6:F:348:THR:HG22	6:F:351:GLU:HG3	2.03	0.41
8:H:243:ILE:HA	8:H:244:PRO:HD3	1.92	0.41
5:e:284:ARG:NH2	5:e:300:ASP:OD2	2.54	0.41
6:f:348:THR:HG22	6:f:351:GLU:HG3	2.02	0.41
7:g:42:CYS:C	7:g:44:ASP:H	2.28	0.41
8:h:228:ILE:HB	8:h:243:ILE:CG1	2.50	0.41
14:n:111:VAL:HG22	14:n:116:THR:HG22	2.03	0.41
8:H:228:ILE:HB	8:H:243:ILE:CG1	2.50	0.41
11:K:129:MET:HA	11:K:134:THR:O	2.20	0.41
14:N:111:VAL:HG22	14:N:116:THR:HG22	2.02	0.41
6:f:377:ILE:O	6:f:389:PHE:HB2	2.20	0.41
8:h:89:THR:HB	8:h:97:CYS:SG	2.60	0.41
10:j:56:LEU:O	10:j:60:GLN:HG3	2.19	0.41
13:m:312:ASP:HB3	13:m:315:THR:HG22	2.03	0.41
3:C:192:GLU:CD	3:C:192:GLU:H	2.28	0.41
4:D:168:VAL:O	4:D:172:MET:HG2	2.20	0.41
4:D:170:GLU:O	4:D:174:LYS:NZ	2.54	0.41
6:F:214:LYS:HG3	6:F:374:ASN:HA	2.01	0.41
9:I:229:GLN:HG3	13:m:303:ASN:HD21	1.85	0.41
3:c:4:ARG:NH1	7:g:10:GLN:HG3	2.35	0.41
5:e:335:ILE:HA	5:e:338:ILE:HD12	2.01	0.41
10:j:21:VAL:HG22	10:j:189:ILE:HG12	2.02	0.41
11:k:13:TYR:CE2	11:k:15:MET:HE3	2.56	0.41
6:F:377:ILE:O	6:F:389:PHE:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:201:HIS:NE2	7:G:206:ASP:HB2	2.35	0.41
13:M:303:ASN:HD21	9:i:229:GLN:HG3	1.85	0.41
6:f:204:GLY:HA3	6:f:352:LEU:HD11	2.03	0.41
7:g:44:ASP:O	7:g:217:CYS:HB2	2.20	0.41
3:C:227:SER:O	9:I:246:ARG:NH1	2.54	0.41
4:D:145:TRP:CE2	4:D:155:ALA:HB2	2.56	0.41
11:K:10:CYS:SG	11:K:162:LEU:HB2	2.60	0.41
11:K:13:TYR:HB3	11:K:195:THR:HG22	2.02	0.41
2:b:41:GLY:HA2	2:b:142:TYR:CD1	2.56	0.41
10:j:87:PHE:CZ	10:j:91:ILE:HD11	2.56	0.41
2:B:116:TYR:O	2:B:120:THR:HG23	2.21	0.41
5:E:109:ASP:OD1	5:E:109:ASP:N	2.53	0.41
8:H:121:GLN:HG2	8:H:128:VAL:HG23	2.03	0.41
9:I:70:ILE:HG12	9:I:105:VAL:HG22	2.02	0.41
13:M:135:THR:N	13:M:150:ASP:OD1	2.41	0.41
1:A:141:ASP:OD1	9:I:101:LYS:NZ	2.53	0.41
1:A:185:GLN:HG3	1:A:190:LEU:HD13	2.02	0.41
3:C:67:SER:OG	10:J:79:GLU:OE1	2.28	0.41
7:G:44:ASP:O	7:G:217:CYS:HB2	2.21	0.41
10:J:87:PHE:CZ	10:J:91:ILE:HD11	2.56	0.41
1:a:59:ARG:HG2	1:a:61:ASP:OD1	2.21	0.41
3:c:17:ARG:NH2	3:c:22:GLU:OE1	2.47	0.41
3:c:21:VAL:O	3:c:25:VAL:HG23	2.21	0.41
3:c:82:VAL:HG12	3:c:140:PHE:CE1	2.56	0.41
11:k:10:CYS:SG	11:k:162:LEU:HB2	2.61	0.41
11:k:83:ALA:HA	11:k:86:MET:HE3	2.03	0.41
9:I:79:ALA:HB2	10:J:129:ALA:HB2	2.02	0.41
2:b:42:VAL:O	2:b:211:VAL:N	2.46	0.41
4:d:145:TRP:CE2	4:d:155:ALA:HB2	2.56	0.41
1:A:59:ARG:HG2	1:A:61:ASP:OD1	2.22	0.40
3:C:24:ALA:O	3:C:28:ILE:HG13	2.22	0.40
4:D:45:VAL:HG22	4:D:205:GLU:HB3	2.04	0.40
5:E:138:LEU:HB2	5:E:149:ALA:HB3	2.04	0.40
10:J:21:VAL:HG22	10:J:189:ILE:HG12	2.03	0.40
13:M:188:GLN:OE1	13:M:192:MET:HE3	2.20	0.40
2:b:137:VAL:HG22	2:b:142:TYR:CD1	2.57	0.40
2:b:143:HIS:HB3	2:b:145:TYR:CE1	2.55	0.40
13:m:261:TYR:OH	13:m:280:ASN:OD1	2.37	0.40
2:B:32:THR:OG1	2:B:163:THR:O	2.30	0.40
5:E:166:LYS:N	5:E:316:GLU:OE1	2.54	0.40
10:J:12:MET:HE1	10:J:167:ALA:HA	2.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:182:MET:HB2	13:M:231:TYR:HB3	2.02	0.40
6:f:235:VAL:HG11	6:f:273:MET:SD	2.62	0.40
11:k:13:TYR:HB3	11:k:195:THR:HG22	2.02	0.40
14:n:176:ARG:HA	14:n:176:ARG:HD3	1.87	0.40
3:C:214:ASP:OD1	3:C:251:ARG:NH1	2.54	0.40
4:D:51:VAL:C	4:D:53:LEU:H	2.29	0.40
6:F:204:GLY:HA3	6:F:352:LEU:HD11	2.03	0.40
11:K:13:TYR:CE2	11:K:15:MET:HE3	2.56	0.40
1:a:141:ASP:OD1	9:i:101:LYS:NZ	2.53	0.40
3:c:144:GLY:HA2	3:c:221:MET:HG2	2.03	0.40
10:j:68:GLN:O	10:j:72:GLU:HG2	2.22	0.40
1:A:72:ASN:HB2	1:A:105:GLU:OE2	2.21	0.40
7:G:82:LEU:O	7:G:86:ARG:HG2	2.22	0.40
1:a:82:PRO:HB2	7:g:121:HIS:CD2	2.57	0.40
3:c:59:GLU:O	3:c:61:MET:N	2.53	0.40
3:c:213:LEU:HD13	3:c:251:ARG:HE	1.87	0.40
4:d:222:LEU:O	4:d:226:VAL:HG13	2.21	0.40
11:k:181:ARG:HD3	11:k:181:ARG:HA	1.71	0.40
6:F:372:VAL:HG12	6:F:391:GLU:HA	2.04	0.40
9:I:153:PHE:HB2	9:I:167:LEU:HD13	2.02	0.40
1:a:185:GLN:HG3	1:a:190:LEU:HD13	2.03	0.40
3:c:45:LEU:HD13	3:c:81:SER:HB2	2.04	0.40
3:c:201:VAL:O	3:c:205:THR:HG23	2.21	0.40
7:g:124:THR:HG22	7:g:131:PRO:HB3	2.03	0.40
8:h:136:LEU:HD23	8:h:136:LEU:HA	1.92	0.40
10:j:120:TYR:CE1	10:j:132:GLU:HG2	2.57	0.40
12:l:115:VAL:HB	12:l:132:LYS:HB2	2.04	0.40

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	A	243/250 (97%)	235 (97%)	8 (3%)	0	100	100
1	a	243/250 (97%)	236 (97%)	7 (3%)	0	100	100
2	B	227/231 (98%)	219 (96%)	8 (4%)	0	100	100
2	b	227/231 (98%)	218 (96%)	9 (4%)	0	100	100
3	C	270/285 (95%)	257 (95%)	13 (5%)	0	100	100
3	c	270/285 (95%)	257 (95%)	13 (5%)	0	100	100
4	D	238/248 (96%)	231 (97%)	7 (3%)	0	100	100
4	d	238/248 (96%)	231 (97%)	7 (3%)	0	100	100
5	E	233/344 (68%)	228 (98%)	5 (2%)	0	100	100
5	e	233/344 (68%)	228 (98%)	5 (2%)	0	100	100
6	F	236/428 (55%)	227 (96%)	9 (4%)	0	100	100
6	f	236/428 (55%)	227 (96%)	9 (4%)	0	100	100
7	G	228/238 (96%)	223 (98%)	5 (2%)	0	100	100
7	g	228/238 (96%)	223 (98%)	5 (2%)	0	100	100
8	H	227/229 (99%)	224 (99%)	3 (1%)	0	100	100
8	h	227/229 (99%)	224 (99%)	3 (1%)	0	100	100
9	I	217/225 (96%)	211 (97%)	6 (3%)	0	100	100
9	i	217/225 (96%)	211 (97%)	6 (3%)	0	100	100
10	J	202/205 (98%)	189 (94%)	13 (6%)	0	100	100
10	j	202/205 (98%)	190 (94%)	12 (6%)	0	100	100
11	K	204/206 (99%)	200 (98%)	4 (2%)	0	100	100
11	k	204/206 (99%)	201 (98%)	3 (2%)	0	100	100
12	L	200/203 (98%)	194 (97%)	6 (3%)	0	100	100
12	l	200/203 (98%)	194 (97%)	6 (3%)	0	100	100
13	M	212/339 (62%)	208 (98%)	4 (2%)	0	100	100
13	m	212/339 (62%)	208 (98%)	4 (2%)	0	100	100
14	N	216/219 (99%)	211 (98%)	5 (2%)	0	100	100
14	n	216/219 (99%)	211 (98%)	5 (2%)	0	100	100
All	All	6306/7300 (86%)	6116 (97%)	190 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	193/197 (98%)	193 (100%)	0	100	100
1	a	193/197 (98%)	193 (100%)	0	100	100
2	B	188/190 (99%)	188 (100%)	0	100	100
2	b	188/190 (99%)	188 (100%)	0	100	100
3	C	229/241 (95%)	229 (100%)	0	100	100
3	c	229/241 (95%)	229 (100%)	0	100	100
4	D	201/208 (97%)	201 (100%)	0	100	100
4	d	201/208 (97%)	200 (100%)	1 (0%)	81	92
5	E	197/301 (65%)	196 (100%)	1 (0%)	81	92
5	e	197/301 (65%)	196 (100%)	1 (0%)	81	92
6	F	200/363 (55%)	200 (100%)	0	100	100
6	f	200/363 (55%)	200 (100%)	0	100	100
7	G	185/190 (97%)	185 (100%)	0	100	100
7	g	185/190 (97%)	185 (100%)	0	100	100
8	H	184/184 (100%)	184 (100%)	0	100	100
8	h	184/184 (100%)	184 (100%)	0	100	100
9	I	180/185 (97%)	180 (100%)	0	100	100
9	i	180/185 (97%)	180 (100%)	0	100	100
10	J	167/168 (99%)	167 (100%)	0	100	100
10	j	167/168 (99%)	167 (100%)	0	100	100
11	K	172/172 (100%)	172 (100%)	0	100	100
11	k	172/172 (100%)	172 (100%)	0	100	100
12	L	162/164 (99%)	162 (100%)	0	100	100
12	l	162/164 (99%)	162 (100%)	0	100	100
13	M	181/288 (63%)	181 (100%)	0	100	100
13	m	181/288 (63%)	181 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	181/182 (100%)	181 (100%)	0	100	100
14	n	181/182 (100%)	181 (100%)	0	100	100
All	All	5240/6066 (86%)	5237 (100%)	3 (0%)	87	96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	328	HIS
4	d	203	ASN
5	e	328	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	100	ASN
4	D	23	GLN
4	D	92	GLN
5	E	197	GLN
5	E	278	GLN
6	F	331	GLN
7	G	54	HIS
7	G	64	ASN
7	G	68	HIS
7	G	147	GLN
8	H	216	HIS
10	J	43	HIS
11	K	22	ASN
11	K	136	GLN
11	K	165	GLN
12	L	123	GLN
12	L	296	HIS
13	M	154	ASN
13	M	160	HIS
13	M	204	ASN
14	N	62	GLN
14	N	94	GLN
14	N	153	ASN
4	d	23	GLN
4	d	54	GLN
4	d	92	GLN

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Continued from previous page...

Mol	Chain	Res	Type
5	e	278	GLN
6	f	331	GLN
7	g	54	HIS
7	g	64	ASN
7	g	147	GLN
8	h	196	ASN
8	h	216	HIS
9	i	115	HIS
10	j	43	HIS
11	k	22	ASN
11	k	136	GLN
12	l	296	HIS
13	m	154	ASN
13	m	163	HIS
13	m	204	ASN
13	m	303	ASN
14	n	62	GLN
14	n	66	ASN
14	n	94	GLN
14	n	153	ASN

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](#)

2 ligands are modelled in this entry.

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	$\# Z > 2$
15	KFC	l	901	-	29,29,29	1.07	2 (6%)	40,40,40	1.02	2 (5%)
15	KFC	L	901	-	29,29,29	1.07	2 (6%)	40,40,40	1.03	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
15	KFC	l	901	-	-	1/12/19/19	0/4/4/4
15	KFC	L	901	-	-	1/12/19/19	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	L	901	KFC	C9-N10	-2.56	1.33	1.37
15	l	901	KFC	C9-N10	-2.50	1.33	1.37
15	l	901	KFC	C16-N14	-2.29	1.35	1.40
15	L	901	KFC	C16-N14	-2.27	1.35	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	L	901	KFC	C11-N10-C9	2.53	121.38	117.56
15	l	901	KFC	C11-N10-C9	2.49	121.32	117.56
15	l	901	KFC	C22-N7-C6	-2.02	118.73	122.56
15	L	901	KFC	C22-N7-C6	-2.01	118.75	122.56

There are no chirality outliers.

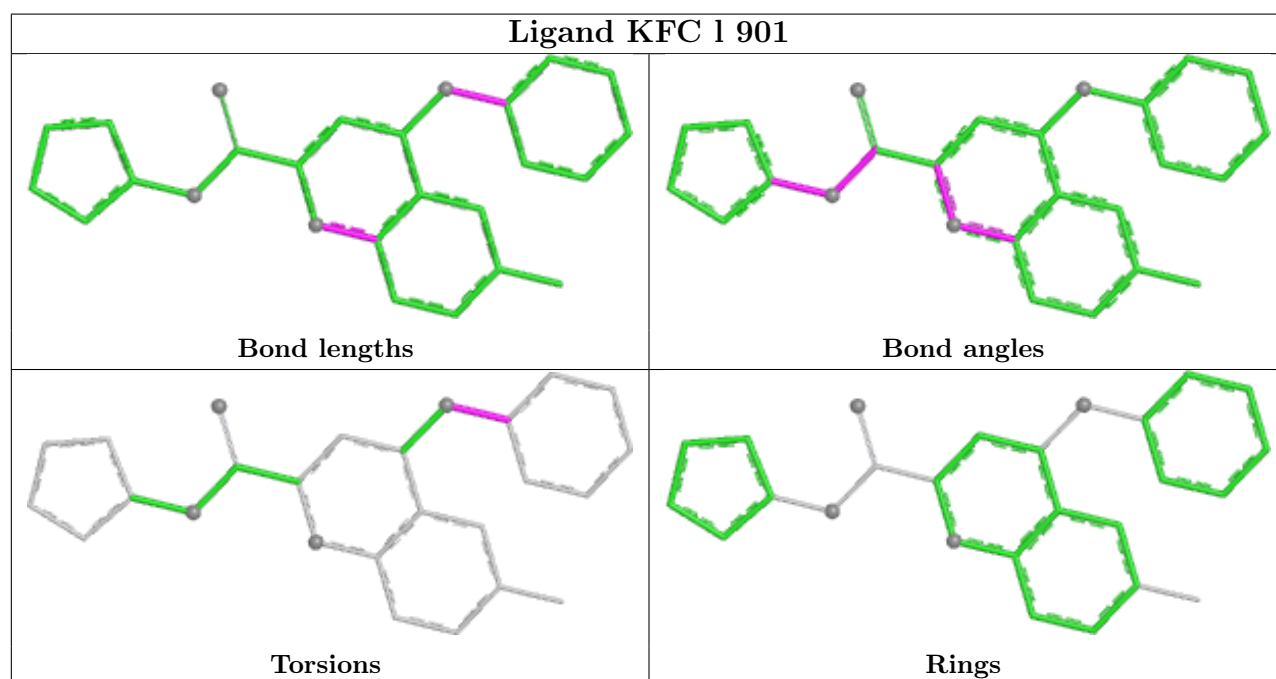
All (2) torsion outliers are listed below:

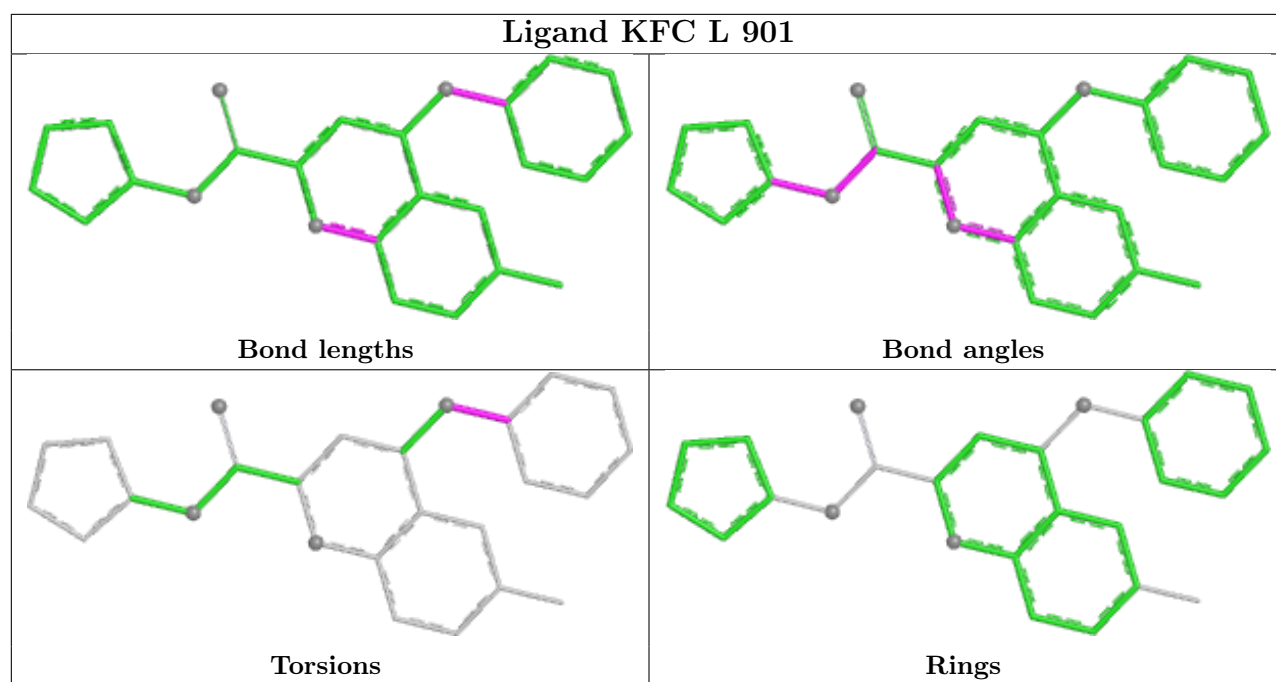
Mol	Chain	Res	Type	Atoms
15	L	901	KFC	C17-C16-N14-C13
15	l	901	KFC	C17-C16-N14-C13

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 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.

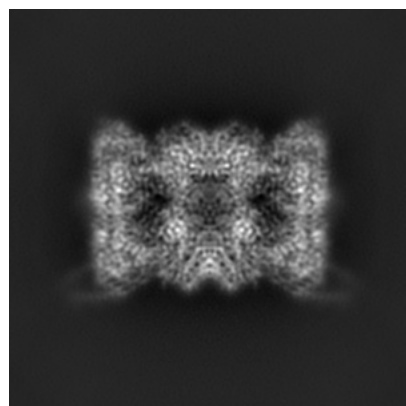
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15025. These allow visual inspection of the internal detail of the map and identification of artifacts.

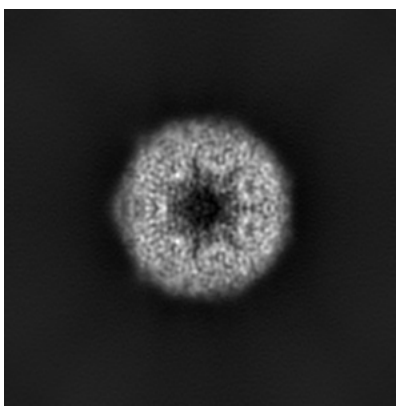
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

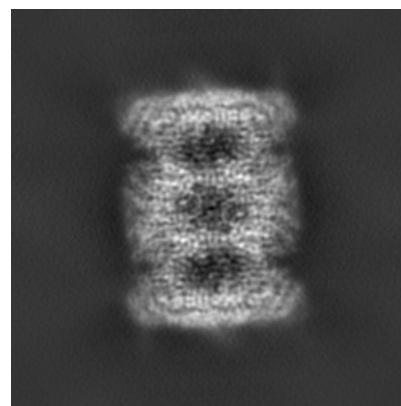
6.1.1 Primary map



X

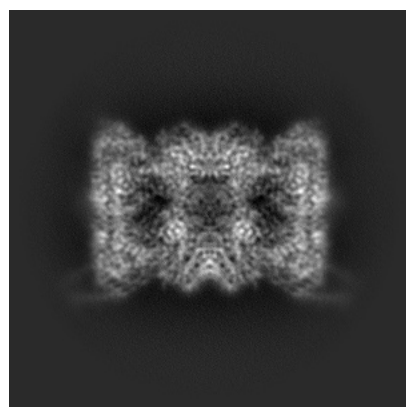


Y

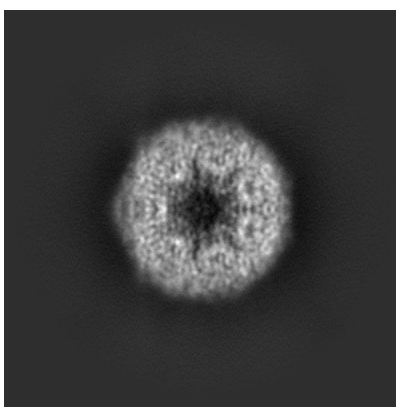


Z

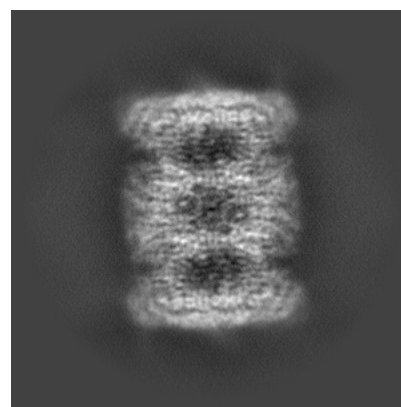
6.1.2 Raw map



X



Y

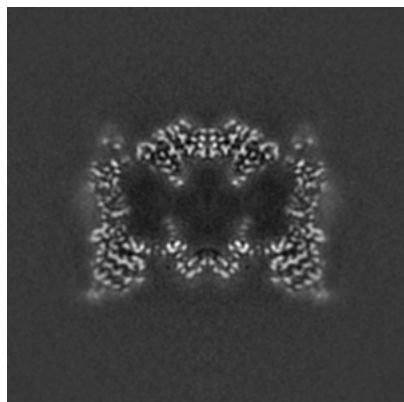


Z

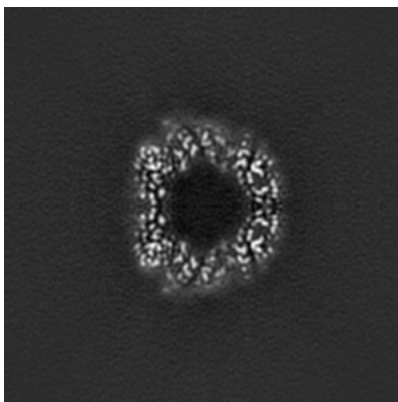
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

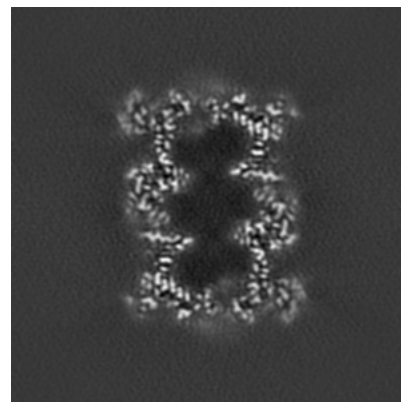
6.2.1 Primary map



X Index: 150

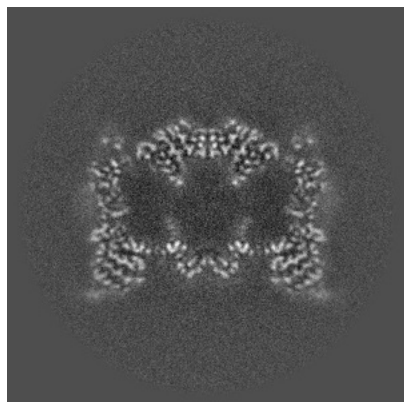


Y Index: 150

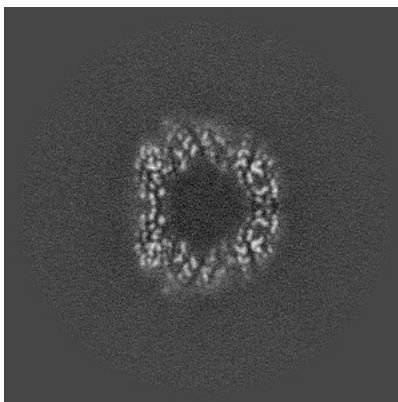


Z Index: 150

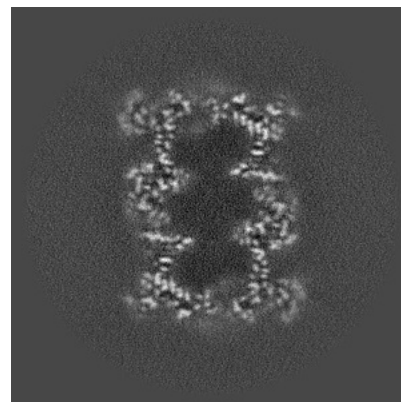
6.2.2 Raw map



X Index: 150



Y Index: 150

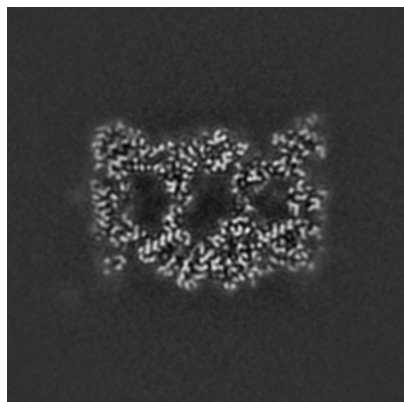


Z Index: 150

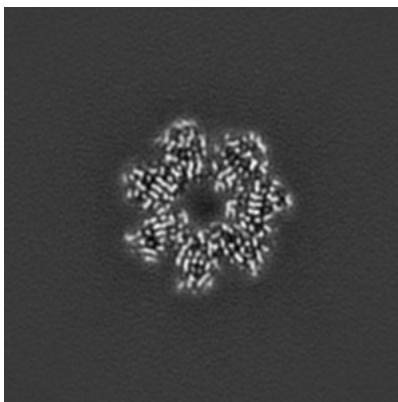
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

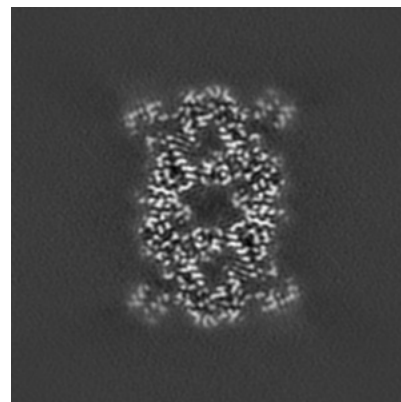
6.3.1 Primary map



X Index: 173

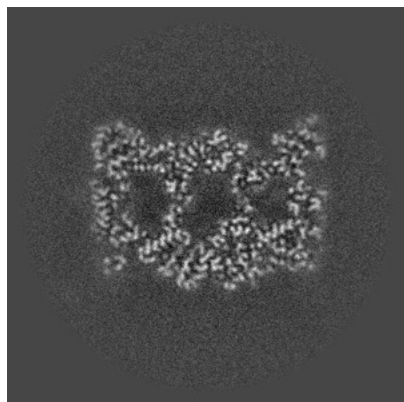


Y Index: 171

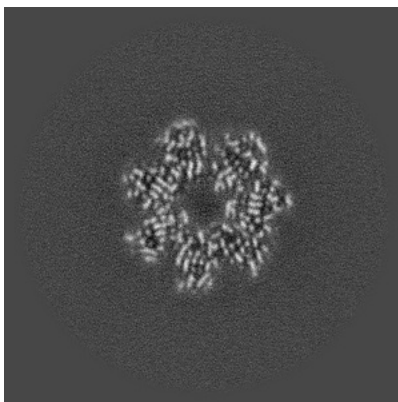


Z Index: 177

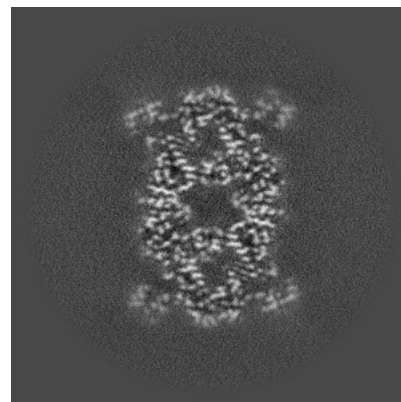
6.3.2 Raw map



X Index: 173



Y Index: 171

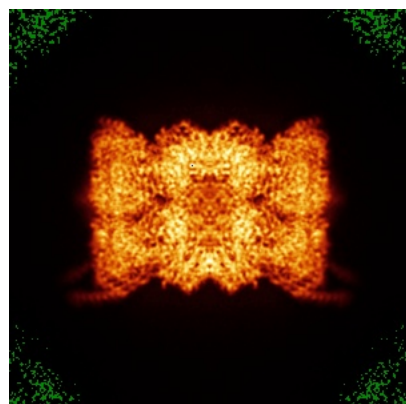


Z Index: 177

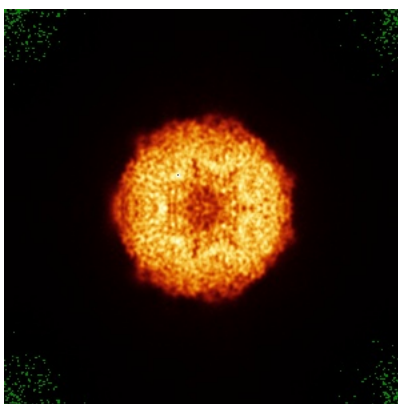
The images above show the largest variance slices of the map in three orthogonal directions.

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

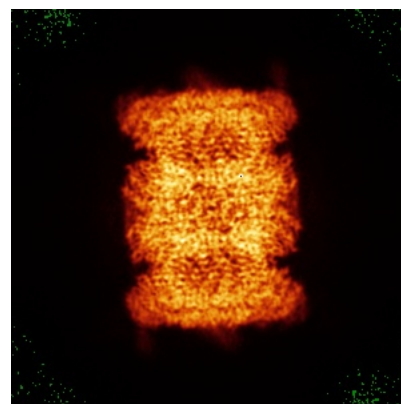
6.4.1 Primary map



X

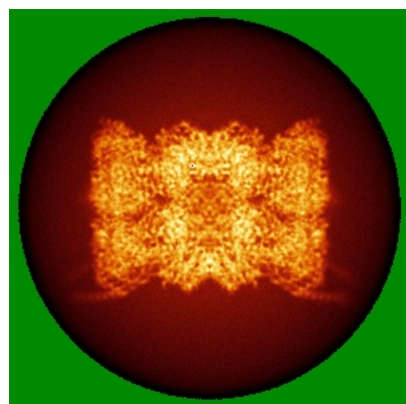


Y

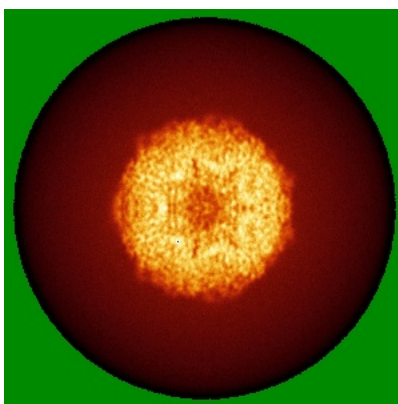


Z

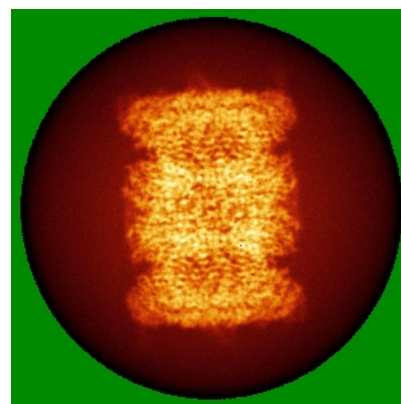
6.4.2 Raw map



X



Y

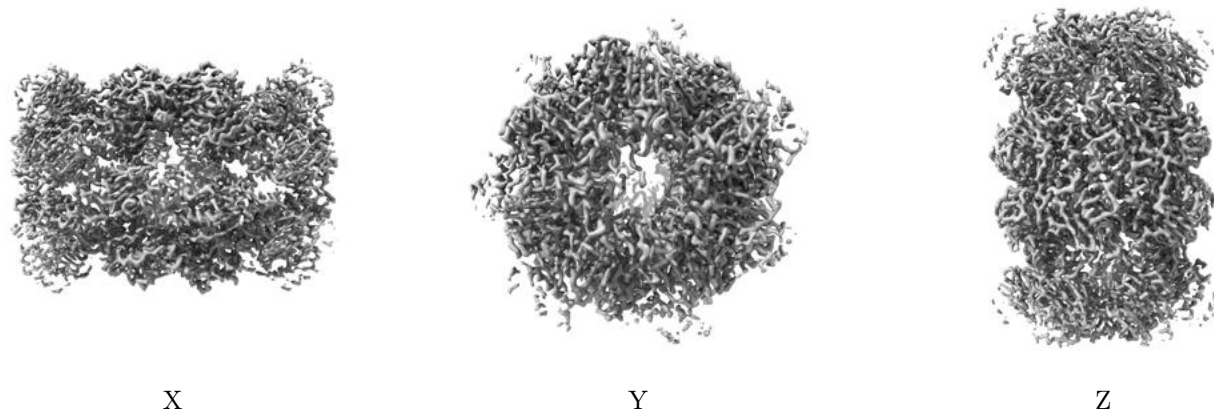


Z

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

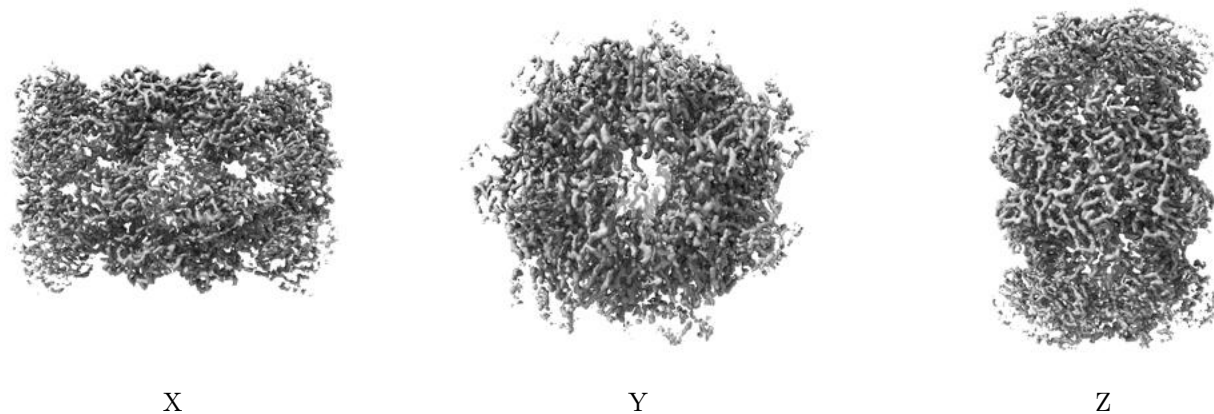
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

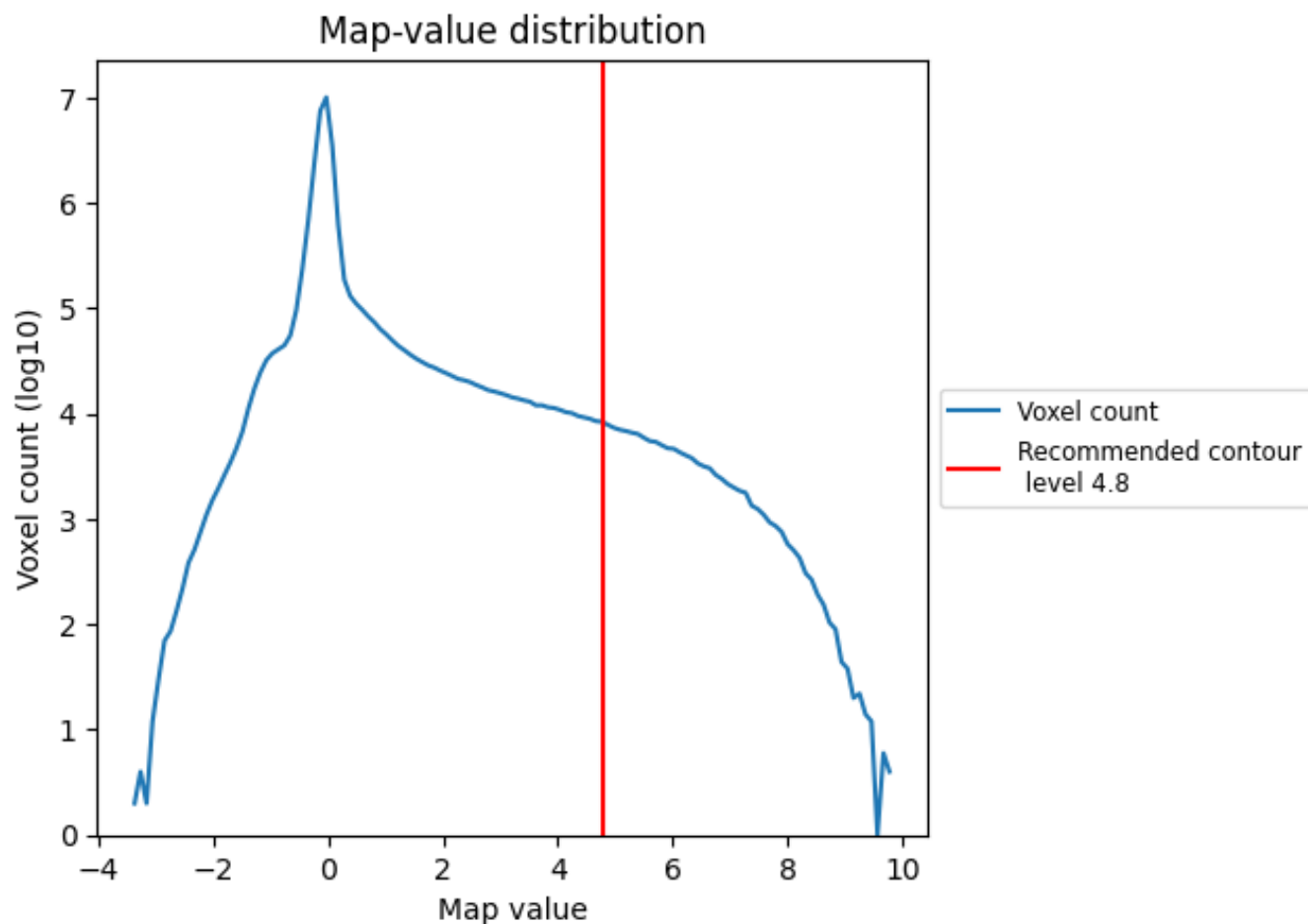
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

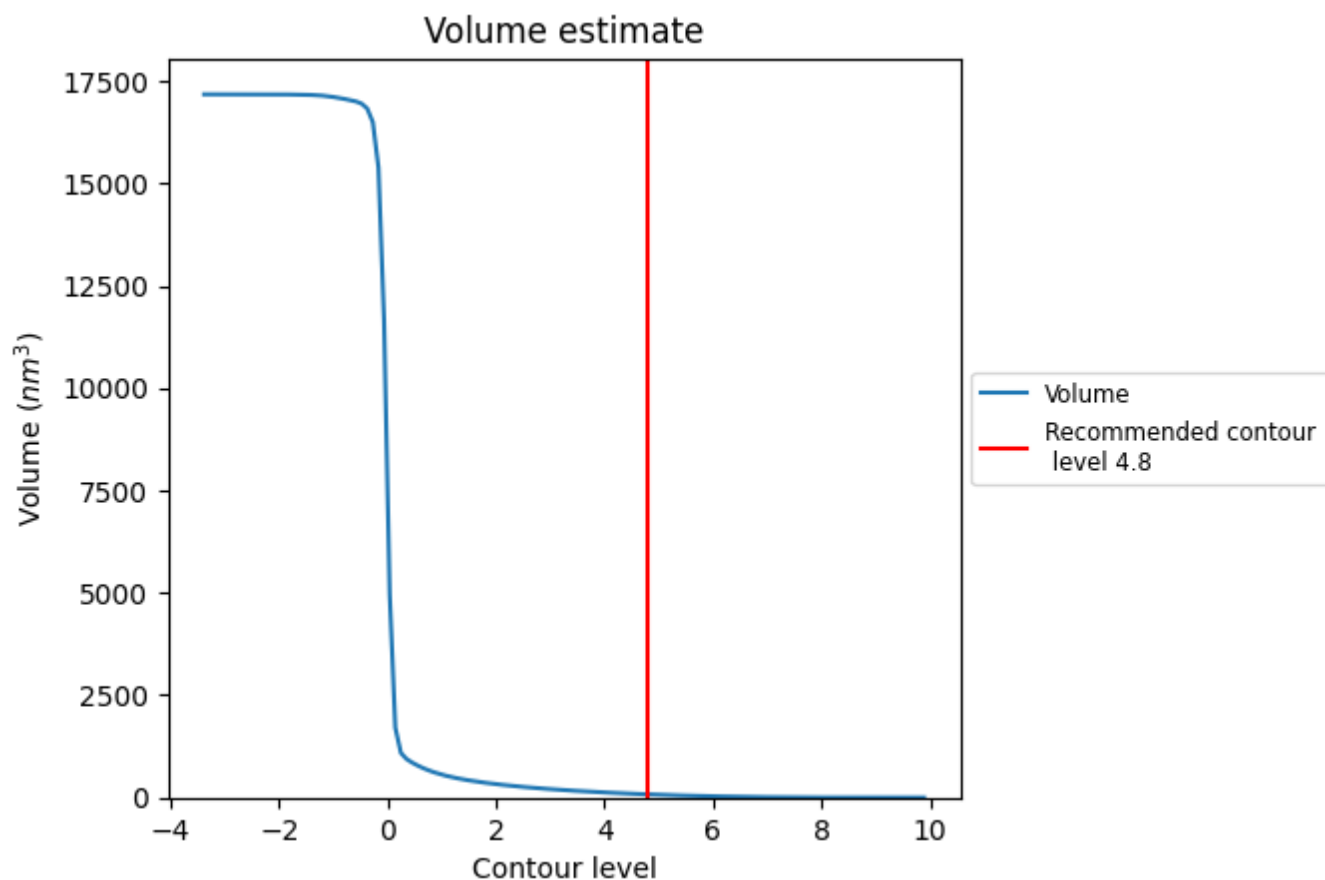
This section contains the results of statistical analysis of the map.

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.

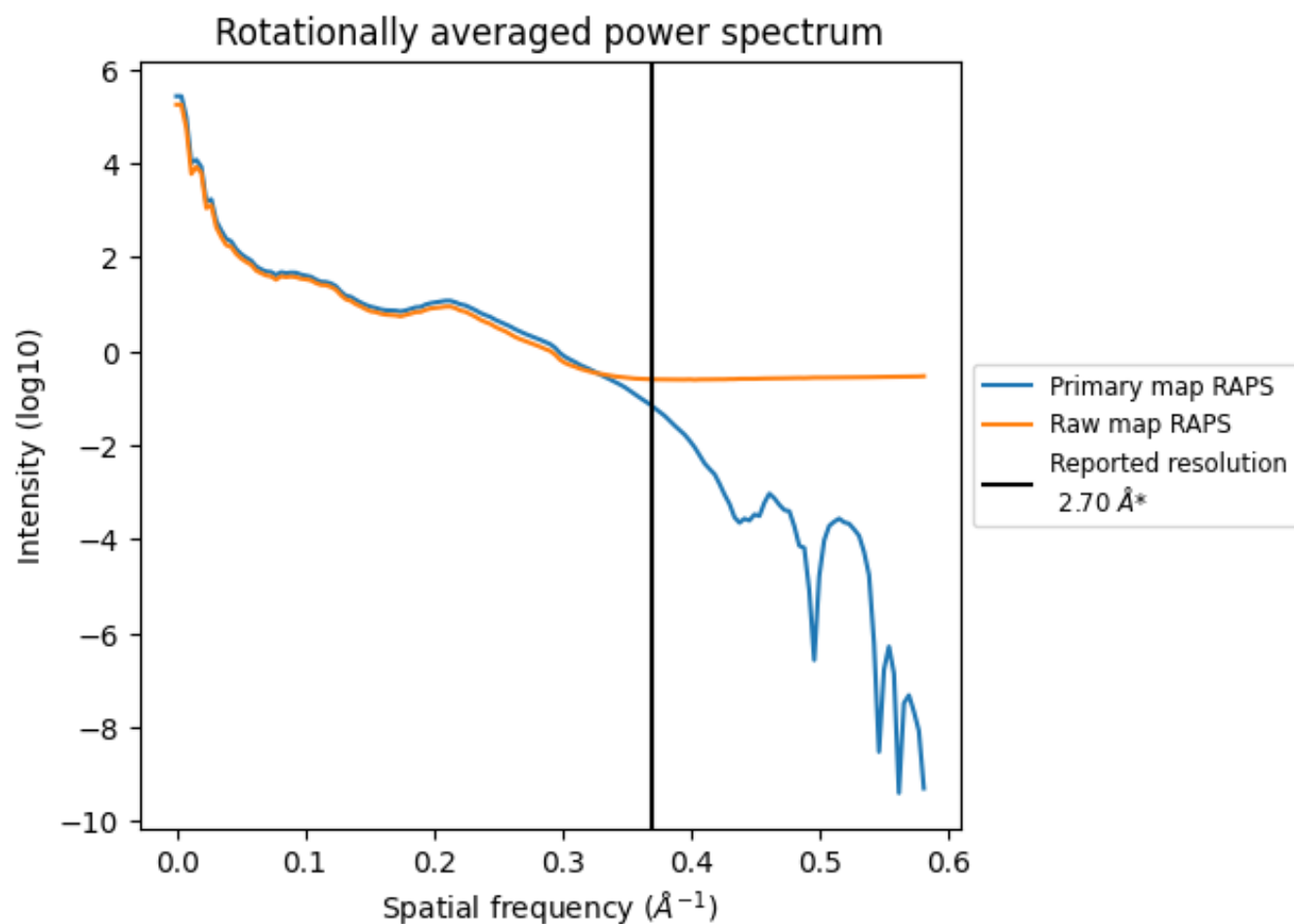
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 78 nm^3 ; this corresponds to an approximate mass of 70 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 ⓘ

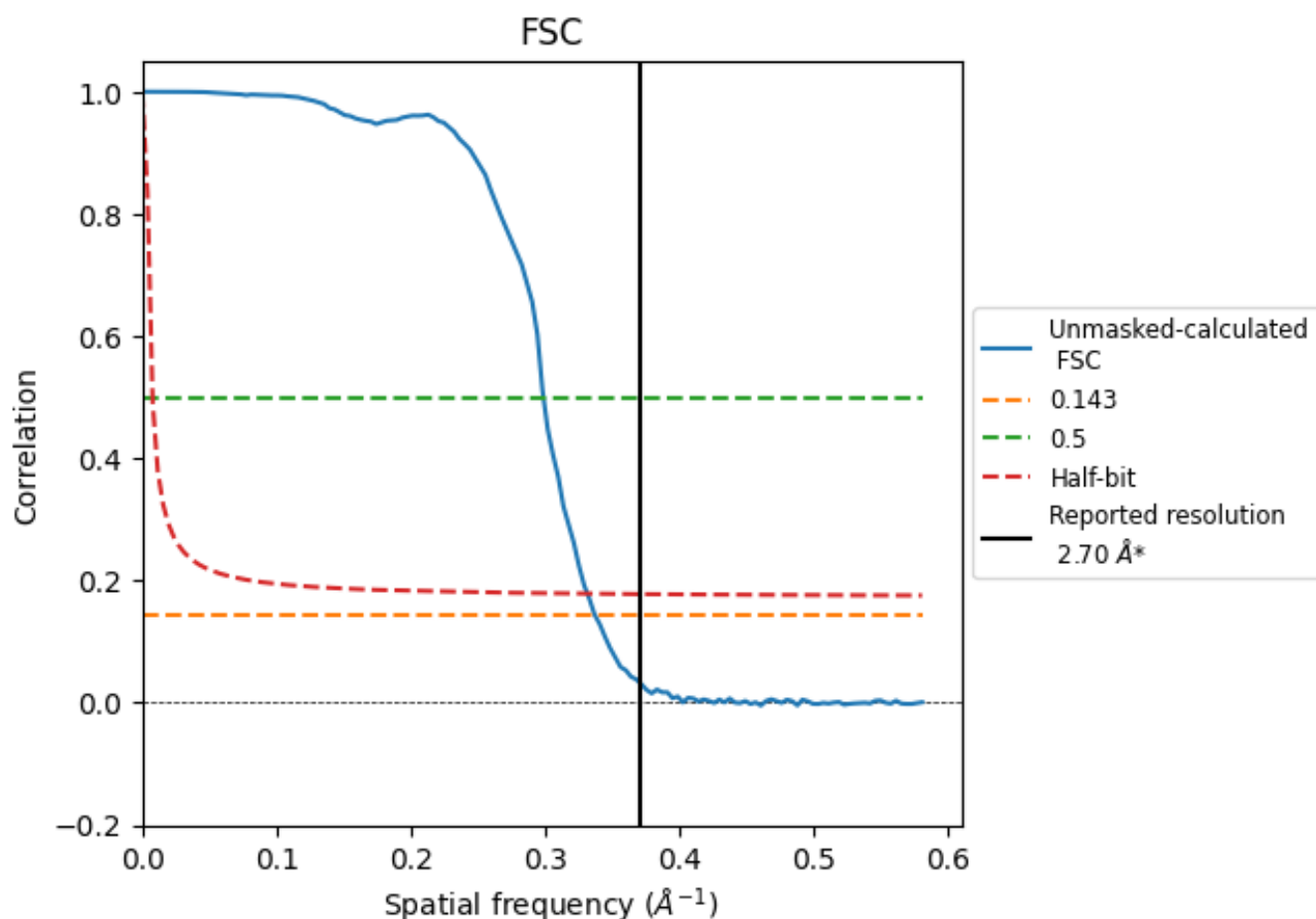


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

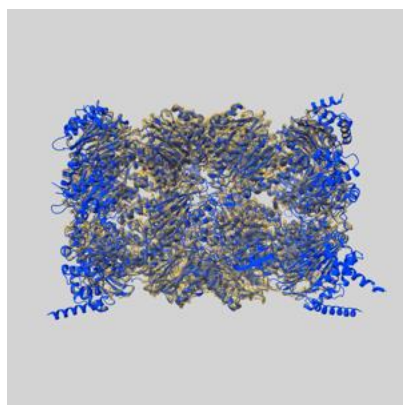
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.96	3.34	3.01

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

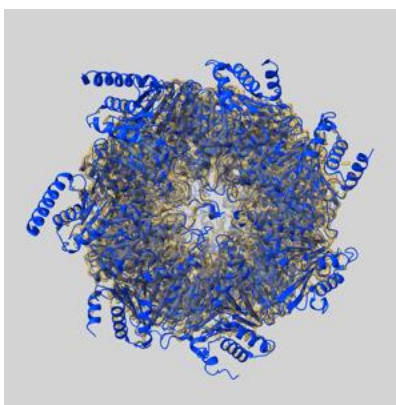
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15025 and PDB model 7ZYJ. Per-residue inclusion information can be found in section [3](#) on page [8](#).

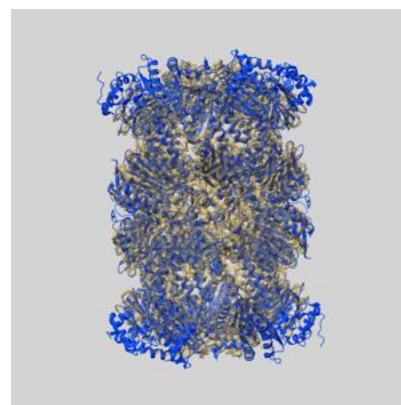
9.1 Map-model overlay [i](#)



X



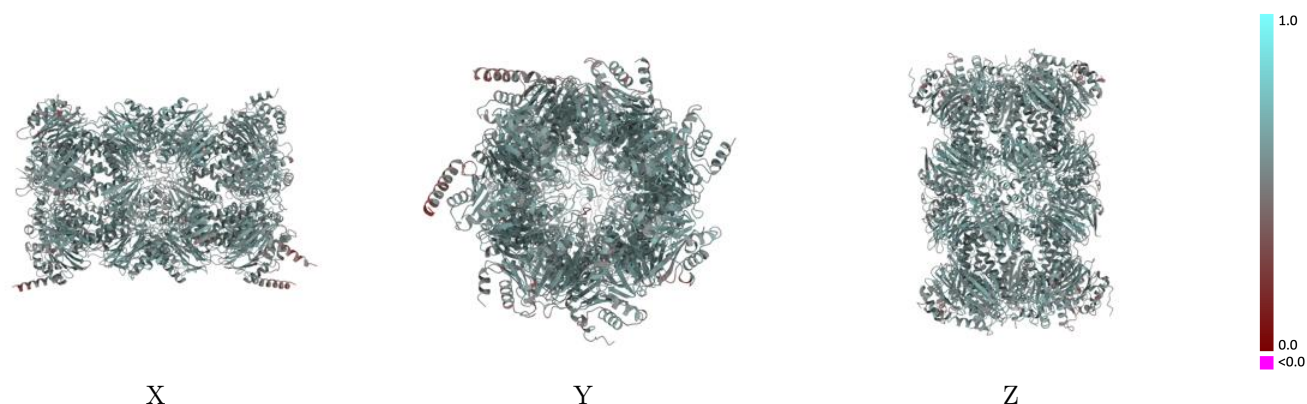
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.8 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](#)

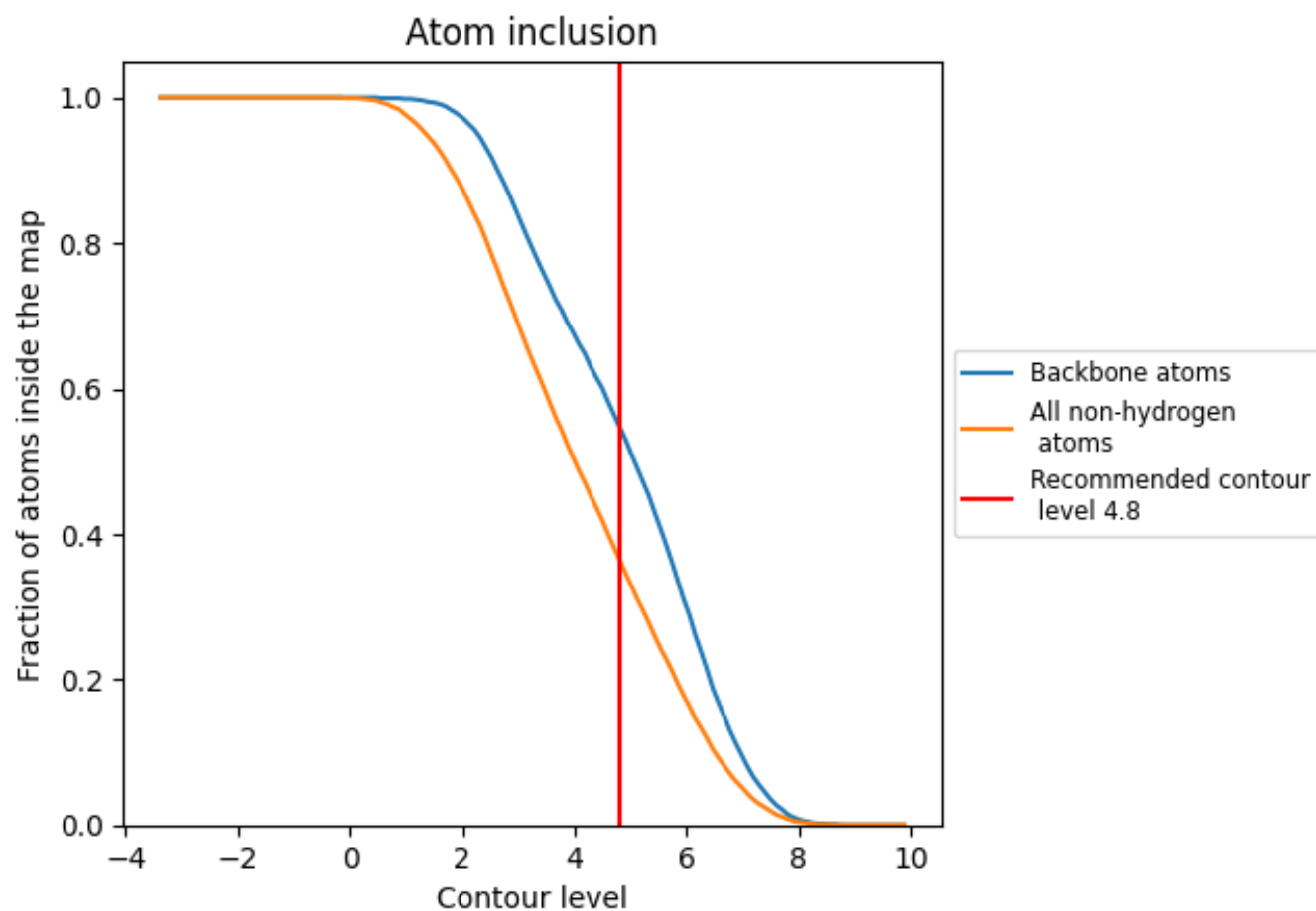


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 55% of all backbone atoms, 36% 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 (4.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3650	 0.5650
A	 0.3280	 0.5620
B	 0.2920	 0.5600
C	 0.2300	 0.5470
D	 0.2670	 0.5400
E	 0.2580	 0.5460
F	 0.2400	 0.5560
G	 0.3180	 0.5570
H	 0.5340	 0.5950
I	 0.3990	 0.5670
J	 0.4520	 0.5690
K	 0.4760	 0.5770
L	 0.5100	 0.5870
M	 0.3810	 0.5650
N	 0.5220	 0.5890
a	 0.3260	 0.5620
b	 0.2940	 0.5600
c	 0.2300	 0.5470
d	 0.2660	 0.5430
e	 0.2590	 0.5440
f	 0.2380	 0.5590
g	 0.3180	 0.5570
h	 0.5350	 0.5980
i	 0.3980	 0.5640
j	 0.4520	 0.5720
k	 0.4770	 0.5790
l	 0.5100	 0.5870
m	 0.3820	 0.5660
n	 0.5220	 0.5910

