



Full wwPDB EM Validation Report ⓘ

Apr 20, 2026 – 08:05 PM JST

PDB ID : 9K58 / pdb_00009k58
EMDB ID : EMD-62084
Title : Structure of substrate-engaged single-cap human proteasome in state EB
Authors : Wu, Z.; Chen, E.; Mao, Y.
Deposited on : 2024-10-21
Resolution : 4.50 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:

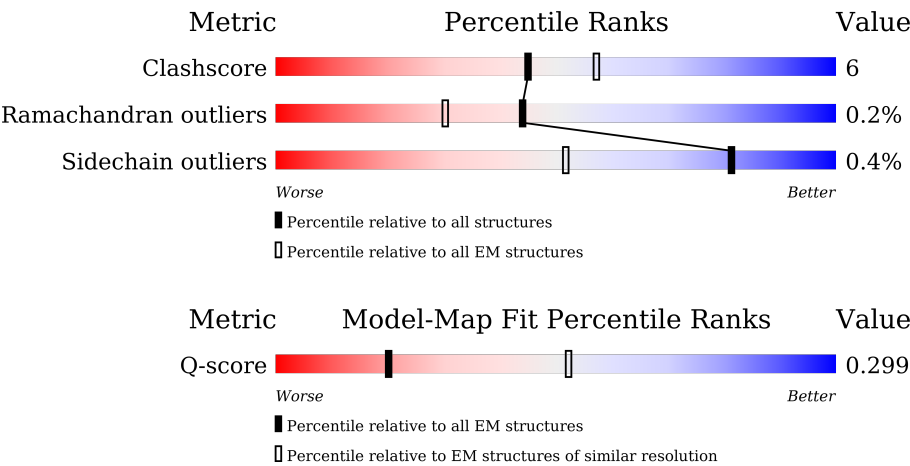
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.50 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	2937 (4.00 - 5.00)

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	433	<div><div>22%</div><div><div></div><div></div><div></div><div></div></div><div>78%</div><div><div></div><div></div><div></div><div></div></div><div>15%</div><div><div></div><div></div><div></div><div></div></div><div>6%</div></div>
2	B	440	<div><div>26%</div><div><div></div><div></div><div></div><div></div></div><div>71%</div><div><div></div><div></div><div></div><div></div></div><div>18%</div><div><div></div><div></div><div></div><div></div></div><div>10%</div></div>
3	C	398	<div><div>38%</div><div><div></div><div></div><div></div><div></div></div><div>72%</div><div><div></div><div></div><div></div><div></div></div><div>22%</div><div><div></div><div></div><div></div><div></div></div><div>• •</div></div>
4	D	418	<div><div>20%</div><div><div></div><div></div><div></div><div></div></div><div>72%</div><div><div></div><div></div><div></div><div></div></div><div>17%</div><div><div></div><div></div><div></div><div></div></div><div>• 9%</div></div>




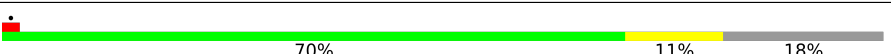
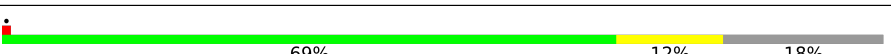
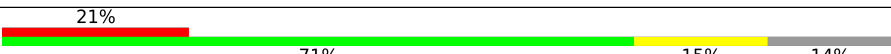
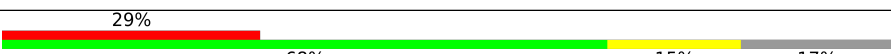
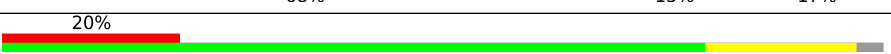

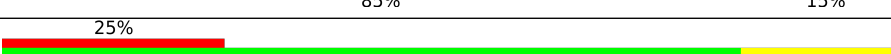
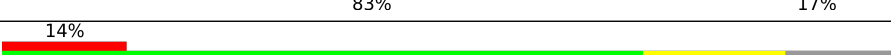
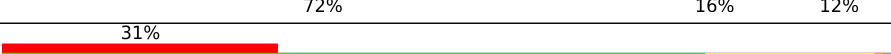
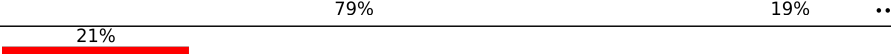
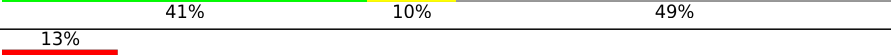





Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	403	
6	F	439	
7	G	246	
7	g	246	
8	H	234	
8	h	234	
9	I	261	
9	i	261	
10	J	248	
10	j	248	
11	K	241	
11	k	241	
12	L	263	
12	l	263	
13	M	255	
13	m	255	
14	N	239	
14	n	239	
15	O	277	
15	o	277	
16	P	205	
16	p	205	
17	Q	201	
17	q	201	
18	R	263	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
18	r	263	
19	S	241	
19	s	241	
20	T	264	
20	t	264	
21	U	953	
22	V	534	
23	W	456	
24	X	422	
25	Y	389	
26	Z	324	
27	a	376	
28	b	377	
29	c	310	
30	d	350	
31	e	70	
32	f	908	
33	u	76	
34	v	28	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 106247 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 26S proteasome regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	406	Total	C	N	O	S	0	0
			3164	1992	555	600	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	397	Total	C	N	O	S	0	0
			3099	1953	525	606	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	381	Total	C	N	O	S	0	0
			2978	1872	536	554	16		

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

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

- Molecule 5 is a protein called Proteasome 26S subunit, ATPase 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	389	Total	C	N	O	S	0	0
			3097	1947	552	581	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	415	Total	C	N	O	S	0	0
			3251	2038	561	634	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	244	Total	C	N	O	S	0	0
			1889	1198	316	362	13		
7	g	244	Total	C	N	O	S	0	0
			1880	1193	318	356	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	232	Total	C	N	O	S	0	0
			1805	1152	305	342	6		
8	h	232	Total	C	N	O	S	0	0
			1805	1154	307	338	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	250	Total	C	N	O	S	0	0
			1955	1234	336	375	10		
9	i	250	Total	C	N	O	S	0	0
			1955	1234	336	375	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	239	Total	C	N	O	S	0	0
			1880	1179	333	363	5		
10	j	239	Total	C	N	O	S	0	0
			1861	1168	332	356	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	234	Total	C	N	O	S	0	0
			1777	1117	295	354	11		
11	k	234	Total	C	N	O	S	0	0
			1782	1119	295	357	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	238	Total	C	N	O	S	0	0
			1866	1169	336	350	11		
12	l	238	Total	C	N	O	S	0	0
			1861	1165	335	350	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	240	Total	C	N	O	S	0	0
			1876	1191	321	353	11		
13	m	240	Total	C	N	O	S	0	0
			1881	1193	321	356	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	202	Total	C	N	O	S	0	0
			1514	949	258	295	12		
14	n	202	Total	C	N	O	S	0	0
			1510	947	258	293	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	220	Total	C	N	O	S	0	0
			1649	1038	279	320	12		
15	o	220	Total	C	N	O	S	0	0
			1659	1044	283	320	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	204	Total	C	N	O	S	0	0
			1587	1010	264	294	19		
16	p	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	199	Total	C	N	O	S	0	0
			1588	1017	270	292	9		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	199	Total	C	N	O	S	0	0
			1588	1017	270	292	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	201	Total	C	N	O	S	0	0
			1559	982	274	294	9		
18	r	201	Total	C	N	O	S	0	0
			1559	982	274	294	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	213	Total	C	N	O	S	0	0
			1641	1041	281	309	10		
19	s	213	Total	C	N	O	S	0	0
			1654	1047	284	313	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	216	Total	C	N	O	S	0	0
			1683	1062	291	318	12		
20	t	216	Total	C	N	O	S	0	0
			1687	1064	291	320	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	818	Total	C	N	O	S	0	0
			6373	4047	1084	1197	45		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	444	Total	C	N	O	S	0	0
			3612	2301	645	653	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	441	Total	C	N	O	S	0	0
			3596	2277	613	682	24		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	422	Total	C	N	O	S	0	0
			3335	2116	567	639	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	389	Total	C	N	O	S	0	0
			3202	2041	545	598	18		

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

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

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

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

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

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

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

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

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

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

- Molecule 31 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	e	50	Total	C	N	O	0	0
			425	260	65	100		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	844	Total	C	N	O	S	0	0
			6529	4126	1108	1250	45		

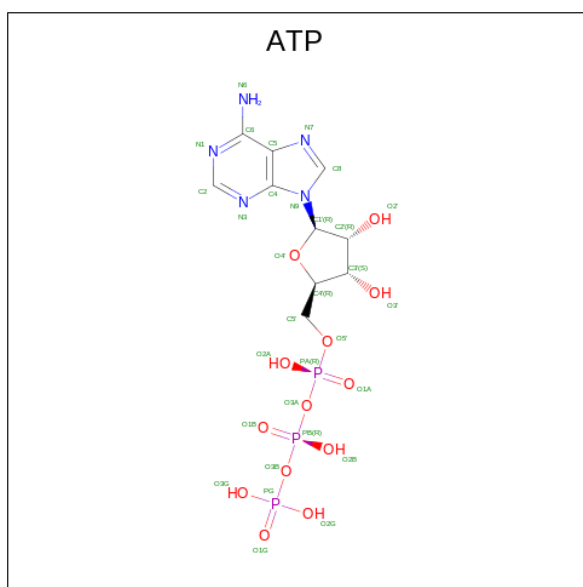
- Molecule 33 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	u	76	Total	C	N	O	S	0	0
			601	378	105	117	1		

- Molecule 34 is a protein called Substrate.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	v	28	Total	C	N	O	0	0
			143	86	29	28		

- Molecule 35 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
36	A	1	Total	Mg	0
			1	1	
36	D	1	Total	Mg	0
			1	1	
36	F	1	Total	Mg	0
			1	1	

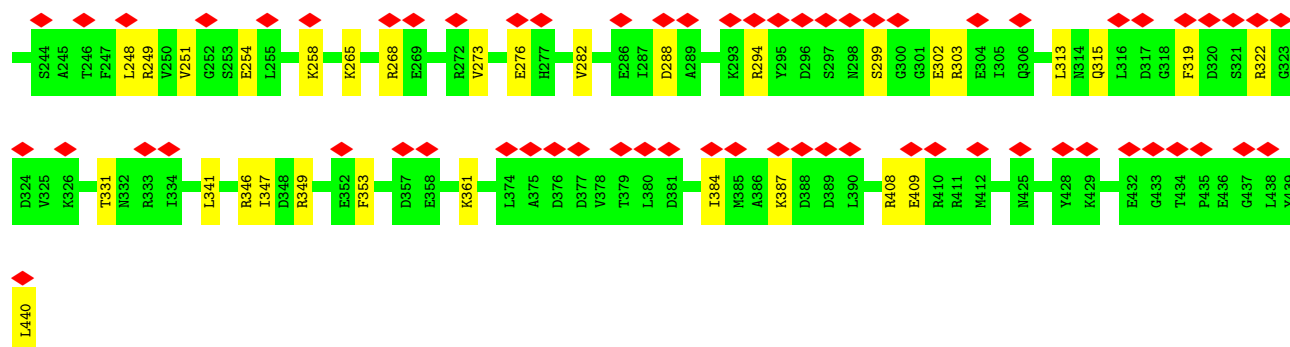
- Molecule 37 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



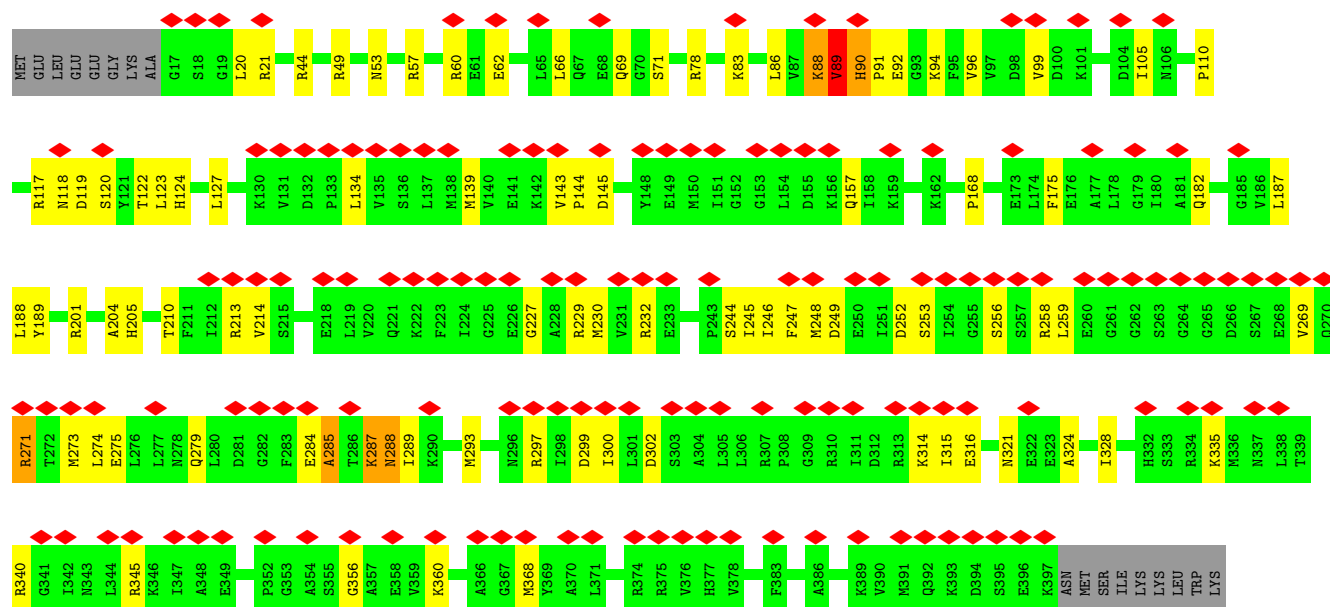
Mol	Chain	Residues	Atoms					AltConf
37	B	1	Total 27	C 10	N 5	O 10	P 2	0
37	E	1	Total 27	C 10	N 5	O 10	P 2	0

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

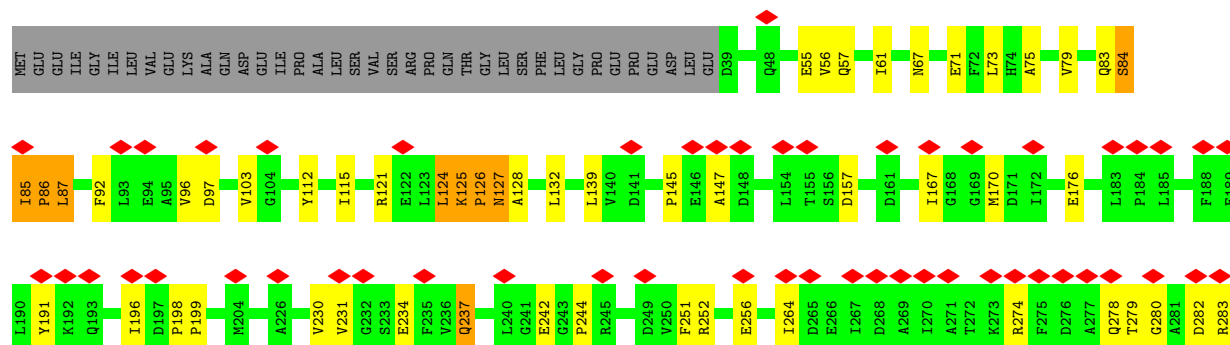
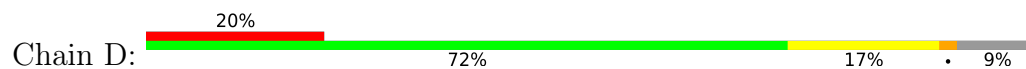
Mol	Chain	Residues	Atoms	AltConf
38	c	1	Total Zn 1 1	0

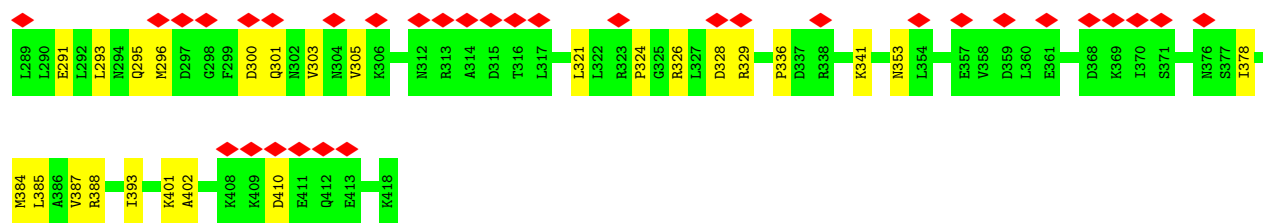


• Molecule 3: 26S proteasome regulatory subunit 8

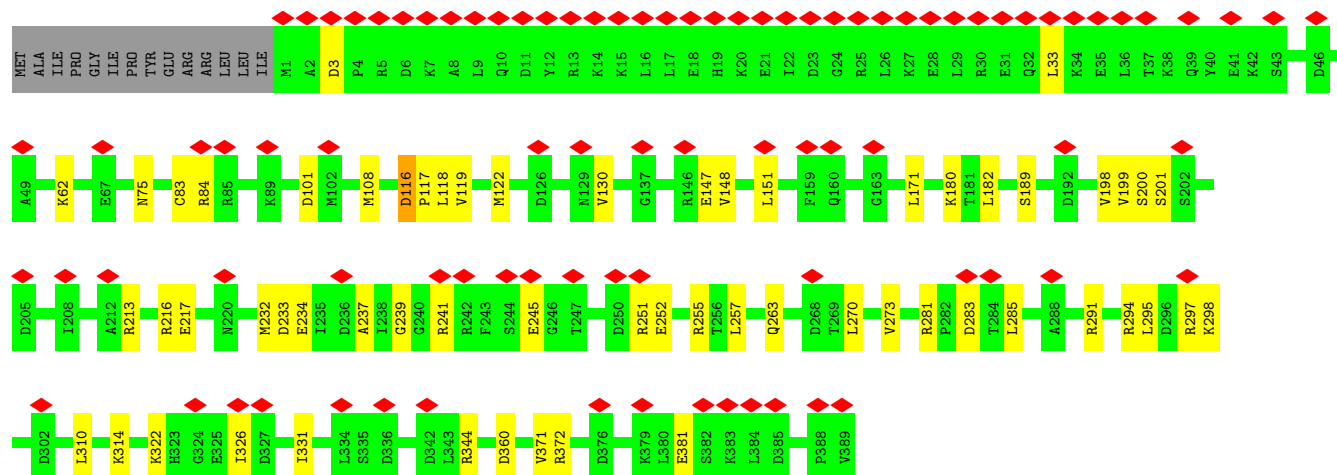
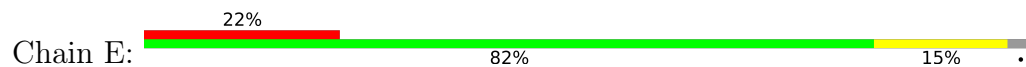


• Molecule 4: 26S proteasome regulatory subunit 6B

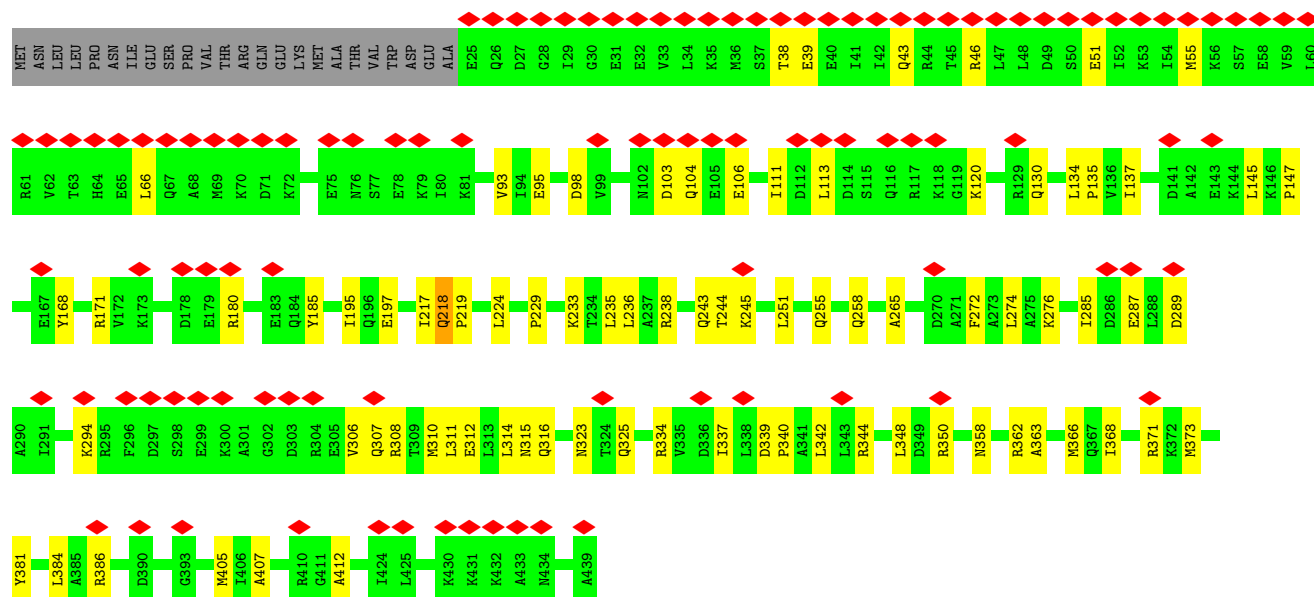
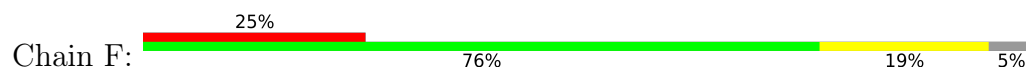




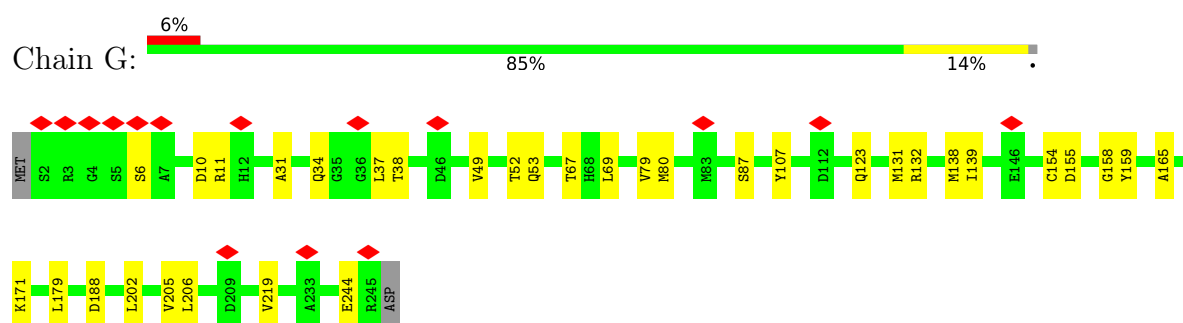
• Molecule 5: Proteasome 26S subunit, ATPase 6



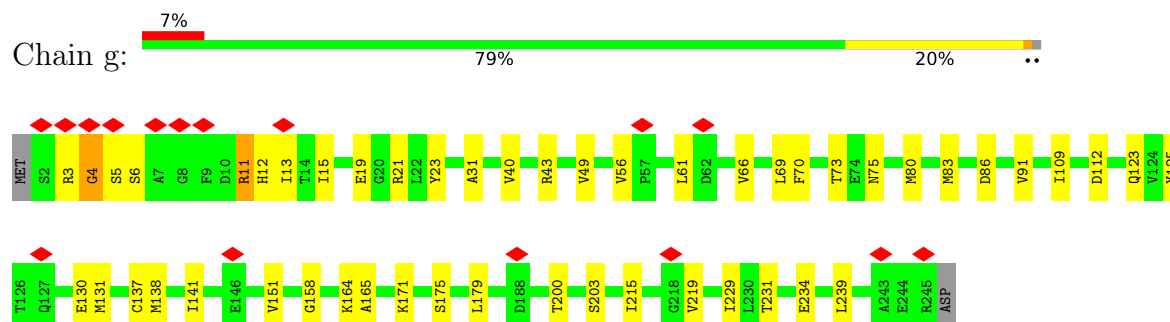
• Molecule 6: 26S proteasome regulatory subunit 6A



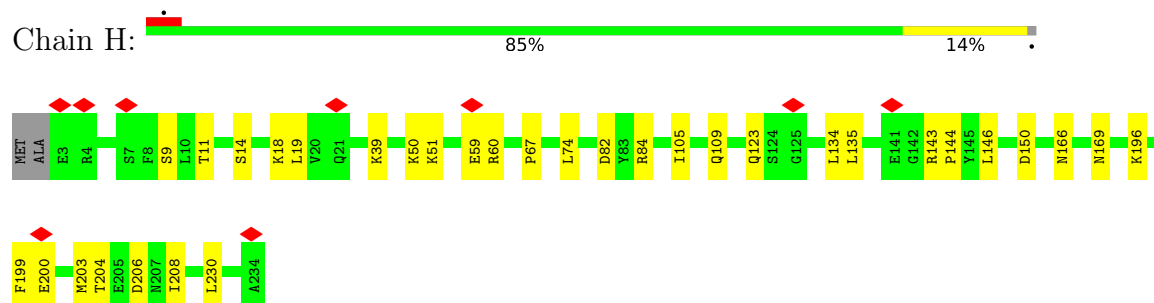
• Molecule 7: Proteasome subunit alpha type-6



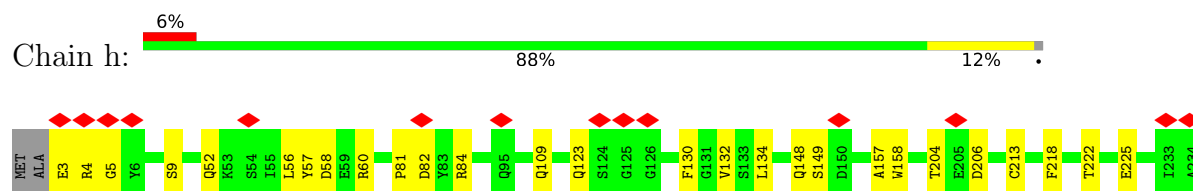
- Molecule 7: Proteasome subunit alpha type-6



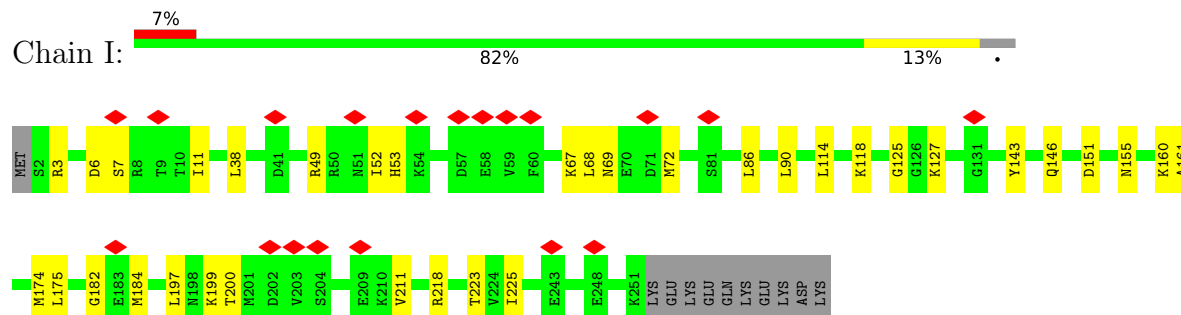
- Molecule 8: Proteasome subunit alpha type-2



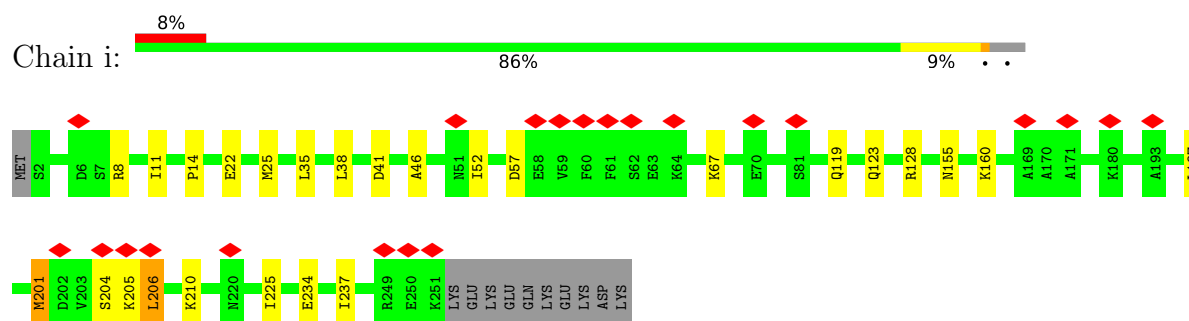
- Molecule 8: Proteasome subunit alpha type-2



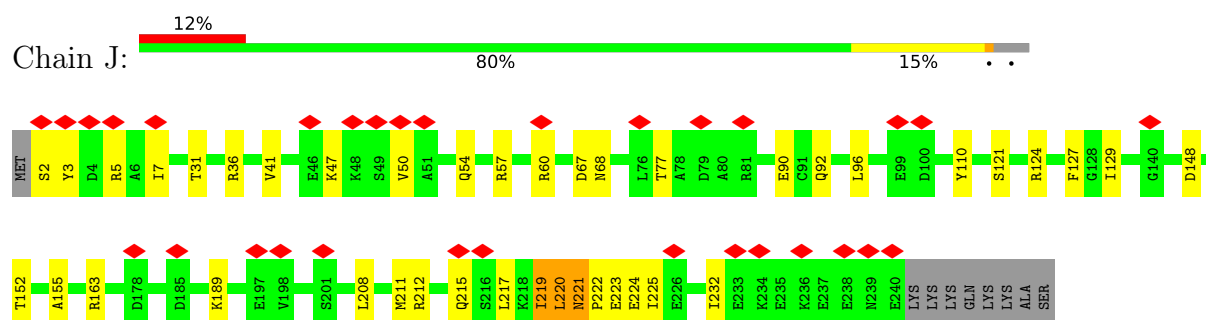
- Molecule 9: Proteasome subunit alpha type-4



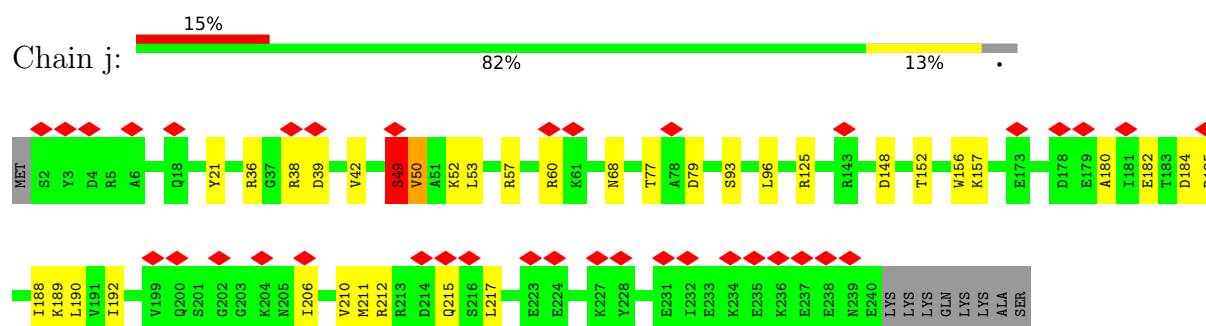
- Molecule 9: Proteasome subunit alpha type-4



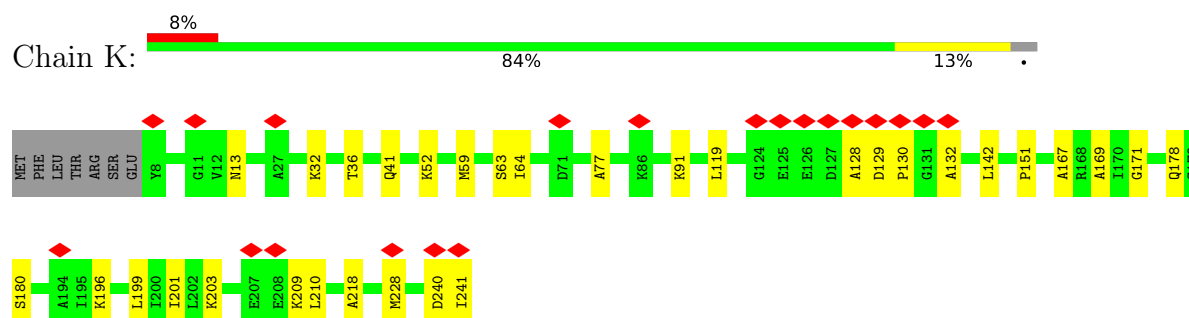
- Molecule 10: Proteasome subunit alpha type-7



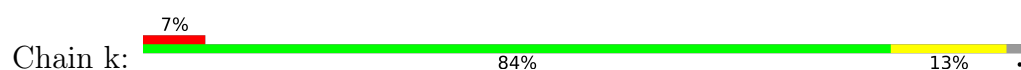
- Molecule 10: Proteasome subunit alpha type-7

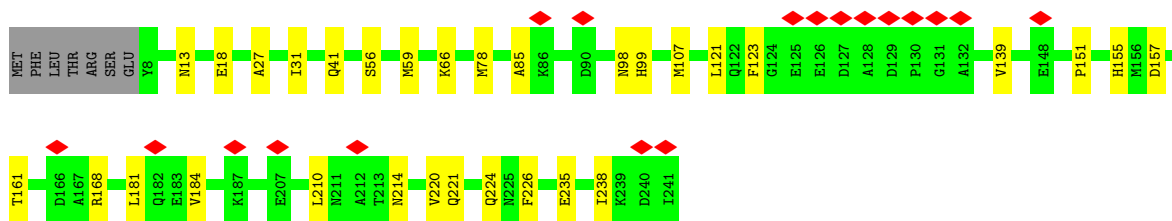


- Molecule 11: Proteasome subunit alpha type-5

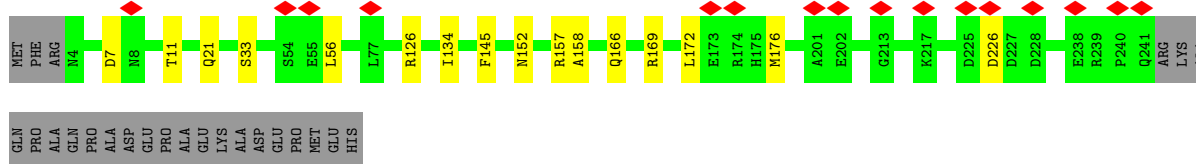
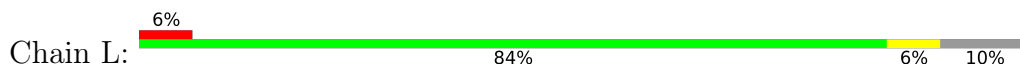


- Molecule 11: Proteasome subunit alpha type-5

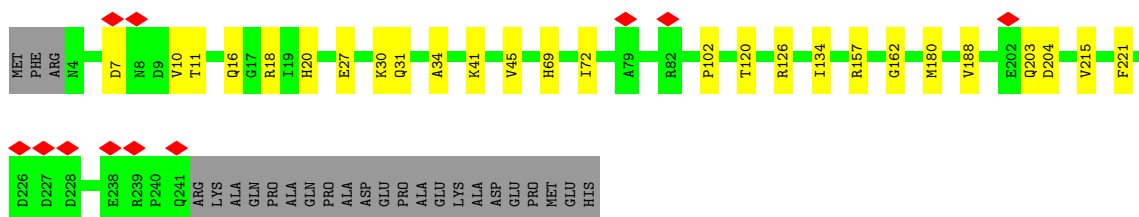
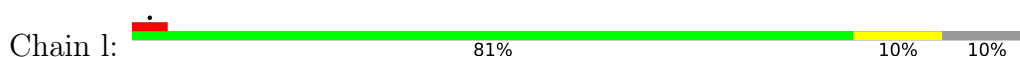




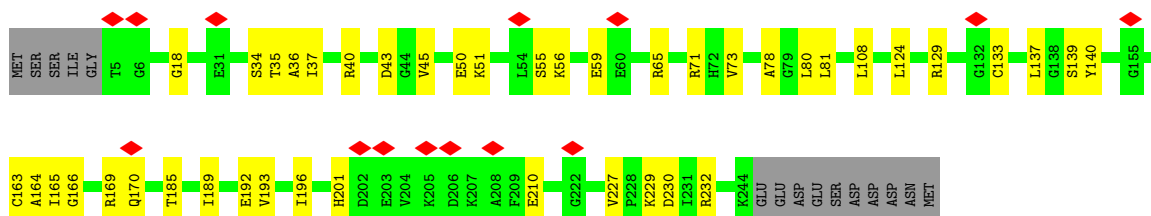
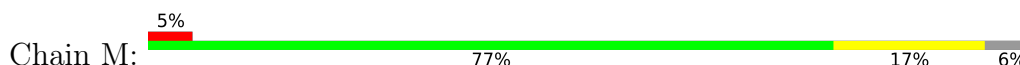
• Molecule 12: Proteasome subunit alpha type-1



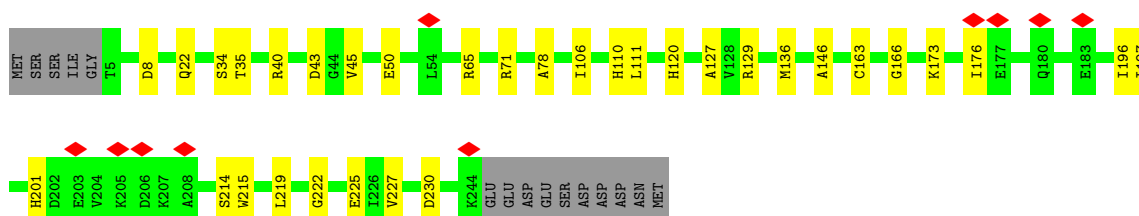
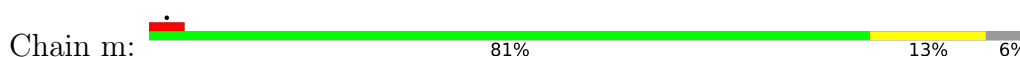
• Molecule 12: Proteasome subunit alpha type-1



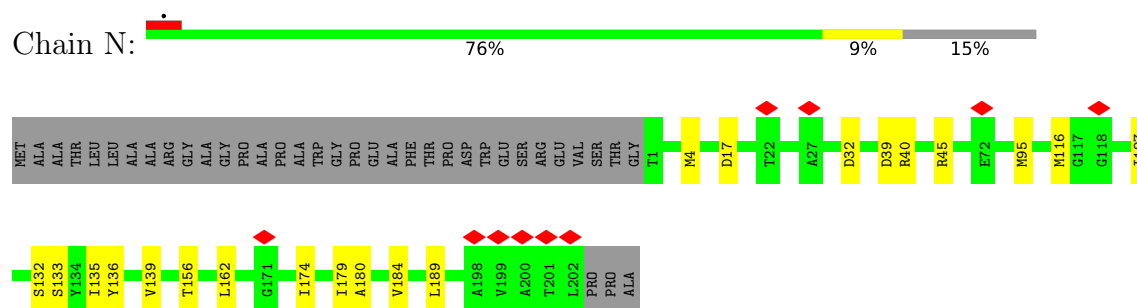
• Molecule 13: Proteasome subunit alpha type-3



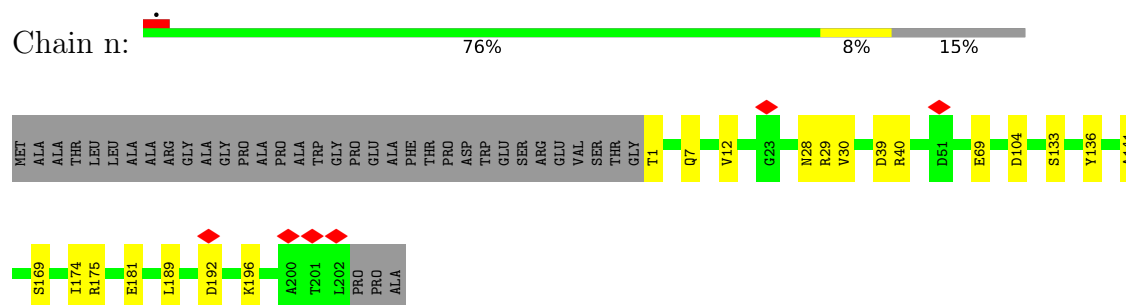
• Molecule 13: Proteasome subunit alpha type-3



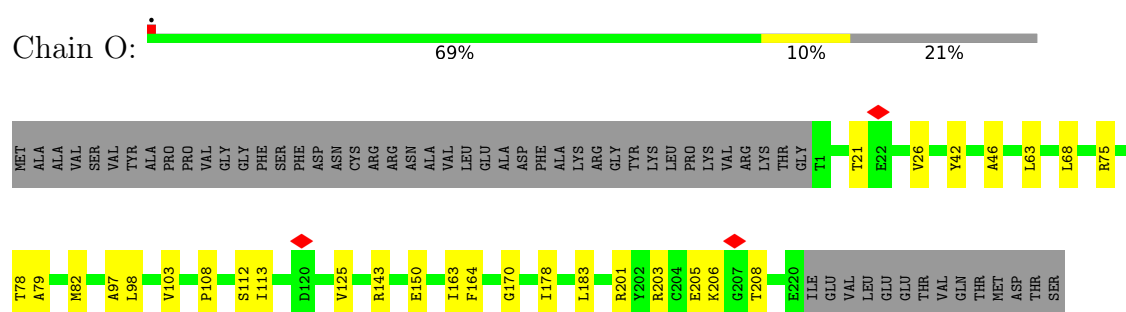
- Molecule 14: Proteasome subunit beta type-6



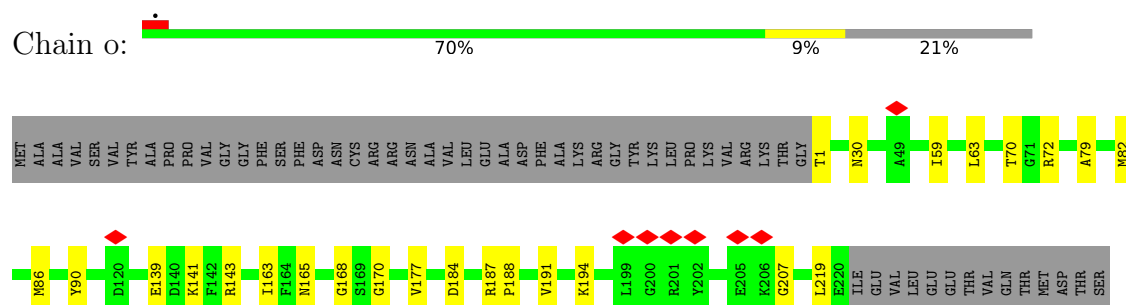
- Molecule 14: Proteasome subunit beta type-6



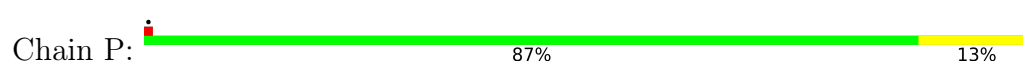
- Molecule 15: Proteasome subunit beta type-7

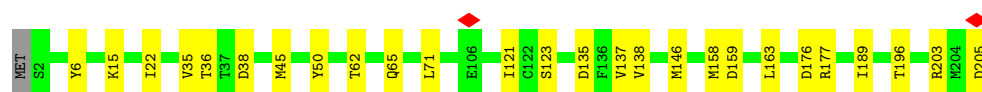


- Molecule 15: Proteasome subunit beta type-7

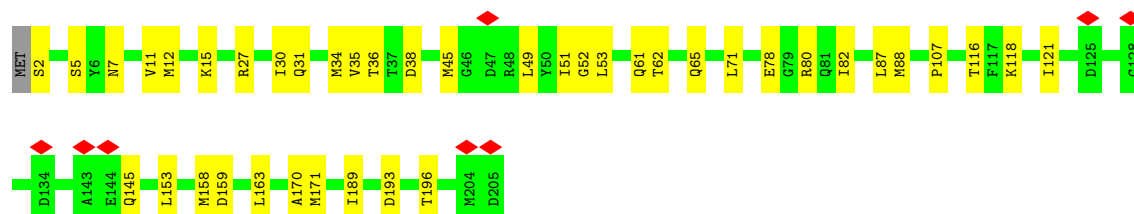
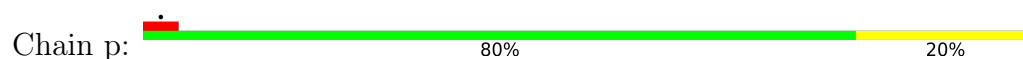


- Molecule 16: Proteasome subunit beta type-3

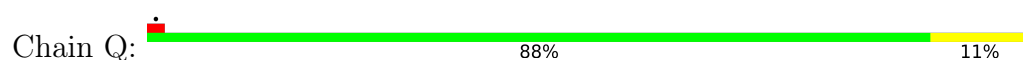




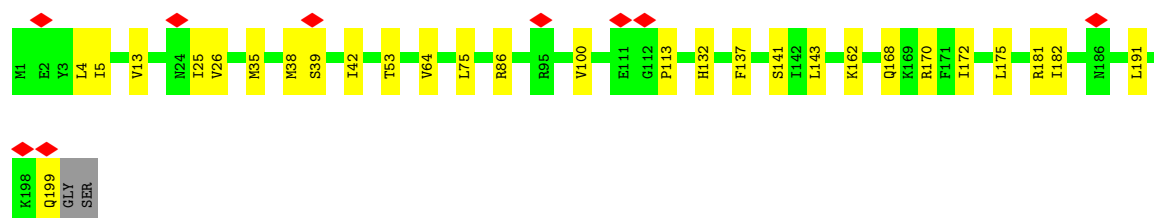
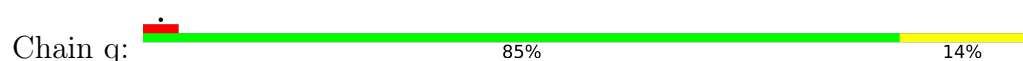
• Molecule 16: Proteasome subunit beta type-3



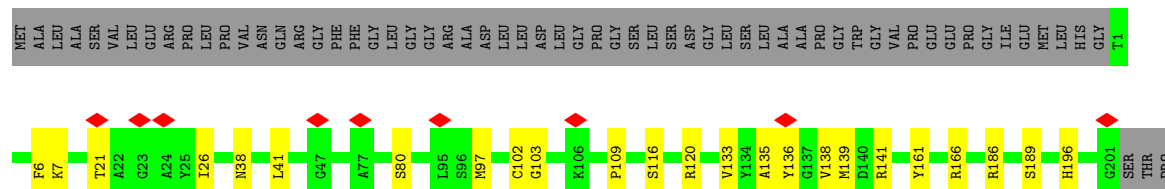
• Molecule 17: Proteasome subunit beta type-2



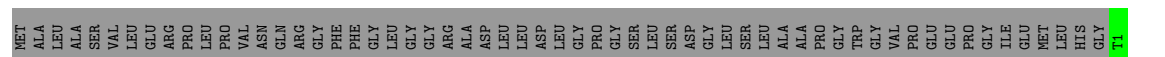
• Molecule 17: Proteasome subunit beta type-2



• Molecule 18: Proteasome subunit beta type-5

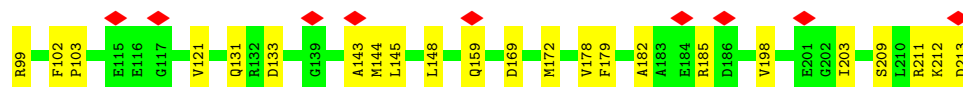
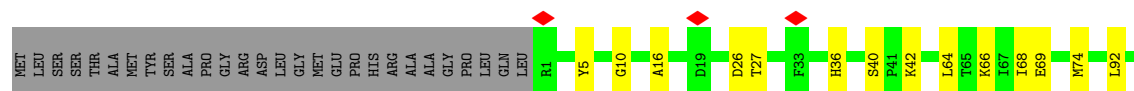
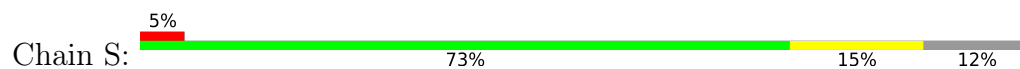


• Molecule 18: Proteasome subunit beta type-5

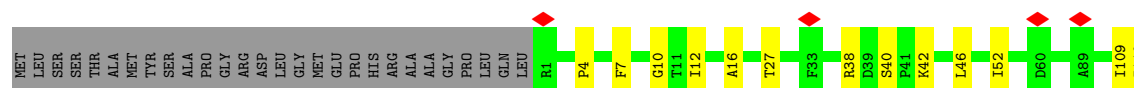
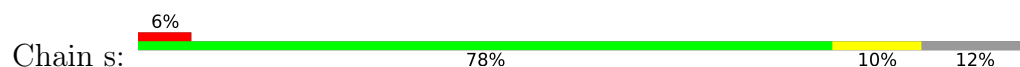




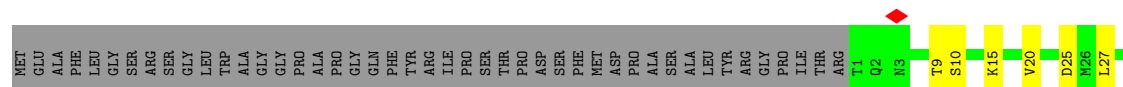
- Molecule 19: Proteasome subunit beta type-1



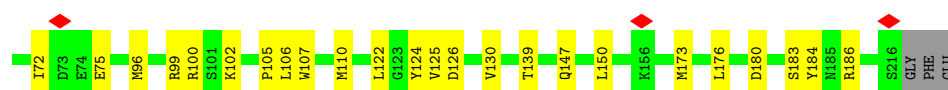
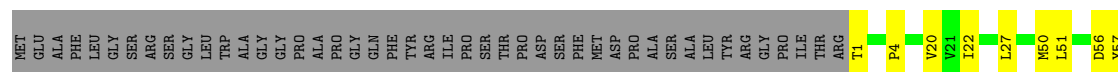
- Molecule 19: Proteasome subunit beta type-1



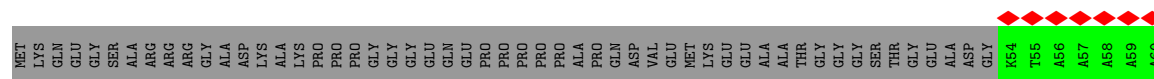
- Molecule 20: Proteasome subunit beta type-4

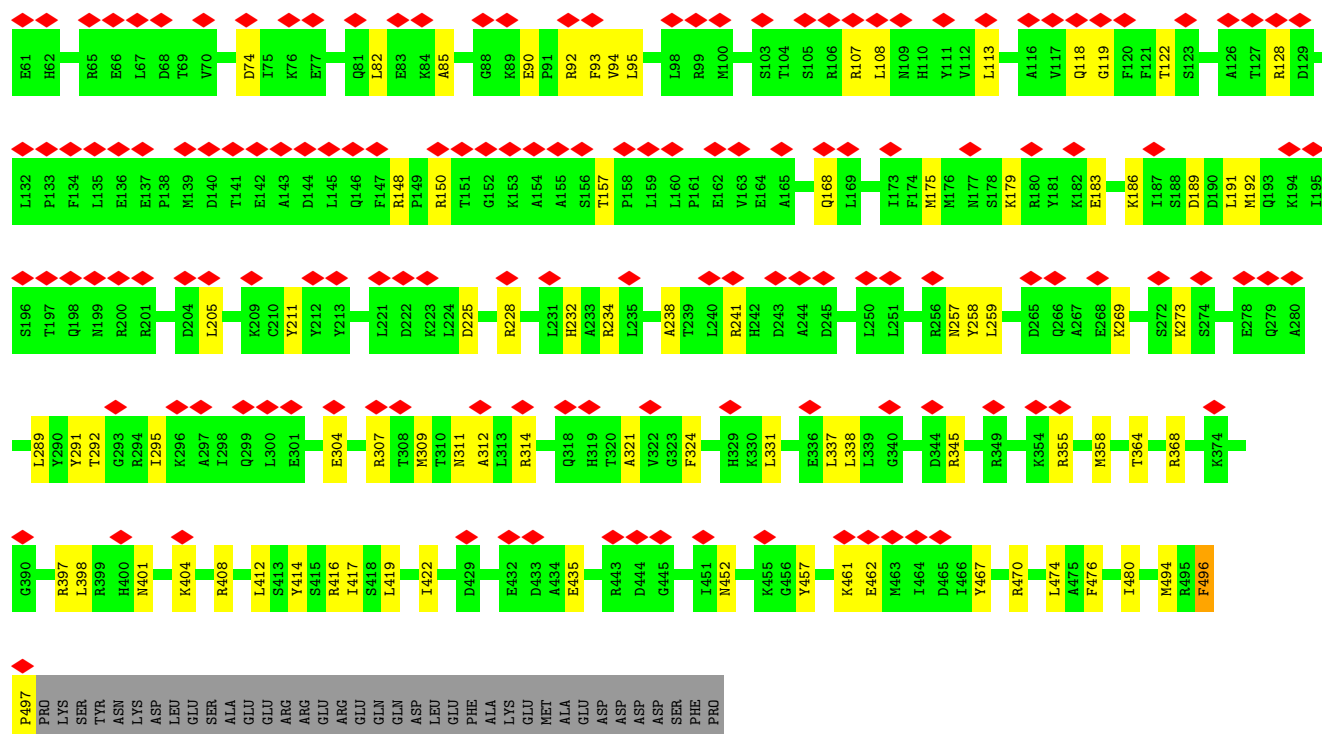


- Molecule 20: Proteasome subunit beta type-4

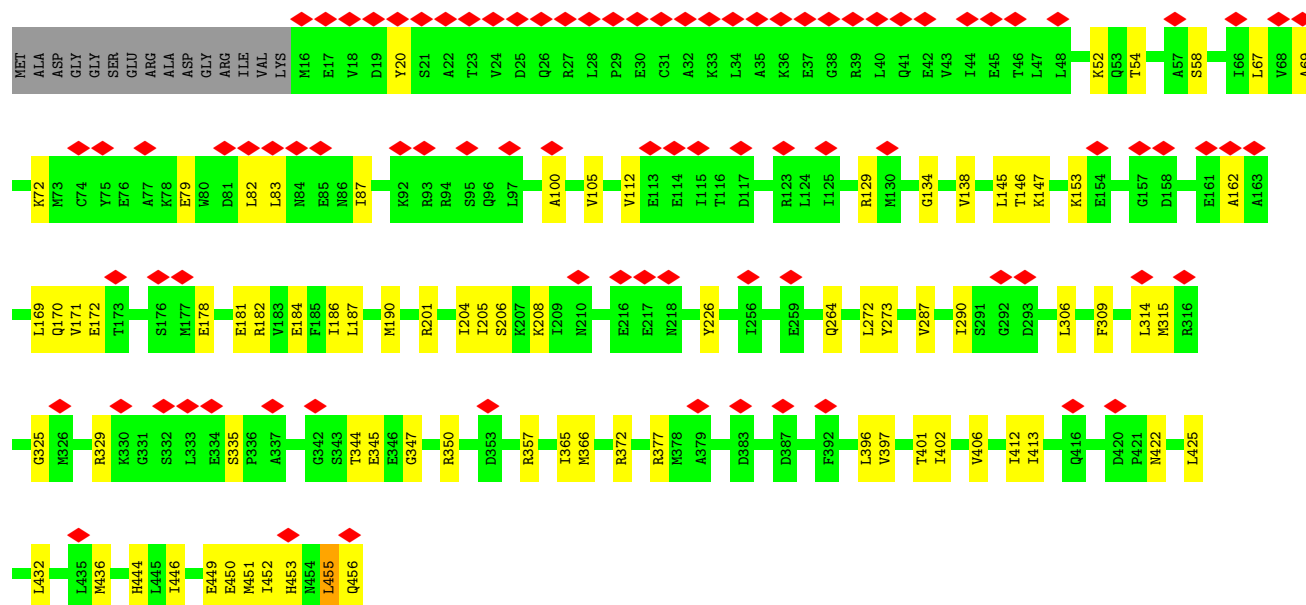
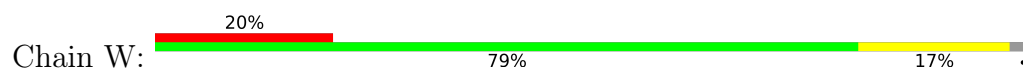


- Molecule 21: 26S proteasome non-ATPase regulatory subunit 1

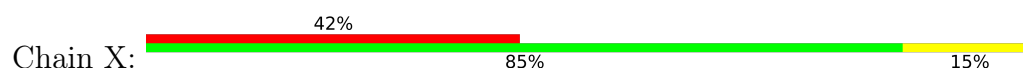


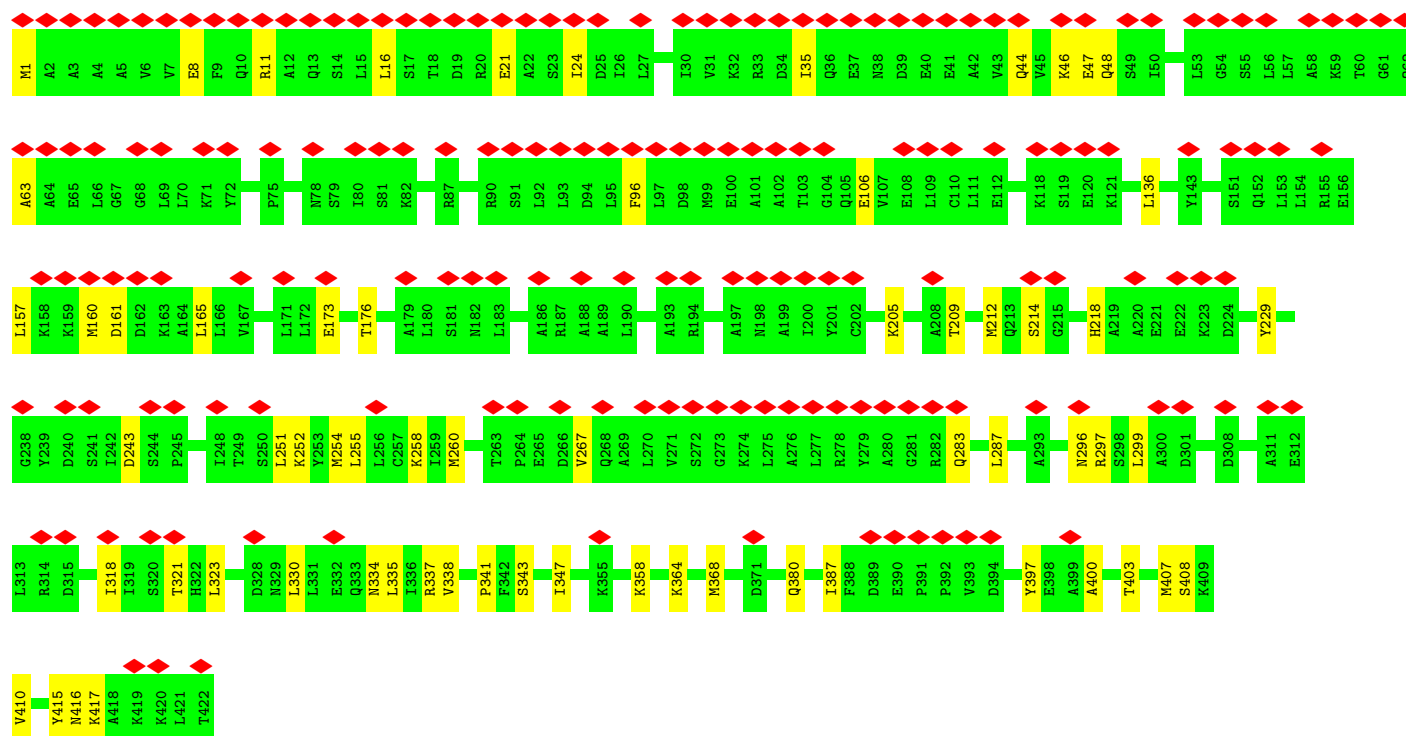


• Molecule 23: 26S proteasome non-ATPase regulatory subunit 12

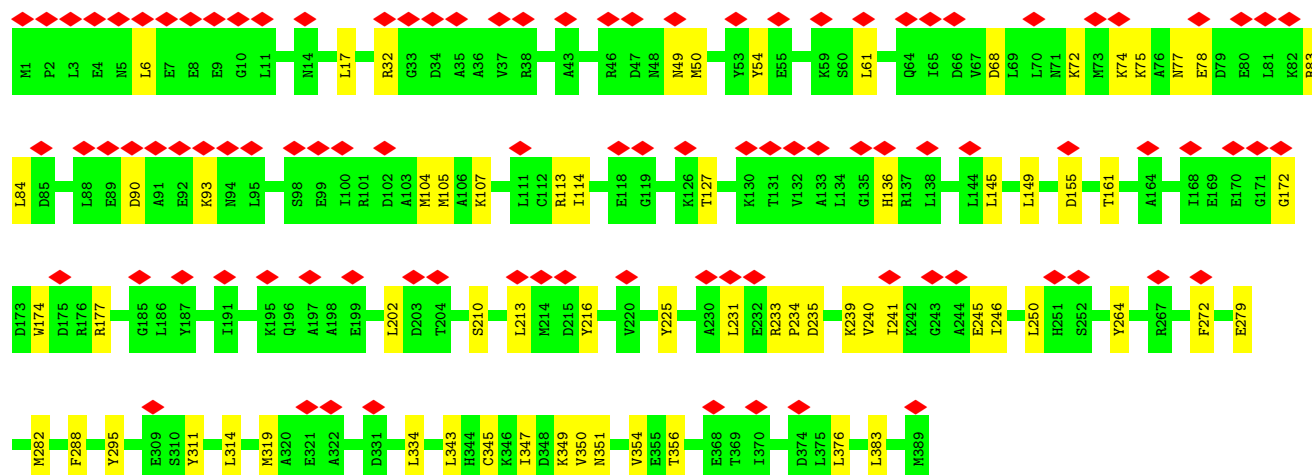
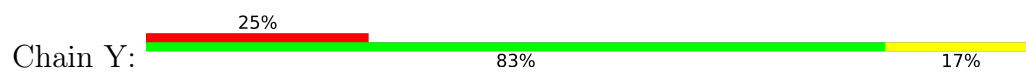


• Molecule 24: 26S proteasome non-ATPase regulatory subunit 11

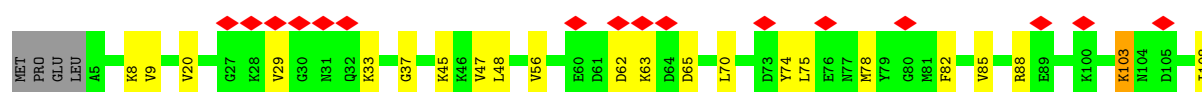


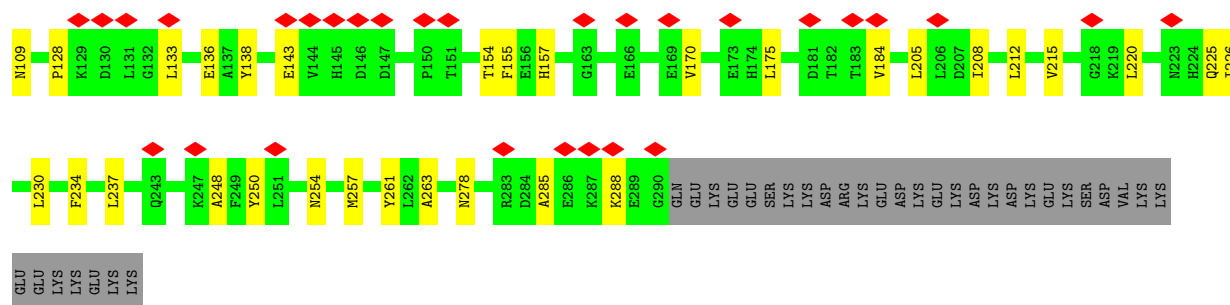


• Molecule 25: 26S proteasome non-ATPase regulatory subunit 6

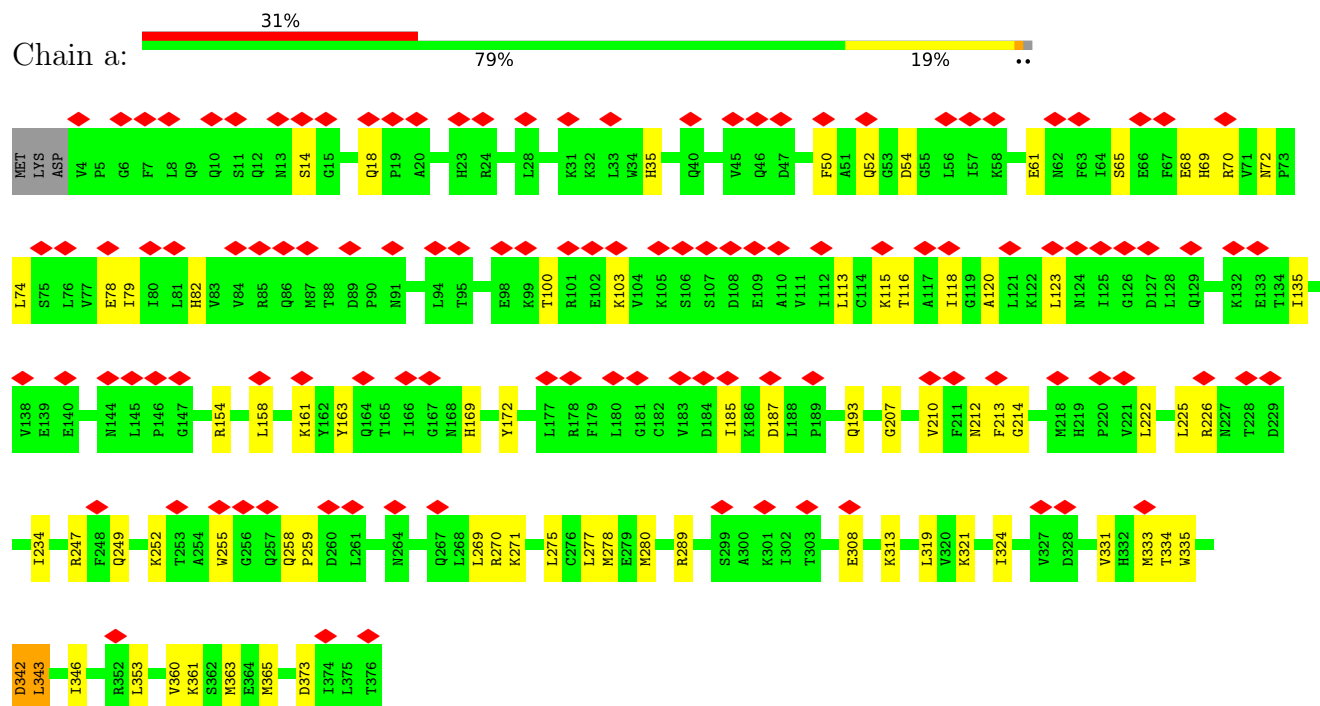


• Molecule 26: 26S proteasome non-ATPase regulatory subunit 7

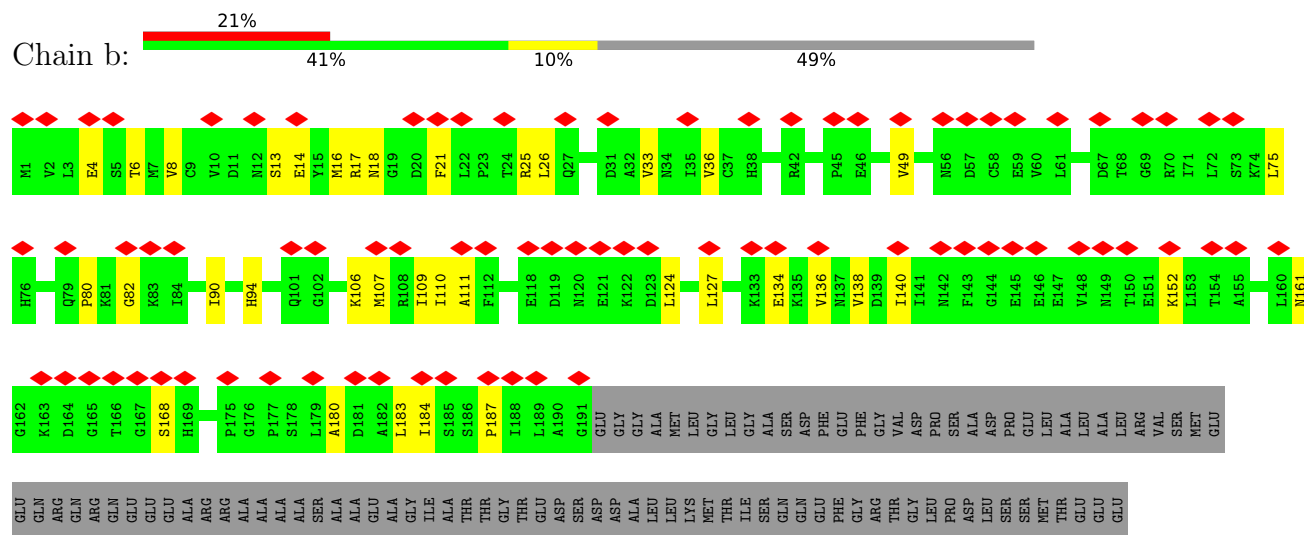


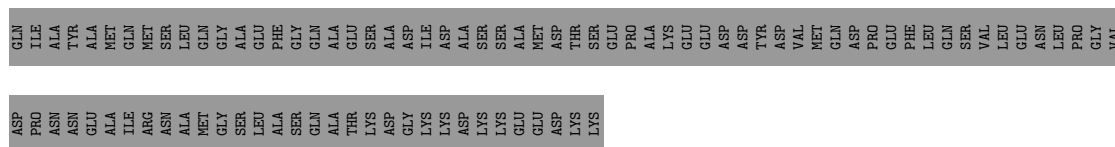


• Molecule 27: 26S proteasome non-ATPase regulatory subunit 13

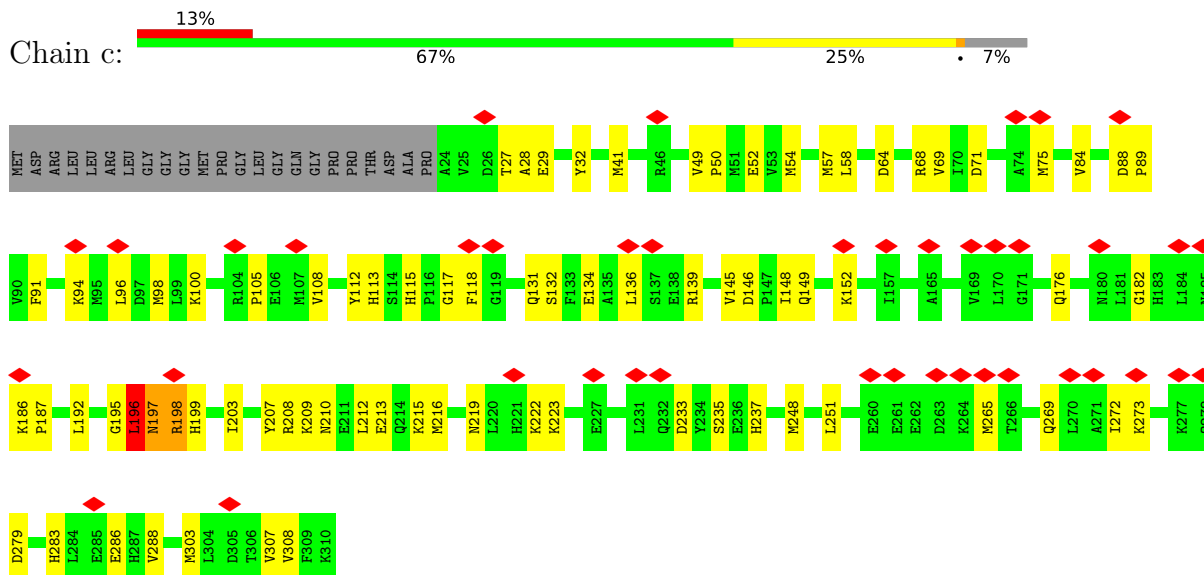


• Molecule 28: 26S proteasome non-ATPase regulatory subunit 4

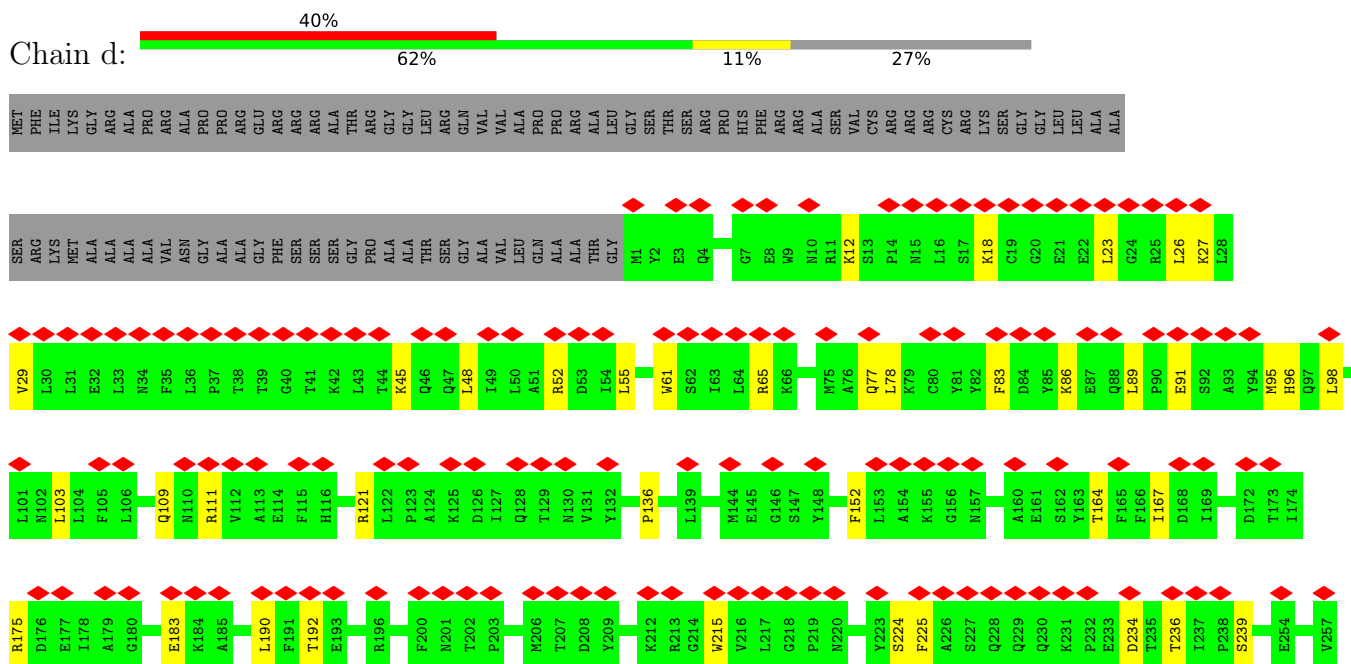




- Molecule 29: 26S proteasome non-ATPase regulatory subunit 14



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

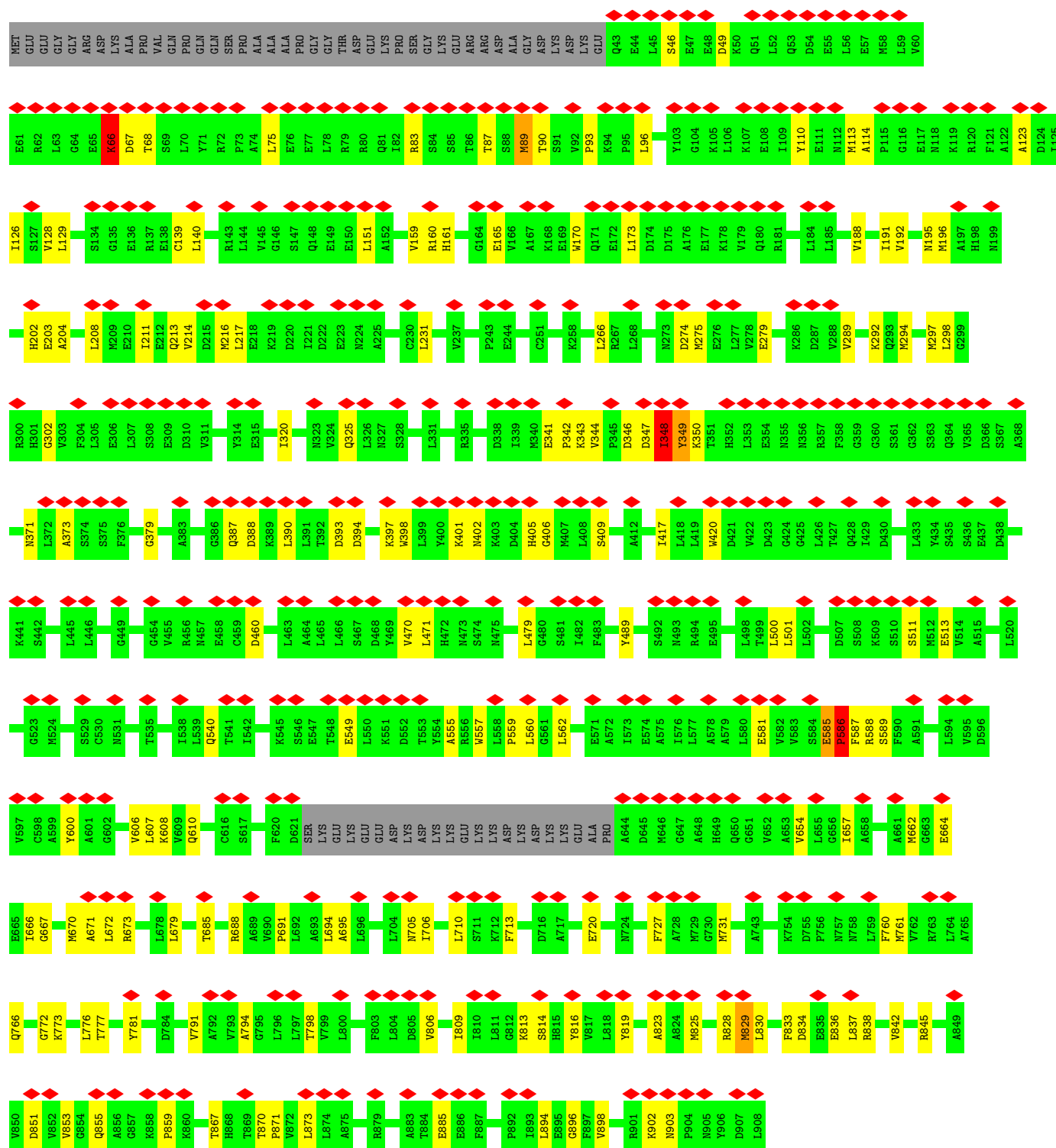
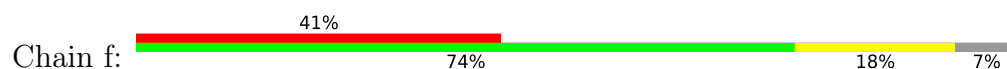


- Molecule 31: 26S proteasome complex subunit SEM1

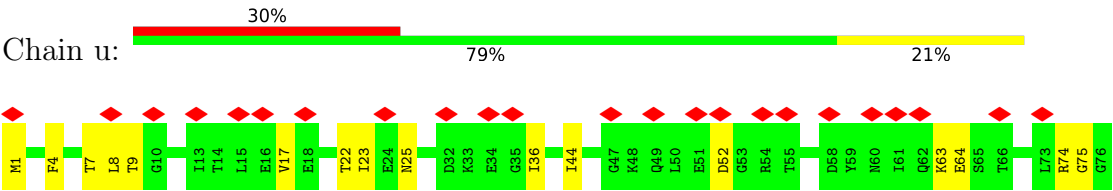




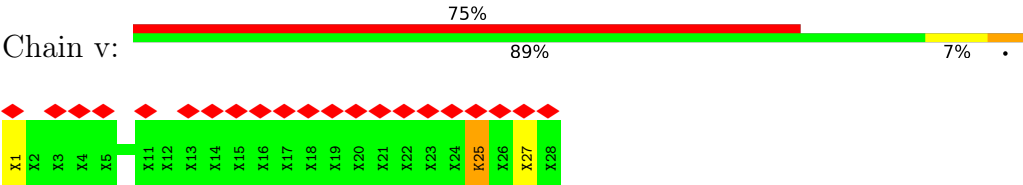
• Molecule 32: 26S proteasome non-ATPase regulatory subunit 2



● Molecule 33: Ubiquitin



● Molecule 34: Substrate



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6862	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.019	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00588	Depositor
Map size (Å)	411.0, 411.0, 411.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.685, 0.685, 0.685	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.24	0/3215	0.59	1/4340 (0.0%)
2	B	0.23	0/3144	0.55	0/4245
3	C	0.23	0/3017	0.57	4/4058 (0.1%)
4	D	0.27	0/3089	0.58	1/4168 (0.0%)
5	E	0.20	0/3145	0.51	0/4233
6	F	0.20	0/3292	0.52	0/4435
7	G	0.24	1/1923 (0.1%)	0.48	0/2601
7	g	0.24	0/1914	0.52	1/2590 (0.0%)
8	H	0.20	0/1844	0.49	0/2499
8	h	0.21	0/1844	0.48	0/2497
9	I	0.23	0/1985	0.53	0/2677
9	i	0.23	0/1985	0.52	1/2677 (0.0%)
10	J	0.21	0/1906	0.48	0/2573
10	j	0.21	0/1887	0.48	0/2549
11	K	0.21	0/1804	0.45	0/2436
11	k	0.19	0/1809	0.46	0/2444
12	L	0.20	0/1901	0.45	0/2570
12	l	0.18	0/1896	0.45	0/2565
13	M	0.19	0/1911	0.47	0/2573
13	m	0.20	0/1916	0.44	0/2580
14	N	0.19	0/1540	0.46	0/2085
14	n	0.19	0/1536	0.42	0/2080
15	O	0.19	0/1676	0.42	0/2271
15	o	0.17	0/1686	0.42	0/2282
16	P	0.19	0/1616	0.48	0/2180
16	p	0.21	0/1620	0.50	0/2184
17	Q	0.19	0/1621	0.42	0/2194
17	q	0.17	0/1621	0.41	0/2194
18	R	0.19	0/1590	0.44	0/2147
18	r	0.18	0/1590	0.43	0/2147
19	S	0.19	0/1671	0.47	0/2252
19	s	0.20	0/1684	0.47	0/2268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	T	0.21	0/1716	0.47	0/2323
20	t	0.20	0/1720	0.46	0/2328
21	U	0.19	0/6488	0.50	0/8782
22	V	0.19	0/3681	0.43	0/4969
23	W	0.17	0/3644	0.45	0/4901
24	X	0.19	0/3381	0.48	0/4558
25	Y	0.19	0/3261	0.50	0/4393
26	Z	0.21	0/2324	0.59	0/3150
27	a	0.24	0/3053	0.57	0/4133
28	b	0.24	0/1478	0.59	0/2001
29	c	0.25	0/2302	0.60	0/3110
30	d	0.21	0/2162	0.57	0/2919
31	e	0.17	0/437	0.49	0/595
32	f	0.23	0/6640	0.55	4/8988 (0.0%)
33	u	0.25	0/607	0.44	0/816
34	v	0.01	0/8	0.05	0/8
All	All	0.21	1/107780 (0.0%)	0.50	12/145568 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	131	MET	C-N	6.38	1.42	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	ARG	N-CA-C	-10.29	100.03	111.14
4	D	86	PRO	N-CA-C	-9.00	103.16	114.68
3	C	288	ASN	CA-C-N	-6.08	114.34	122.98
3	C	288	ASN	C-N-CA	-6.08	114.34	122.98
32	f	89	MET	CA-C-N	5.88	136.85	126.45
32	f	89	MET	C-N-CA	5.88	136.85	126.45
32	f	859	PRO	N-CA-C	5.50	120.83	111.03
9	i	201	MET	CA-CB-CG	5.39	124.87	114.10
7	g	109	ILE	N-CA-C	5.34	114.19	108.95
32	f	586	PRO	N-CA-CB	-5.29	97.70	103.25
3	C	285	ALA	CA-C-N	5.20	131.48	121.54
3	C	285	ALA	C-N-CA	5.20	131.48	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3164	0	3201	44	0
2	B	3099	0	3143	59	0
3	C	2978	0	3075	68	0
4	D	3039	0	3075	67	0
5	E	3097	0	3174	41	0
6	F	3251	0	3319	60	0
7	G	1889	0	1885	22	0
7	g	1880	0	1875	32	0
8	H	1805	0	1784	20	0
8	h	1805	0	1798	19	0
9	I	1955	0	1955	19	0
9	i	1955	0	1955	18	0
10	J	1880	0	1892	31	0
10	j	1861	0	1865	24	0
11	K	1777	0	1762	23	0
11	k	1782	0	1766	18	0
12	L	1866	0	1852	12	0
12	l	1861	0	1839	15	0
13	M	1876	0	1861	27	0
13	m	1881	0	1868	22	0
14	N	1514	0	1487	12	0
14	n	1510	0	1483	14	0
15	O	1649	0	1659	17	0
15	o	1659	0	1681	15	0
16	P	1587	0	1598	20	0
16	p	1591	0	1609	29	0
17	Q	1588	0	1584	24	0
17	q	1588	0	1584	19	0
18	R	1559	0	1523	16	0
18	r	1559	0	1523	12	0
19	S	1641	0	1639	25	0
19	s	1654	0	1656	15	0
20	T	1683	0	1662	22	0
20	t	1687	0	1666	20	0
21	U	6373	0	6409	87	0
22	V	3612	0	3682	58	0
23	W	3596	0	3713	52	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	X	3335	0	3435	38	0
25	Y	3202	0	3204	43	0
26	Z	2281	0	2312	41	0
27	a	2995	0	3012	52	0
28	b	1458	0	1505	26	0
29	c	2260	0	2276	62	0
30	d	2116	0	2146	24	0
31	e	425	0	328	7	0
32	f	6529	0	6541	112	0
33	u	601	0	629	16	0
34	v	143	0	46	2	0
35	A	31	0	12	1	0
35	D	31	0	12	0	0
35	F	31	0	12	1	0
36	A	1	0	0	0	0
36	D	1	0	0	0	0
36	F	1	0	0	0	0
37	B	27	0	12	3	0
37	E	27	0	12	3	0
38	c	1	0	0	0	0
All	All	106247	0	106596	1341	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 6.

All (1341) 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)
32:f:585:GLU:HB2	32:f:586:PRO:HD2	1.49	0.93
3:C:44:ARG:HG3	22:V:496:PHE:HE2	1.38	0.88
29:c:192:LEU:HA	29:c:196:LEU:HB2	1.59	0.83
3:C:90:HIS:HB3	3:C:91:PRO:HD3	1.63	0.80
7:g:130:GLU:HG2	8:h:5:GLY:HA2	1.63	0.80
29:c:89:PRO:HG2	33:u:44:ILE:HD11	1.64	0.79
1:A:346:PRO:HG2	1:A:350:GLY:HA3	1.65	0.79
10:J:220:LEU:HD12	10:J:225:ILE:HG13	1.63	0.78
29:c:52:GLU:HG3	33:u:75:GLY:O	1.84	0.78
28:b:16:MET:HE3	28:b:25:ARG:HB3	1.67	0.76
24:X:35:ILE:HD12	24:X:46:LYS:HD2	1.68	0.76
29:c:96:LEU:HD12	33:u:8:LEU:HD22	1.67	0.75
2:B:68:ILE:HG23	32:f:670:MET:HE1	1.70	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:r:125:THR:HB	18:r:139:MET:HE3	1.71	0.72
4:D:126:PRO:HG2	4:D:128:ALA:HB2	1.69	0.72
18:r:88:TYR:HA	18:r:91:LYS:HE3	1.71	0.72
4:D:84:SER:C	4:D:86:PRO:HD3	2.14	0.71
7:g:125:TYR:HD1	7:g:131:MET:HE3	1.55	0.71
10:J:92:GLN:HE22	17:Q:65:GLN:HB3	1.54	0.71
19:S:148:LEU:HD23	19:S:178:VAL:HG12	1.71	0.70
4:D:125:LYS:N	4:D:126:PRO:HD3	2.06	0.70
9:I:143:TYR:HB2	9:I:146:GLN:HE21	1.55	0.70
21:U:540:GLN:HB3	29:c:68:ARG:HH22	1.57	0.69
11:K:91:LYS:HG2	11:K:119:LEU:HD11	1.74	0.69
19:s:27:THR:HB	19:s:40:SER:H	1.57	0.69
20:T:215:ILE:HG13	14:n:175:ARG:HH22	1.57	0.69
29:c:96:LEU:CD1	33:u:8:LEU:HD22	2.24	0.68
6:F:217:ILE:HG13	6:F:218:GLN:H	1.60	0.67
23:W:314:LEU:HD21	23:W:366:MET:HE3	1.75	0.67
30:d:86:LYS:HG2	30:d:89:LEU:HD13	1.76	0.67
16:p:51:ILE:HD11	16:p:87:LEU:HD21	1.76	0.67
21:U:208:LEU:HD23	21:U:210:LYS:H	1.57	0.67
32:f:829:MET:HE1	32:f:871:PRO:HB2	1.77	0.67
2:B:53:THR:HB	2:B:54:PRO:HD2	1.76	0.67
7:g:5:SER:HA	7:g:19:GLU:OE2	1.95	0.67
16:P:15:LYS:HE3	16:P:121:ILE:HG12	1.77	0.66
23:W:397:VAL:HG11	24:X:341:PRO:HB3	1.78	0.66
8:H:74:LEU:HD12	8:H:134:LEU:HD12	1.77	0.66
13:m:34:SER:HG	13:m:65:ARG:HH12	1.44	0.66
19:S:27:THR:HB	19:S:40:SER:H	1.60	0.66
10:j:38:ARG:HH22	10:j:182:GLU:HG3	1.61	0.66
10:j:36:ARG:HH21	10:j:157:LYS:HG2	1.61	0.66
29:c:131:GLN:HA	29:c:134:GLU:HG2	1.78	0.65
1:A:208:PRO:HA	6:F:405:MET:HE1	1.78	0.65
3:C:83:LYS:HG2	3:C:105:ILE:HD11	1.78	0.65
5:E:101:ASP:HB2	5:E:108:MET:HE3	1.78	0.65
29:c:283:HIS:HA	29:c:286:GLU:HG2	1.79	0.65
11:K:13:ASN:HB3	12:L:126:ARG:HB3	1.77	0.65
16:P:62:THR:HG23	17:Q:86:ARG:HH12	1.62	0.65
2:B:294:ARG:HH22	2:B:302:GLU:HB3	1.61	0.65
27:a:135:ILE:HG12	27:a:158:LEU:HD13	1.78	0.64
27:a:342:ASP:O	27:a:346:ILE:HG13	1.98	0.64
14:n:174:ILE:HB	14:n:189:LEU:HB2	1.79	0.64
22:V:82:LEU:HD23	22:V:94:VAL:HG12	1.78	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:203:LYS:HB3	11:K:210:LEU:HD22	1.80	0.64
22:V:108:LEU:HD21	22:V:113:LEU:HG	1.78	0.64
2:B:155:LYS:HD2	2:B:156:VAL:HG13	1.79	0.64
29:c:28:ALA:H	29:c:176:GLN:HE22	1.45	0.63
26:Z:109:ASN:HD22	26:Z:155:PHE:HE1	1.47	0.63
27:a:72:ASN:H	28:b:17:ARG:HH22	1.47	0.63
10:j:211:MET:HE3	10:j:217:LEU:HB2	1.81	0.63
11:K:77:ALA:HB3	11:K:142:LEU:HB2	1.80	0.63
32:f:694:LEU:HD11	32:f:710:LEU:HD21	1.81	0.63
3:C:44:ARG:HG3	22:V:496:PHE:CE2	2.28	0.63
6:F:276:LYS:HE3	6:F:325:GLN:HE21	1.63	0.63
15:O:78:THR:HG22	15:O:82:MET:HE2	1.81	0.62
2:B:319:PHE:HB3	2:B:322:ARG:HH12	1.65	0.62
4:D:83:GLN:C	4:D:85:ILE:H	2.07	0.62
5:E:198:VAL:HB	5:E:232:MET:HG2	1.80	0.62
4:D:199:PRO:HB3	4:D:328:ASP:HB2	1.82	0.62
15:o:177:VAL:HB	15:o:184:ASP:HB3	1.81	0.62
16:P:158:MET:HE3	16:P:163:LEU:HA	1.81	0.62
17:q:38:MET:HE1	17:q:64:VAL:HG21	1.81	0.62
28:b:90:ILE:HD13	28:b:127:LEU:HD13	1.81	0.62
21:U:367:THR:HG22	21:U:400:ALA:HB2	1.82	0.62
21:U:417:LYS:HE3	21:U:421:GLN:HE22	1.63	0.62
26:Z:82:PHE:HA	26:Z:85:VAL:HG12	1.82	0.62
32:f:585:GLU:O	32:f:587:PHE:N	2.33	0.62
4:D:92:PHE:HE2	4:D:125:LYS:HD2	1.65	0.62
21:U:797:MET:HE2	21:U:880:ASN:HD22	1.65	0.62
18:R:7:LYS:HE3	18:R:109:PRO:HB2	1.81	0.61
32:f:320:ILE:HA	32:f:325:GLN:HE22	1.64	0.61
3:C:117:ARG:HB3	3:C:122:THR:H	1.65	0.61
2:B:171:VAL:O	2:B:175:LYS:HB3	2.01	0.61
22:V:85:ALA:HB2	22:V:93:PHE:HB2	1.82	0.61
23:W:372:ARG:HB3	23:W:412:ILE:HD11	1.81	0.61
4:D:124:LEU:C	4:D:126:PRO:HD3	2.25	0.61
23:W:449:GLU:HA	23:W:452:ILE:HD12	1.81	0.61
15:o:70:THR:HG23	15:o:72:ARG:H	1.65	0.61
26:Z:208:ILE:HG23	27:a:353:LEU:HD21	1.82	0.61
4:D:385:LEU:HD12	4:D:388:ARG:HD3	1.82	0.61
13:M:65:ARG:HH21	13:M:78:ALA:HA	1.66	0.61
32:f:585:GLU:HB2	32:f:586:PRO:CD	2.29	0.61
2:B:51:LEU:HD23	32:f:666:ILE:HG12	1.83	0.60
17:q:25:ILE:HG22	17:q:26:VAL:HG13	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:ASN:HA	1:A:136:GLU:HG2	1.82	0.60
3:C:232:ARG:HH12	3:C:275:GLU:HB3	1.65	0.60
14:N:4:MET:HE1	14:N:156:THR:HA	1.82	0.60
29:c:195:GLY:O	29:c:198:ARG:HB2	2.01	0.60
4:D:127:ASN:HB3	4:D:252:ARG:HH11	1.65	0.60
3:C:189:TYR:HE2	3:C:314:LYS:HB3	1.67	0.60
4:D:103:VAL:HG11	4:D:139:LEU:HD21	1.83	0.60
9:i:52:ILE:HD12	9:i:210:LYS:HE2	1.84	0.60
3:C:232:ARG:HH21	3:C:279:GLN:HB2	1.67	0.60
6:F:93:VAL:HG21	6:F:145:LEU:HD12	1.84	0.60
6:F:366:MET:HE1	6:F:384:LEU:HB2	1.84	0.60
30:d:103:LEU:HD22	30:d:136:PRO:HB2	1.83	0.60
8:h:134:LEU:H	8:h:149:SER:HB3	1.67	0.60
9:I:38:LEU:HD23	9:I:160:LYS:HG2	1.84	0.60
1:A:112:ILE:HG12	1:A:122:VAL:HG22	1.83	0.59
21:U:772:TRP:HD1	21:U:775:LEU:HB2	1.67	0.59
28:b:111:ALA:HB3	28:b:140:ILE:HA	1.84	0.59
6:F:265:ALA:HA	6:F:312:GLU:HG2	1.85	0.59
32:f:654:VAL:HA	32:f:657:ILE:HD12	1.84	0.59
4:D:282:ASP:HA	4:D:285:VAL:HG22	1.85	0.59
10:j:38:ARG:NH1	10:j:182:GLU:O	2.36	0.59
7:g:141:ILE:HG22	7:g:151:VAL:HG22	1.83	0.59
20:t:51:LEU:HD11	20:t:110:MET:HE3	1.84	0.59
23:W:146:THR:HG21	23:W:169:LEU:HD21	1.84	0.59
25:Y:311:TYR:HB2	25:Y:314:LEU:HD12	1.85	0.59
4:D:92:PHE:HA	4:D:103:VAL:HG12	1.85	0.59
16:P:176:ASP:OD2	19:s:157:ASN:ND2	2.36	0.59
19:S:159:GLN:NE2	15:o:207:GLY:O	2.36	0.59
29:c:136:LEU:HD11	33:u:7:THR:HG21	1.85	0.59
32:f:275:MET:HE3	32:f:279:GLU:HG3	1.84	0.59
23:W:171:VAL:HG12	23:W:182:ARG:HG3	1.85	0.58
7:G:49:VAL:HG22	7:G:219:VAL:HG22	1.85	0.58
19:S:144:MET:HE1	19:S:185:ARG:HB2	1.84	0.58
19:S:198:VAL:HG22	19:S:203:ILE:HG12	1.85	0.58
27:a:249:GLN:HA	27:a:252:LYS:HB2	1.85	0.58
2:B:223:ILE:HG12	2:B:347:ILE:HG21	1.85	0.58
3:C:258:ARG:NH1	3:C:302:ASP:OD2	2.36	0.58
5:E:199:VAL:HG13	5:E:201:SER:H	1.67	0.58
4:D:126:PRO:HG2	4:D:128:ALA:CB	2.32	0.58
5:E:381:GLU:HB2	6:F:340:PRO:HB3	1.85	0.58
32:f:140:LEU:HD23	32:f:165:GLU:HB3	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:201:ARG:HD3	15:O:203:ARG:H	1.69	0.58
16:P:65:GLN:OE1	17:Q:86:ARG:NH2	2.36	0.58
21:U:30:VAL:HA	21:U:33:ASP:HB2	1.86	0.58
27:a:289:ARG:HB3	27:a:333:MET:HB2	1.86	0.58
30:d:152:PHE:HE1	30:d:175:ARG:HH12	1.52	0.58
20:t:99:ARG:HA	20:t:102:LYS:HZ3	1.69	0.58
23:W:273:TYR:OH	23:W:350:ARG:NH2	2.36	0.58
1:A:307:ASP:HB2	1:A:336:ARG:HE	1.68	0.58
4:D:244:PRO:HB3	4:D:291:GLU:HG3	1.85	0.58
22:V:345:ARG:HH21	31:e:43:TRP:HA	1.67	0.58
24:X:297:ARG:HH11	24:X:337:ARG:HE	1.52	0.58
28:b:8:VAL:HG22	28:b:110:ILE:HD11	1.86	0.58
9:i:8:ARG:HD3	9:i:11:ILE:HD13	1.86	0.58
11:k:210:LEU:HA	11:k:214:ASN:HD21	1.68	0.58
21:U:322:THR:HA	21:U:325:MET:HG3	1.86	0.58
25:Y:233:ARG:NH2	25:Y:264:TYR:O	2.36	0.58
15:O:112:SER:HB3	15:O:125:VAL:HG11	1.86	0.57
17:Q:144:ASP:OD2	18:r:166:ARG:NH2	2.36	0.57
32:f:208:LEU:HB3	32:f:217:LEU:HD11	1.86	0.57
16:p:189:ILE:HB	16:p:196:THR:HB	1.85	0.57
25:Y:314:LEU:HD21	25:Y:319:MET:HE3	1.85	0.57
11:k:13:ASN:HB2	12:l:126:ARG:HG2	1.86	0.57
1:A:209:PRO:HD3	6:F:405:MET:HE1	1.86	0.57
2:B:141:LYS:HA	2:B:144:LEU:HD12	1.84	0.57
22:V:74:ASP:OD2	22:V:107:ARG:NH2	2.37	0.57
32:f:75:LEU:HD21	32:f:113:MET:HE1	1.86	0.57
16:p:78:GLU:HB3	16:p:80:ARG:HG2	1.86	0.57
5:E:171:LEU:HD23	5:E:298:LYS:HG3	1.87	0.57
11:K:196:LYS:HE2	11:K:241:ILE:HG21	1.85	0.57
15:O:163:ILE:HG12	15:O:170:GLY:HA2	1.87	0.57
28:b:94:HIS:NE2	28:b:134:GLU:OE1	2.36	0.57
5:E:119:VAL:HA	5:E:122:MET:HE2	1.87	0.57
23:W:344:THR:HG23	23:W:347:GLY:H	1.69	0.57
1:A:78:TRP:HA	1:A:81:ALA:HB3	1.86	0.57
7:G:244:GLU:O	23:W:52:LYS:NZ	2.37	0.57
8:H:39:LYS:HB2	8:H:146:LEU:HD12	1.87	0.57
27:a:210:VAL:HA	27:a:213:PHE:CE1	2.40	0.57
4:D:92:PHE:CE2	4:D:125:LYS:HD2	2.39	0.57
21:U:678:ASP:O	21:U:684:ARG:NH1	2.38	0.57
26:Z:45:LYS:HB3	26:Z:47:VAL:HG12	1.87	0.57
26:Z:250:TYR:O	26:Z:254:ASN:ND2	2.37	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:j:49:SER:O	10:j:50:VAL:C	2.47	0.57
3:C:269:VAL:HG12	3:C:273:MET:HE1	1.87	0.57
26:Z:128:PRO:O	29:c:215:LYS:NZ	2.38	0.57
29:c:94:LYS:HG2	29:c:98:MET:HE2	1.86	0.57
32:f:371:ASN:ND2	32:f:401:LYS:O	2.37	0.57
33:u:4:PHE:HE2	33:u:64:GLU:HG2	1.69	0.57
3:C:340:ARG:HG2	25:Y:6:LEU:HD13	1.86	0.57
15:O:21:THR:HG22	15:O:26:VAL:HA	1.85	0.57
21:U:12:LEU:HD11	21:U:27:LEU:HD21	1.85	0.57
25:Y:74:LYS:NZ	25:Y:78:GLU:OE2	2.38	0.57
29:c:182:GLY:HA2	29:c:186:LYS:HD3	1.86	0.57
20:t:22:ILE:HG12	20:t:50:MET:HE3	1.86	0.57
7:G:132:ARG:HH12	13:M:124:LEU:HA	1.70	0.57
13:M:40:ARG:HG2	13:M:45:VAL:HG22	1.85	0.57
19:S:66:LYS:HA	19:S:69:GLU:HG2	1.85	0.57
32:f:842:VAL:H	32:f:870:THR:HG22	1.69	0.57
3:C:49:ARG:HD2	21:U:639:LEU:HD21	1.87	0.56
7:g:73:THR:HG23	7:g:75:ASN:H	1.70	0.56
12:l:45:VAL:HG11	12:l:188:VAL:HG22	1.87	0.56
3:C:284:GLU:O	3:C:287:LYS:HG3	2.05	0.56
5:E:198:VAL:HG12	5:E:200:SER:H	1.69	0.56
6:F:180:ARG:HH12	6:F:245:LYS:HA	1.68	0.56
7:G:123:GLN:NE2	8:H:82:ASP:OD1	2.39	0.56
11:K:41:GLN:NE2	11:K:151:PRO:O	2.39	0.56
29:c:113:HIS:NE2	29:c:115:HIS:HE1	1.90	0.56
7:G:67:THR:HG22	7:G:69:LEU:H	1.70	0.56
11:K:52:LYS:NZ	11:K:64:ILE:O	2.39	0.56
30:d:52:ARG:NH1	30:d:95:MET:SD	2.78	0.56
8:h:109:GLN:NE2	16:p:78:GLU:OE2	2.38	0.56
20:t:96:MET:HE1	20:t:106:LEU:HD12	1.87	0.56
1:A:345:LEU:O	1:A:346:PRO:C	2.49	0.56
6:F:314:LEU:HD21	6:F:342:LEU:HA	1.88	0.56
9:I:182:GLY:H	9:I:184:MET:HE1	1.70	0.56
27:a:360:VAL:HG22	29:c:308:VAL:HG13	1.87	0.56
30:d:91:GLU:OE2	30:d:96:HIS:NE2	2.39	0.56
18:R:102:CYS:SG	18:R:103:GLY:N	2.78	0.56
5:E:75:ASN:ND2	6:F:130:GLN:OE1	2.38	0.56
5:E:182:LEU:HD22	37:E:401:ADP:H2'	1.86	0.56
7:g:69:LEU:HD11	7:g:229:ILE:HD13	1.87	0.56
10:j:68:ASN:HA	10:j:211:MET:HE1	1.88	0.56
15:o:30:ASN:O	15:o:187:ARG:NH2	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:366:MET:HE3	6:F:381:TYR:HD1	1.71	0.56
27:a:361:LYS:HD3	27:a:365:MET:HE2	1.87	0.56
4:D:384:MET:HA	4:D:387:VAL:HG12	1.88	0.55
15:O:143:ARG:NH2	15:O:150:GLU:OE1	2.38	0.55
24:X:209:THR:HA	24:X:212:MET:HE3	1.87	0.55
17:q:168:GLN:NE2	17:q:175:LEU:O	2.39	0.55
8:H:143:ARG:NH1	8:H:144:PRO:O	2.37	0.55
19:S:64:LEU:O	19:S:68:ILE:HG12	2.07	0.55
21:U:616:ARG:NH1	21:U:620:GLU:OE2	2.39	0.55
23:W:446:ILE:HB	26:Z:226:ILE:HD11	1.88	0.55
8:h:58:ASP:OD1	8:h:60:ARG:NH1	2.40	0.55
18:r:99:THR:OG1	18:r:114:VAL:O	2.23	0.55
5:E:33:LEU:HD21	6:F:66:LEU:HB2	1.87	0.55
16:P:189:ILE:HB	16:P:196:THR:HB	1.89	0.55
7:g:43:ARG:HH21	7:g:164:LYS:HG2	1.71	0.55
7:g:165:ALA:HB1	7:g:179:LEU:HD13	1.89	0.55
18:R:166:ARG:NH1	16:p:34:MET:O	2.39	0.55
23:W:79:GLU:HB3	23:W:82:LEU:HB3	1.88	0.55
25:Y:72:LYS:HA	25:Y:75:LYS:HE3	1.88	0.55
27:a:270:ARG:HH21	27:a:313:LYS:HG3	1.71	0.55
16:p:71:LEU:HD11	16:p:82:ILE:HG21	1.87	0.55
1:A:376:LEU:HB3	1:A:417:ILE:HD11	1.88	0.55
16:P:159:ASP:N	16:P:159:ASP:OD1	2.39	0.55
20:T:184:TYR:HE2	20:T:186:ARG:HD3	1.72	0.55
7:g:137:CYS:SG	7:g:138:MET:N	2.79	0.55
1:A:38:GLN:OE1	32:f:160:ARG:NH2	2.40	0.55
9:I:90:LEU:HD21	9:I:114:LEU:HB2	1.87	0.55
12:L:152:ASN:HD21	13:M:81:LEU:HD12	1.72	0.55
20:T:122:LEU:HG	20:T:137:LEU:HD12	1.89	0.55
21:U:522:GLY:O	21:U:559:ARG:NH2	2.40	0.55
18:R:135:ALA:O	18:R:139:MET:HB2	2.06	0.55
2:B:233:THR:N	37:B:501:ADP:O1A	2.39	0.54
28:b:26:LEU:HD11	28:b:80:PRO:HG3	1.89	0.54
10:j:93:SER:HA	10:j:96:LEU:HD12	1.89	0.54
11:k:121:LEU:HD12	11:k:123:PHE:HE1	1.72	0.54
6:F:294:LYS:HA	6:F:339:ASP:HB3	1.89	0.54
26:Z:37:GLY:HA2	26:Z:56:VAL:HG12	1.90	0.54
10:j:192:ILE:HD12	10:j:206:ILE:HD12	1.90	0.54
33:u:22:THR:OG1	33:u:25:ASN:OD1	2.25	0.54
3:C:57:ARG:NH2	21:U:643:SER:O	2.41	0.54
3:C:157:GLN:NE2	3:C:316:GLU:OE2	2.39	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:808:PRO:HD3	21:U:874:ASN:HA	1.90	0.54
32:f:387:GLN:NE2	32:f:388:ASP:OD1	2.40	0.54
16:p:45:MET:HE2	16:p:71:LEU:HD13	1.89	0.54
20:t:1:THR:N	20:t:105:PRO:O	2.37	0.54
20:t:110:MET:HB2	20:t:125:VAL:HB	1.89	0.54
15:O:98:LEU:HB2	15:O:113:ILE:HB	1.89	0.54
21:U:643:SER:O	21:U:649:ARG:NH1	2.39	0.54
22:V:355:ARG:NH2	31:e:31:ASP:O	2.38	0.54
24:X:380:GLN:HB2	25:Y:314:LEU:HA	1.89	0.54
32:f:777:THR:HB	32:f:828:ARG:HD3	1.89	0.54
32:f:894:LEU:HD13	32:f:898:VAL:HG21	1.90	0.54
9:i:234:GLU:HA	9:i:237:ILE:HG12	1.88	0.54
19:s:4:PRO:HB2	20:t:100:ARG:HH21	1.72	0.54
10:J:36:ARG:HA	10:J:41:VAL:HG12	1.88	0.54
22:V:452:ASN:HB3	22:V:457:TYR:HB2	1.89	0.54
2:B:234:LEU:HD11	37:B:501:ADP:H2'	1.88	0.54
2:B:313:LEU:O	2:B:346:ARG:NH1	2.40	0.54
21:U:35:TRP:CD1	22:V:273:LYS:HZ3	2.26	0.54
21:U:611:ASN:HB3	21:U:614:VAL:HG12	1.89	0.54
22:V:337:LEU:HD21	22:V:364:THR:HG23	1.88	0.54
30:d:234:ASP:OD2	30:d:236:THR:OG1	2.25	0.54
11:K:167:ALA:HB3	12:L:56:LEU:HD13	1.90	0.54
13:M:227:VAL:O	13:M:232:ARG:NH2	2.39	0.54
19:S:36:HIS:O	20:T:151:ARG:NH2	2.40	0.54
32:f:685:THR:HA	32:f:688:ARG:HD2	1.88	0.54
7:g:31:ALA:HB1	7:g:83:MET:HE1	1.90	0.54
7:g:165:ALA:HB3	8:h:56:LEU:HD22	1.90	0.54
3:C:62:GLU:HG2	3:C:66:LEU:HD13	1.89	0.54
6:F:43:GLN:HA	6:F:46:ARG:HG2	1.89	0.54
6:F:235:LEU:HD21	35:F:501:ATP:H2'	1.89	0.54
29:c:115:HIS:HB3	29:c:118:PHE:HB2	1.90	0.54
7:g:123:GLN:NE2	8:h:82:ASP:OD1	2.41	0.54
9:I:3:ARG:HG2	10:J:5:ARG:HH12	1.73	0.54
9:I:155:ASN:OD1	10:J:77:THR:OG1	2.24	0.54
32:f:772:GLY:HA3	32:f:776:LEU:HD23	1.89	0.54
11:k:221:GLN:OE1	11:k:224:GLN:NE2	2.41	0.54
16:p:35:VAL:HG12	16:p:36:THR:HG23	1.88	0.54
1:A:296:GLN:HA	1:A:299:MET:HG2	1.90	0.54
3:C:60:ARG:NH2	4:D:71:GLU:OE2	2.41	0.54
3:C:188:LEU:HD23	3:C:315:ILE:HB	1.90	0.54
32:f:557:TRP:HA	32:f:560:LEU:HD12	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:225:ASP:OD1	22:V:225:ASP:N	2.41	0.53
22:V:289:LEU:HB3	22:V:312:ALA:HB2	1.90	0.53
29:c:198:ARG:O	29:c:199:HIS:HB2	2.08	0.53
7:g:3:ARG:O	7:g:4:GLY:C	2.51	0.53
6:F:363:ALA:HA	6:F:366:MET:HE2	1.90	0.53
20:T:126:ASP:OD1	20:T:130:VAL:N	2.41	0.53
8:h:148:GLN:OE1	8:h:158:TRP:NE1	2.41	0.53
12:l:120:THR:O	13:m:129:ARG:NH1	2.41	0.53
2:B:224:LEU:HD21	2:B:235:LEU:HD22	1.91	0.53
14:N:32:ASP:O	14:N:45:ARG:NH2	2.41	0.53
15:O:46:ALA:HB3	15:O:97:ALA:HB3	1.90	0.53
23:W:451:MET:O	23:W:455:LEU:HG	2.08	0.53
7:g:11:ARG:HH22	7:g:12:HIS:CE1	2.27	0.53
3:C:287:LYS:HZ1	3:C:289:ILE:HD12	1.73	0.53
23:W:170:GLN:NE2	23:W:172:GLU:OE2	2.42	0.53
7:g:21:ARG:NH2	7:g:23:TYR:OH	2.42	0.53
9:i:123:GLN:HA	10:j:125:ARG:HE	1.73	0.53
1:A:105:ASP:HB2	1:A:110:LYS:HB2	1.91	0.53
3:C:144:PRO:O	3:C:205:HIS:ND1	2.41	0.53
4:D:56:VAL:HG21	21:U:599:ILE:HG23	1.91	0.53
7:G:80:MET:HG3	7:G:87:SER:HB3	1.90	0.53
27:a:210:VAL:HG12	27:a:213:PHE:CE2	2.43	0.53
32:f:902:LYS:NZ	32:f:903:ASN:O	2.42	0.53
1:A:227:ARG:NH2	2:B:319:PHE:O	2.41	0.53
19:S:36:HIS:HD1	20:T:132:TYR:HH	1.51	0.53
23:W:172:GLU:HA	23:W:182:ARG:HD3	1.91	0.53
30:d:109:GLN:O	30:d:111:ARG:NH1	2.42	0.53
1:A:224:LEU:HD11	35:A:501:ATP:H2'	1.91	0.53
8:H:14:SER:OG	8:H:18:LYS:N	2.42	0.53
27:a:247:ARG:HH22	27:a:269:LEU:HD22	1.74	0.53
32:f:343:LYS:HE2	32:f:773:LYS:HG2	1.90	0.53
19:s:148:LEU:HD23	19:s:178:VAL:HG12	1.89	0.53
20:t:27:LEU:HD22	20:t:184:TYR:HB2	1.90	0.53
3:C:20:LEU:HD12	3:C:21:ARG:HG3	1.90	0.53
9:i:119:GLN:NE2	10:j:79:ASP:OD1	2.42	0.53
20:T:86:ARG:NH1	20:T:133:GLU:OE2	2.41	0.53
21:U:527:GLN:HG2	21:U:528:ALA:N	2.24	0.53
21:U:798:PRO:O	21:U:880:ASN:ND2	2.42	0.53
30:d:164:THR:HA	30:d:167:ILE:HG12	1.90	0.53
3:C:182:GLN:NE2	3:C:285:ALA:O	2.38	0.53
10:J:50:VAL:HB	10:J:54:GLN:HB2	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:37:ILE:HD11	13:M:193:VAL:HG13	1.90	0.53
16:P:62:THR:OG1	17:Q:85:ARG:NH2	2.41	0.53
20:T:151:ARG:NH1	15:o:165:ASN:OD1	2.41	0.53
5:E:322:LYS:HD3	5:E:326:ILE:HG13	1.91	0.52
27:a:35:HIS:CE1	28:b:17:ARG:HH21	2.27	0.52
12:l:16:GLN:HG3	12:l:18:ARG:HH21	1.73	0.52
19:S:68:ILE:HD11	19:S:92:LEU:HD13	1.90	0.52
23:W:201:ARG:HD3	23:W:204:ILE:HD11	1.90	0.52
27:a:226:ARG:HB3	27:a:234:ILE:HD11	1.90	0.52
8:h:204:THR:OG1	8:h:206:ASP:OD1	2.25	0.52
14:n:39:ASP:OD2	14:n:40:ARG:NH1	2.40	0.52
15:o:191:VAL:O	15:o:194:LYS:NZ	2.40	0.52
1:A:304:ASN:ND2	6:F:287:GLU:OE2	2.42	0.52
2:B:361:LYS:NZ	2:B:387:LYS:O	2.42	0.52
10:J:211:MET:HE1	10:J:217:LEU:HB3	1.91	0.52
22:V:461:LYS:NZ	22:V:462:GLU:O	2.43	0.52
7:g:125:TYR:CD1	7:g:131:MET:HE3	2.42	0.52
12:l:215:VAL:HB	12:l:221:PHE:HD1	1.73	0.52
22:V:496:PHE:HB2	22:V:497:PRO:HD3	1.91	0.52
16:P:203:ARG:NH2	16:P:205:ASP:OD2	2.40	0.52
21:U:173:VAL:HG22	21:U:176:MET:HE2	1.91	0.52
24:X:299:LEU:H	24:X:334:ASN:HD21	1.58	0.52
25:Y:246:ILE:HG22	25:Y:250:LEU:HD23	1.91	0.52
32:f:348:ILE:O	32:f:349:TYR:C	2.52	0.52
32:f:460:ASP:OD1	32:f:489:TYR:OH	2.27	0.52
9:i:38:LEU:HD12	9:i:160:LYS:HA	1.90	0.52
6:F:373:MET:SD	6:F:373:MET:N	2.78	0.52
8:H:166:ASN:OD1	8:H:169:ASN:ND2	2.37	0.52
13:M:36:ALA:HB3	13:M:165:ILE:HG13	1.91	0.52
23:W:377:ARG:NH2	27:a:308:GLU:OE1	2.43	0.52
27:a:100:THR:HA	27:a:103:LYS:HG2	1.92	0.52
32:f:600:TYR:HE2	32:f:608:LYS:HE3	1.73	0.52
6:F:51:GLU:HG2	6:F:55:MET:HE2	1.92	0.52
22:V:416:ARG:NH2	25:Y:351:ASN:OD1	2.43	0.52
29:c:279:ASP:OD1	29:c:279:ASP:N	2.42	0.52
7:g:11:ARG:HB3	7:g:11:ARG:CZ	2.38	0.52
4:D:378:ILE:HG23	4:D:402:ALA:HB1	1.92	0.52
27:a:115:LYS:HA	27:a:118:ILE:HD12	1.92	0.52
1:A:286:ASP:OD2	6:F:334:ARG:NH1	2.43	0.52
3:C:86:LEU:HD21	3:C:94:LYS:HD2	1.92	0.52
8:H:59:GLU:OE2	8:H:60:ARG:NH1	2.43	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:13:ASP:OD1	21:U:44:LYS:NZ	2.43	0.52
26:Z:9:VAL:HG12	26:Z:48:LEU:HB3	1.91	0.52
15:o:141:LYS:O	15:o:143:ARG:NH1	2.42	0.52
2:B:49:LEU:HD11	32:f:673:ARG:HE	1.75	0.52
6:F:224:LEU:HB2	6:F:348:LEU:HD23	1.91	0.52
21:U:133:ILE:HB	21:U:137:MET:HE2	1.92	0.52
23:W:401:THR:HG23	23:W:402:ILE:HD12	1.92	0.52
23:W:406:VAL:HA	23:W:413:ILE:HG22	1.92	0.52
24:X:408:SER:HB2	25:Y:376:LEU:HD11	1.91	0.52
32:f:342:PRO:HB3	32:f:390:LEU:HB2	1.92	0.52
5:E:270:LEU:HD12	5:E:273:VAL:HG21	1.93	0.51
7:g:86:ASP:OD1	13:m:120:HIS:NE2	2.41	0.51
17:q:13:VAL:HG13	17:q:113:PRO:HB2	1.91	0.51
4:D:67:ASN:HD22	21:U:607:VAL:HG12	1.76	0.51
37:E:401:ADP:O2B	6:F:344:ARG:NH1	2.43	0.51
21:U:448:LEU:HA	21:U:483:LEU:HD22	1.91	0.51
26:Z:133:LEU:HD12	29:c:223:LYS:HA	1.92	0.51
5:E:234:GLU:HG2	6:F:311:LEU:HD22	1.93	0.51
3:C:297:ARG:HH21	3:C:299:ASP:HB2	1.75	0.51
27:a:35:HIS:NE2	28:b:14:GLU:O	2.44	0.51
28:b:180:ALA:HA	28:b:183:LEU:HB2	1.93	0.51
10:j:42:VAL:HG22	10:j:210:VAL:HG22	1.93	0.51
7:G:34:GLN:NE2	13:M:18:GLY:O	2.43	0.51
21:U:607:VAL:O	21:U:615:ARG:NH1	2.41	0.51
22:V:90:GLU:OE1	22:V:92:ARG:NH1	2.44	0.51
23:W:205:ILE:HA	23:W:208:LYS:HE3	1.93	0.51
32:f:851:ASP:O	32:f:855:GLN:NE2	2.44	0.51
13:m:35:THR:HA	13:m:166:GLY:HA3	1.91	0.51
3:C:134:LEU:HD22	3:C:230:MET:HA	1.92	0.51
21:U:415:HIS:O	21:U:450:HIS:NE2	2.43	0.51
22:V:309:MET:HE2	22:V:331:LEU:HD22	1.92	0.51
25:Y:105:MET:HG3	25:Y:136:HIS:NE2	2.26	0.51
17:q:53:THR:HG22	17:q:100:VAL:HG12	1.92	0.51
4:D:231:VAL:HG11	5:E:216:ARG:HH21	1.74	0.51
16:P:45:MET:HE2	16:P:71:LEU:HD22	1.92	0.51
17:Q:25:ILE:HG22	17:Q:26:VAL:HG13	1.91	0.51
29:c:187:PRO:HB3	29:c:196:LEU:HD21	1.92	0.51
32:f:343:LYS:HG3	32:f:773:LYS:HE2	1.93	0.51
7:G:10:ASP:OD1	7:G:10:ASP:N	2.43	0.51
20:T:179:ARG:NH2	15:o:139:GLU:OE2	2.44	0.51
8:h:213:CYS:HB2	8:h:218:PHE:HD1	1.75	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:118:MET:SD	17:Q:118:MET:N	2.84	0.51
21:U:898:CYS:SG	21:U:899:ARG:N	2.84	0.51
22:V:476:PHE:HD2	26:Z:257:MET:HE3	1.75	0.51
30:d:55:LEU:HD13	30:d:77:GLN:HG3	1.93	0.51
4:D:231:VAL:HB	4:D:234:GLU:HB3	1.91	0.51
9:I:68:LEU:HB3	9:I:72:MET:HB2	1.92	0.51
29:c:196:LEU:C	29:c:198:ARG:H	2.18	0.51
32:f:341:GLU:OE2	32:f:343:LYS:NZ	2.36	0.51
9:i:67:LYS:HE3	9:i:225:ILE:HD12	1.93	0.51
14:n:192:ASP:OD1	14:n:196:LYS:NZ	2.44	0.51
3:C:252:ASP:OD1	3:C:252:ASP:N	2.44	0.50
7:G:37:LEU:HD22	7:G:53:GLN:HG3	1.91	0.50
26:Z:234:PHE:HA	26:Z:237:LEU:HD23	1.93	0.50
29:c:212:LEU:HG	29:c:216:MET:HE1	1.93	0.50
32:f:139:CYS:SG	32:f:161:HIS:NE2	2.84	0.50
2:B:74:MET:HB2	32:f:610:GLN:HE22	1.76	0.50
3:C:69:GLN:HB3	3:C:118:ASN:HD21	1.76	0.50
13:M:230:ASP:N	13:M:230:ASP:OD1	2.44	0.50
15:O:63:LEU:HD11	15:O:79:ALA:HB2	1.92	0.50
26:Z:65:ASP:OD1	26:Z:65:ASP:N	2.43	0.50
28:b:107:MET:HB3	28:b:136:VAL:HG13	1.92	0.50
11:k:56:SER:HB3	11:k:59:MET:HE3	1.93	0.50
15:o:1:THR:N	15:o:168:GLY:O	2.44	0.50
16:p:2:SER:N	16:p:5:SER:HG	2.09	0.50
2:B:249:ARG:HH22	2:B:251:VAL:HG23	1.76	0.50
21:U:516:LEU:HD23	21:U:532:MET:HE3	1.93	0.50
25:Y:282:MET:HB2	25:Y:288:PHE:HE1	1.76	0.50
32:f:585:GLU:CB	32:f:586:PRO:HD2	2.32	0.50
8:h:123:GLN:OE1	9:i:128:ARG:NE	2.45	0.50
13:m:50:GLU:OE2	13:m:201:HIS:ND1	2.36	0.50
4:D:121:ARG:HA	4:D:124:LEU:HD23	1.93	0.50
6:F:103:ASP:OD1	6:F:104:GLN:N	2.45	0.50
8:H:51:LYS:NZ	8:H:199:PHE:O	2.43	0.50
9:I:161:ALA:HB1	9:I:175:LEU:HD13	1.93	0.50
21:U:167:ILE:HB	21:U:177:LEU:HD11	1.94	0.50
23:W:190:MET:HE2	23:W:206:SER:HA	1.93	0.50
24:X:296:ASN:O	24:X:337:ARG:NH1	2.44	0.50
25:Y:32:ARG:NH2	25:Y:61:LEU:O	2.45	0.50
8:h:222:THR:HG23	8:h:225:GLU:H	1.77	0.50
10:j:180:ALA:HB1	10:j:190:LEU:HD11	1.93	0.50
2:B:268:ARG:HA	2:B:315:GLN:HE22	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:372:ARG:HD3	13:M:170:GLN:HB2	1.92	0.50
29:c:108:VAL:HG23	33:u:9:THR:HG22	1.93	0.50
32:f:409:SER:O	32:f:819:TYR:OH	2.26	0.50
17:q:4:LEU:HB2	17:q:132:HIS:HB2	1.93	0.50
4:D:97:ASP:OD1	4:D:97:ASP:N	2.43	0.50
10:J:148:ASP:OD1	10:J:152:THR:N	2.45	0.50
21:U:801:GLN:HB3	21:U:877:LEU:HD12	1.92	0.50
21:U:802:TYR:HB2	21:U:878:LEU:HB2	1.93	0.50
3:C:53:ASN:ND2	21:U:642:GLU:O	2.44	0.50
4:D:145:PRO:HB2	4:D:256:GLU:HG3	1.93	0.50
10:J:189:LYS:HA	10:J:232:ILE:HD11	1.94	0.50
14:N:40:ARG:NH1	14:N:180:ALA:O	2.45	0.50
16:P:177:ARG:NH2	19:s:150:ASP:OD2	2.40	0.50
17:Q:83:PHE:O	17:Q:87:ASN:ND2	2.44	0.50
24:X:251:LEU:HA	24:X:254:MET:HE2	1.93	0.50
32:f:151:LEU:HD23	32:f:159:VAL:HG22	1.94	0.50
4:D:191:TYR:HA	4:D:196:ILE:HD12	1.93	0.50
6:F:229:PRO:HA	6:F:233:LYS:HZ1	1.76	0.50
7:G:107:TYR:OH	15:O:75:ARG:NH1	2.45	0.50
11:K:129:ASP:N	11:K:130:PRO:HD2	2.27	0.50
19:S:209:SER:OG	19:S:212:LYS:NZ	2.42	0.50
22:V:228:ARG:NH2	22:V:257:ASN:O	2.45	0.50
26:Z:74:TYR:OH	29:c:98:MET:O	2.28	0.50
8:h:52:GLN:HE21	8:h:57:TYR:HD2	1.57	0.50
33:u:23:ILE:HB	33:u:52:ASP:HA	1.92	0.50
4:D:92:PHE:O	4:D:127:ASN:HA	2.12	0.50
8:H:9:SER:OG	8:H:123:GLN:O	2.30	0.50
8:H:67:PRO:HG2	15:O:68:LEU:HD11	1.94	0.50
21:U:198:LEU:HD21	21:U:219:CYS:HB2	1.92	0.50
24:X:407:MET:HA	24:X:410:VAL:HG12	1.93	0.50
13:m:215:TRP:CD1	13:m:227:VAL:HG22	2.46	0.50
2:B:76:GLU:O	2:B:80:ARG:HG2	2.12	0.49
2:B:237:LYS:O	2:B:241:ASN:ND2	2.45	0.49
19:S:169:ASP:HA	19:S:172:MET:HE2	1.94	0.49
23:W:264:GLN:OE1	23:W:335:SER:OG	2.30	0.49
4:D:278:GLN:HE22	4:D:283:ARG:HD3	1.77	0.49
11:K:180:SER:HB3	11:K:201:ILE:HD12	1.94	0.49
22:V:408:ARG:HD3	22:V:412:LEU:HD23	1.94	0.49
26:Z:212:LEU:HA	26:Z:215:VAL:HG12	1.93	0.49
30:d:183:GLU:OE2	30:d:215:TRP:NE1	2.42	0.49
32:f:794:ALA:O	32:f:798:THR:HG23	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:81:PRO:HA	8:h:84:ARG:HE	1.76	0.49
9:i:201:MET:HE1	9:i:204:SER:O	2.12	0.49
20:t:126:ASP:OD1	20:t:130:VAL:N	2.45	0.49
3:C:90:HIS:CB	3:C:91:PRO:HD3	2.38	0.49
13:M:35:THR:HA	13:M:166:GLY:HA3	1.95	0.49
14:N:162:LEU:HD11	14:n:141:ALA:HB2	1.94	0.49
29:c:29:GLU:HB2	29:c:203:ILE:HD11	1.94	0.49
29:c:132:SER:HA	33:u:36:ILE:HD12	1.93	0.49
29:c:303:MET:HE1	30:d:239:SER:HA	1.93	0.49
12:l:203:GLN:NE2	12:l:204:ASP:O	2.45	0.49
16:p:12:MET:SD	16:p:12:MET:N	2.85	0.49
2:B:109:VAL:HG11	3:C:94:LYS:HE2	1.93	0.49
6:F:386:ARG:HE	12:L:166:GLN:HE21	1.61	0.49
13:M:185:THR:O	13:M:189:ILE:HG12	2.13	0.49
22:V:311:ASN:OD1	22:V:314:ARG:NH1	2.42	0.49
24:X:364:LYS:HE3	24:X:368:MET:HE3	1.94	0.49
32:f:606:VAL:O	32:f:610:GLN:HG2	2.13	0.49
9:i:46:ALA:HB1	9:i:197:LEU:HD11	1.93	0.49
2:B:204:PRO:HG3	2:B:211:TYR:HE2	1.77	0.49
5:E:213:ARG:NH1	5:E:217:GLU:OE2	2.45	0.49
23:W:425:LEU:HD13	26:Z:248:ALA:HB1	1.95	0.49
32:f:885:GLU:OE2	32:f:903:ASN:ND2	2.45	0.49
1:A:362:MET:HE2	2:B:216:ILE:HG12	1.95	0.49
3:C:99:VAL:HG12	3:C:123:LEU:HD12	1.95	0.49
8:H:11:THR:HG22	8:H:19:LEU:HD12	1.94	0.49
20:T:27:LEU:HD22	20:T:184:TYR:HB2	1.94	0.49
32:f:511:SER:OG	32:f:513:GLU:OE1	2.30	0.49
32:f:836:GLU:O	32:f:838:ARG:NH1	2.45	0.49
11:k:98:ASN:OD1	18:r:61:ARG:NH2	2.46	0.49
1:A:55:LEU:HD11	2:B:76:GLU:HG2	1.95	0.49
7:G:31:ALA:HA	7:G:34:GLN:HE22	1.78	0.49
10:J:96:LEU:HD22	17:Q:62:LYS:HZ2	1.78	0.49
21:U:78:LEU:HD11	21:U:104:CYS:HB2	1.94	0.49
22:V:494:MET:HB2	26:Z:278:ASN:HD22	1.78	0.49
27:a:278:MET:HB3	27:a:319:LEU:HD13	1.95	0.49
32:f:394:ASP:O	32:f:397:LYS:NZ	2.46	0.49
1:A:393:GLY:HA3	2:B:216:ILE:HD13	1.94	0.49
4:D:336:PRO:HB2	4:D:341:LYS:HE3	1.94	0.49
10:J:155:ALA:H	11:K:63:SER:HB2	1.78	0.49
25:Y:49:ASN:OD1	25:Y:77:ASN:ND2	2.45	0.49
32:f:555:ALA:O	32:f:587:PHE:HZ	1.96	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:791:VAL:HG12	32:f:823:ALA:HB1	1.94	0.49
11:k:41:GLN:NE2	11:k:151:PRO:O	2.46	0.49
6:F:39:GLU:HB3	6:F:43:GLN:HB2	1.94	0.49
15:O:103:VAL:HG22	15:O:108:PRO:HB3	1.95	0.49
16:P:135:ASP:OD1	16:P:135:ASP:N	2.44	0.49
18:R:133:VAL:HG21	17:q:137:PHE:HB3	1.93	0.49
21:U:265:ILE:HA	21:U:268:LEU:HD12	1.93	0.49
22:V:496:PHE:H	22:V:497:PRO:HD2	1.77	0.49
24:X:8:GLU:OE1	24:X:11:ARG:NH1	2.45	0.49
27:a:193:GLN:HB3	27:a:225:LEU:HD13	1.94	0.49
29:c:96:LEU:HD12	33:u:8:LEU:CD2	2.41	0.49
32:f:349:TYR:CZ	32:f:350:LYS:HG2	2.48	0.49
32:f:470:VAL:HG11	32:f:500:LEU:HD21	1.95	0.49
2:B:223:ILE:HD11	2:B:347:ILE:HD13	1.95	0.49
6:F:289:ASP:OD1	6:F:289:ASP:N	2.45	0.49
9:I:86:LEU:HD22	9:I:114:LEU:HD11	1.95	0.49
25:Y:50:MET:O	25:Y:54:TYR:N	2.45	0.49
27:a:65:SER:HA	27:a:68:GLU:HB2	1.95	0.49
27:a:120:ALA:HB2	27:a:154:ARG:HH21	1.78	0.49
32:f:405:HIS:ND1	32:f:813:LYS:O	2.44	0.49
32:f:691:PRO:HA	32:f:694:LEU:HG	1.95	0.49
7:g:70:PHE:HD2	7:g:91:VAL:HG21	1.77	0.49
11:k:85:ALA:HB2	11:k:139:VAL:HG11	1.95	0.49
5:E:83:CYS:SG	5:E:84:ARG:N	2.86	0.48
23:W:422:ASN:HD21	29:c:235:SER:HA	1.78	0.48
25:Y:272:PHE:HB3	31:e:52:PHE:HZ	1.78	0.48
26:Z:175:LEU:HD11	29:c:209:LYS:HE3	1.93	0.48
20:t:180:ASP:HB3	20:t:183:SER:HB3	1.93	0.48
1:A:306:LEU:HD12	1:A:312:ARG:HD3	1.94	0.48
3:C:117:ARG:HE	3:C:124:HIS:CE1	2.31	0.48
4:D:291:GLU:O	4:D:295:GLN:HG3	2.13	0.48
6:F:180:ARG:NH1	6:F:244:THR:O	2.46	0.48
9:I:49:ARG:NH2	9:I:211:VAL:O	2.46	0.48
10:J:47:LYS:HE2	10:J:47:LYS:HB3	1.65	0.48
24:X:335:LEU:HA	24:X:338:VAL:HG22	1.95	0.48
32:f:93:PRO:HB2	32:f:96:LEU:HB2	1.94	0.48
7:g:13:ILE:HG13	7:g:15:ILE:HG12	1.95	0.48
12:l:34:ALA:HA	12:l:162:GLY:HA3	1.95	0.48
17:q:35:MET:HE3	17:q:181:ARG:HD2	1.95	0.48
7:G:158:GLY:O	8:H:84:ARG:NH2	2.46	0.48
8:H:50:LYS:NZ	8:H:59:GLU:O	2.44	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:226:ASP:OD1	12:L:226:ASP:N	2.46	0.48
16:p:7:ASN:O	16:p:27:ARG:NH1	2.46	0.48
2:B:440:LEU:HD22	10:J:77:THR:HG21	1.95	0.48
3:C:229:ARG:HE	3:C:232:ARG:HG3	1.79	0.48
21:U:450:HIS:HB2	21:U:457:ILE:HD13	1.94	0.48
27:a:123:LEU:HD21	27:a:161:LYS:HD3	1.94	0.48
7:g:11:ARG:HH12	7:g:12:HIS:CE1	2.31	0.48
12:l:27:GLU:HA	12:l:30:LYS:HD3	1.96	0.48
10:J:57:ARG:O	10:J:60:ARG:NH1	2.46	0.48
21:U:146:LYS:HE2	21:U:148:LYS:HB2	1.95	0.48
21:U:570:LEU:HD22	21:U:578:LEU:HG	1.95	0.48
21:U:625:ILE:HG13	21:U:626:LEU:HG	1.95	0.48
24:X:343:SER:HA	24:X:387:ILE:HB	1.94	0.48
27:a:72:ASN:N	28:b:17:ARG:HH22	2.12	0.48
28:b:124:LEU:HD21	28:b:152:LYS:HB3	1.95	0.48
32:f:549:GLU:HG3	32:f:587:PHE:CG	2.48	0.48
32:f:727:PHE:HE1	32:f:806:VAL:HG21	1.78	0.48
1:A:309:PHE:H	6:F:238:ARG:HH21	1.62	0.48
2:B:222:VAL:HG22	2:B:349:ARG:HB2	1.96	0.48
11:K:130:PRO:O	11:K:132:ALA:N	2.43	0.48
19:S:143:ALA:HB1	16:p:145:GLN:HE21	1.77	0.48
21:U:528:ALA:O	21:U:532:MET:HG3	2.13	0.48
26:Z:20:VAL:HG11	29:c:213:GLU:HB3	1.95	0.48
32:f:581:GLU:HA	32:f:588:ARG:HD2	1.95	0.48
10:j:148:ASP:OD2	10:j:152:THR:OG1	2.26	0.48
16:p:11:VAL:HG11	16:p:52:GLY:HA3	1.96	0.48
23:W:20:TYR:HD2	23:W:54:THR:HG22	1.77	0.48
23:W:147:LYS:NZ	23:W:184:GLU:OE1	2.38	0.48
32:f:96:LEU:HD11	32:f:128:VAL:HG12	1.95	0.48
12:l:69:HIS:CE1	12:l:102:PRO:HB3	2.48	0.48
3:C:119:ASP:OD2	3:C:120:SER:N	2.45	0.48
3:C:244:SER:H	3:C:289:ILE:HG12	1.77	0.48
23:W:105:VAL:HG11	23:W:138:VAL:HG12	1.93	0.48
25:Y:84:LEU:HD13	25:Y:107:LYS:HA	1.96	0.48
7:g:200:THR:HA	7:g:203:SER:HB3	1.94	0.48
2:B:102:LEU:HD22	2:B:138:PHE:HE2	1.79	0.48
3:C:232:ARG:NH2	3:C:275:GLU:O	2.43	0.48
4:D:293:LEU:HD22	4:D:326:ARG:NH2	2.29	0.48
4:D:296:MET:HE1	4:D:326:ARG:HB3	1.95	0.48
6:F:197:GLU:OE1	6:F:350:ARG:NH2	2.47	0.48
18:R:186:ARG:HH22	18:R:189:SER:HB2	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:186:ILE:O	23:W:190:MET:HG3	2.14	0.48
26:Z:215:VAL:HB	26:Z:220:LEU:HD23	1.95	0.48
29:c:32:TYR:HE1	29:c:208:ARG:HE	1.61	0.48
32:f:298:LEU:O	32:f:302:GLY:N	2.46	0.48
2:B:258:LYS:HE2	34:v:1:UNK:H	1.79	0.48
11:K:36:THR:HA	11:K:171:GLY:HA3	1.96	0.47
21:U:364:VAL:O	21:U:367:THR:OG1	2.30	0.47
22:V:234:ARG:HH22	22:V:241:ARG:HH22	1.61	0.47
29:c:219:ASN:HB2	29:c:222:LYS:HD3	1.96	0.47
3:C:53:ASN:HD21	21:U:643:SER:HA	1.78	0.47
3:C:143:VAL:O	3:C:201:ARG:NH2	2.44	0.47
10:J:220:LEU:CD1	10:J:224:GLU:HB2	2.44	0.47
11:K:59:MET:HE3	11:K:64:ILE:HD11	1.96	0.47
11:K:169:ALA:N	11:K:178:GLN:OE1	2.47	0.47
12:L:7:ASP:O	12:L:21:GLN:NE2	2.42	0.47
13:M:50:GLU:OE2	13:M:201:HIS:ND1	2.40	0.47
16:P:123:SER:HB3	16:P:137:VAL:HB	1.95	0.47
26:Z:208:ILE:HD11	26:Z:230:LEU:HD11	1.95	0.47
27:a:343:LEU:HA	27:a:346:ILE:HD12	1.95	0.47
16:p:61:GLN:HE22	16:p:65:GLN:HE21	1.61	0.47
5:E:245:GLU:OE1	5:E:251:ARG:NH2	2.47	0.47
5:E:281:ARG:HH21	5:E:283:ASP:HB2	1.79	0.47
5:E:331:ILE:HG23	5:E:371:VAL:HG21	1.96	0.47
12:L:11:THR:HA	13:M:129:ARG:HD3	1.97	0.47
13:M:163:CYS:SG	13:M:164:ALA:N	2.87	0.47
32:f:123:ALA:HA	32:f:126:ILE:HD12	1.95	0.47
12:l:72:ILE:HG22	12:l:134:ILE:HG12	1.95	0.47
2:B:214:MET:HB3	2:B:216:ILE:HD12	1.96	0.47
3:C:78:ARG:HH11	3:C:110:PRO:HB3	1.80	0.47
5:E:180:LYS:NZ	37:E:401:ADP:O3B	2.36	0.47
6:F:368:ILE:HG23	6:F:371:ARG:HH22	1.79	0.47
10:J:31:THR:OG1	10:J:163:ARG:O	2.26	0.47
10:J:90:GLU:HG3	10:J:110:TYR:CZ	2.48	0.47
24:X:173:GLU:HA	24:X:176:THR:HG22	1.96	0.47
25:Y:231:LEU:HD12	25:Y:234:PRO:HG2	1.96	0.47
32:f:208:LEU:HD13	32:f:217:LEU:HG	1.97	0.47
13:m:230:ASP:OD1	13:m:230:ASP:N	2.47	0.47
2:B:133:VAL:HB	2:B:158:ALA:HA	1.96	0.47
5:E:237:ALA:HA	6:F:308:ARG:HE	1.79	0.47
6:F:307:GLN:HA	6:F:310:MET:HG3	1.97	0.47
10:J:127:PHE:HB3	10:J:129:ILE:HG22	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:73:VAL:HG22	13:M:139:SER:HB2	1.96	0.47
18:R:38:ASN:OD1	18:R:41:LEU:N	2.47	0.47
21:U:62:LEU:HD12	21:U:84:ALA:HB1	1.96	0.47
16:p:153:LEU:HD12	16:p:170:ALA:HB2	1.96	0.47
16:P:138:VAL:HG11	16:P:146:MET:HB3	1.96	0.47
21:U:696:ILE:HD11	21:U:746:ILE:HG12	1.96	0.47
24:X:21:GLU:HA	24:X:24:ILE:HD12	1.96	0.47
27:a:252:LYS:HD2	27:a:255:TRP:CD1	2.49	0.47
9:i:14:PRO:HA	10:j:21:TYR:CZ	2.49	0.47
1:A:398:ARG:HG3	1:A:399:ALA:N	2.30	0.47
4:D:176:GLU:OE2	4:D:329:ARG:NH1	2.48	0.47
12:L:158:ALA:HB1	12:L:172:LEU:HD13	1.95	0.47
16:P:35:VAL:HG12	16:P:36:THR:HG23	1.97	0.47
17:Q:27:GLN:HG3	17:q:172:ILE:HG22	1.95	0.47
21:U:36:ALA:HB1	22:V:269:LYS:HB3	1.97	0.47
21:U:52:GLU:OE1	21:U:57:ARG:NH1	2.48	0.47
21:U:500:ASN:HA	21:U:503:GLN:NE2	2.29	0.47
23:W:287:VAL:HA	23:W:290:ILE:HG22	1.96	0.47
27:a:61:GLU:HG3	27:a:79:ILE:HD13	1.97	0.47
27:a:72:ASN:HD21	27:a:74:LEU:HD12	1.80	0.47
29:c:64:ASP:O	29:c:139:ARG:NH1	2.47	0.47
29:c:88:ASP:N	29:c:88:ASP:OD1	2.44	0.47
9:i:204:SER:O	9:i:205:LYS:C	2.58	0.47
16:p:158:MET:HG3	16:p:163:LEU:HB2	1.95	0.47
17:q:64:VAL:HG13	17:q:75:LEU:HD12	1.96	0.47
18:r:182:ASP:OD1	18:r:182:ASP:N	2.47	0.47
22:V:238:ALA:HA	22:V:241:ARG:HG2	1.96	0.47
8:H:51:LYS:NZ	8:H:200:GLU:O	2.48	0.47
9:I:197:LEU:HA	9:I:200:THR:HG22	1.95	0.47
10:J:92:GLN:NE2	17:Q:62:LYS:O	2.42	0.47
21:U:373:ASN:HD22	21:U:385:PHE:HB3	1.78	0.47
22:V:175:MET:HE2	22:V:183:GLU:HB2	1.97	0.47
25:Y:225:TYR:O	25:Y:295:TYR:OH	2.26	0.47
31:e:16:ASP:OD1	31:e:16:ASP:N	2.46	0.47
4:D:85:ILE:N	4:D:86:PRO:CD	2.78	0.47
4:D:147:ALA:HA	5:E:62:LYS:HD3	1.97	0.47
20:t:124:TYR:HE1	20:t:139:THR:HG22	1.80	0.47
1:A:297:ARG:HH22	6:F:306:VAL:HG21	1.79	0.46
7:G:165:ALA:HB1	7:G:179:LEU:HD13	1.97	0.46
8:H:204:THR:OG1	8:H:206:ASP:OD2	2.33	0.46
12:L:134:ILE:HB	12:L:145:PHE:HB2	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:42:TYR:HE2	15:O:183:LEU:HD11	1.80	0.46
17:Q:197:PRO:HD2	17:q:199:GLN:H	1.79	0.46
24:X:252:LYS:HD2	24:X:283:GLN:HG2	1.97	0.46
32:f:830:LEU:HD12	32:f:896:GLY:O	2.15	0.46
16:P:38:ASP:OD1	16:P:38:ASP:N	2.48	0.46
19:s:125:ASP:OD1	19:s:129:SER:N	2.47	0.46
4:D:410:ASP:OD1	4:D:410:ASP:N	2.48	0.46
6:F:294:LYS:N	6:F:337:ILE:O	2.47	0.46
13:M:51:LYS:O	13:M:210:GLU:N	2.46	0.46
13:M:229:LYS:HA	13:M:232:ARG:HG2	1.97	0.46
19:S:16:ALA:HB2	19:S:121:VAL:HG23	1.95	0.46
19:S:131:GLN:NE2	19:S:133:ASP:OD2	2.49	0.46
22:V:95:LEU:HD21	22:V:205:LEU:HD22	1.97	0.46
22:V:118:GLN:HG3	22:V:128:ARG:HH22	1.80	0.46
24:X:157:LEU:HD21	24:X:165:LEU:HD23	1.98	0.46
27:a:14:SER:N	27:a:18:GLN:HE21	2.13	0.46
28:b:109:ILE:HB	28:b:138:VAL:HA	1.97	0.46
32:f:667:GLY:O	32:f:671:ALA:CB	2.64	0.46
10:j:212:ARG:HG3	10:j:215:GLN:HB2	1.96	0.46
33:u:63:LYS:HD3	33:u:64:GLU:HB2	1.98	0.46
5:E:239:GLY:HA2	5:E:257:LEU:HD12	1.98	0.46
21:U:428:PRO:HG3	21:U:439:GLU:HB3	1.98	0.46
21:U:699:THR:OG1	21:U:810:THR:O	2.31	0.46
23:W:396:LEU:HD13	23:W:402:ILE:HB	1.98	0.46
25:Y:347:ILE:HG13	25:Y:354:VAL:HG22	1.97	0.46
27:a:321:LYS:HB2	27:a:335:TRP:HB3	1.97	0.46
32:f:586:PRO:O	32:f:589:SER:N	2.49	0.46
7:g:80:MET:SD	7:g:80:MET:N	2.89	0.46
2:B:232:LYS:NZ	2:B:331:THR:O	2.45	0.46
3:C:335:LYS:HE3	25:Y:172:GLY:HA3	1.98	0.46
17:Q:18:ASP:OD1	17:Q:18:ASP:N	2.49	0.46
19:S:26:ASP:HB3	19:S:179:PHE:HZ	1.80	0.46
25:Y:104:MET:HE1	25:Y:127:THR:HA	1.98	0.46
25:Y:334:LEU:HD22	25:Y:343:LEU:HD21	1.97	0.46
11:k:18:GLU:O	12:l:31:GLN:NE2	2.46	0.46
2:B:230:THR:HG21	2:B:353:PHE:HB3	1.98	0.46
6:F:195:ILE:HG12	6:F:236:LEU:HD21	1.97	0.46
12:L:157:ARG:NE	13:M:59:GLU:OE2	2.44	0.46
32:f:96:LEU:HD13	32:f:129:LEU:HD13	1.98	0.46
32:f:559:PRO:HA	32:f:562:LEU:HB2	1.98	0.46
11:k:235:GLU:HA	11:k:238:ILE:HG22	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:265:LYS:HD2	2:B:268:ARG:HH12	1.80	0.46
4:D:83:GLN:C	4:D:85:ILE:N	2.73	0.46
12:L:166:GLN:OE1	12:L:169:ARG:NH2	2.47	0.46
32:f:470:VAL:HG13	32:f:471:LEU:HG	1.98	0.46
32:f:833:PHE:HB3	32:f:837:LEU:HA	1.97	0.46
16:p:30:ILE:HG22	16:p:31:GLN:H	1.81	0.46
5:E:200:SER:OG	5:E:233:ASP:O	2.27	0.46
6:F:358:ASN:O	6:F:362:ARG:NH1	2.49	0.46
13:M:192:GLU:O	13:M:196:ILE:HG12	2.15	0.46
25:Y:90:ASP:HA	25:Y:93:LYS:HE3	1.97	0.46
28:b:184:ILE:HA	28:b:187:PRO:HD2	1.97	0.46
30:d:55:LEU:HB2	30:d:78:LEU:HD21	1.96	0.46
32:f:586:PRO:O	32:f:587:PHE:C	2.58	0.46
32:f:705:ASN:OD1	32:f:705:ASN:N	2.49	0.46
11:k:99:HIS:HB2	11:k:107:MET:HE2	1.98	0.46
2:B:125:THR:OG1	2:B:127:VAL:HG22	2.15	0.46
2:B:248:LEU:HD12	2:B:282:VAL:HG12	1.97	0.46
4:D:126:PRO:C	4:D:128:ALA:N	2.72	0.46
7:G:202:LEU:HA	7:G:205:VAL:HG22	1.98	0.46
11:K:130:PRO:C	11:K:132:ALA:H	2.22	0.46
17:Q:137:PHE:HB3	18:r:133:VAL:HG21	1.97	0.46
27:a:321:LYS:O	27:a:334:THR:OG1	2.33	0.46
1:A:114:ASN:HB3	1:A:120:LYS:HG2	1.98	0.46
4:D:279:THR:HG23	4:D:280:GLY:H	1.81	0.46
6:F:38:THR:HG22	6:F:39:GLU:HG2	1.98	0.46
6:F:251:LEU:HD23	6:F:285:ILE:HG22	1.97	0.46
11:K:218:ALA:HB2	11:K:228:MET:HE2	1.97	0.46
21:U:334:ALA:O	21:U:338:HIS:ND1	2.49	0.46
24:X:347:ILE:HD12	24:X:358:LYS:HD3	1.98	0.46
27:a:252:LYS:HA	27:a:255:TRP:HD1	1.81	0.46
31:e:50:ASP:OD1	31:e:50:ASP:N	2.46	0.46
3:C:139:MET:HG3	3:C:214:VAL:HG22	1.98	0.45
10:J:220:LEU:HD11	10:J:224:GLU:HB2	1.97	0.45
3:C:271:ARG:HA	3:C:274:LEU:HD12	1.98	0.45
14:N:135:ILE:HG22	14:N:139:VAL:HG13	1.98	0.45
20:T:15:LYS:HG2	20:T:20:VAL:HG12	1.97	0.45
29:c:57:MET:HB2	29:c:69:VAL:HG21	1.97	0.45
29:c:233:ASP:O	29:c:237:HIS:HB2	2.16	0.45
30:d:26:LEU:HA	30:d:29:VAL:HG12	1.98	0.45
30:d:45:LYS:HA	30:d:48:LEU:HB2	1.97	0.45
30:d:61:TRP:HB3	30:d:65:ARG:HH21	1.80	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:52:GLN:HB3	8:h:57:TYR:HD2	1.81	0.45
1:A:101:ILE:HG23	1:A:137:GLY:H	1.81	0.45
2:B:116:ILE:HG13	2:B:121:ALA:HA	1.98	0.45
7:G:155:ASP:OD1	7:G:159:TYR:N	2.43	0.45
10:J:208:LEU:O	10:J:220:LEU:HB2	2.16	0.45
25:Y:155:ASP:N	25:Y:155:ASP:OD1	2.46	0.45
26:Z:29:VAL:HG11	26:Z:33:LYS:HG2	1.98	0.45
29:c:84:VAL:O	33:u:74:ARG:HG2	2.16	0.45
1:A:413:VAL:HA	1:A:416:VAL:HG22	1.97	0.45
3:C:88:LYS:HE3	3:C:88:LYS:HB3	1.57	0.45
4:D:127:ASN:HB3	4:D:252:ARG:NH1	2.29	0.45
30:d:83:PHE:HB2	30:d:121:ARG:HH22	1.82	0.45
20:t:56:ASP:OD1	20:t:57:TYR:N	2.50	0.45
2:B:116:ILE:O	2:B:117:ASP:HB3	2.16	0.45
4:D:84:SER:HB3	4:D:86:PRO:HD3	1.97	0.45
4:D:85:ILE:N	4:D:86:PRO:HD3	2.30	0.45
4:D:115:ILE:HG22	4:D:139:LEU:HD12	1.98	0.45
5:E:148:VAL:HB	5:E:297:ARG:HH22	1.81	0.45
7:G:79:VAL:HG12	7:G:139:ILE:HB	1.99	0.45
22:V:470:ARG:HB3	26:Z:250:TYR:CZ	2.50	0.45
23:W:290:ILE:HG23	23:W:306:LEU:HD21	1.99	0.45
25:Y:49:ASN:HB3	25:Y:114:ILE:HG22	1.97	0.45
26:Z:103:LYS:HD2	26:Z:103:LYS:HA	1.52	0.45
27:a:169:HIS:HB3	27:a:207:GLY:HA2	1.98	0.45
32:f:188:VAL:HG21	32:f:211:ILE:HD12	1.99	0.45
1:A:51:ASP:HA	1:A:54:GLN:HG3	1.98	0.45
1:A:156:LYS:HE3	1:A:156:LYS:HA	1.99	0.45
1:A:179:GLY:O	1:A:346:PRO:HG3	2.16	0.45
2:B:251:VAL:HB	2:B:254:GLU:HB2	1.98	0.45
17:Q:27:GLN:O	17:q:170:ARG:NH1	2.49	0.45
19:S:10:GLY:HA3	19:S:42:LYS:HE2	1.98	0.45
22:V:119:GLY:HA2	22:V:148:ARG:HD3	1.98	0.45
26:Z:138:TYR:HB3	26:Z:155:PHE:HB3	1.97	0.45
27:a:78:GLU:O	27:a:82:HIS:ND1	2.40	0.45
7:g:231:THR:OG1	7:g:234:GLU:OE1	2.24	0.45
1:A:395:PHE:HZ	1:A:415:LYS:HD3	1.81	0.45
8:H:196:LYS:HD3	8:H:203:MET:HE3	1.98	0.45
19:S:5:TYR:OH	19:S:103:PRO:O	2.29	0.45
21:U:108:TYR:OH	21:U:159:ARG:NH2	2.47	0.45
21:U:342:LEU:HD13	21:U:379:GLY:HA3	1.98	0.45
26:Z:8:LYS:HG3	26:Z:47:VAL:HG23	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:89:MET:O	32:f:90:THR:HG22	2.17	0.45
32:f:151:LEU:HB3	32:f:159:VAL:HG22	1.97	0.45
32:f:809:ILE:HG23	32:f:814:SER:HB2	1.98	0.45
14:n:30:VAL:O	14:n:175:ARG:NH2	2.49	0.45
20:t:176:LEU:O	20:t:180:ASP:HB2	2.16	0.45
3:C:88:LYS:HA	3:C:94:LYS:HA	1.98	0.45
7:G:138:MET:SD	7:G:154:CYS:HB2	2.57	0.45
28:b:6:THR:HB	28:b:49:VAL:HG22	1.98	0.45
32:f:347:ASP:O	32:f:348:ILE:HG13	2.16	0.45
32:f:393:ASP:OD1	32:f:393:ASP:N	2.48	0.45
32:f:727:PHE:CE2	32:f:761:MET:HB2	2.52	0.45
8:h:130:PHE:HB3	8:h:132:VAL:HG22	1.99	0.45
2:B:107:MET:HB3	3:C:96:VAL:HB	1.99	0.45
2:B:313:LEU:HD12	2:B:341:LEU:HD22	1.98	0.45
15:O:205:GLU:O	15:O:208:THR:OG1	2.29	0.45
27:a:54:ASP:N	27:a:54:ASP:OD1	2.50	0.45
13:m:40:ARG:NE	13:m:146:ALA:O	2.41	0.45
2:B:273:VAL:HA	2:B:276:GLU:HG3	1.99	0.45
3:C:230:MET:SD	3:C:230:MET:N	2.90	0.45
3:C:246:ILE:HG22	3:C:248:MET:HE3	1.98	0.45
10:J:2:SER:OG	10:J:3:TYR:N	2.47	0.45
22:V:118:GLN:HG3	22:V:128:ARG:NH2	2.32	0.45
24:X:229:TYR:CZ	24:X:258:LYS:HE2	2.52	0.45
27:a:363:MET:SD	29:c:307:VAL:HG11	2.56	0.45
2:B:229:GLY:HA2	37:B:501:ADP:H5'1	1.99	0.44
8:H:105:ILE:HD11	8:H:109:GLN:HB2	1.99	0.44
18:R:97:MET:H	18:R:116:SER:HB3	1.83	0.44
20:T:9:THR:OG1	20:T:10:SER:N	2.49	0.44
22:V:304:GLU:HA	22:V:307:ARG:HG2	1.99	0.44
22:V:397:ARG:O	22:V:401:ASN:ND2	2.50	0.44
24:X:255:LEU:HD22	24:X:267:VAL:HG22	1.98	0.44
24:X:299:LEU:HD12	24:X:330:LEU:HD23	1.98	0.44
7:g:158:GLY:O	8:h:84:ARG:NH2	2.50	0.44
8:h:9:SER:OG	8:h:123:GLN:O	2.32	0.44
9:i:41:ASP:OD1	9:i:41:ASP:N	2.50	0.44
16:p:193:ASP:OD1	16:p:193:ASP:N	2.50	0.44
19:s:16:ALA:HB2	19:s:121:VAL:HG23	1.98	0.44
3:C:89:VAL:HB	3:C:90:HIS:H	1.60	0.44
3:C:249:ASP:OD1	3:C:249:ASP:N	2.50	0.44
4:D:83:GLN:HB3	4:D:87:LEU:HD11	1.99	0.44
5:E:310:LEU:HD11	5:E:314:LYS:HE3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:141:ARG:HH21	17:q:162:LYS:HZ2	1.65	0.44
21:U:161:ASP:OD1	21:U:161:ASP:N	2.48	0.44
21:U:386:LEU:HD12	21:U:393:LEU:HD11	2.00	0.44
21:U:609:ASP:O	21:U:615:ARG:NH1	2.40	0.44
25:Y:279:GLU:HA	25:Y:282:MET:HE2	1.98	0.44
30:d:236:THR:O	30:d:239:SER:OG	2.23	0.44
14:n:7:GLN:HA	14:n:12:VAL:HG12	1.98	0.44
20:t:147:GLN:HA	20:t:150:LEU:HD12	1.98	0.44
9:I:11:ILE:HG22	10:J:7:ILE:HG23	1.99	0.44
11:K:209:LYS:HD2	11:K:209:LYS:HA	1.84	0.44
21:U:111:GLN:O	21:U:115:ASN:ND2	2.51	0.44
25:Y:240:VAL:HG23	25:Y:241:ILE:HG13	1.99	0.44
26:Z:143:GLU:OE2	26:Z:154:THR:N	2.49	0.44
29:c:196:LEU:C	29:c:198:ARG:N	2.75	0.44
2:B:288:ASP:OD1	2:B:288:ASP:N	2.48	0.44
4:D:157:ASP:OD1	4:D:157:ASP:N	2.48	0.44
9:I:6:ASP:OD1	9:I:7:SER:N	2.50	0.44
14:N:179:ILE:HG12	14:N:184:VAL:HG22	1.99	0.44
7:g:215:ILE:HD11	7:g:239:LEU:HD11	2.00	0.44
1:A:164:MET:HB2	1:A:239:ARG:O	2.18	0.44
11:K:240:ASP:OD1	11:K:240:ASP:N	2.50	0.44
21:U:98:GLU:HA	21:U:101:ILE:HG12	2.00	0.44
23:W:201:ARG:HA	23:W:204:ILE:HG12	1.98	0.44
14:n:40:ARG:NH2	14:n:181:GLU:O	2.38	0.44
2:B:170:LEU:HD11	2:B:273:VAL:HG21	2.00	0.44
3:C:368:MET:HE3	3:C:368:MET:O	2.18	0.44
14:N:133:SER:HA	14:N:136:TYR:HD2	1.81	0.44
21:U:12:LEU:O	21:U:20:LYS:NZ	2.50	0.44
25:Y:202:LEU:HD13	25:Y:239:LYS:HD2	2.00	0.44
32:f:289:VAL:HA	32:f:292:LYS:HG2	1.99	0.44
32:f:679:LEU:HD13	32:f:713:PHE:HE2	1.82	0.44
32:f:828:ARG:NH2	32:f:873:LEU:HD12	2.33	0.44
20:t:173:MET:HB2	20:t:173:MET:HE3	1.80	0.44
2:B:169:PRO:O	2:B:172:THR:OG1	2.31	0.44
3:C:321:ASN:H	3:C:324:ALA:HB3	1.83	0.44
6:F:113:LEU:HG	6:F:135:PRO:HG3	2.00	0.44
13:M:71:ARG:HD3	20:T:72:ILE:HD11	1.98	0.44
16:P:22:ILE:HD11	16:P:50:TYR:HD2	1.83	0.44
20:T:79:ASP:OD1	20:T:79:ASP:N	2.49	0.44
21:U:235:LYS:HA	21:U:235:LYS:HD3	1.76	0.44
23:W:309:PHE:HD1	23:W:315:MET:HE1	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:214:SER:O	24:X:218:HIS:ND1	2.41	0.44
5:E:360:ASP:N	5:E:360:ASP:OD1	2.50	0.44
19:S:211:ARG:NH2	19:S:213:ASP:OD2	2.51	0.44
22:V:419:LEU:HA	22:V:422:ILE:HG22	1.99	0.44
23:W:453:HIS:HA	26:Z:103:LYS:NZ	2.32	0.44
29:c:146:ASP:OD2	29:c:149:GLN:N	2.39	0.44
17:q:5:ILE:HD11	17:q:143:LEU:HD21	1.99	0.44
5:E:291:ARG:HE	5:E:294:ARG:NH1	2.15	0.44
10:J:221:ASN:HD21	10:J:224:GLU:HG3	1.83	0.44
22:V:321:ALA:HB1	22:V:324:PHE:HB3	2.00	0.44
23:W:444:HIS:CE1	26:Z:208:ILE:HB	2.52	0.44
24:X:205:LYS:NZ	24:X:243:ASP:OD2	2.51	0.44
32:f:110:TYR:HB3	32:f:126:ILE:HD11	1.99	0.44
32:f:151:LEU:HD22	32:f:191:ILE:HG12	2.00	0.44
7:g:56:VAL:HG23	7:g:61:LEU:HD22	2.00	0.44
9:i:155:ASN:OD1	10:j:77:THR:OG1	2.36	0.44
11:k:181:LEU:HA	11:k:184:VAL:HG22	1.99	0.44
2:B:299:SER:HA	2:B:303:ARG:HB2	2.00	0.43
3:C:91:PRO:HD2	3:C:92:GLU:HG3	1.99	0.43
3:C:187:LEU:HD13	3:C:293:MET:HE2	1.99	0.43
17:Q:30:ASP:OD1	17:Q:30:ASP:N	2.49	0.43
18:R:21:THR:HG22	18:R:26:ILE:HG12	1.99	0.43
22:V:259:LEU:HD12	22:V:291:TYR:HD2	1.83	0.43
23:W:153:LYS:HB3	23:W:162:ALA:HB2	1.99	0.43
24:X:160:MET:HG3	24:X:161:ASP:H	1.83	0.43
27:a:252:LYS:HA	27:a:255:TRP:CD1	2.52	0.43
29:c:210:ASN:HB2	29:c:213:GLU:HG3	1.99	0.43
14:n:104:ASP:OD1	14:n:104:ASP:N	2.51	0.43
16:p:116:THR:HG22	16:p:118:LYS:HE3	2.00	0.43
5:E:3:ASP:OD1	5:E:3:ASP:N	2.50	0.43
6:F:98:ASP:N	6:F:98:ASP:OD1	2.50	0.43
21:U:807:LYS:HA	21:U:808:PRO:HD3	1.83	0.43
25:Y:83:ARG:HA	25:Y:83:ARG:HD2	1.89	0.43
28:b:33:VAL:HG11	28:b:75:LEU:HD21	2.00	0.43
30:d:224:SER:OG	30:d:225:PHE:N	2.51	0.43
9:i:201:MET:SD	9:i:206:LEU:N	2.91	0.43
10:j:148:ASP:OD1	10:j:152:THR:N	2.52	0.43
15:o:187:ARG:HA	15:o:188:PRO:HA	1.88	0.43
19:s:46:LEU:HD11	19:s:52:ILE:HD12	2.00	0.43
4:D:237:GLN:HB2	4:D:242:GLU:OE2	2.19	0.43
4:D:293:LEU:HD21	4:D:321:LEU:HD22	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:216:ARG:HG3	5:E:263:GLN:HE22	1.84	0.43
5:E:241:ARG:NE	5:E:285:LEU:O	2.52	0.43
18:R:80:SER:OG	18:R:120:ARG:NH1	2.50	0.43
21:U:803:LYS:NZ	21:U:804:SER:O	2.44	0.43
25:Y:68:ASP:OD1	25:Y:68:ASP:N	2.51	0.43
25:Y:113:ARG:HD2	25:Y:113:ARG:HA	1.78	0.43
27:a:222:LEU:HA	27:a:225:LEU:HD12	2.01	0.43
29:c:265:MET:HE1	29:c:273:LYS:HD3	1.99	0.43
29:c:269:GLN:HA	29:c:272:ILE:HG22	2.00	0.43
20:t:56:ASP:HB2	20:t:107:TRP:HB3	2.01	0.43
3:C:285:ALA:C	3:C:287:LYS:H	2.27	0.43
3:C:287:LYS:HB2	3:C:288:ASN:H	1.57	0.43
5:E:252:GLU:HG2	5:E:255:ARG:NH2	2.33	0.43
21:U:35:TRP:HD1	22:V:273:LYS:HZ3	1.64	0.43
22:V:461:LYS:HD2	22:V:461:LYS:HA	1.75	0.43
22:V:470:ARG:HH21	22:V:474:LEU:HG	1.82	0.43
23:W:69:ALA:HA	23:W:72:LYS:HG2	2.01	0.43
24:X:400:ALA:O	24:X:403:THR:OG1	2.31	0.43
25:Y:174:TRP:CD1	25:Y:177:ARG:HH21	2.36	0.43
29:c:75:MET:HA	29:c:91:PHE:CE2	2.53	0.43
9:i:22:GLU:HA	9:i:25:MET:HG3	2.00	0.43
12:l:41:LYS:HD2	12:l:41:LYS:HA	1.82	0.43
13:m:173:LYS:HA	13:m:176:ILE:HG12	1.99	0.43
16:p:53:LEU:HG	16:p:107:PRO:HB3	2.01	0.43
1:A:72:LEU:HD11	2:B:103:ARG:HH22	1.82	0.43
3:C:71:SER:O	4:D:112:TYR:N	2.51	0.43
6:F:95:GLU:HA	6:F:147:PRO:HG3	2.00	0.43
6:F:218:GLN:HG2	6:F:219:PRO:HD2	2.00	0.43
9:I:118:LYS:NZ	9:I:151:ASP:O	2.51	0.43
21:U:356:THR:O	21:U:360:VAL:HG13	2.17	0.43
28:b:4:GLU:HA	28:b:106:LYS:H	1.83	0.43
29:c:27:THR:HB	29:c:176:GLN:HE22	1.83	0.43
29:c:100:LYS:HB2	29:c:105:PRO:HB3	2.00	0.43
30:d:190:LEU:HD22	30:d:192:THR:HG22	2.00	0.43
11:k:155:HIS:CD2	11:k:168:ARG:HG2	2.54	0.43
13:m:50:GLU:HB2	13:m:197:ILE:HD11	2.01	0.43
13:m:176:ILE:HG22	13:m:196:ILE:HD13	2.00	0.43
6:F:217:ILE:HG13	6:F:218:GLN:N	2.29	0.43
9:I:218:ARG:NH1	9:I:223:THR:OG1	2.52	0.43
10:J:212:ARG:HD2	10:J:215:GLN:NE2	2.33	0.43
13:M:108:LEU:HD11	13:M:137:LEU:HB3	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:95:MET:HG3	14:N:116:MET:HE2	1.99	0.43
25:Y:349:LYS:O	25:Y:351:ASN:N	2.51	0.43
27:a:70:ARG:HH21	28:b:18:ASN:HA	1.83	0.43
32:f:672:LEU:HD11	32:f:706:ILE:HG12	2.01	0.43
2:B:227:PRO:O	2:B:230:THR:OG1	2.32	0.43
16:P:177:ARG:HG2	19:s:147:PRO:HG3	2.01	0.43
19:S:99:ARG:HH21	19:S:102:PHE:HD2	1.65	0.43
20:T:195:LYS:HE2	20:T:195:LYS:HB2	1.87	0.43
22:V:119:GLY:O	22:V:122:THR:OG1	2.30	0.43
23:W:187:LEU:HD21	23:W:226:TYR:HB2	2.01	0.43
27:a:324:ILE:HG13	27:a:331:VAL:HG13	2.00	0.43
29:c:117:GLY:HA2	29:c:149:GLN:HE22	1.84	0.43
16:p:15:LYS:HE3	16:p:121:ILE:HG12	2.01	0.43
18:r:38:ASN:OD1	18:r:41:LEU:N	2.51	0.43
34:v:25:LYS:O	34:v:27:UNK:N	2.51	0.43
4:D:125:LYS:N	4:D:126:PRO:CD	2.80	0.43
14:N:174:ILE:HB	14:N:189:LEU:HB2	2.01	0.43
18:R:161:TYR:OH	18:R:196:HIS:ND1	2.33	0.43
21:U:261:LEU:HA	21:U:264:VAL:HG12	1.99	0.43
21:U:794:ASP:OD1	21:U:794:ASP:N	2.51	0.43
25:Y:145:LEU:HD21	25:Y:161:THR:HG23	2.00	0.43
25:Y:149:LEU:HD23	25:Y:149:LEU:HA	1.91	0.43
27:a:14:SER:H	27:a:18:GLN:HE21	1.66	0.43
31:e:59:GLU:O	31:e:63:HIS:ND1	2.51	0.43
32:f:173:LEU:HD23	32:f:173:LEU:HA	1.88	0.43
32:f:231:LEU:HB3	32:f:853:VAL:HG22	1.99	0.43
16:p:61:GLN:HE22	16:p:65:GLN:NE2	2.17	0.43
20:t:72:ILE:HA	20:t:75:GLU:HG2	2.00	0.43
4:D:124:LEU:HD13	4:D:124:LEU:HA	1.81	0.43
21:U:692:ALA:HB2	21:U:733:ALA:HB1	2.01	0.43
26:Z:62:ASP:OD1	26:Z:63:LYS:N	2.51	0.43
27:a:35:HIS:HE1	28:b:17:ARG:HH21	1.64	0.43
27:a:113:LEU:HA	27:a:116:THR:HG23	2.01	0.43
27:a:163:TYR:CZ	27:a:172:TYR:HB2	2.54	0.43
29:c:41:MET:HB3	29:c:145:VAL:HG21	2.00	0.43
29:c:54:MET:HE1	33:u:75:GLY:HA3	2.00	0.43
16:p:38:ASP:OD1	16:p:38:ASP:N	2.52	0.43
16:P:6:TYR:OH	17:Q:120:TYR:OH	2.32	0.43
22:V:189:ASP:HA	22:V:192:MET:HG2	1.99	0.43
23:W:112:VAL:HG21	23:W:145:LEU:HD21	2.01	0.43
23:W:425:LEU:HD12	23:W:425:LEU:HA	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:318:ILE:HG22	24:X:321:THR:HB	2.00	0.43
26:Z:263:ALA:HB1	29:c:288:VAL:HG13	2.00	0.43
27:a:185:ILE:HG23	27:a:187:ASP:HB3	2.00	0.43
29:c:64:ASP:OD1	29:c:64:ASP:N	2.50	0.43
32:f:66:LYS:HD2	32:f:67:ASP:H	1.84	0.43
32:f:202:HIS:CE1	32:f:203:GLU:HG2	2.53	0.43
7:g:171:LYS:O	7:g:175:SER:OG	2.30	0.43
10:j:185:ASP:OD1	10:j:185:ASP:N	2.51	0.43
13:m:65:ARG:HH21	13:m:78:ALA:HA	1.83	0.43
16:p:62:THR:HG23	17:q:86:ARG:HH12	1.84	0.43
33:u:1:MET:N	33:u:17:VAL:O	2.46	0.43
1:A:117:GLN:NE2	2:B:127:VAL:O	2.51	0.42
1:A:312:ARG:NH1	1:A:315:ILE:O	2.52	0.42
3:C:256:SER:HB2	3:C:273:MET:HE1	2.00	0.42
3:C:287:LYS:HB2	3:C:287:LYS:HE2	1.72	0.42
19:S:145:LEU:HD21	19:S:182:ALA:HB2	1.99	0.42
25:Y:17:LEU:HD23	25:Y:17:LEU:HA	1.92	0.42
27:a:271:LYS:O	27:a:275:LEU:HB2	2.18	0.42
30:d:78:LEU:HD13	30:d:98:LEU:HD21	2.00	0.42
32:f:266:LEU:HA	32:f:266:LEU:HD12	1.85	0.42
8:h:3:GLU:OE2	13:m:127:ALA:HB3	2.18	0.42
10:j:184:ASP:O	10:j:188:ILE:HG12	2.19	0.42
11:k:66:LYS:HA	11:k:78:MET:HE2	2.01	0.42
3:C:204:ALA:HA	3:C:245:ILE:HD12	2.01	0.42
4:D:274:ARG:HD3	5:E:245:GLU:HB3	2.00	0.42
12:L:172:LEU:O	12:L:176:MET:HB3	2.20	0.42
24:X:63:ALA:HB1	24:X:96:PHE:HE1	1.83	0.42
30:d:12:LYS:HD2	30:d:12:LYS:HA	1.81	0.42
12:l:7:ASP:HB3	12:l:20:HIS:HD1	1.85	0.42
19:s:10:GLY:HA3	19:s:42:LYS:HE2	2.01	0.42
19:s:12:ILE:HG13	19:s:109:ILE:HD12	2.01	0.42
4:D:67:ASN:ND2	21:U:607:VAL:O	2.52	0.42
15:O:164:PHE:O	19:s:38:ARG:NH2	2.52	0.42
19:S:26:ASP:OD1	19:S:26:ASP:N	2.51	0.42
21:U:320:ASP:HB3	21:U:321:GLN:H	1.74	0.42
32:f:214:VAL:HA	32:f:217:LEU:HD13	2.01	0.42
32:f:664:GLU:OE2	32:f:667:GLY:N	2.49	0.42
13:m:136:MET:HE2	13:m:163:CYS:SG	2.58	0.42
19:s:7:PHE:HZ	19:s:140:SER:HB2	1.84	0.42
1:A:362:MET:HE1	1:A:389:CYS:HB3	2.01	0.42
23:W:67:LEU:HD22	23:W:100:ALA:HB1	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:415:TYR:HB2	25:Y:383:LEU:HD21	2.01	0.42
29:c:49:VAL:HG23	29:c:148:ILE:HD11	2.00	0.42
32:f:294:MET:HA	32:f:297:MET:HG3	2.01	0.42
32:f:662:MET:O	32:f:781:TYR:OH	2.22	0.42
32:f:670:MET:HE2	32:f:670:MET:HB3	1.85	0.42
9:i:35:LEU:HG	9:i:46:ALA:HB3	2.01	0.42
10:j:39:ASP:OD1	10:j:39:ASP:N	2.52	0.42
12:l:10:VAL:HG13	12:l:11:THR:HG23	2.01	0.42
6:F:407:ALA:O	6:F:412:ALA:N	2.53	0.42
13:M:139:SER:OG	13:M:140:TYR:N	2.51	0.42
14:N:17:ASP:OD1	14:N:17:ASP:N	2.51	0.42
15:O:42:TYR:HB2	15:O:178:ILE:HD11	1.99	0.42
21:U:581:SER:O	21:U:585:THR:N	2.52	0.42
24:X:260:MET:HE2	24:X:260:MET:HB3	1.92	0.42
25:Y:345:CYS:HA	25:Y:356:THR:HA	2.00	0.42
26:Z:205:LEU:HA	26:Z:208:ILE:HG22	2.02	0.42
9:I:125:GLY:O	9:I:127:LYS:NZ	2.50	0.42
11:K:196:LYS:HE2	11:K:241:ILE:HD13	2.01	0.42
16:P:6:TYR:HH	17:Q:120:TYR:HH	1.62	0.42
26:Z:70:LEU:HD11	26:Z:108:ILE:HG23	2.02	0.42
28:b:33:VAL:HA	28:b:36:VAL:HG22	2.02	0.42
29:c:58:LEU:HB3	29:c:71:ASP:HB3	2.01	0.42
32:f:398:TRP:HA	32:f:401:LYS:HD3	2.02	0.42
13:m:8:ASP:OD1	13:m:8:ASP:N	2.49	0.42
17:q:39:SER:HB3	17:q:42:ILE:HB	2.02	0.42
18:r:96:SER:C	18:r:97:MET:HE2	2.45	0.42
1:A:41:TYR:HB3	1:A:45:ILE:HG12	2.01	0.42
2:B:408:ARG:HG3	2:B:409:GLU:HG3	2.02	0.42
4:D:393:ILE:HD12	23:W:134:GLY:HA2	2.01	0.42
10:J:221:ASN:ND2	10:J:224:GLU:HG3	2.35	0.42
11:K:32:LYS:HD3	11:K:32:LYS:HA	1.84	0.42
13:M:80:LEU:H	13:M:133:CYS:HB3	1.84	0.42
18:R:138:VAL:HG23	17:q:141:SER:HB3	2.02	0.42
20:T:53:ALA:HB2	20:T:110:MET:HG3	2.00	0.42
20:T:211:ILE:HG23	14:n:30:VAL:HG11	2.01	0.42
21:U:128:GLN:O	21:U:132:GLY:N	2.53	0.42
23:W:129:ARG:HH22	23:W:146:THR:HA	1.84	0.42
24:X:16:LEU:HD23	24:X:16:LEU:HA	1.92	0.42
24:X:44:GLN:O	24:X:48:GLN:HG3	2.19	0.42
27:a:277:LEU:HA	27:a:280:MET:HG2	2.02	0.42
32:f:213:GLN:HB3	32:f:216:MET:HE2	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:379:GLY:HA2	32:f:417:ILE:HD11	2.02	0.42
32:f:695:ALA:HB1	32:f:731:MET:HG3	2.02	0.42
11:k:157:ASP:OD1	11:k:161:THR:N	2.53	0.42
13:m:71:ARG:NH2	13:m:222:GLY:O	2.51	0.42
16:p:45:MET:HG2	16:p:49:LEU:O	2.19	0.42
2:B:168:ASP:OD1	2:B:168:ASP:N	2.52	0.42
3:C:345:ARG:HE	3:C:345:ARG:HB3	1.71	0.42
4:D:57:GLN:O	4:D:61:ILE:HG12	2.20	0.42
18:R:6:PHE:HB3	18:R:139:MET:HE2	2.01	0.42
21:U:194:ARG:O	21:U:198:LEU:HB2	2.20	0.42
22:V:150:ARG:NH1	22:V:157:THR:O	2.53	0.42
32:f:402:ASN:HB3	32:f:406:GLY:HA3	2.01	0.42
32:f:479:LEU:HD11	32:f:816:TYR:CZ	2.55	0.42
32:f:845:ARG:HG2	32:f:867:THR:HG22	2.02	0.42
3:C:227:GLY:HA3	3:C:271:ARG:HH12	1.84	0.42
17:Q:166:GLU:HB2	18:r:141:ARG:HH21	1.85	0.42
19:S:74:MET:HE3	19:S:74:MET:O	2.20	0.42
21:U:638:SER:O	21:U:641:SER:OG	2.30	0.42
22:V:414:TYR:CG	22:V:417:ILE:HD11	2.55	0.42
32:f:195:ASN:HB3	32:f:204:ALA:HB2	2.01	0.42
16:p:88:MET:HE3	16:p:88:MET:HB3	1.86	0.42
1:A:99:THR:HG22	1:A:115:VAL:HA	2.01	0.42
1:A:333:ARG:HH21	1:A:336:ARG:NH2	2.17	0.42
3:C:127:LEU:HD22	4:D:96:VAL:HG21	2.01	0.42
3:C:213:ARG:HA	3:C:247:PHE:HB3	2.01	0.42
3:C:360:LYS:NZ	4:D:324:PRO:HG3	2.35	0.42
6:F:185:TYR:CE2	6:F:243:GLN:HG3	2.54	0.42
13:M:55:SER:OG	13:M:56:LYS:N	2.53	0.42
19:S:145:LEU:HD22	19:S:178:VAL:HB	2.01	0.42
21:U:14:GLU:HG3	21:U:16:GLU:HG2	2.01	0.42
22:V:183:GLU:O	22:V:186:LYS:HG3	2.19	0.42
26:Z:136:GLU:OE2	26:Z:157:HIS:ND1	2.53	0.42
29:c:248:MET:HA	29:c:251:LEU:HB2	2.02	0.42
32:f:688:ARG:HG2	32:f:720:GLU:HB3	2.00	0.42
13:m:43:ASP:OD1	13:m:43:ASP:N	2.52	0.42
13:m:106:ILE:HD13	13:m:111:LEU:HD13	2.02	0.42
1:A:249:TYR:N	1:A:252:GLU:OE2	2.53	0.41
6:F:106:GLU:CD	26:Z:88:ARG:HH21	2.27	0.41
6:F:134:LEU:HD12	6:F:135:PRO:HD2	2.02	0.41
7:G:171:LYS:HE3	7:G:206:LEU:HD21	2.01	0.41
20:T:44:ARG:NH2	20:T:47:ASN:OD1	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:110:MET:SD	20:T:110:MET:N	2.93	0.41
21:U:505:ASP:HB3	21:U:508:THR:HG22	2.02	0.41
21:U:636:VAL:HG23	21:U:637:VAL:HG23	2.01	0.41
21:U:791:LEU:HB3	21:U:913:ILE:HD13	2.01	0.41
22:V:211:TYR:OH	22:V:234:ARG:NE	2.52	0.41
25:Y:235:ASP:O	25:Y:239:LYS:NZ	2.53	0.41
7:g:61:LEU:HD21	7:g:66:VAL:HG11	2.01	0.41
19:s:52:ILE:HG13	19:s:110:ILE:HG12	2.01	0.41
4:D:103:VAL:HG21	4:D:132:LEU:HD21	2.03	0.41
10:J:96:LEU:HD22	17:Q:62:LYS:HD3	2.02	0.41
21:U:714:SER:HA	21:U:717:ILE:HG22	2.02	0.41
29:c:136:LEU:HD21	33:u:7:THR:HB	2.01	0.41
32:f:607:LEU:HA	32:f:610:GLN:HG2	2.00	0.41
10:j:185:ASP:O	10:j:189:LYS:HG2	2.20	0.41
4:D:251:PHE:HD2	4:D:295:GLN:OE1	2.02	0.41
7:G:34:GLN:OE1	7:G:34:GLN:N	2.53	0.41
13:M:43:ASP:OD1	13:M:43:ASP:N	2.54	0.41
20:T:92:LEU:HD23	20:T:92:LEU:HA	1.90	0.41
21:U:452:ASN:H	21:U:486:MET:HE1	1.85	0.41
23:W:455:LEU:HB2	23:W:456:GLN:NE2	2.36	0.41
27:a:50:PHE:HD2	27:a:52:GLN:HB3	1.85	0.41
32:f:192:VAL:HG12	32:f:196:MET:HE2	2.02	0.41
8:h:157:ALA:HB1	9:i:57:ASP:HB3	2.03	0.41
20:t:184:TYR:HE2	20:t:186:ARG:HH11	1.66	0.41
1:A:215:PHE:CG	1:A:324:PRO:HG3	2.56	0.41
5:E:199:VAL:HG23	6:F:315:ASN:HD22	1.85	0.41
5:E:295:LEU:HD23	5:E:295:LEU:HA	1.86	0.41
7:G:6:SER:OG	7:G:11:ARG:NH1	2.51	0.41
9:I:174:MET:HE1	9:I:199:LYS:HD2	2.02	0.41
10:J:67:ASP:OD1	10:J:68:ASN:N	2.53	0.41
13:M:166:GLY:H	13:M:169:ARG:HE	1.69	0.41
23:W:450:GLU:OE2	26:Z:225:GLN:NE2	2.48	0.41
26:Z:285:ALA:HA	26:Z:288:LYS:HG2	2.02	0.41
28:b:13:SER:OG	28:b:82:GLY:O	2.35	0.41
29:c:41:MET:HE1	29:c:112:TYR:CD1	2.56	0.41
10:j:57:ARG:O	10:j:60:ARG:NH2	2.53	0.41
15:o:63:LEU:HD11	15:o:79:ALA:HB2	2.01	0.41
4:D:85:ILE:O	4:D:85:ILE:HG22	2.20	0.41
5:E:84:ARG:NE	29:c:50:PRO:HG3	2.35	0.41
5:E:147:GLU:HG3	5:E:151:LEU:HD12	2.03	0.41
17:Q:66:LEU:HA	17:Q:69:MET:HG2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:141:ARG:HH21	17:q:162:LYS:NZ	2.19	0.41
20:T:25:ASP:HA	20:T:187:PHE:HA	2.01	0.41
21:U:560:MET:SD	21:U:590:TYR:HA	2.60	0.41
22:V:338:LEU:HG	22:V:398:LEU:HD12	2.02	0.41
23:W:357:ARG:HA	23:W:357:ARG:HD3	1.83	0.41
25:Y:210:SER:HB3	25:Y:213:LEU:HD23	2.01	0.41
26:Z:75:LEU:HA	26:Z:78:MET:HE2	2.01	0.41
26:Z:170:VAL:HG22	29:c:152:LYS:HA	2.03	0.41
32:f:46:SER:HB3	32:f:49:ASP:HB2	2.03	0.41
15:o:86:MET:HE3	15:o:90:TYR:HE2	1.86	0.41
15:o:219:LEU:N	16:p:193:ASP:O	2.50	0.41
20:t:20:VAL:HG11	20:t:122:LEU:HD13	2.01	0.41
2:B:91:LYS:HA	2:B:94:GLU:HB3	2.03	0.41
2:B:136:LEU:HD12	2:B:160:ILE:HG13	2.03	0.41
5:E:116:ASP:O	5:E:118:LEU:N	2.54	0.41
6:F:111:ILE:HG12	6:F:113:LEU:H	1.86	0.41
6:F:323:ASN:OD1	6:F:323:ASN:N	2.54	0.41
11:K:130:PRO:C	11:K:132:ALA:N	2.79	0.41
17:Q:26:VAL:HG21	18:R:136:TYR:HE2	1.85	0.41
17:Q:38:MET:HE1	17:Q:61:GLN:HB3	2.03	0.41
21:U:469:SER:OG	21:U:470:ASN:N	2.53	0.41
27:a:258:GLN:HB2	27:a:259:PRO:HD3	2.02	0.41
32:f:420:TRP:CZ2	32:f:825:MET:HE1	2.55	0.41
7:g:49:VAL:HA	7:g:219:VAL:HG12	2.03	0.41
18:r:80:SER:OG	18:r:120:ARG:NH2	2.47	0.41
1:A:354:ILE:HG22	1:A:385:ILE:HG21	2.02	0.41
1:A:415:LYS:HA	1:A:418:LYS:NZ	2.36	0.41
5:E:199:VAL:HG23	6:F:315:ASN:ND2	2.35	0.41
8:H:208:ILE:HD11	8:H:230:LEU:HD21	2.03	0.41
9:I:67:LYS:HE3	9:I:225:ILE:HD12	2.02	0.41
14:N:39:ASP:N	14:N:39:ASP:OD1	2.51	0.41
14:N:127:ILE:HD12	14:N:132:SER:HB2	2.01	0.41
21:U:214:ILE:HB	21:U:904:LYS:HZ3	1.85	0.41
28:b:13:SER:OG	28:b:14:GLU:N	2.53	0.41
30:d:23:LEU:O	30:d:27:LYS:HG2	2.20	0.41
32:f:349:TYR:HB2	32:f:766:GLN:NE2	2.35	0.41
10:j:156:TRP:CE2	11:k:59:MET:HE1	2.55	0.41
6:F:272:PHE:HD2	6:F:316:GLN:HB3	1.85	0.41
10:J:221:ASN:O	10:J:223:GLU:N	2.54	0.41
23:W:272:LEU:HD23	23:W:272:LEU:HA	1.93	0.41
23:W:325:GLY:O	23:W:329:ARG:HB2	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:86:LYS:HD3	30:d:89:LEU:HD22	2.02	0.41
13:m:110:HIS:ND1	14:n:69:GLU:OE1	2.54	0.41
3:C:168:PRO:HG3	3:C:175:PHE:HE2	1.85	0.41
3:C:253:SER:HB3	3:C:300:ILE:HD11	2.03	0.41
4:D:73:LEU:HD13	26:Z:184:VAL:HG21	2.03	0.41
4:D:191:TYR:HB3	4:D:198:PRO:HG3	2.03	0.41
4:D:230:VAL:HB	4:D:264:ILE:HG13	2.03	0.41
4:D:300:ASP:O	4:D:301:GLN:HG3	2.21	0.41
6:F:171:ARG:NH1	6:F:258:GLN:OE1	2.53	0.41
6:F:255:GLN:O	6:F:258:GLN:NE2	2.53	0.41
8:H:150:ASP:OD1	8:H:150:ASP:N	2.50	0.41
10:J:121:SER:HB3	10:J:124:ARG:HD2	2.01	0.41
11:K:199:LEU:HD12	11:K:210:LEU:HD21	2.02	0.41
21:U:900:TYR:HB3	21:U:914:LEU:HD11	2.02	0.41
22:V:480:ILE:HD11	26:Z:261:TYR:HA	2.03	0.41
23:W:54:THR:O	23:W:58:SER:N	2.54	0.41
23:W:178:GLU:OE2	23:W:181:GLU:N	2.54	0.41
29:c:197:ASN:O	29:c:199:HIS:N	2.54	0.41
29:c:207:TYR:HB3	29:c:209:LYS:HZ1	1.86	0.41
32:f:344:VAL:HG23	32:f:346:ASP:H	1.86	0.41
32:f:501:LEU:HD23	32:f:501:LEU:HA	1.90	0.41
12:l:157:ARG:HH21	12:l:180:MET:HE3	1.86	0.41
13:m:45:VAL:HG23	13:m:146:ALA:HB1	2.03	0.41
1:A:161:VAL:HA	1:A:164:MET:HG2	2.03	0.41
22:V:355:ARG:HA	22:V:358:MET:HG3	2.03	0.41
22:V:419:LEU:HD22	22:V:435:GLU:HG3	2.02	0.41
24:X:106:GLU:HB3	24:X:136:LEU:HD21	2.03	0.41
32:f:68:THR:HG21	32:f:114:ALA:HB2	2.03	0.41
14:n:28:ASN:OD1	14:n:29:ARG:N	2.53	0.41
15:o:59:ILE:HD12	15:o:82:MET:HB3	2.02	0.41
20:t:4:PRO:HG3	20:t:107:TRP:CE2	2.56	0.41
2:B:45:ALA:HA	32:f:673:ARG:HH22	1.86	0.40
4:D:75:ALA:O	4:D:79:VAL:HG23	2.21	0.40
7:G:188:ASP:OD1	7:G:188:ASP:N	2.52	0.40
8:H:135:LEU:HD23	8:H:135:LEU:HA	1.91	0.40
10:J:220:LEU:HD22	10:J:220:LEU:HA	1.96	0.40
22:V:168:GLN:HB2	22:V:191:LEU:HD21	2.02	0.40
22:V:179:LYS:HE2	22:V:179:LYS:HB2	1.91	0.40
22:V:292:THR:HA	22:V:295:ILE:HD12	2.03	0.40
23:W:314:LEU:HD23	23:W:365:ILE:HD11	2.02	0.40
23:W:432:LEU:O	23:W:436:MET:HB2	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:44:GLN:O	24:X:47:GLU:HG3	2.21	0.40
27:a:373:ASP:OD1	27:a:373:ASP:N	2.53	0.40
32:f:373:ALA:HB2	32:f:760:PHE:HD1	1.86	0.40
2:B:361:LYS:HB3	2:B:384:ILE:HG12	2.02	0.40
4:D:167:ILE:HD11	4:D:170:MET:HG3	2.04	0.40
4:D:303:VAL:HG12	4:D:305:VAL:HG23	2.03	0.40
5:E:130:VAL:O	5:E:189:SER:OG	2.39	0.40
6:F:168:TYR:HD2	6:F:274:LEU:HD12	1.86	0.40
6:F:236:LEU:HA	6:F:236:LEU:HD23	1.82	0.40
7:G:38:THR:O	7:G:52:THR:OG1	2.30	0.40
21:U:33:ASP:O	21:U:35:TRP:N	2.53	0.40
22:V:401:ASN:HA	22:V:404:LYS:NZ	2.37	0.40
28:b:161:ASN:ND2	28:b:168:SER:O	2.54	0.40
15:o:163:ILE:HG12	15:o:170:GLY:HA2	2.01	0.40
3:C:328:ILE:HG21	3:C:356:GLY:HA2	2.03	0.40
4:D:385:LEU:HD21	4:D:401:LYS:HD2	2.03	0.40
9:I:69:ASN:OD1	9:I:72:MET:N	2.52	0.40
19:S:64:LEU:HD21	19:S:92:LEU:HD11	2.02	0.40
20:T:43:MET:HG3	20:T:64:LYS:HG3	2.04	0.40
21:U:229:VAL:HA	21:U:232:ILE:HG12	2.02	0.40
22:V:232:HIS:HE2	22:V:258:TYR:HH	1.69	0.40
22:V:368:ARG:NH1	31:e:43:TRP:O	2.47	0.40
22:V:467:TYR:OH	24:X:397:TYR:OH	2.30	0.40
27:a:69:HIS:CD2	27:a:69:HIS:N	2.89	0.40
28:b:21:PHE:HD2	28:b:25:ARG:HG2	1.86	0.40
32:f:170:TRP:HA	32:f:173:LEU:HG	2.03	0.40
10:j:52:LYS:HG3	10:j:53:LEU:HD12	2.04	0.40
11:k:220:VAL:HG22	11:k:226:PHE:HD1	1.86	0.40
16:p:171:MET:HE2	16:p:171:MET:HB3	1.83	0.40
17:q:182:ILE:HD11	17:q:191:LEU:HD11	2.03	0.40
18:r:148:GLU:OE2	18:r:151:GLN:N	2.54	0.40
19:s:211:ARG:NH2	19:s:213:ASP:OD2	2.55	0.40
1:A:52:ILE:HD11	2:B:68:ILE:HG22	2.03	0.40
3:C:258:ARG:HG3	3:C:259:LEU:H	1.86	0.40
6:F:120:LYS:HB2	6:F:137:ILE:HD11	2.02	0.40
23:W:83:LEU:O	23:W:87:ILE:HG12	2.22	0.40
24:X:252:LYS:HA	24:X:287:LEU:HD11	2.04	0.40
27:a:212:ASN:OD1	27:a:213:PHE:N	2.55	0.40
32:f:83:ARG:O	32:f:87:THR:OG1	2.35	0.40
32:f:834:ASP:OD1	32:f:838:ARG:N	2.42	0.40
7:g:112:ASP:OD1	7:g:112:ASP:N	2.53	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:m:215:TRP:CH2	13:m:219:LEU:HD11	2.57	0.40
14:n:133:SER:HA	14:n:136:TYR:HD2	1.86	0.40
16:p:159:ASP:N	16:p:159:ASP:OD1	2.45	0.40
15:O:206:LYS:HE2	15:O:206:LYS:HB2	1.95	0.40
17:Q:11:ASP:N	17:Q:11:ASP:OD1	2.54	0.40
24:X:323:LEU:HD23	24:X:323:LEU:HA	1.91	0.40
24:X:416:ASN:OD1	24:X:417:LYS:N	2.55	0.40
25:Y:216:TYR:OH	25:Y:245:GLU:OE2	2.40	0.40
25:Y:334:LEU:HD12	25:Y:347:ILE:HD12	2.03	0.40
28:b:14:GLU:O	28:b:17:ARG:HG3	2.22	0.40
30:d:18:LYS:HE2	30:d:18:LYS:HB2	1.88	0.40
32:f:274:ASP:OD1	32:f:274:ASP:N	2.55	0.40
7:g:40:VAL:HG13	7:g:179:LEU:HD11	2.03	0.40
11:k:27:ALA:O	11:k:31:ILE:HG13	2.22	0.40
13:m:214:SER:OG	13:m:225:GLU:O	2.40	0.40
14:n:1:THR:N	14:n:169:SER:O	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	404/433 (93%)	361 (89%)	41 (10%)	2 (0%)	24	63
2	B	395/440 (90%)	349 (88%)	43 (11%)	3 (1%)	16	53
3	C	379/398 (95%)	330 (87%)	47 (12%)	2 (0%)	24	63
4	D	378/418 (90%)	324 (86%)	51 (14%)	3 (1%)	16	53
5	E	387/403 (96%)	351 (91%)	35 (9%)	1 (0%)	36	71
6	F	413/439 (94%)	378 (92%)	35 (8%)	0	100	100
7	G	242/246 (98%)	233 (96%)	9 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	g	242/246 (98%)	222 (92%)	19 (8%)	1 (0%)	30	67
8	H	230/234 (98%)	220 (96%)	10 (4%)	0	100	100
8	h	230/234 (98%)	219 (95%)	11 (5%)	0	100	100
9	I	248/261 (95%)	240 (97%)	7 (3%)	1 (0%)	30	67
9	i	248/261 (95%)	241 (97%)	7 (3%)	0	100	100
10	J	237/248 (96%)	223 (94%)	12 (5%)	2 (1%)	16	53
10	j	237/248 (96%)	226 (95%)	9 (4%)	2 (1%)	16	53
11	K	232/241 (96%)	221 (95%)	10 (4%)	1 (0%)	30	67
11	k	232/241 (96%)	226 (97%)	6 (3%)	0	100	100
12	L	236/263 (90%)	228 (97%)	8 (3%)	0	100	100
12	l	236/263 (90%)	228 (97%)	8 (3%)	0	100	100
13	M	238/255 (93%)	232 (98%)	6 (2%)	0	100	100
13	m	238/255 (93%)	232 (98%)	6 (2%)	0	100	100
14	N	200/239 (84%)	194 (97%)	6 (3%)	0	100	100
14	n	200/239 (84%)	195 (98%)	5 (2%)	0	100	100
15	O	218/277 (79%)	213 (98%)	5 (2%)	0	100	100
15	o	218/277 (79%)	212 (97%)	6 (3%)	0	100	100
16	P	202/205 (98%)	193 (96%)	9 (4%)	0	100	100
16	p	202/205 (98%)	189 (94%)	13 (6%)	0	100	100
17	Q	197/201 (98%)	191 (97%)	6 (3%)	0	100	100
17	q	197/201 (98%)	188 (95%)	9 (5%)	0	100	100
18	R	199/263 (76%)	191 (96%)	8 (4%)	0	100	100
18	r	199/263 (76%)	194 (98%)	5 (2%)	0	100	100
19	S	211/241 (88%)	202 (96%)	9 (4%)	0	100	100
19	s	211/241 (88%)	204 (97%)	7 (3%)	0	100	100
20	T	214/264 (81%)	207 (97%)	7 (3%)	0	100	100
20	t	214/264 (81%)	204 (95%)	10 (5%)	0	100	100
21	U	812/953 (85%)	767 (94%)	45 (6%)	0	100	100
22	V	442/534 (83%)	434 (98%)	7 (2%)	1 (0%)	43	77
23	W	439/456 (96%)	433 (99%)	6 (1%)	0	100	100
24	X	420/422 (100%)	401 (96%)	19 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	Y	387/389 (100%)	361 (93%)	25 (6%)	1 (0%)	36	71
26	Z	284/324 (88%)	255 (90%)	29 (10%)	0	100	100
27	a	371/376 (99%)	339 (91%)	31 (8%)	1 (0%)	36	71
28	b	189/377 (50%)	167 (88%)	22 (12%)	0	100	100
29	c	285/310 (92%)	259 (91%)	24 (8%)	2 (1%)	18	55
30	d	255/350 (73%)	213 (84%)	42 (16%)	0	100	100
31	e	48/70 (69%)	41 (85%)	7 (15%)	0	100	100
32	f	840/908 (92%)	796 (95%)	39 (5%)	5 (1%)	21	58
33	u	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
34	v	1/28 (4%)	1 (100%)	0	0	100	100
All	All	13411/14980 (90%)	12599 (94%)	784 (6%)	28 (0%)	44	77

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	54	PRO
4	D	85	ILE
9	I	53	HIS
29	c	196	LEU
32	f	349	TYR
32	f	586	PRO
10	j	50	VAL
1	A	347	ASP
2	B	117	ASP
4	D	126	PRO
10	J	219	ILE
29	c	198	ARG
32	f	66	LYS
7	g	4	GLY
1	A	346	PRO
3	C	90	HIS
4	D	237	GLN
11	K	128	ALA
22	V	496	PHE
32	f	348	ILE
32	f	585	GLU
3	C	89	VAL
5	E	117	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	j	49	SER
2	B	55	HIS
25	Y	350	VAL
27	a	214	GLY
10	J	222	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	342/372 (92%)	338 (99%)	4 (1%)	63	73
2	B	345/385 (90%)	344 (100%)	1 (0%)	86	84
3	C	326/346 (94%)	320 (98%)	6 (2%)	51	67
4	D	333/366 (91%)	326 (98%)	7 (2%)	47	65
5	E	341/353 (97%)	339 (99%)	2 (1%)	78	80
6	F	357/379 (94%)	356 (100%)	1 (0%)	86	84
7	G	205/210 (98%)	205 (100%)	0	100	100
7	g	202/210 (96%)	200 (99%)	2 (1%)	68	76
8	H	188/191 (98%)	188 (100%)	0	100	100
8	h	188/191 (98%)	187 (100%)	1 (0%)	81	81
9	I	206/221 (93%)	205 (100%)	1 (0%)	81	81
9	i	206/221 (93%)	205 (100%)	1 (0%)	81	81
10	J	201/211 (95%)	198 (98%)	3 (2%)	57	70
10	j	196/211 (93%)	195 (100%)	1 (0%)	81	81
11	K	193/203 (95%)	193 (100%)	0	100	100
11	k	195/203 (96%)	195 (100%)	0	100	100
12	L	202/224 (90%)	201 (100%)	1 (0%)	81	81
12	l	201/224 (90%)	201 (100%)	0	100	100
13	M	196/212 (92%)	195 (100%)	1 (0%)	81	81
13	m	198/212 (93%)	197 (100%)	1 (0%)	81	81

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	157/181 (87%)	157 (100%)	0	100	100
14	n	156/181 (86%)	156 (100%)	0	100	100
15	O	179/228 (78%)	179 (100%)	0	100	100
15	o	181/228 (79%)	181 (100%)	0	100	100
16	P	172/174 (99%)	172 (100%)	0	100	100
16	p	173/174 (99%)	173 (100%)	0	100	100
17	Q	168/171 (98%)	167 (99%)	1 (1%)	78	80
17	q	168/171 (98%)	168 (100%)	0	100	100
18	R	156/202 (77%)	156 (100%)	0	100	100
18	r	156/202 (77%)	156 (100%)	0	100	100
19	S	175/199 (88%)	175 (100%)	0	100	100
19	s	178/199 (89%)	178 (100%)	0	100	100
20	T	178/215 (83%)	178 (100%)	0	100	100
20	t	179/215 (83%)	179 (100%)	0	100	100
21	U	696/816 (85%)	695 (100%)	1 (0%)	88	88
22	V	390/460 (85%)	390 (100%)	0	100	100
23	W	406/416 (98%)	404 (100%)	2 (0%)	81	81
24	X	362/362 (100%)	361 (100%)	1 (0%)	86	84
25	Y	344/344 (100%)	344 (100%)	0	100	100
26	Z	257/295 (87%)	256 (100%)	1 (0%)	84	82
27	a	333/336 (99%)	331 (99%)	2 (1%)	78	80
28	b	167/312 (54%)	167 (100%)	0	100	100
29	c	252/268 (94%)	250 (99%)	2 (1%)	73	77
30	d	231/294 (79%)	231 (100%)	0	100	100
31	e	44/63 (70%)	44 (100%)	0	100	100
32	f	711/763 (93%)	706 (99%)	5 (1%)	76	79
33	u	68/68 (100%)	68 (100%)	0	100	100
34	v	1/1 (100%)	0	1 (100%)	0	0
All	All	11459/12683 (90%)	11410 (100%)	49 (0%)	81	82

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	ASP
1	A	373	LEU
1	A	398	ARG
1	A	403	ILE
2	B	125	THR
3	C	88	LYS
3	C	89	VAL
3	C	145	ASP
3	C	210	THR
3	C	271	ARG
3	C	287	LYS
4	D	55	GLU
4	D	84	SER
4	D	87	LEU
4	D	124	LEU
4	D	125	LYS
4	D	127	ASN
4	D	353	ASN
5	E	116	ASP
5	E	344	ARG
6	F	218	GLN
9	I	52	ILE
10	J	219	ILE
10	J	220	LEU
10	J	221	ASN
12	L	33	SER
13	M	34	SER
17	Q	179	SER
21	U	527	GLN
23	W	345	GLU
23	W	455	LEU
24	X	1	MET
26	Z	103	LYS
27	a	342	ASP
27	a	343	LEU
29	c	196	LEU
29	c	197	ASN
32	f	66	LYS
32	f	348	ILE
32	f	540	GLN
32	f	586	PRO
32	f	829	MET
7	g	6	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	g	11	ARG
8	h	4	ARG
9	i	206	LEU
10	j	49	SER
13	m	22	GLN
34	v	25	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (118) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	197	HIS
1	A	203	ASN
1	A	414	ASN
2	B	55	HIS
2	B	181	GLN
2	B	277	HIS
3	C	53	ASN
3	C	279	GLN
3	C	343	ASN
4	D	67	ASN
4	D	83	GLN
4	D	127	ASN
4	D	187	HIS
4	D	257	ASN
5	E	10	GLN
5	E	45	ASN
5	E	190	GLN
5	E	220	ASN
5	E	225	HIS
5	E	262	ASN
5	E	307	GLN
5	E	323	HIS
6	F	92	ASN
7	G	24	GLN
7	G	75	ASN
7	G	128	ASN
8	H	109	GLN
9	I	109	GLN
9	I	142	HIS
9	I	146	GLN
9	I	240	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	J	200	GLN
11	K	41	GLN
11	K	97	GLN
11	K	204	GLN
12	L	59	HIS
12	L	60	GLN
12	L	86	ASN
14	N	123	GLN
15	O	91	GLN
16	P	7	ASN
17	Q	32	HIS
17	Q	82	ASN
17	Q	99	HIS
17	Q	168	GLN
20	T	157	GLN
21	U	28	ASN
21	U	111	GLN
21	U	267	ASN
21	U	340	GLN
21	U	491	GLN
21	U	541	HIS
21	U	604	HIS
21	U	718	ASN
22	V	81	GLN
23	W	84	ASN
23	W	167	GLN
23	W	236	HIS
23	W	361	HIS
23	W	399	ASN
23	W	422	ASN
24	X	178	HIS
24	X	334	ASN
25	Y	77	ASN
25	Y	160	ASN
25	Y	258	GLN
25	Y	365	GLN
25	Y	367	GLN
26	Z	32	GLN
26	Z	96	HIS
26	Z	189	GLN
27	a	46	GLN
27	a	86	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	a	257	GLN
28	b	27	GLN
28	b	79	GLN
28	b	149	ASN
28	b	169	HIS
29	c	115	HIS
29	c	176	GLN
29	c	237	HIS
30	d	220	ASN
32	f	171	GLN
32	f	273	ASN
32	f	325	GLN
32	f	329	ASN
32	f	428	GLN
32	f	565	ASN
32	f	592	ASN
32	f	610	GLN
32	f	650	GLN
32	f	786	GLN
32	f	790	GLN
7	g	12	HIS
7	g	193	GLN
8	h	21	GLN
9	i	20	GLN
9	i	84	ASN
9	i	142	HIS
9	i	167	ASN
9	i	230	GLN
10	j	85	ASN
10	j	175	ASN
11	k	41	GLN
11	k	224	GLN
11	k	227	HIS
12	l	175	HIS
13	m	180	GLN
14	n	106	GLN
15	o	116	HIS
15	o	193	ASN
16	p	31	GLN
16	p	61	GLN
17	q	99	HIS
19	s	146	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
20	t	61	GLN
20	t	108	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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$
37	ADP	E	401	-	27,29,29	1.36	4 (14%)	42,45,45	2.02	9 (21%)
35	ATP	A	501	36	29,33,33	0.30	0	44,52,52	0.47	1 (2%)
37	ADP	B	501	-	27,29,29	1.36	4 (14%)	42,45,45	2.02	10 (23%)
35	ATP	D	501	36	29,33,33	0.31	0	44,52,52	0.47	0
35	ATP	F	501	36	29,33,33	0.30	0	44,52,52	0.51	1 (2%)

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
37	ADP	E	401	-	-	3/16/32/32	0/3/3/3
35	ATP	A	501	36	-	2/22/38/38	0/3/3/3
37	ADP	B	501	-	-	2/16/32/32	0/3/3/3
35	ATP	D	501	36	-	5/22/38/38	0/3/3/3
35	ATP	F	501	36	-	2/22/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	E	401	ADP	C5-C4	4.59	1.47	1.39
37	B	501	ADP	C5-C4	4.57	1.47	1.39
37	B	501	ADP	C5-C6	2.59	1.48	1.41
37	E	401	ADP	C5-C6	2.56	1.48	1.41
37	E	401	ADP	C5-N7	-2.36	1.34	1.39
37	B	501	ADP	C5-N7	-2.33	1.34	1.39
37	B	501	ADP	C8-N7	2.28	1.35	1.31
37	E	401	ADP	C8-N7	2.25	1.35	1.31

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	E	401	ADP	C5-C4-N3	-6.63	118.10	126.75
37	B	501	ADP	C5-C4-N3	-6.53	118.23	126.75
37	E	401	ADP	N3-C4-N9	5.30	135.82	127.08
37	B	501	ADP	N3-C4-N9	5.16	135.59	127.08
37	E	401	ADP	C2-N3-C4	3.90	120.97	111.75
37	B	501	ADP	PA-O3A-PB	-3.83	119.69	132.83
37	E	401	ADP	PA-O3A-PB	-3.83	119.70	132.83
37	B	501	ADP	C2-N3-C4	3.81	120.76	111.75
37	B	501	ADP	C4-C5-N7	-3.29	106.61	110.62
37	E	401	ADP	C4-C5-N7	-3.09	106.86	110.62
37	E	401	ADP	N3-C2-N1	-2.97	123.96	128.60
37	B	501	ADP	C5-N7-C8	2.92	107.65	103.51
37	B	501	ADP	N3-C2-N1	-2.90	124.07	128.60
37	B	501	ADP	C3'-C2'-C1'	2.82	106.78	101.43
37	E	401	ADP	C3'-C2'-C1'	2.66	106.47	101.43
37	E	401	ADP	C5-N7-C8	2.60	107.20	103.51
37	B	501	ADP	C4-N9-C8	2.51	108.45	105.73
37	E	401	ADP	C4-N9-C8	2.33	108.25	105.73
35	F	501	ATP	PB-O3B-PG	2.06	139.90	132.83
37	B	501	ADP	N9-C8-N7	-2.05	111.12	113.91
35	A	501	ATP	PB-O3B-PG	2.03	139.79	132.83

There are no chirality outliers.

All (14) torsion outliers are listed below:

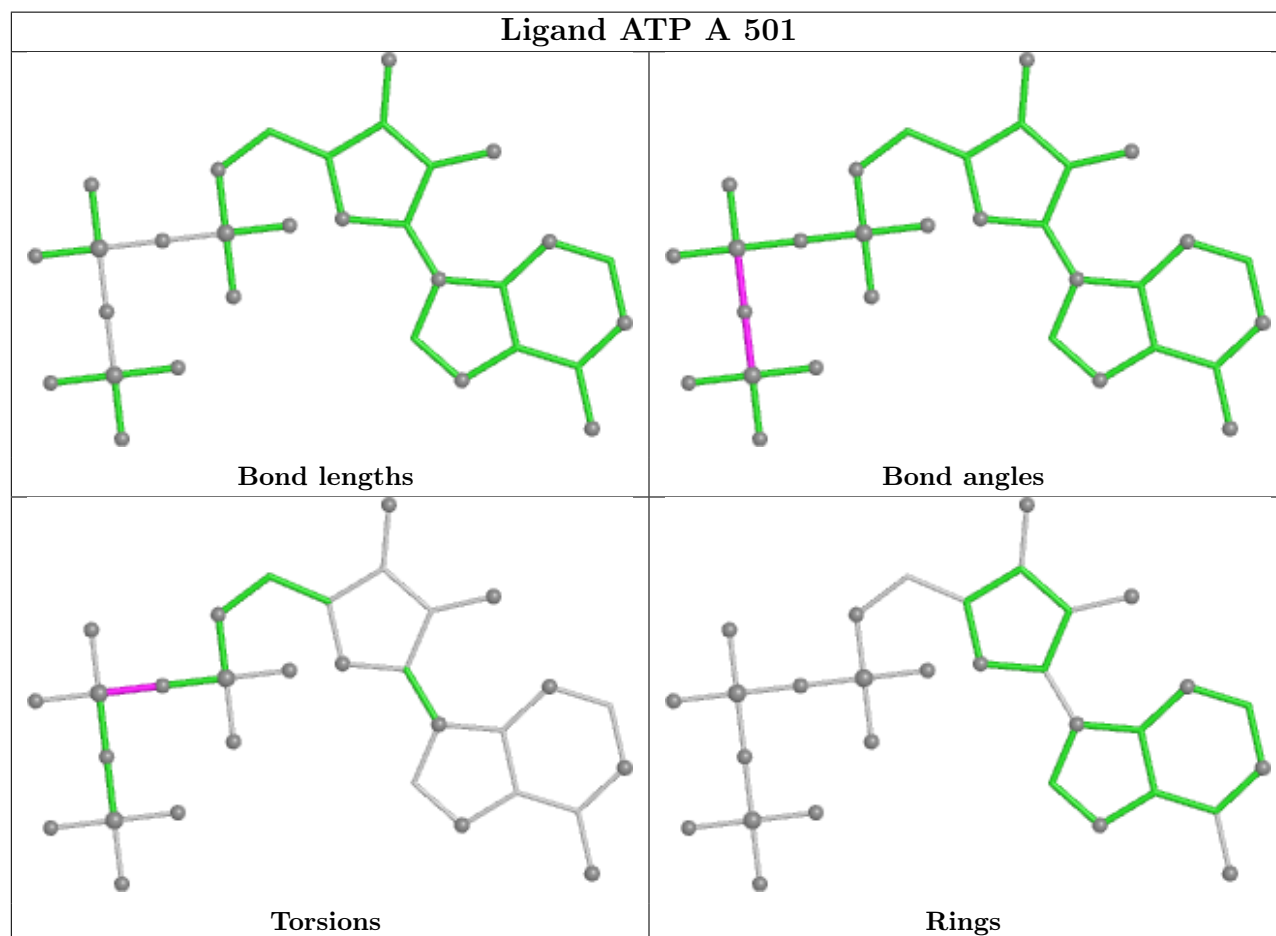
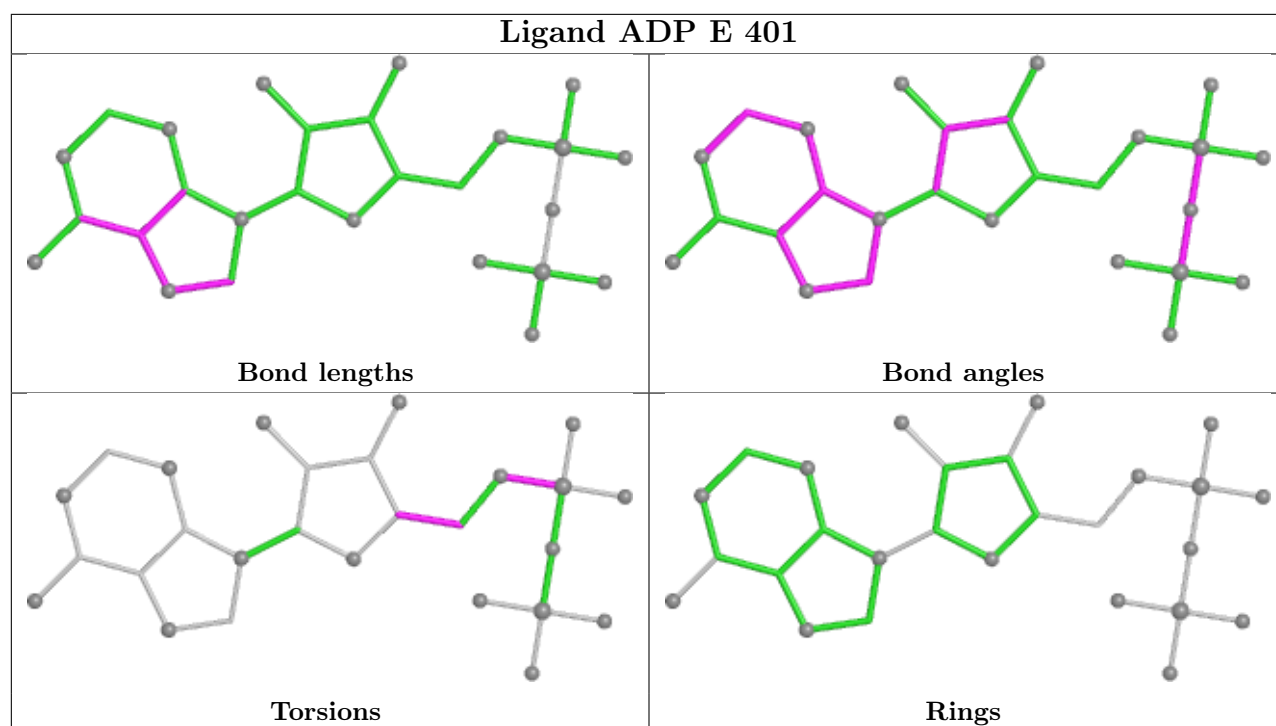
Mol	Chain	Res	Type	Atoms
35	D	501	ATP	C5'-O5'-PA-O3A
35	D	501	ATP	C4'-C5'-O5'-PA
35	D	501	ATP	C3'-C4'-C5'-O5'
35	F	501	ATP	C5'-O5'-PA-O3A
35	D	501	ATP	O4'-C4'-C5'-O5'
37	E	401	ADP	O4'-C4'-C5'-O5'
37	B	501	ADP	O4'-C4'-C5'-O5'
37	B	501	ADP	C3'-C4'-C5'-O5'
37	E	401	ADP	C3'-C4'-C5'-O5'
35	D	501	ATP	C5'-O5'-PA-O1A
35	F	501	ATP	C5'-O5'-PA-O1A
35	A	501	ATP	PA-O3A-PB-O1B
35	A	501	ATP	PA-O3A-PB-O2B
37	E	401	ADP	C5'-O5'-PA-O1A

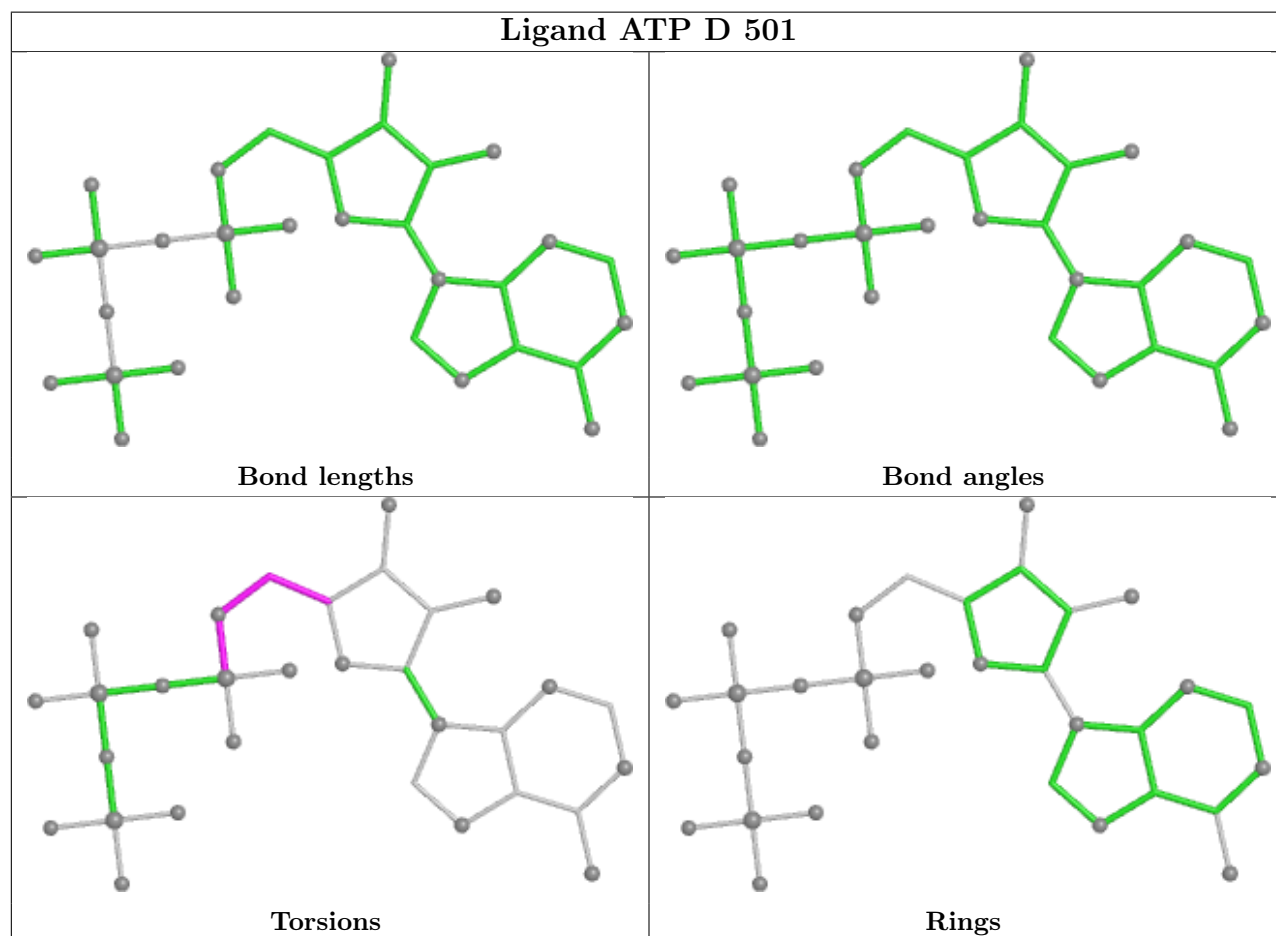
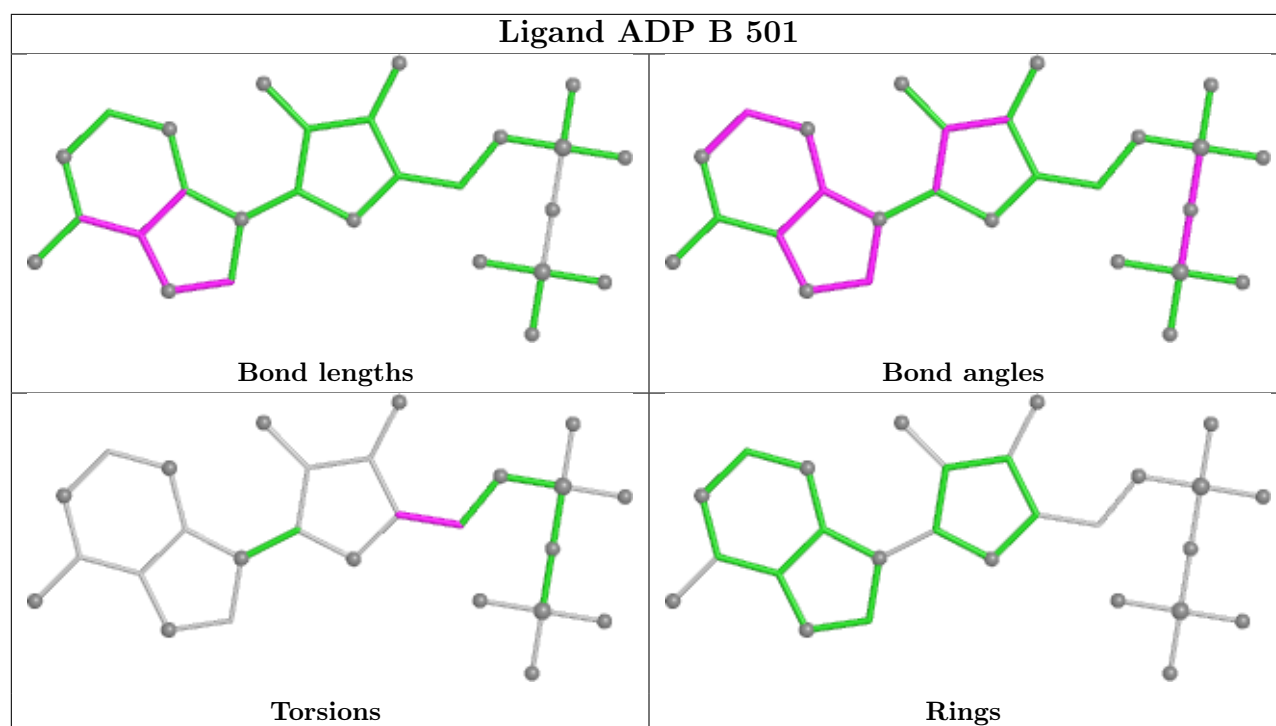
There are no ring outliers.

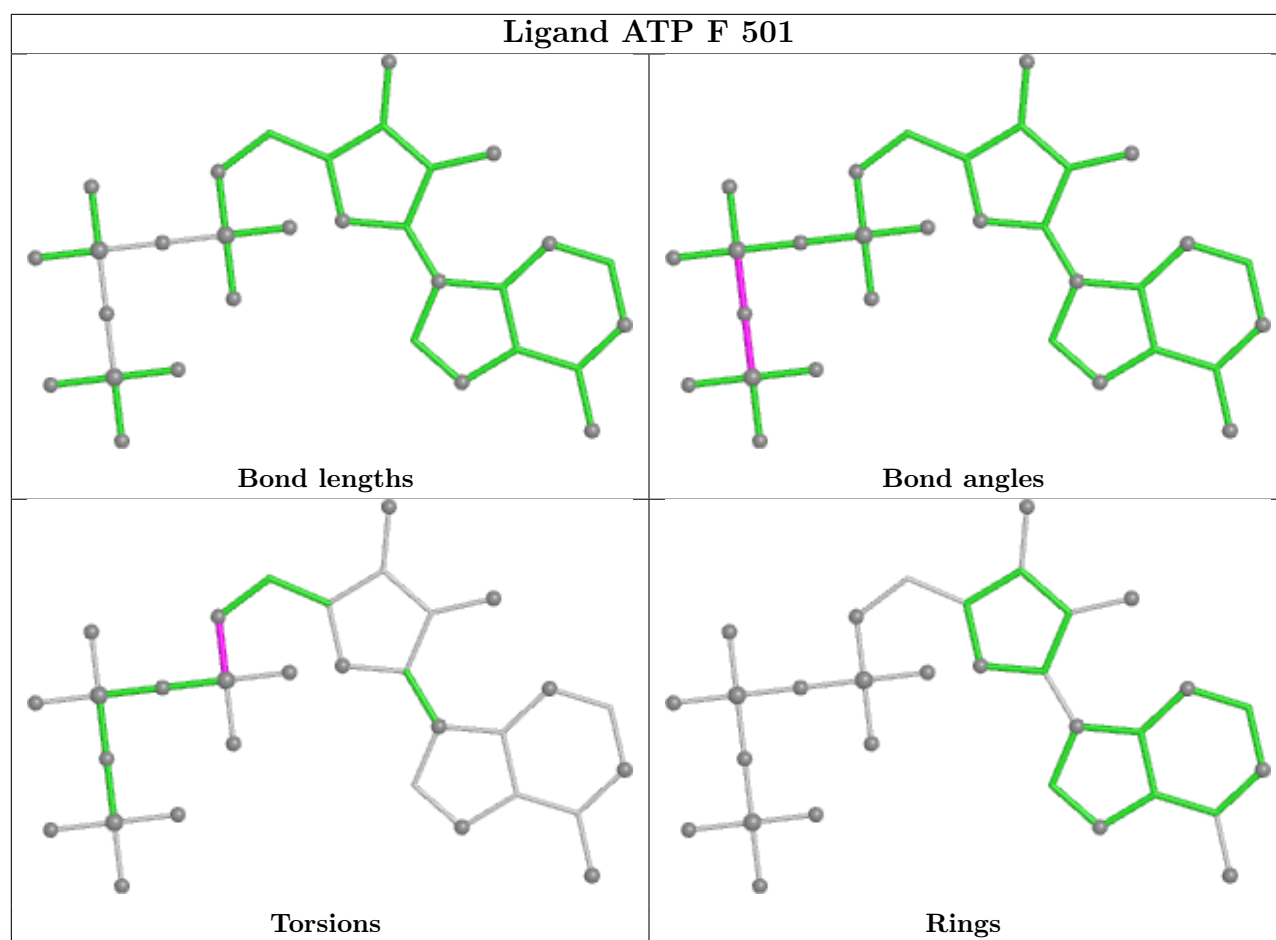
4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
37	E	401	ADP	3	0
35	A	501	ATP	1	0
37	B	501	ADP	3	0
35	F	501	ATP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

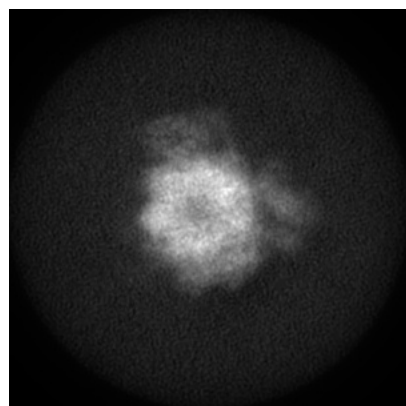
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62084. These allow visual inspection of the internal detail of the map and identification of artifacts.

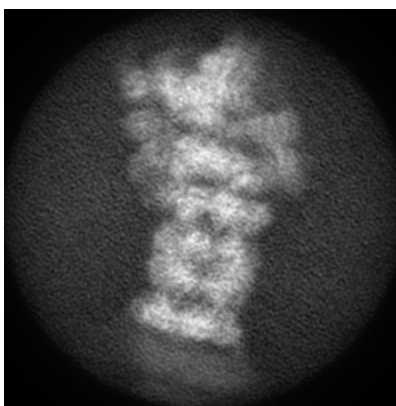
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

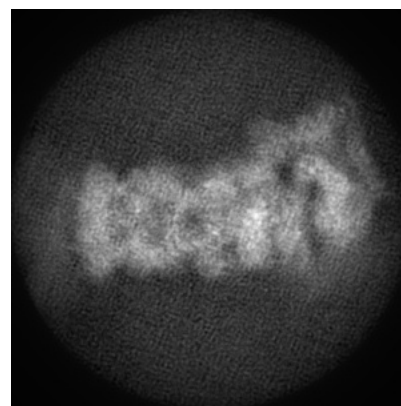
6.1.1 Primary map



X

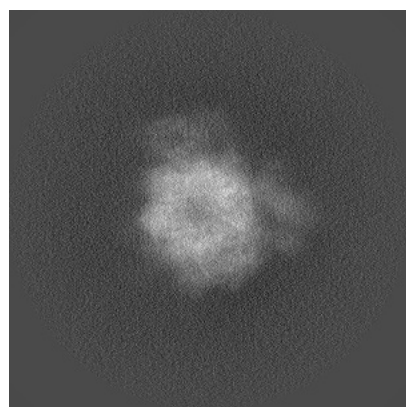


Y

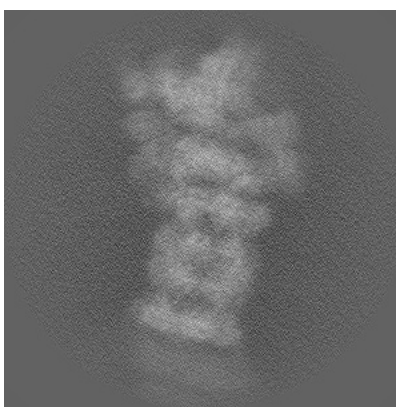


Z

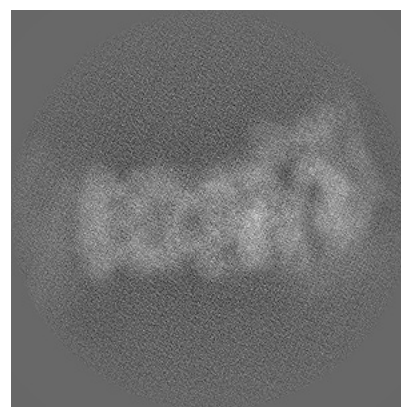
6.1.2 Raw map



X



Y

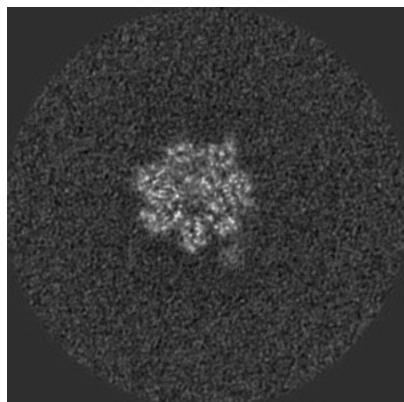


Z

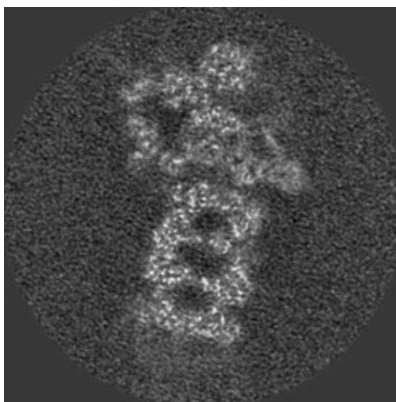
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

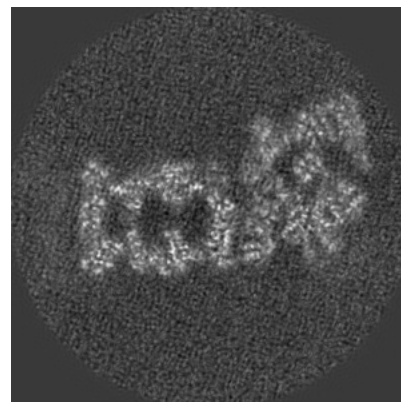
6.2.1 Primary map



X Index: 300

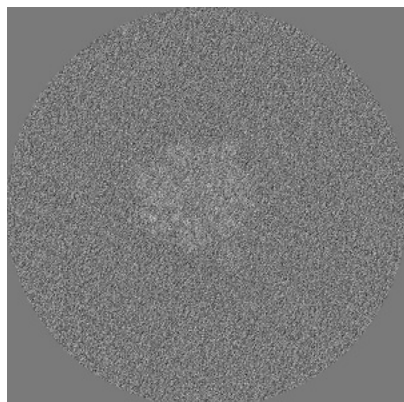


Y Index: 300

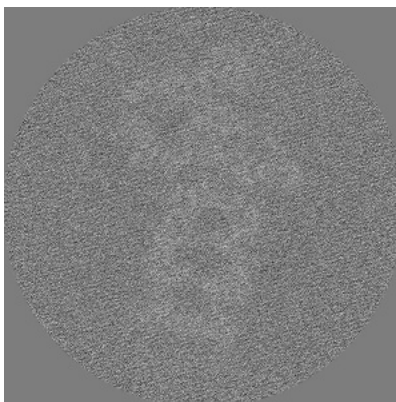


Z Index: 300

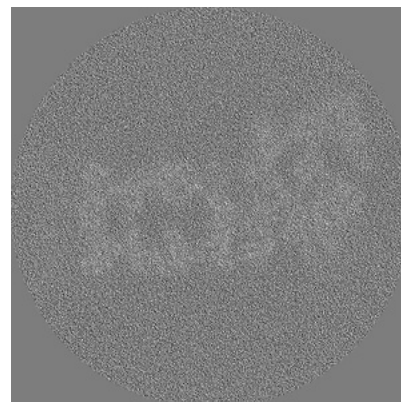
6.2.2 Raw map



X Index: 300



Y Index: 300

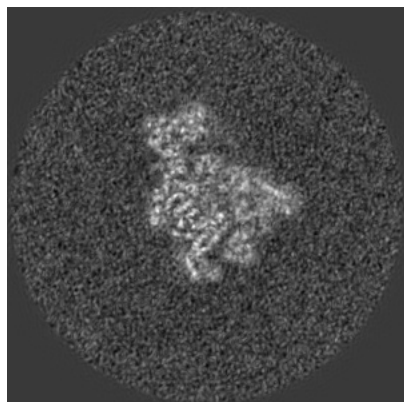


Z Index: 300

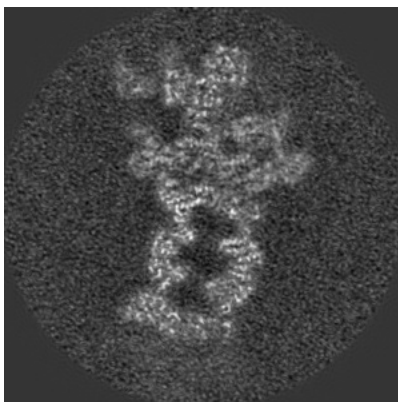
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

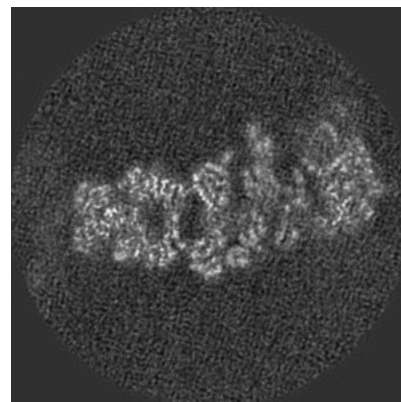
6.3.1 Primary map



X Index: 372

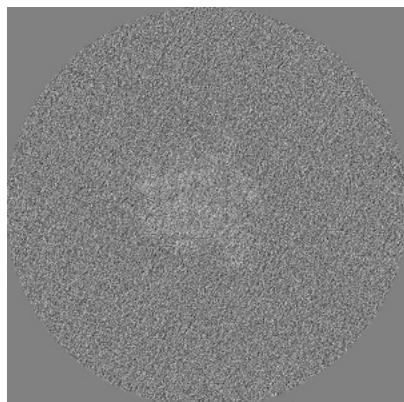


Y Index: 286

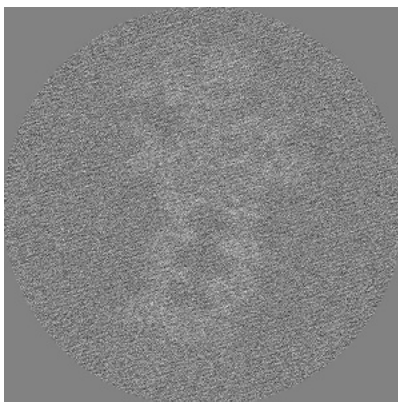


Z Index: 329

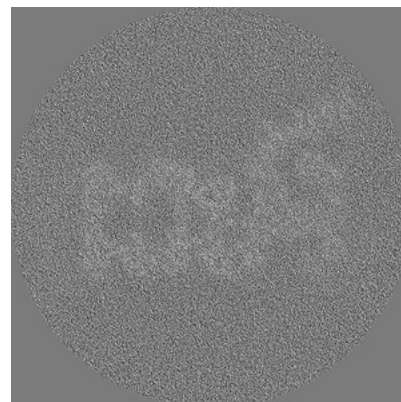
6.3.2 Raw map



X Index: 311



Y Index: 288

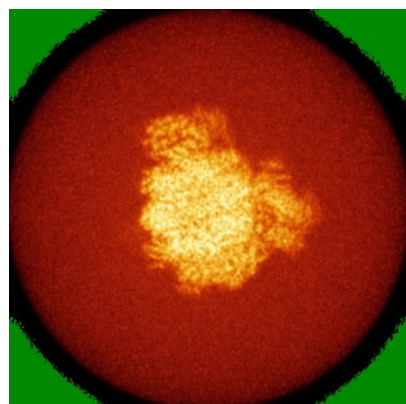


Z Index: 284

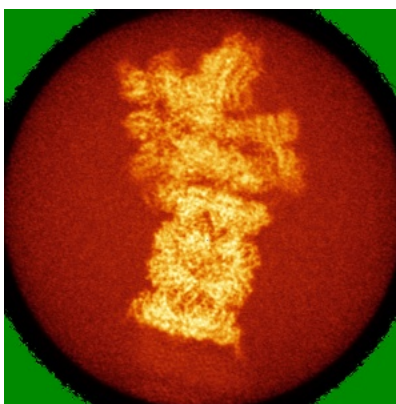
The images above show the largest variance slices of the map in three orthogonal directions.

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

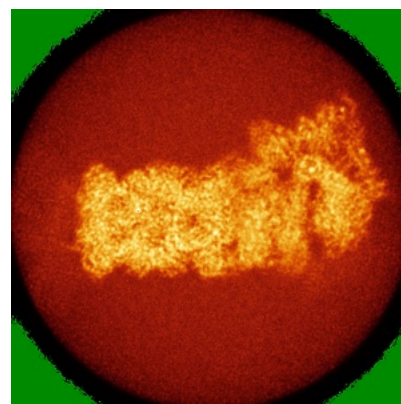
6.4.1 Primary map



X

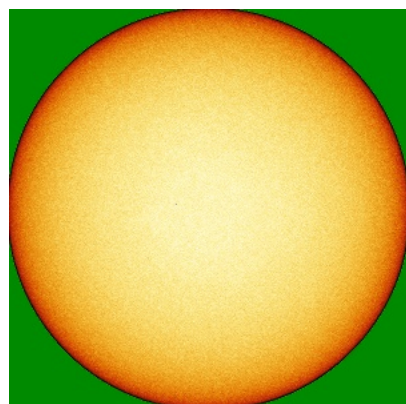


Y

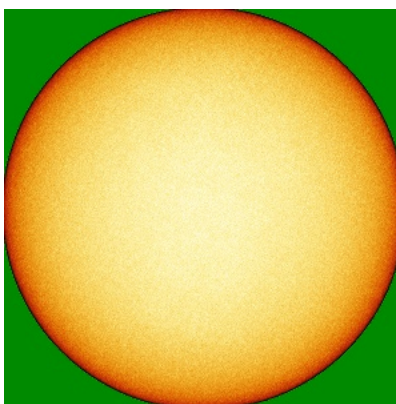


Z

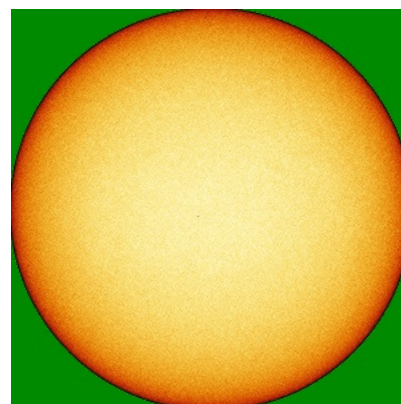
6.4.2 Raw map



X



Y

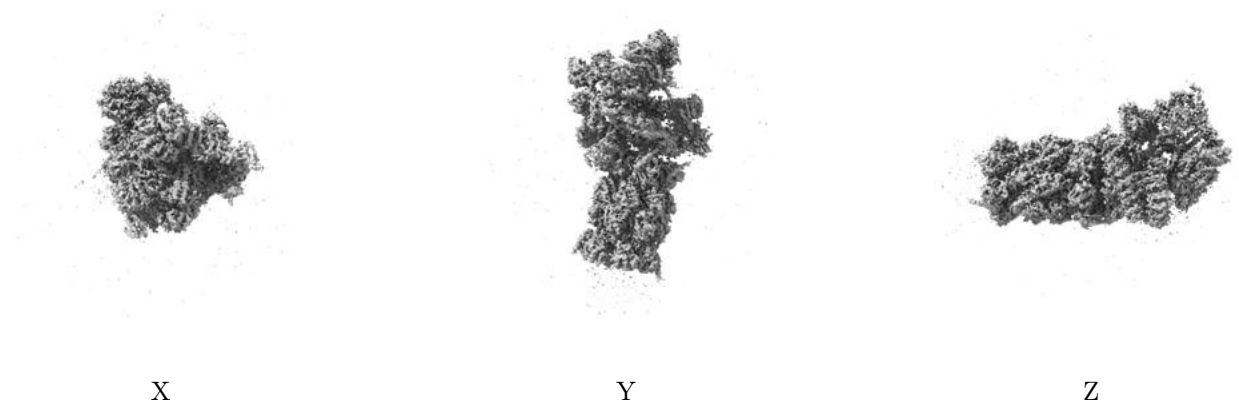


Z

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.

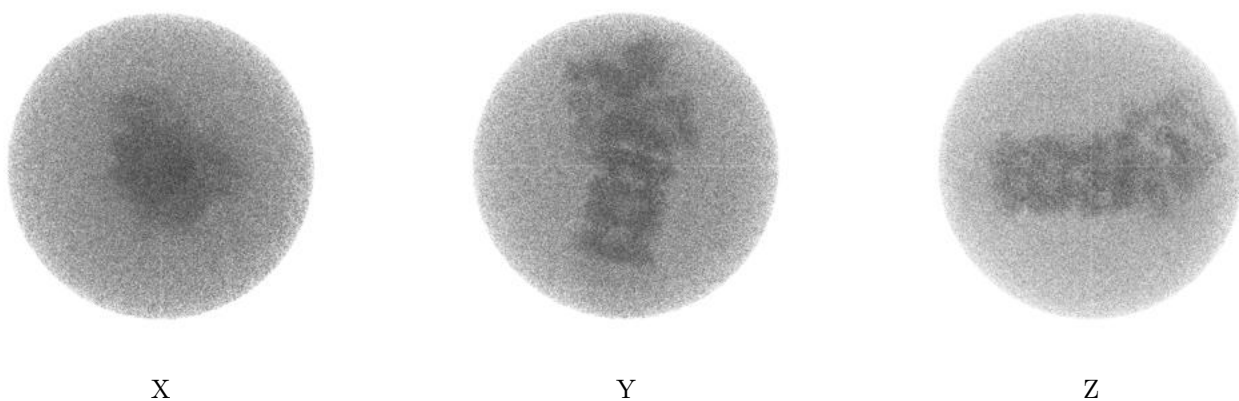
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00588. 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.

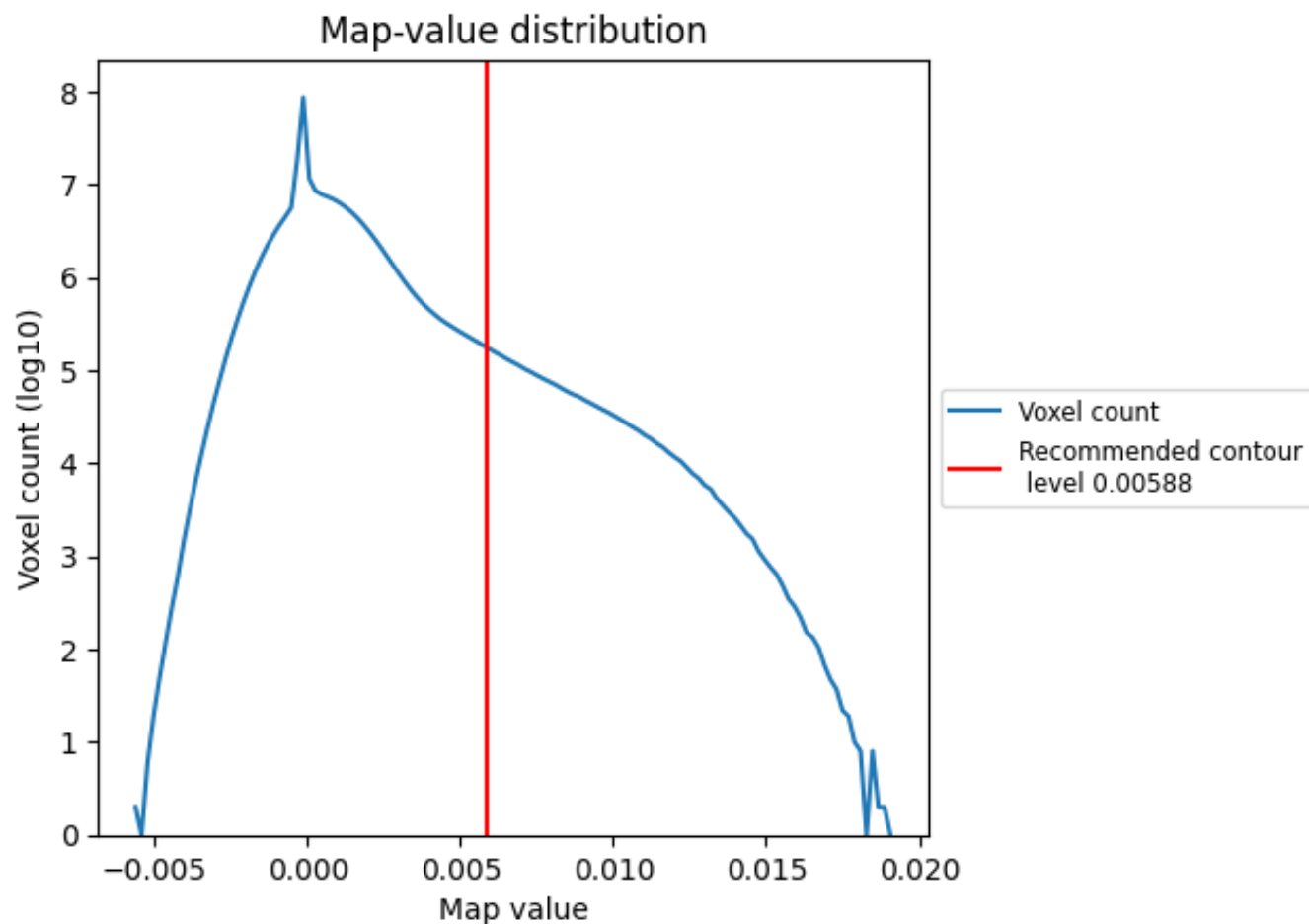
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

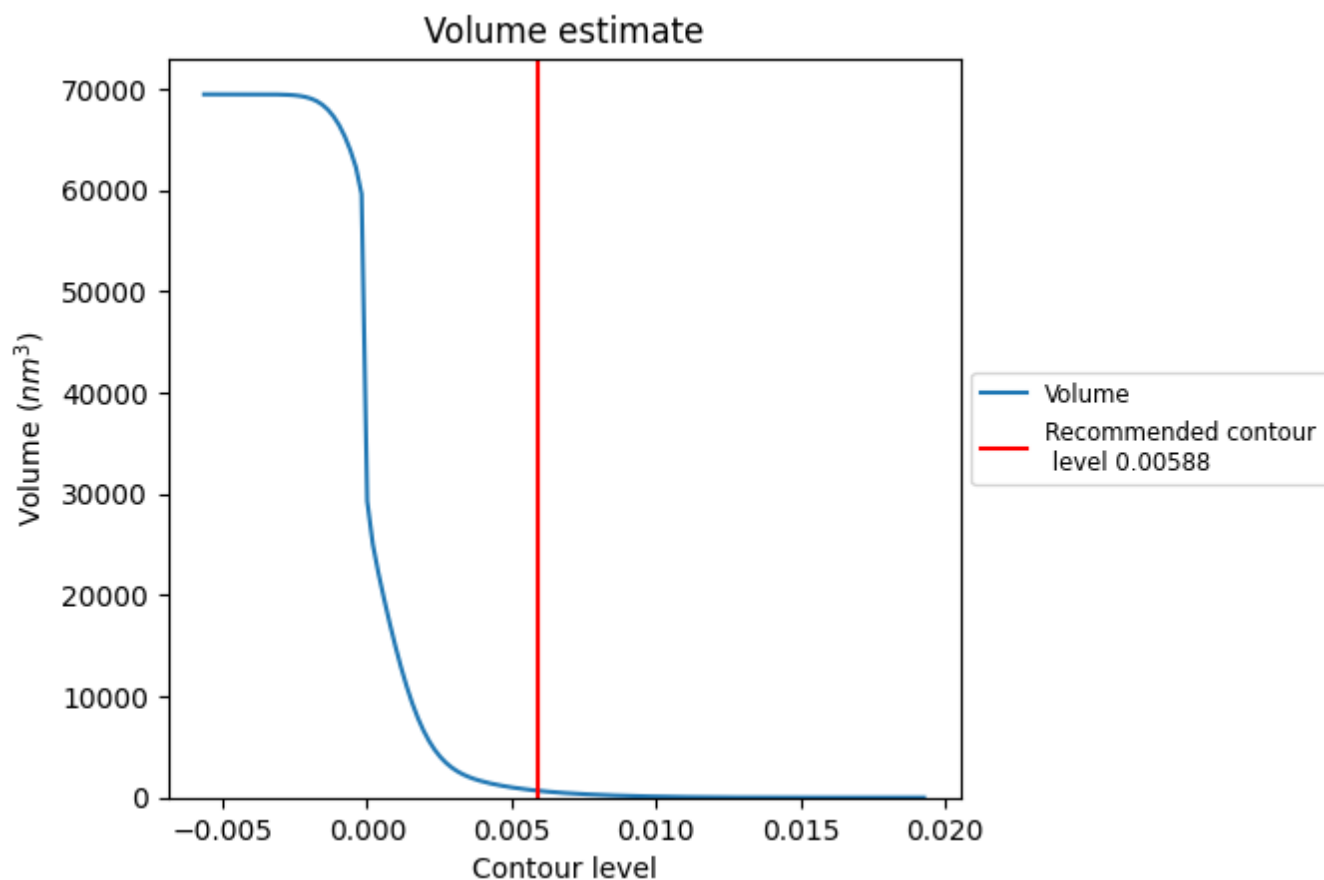
This section contains the results of statistical analysis of the map.

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.

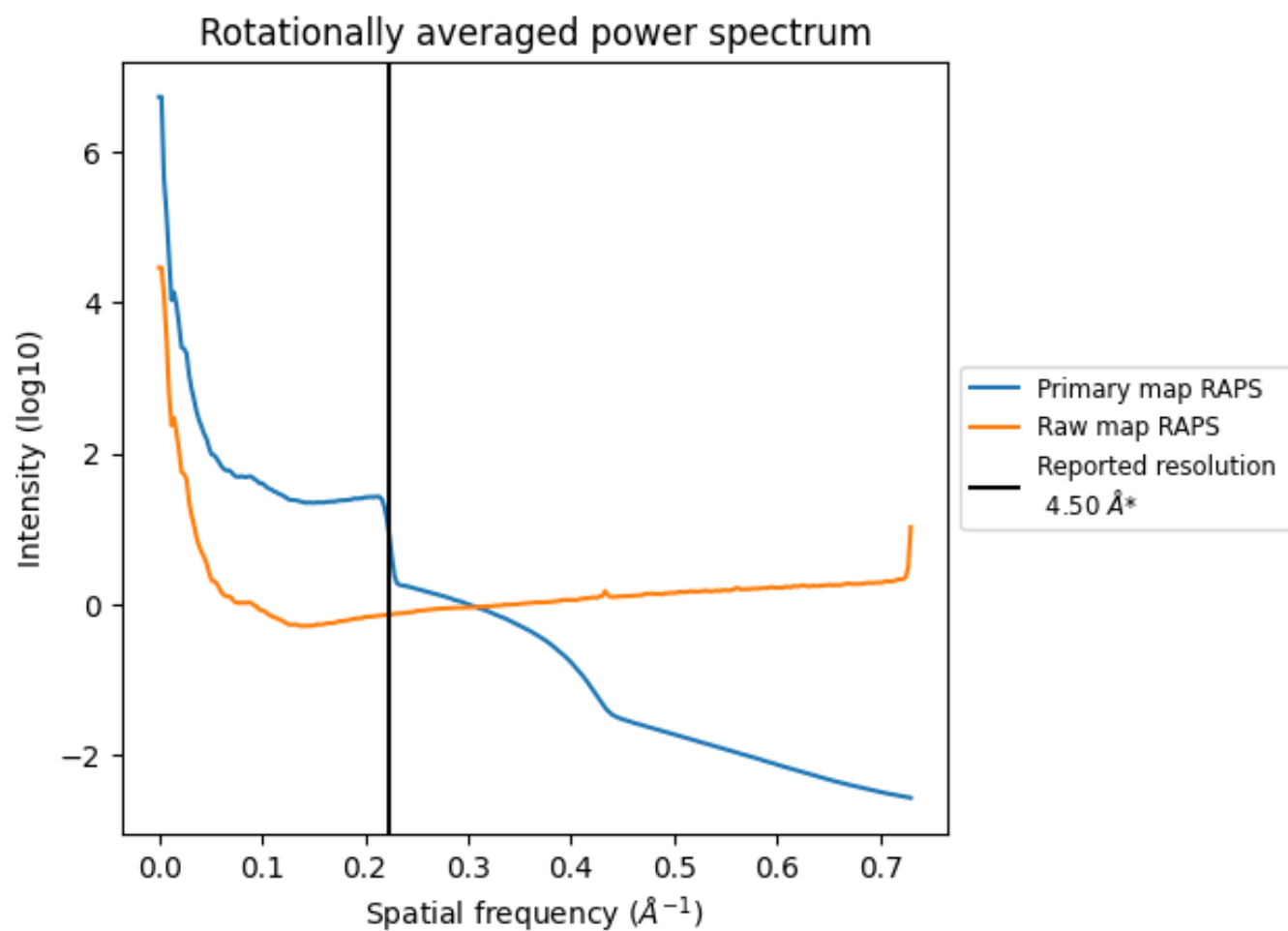
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 688 nm³; this corresponds to an approximate mass of 621 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 ⓘ

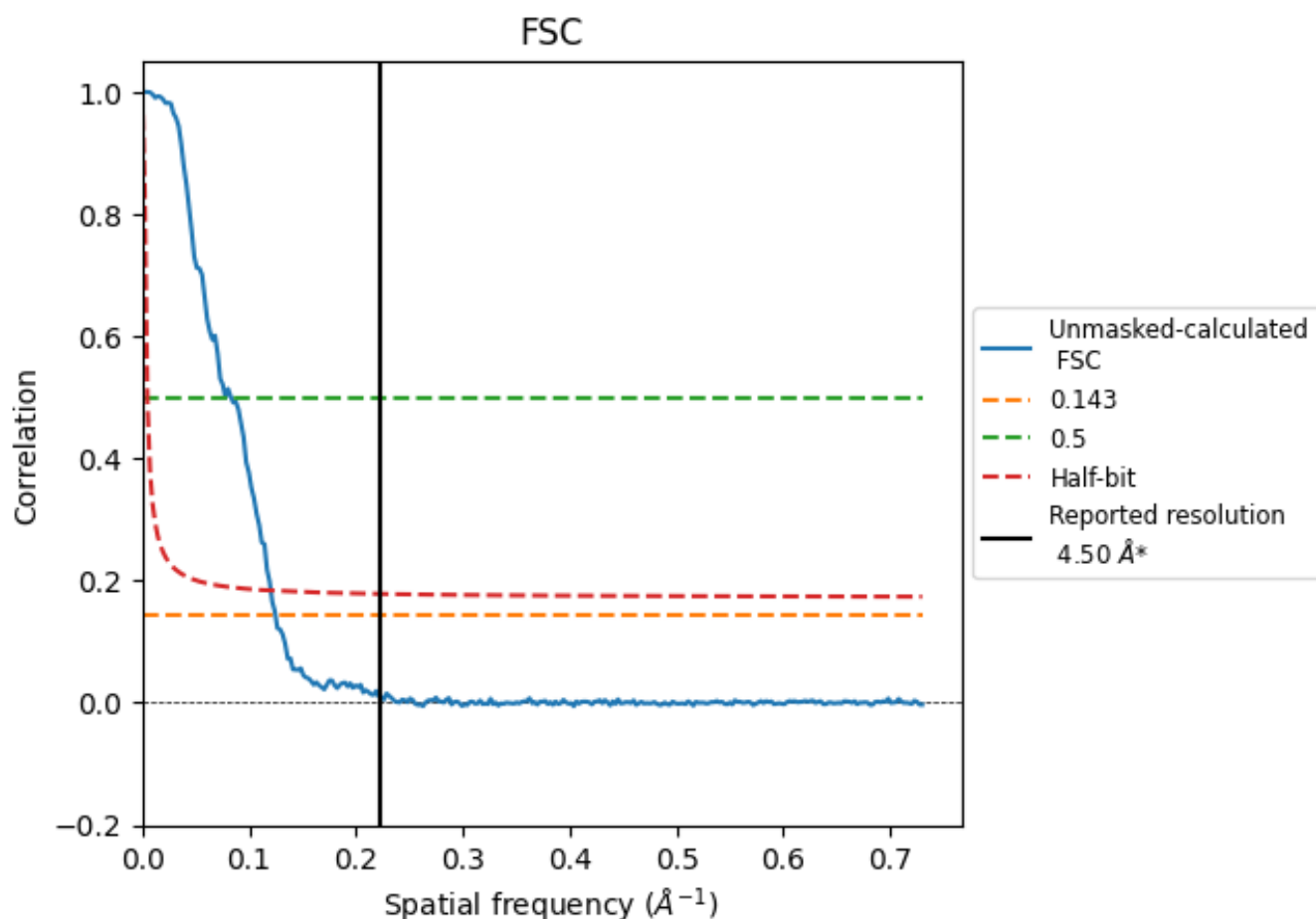


*Reported resolution corresponds to spatial frequency of 0.222 \AA^{-1}

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 0.222 \AA^{-1}

8.2 Resolution estimates [i](#)

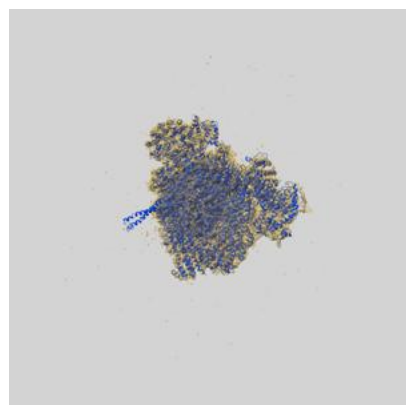
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.02	12.87	8.31

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.02 differs from the reported value 4.5 by more than 10 %

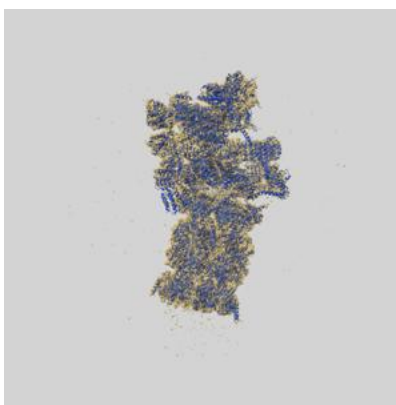
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-62084 and PDB model 9K58. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

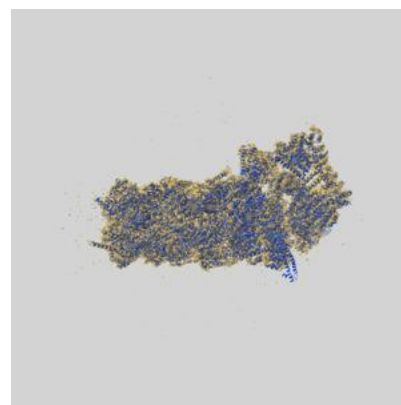
9.1 Map-model overlay [i](#)



X



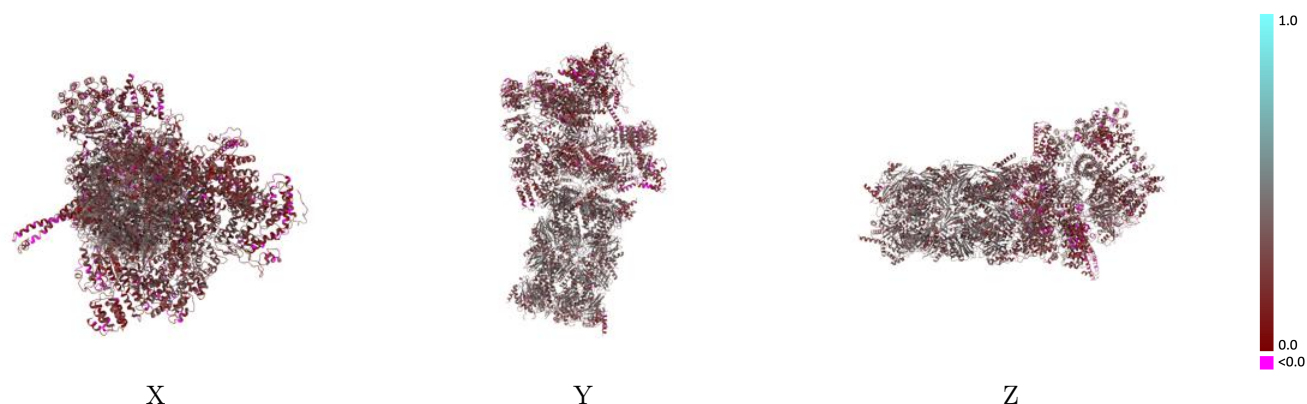
Y



Z

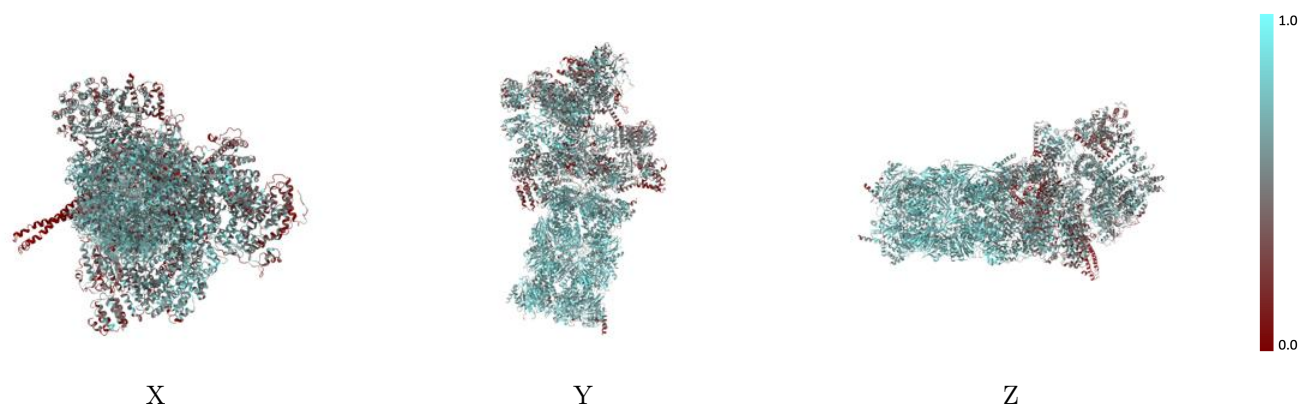
The images above show the 3D surface view of the map at the recommended contour level 0.00588 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



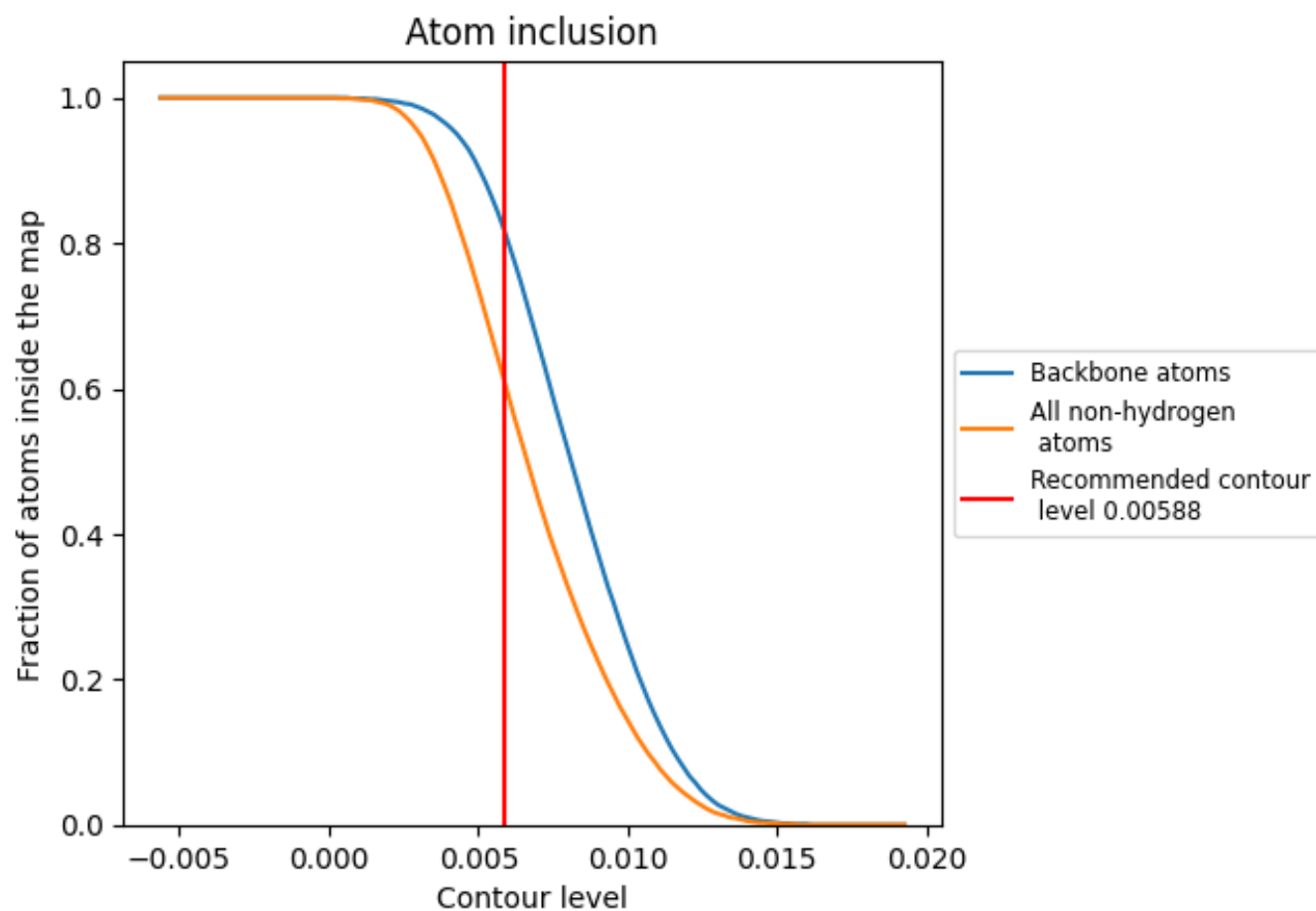
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00588).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





























The table lists the average atom inclusion at the recommended contour level (0.00588) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6100	 0.2990
A	 0.5490	 0.2770
B	 0.5110	 0.2630
C	 0.4650	 0.2390
D	 0.5650	 0.2890
E	 0.5620	 0.2890
F	 0.5300	 0.2890
G	 0.6970	 0.3580
H	 0.7220	 0.3630
I	 0.6820	 0.3340
J	 0.6450	 0.3100
K	 0.6740	 0.3470
L	 0.7270	 0.3620
M	 0.7080	 0.3400
N	 0.7540	 0.3660
O	 0.7610	 0.3640
P	 0.7640	 0.3780
Q	 0.7660	 0.3620
R	 0.7720	 0.3560
S	 0.7440	 0.3650
T	 0.7610	 0.3700
U	 0.5520	 0.2590
V	 0.4900	 0.2460
W	 0.5600	 0.2640
X	 0.4610	 0.2560
Y	 0.5660	 0.2360
Z	 0.6080	 0.3000
a	 0.5160	 0.2300
b	 0.4330	 0.2630
c	 0.6210	 0.3180
d	 0.3720	 0.1890
e	 0.4080	 0.2260
f	 0.4310	 0.2110
g	 0.7100	 0.3460
h	 0.7130	 0.3390



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.6820	 0.3420
j	 0.6350	 0.3120
k	 0.6780	 0.3420
l	 0.7280	 0.3440
m	 0.7260	 0.3450
n	 0.7490	 0.3680
o	 0.7540	 0.3680
p	 0.7480	 0.3520
q	 0.7520	 0.3490
r	 0.7680	 0.3570
s	 0.7210	 0.3530
t	 0.7710	 0.3540
u	 0.5240	 0.2470
v	 0.2940	 0.1980