



Full wwPDB EM Validation Report ⓘ

Apr 21, 2026 – 01:07 PM JST

PDB ID : 9K4U / pdb_00009k4u
EMDB ID : EMD-62070
Title : Structure of substrate-engaged human 26S proteasome RP-CP subcomplex in state EC1
Authors : Wu, Z.; Chen, E.; Mao, Y.
Deposited on : 2024-10-21
Resolution : 3.40 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

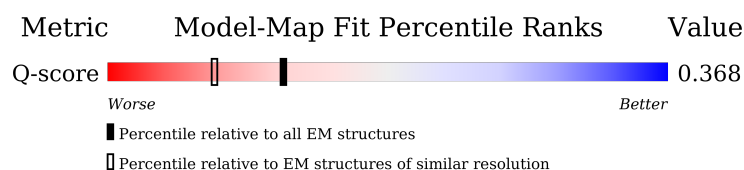
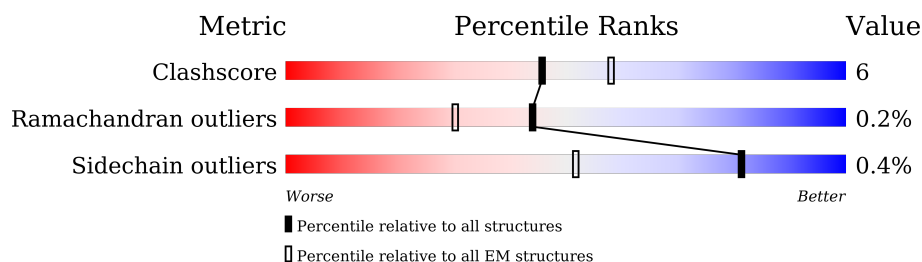
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



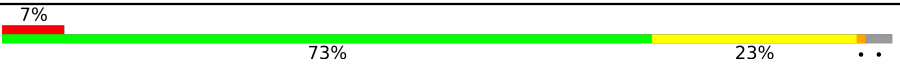

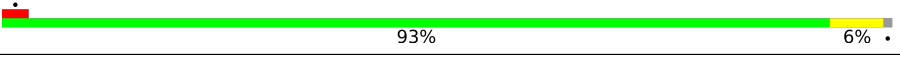
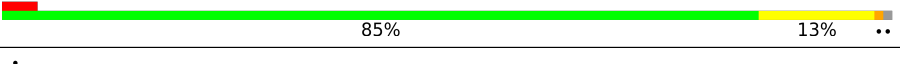
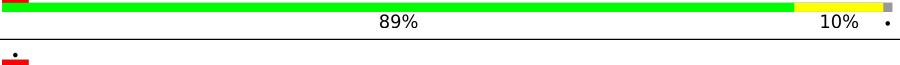
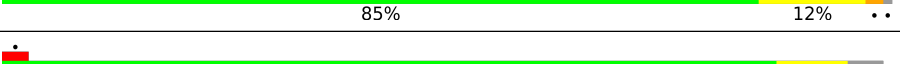
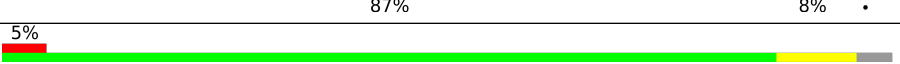
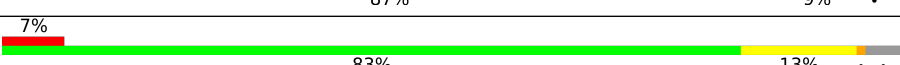
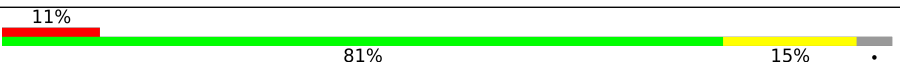

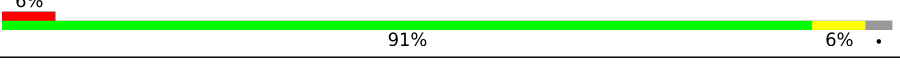




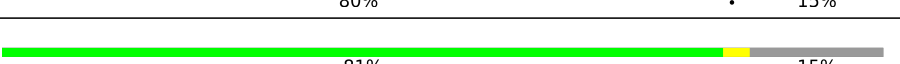
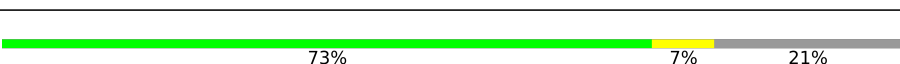
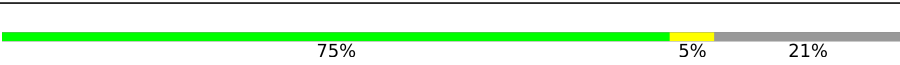
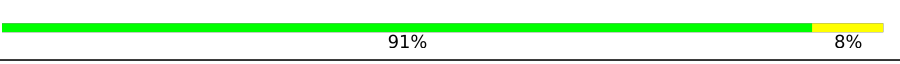
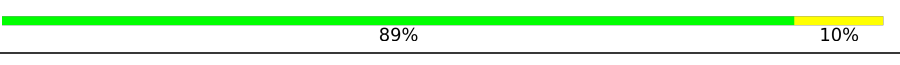
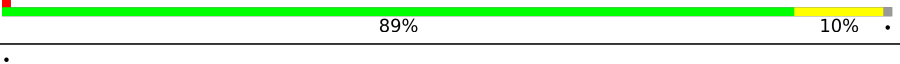
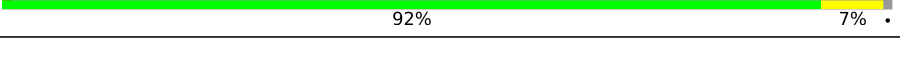
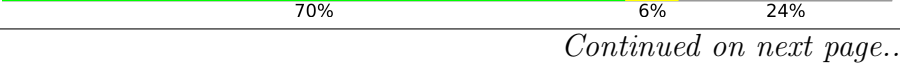


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	
2	B	440	
3	C	398	
4	D	418	

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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	

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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	24	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 106690 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	402	Total	C	N	O	S	0	0
			3135	1973	551	594	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	399	Total	C	N	O	S	0	0
			3122	1967	529	611	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	396	Total	C	N	O	S	0	0
			3105	1954	558	576	17		

- 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
			3040	1923	524	580	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	395	Total	C	N	O	S	0	0
			3098	1951	533	596	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	1	0
			1958	1236	336	376	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		

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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	878	Total	C	N	O	S	0	0
			6867	4352	1163	1306	46		

- 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		

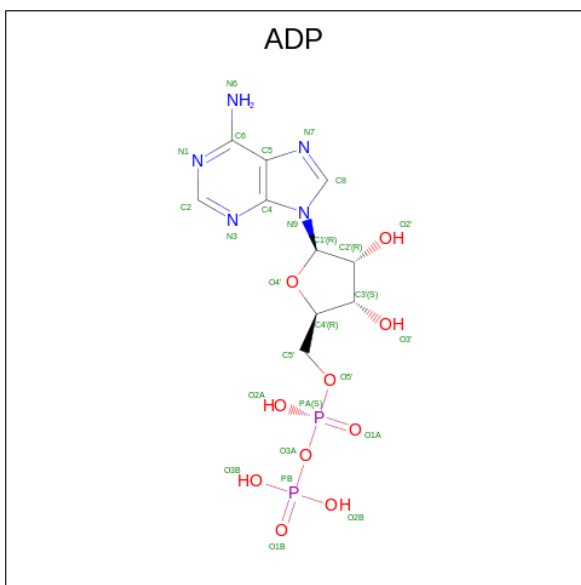
- Molecule 33 is a protein called Ubiquitin.

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.

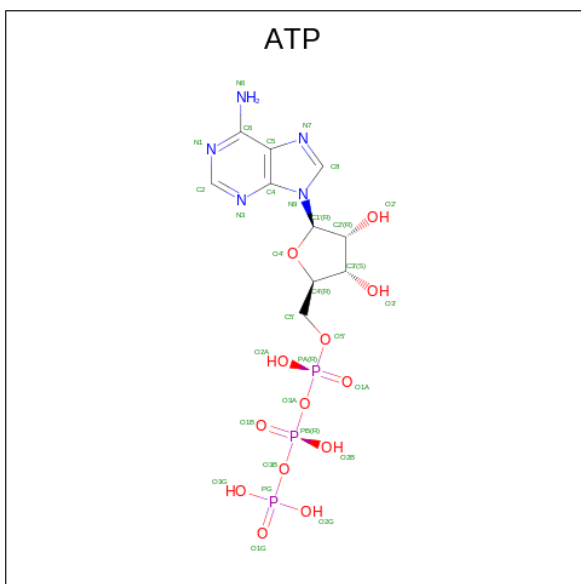
Mol	Chain	Residues	Atoms				AltConf	Trace
34	v	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 36 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{13}\text{P}_3$) (labeled as "Ligand of Interest" by depositor).



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

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

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
37	C	1	Total	Mg	0
			1	1	
37	D	1	Total	Mg	0
			1	1	
37	E	1	Total	Mg	0
			1	1	

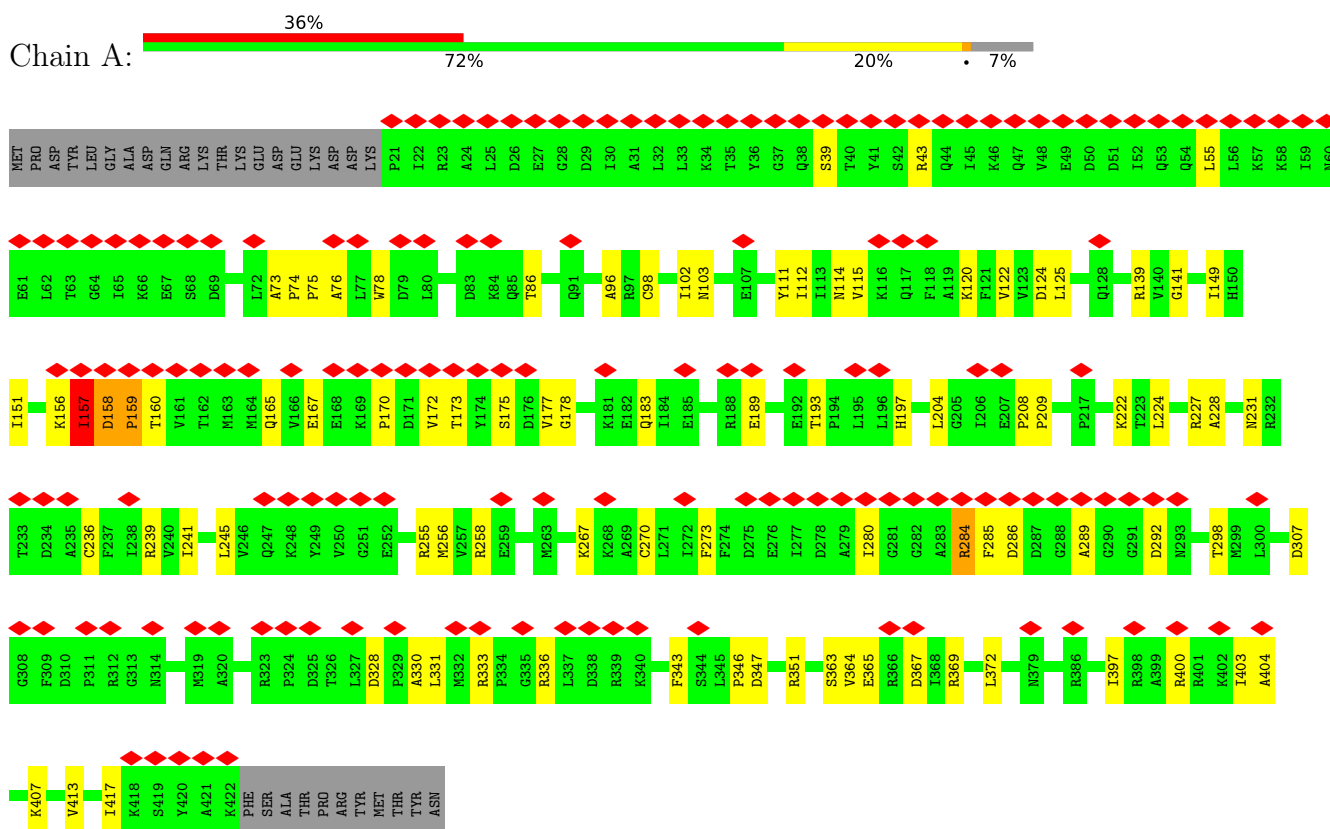
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

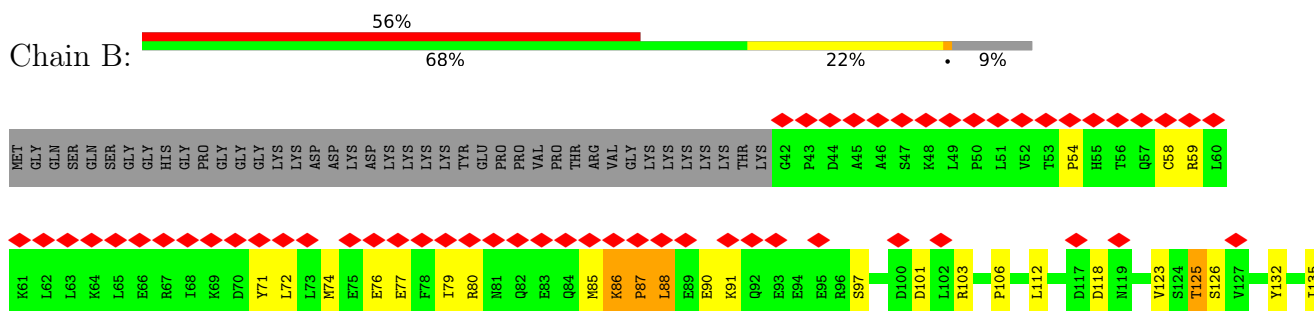
3 Residue-property plots

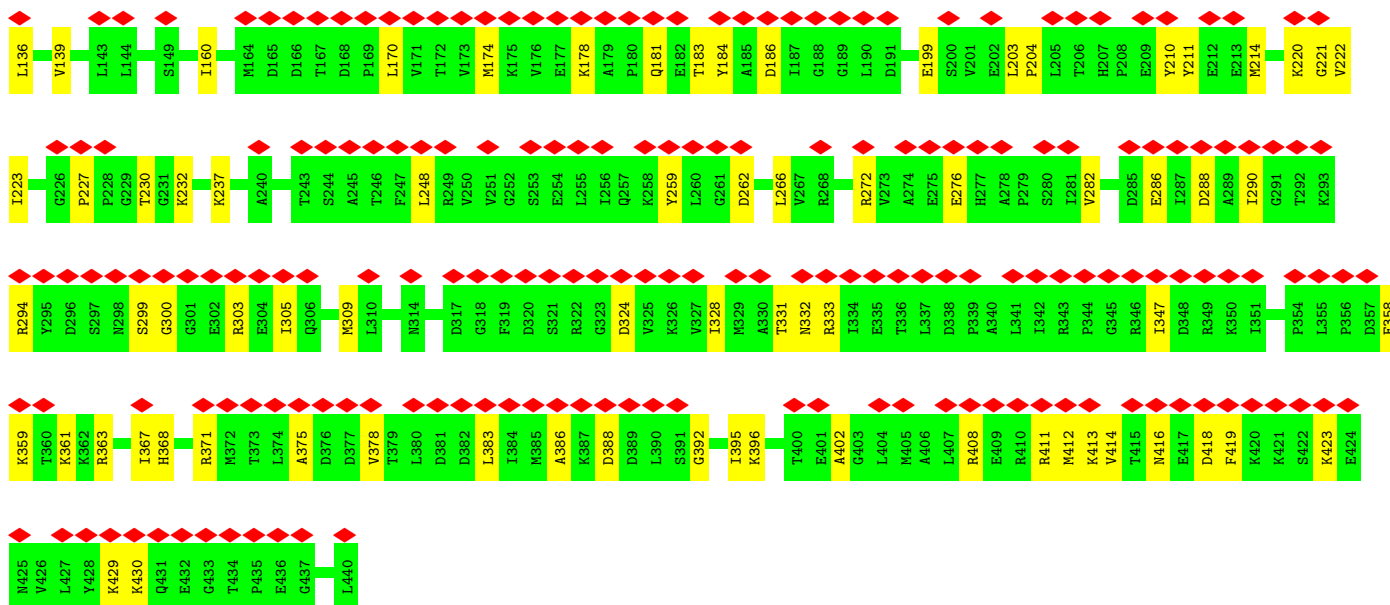
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 26S proteasome regulatory subunit 7

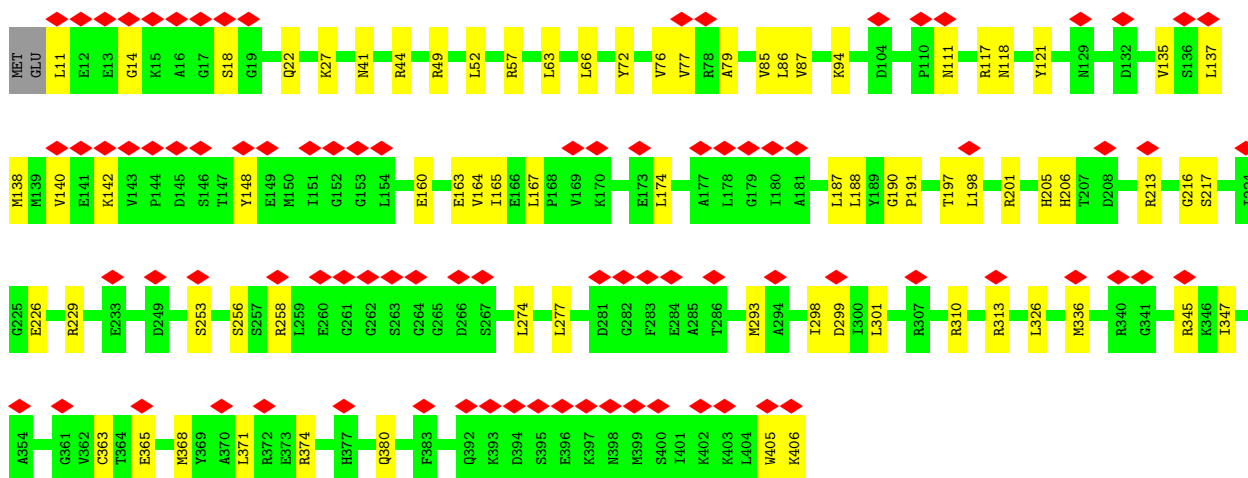
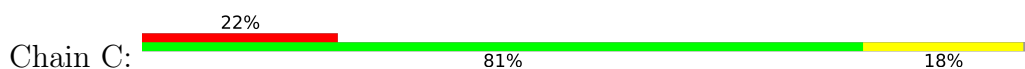


• Molecule 2: 26S proteasome regulatory subunit 4

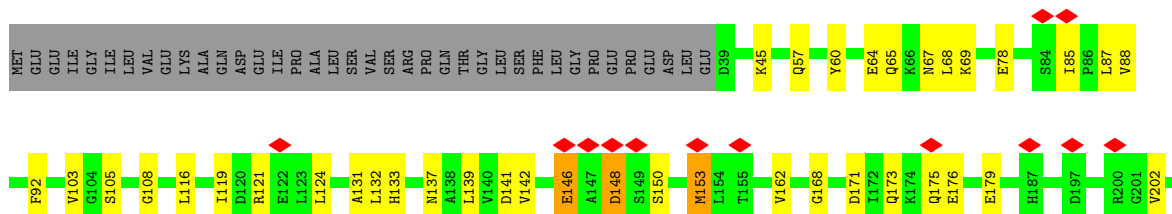
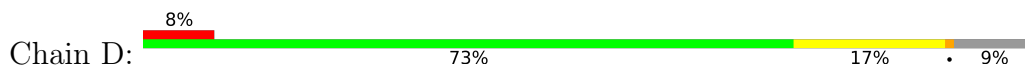


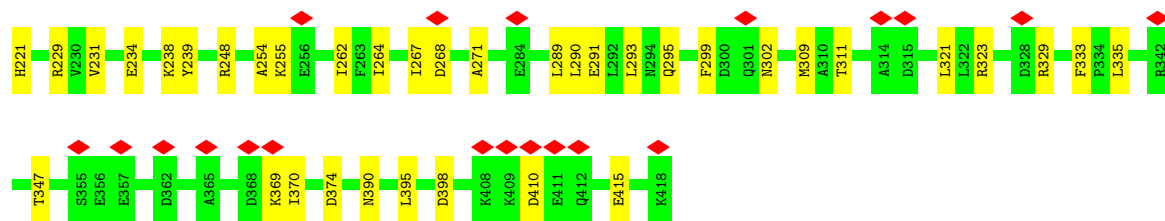


• Molecule 3: 26S proteasome regulatory subunit 8

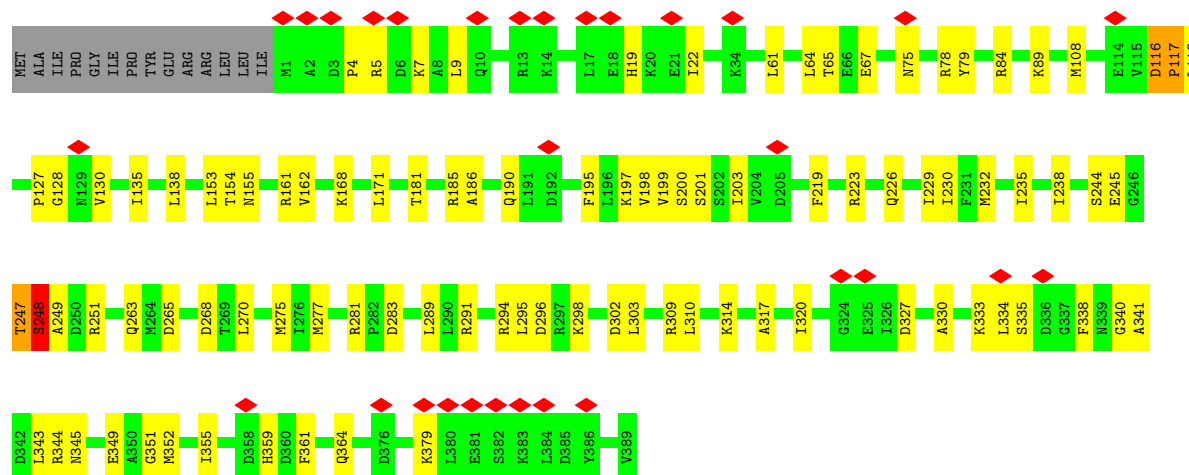
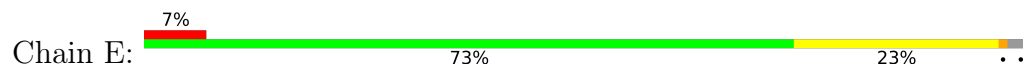


• Molecule 4: 26S proteasome regulatory subunit 6B

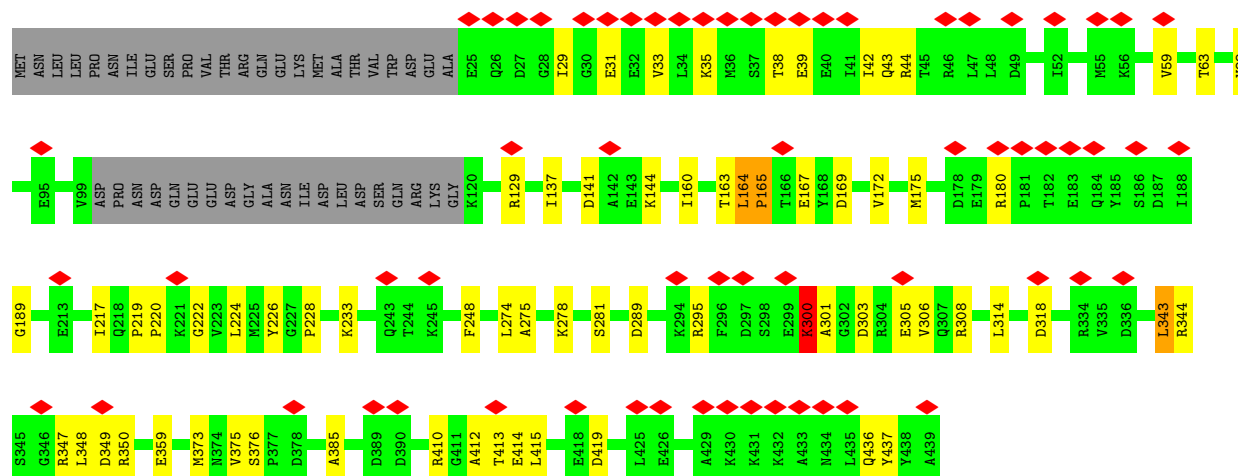
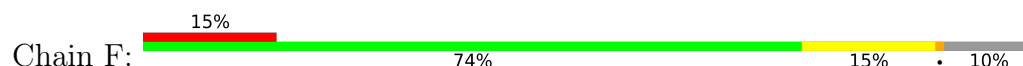




• Molecule 5: Proteasome 26S subunit, ATPase 6



• Molecule 6: 26S proteasome regulatory subunit 6A

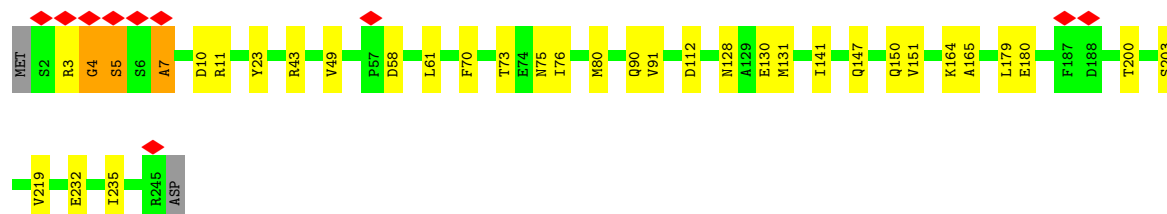
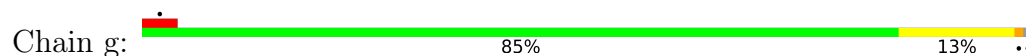


• Molecule 7: Proteasome subunit alpha type-6

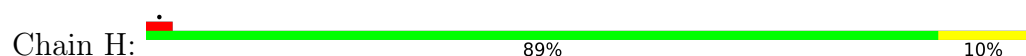




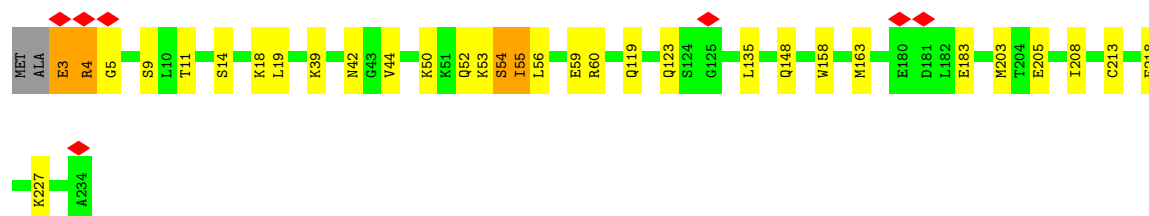
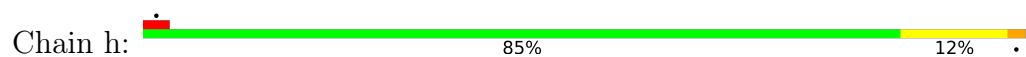
- Molecule 7: Proteasome subunit alpha type-6



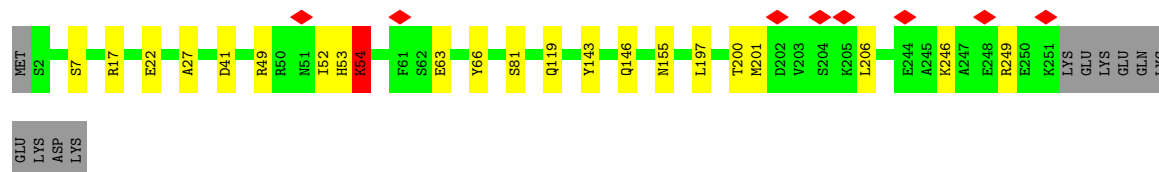
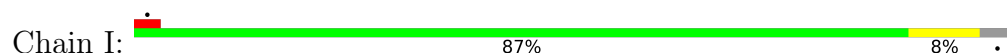
- Molecule 8: Proteasome subunit alpha type-2



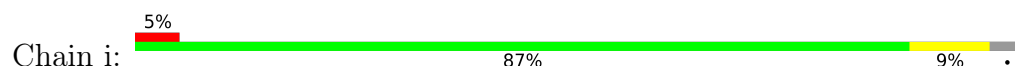
- Molecule 8: Proteasome subunit alpha type-2



- Molecule 9: Proteasome subunit alpha type-4

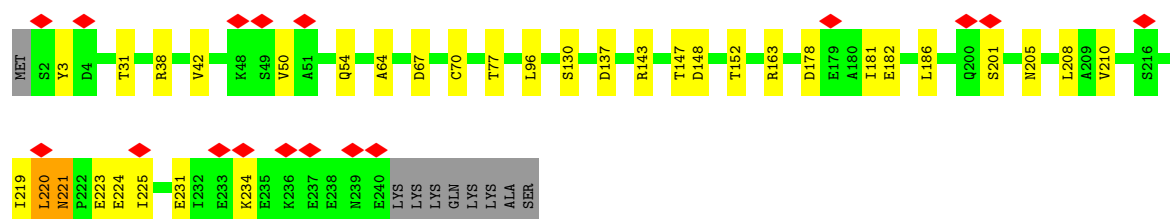
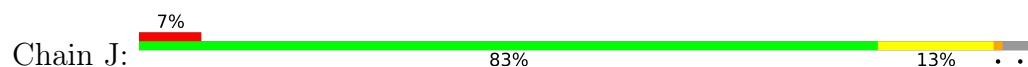


- Molecule 9: Proteasome subunit alpha type-4

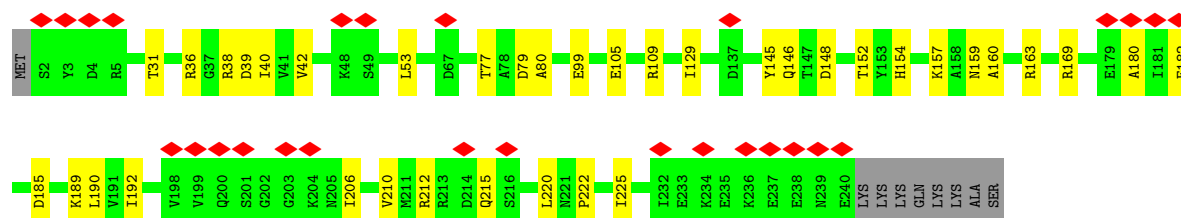
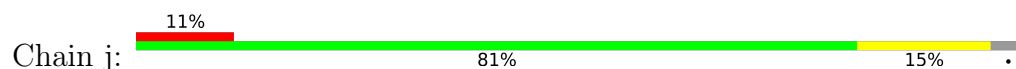




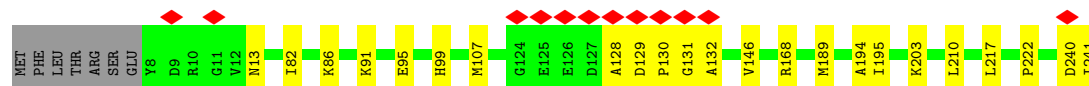
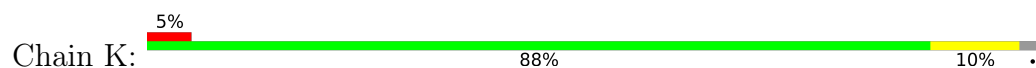
- Molecule 10: Proteasome subunit alpha type-7



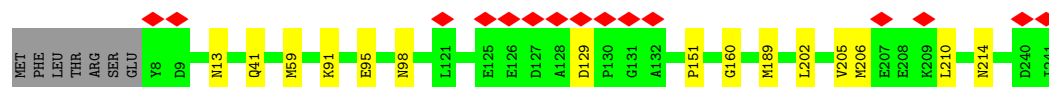
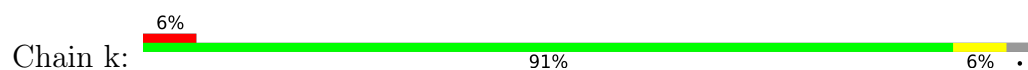
- Molecule 10: Proteasome subunit alpha type-7



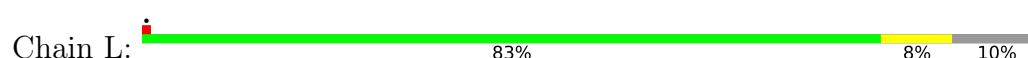
- Molecule 11: Proteasome subunit alpha type-5

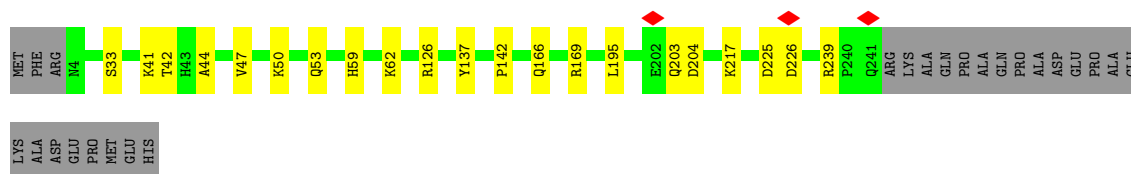


- Molecule 11: Proteasome subunit alpha type-5

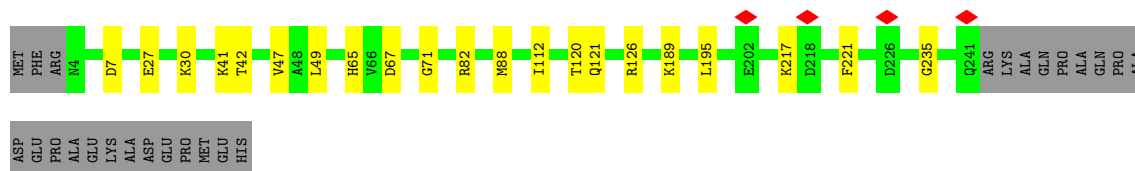
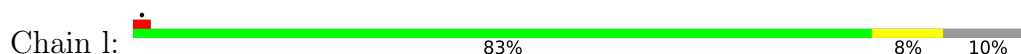


- Molecule 12: Proteasome subunit alpha type-1

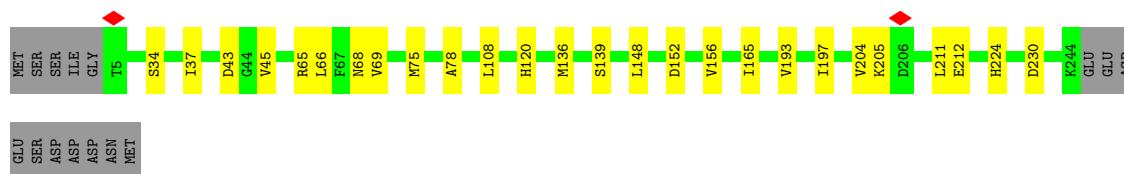
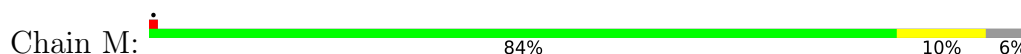




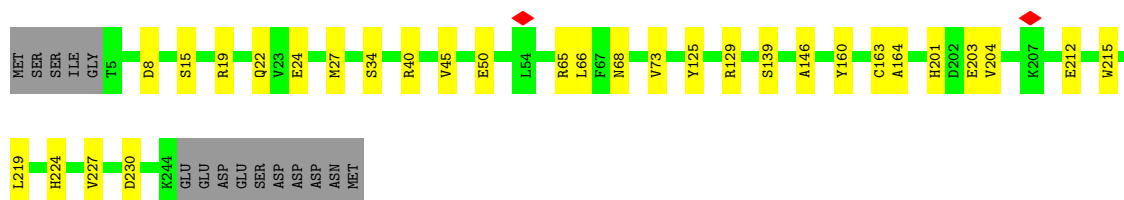
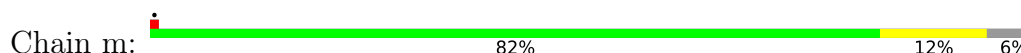
• Molecule 12: Proteasome subunit alpha type-1



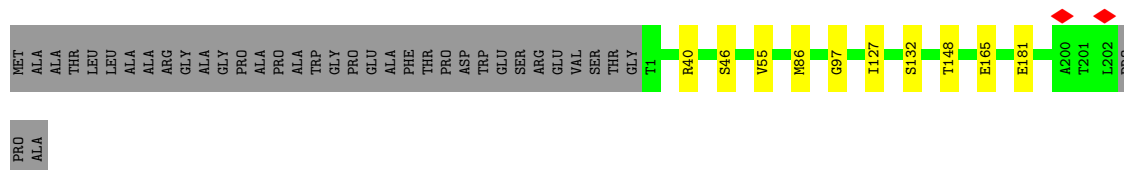
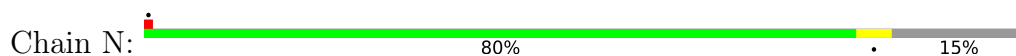
• Molecule 13: Proteasome subunit alpha type-3



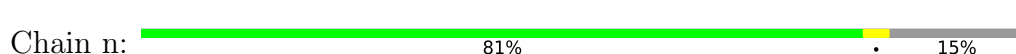
• Molecule 13: Proteasome subunit alpha type-3

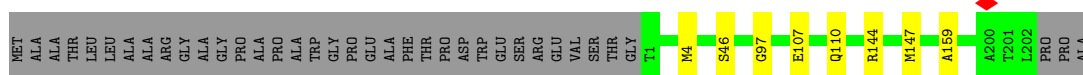


• Molecule 14: Proteasome subunit beta type-6



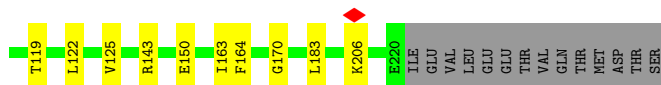
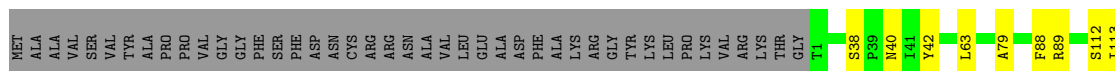
• Molecule 14: Proteasome subunit beta type-6





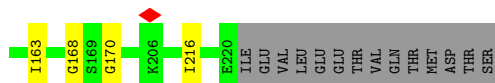
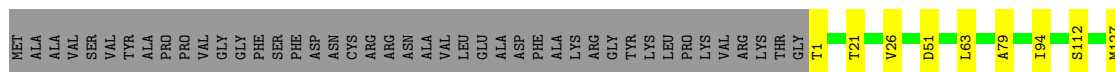
- Molecule 15: Proteasome subunit beta type-7

Chain O:
73% 7% 21%



- Molecule 15: Proteasome subunit beta type-7

Chain o:
75% 5% 21%



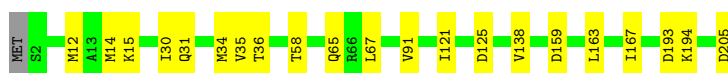
- Molecule 16: Proteasome subunit beta type-3

Chain P:
91% 8%



- Molecule 16: Proteasome subunit beta type-3

Chain p:
89% 10%



- Molecule 17: Proteasome subunit beta type-2

Chain Q:
89% 10%



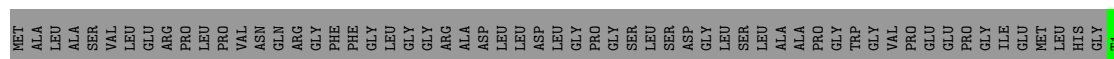
- Molecule 17: Proteasome subunit beta type-2

Chain q:
92% 7%



- Molecule 18: Proteasome subunit beta type-5

Chain R: 70% 6% 24%



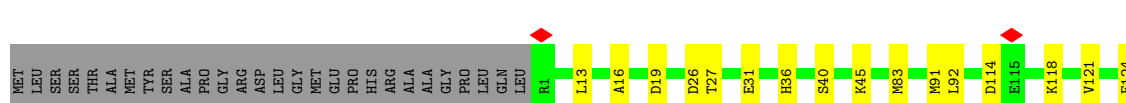
- Molecule 18: Proteasome subunit beta type-5

Chain r: 68% 8% 24%



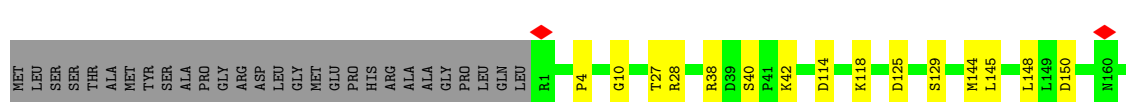
- Molecule 19: Proteasome subunit beta type-1

Chain S: 78% 10% 12%



- Molecule 19: Proteasome subunit beta type-1

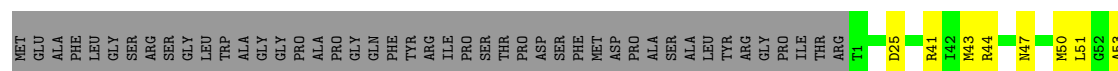
Chain s: 78% 10% 12%



- Molecule 20: Proteasome subunit beta type-4

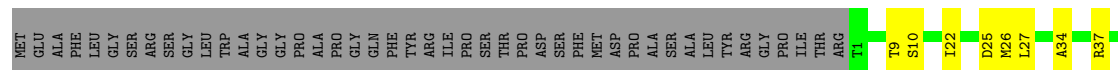
Chain T: 75% 7% 18%





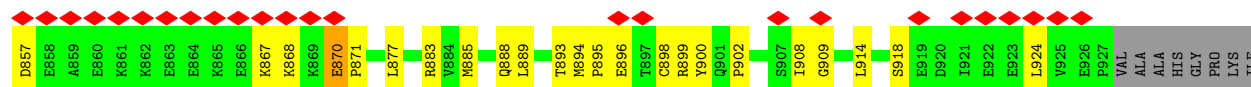
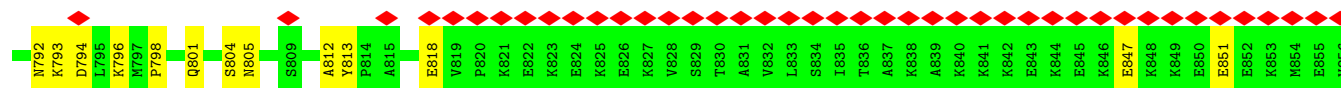
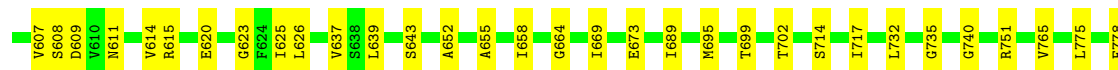
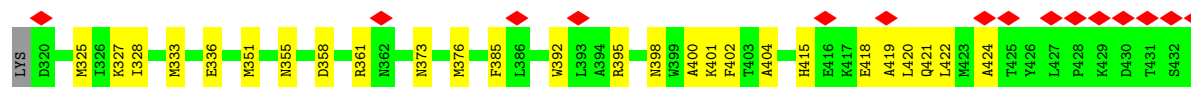
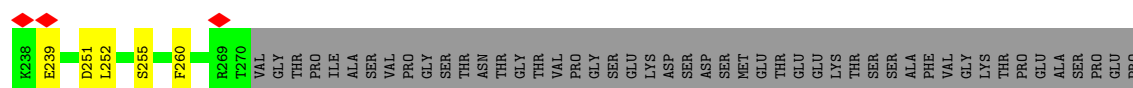
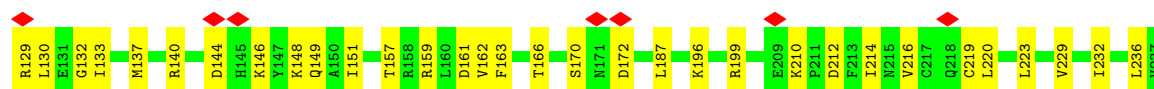
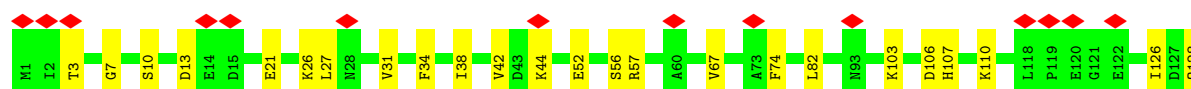
• Molecule 20: Proteasome subunit beta type-4

Chain t: 74% 8% 18%



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

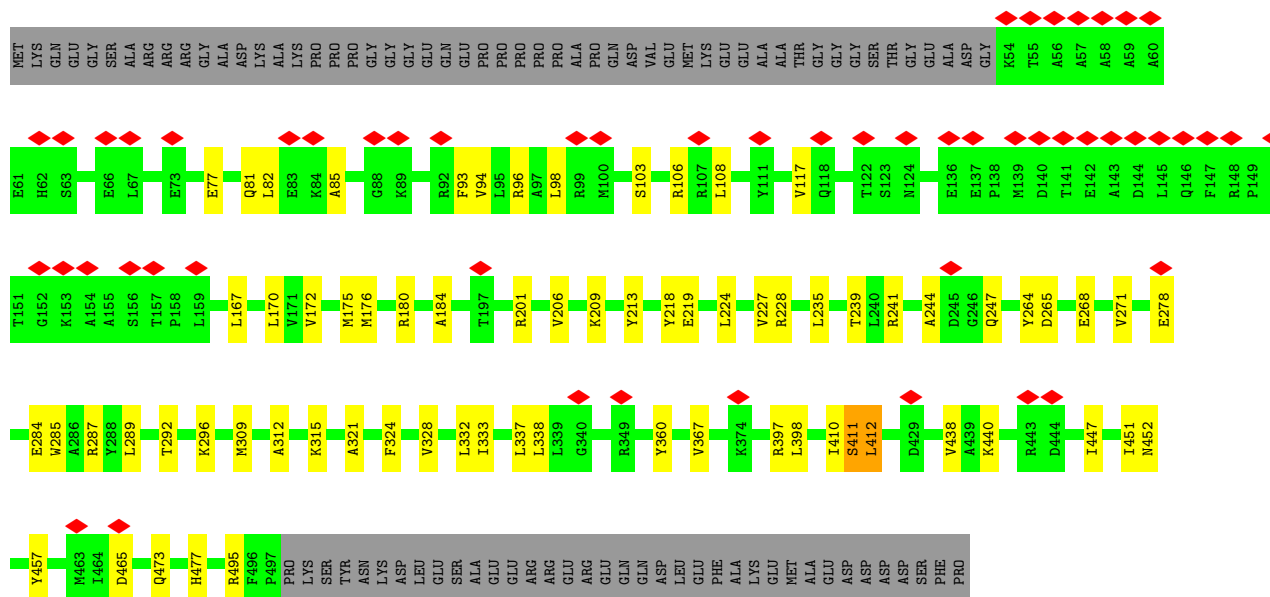
Chain U: 11% 73% 19% 8%



GLU
GLU
GLU
GLU
GLN
GLU
PRO
GLU
PRO
PHE
GLU
TYR
ASP
ASP

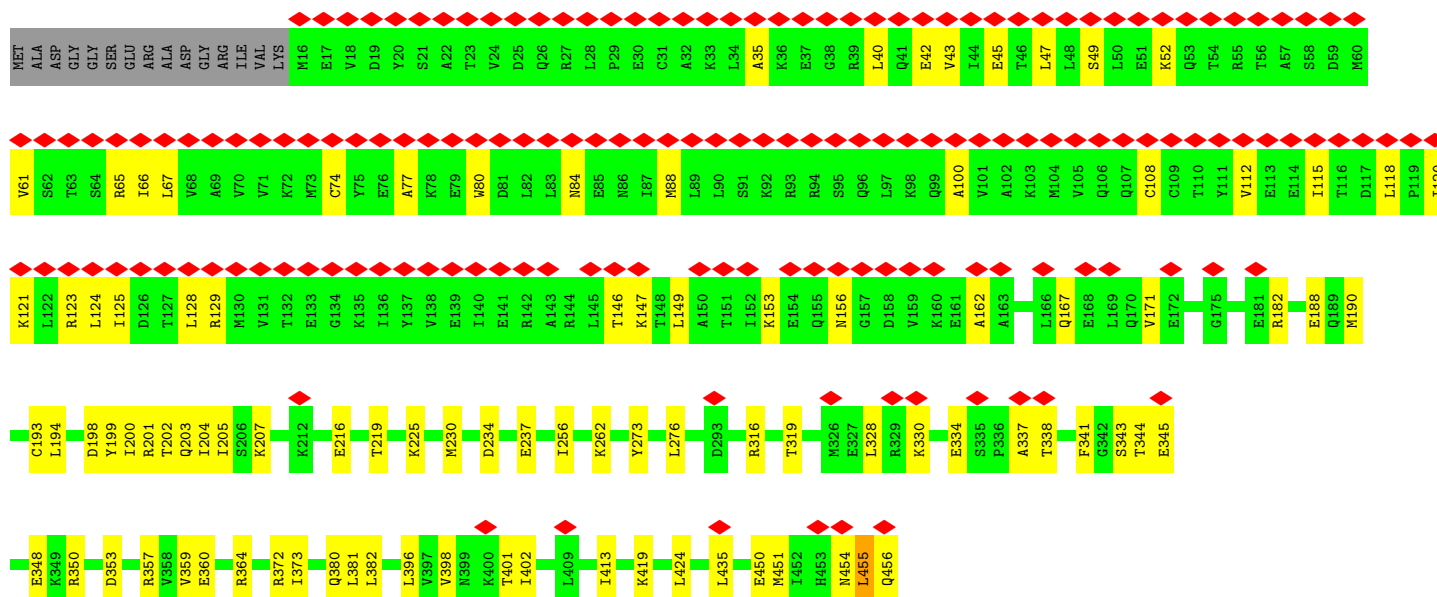
• Molecule 22: 26S proteasome non-ATPase regulatory subunit 3

Chain V: 10% 70% 13% 17%



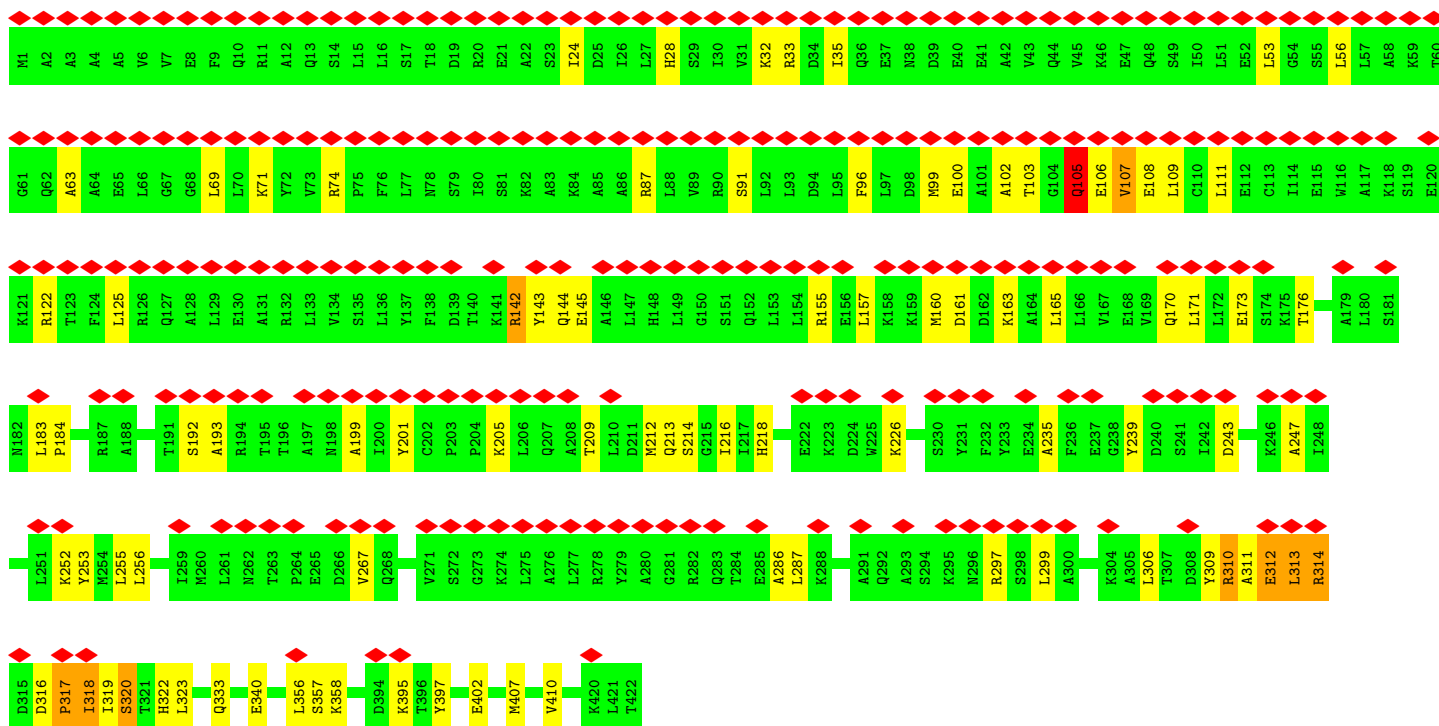
• Molecule 23: 26S proteasome non-ATPase regulatory subunit 12

Chain W: 36% 75% 21%

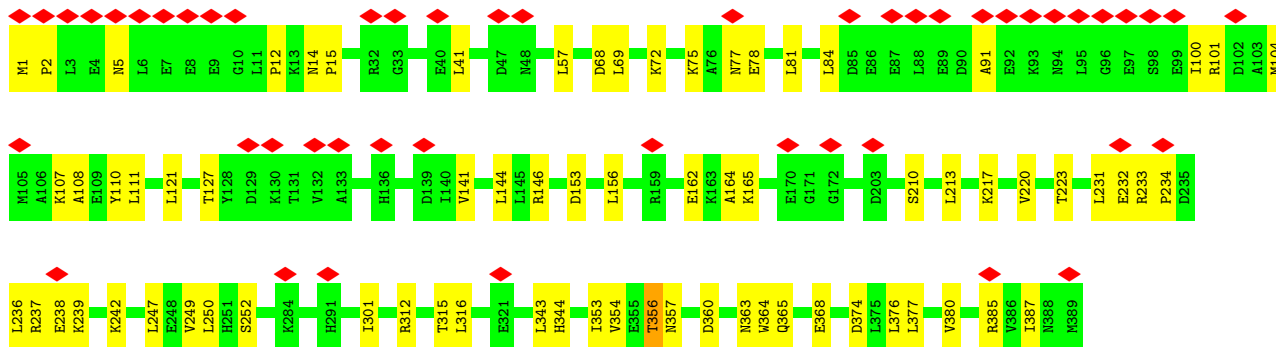
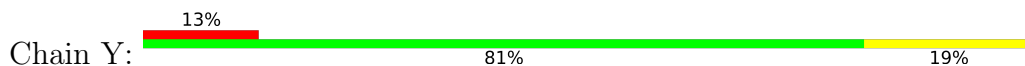


• Molecule 24: 26S proteasome non-ATPase regulatory subunit 11

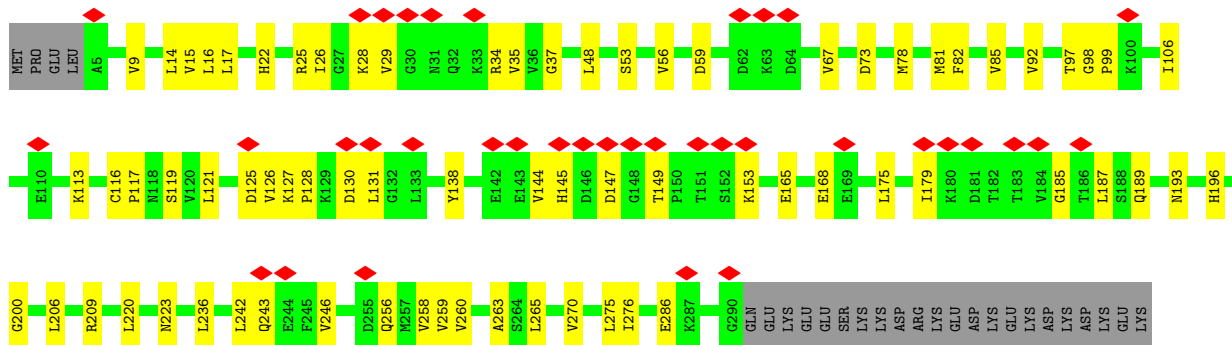
Chain X: 60% 78% 19%

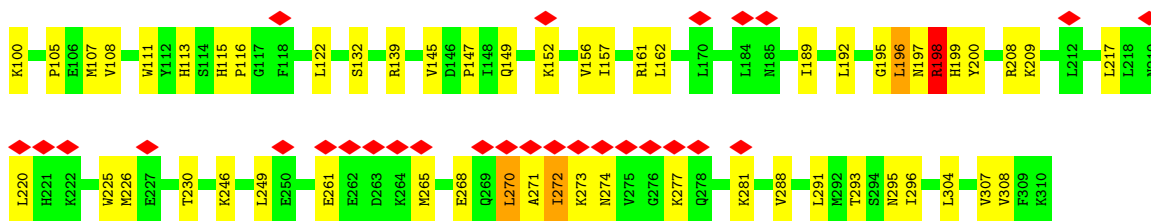


• Molecule 25: 26S proteasome non-ATPase regulatory subunit 6

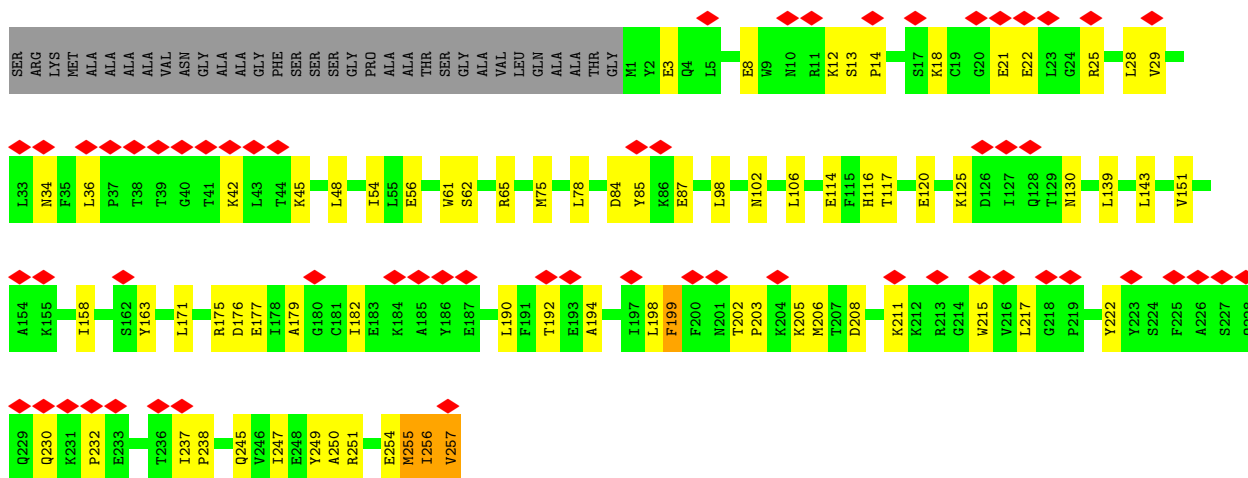
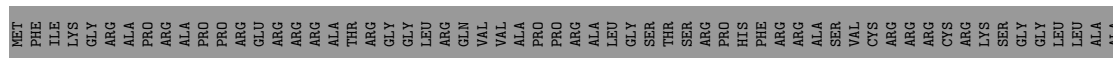


• Molecule 26: 26S proteasome non-ATPase regulatory subunit 7

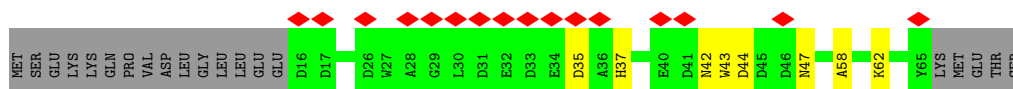




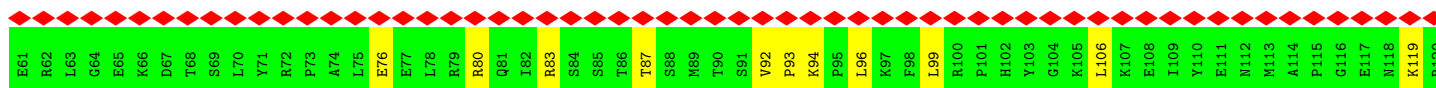
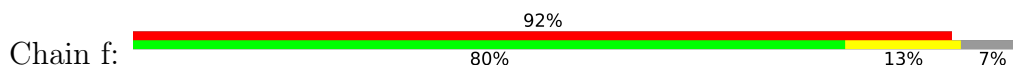
- Molecule 30: 26S proteasome non-ATPase regulatory subunit 8



- Molecule 31: 26S proteasome complex subunit SEM1

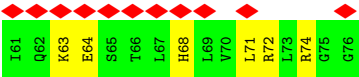
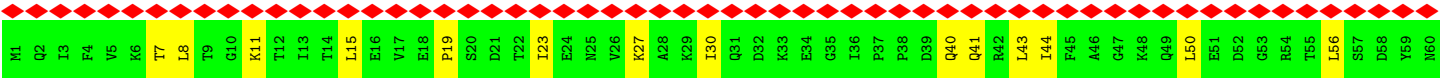


- Molecule 32: 26S proteasome non-ATPase regulatory subunit 2

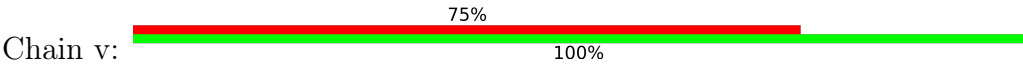


- Molecule 33: Ubiquitin

Chain u:



● Molecule 34: Substrate



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68506	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	0.022	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00603	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: MG, ATP, ADP, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.21	0/3185	0.52	2/4299 (0.0%)
2	B	0.20	0/3168	0.57	4/4276 (0.1%)
3	C	0.22	0/3146	0.53	0/4226
4	D	0.25	0/3090	0.61	3/4168 (0.1%)
5	E	0.25	0/3145	0.57	4/4233 (0.1%)
6	F	0.24	0/3137	0.54	0/4223
7	G	0.26	0/1923	0.47	0/2601
7	g	0.28	0/1914	0.48	0/2590
8	H	0.27	0/1844	0.49	0/2499
8	h	0.26	0/1844	0.44	0/2497
9	I	0.27	0/1991	0.53	1/2685 (0.0%)
9	i	0.24	0/1985	0.47	1/2677 (0.0%)
10	J	0.26	0/1906	0.51	0/2573
10	j	0.23	0/1887	0.48	0/2549
11	K	0.26	0/1804	0.44	0/2436
11	k	0.23	0/1809	0.43	0/2444
12	L	0.24	0/1901	0.42	0/2570
12	l	0.25	0/1896	0.45	0/2565
13	M	0.23	0/1911	0.40	0/2573
13	m	0.24	0/1916	0.42	0/2580
14	N	0.26	0/1540	0.41	0/2085
14	n	0.26	0/1536	0.39	0/2080
15	O	0.27	0/1676	0.44	0/2271
15	o	0.26	0/1686	0.43	0/2282
16	P	0.27	0/1616	0.50	0/2180
16	p	0.26	0/1620	0.45	0/2184
17	Q	0.27	0/1621	0.40	0/2194
17	q	0.27	0/1621	0.42	0/2194
18	R	0.28	0/1590	0.45	0/2147
18	r	0.29	0/1590	0.45	0/2147
19	S	0.27	0/1671	0.46	0/2252
19	s	0.27	0/1684	0.49	0/2268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	T	0.26	0/1716	0.42	0/2323
20	t	0.27	0/1720	0.43	0/2328
21	U	0.24	0/6984	0.54	0/9435
22	V	0.20	0/3681	0.45	0/4969
23	W	0.21	0/3644	0.50	0/4901
24	X	0.27	0/3381	0.56	1/4558 (0.0%)
25	Y	0.23	0/3261	0.53	1/4393 (0.0%)
26	Z	0.25	0/2324	0.62	3/3150 (0.1%)
27	a	0.22	0/3053	0.57	0/4133
28	b	0.19	0/1478	0.51	0/2001
29	c	0.28	0/2302	0.63	0/3110
30	d	0.26	0/2162	0.59	0/2919
31	e	0.25	0/437	0.69	0/595
32	f	0.19	0/6640	0.49	0/8988
33	u	0.18	0/607	0.44	0/816
All	All	0.24	0/108243	0.50	20/146167 (0.0%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	X	317	PRO	N-CA-C	-9.30	99.93	112.48
5	E	116	ASP	CA-C-N	8.87	130.93	119.84
5	E	116	ASP	C-N-CA	8.87	130.93	119.84
2	B	86	LYS	CA-C-N	8.84	130.89	119.84
2	B	86	LYS	C-N-CA	8.84	130.89	119.84
25	Y	356	THR	N-CA-C	8.71	123.35	110.46
4	D	153	MET	N-CA-C	6.24	117.96	111.03
1	A	115	VAL	N-CA-C	-6.13	106.75	113.43
1	A	159	PRO	N-CA-C	-6.12	99.86	112.47
9	I	52	ILE	N-CA-C	-5.94	107.13	112.12
2	B	178	LYS	CA-C-N	5.90	128.59	120.39
2	B	178	LYS	C-N-CA	5.90	128.59	120.39
26	Z	92	VAL	N-CA-C	-5.49	108.50	113.71
26	Z	179	ILE	CA-C-N	5.33	131.72	121.54
26	Z	179	ILE	C-N-CA	5.33	131.72	121.54
4	D	153	MET	CA-C-N	-5.04	114.40	122.17
4	D	153	MET	C-N-CA	-5.04	114.40	122.17
9	i	241	GLU	N-CA-CB	5.04	118.61	110.40
5	E	302	ASP	CA-C-N	5.01	128.27	120.60
5	E	302	ASP	C-N-CA	5.01	128.27	120.60

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	3135	0	3175	73	0
2	B	3122	0	3174	76	0
3	C	3105	0	3219	51	0
4	D	3040	0	3076	62	0
5	E	3097	0	3173	68	0
6	F	3098	0	3187	55	0
7	G	1889	0	1885	12	0
7	g	1880	0	1875	24	0
8	H	1805	0	1784	16	0
8	h	1805	0	1798	20	0
9	I	1958	0	1960	13	0
9	i	1955	0	1955	14	0
10	J	1880	0	1892	25	0
10	j	1861	0	1865	25	0
11	K	1777	0	1762	14	0
11	k	1782	0	1766	11	0
12	L	1866	0	1852	14	0
12	l	1861	0	1839	15	0
13	M	1876	0	1861	15	0
13	m	1881	0	1868	21	0
14	N	1514	0	1487	5	0
14	n	1510	0	1483	4	0
15	O	1649	0	1659	11	0
15	o	1659	0	1681	8	0
16	P	1587	0	1598	13	0
16	p	1591	0	1609	18	0
17	Q	1588	0	1584	16	0
17	q	1588	0	1584	11	0
18	R	1559	0	1523	11	0
18	r	1559	0	1523	14	0
19	S	1641	0	1639	15	0
19	s	1654	0	1656	14	0
20	T	1683	0	1662	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	t	1687	0	1666	13	0
21	U	6867	0	6929	120	0
22	V	3612	0	3682	46	0
23	W	3596	0	3713	61	0
24	X	3335	0	3435	82	0
25	Y	3202	0	3204	61	0
26	Z	2281	0	2312	52	0
27	a	2995	0	3012	46	0
28	b	1458	0	1505	29	0
29	c	2260	0	2276	59	0
30	d	2116	0	2146	50	0
31	e	425	0	328	5	0
32	f	6529	0	6541	72	0
33	u	601	0	629	13	0
34	v	120	0	32	0	0
35	A	27	0	12	2	0
35	F	27	0	12	1	0
36	C	31	0	12	3	0
36	D	31	0	12	1	0
36	E	31	0	12	3	0
37	C	1	0	0	0	0
37	D	1	0	0	0	0
37	E	1	0	0	0	0
38	c	1	0	0	0	0
All	All	106690	0	107124	1327	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 (1327) 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)
24:X:142:ARG:HG2	24:X:145:GLU:OE2	1.43	1.16
25:Y:236:LEU:HD12	25:Y:239:LYS:HZ1	1.22	1.02
24:X:317:PRO:HD2	24:X:319:ILE:HG12	1.42	1.00
24:X:183:LEU:HB3	24:X:184:PRO:HD3	1.43	0.98
23:W:451:MET:HE3	23:W:455:LEU:HD11	1.45	0.96
2:B:88:LEU:HD22	2:B:91:LYS:HG2	1.50	0.92
6:F:163:THR:HG22	6:F:165:PRO:HD3	1.51	0.92
22:V:411:SER:HB3	22:V:447:ILE:HG12	1.54	0.88
24:X:107:VAL:O	24:X:111:LEU:HD13	1.74	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:236:LEU:HD12	25:Y:239:LYS:NZ	1.91	0.84
24:X:309:TYR:HB2	24:X:313:LEU:HD23	1.60	0.84
24:X:102:ALA:O	24:X:106:GLU:HG2	1.78	0.83
24:X:318:ILE:HG22	24:X:322:HIS:HE1	1.43	0.82
22:V:397:ARG:HH21	30:d:116:HIS:HB3	1.46	0.80
10:J:221:ASN:HD21	10:J:223:GLU:HB3	1.45	0.80
21:U:140:ARG:O	21:U:144:ASP:HB2	1.83	0.79
25:Y:236:LEU:CD1	25:Y:239:LYS:HZ1	1.96	0.78
25:Y:236:LEU:CD1	25:Y:239:LYS:NZ	2.48	0.77
27:a:284:ARG:HD3	27:a:288:HIS:H	1.51	0.76
3:C:77:VAL:HG22	3:C:111:ASN:H	1.52	0.75
2:B:368:HIS:ND1	2:B:395:ILE:HB	2.02	0.74
2:B:368:HIS:HE1	2:B:392:GLY:O	1.70	0.74
29:c:268:GLU:OE2	29:c:271:ALA:HB2	1.88	0.74
20:t:22:ILE:HG12	20:t:50:MET:HE3	1.69	0.72
6:F:343:LEU:O	6:F:349:ASP:N	2.22	0.72
1:A:158:ASP:HB2	1:A:160:THR:HG22	1.70	0.71
24:X:309:TYR:HB3	24:X:312:GLU:HB2	1.72	0.71
4:D:45:LYS:HG2	21:U:187:LEU:HD13	1.72	0.71
10:J:208:LEU:HB3	10:J:220:LEU:HB2	1.72	0.71
19:s:4:PRO:HB2	20:t:100:ARG:HH21	1.54	0.71
26:Z:206:LEU:HD13	26:Z:209:ARG:HH12	1.55	0.71
9:I:143:TYR:HB2	9:I:146:GLN:HE21	1.56	0.70
29:c:79:GLY:HA3	29:c:84:VAL:HA	1.73	0.70
24:X:102:ALA:C	24:X:106:GLU:HG2	2.16	0.70
8:h:55:ILE:O	8:h:55:ILE:HG13	1.92	0.70
1:A:165:GLN:NE2	1:A:236:CYS:SG	2.65	0.70
2:B:368:HIS:CE1	2:B:392:GLY:O	2.45	0.70
27:a:243:GLY:HA3	27:a:279:GLU:HG3	1.74	0.69
10:J:221:ASN:HD22	10:J:224:GLU:HG3	1.58	0.69
28:b:161:ASN:HD21	28:b:168:SER:H	1.41	0.69
12:l:27:GLU:HA	12:l:30:LYS:HD2	1.75	0.68
1:A:158:ASP:HB2	1:A:160:THR:CG2	2.23	0.68
1:A:363:SER:H	2:B:214:MET:HB2	1.59	0.68
2:B:86:LYS:HD2	2:B:86:LYS:O	1.93	0.68
36:D:501:ATP:O1G	5:E:294:ARG:NH2	2.27	0.68
5:E:247:THR:O	5:E:249:ALA:N	2.26	0.68
26:Z:256:GLN:O	29:c:295:ASN:ND2	2.27	0.67
10:j:36:ARG:HH21	10:j:157:LYS:HG2	1.58	0.67
29:c:75:MET:HE3	29:c:87:VAL:HG22	1.75	0.67
4:D:231:VAL:HB	4:D:234:GLU:HB2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:318:ILE:HG22	24:X:322:HIS:CE1	2.29	0.66
11:k:210:LEU:HA	11:k:214:ASN:HD21	1.60	0.66
29:c:107:MET:HE3	29:c:108:VAL:HG22	1.75	0.66
32:f:833:PHE:HB3	32:f:837:LEU:HA	1.77	0.66
6:F:172:VAL:HA	6:F:175:MET:HE2	1.77	0.66
19:S:148:LEU:HD23	19:S:178:VAL:HG12	1.77	0.66
25:Y:238:GLU:HA	25:Y:242:LYS:HB2	1.78	0.66
26:Z:263:ALA:HB1	29:c:288:VAL:HG13	1.78	0.66
11:K:130:PRO:C	11:K:132:ALA:H	2.03	0.65
29:c:261:GLU:HG2	29:c:265:MET:HE1	1.78	0.65
4:D:148:ASP:HA	5:E:61:LEU:HD13	1.77	0.65
25:Y:220:VAL:HG21	25:Y:249:VAL:HG21	1.79	0.65
25:Y:236:LEU:HG	25:Y:239:LYS:NZ	2.11	0.65
29:c:85:GLU:HA	33:u:74:ARG:HG3	1.78	0.65
27:a:347:LYS:HD3	27:a:350:LYS:HZ1	1.61	0.64
26:Z:145:HIS:HB3	26:Z:149:THR:OG1	1.97	0.64
6:F:137:ILE:HG23	6:F:160:ILE:HD12	1.77	0.64
10:J:208:LEU:HD22	10:J:220:LEU:HG	1.80	0.64
8:h:135:LEU:HG	8:h:163:MET:HE2	1.80	0.64
4:D:85:ILE:HG13	29:c:152:LYS:HE2	1.78	0.64
22:V:292:THR:HG22	22:V:296:LYS:HE2	1.80	0.64
4:D:67:ASN:HD22	21:U:607:VAL:HG12	1.62	0.64
17:Q:65:GLN:HA	17:Q:68:LYS:HE3	1.79	0.64
21:U:801:GLN:HB3	21:U:877:LEU:HB3	1.80	0.64
22:V:309:MET:HE1	22:V:332:LEU:HB2	1.80	0.63
1:A:157:ILE:O	1:A:158:ASP:C	2.41	0.63
6:F:35:LYS:HD3	6:F:39:GLU:H	1.63	0.63
4:D:229:ARG:NH1	5:E:268:ASP:OD1	2.32	0.63
5:E:345:ASN:ND2	6:F:349:ASP:OD2	2.31	0.63
10:J:96:LEU:HB2	17:Q:62:LYS:HE3	1.79	0.63
24:X:142:ARG:HG2	24:X:145:GLU:CD	2.22	0.63
10:J:38:ARG:HH21	10:J:181:ILE:HG13	1.63	0.63
23:W:61:VAL:O	23:W:65:ARG:NH1	2.32	0.63
23:W:401:THR:HG23	23:W:402:ILE:HD12	1.80	0.63
24:X:106:GLU:HA	24:X:106:GLU:OE1	1.99	0.63
21:U:796:LYS:HA	21:U:924:LEU:HD11	1.81	0.63
23:W:199:TYR:O	23:W:203:GLN:HB2	1.99	0.63
11:k:13:ASN:HB2	12:l:126:ARG:HG2	1.80	0.63
32:f:76:GLU:HB3	32:f:80:ARG:HH21	1.62	0.63
20:t:27:LEU:HD11	20:t:34:ALA:HB1	1.81	0.63
21:U:751:ARG:NH1	21:U:908:ILE:O	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:38:THR:HG22	6:F:39:GLU:HG2	1.81	0.62
15:O:163:ILE:HG12	15:O:170:GLY:HA2	1.80	0.62
21:U:522:GLY:O	21:U:559:ARG:NH2	2.31	0.62
23:W:188:GLU:OE2	23:W:225:LYS:NZ	2.32	0.62
28:b:26:LEU:HD11	28:b:80:PRO:HG3	1.81	0.62
7:g:128:ASN:HB2	7:g:131:MET:HE1	1.81	0.62
21:U:133:ILE:HG12	21:U:137:MET:HE1	1.81	0.62
21:U:216:VAL:HA	21:U:220:LEU:HB2	1.81	0.62
27:a:35:HIS:NE2	28:b:14:GLU:O	2.33	0.62
28:b:100:ARG:NH1	28:b:102:GLY:O	2.32	0.62
19:s:148:LEU:HD23	19:s:178:VAL:HG12	1.80	0.62
1:A:255:ARG:HG3	1:A:258:ARG:HH21	1.65	0.62
2:B:272:ARG:O	2:B:276:GLU:HB2	2.00	0.62
23:W:198:ASP:O	23:W:202:THR:N	2.20	0.62
26:Z:126:VAL:HG13	26:Z:127:LYS:HD3	1.82	0.62
23:W:328:LEU:HD13	23:W:337:ALA:HB1	1.82	0.62
23:W:345:GLU:HA	23:W:348:GLU:HB3	1.82	0.62
1:A:330:ALA:O	1:A:336:ARG:NH1	2.33	0.62
27:a:321:LYS:HE2	27:a:336:VAL:HG21	1.82	0.62
12:l:121:GLN:HG3	13:m:129:ARG:HG2	1.82	0.62
1:A:178:GLY:H	35:A:501:ADP:HN62	1.47	0.61
11:K:189:MET:HE2	11:K:194:ALA:HA	1.81	0.61
4:D:103:VAL:HG11	4:D:139:LEU:HD21	1.82	0.61
5:E:352:MET:HA	5:E:355:ILE:HD12	1.82	0.61
21:U:625:ILE:HG13	21:U:626:LEU:HG	1.82	0.61
24:X:253:TYR:OH	24:X:317:PRO:HB2	1.99	0.61
29:c:268:GLU:OE2	29:c:271:ALA:CB	2.47	0.61
2:B:408:ARG:NH1	3:C:163:GLU:OE1	2.32	0.61
21:U:373:ASN:HA	21:U:376:MET:HE3	1.83	0.61
3:C:298:ILE:HG23	3:C:301:LEU:HD21	1.81	0.61
5:E:197:LYS:HZ3	5:E:199:VAL:HG12	1.66	0.61
24:X:173:GLU:HA	24:X:176:THR:HG22	1.82	0.61
24:X:255:LEU:HD22	24:X:267:VAL:HG13	1.81	0.61
25:Y:236:LEU:CG	25:Y:239:LYS:NZ	2.63	0.61
16:p:65:GLN:OE1	17:q:86:ARG:NH2	2.34	0.61
25:Y:231:LEU:HD21	25:Y:236:LEU:HD12	1.81	0.61
32:f:781:TYR:HB3	32:f:785:ARG:HA	1.83	0.61
10:j:192:ILE:HD12	10:j:206:ILE:HD12	1.81	0.61
4:D:370:ILE:HG23	4:D:374:ASP:HB2	1.83	0.61
32:f:96:LEU:HD12	32:f:132:THR:HG23	1.83	0.61
2:B:88:LEU:HD22	2:B:91:LYS:H	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:885:MET:HB2	21:U:888:GLN:HG2	1.83	0.60
2:B:186:ASP:O	2:B:363:ARG:NH1	2.34	0.60
24:X:213:GLN:HA	24:X:216:ILE:HB	1.83	0.60
24:X:306:LEU:HA	24:X:313:LEU:HD21	1.83	0.60
25:Y:231:LEU:HD21	25:Y:239:LYS:HZ1	1.65	0.60
26:Z:165:GLU:H	26:Z:168:GLU:HB3	1.66	0.60
1:A:73:ALA:O	1:A:78:TRP:NE1	2.35	0.60
10:J:42:VAL:HG22	10:J:210:VAL:HG12	1.83	0.60
21:U:664:GLY:HA2	21:U:695:MET:HE1	1.84	0.60
28:b:55:ALA:HB1	28:b:82:GLY:HA3	1.84	0.60
7:g:43:ARG:HH21	7:g:164:LYS:HG2	1.65	0.60
1:A:112:ILE:HG12	1:A:122:VAL:HG22	1.83	0.60
5:E:235:ILE:HG13	5:E:277:MET:HE3	1.84	0.60
18:R:19:ARG:NH2	16:p:205:ASP:OD1	2.34	0.60
22:V:278:GLU:HA	22:V:285:TRP:HZ2	1.66	0.60
26:Z:187:LEU:HG	29:c:293:THR:HG22	1.83	0.60
27:a:255:TRP:O	27:a:258:GLN:NE2	2.31	0.60
5:E:67:GLU:OE2	5:E:89:LYS:NZ	2.34	0.60
27:a:182:CYS:SG	27:a:183:VAL:N	2.74	0.60
32:f:378:ASN:OD1	32:f:382:ASN:ND2	2.35	0.60
18:R:90:TYR:HA	18:R:93:MET:HE3	1.83	0.60
29:c:192:LEU:HA	29:c:196:LEU:HB2	1.82	0.60
11:K:91:LYS:NZ	11:K:95:GLU:OE2	2.34	0.60
28:b:25:ARG:NH1	28:b:145:GLU:OE1	2.34	0.60
25:Y:217:LYS:NZ	25:Y:249:VAL:O	2.34	0.59
4:D:267:ILE:HB	4:D:311:THR:HG22	1.84	0.59
24:X:214:SER:O	24:X:218:HIS:ND1	2.35	0.59
8:h:59:GLU:HG2	8:h:60:ARG:HD2	1.84	0.59
21:U:792:ASN:HB3	21:U:914:LEU:H	1.67	0.59
23:W:198:ASP:HB3	23:W:201:ARG:HB3	1.84	0.59
25:Y:210:SER:HB3	25:Y:213:LEU:HD23	1.84	0.59
30:d:78:LEU:HD13	30:d:98:LEU:HD21	1.83	0.59
1:A:413:VAL:HG13	1:A:417:ILE:HD12	1.84	0.59
23:W:40:LEU:HD21	23:W:74:CYS:HA	1.84	0.59
21:U:251:ASP:O	21:U:255:SER:HB3	2.02	0.59
22:V:477:HIS:HD1	30:d:249:TYR:HH	1.50	0.59
4:D:148:ASP:HB3	5:E:78:ARG:NE	2.18	0.59
1:A:165:GLN:NE2	1:A:167:GLU:OE2	2.36	0.59
1:A:347:ASP:O	1:A:351:ARG:NH2	2.36	0.59
5:E:64:LEU:HG	5:E:65:THR:HG23	1.84	0.59
9:i:180:LYS:HB2	9:i:184:MET:HE3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:318:ASP:OD1	6:F:347:ARG:NH1	2.35	0.59
1:A:156:LYS:O	1:A:157:ILE:C	2.46	0.58
21:U:765:VAL:HG11	21:U:778:PHE:HD2	1.68	0.58
32:f:679:LEU:HB2	32:f:690:VAL:HG11	1.85	0.58
15:o:163:ILE:HG12	15:o:170:GLY:HA2	1.84	0.58
3:C:135:VAL:HG12	3:C:138:MET:HE3	1.84	0.58
5:E:75:ASN:ND2	6:F:129:ARG:O	2.36	0.58
5:E:291:ARG:HH21	5:E:294:ARG:HH21	1.51	0.58
21:U:896:GLU:O	21:U:899:ARG:NH2	2.36	0.58
7:g:141:ILE:HG22	7:g:151:VAL:HG22	1.85	0.58
10:j:38:ARG:NH2	10:j:182:GLU:O	2.36	0.58
5:E:135:ILE:HD11	5:E:138:LEU:HD23	1.85	0.58
28:b:22:LEU:HD23	28:b:177:PRO:HG3	1.84	0.58
30:d:25:ARG:HE	30:d:28:LEU:HD12	1.68	0.58
32:f:240:VAL:O	32:f:245:ASN:ND2	2.34	0.58
11:k:41:GLN:NE2	11:k:151:PRO:O	2.37	0.58
12:l:189:LYS:NZ	12:l:235:GLY:O	2.36	0.58
2:B:259:TYR:HB2	2:B:262:ASP:HB2	1.86	0.58
24:X:320:SER:HA	24:X:323:LEU:HD12	1.85	0.58
26:Z:185:GLY:HA3	26:Z:189:GLN:HB3	1.84	0.58
16:p:12:MET:HB2	16:p:138:VAL:HG12	1.84	0.58
15:O:206:LYS:HD2	16:P:161:ASP:HB3	1.83	0.58
4:D:92:PHE:HA	4:D:103:VAL:HG12	1.86	0.58
26:Z:59:ASP:OD2	28:b:99:HIS:NE2	2.35	0.58
32:f:861:THR:HB	32:f:879:ARG:HH11	1.68	0.58
4:D:119:ILE:O	4:D:121:ARG:NH1	2.37	0.58
20:T:63:LEU:HD21	20:T:106:LEU:HD13	1.85	0.58
26:Z:34:ARG:NE	26:Z:97:THR:O	2.37	0.58
29:c:100:LYS:HG2	29:c:105:PRO:HB3	1.86	0.58
13:M:152:ASP:OD1	13:M:156:VAL:N	2.37	0.58
21:U:327:LYS:NZ	21:U:794:ASP:OD2	2.36	0.58
2:B:88:LEU:HD22	2:B:91:LYS:CG	2.30	0.57
29:c:89:PRO:HB2	33:u:44:ILE:HD11	1.86	0.57
24:X:310:ARG:HB3	24:X:314:ARG:HH21	1.70	0.57
15:o:1:THR:N	15:o:168:GLY:O	2.38	0.57
16:P:65:GLN:OE1	17:Q:86:ARG:NH2	2.37	0.57
24:X:256:LEU:HD13	24:X:319:ILE:HB	1.85	0.57
5:E:4:PRO:HG2	5:E:7:LYS:H	1.70	0.57
24:X:310:ARG:O	24:X:311:ALA:C	2.48	0.57
27:a:252:LYS:HA	27:a:255:TRP:HB3	1.87	0.57
3:C:198:LEU:HG	3:C:201:ARG:HH21	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:807:ARG:HA	32:f:811:LEU:HD12	1.87	0.57
19:S:27:THR:HB	19:S:40:SER:H	1.70	0.57
6:F:224:LEU:HB2	6:F:348:LEU:HD21	1.87	0.57
21:U:107:HIS:HA	21:U:110:LYS:HE3	1.87	0.57
24:X:96:PHE:CZ	24:X:109:LEU:HD12	2.39	0.57
26:Z:9:VAL:HG12	26:Z:48:LEU:HB3	1.86	0.57
26:Z:242:LEU:HG	26:Z:243:GLN:OE1	2.05	0.57
21:U:620:GLU:HA	21:U:655:ALA:HB2	1.87	0.56
24:X:310:ARG:HB3	24:X:314:ARG:HE	1.70	0.56
11:k:160:GLY:O	12:l:82:ARG:NH2	2.38	0.56
5:E:223:ARG:O	5:E:226:GLN:NE2	2.37	0.56
7:G:165:ALA:HB3	8:H:56:LEU:HD22	1.86	0.56
30:d:230:GLN:HG2	30:d:232:PRO:HD3	1.87	0.56
32:f:368:ALA:HA	32:f:371:ASN:HD21	1.69	0.56
3:C:41:ASN:OD1	3:C:44:ARG:NH2	2.38	0.56
5:E:198:VAL:HG12	5:E:200:SER:H	1.70	0.56
24:X:286:ALA:HB2	24:X:312:GLU:HB3	1.87	0.56
25:Y:236:LEU:O	25:Y:236:LEU:HD23	2.04	0.56
29:c:76:PRO:HG2	29:c:87:VAL:HG21	1.87	0.56
31:e:35:ASP:HB3	31:e:37:HIS:HD1	1.69	0.56
9:i:143:TYR:HB2	9:i:146:GLN:HE21	1.70	0.56
10:j:31:THR:OG1	10:j:163:ARG:O	2.23	0.56
1:A:86:THR:HG22	2:B:136:LEU:HD12	1.88	0.56
5:E:171:LEU:HB3	5:E:298:LYS:HG2	1.87	0.56
5:E:310:LEU:HG	5:E:314:LYS:HE3	1.87	0.56
15:O:143:ARG:NH2	15:O:150:GLU:OE1	2.39	0.56
8:h:14:SER:HB3	8:h:18:LYS:H	1.70	0.56
5:E:201:SER:O	6:F:308:ARG:NH2	2.38	0.56
5:E:265:ASP:OD2	5:E:291:ARG:NH2	2.39	0.56
12:l:88:MET:HE3	12:l:112:ILE:HG13	1.87	0.56
2:B:358:GLU:HG2	2:B:361:LYS:HD2	1.88	0.56
15:O:164:PHE:O	19:s:38:ARG:NH2	2.37	0.56
23:W:40:LEU:HD22	23:W:77:ALA:HB3	1.86	0.56
1:A:103:ASN:ND2	6:F:167:GLU:OE2	2.39	0.56
30:d:114:GLU:HA	30:d:117:THR:HG22	1.88	0.56
3:C:216:GLY:O	3:C:253:SER:OG	2.22	0.56
6:F:300:LYS:HD3	6:F:301:ALA:H	1.71	0.56
10:J:38:ARG:NH2	10:J:178:ASP:O	2.38	0.56
24:X:87:ARG:NH1	24:X:91:SER:OG	2.39	0.56
29:c:296:ILE:HG21	30:d:250:ALA:HB2	1.86	0.56
2:B:222:VAL:HB	2:B:328:ILE:HG12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:375:VAL:HG22	6:F:415:LEU:HD12	1.88	0.56
22:V:333:ILE:HG21	22:V:360:TYR:HB3	1.88	0.56
23:W:372:ARG:NH1	27:a:325:ASP:OD2	2.39	0.56
25:Y:78:GLU:HA	25:Y:81:LEU:HB2	1.88	0.56
27:a:8:LEU:HD11	27:a:26:GLU:HB3	1.87	0.56
27:a:205:LEU:O	27:a:271:LYS:NZ	2.38	0.56
10:j:42:VAL:HG22	10:j:210:VAL:HG22	1.88	0.56
25:Y:12:PRO:O	25:Y:146:ARG:NH1	2.38	0.56
26:Z:78:MET:HA	26:Z:81:MET:HG2	1.88	0.56
32:f:320:ILE:HA	32:f:325:GLN:HE22	1.70	0.56
32:f:531:ASN:O	32:f:565:ASN:ND2	2.38	0.56
5:E:244:SER:OG	5:E:245:GLU:N	2.39	0.55
26:Z:113:LYS:NZ	26:Z:117:PRO:O	2.31	0.55
32:f:402:ASN:HB2	32:f:407:MET:HB3	1.86	0.55
11:K:203:LYS:HB2	11:K:210:LEU:HD22	1.88	0.55
1:A:239:ARG:HG2	1:A:273:PHE:HD2	1.71	0.55
24:X:319:ILE:HG13	24:X:320:SER:N	2.19	0.55
1:A:245:LEU:HD21	1:A:298:THR:HG21	1.88	0.55
2:B:54:PRO:HA	32:f:854:GLY:HA3	1.88	0.55
3:C:406:LYS:NZ	9:I:66:TYR:OH	2.38	0.55
22:V:85:ALA:HB2	22:V:93:PHE:HB2	1.88	0.55
11:k:91:LYS:NZ	11:k:95:GLU:OE1	2.38	0.55
7:G:158:GLY:O	8:H:84:ARG:NH2	2.39	0.55
9:i:220:ASN:O	9:i:222:LYS:NZ	2.39	0.55
26:Z:17:LEU:HD11	29:c:217:LEU:HD12	1.88	0.55
29:c:198:ARG:HH11	29:c:199:HIS:CD2	2.25	0.55
17:q:1:MET:HE2	17:q:133:GLY:HA2	1.87	0.55
3:C:57:ARG:NH2	21:U:643:SER:O	2.40	0.55
22:V:98:LEU:HD21	22:V:206:VAL:HG22	1.88	0.55
22:V:289:LEU:HB3	22:V:312:ALA:HB2	1.89	0.55
2:B:88:LEU:CD2	2:B:91:LYS:HG2	2.32	0.55
12:L:203:GLN:O	12:L:239:ARG:NH2	2.40	0.55
22:V:284:GLU:OE2	22:V:287:ARG:NH1	2.38	0.55
25:Y:301:ILE:HD11	25:Y:343:LEU:HB2	1.88	0.55
15:o:112:SER:HB2	15:o:127:MET:HE3	1.88	0.55
1:A:122:VAL:HB	6:F:88:TYR:HB2	1.89	0.55
18:R:166:ARG:NH1	16:p:34:MET:O	2.39	0.55
21:U:894:MET:HE2	21:U:902:PRO:HG2	1.88	0.55
25:Y:231:LEU:CD2	25:Y:236:LEU:HD12	2.37	0.55
30:d:21:GLU:OE2	30:d:25:ARG:NH1	2.38	0.55
13:m:34:SER:OG	13:m:65:ARG:NH1	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:172:VAL:HG12	22:V:176:MET:HE2	1.88	0.54
32:f:547:GLU:O	32:f:551:LYS:NZ	2.41	0.54
10:j:99:GLU:OE2	18:r:120:ARG:NH2	2.40	0.54
13:m:203:GLU:HG2	13:m:204:VAL:HG13	1.89	0.54
1:A:239:ARG:HH21	1:A:241:ILE:HD11	1.73	0.54
3:C:368:MET:HG3	4:D:329:ARG:HH22	1.70	0.54
21:U:805:ASN:OD1	21:U:893:THR:OG1	2.25	0.54
25:Y:121:LEU:HD23	25:Y:144:LEU:HD22	1.89	0.54
20:t:25:ASP:OD1	20:t:41:ARG:NH2	2.38	0.54
5:E:309:ARG:HG2	5:E:343:LEU:HD11	1.89	0.54
6:F:305:GLU:HG3	6:F:306:VAL:HG23	1.89	0.54
21:U:52:GLU:HA	21:U:57:ARG:HH21	1.71	0.54
32:f:560:LEU:HD21	32:f:798:THR:HA	1.88	0.54
22:V:440:LYS:NZ	30:d:143:LEU:O	2.38	0.54
26:Z:81:MET:HB2	29:c:91:PHE:HE1	1.72	0.54
32:f:567:LEU:HG	32:f:598:CYS:O	2.08	0.54
2:B:332:ASN:OD1	2:B:333:ARG:N	2.40	0.54
3:C:160:GLU:OE1	3:C:313:ARG:NH2	2.40	0.54
3:C:217:SER:OG	4:D:291:GLU:OE1	2.22	0.54
8:H:192:ILE:HG23	8:H:203:MET:HE1	1.90	0.54
9:i:119:GLN:NE2	10:j:79:ASP:OD1	2.41	0.54
12:l:41:LYS:HG3	12:l:42:THR:HG23	1.90	0.54
1:A:125:LEU:HA	1:A:149:ILE:HB	1.89	0.54
6:F:410:ARG:NH2	6:F:419:ASP:OD2	2.40	0.54
21:U:162:VAL:O	21:U:166:THR:OG1	2.22	0.54
32:f:783:SER:HB2	32:f:787:LEU:HD13	1.89	0.54
15:o:216:ILE:HD11	16:p:194:LYS:HD2	1.89	0.54
24:X:183:LEU:HB3	24:X:184:PRO:CD	2.30	0.54
28:b:107:MET:HB3	28:b:136:VAL:HG13	1.90	0.54
19:s:27:THR:HB	19:s:40:SER:H	1.72	0.54
3:C:187:LEU:HA	3:C:293:MET:HB2	1.90	0.54
20:T:44:ARG:NH2	20:T:47:ASN:OD1	2.40	0.54
25:Y:231:LEU:CG	25:Y:236:LEU:HD12	2.38	0.54
32:f:679:LEU:O	32:f:687:ARG:NE	2.39	0.54
22:V:96:ARG:NH1	26:Z:286:GLU:OE2	2.41	0.54
20:t:44:ARG:NH2	20:t:47:ASN:OD1	2.41	0.54
32:f:809:ILE:HG23	32:f:814:SER:HB2	1.89	0.53
8:h:42:ASN:ND2	8:h:183:GLU:OE2	2.42	0.53
13:m:40:ARG:NE	13:m:146:ALA:O	2.36	0.53
13:m:68:ASN:OD1	13:m:224:HIS:ND1	2.40	0.53
19:s:144:MET:HE1	19:s:185:ARG:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:402:ALA:HB1	2:B:414:VAL:HG11	1.89	0.53
22:V:473:GLN:NE2	30:d:245:GLN:OE1	2.40	0.53
25:Y:247:LEU:HD12	25:Y:250:LEU:HD21	1.91	0.53
27:a:254:ALA:HA	27:a:261:LEU:HD23	1.88	0.53
28:b:181:ASP:HA	28:b:184:ILE:HG12	1.91	0.53
1:A:307:ASP:OD2	1:A:333:ARG:NH2	2.41	0.53
5:E:309:ARG:NH1	5:E:335:SER:O	2.42	0.53
21:U:82:LEU:O	21:U:129:ARG:NH2	2.37	0.53
23:W:396:LEU:HB3	23:W:402:ILE:HD13	1.89	0.53
25:Y:364:TRP:NE1	25:Y:368:GLU:OE2	2.42	0.53
30:d:75:MET:HE2	30:d:102:ASN:HB2	1.90	0.53
7:g:165:ALA:HB1	7:g:179:LEU:HD13	1.90	0.53
17:q:44:LEU:HD11	17:q:102:LEU:HD22	1.89	0.53
36:C:501:ATP:O2G	4:D:323:ARG:NH1	2.42	0.53
26:Z:28:LYS:HD2	26:Z:29:VAL:HG13	1.91	0.53
6:F:373:MET:SD	6:F:373:MET:N	2.82	0.53
21:U:74:PHE:HB3	21:U:103:LYS:HD2	1.90	0.53
23:W:316:ARG:HB2	23:W:319:THR:OG1	2.09	0.53
7:g:147:GLN:OE1	7:g:150:GLN:NE2	2.38	0.53
1:A:170:PRO:HG2	1:A:231:ASN:HB3	1.91	0.53
5:E:5:ARG:HB2	6:F:33:VAL:HG22	1.91	0.53
32:f:150:GLU:HG3	32:f:152:ALA:H	1.72	0.53
8:h:9:SER:OG	8:h:123:GLN:O	2.26	0.53
1:A:284:ARG:HH21	1:A:286:ASP:HA	1.73	0.53
6:F:164:LEU:HG	6:F:164:LEU:O	2.07	0.53
17:Q:144:ASP:OD2	18:r:166:ARG:NH2	2.42	0.53
23:W:450:GLU:OE2	26:Z:223:ASN:ND2	2.41	0.53
30:d:203:PRO:HG2	30:d:205:LYS:HB3	1.90	0.53
4:D:264:ILE:HD12	4:D:309:MET:HE1	1.91	0.53
10:J:208:LEU:HB3	10:J:220:LEU:CB	2.39	0.53
11:K:130:PRO:C	11:K:132:ALA:N	2.66	0.53
12:l:120:THR:O	13:m:129:ARG:NH1	2.42	0.53
2:B:183:THR:HG22	2:B:184:TYR:HD2	1.74	0.53
3:C:140:VAL:HG22	3:C:142:LYS:HG3	1.91	0.53
12:L:33:SER:OG	12:L:62:LYS:NZ	2.36	0.53
21:U:415:HIS:HB3	21:U:418:GLU:HB3	1.91	0.53
21:U:714:SER:HA	21:U:717:ILE:HG22	1.89	0.53
23:W:35:ALA:HB2	23:W:43:VAL:HG21	1.91	0.53
25:Y:312:ARG:HA	25:Y:356:THR:HG22	1.90	0.53
16:p:12:MET:HE3	16:p:167:ILE:HG13	1.91	0.53
3:C:365:GLU:OE2	4:D:329:ARG:NH1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:198:VAL:HG22	19:S:203:ILE:HG12	1.90	0.52
28:b:14:GLU:N	28:b:82:GLY:O	2.41	0.52
32:f:92:VAL:HG13	32:f:94:LYS:HE2	1.91	0.52
32:f:188:VAL:HG21	32:f:211:ILE:HD12	1.91	0.52
17:q:168:GLN:NE2	17:q:175:LEU:O	2.42	0.52
1:A:204:LEU:HD12	6:F:413:THR:HA	1.91	0.52
2:B:368:HIS:CE1	2:B:396:LYS:HG3	2.44	0.52
8:H:204:THR:OG1	8:H:206:ASP:OD1	2.26	0.52
25:Y:41:LEU:HD21	25:Y:57:LEU:HD11	1.91	0.52
32:f:56:LEU:HD22	32:f:99:LEU:HD11	1.91	0.52
10:j:40:ILE:HG22	10:j:212:ARG:HG3	1.91	0.52
2:B:383:LEU:HD11	2:B:419:PHE:HB3	1.91	0.52
5:E:333:LYS:HG3	5:E:334:LEU:HD12	1.90	0.52
13:M:37:ILE:HD11	13:M:193:VAL:HG13	1.91	0.52
25:Y:360:ASP:OD1	25:Y:363:ASN:ND2	2.42	0.52
4:D:176:GLU:OE2	4:D:329:ARG:NH1	2.43	0.52
24:X:310:ARG:NH1	24:X:310:ARG:HA	2.25	0.52
13:m:50:GLU:OE2	13:m:201:HIS:ND1	2.39	0.52
19:s:172:MET:HE1	19:s:195:ILE:HG21	1.90	0.52
2:B:411:ARG:NH2	2:B:418:ASP:OD2	2.41	0.52
6:F:222:GLY:HA3	6:F:348:LEU:HA	1.92	0.52
22:V:338:LEU:HG	22:V:398:LEU:HD12	1.92	0.52
24:X:163:LYS:NZ	24:X:199:ALA:O	2.42	0.52
28:b:65:THR:HG21	28:b:70:ARG:HD2	1.91	0.52
13:m:8:ASP:O	13:m:22:GLN:NE2	2.35	0.52
3:C:326:LEU:HD22	3:C:345:ARG:HD3	1.91	0.52
21:U:26:LYS:HD3	30:d:34:ASN:HD21	1.74	0.52
22:V:201:ARG:NH1	22:V:241:ARG:O	2.43	0.52
25:Y:77:ASN:OD1	25:Y:110:TYR:OH	2.28	0.52
31:e:44:ASP:OD1	31:e:47:ASN:ND2	2.42	0.52
20:t:26:MET:HE1	20:t:202:PRO:HB3	1.92	0.52
9:I:49:ARG:NH2	9:I:63:GLU:OE2	2.43	0.52
13:M:136:MET:HE3	13:M:165:ILE:HG12	1.90	0.52
21:U:42:VAL:HG11	21:U:67:VAL:HG11	1.92	0.52
24:X:96:PHE:CE2	24:X:109:LEU:HD12	2.45	0.52
24:X:311:ALA:O	24:X:312:GLU:C	2.53	0.52
25:Y:236:LEU:HG	25:Y:239:LYS:HZ3	1.73	0.52
10:j:160:ALA:O	10:j:169:ARG:NH2	2.42	0.52
2:B:368:HIS:CE1	2:B:395:ILE:HB	2.43	0.52
3:C:86:LEU:HD21	3:C:94:LYS:HD2	1.92	0.52
6:F:376:SER:HB3	6:F:414:GLU:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:164:VAL:HG21	3:C:313:ARG:HG3	1.92	0.52
19:S:92:LEU:HD23	19:S:124:PHE:HE2	1.74	0.52
26:Z:243:GLN:H	26:Z:246:VAL:HG12	1.75	0.52
29:c:139:ARG:HD3	29:c:161:ARG:HH12	1.74	0.52
19:s:166:LEU:HD21	19:s:171:ALA:HB2	1.92	0.52
33:u:15:LEU:HD11	33:u:30:ILE:HD11	1.91	0.52
3:C:371:LEU:O	3:C:374:ARG:NH1	2.42	0.51
25:Y:387:ILE:HD12	26:Z:275:LEU:HD22	1.92	0.51
7:g:5:SER:HB2	7:g:23:TYR:OH	2.10	0.51
8:h:119:GLN:HG3	9:i:81:SER:HB2	1.92	0.51
10:j:180:ALA:HB1	10:j:190:LEU:HD11	1.92	0.51
2:B:386:ALA:HB3	2:B:423:LYS:HE3	1.92	0.51
3:C:253:SER:HB3	4:D:290:LEU:HD12	1.91	0.51
20:T:51:LEU:HD11	20:T:92:LEU:HD11	1.93	0.51
21:U:699:THR:O	21:U:702:THR:OG1	2.27	0.51
21:U:373:ASN:HD22	21:U:385:PHE:HD2	1.57	0.51
8:h:39:LYS:HG3	8:h:44:VAL:HG22	1.92	0.51
1:A:364:VAL:HA	1:A:404:ALA:H	1.76	0.51
2:B:368:HIS:ND1	2:B:395:ILE:CG2	2.73	0.51
2:B:368:HIS:ND1	2:B:395:ILE:CB	2.73	0.51
21:U:599:ILE:HD13	21:U:625:ILE:HD11	1.93	0.51
27:a:156:TYR:HE2	27:a:196:ARG:HH12	1.56	0.51
32:f:368:ALA:HA	32:f:371:ASN:ND2	2.25	0.51
13:m:66:LEU:HD12	13:m:212:GLU:HG2	1.93	0.51
13:m:230:ASP:OD1	13:m:230:ASP:N	2.44	0.51
5:E:281:ARG:NH1	6:F:295:ARG:O	2.43	0.51
25:Y:162:GLU:HA	25:Y:165:LYS:HB2	1.91	0.51
8:h:203:MET:HE2	8:h:208:ILE:HG21	1.92	0.51
16:p:14:MET:HE3	16:p:163:LEU:HD12	1.93	0.51
1:A:55:LEU:HD11	2:B:76:GLU:HG2	1.93	0.51
3:C:137:LEU:HD11	3:C:213:ARG:HE	1.74	0.51
5:E:349:GLU:OE2	6:F:350:ARG:NH1	2.43	0.51
19:S:211:ARG:NH2	19:S:213:ASP:OD2	2.44	0.51
24:X:71:LYS:HA	24:X:74:ARG:HE	1.75	0.51
33:u:30:ILE:HB	33:u:41:GLN:HE22	1.76	0.51
5:E:181:THR:OG1	36:E:401:ATP:O1B	2.28	0.51
13:M:68:ASN:OD1	13:M:224:HIS:ND1	2.43	0.51
19:S:125:ASP:OD1	19:S:129:SER:N	2.44	0.51
32:f:99:LEU:HD23	32:f:106:LEU:HD11	1.92	0.51
16:p:35:VAL:HG12	16:p:36:THR:HG23	1.93	0.51
20:t:51:LEU:HD11	20:t:110:MET:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:84:ARG:HD3	5:E:108:MET:HE3	1.93	0.51
25:Y:69:LEU:HD12	25:Y:72:LYS:HE2	1.93	0.51
8:H:74:LEU:HD12	8:H:87:VAL:HG22	1.92	0.51
22:V:82:LEU:HD23	22:V:94:VAL:HG12	1.93	0.51
24:X:63:ALA:HB1	24:X:96:PHE:HE1	1.76	0.51
2:B:58:CYS:SG	2:B:59:ARG:N	2.84	0.51
5:E:161:ARG:HG3	5:E:162:VAL:HG23	1.93	0.51
23:W:120:ILE:HG12	23:W:123:ARG:HH21	1.76	0.51
27:a:230:ARG:HB3	27:a:232:TRP:HD1	1.75	0.51
10:j:39:ASP:OD1	10:j:39:ASP:N	2.44	0.51
6:F:43:GLN:HG2	6:F:44:ARG:HH21	1.75	0.50
12:L:166:GLN:OE1	12:L:169:ARG:NH2	2.43	0.50
21:U:376:MET:HA	21:U:740:GLY:H	1.74	0.50
23:W:194:LEU:HG	23:W:202:THR:HG21	1.92	0.50
4:D:162:VAL:O	4:D:221:HIS:ND1	2.41	0.50
21:U:902:PRO:HA	21:U:914:LEU:HA	1.94	0.50
25:Y:231:LEU:HD12	25:Y:234:PRO:HD2	1.92	0.50
30:d:8:GLU:H	30:d:18:LYS:HE3	1.76	0.50
4:D:202:VAL:HG13	4:D:329:ARG:HB2	1.92	0.50
36:E:401:ATP:O2G	6:F:347:ARG:NH2	2.44	0.50
10:J:50:VAL:HB	10:J:54:GLN:HB2	1.93	0.50
16:P:193:ASP:OD1	16:P:193:ASP:N	2.42	0.50
17:Q:35:MET:SD	17:Q:181:ARG:NH1	2.78	0.50
17:Q:137:PHE:HB3	18:r:133:VAL:HG21	1.92	0.50
26:Z:259:VAL:HB	29:c:291:LEU:HD21	1.93	0.50
29:c:75:MET:HG2	29:c:76:PRO:HD2	1.92	0.50
19:s:125:ASP:OD1	19:s:129:SER:N	2.44	0.50
21:U:870:GLU:N	21:U:871:PRO:CD	2.74	0.50
21:U:889:LEU:HD13	21:U:909:GLY:H	1.77	0.50
10:j:146:GLN:OE1	10:j:159:ASN:ND2	2.45	0.50
19:s:198:VAL:HG22	19:s:203:ILE:HG12	1.94	0.50
8:H:203:MET:HA	8:H:207:ASN:HD21	1.77	0.50
22:V:337:LEU:HD22	22:V:367:VAL:HG11	1.93	0.50
23:W:167:GLN:NE2	23:W:193:CYS:SG	2.68	0.50
23:W:419:LYS:HD2	23:W:424:LEU:HD13	1.92	0.50
24:X:310:ARG:O	24:X:314:ARG:HB3	2.11	0.50
7:g:49:VAL:HG22	7:g:219:VAL:HG12	1.93	0.50
7:g:73:THR:HG23	7:g:75:ASN:H	1.75	0.50
2:B:223:ILE:HG13	2:B:347:ILE:HG21	1.92	0.50
14:N:55:VAL:HG22	14:N:86:MET:HE2	1.92	0.50
20:T:53:ALA:HB2	20:T:110:MET:HG3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:j:109:ARG:NH2	18:r:70:ASN:OD1	2.42	0.50
12:L:50:LYS:HB3	12:L:59:HIS:HB3	1.93	0.50
21:U:21:GLU:OE2	21:U:56:SER:OG	2.29	0.50
17:q:11:ASP:N	17:q:11:ASP:OD1	2.44	0.50
2:B:367:ILE:O	2:B:371:ARG:NH1	2.45	0.50
6:F:228:PRO:O	6:F:233:LYS:NZ	2.45	0.50
13:M:230:ASP:N	13:M:230:ASP:OD1	2.44	0.50
21:U:146:LYS:HB3	21:U:149:GLN:HG2	1.92	0.50
21:U:497:LEU:HB2	21:U:516:LEU:HD13	1.94	0.50
29:c:162:LEU:HD12	29:c:200:TYR:HB3	1.93	0.50
18:r:97:MET:O	18:r:116:SER:N	2.45	0.50
1:A:156:LYS:O	1:A:158:ASP:N	2.45	0.50
8:H:93:LEU:HD13	8:H:113:ARG:HB3	1.93	0.50
21:U:251:ASP:O	21:U:255:SER:CB	2.60	0.50
21:U:798:PRO:HG3	21:U:914:LEU:HD22	1.94	0.50
24:X:142:ARG:NH1	24:X:145:GLU:OE2	2.45	0.50
26:Z:130:ASP:OD1	26:Z:131:LEU:N	2.43	0.50
18:R:114:VAL:HG22	18:R:120:ARG:HG3	1.93	0.49
21:U:510:GLU:HG3	21:U:543:LYS:HB3	1.93	0.49
23:W:435:LEU:HD23	26:Z:236:LEU:HD22	1.93	0.49
9:i:234:GLU:HA	9:i:237:ILE:HG12	1.94	0.49
1:A:111:TYR:HE2	1:A:125:LEU:HD23	1.76	0.49
1:A:173:THR:HG22	1:A:175:SER:H	1.76	0.49
4:D:133:HIS:HB3	4:D:137:ASN:H	1.76	0.49
4:D:335:LEU:HD12	4:D:369:LYS:HE2	1.94	0.49
11:K:130:PRO:O	11:K:132:ALA:N	2.42	0.49
25:Y:376:LEU:HD22	26:Z:265:LEU:HD23	1.94	0.49
2:B:170:LEU:HG	2:B:266:LEU:HD11	1.93	0.49
2:B:220:LYS:NZ	2:B:324:ASP:OD1	2.40	0.49
21:U:196:LYS:HA	21:U:199:ARG:HG2	1.94	0.49
23:W:153:LYS:HB2	23:W:162:ALA:HB2	1.94	0.49
2:B:79:ILE:HD12	32:f:677:HIS:CE1	2.47	0.49
3:C:256:SER:HA	3:C:301:LEU:HA	1.94	0.49
7:G:141:ILE:HG22	7:G:151:VAL:HG22	1.95	0.49
10:J:182:GLU:HB2	10:J:186:LEU:HD12	1.94	0.49
24:X:103:THR:HA	24:X:106:GLU:HB2	1.95	0.49
29:c:226:MET:O	29:c:230:THR:OG1	2.28	0.49
16:p:193:ASP:OD1	16:p:193:ASP:N	2.44	0.49
1:A:346:PRO:O	1:A:351:ARG:NH1	2.45	0.49
3:C:63:LEU:HD11	4:D:78:GLU:HG2	1.94	0.49
9:I:155:ASN:OD1	10:J:77:THR:OG1	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:192:VAL:HG11	16:p:205:ASP:HB3	1.95	0.49
21:U:568:GLU:OE2	21:U:572:ARG:NH2	2.45	0.49
22:V:228:ARG:NH1	30:d:85:TYR:OH	2.46	0.49
25:Y:72:LYS:HA	25:Y:75:LYS:HE3	1.94	0.49
27:a:133:GLU:HA	27:a:136:GLU:HG3	1.94	0.49
2:B:388:ASP:OD1	2:B:388:ASP:N	2.43	0.49
3:C:52:LEU:HB3	4:D:68:LEU:HD22	1.95	0.49
36:C:501:ATP:O2B	4:D:323:ARG:NH2	2.34	0.49
4:D:57:GLN:HA	4:D:60:TYR:CE1	2.47	0.49
32:f:417:ILE:HG22	32:f:418:LEU:HD12	1.94	0.49
12:l:49:LEU:HG	12:l:195:LEU:HD21	1.94	0.49
2:B:125:THR:OG1	2:B:126:SER:N	2.45	0.49
4:D:69:LYS:HD2	30:d:257:VAL:HG21	1.94	0.49
4:D:175:GLN:NE2	4:D:179:GLU:OE1	2.44	0.49
26:Z:106:ILE:HD12	26:Z:153:LYS:HB2	1.95	0.49
8:h:4:ARG:C	8:h:4:ARG:HE	2.21	0.49
1:A:236:CYS:HB3	1:A:270:CYS:HA	1.95	0.49
2:B:135:ILE:HG12	2:B:139:VAL:HG21	1.94	0.49
3:C:299:ASP:OD1	3:C:299:ASP:N	2.44	0.49
5:E:219:PHE:HD2	5:E:263:GLN:HB3	1.77	0.49
21:U:558:GLY:N	21:U:588:MET:O	2.41	0.49
23:W:121:LYS:O	23:W:125:ILE:HG12	2.13	0.49
23:W:147:LYS:HE3	23:W:188:GLU:HG3	1.93	0.49
25:Y:374:ASP:OD1	25:Y:374:ASP:N	2.45	0.49
16:p:30:ILE:HG22	16:p:31:GLN:H	1.78	0.49
2:B:77:GLU:HA	2:B:80:ARG:HE	1.77	0.49
3:C:66:LEU:HD22	4:D:116:LEU:HD21	1.94	0.49
6:F:165:PRO:O	6:F:167:GLU:HG2	2.13	0.49
21:U:541:HIS:HB2	21:U:544:ILE:HG22	1.95	0.49
4:D:64:GLU:HA	21:U:607:VAL:HG11	1.95	0.49
6:F:343:LEU:O	6:F:349:ASP:HA	2.13	0.49
15:O:88:PHE:HD2	15:O:89:ARG:HH11	1.61	0.49
21:U:351:MET:HE1	21:U:818:GLU:HA	1.95	0.49
23:W:328:LEU:HD12	23:W:341:PHE:HB2	1.95	0.49
25:Y:231:LEU:HG	25:Y:236:LEU:HD12	1.93	0.49
29:c:272:ILE:C	29:c:274:ASN:H	2.20	0.49
32:f:326:LEU:HB3	32:f:420:TRP:HE1	1.77	0.49
2:B:199:GLU:O	2:B:211:TYR:OH	2.30	0.48
6:F:31:GLU:HA	6:F:35:LYS:HZ3	1.77	0.48
21:U:501:LEU:HD11	21:U:548:LEU:HD11	1.95	0.48
21:U:212:ASP:HB3	21:U:214:ILE:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:475:HIS:CE1	21:U:507:VAL:HG22	2.48	0.48
23:W:373:ILE:HG23	23:W:413:ILE:HB	1.95	0.48
27:a:219:HIS:CD2	27:a:221:VAL:HG22	2.48	0.48
32:f:446:LEU:HD12	32:f:480:GLY:HA2	1.95	0.48
32:f:822:VAL:HA	32:f:825:MET:HB2	1.94	0.48
2:B:375:ALA:HB2	2:B:413:LYS:HB3	1.94	0.48
4:D:153:MET:HE2	4:D:229:ARG:H	1.78	0.48
4:D:398:ASP:OD1	4:D:398:ASP:N	2.45	0.48
8:H:177:ARG:HH22	8:H:190:THR:HA	1.78	0.48
25:Y:231:LEU:HG	25:Y:236:LEU:CD1	2.43	0.48
32:f:542:ILE:HA	32:f:545:LYS:HD2	1.95	0.48
14:n:144:ARG:H	14:n:147:MET:HE3	1.78	0.48
1:A:284:ARG:HH12	1:A:289:ALA:H	1.60	0.48
21:U:31:VAL:HG23	21:U:38:ILE:HD12	1.96	0.48
21:U:847:GLU:O	21:U:851:GLU:N	2.46	0.48
19:s:145:LEU:HD22	19:s:178:VAL:HB	1.96	0.48
1:A:346:PRO:HB2	1:A:351:ARG:HG3	1.94	0.48
2:B:203:LEU:HD21	2:B:210:TYR:HD2	1.78	0.48
6:F:180:ARG:HH12	6:F:248:PHE:HB3	1.78	0.48
10:J:64:ALA:HA	10:J:70:CYS:HA	1.94	0.48
15:O:42:TYR:HE2	15:O:183:LEU:HD11	1.79	0.48
23:W:125:ILE:HG21	23:W:149:LEU:HB2	1.95	0.48
10:J:31:THR:OG1	10:J:163:ARG:O	2.30	0.48
32:f:685:THR:HG22	32:f:688:ARG:HH21	1.79	0.48
7:g:7:ALA:N	7:g:10:ASP:OD2	2.47	0.48
7:g:58:ASP:OD1	7:g:58:ASP:N	2.46	0.48
4:D:410:ASP:OD1	4:D:410:ASP:N	2.44	0.48
6:F:226:TYR:HA	6:F:233:LYS:HE3	1.94	0.48
12:L:204:ASP:N	12:L:204:ASP:OD1	2.46	0.48
24:X:142:ARG:HH11	24:X:145:GLU:HG3	1.79	0.48
7:g:3:ARG:O	7:g:4:GLY:C	2.56	0.48
15:o:21:THR:HG22	15:o:26:VAL:HA	1.94	0.48
1:A:365:GLU:HG2	1:A:367:ASP:H	1.77	0.48
21:U:128:GLN:O	21:U:132:GLY:N	2.46	0.48
21:U:333:MET:SD	21:U:333:MET:N	2.84	0.48
21:U:505:ASP:HB3	21:U:508:THR:HG22	1.95	0.48
22:V:175:MET:HG2	22:V:184:ALA:HB2	1.96	0.48
23:W:129:ARG:NH1	23:W:146:THR:OG1	2.46	0.48
24:X:143:TYR:HD2	24:X:144:GLN:HG2	1.78	0.48
24:X:310:ARG:C	24:X:314:ARG:HB3	2.39	0.48
7:g:180:GLU:HG2	8:h:55:ILE:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:r:7:LYS:HD2	18:r:109:PRO:HB2	1.96	0.48
4:D:65:GLN:HB3	30:d:257:VAL:OXT	2.13	0.48
25:Y:220:VAL:HA	25:Y:223:THR:HG22	1.95	0.48
26:Z:16:LEU:HD11	29:c:220:LEU:HD22	1.96	0.48
26:Z:82:PHE:HA	26:Z:85:VAL:HG12	1.95	0.48
27:a:373:ASP:OD2	30:d:251:ARG:NH2	2.42	0.48
30:d:125:LYS:HE3	30:d:130:ASN:HB2	1.95	0.48
32:f:348:ILE:HD13	32:f:381:VAL:HG21	1.95	0.48
15:o:63:LEU:HD11	15:o:79:ALA:HB2	1.95	0.48
33:u:7:THR:OG1	33:u:11:LYS:O	2.29	0.48
2:B:204:PRO:HG3	2:B:211:TYR:HE2	1.79	0.48
3:C:167:LEU:HD11	3:C:174:LEU:HD12	1.95	0.48
3:C:226:GLU:HG3	3:C:229:ARG:HH12	1.78	0.48
5:E:230:ILE:HB	5:E:275:MET:HG3	1.95	0.48
9:I:197:LEU:HA	9:I:200:THR:HG22	1.96	0.48
21:U:157:THR:HG23	21:U:159:ARG:H	1.79	0.48
28:b:161:ASN:HB2	28:b:166:THR:H	1.78	0.48
29:c:116:PRO:HA	29:c:147:PRO:HD2	1.96	0.48
2:B:214:MET:SD	2:B:214:MET:N	2.87	0.47
2:B:227:PRO:HB2	2:B:230:THR:HB	1.96	0.47
15:O:38:SER:OG	15:O:40:ASN:OD1	2.28	0.47
21:U:497:LEU:O	21:U:501:LEU:N	2.39	0.47
22:V:108:LEU:HD11	22:V:170:LEU:HG	1.96	0.47
23:W:316:ARG:NH1	23:W:380:GLN:O	2.42	0.47
23:W:359:VAL:HG23	23:W:382:LEU:HD22	1.96	0.47
23:W:398:VAL:HG12	24:X:340:GLU:HB2	1.96	0.47
30:d:202:THR:HA	30:d:206:MET:HG2	1.96	0.47
20:t:63:LEU:HD12	20:t:110:MET:HE1	1.96	0.47
33:u:63:LYS:HG2	33:u:64:GLU:HG3	1.95	0.47
1:A:165:GLN:HG2	1:A:167:GLU:HG3	1.96	0.47
1:A:407:LYS:H	1:A:407:LYS:HD2	1.79	0.47
6:F:375:VAL:HG13	6:F:415:LEU:HB2	1.96	0.47
18:R:7:LYS:O	18:R:143:TYR:OH	2.25	0.47
20:T:43:MET:HE2	20:T:51:LEU:HD22	1.96	0.47
21:U:796:LYS:HZ3	21:U:798:PRO:HB3	1.79	0.47
24:X:212:MET:HE2	24:X:235:ALA:HB1	1.95	0.47
26:Z:270:VAL:HG22	29:c:281:LYS:HZ2	1.78	0.47
27:a:135:ILE:HG12	27:a:158:LEU:HD13	1.96	0.47
5:E:168:LYS:N	5:E:296:ASP:OD2	2.46	0.47
5:E:327:ASP:H	5:E:364:GLN:HG3	1.77	0.47
11:K:129:ASP:N	11:K:130:PRO:HD2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:161:ASN:HD22	28:b:166:THR:HB	1.79	0.47
29:c:57:MET:HA	29:c:72:VAL:HG22	1.95	0.47
10:j:148:ASP:OD1	10:j:152:THR:N	2.45	0.47
20:t:27:LEU:HD22	20:t:184:TYR:HB2	1.95	0.47
33:u:23:ILE:HD12	33:u:50:LEU:HD23	1.96	0.47
13:M:197:ILE:HG21	13:M:211:LEU:HD13	1.96	0.47
32:f:267:ARG:HG3	32:f:787:LEU:HD21	1.96	0.47
16:p:58:THR:O	17:q:85:ARG:NH2	2.46	0.47
7:G:86:ASP:OD1	13:M:120:HIS:NE2	2.47	0.47
21:U:699:THR:HG21	21:U:812:ALA:H	1.79	0.47
26:Z:175:LEU:O	29:c:209:LYS:NZ	2.40	0.47
27:a:54:ASP:HA	27:a:57:ILE:HG22	1.96	0.47
27:a:230:ARG:HB3	27:a:232:TRP:CD1	2.49	0.47
27:a:360:VAL:HG22	29:c:308:VAL:HG13	1.96	0.47
21:U:333:MET:HA	21:U:336:GLU:HB3	1.96	0.47
24:X:103:THR:C	24:X:105:GLN:H	2.21	0.47
18:r:33:LYS:HA	18:r:45:MET:HE3	1.96	0.47
33:u:19:PRO:HA	33:u:56:LEU:HB3	1.97	0.47
1:A:222:LYS:HA	1:A:343:PHE:HE2	1.79	0.47
1:A:224:LEU:HD11	35:A:501:ADP:H2'	1.96	0.47
2:B:88:LEU:HD23	2:B:90:GLU:H	1.79	0.47
3:C:197:THR:OG1	36:C:501:ATP:O1B	2.33	0.47
12:L:41:LYS:HG3	12:L:42:THR:HG23	1.96	0.47
21:U:867:LYS:HG3	21:U:868:LYS:H	1.80	0.47
22:V:175:MET:HG3	22:V:180:ARG:HB2	1.96	0.47
23:W:276:LEU:HD22	23:W:353:ASP:HB3	1.97	0.47
25:Y:68:ASP:OD1	25:Y:68:ASP:N	2.46	0.47
26:Z:67:VAL:HG12	28:b:95:LEU:HD22	1.96	0.47
30:d:8:GLU:O	30:d:13:SER:OG	2.23	0.47
32:f:486:GLY:HA3	32:f:521:ALA:HB1	1.97	0.47
1:A:177:VAL:HG21	1:A:228:ALA:HB2	1.97	0.47
20:T:98:SER:O	20:T:102:LYS:NZ	2.47	0.47
21:U:669:ILE:O	21:U:673:GLU:N	2.46	0.47
27:a:273:GLN:HB3	27:a:310:LEU:HD11	1.95	0.47
32:f:267:ARG:HD3	32:f:787:LEU:HD11	1.97	0.47
11:k:202:LEU:O	11:k:206:MET:HG2	2.15	0.47
4:D:293:LEU:HD21	4:D:321:LEU:HD22	1.95	0.47
5:E:303:LEU:HD23	5:E:338:PHE:HB3	1.97	0.47
7:G:112:ASP:OD1	7:G:112:ASP:N	2.48	0.47
16:P:159:ASP:N	16:P:159:ASP:OD1	2.44	0.47
22:V:218:TYR:CD2	22:V:227:VAL:HG21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:465:ASP:N	22:V:465:ASP:OD1	2.45	0.47
26:Z:193:ASN:HA	26:Z:196:HIS:CE1	2.50	0.47
27:a:201:GLY:HA3	27:a:233:LEU:HD21	1.97	0.47
32:f:193:PRO:HA	32:f:196:MET:HG2	1.97	0.47
13:m:24:GLU:HA	13:m:27:MET:HG3	1.96	0.47
1:A:55:LEU:HD23	2:B:72:LEU:HB3	1.97	0.47
1:A:292:ASP:OD1	2:B:303:ARG:NH2	2.48	0.47
2:B:97:SER:O	2:B:101:ASP:N	2.45	0.47
8:H:111:VAL:HG22	8:H:136:ILE:HD12	1.96	0.47
21:U:536:ALA:HB2	21:U:548:LEU:HD22	1.95	0.47
21:U:792:ASN:OD1	21:U:793:LYS:N	2.42	0.47
22:V:98:LEU:HD12	22:V:209:LYS:HD2	1.97	0.47
1:A:165:GLN:HE22	1:A:267:LYS:HD2	1.80	0.46
4:D:390:ASN:O	23:W:201:ARG:NE	2.47	0.46
6:F:42:ILE:HG13	27:a:66:GLU:HG2	1.97	0.46
11:k:98:ASN:OD1	18:r:61:ARG:NH2	2.48	0.46
3:C:72:TYR:HE1	3:C:121:TYR:HE1	1.63	0.46
3:C:258:ARG:HH22	3:C:274:LEU:HD13	1.80	0.46
11:K:13:ASN:HB3	12:L:126:ARG:HB3	1.96	0.46
22:V:309:MET:SD	22:V:328:VAL:HG13	2.55	0.46
25:Y:377:LEU:HA	25:Y:380:VAL:HG22	1.96	0.46
30:d:45:LYS:HA	30:d:48:LEU:HB2	1.97	0.46
18:r:115:ASP:OD1	18:r:119:ASN:N	2.46	0.46
3:C:11:LEU:HD13	3:C:14:GLY:HA3	1.98	0.46
5:E:9:LEU:HD11	6:F:29:ILE:HA	1.97	0.46
5:E:341:ALA:HA	5:E:344:ARG:HG2	1.96	0.46
8:H:119:GLN:HG3	9:I:81:SER:HB2	1.97	0.46
14:N:46:SER:OG	14:N:97:GLY:O	2.32	0.46
16:P:177:ARG:NH2	19:s:150:ASP:OD2	2.39	0.46
18:R:64:ARG:NH1	18:R:67:GLU:OE1	2.47	0.46
21:U:219:CYS:O	21:U:223:LEU:N	2.39	0.46
23:W:47:LEU:HD12	23:W:66:ILE:HG23	1.97	0.46
28:b:25:ARG:HH22	28:b:145:GLU:HB3	1.81	0.46
3:C:76:VAL:HG22	3:C:87:VAL:HA	1.98	0.46
4:D:131:ALA:HB3	4:D:141:ASP:H	1.80	0.46
21:U:900:TYR:HE1	21:U:918:SER:HB2	1.80	0.46
24:X:160:MET:HG2	24:X:161:ASP:H	1.80	0.46
7:g:180:GLU:HG3	8:h:54:SER:HB2	1.97	0.46
1:A:193:THR:O	1:A:197:HIS:N	2.43	0.46
1:A:328:ASP:HB3	1:A:331:LEU:HB2	1.98	0.46
4:D:255:LYS:HD3	4:D:302:ASN:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:203:ILE:HD11	5:E:238:ILE:HD13	1.97	0.46
5:E:317:ALA:HA	5:E:320:ILE:HD13	1.98	0.46
24:X:205:LYS:NZ	24:X:243:ASP:OD2	2.48	0.46
26:Z:260:VAL:HG13	29:c:295:ASN:HD22	1.80	0.46
27:a:369:HIS:O	27:a:372:HIS:ND1	2.41	0.46
32:f:710:LEU:O	32:f:714:SER:OG	2.29	0.46
1:A:124:ASP:OD1	1:A:125:LEU:N	2.48	0.46
5:E:330:ALA:HA	5:E:333:LYS:HG2	1.97	0.46
6:F:278:LYS:HB2	6:F:281:SER:HB3	1.97	0.46
13:M:69:VAL:HG11	13:M:75:MET:HE3	1.98	0.46
22:V:218:TYR:HD2	22:V:227:VAL:HG21	1.81	0.46
23:W:454:ASN:HB3	26:Z:220:LEU:HB2	1.96	0.46
8:h:11:THR:HG22	8:h:19:LEU:HD22	1.98	0.46
12:l:47:VAL:HG12	12:l:195:LEU:HD22	1.97	0.46
1:A:98:CYS:SG	1:A:139:ARG:NH1	2.89	0.46
2:B:248:LEU:HD12	2:B:282:VAL:HG22	1.98	0.46
21:U:540:GLN:HB3	29:c:68:ARG:HH22	1.81	0.46
24:X:53:LEU:HD22	24:X:69:LEU:HD22	1.97	0.46
25:Y:374:ASP:HA	25:Y:377:LEU:HB2	1.98	0.46
29:c:107:MET:HE1	33:u:8:LEU:HG	1.97	0.46
9:i:72:MET:HE2	9:i:72:MET:HB3	1.79	0.46
19:s:10:GLY:HA3	19:s:42:LYS:HE2	1.97	0.46
5:E:198:VAL:HB	5:E:232:MET:HG2	1.98	0.46
5:E:351:GLY:HA3	6:F:217:ILE:HD13	1.97	0.46
10:J:221:ASN:ND2	10:J:223:GLU:HB3	2.21	0.46
23:W:190:MET:HE1	23:W:205:ILE:HB	1.98	0.46
24:X:96:PHE:CE2	24:X:109:LEU:CD1	2.99	0.46
27:a:131:THR:HA	27:a:134:THR:HG22	1.97	0.46
27:a:370:GLN:HG3	30:d:247:ILE:HG21	1.98	0.46
30:d:198:LEU:C	30:d:199:PHE:CG	2.94	0.46
32:f:560:LEU:HD13	32:f:801:VAL:HG21	1.97	0.46
9:i:155:ASN:OD1	10:j:77:THR:OG1	2.34	0.46
13:m:215:TRP:HE1	13:m:227:VAL:HA	1.81	0.46
1:A:397:ILE:O	1:A:400:ARG:NH2	2.48	0.46
2:B:367:ILE:HG22	2:B:371:ARG:HH22	1.81	0.46
6:F:141:ASP:OD1	6:F:144:LYS:NZ	2.37	0.46
12:L:226:ASP:OD1	12:L:226:ASP:N	2.47	0.46
19:S:13:LEU:HD11	19:S:149:LEU:HD11	1.97	0.46
24:X:24:ILE:HG12	24:X:56:LEU:HD13	1.97	0.46
25:Y:387:ILE:HG21	26:Z:276:ILE:HD11	1.98	0.46
29:c:145:VAL:HG22	29:c:157:ILE:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:GLU:O	1:A:193:THR:OG1	2.34	0.46
27:a:97:LEU:HD22	27:a:118:ILE:HG13	1.98	0.46
32:f:594:LEU:HB2	32:f:652:VAL:HG21	1.98	0.46
8:h:50:LYS:HG2	8:h:52:GLN:HE21	1.81	0.46
1:A:284:ARG:HE	1:A:286:ASP:HA	1.81	0.45
2:B:290:ILE:HG13	2:B:305:ILE:HG23	1.98	0.45
2:B:294:ARG:HE	2:B:309:MET:HE1	1.80	0.45
3:C:205:HIS:HD2	3:C:206:HIS:CD2	2.34	0.45
21:U:609:ASP:O	21:U:615:ARG:NH1	2.47	0.45
25:Y:84:LEU:HD13	25:Y:107:LYS:HA	1.98	0.45
8:h:3:GLU:N	13:m:125:TYR:HB3	2.32	0.45
10:J:201:SER:OG	10:J:205:ASN:ND2	2.42	0.45
15:O:63:LEU:HD11	15:O:79:ALA:HB2	1.98	0.45
21:U:327:LYS:HG2	21:U:333:MET:HE1	1.98	0.45
24:X:407:MET:HA	24:X:410:VAL:HG22	1.98	0.45
27:a:363:MET:HE1	29:c:304:LEU:HD13	1.98	0.45
7:g:112:ASP:OD1	7:g:112:ASP:N	2.45	0.45
4:D:271:ALA:HA	4:D:289:LEU:HD12	1.97	0.45
10:J:231:GLU:O	10:J:234:LYS:HG3	2.16	0.45
13:M:65:ARG:HH21	13:M:78:ALA:HA	1.82	0.45
21:U:236:LEU:HA	21:U:239:GLU:HG2	1.99	0.45
21:U:857:ASP:OD1	21:U:857:ASP:N	2.48	0.45
22:V:117:VAL:HG22	22:V:167:LEU:HD21	1.98	0.45
24:X:28:HIS:O	24:X:32:LYS:HB2	2.16	0.45
24:X:316:ASP:C	24:X:318:ILE:N	2.73	0.45
2:B:288:ASP:N	2:B:288:ASP:OD1	2.47	0.45
3:C:148:TYR:HB2	3:C:206:HIS:CD2	2.50	0.45
3:C:188:LEU:N	3:C:293:MET:O	2.46	0.45
5:E:359:HIS:ND1	5:E:361:PHE:O	2.49	0.45
19:S:114:ASP:OD1	19:S:118:LYS:N	2.47	0.45
21:U:376:MET:HE2	21:U:735:GLY:HA2	1.97	0.45
21:U:400:ALA:O	21:U:404:ALA:N	2.38	0.45
26:Z:22:HIS:HA	26:Z:25:ARG:HE	1.81	0.45
32:f:119:LYS:HE2	32:f:119:LYS:HB3	1.78	0.45
32:f:408:LEU:HB3	32:f:439:TYR:HB3	1.98	0.45
19:s:114:ASP:OD1	19:s:118:LYS:N	2.35	0.45
2:B:221:GLY:HA3	2:B:347:ILE:HG12	1.99	0.45
12:L:137:TYR:HH	12:L:217:LYS:HZ3	1.58	0.45
22:V:219:GLU:HA	22:V:224:LEU:HD11	1.98	0.45
24:X:170:GLN:HB3	24:X:193:ALA:HB2	1.99	0.45
32:f:570:GLY:H	32:f:599:ALA:HB1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:130:SER:OG	10:J:147:THR:O	2.30	0.45
24:X:239:TYR:HB3	24:X:247:ALA:HB2	1.97	0.45
24:X:299:LEU:HD21	24:X:356:LEU:HD22	1.99	0.45
28:b:51:LEU:HD11	28:b:61:LEU:HD23	1.99	0.45
30:d:22:GLU:HB2	30:d:61:TRP:HZ3	1.81	0.45
32:f:233:LEU:HD13	32:f:252:ALA:HB2	1.99	0.45
19:s:28:ARG:NH2	19:s:213:ASP:OXT	2.49	0.45
33:u:44:ILE:HB	33:u:68:HIS:HB2	1.98	0.45
7:G:46:ASP:OD1	7:G:46:ASP:N	2.48	0.45
9:I:201:MET:HE3	9:I:206:LEU:HD11	1.99	0.45
21:U:392:TRP:HA	21:U:395:ARG:HH21	1.81	0.45
21:U:402:PHE:HB2	21:U:437:TYR:HB3	1.99	0.45
21:U:475:HIS:NE2	21:U:507:VAL:O	2.50	0.45
27:a:6:GLY:HA2	27:a:9:GLN:HB2	1.98	0.45
9:i:140:ASP:OD1	9:i:140:ASP:N	2.48	0.45
10:j:185:ASP:O	10:j:189:LYS:HG2	2.17	0.45
18:r:135:ALA:O	18:r:139:MET:HB2	2.17	0.45
4:D:124:LEU:HD21	4:D:142:VAL:HG21	1.99	0.45
8:H:197:GLU:HB3	24:X:201:TYR:HE1	1.82	0.45
12:L:47:VAL:HG12	12:L:195:LEU:HD22	1.99	0.45
23:W:80:TRP:HB3	23:W:123:ARG:HH22	1.80	0.45
24:X:314:ARG:O	24:X:314:ARG:HG2	2.16	0.45
28:b:20:ASP:HB3	28:b:25:ARG:HH21	1.81	0.45
32:f:743:ALA:HA	32:f:746:ARG:HB2	1.99	0.45
32:f:745:LEU:HD23	32:f:748:LEU:HD12	1.98	0.45
4:D:171:ASP:OD1	4:D:171:ASP:N	2.47	0.45
4:D:268:ASP:OD1	4:D:268:ASP:N	2.49	0.45
5:E:116:ASP:HA	5:E:117:PRO:HD2	1.59	0.45
21:U:689:ILE:HG12	21:U:732:LEU:HD22	1.99	0.45
22:V:176:MET:HE1	22:V:213:TYR:CD1	2.51	0.45
24:X:170:GLN:OE1	24:X:192:SER:OG	2.28	0.45
24:X:316:ASP:C	24:X:318:ILE:H	2.25	0.45
25:Y:91:ALA:HB1	25:Y:100:ILE:HG22	1.97	0.45
26:Z:200:GLY:HA3	29:c:225:TRP:HE1	1.82	0.45
31:e:42:ASN:OD1	31:e:43:TRP:N	2.47	0.45
16:p:67:LEU:HD11	16:p:91:VAL:HG22	1.97	0.45
3:C:18:SER:HA	3:C:22:GLN:HB2	1.99	0.45
3:C:405:TRP:CH2	9:I:27:ALA:HB1	2.52	0.45
11:K:168:ARG:NH2	12:L:53:GLN:OE1	2.49	0.45
21:U:13:ASP:OD1	21:U:44:LYS:NZ	2.47	0.45
21:U:151:ILE:HD11	21:U:163:PHE:HD2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:141:ILE:HG21	28:b:183:LEU:HD21	1.99	0.45
32:f:93:PRO:HB2	32:f:96:LEU:HD23	1.99	0.45
32:f:217:LEU:HD21	32:f:229:VAL:HG11	1.99	0.45
32:f:688:ARG:HA	32:f:721:VAL:HG22	1.99	0.45
21:U:804:SER:OG	21:U:805:ASN:N	2.50	0.44
22:V:268:GLU:HA	22:V:271:VAL:HG22	1.99	0.44
23:W:84:ASN:O	23:W:88:MET:HG3	2.16	0.44
23:W:230:MET:HB2	23:W:230:MET:HE2	1.84	0.44
27:a:276:CYS:O	27:a:280:MET:HE2	2.18	0.44
30:d:29:VAL:HG11	30:d:54:ILE:HD11	1.98	0.44
30:d:194:ALA:HA	30:d:198:LEU:HB2	1.98	0.44
14:n:46:SER:OG	14:n:97:GLY:O	2.35	0.44
5:E:248:SER:O	5:E:251:ARG:N	2.46	0.44
22:V:264:TYR:HE2	30:d:120:GLU:HG2	1.82	0.44
23:W:360:GLU:HG2	23:W:364:ARG:HH21	1.82	0.44
26:Z:26:ILE:HD11	26:Z:35:VAL:HG22	1.98	0.44
1:A:96:ALA:HB3	2:B:132:TYR:HD2	1.82	0.44
2:B:378:VAL:HA	2:B:416:ASN:HB2	1.98	0.44
10:J:148:ASP:OD1	10:J:152:THR:N	2.46	0.44
11:K:82:ILE:O	11:K:86:LYS:NZ	2.50	0.44
12:L:44:ALA:HB2	12:L:142:PRO:HB3	1.98	0.44
17:Q:65:GLN:HA	17:Q:68:LYS:HG2	1.99	0.44
22:V:452:ASN:HD22	22:V:457:TYR:HD2	1.64	0.44
23:W:316:ARG:CB	23:W:319:THR:OG1	2.65	0.44
24:X:33:ARG:HH12	24:X:35:ILE:HD13	1.82	0.44
26:Z:37:GLY:HA2	26:Z:56:VAL:HG12	1.99	0.44
27:a:84:VAL:HA	27:a:87:MET:HG3	1.99	0.44
32:f:208:LEU:HD13	32:f:217:LEU:HD12	1.99	0.44
1:A:74:PRO:HA	1:A:75:PRO:HD3	1.86	0.44
5:E:295:LEU:HD13	5:E:295:LEU:HA	1.88	0.44
6:F:343:LEU:O	6:F:349:ASP:CA	2.65	0.44
13:M:66:LEU:HD12	13:M:212:GLU:HG2	1.97	0.44
21:U:611:ASN:HB3	21:U:614:VAL:HG12	1.99	0.44
29:c:273:LYS:HG2	29:c:277:LYS:HD3	2.00	0.44
32:f:540:GLN:HA	32:f:543:MET:HG2	2.00	0.44
8:h:205:GLU:HG2	8:h:227:LYS:HB2	1.99	0.44
2:B:106:PRO:HB3	3:C:121:TYR:HB2	1.98	0.44
21:U:126:ILE:HB	21:U:130:LEU:HD11	1.99	0.44
23:W:216:GLU:O	23:W:219:THR:OG1	2.32	0.44
24:X:143:TYR:CE2	25:Y:252:SER:HB2	2.52	0.44
26:Z:147:ASP:OD1	26:Z:147:ASP:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:115:LYS:HD3	27:a:118:ILE:HD12	2.00	0.44
30:d:62:SER:HA	30:d:65:ARG:HG2	1.99	0.44
32:f:466:LEU:HB3	32:f:485:LEU:HD12	1.99	0.44
2:B:286:GLU:HA	2:B:331:THR:HG22	1.99	0.44
2:B:358:GLU:HA	2:B:361:LYS:HB2	1.99	0.44
4:D:173:GLN:HB3	4:D:333:PHE:HE1	1.82	0.44
10:J:220:LEU:HD12	10:J:225:ILE:HG13	1.98	0.44
14:N:40:ARG:NH2	14:N:181:GLU:O	2.41	0.44
17:Q:11:ASP:N	17:Q:11:ASP:OD1	2.50	0.44
20:T:25:ASP:OD1	20:T:41:ARG:NH2	2.45	0.44
21:U:26:LYS:HE3	30:d:36:LEU:HB2	2.00	0.44
21:U:870:GLU:N	21:U:871:PRO:HD2	2.32	0.44
32:f:83:ARG:O	32:f:87:THR:OG1	2.25	0.44
9:i:46:ALA:HB1	9:i:197:LEU:HD11	2.00	0.44
10:j:148:ASP:OD2	10:j:152:THR:OG1	2.36	0.44
2:B:103:ARG:HD3	2:B:160:ILE:HG21	1.99	0.44
5:E:168:LYS:HE3	5:E:270:LEU:HD23	2.00	0.44
27:a:261:LEU:HA	27:a:261:LEU:HD12	1.78	0.44
32:f:535:THR:HG23	32:f:562:LEU:HG	2.00	0.44
17:q:35:MET:HG2	17:q:45:LEU:HG	2.00	0.44
1:A:245:LEU:HD13	1:A:280:ILE:HD12	1.99	0.44
21:U:252:LEU:HD11	21:U:260:PHE:HE2	1.82	0.44
22:V:77:GLU:OE1	22:V:81:GLN:NE2	2.50	0.44
24:X:252:LYS:HA	24:X:287:LEU:HD11	2.00	0.44
24:X:357:SER:OG	24:X:358:LYS:N	2.50	0.44
25:Y:344:HIS:HB3	25:Y:357:ASN:OD1	2.18	0.44
15:o:51:ASP:HB3	15:o:94:ILE:HG23	2.00	0.44
20:t:69:GLN:HA	20:t:72:ILE:HG22	1.98	0.44
2:B:88:LEU:CD2	2:B:91:LYS:H	2.28	0.44
2:B:411:ARG:NH1	2:B:413:LYS:O	2.51	0.44
5:E:199:VAL:HG23	5:E:201:SER:H	1.83	0.44
6:F:314:LEU:O	6:F:347:ARG:NH1	2.51	0.44
11:K:99:HIS:HB2	11:K:107:MET:HE3	2.00	0.44
18:R:100:MET:HE2	18:R:128:VAL:HG23	2.00	0.44
19:S:16:ALA:HB2	19:S:121:VAL:HG23	1.99	0.44
21:U:358:ASP:O	21:U:361:ARG:NH2	2.51	0.44
22:V:244:ALA:HA	22:V:247:GLN:HE21	1.83	0.44
23:W:343:SER:OG	23:W:344:THR:N	2.51	0.44
24:X:157:LEU:HD21	24:X:165:LEU:HD23	2.00	0.44
27:a:222:LEU:HB2	27:a:226:ARG:NH2	2.33	0.44
28:b:122:LYS:HA	28:b:125:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:149:GLN:HB3	29:c:156:VAL:HG21	2.00	0.44
30:d:190:LEU:HD23	30:d:192:THR:H	1.82	0.44
12:l:88:MET:HG2	12:l:112:ILE:HD11	2.00	0.44
33:u:40:GLN:HA	33:u:72:ARG:HB2	2.00	0.44
10:J:208:LEU:HD22	10:J:220:LEU:CG	2.48	0.43
21:U:607:VAL:O	21:U:615:ARG:NH1	2.45	0.43
25:Y:153:ASP:HB3	25:Y:156:LEU:HB3	2.00	0.43
25:Y:237:ARG:O	25:Y:242:LYS:N	2.33	0.43
8:h:213:CYS:HB2	8:h:218:PHE:HD1	1.82	0.43
1:A:102:ILE:HD12	1:A:112:ILE:HG22	2.00	0.43
6:F:303:ASP:OD1	6:F:303:ASP:N	2.50	0.43
13:M:108:LEU:HD22	13:M:139:SER:HB3	1.99	0.43
16:P:38:ASP:OD1	16:P:38:ASP:N	2.51	0.43
23:W:49:SER:HA	23:W:52:LYS:HE3	1.98	0.43
24:X:395:LYS:NZ	29:c:246:LYS:HD3	2.32	0.43
28:b:156:PHE:O	28:b:160:LEU:HB2	2.17	0.43
7:g:61:LEU:HA	13:m:160:TYR:HD1	1.82	0.43
16:p:14:MET:HE2	16:p:167:ILE:HB	2.00	0.43
2:B:77:GLU:HA	2:B:80:ARG:NE	2.34	0.43
2:B:227:PRO:O	2:B:232:LYS:NZ	2.51	0.43
5:E:247:THR:O	5:E:247:THR:OG1	2.34	0.43
6:F:359:GLU:HB3	6:F:385:ALA:HB1	2.01	0.43
10:J:137:ASP:OD2	10:J:143:ARG:NE	2.46	0.43
23:W:108:CYS:HB3	23:W:128:LEU:HD11	2.00	0.43
23:W:334:GLU:OE2	23:W:338:THR:OG1	2.36	0.43
24:X:183:LEU:CB	24:X:184:PRO:HD3	2.25	0.43
12:l:65:HIS:NE2	12:l:67:ASP:O	2.51	0.43
6:F:289:ASP:OD1	6:F:289:ASP:N	2.48	0.43
21:U:38:ILE:O	21:U:42:VAL:HG13	2.19	0.43
25:Y:104:MET:HE3	25:Y:127:THR:HA	2.00	0.43
25:Y:316:LEU:HB3	25:Y:354:VAL:HG23	2.01	0.43
14:n:4:MET:HE1	14:n:159:ALA:HB3	2.00	0.43
16:p:159:ASP:OD1	16:p:159:ASP:N	2.49	0.43
3:C:277:LEU:O	3:C:310:ARG:NH1	2.52	0.43
17:Q:13:VAL:HG11	17:Q:105:ALA:HB1	2.01	0.43
21:U:3:THR:HG22	21:U:34:PHE:CZ	2.54	0.43
21:U:421:GLN:HA	21:U:424:ALA:HB3	2.00	0.43
26:Z:121:LEU:HD11	26:Z:138:TYR:HD2	1.83	0.43
29:c:45:GLY:HA2	29:c:53:VAL:HG21	2.00	0.43
10:j:185:ASP:OD1	10:j:185:ASP:N	2.50	0.43
17:q:88:LEU:HD23	17:q:118:MET:HE2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:r:41:LEU:HD23	18:r:103:GLY:HA3	2.00	0.43
1:A:157:ILE:O	1:A:159:PRO:N	2.52	0.43
7:G:165:ALA:HB1	7:G:179:LEU:HD13	2.00	0.43
13:M:45:VAL:HG11	13:M:148:LEU:HD13	2.01	0.43
22:V:235:LEU:O	22:V:239:THR:OG1	2.30	0.43
26:Z:125:ASP:HB3	26:Z:128:PRO:HD2	2.00	0.43
27:a:118:ILE:O	27:a:122:LYS:HB2	2.18	0.43
30:d:171:LEU:O	30:d:175:ARG:HG2	2.18	0.43
32:f:720:GLU:OE2	32:f:807:ARG:NH1	2.47	0.43
7:g:200:THR:HA	7:g:203:SER:HB3	2.00	0.43
14:n:107:GLU:HG2	14:n:110:GLN:NE2	2.34	0.43
1:A:183:GLN:HG2	1:A:343:PHE:CD1	2.54	0.43
2:B:359:LYS:H	2:B:359:LYS:HD2	1.83	0.43
3:C:27:LYS:NZ	21:U:106:ASP:OD1	2.50	0.43
16:P:125:ASP:OD1	16:P:125:ASP:N	2.52	0.43
21:U:420:LEU:O	21:U:424:ALA:N	2.51	0.43
22:V:438:VAL:HG12	22:V:451:ILE:HD11	2.00	0.43
23:W:171:VAL:HG11	23:W:182:ARG:HA	2.01	0.43
23:W:273:TYR:OH	23:W:350:ARG:NH2	2.52	0.43
25:Y:108:ALA:HA	25:Y:111:LEU:HD12	2.00	0.43
27:a:50:PHE:HD2	27:a:52:GLN:HB3	1.83	0.43
29:c:113:HIS:NE2	29:c:115:HIS:CE1	2.87	0.43
30:d:139:LEU:HD11	30:d:151:VAL:HG13	2.01	0.43
2:B:429:LYS:HG3	2:B:430:LYS:HG3	2.01	0.43
3:C:118:ASN:N	3:C:118:ASN:OD1	2.50	0.43
18:R:105:ASP:OD1	18:R:105:ASP:N	2.50	0.43
22:V:410:ILE:C	22:V:412:LEU:N	2.77	0.43
27:a:70:ARG:NH2	28:b:16:MET:O	2.51	0.43
27:a:103:LYS:HG3	27:a:104:VAL:HG23	2.00	0.43
27:a:278:MET:HA	27:a:281:THR:HG22	2.00	0.43
32:f:138:GLU:HA	32:f:141:LYS:HE2	2.00	0.43
32:f:540:GLN:HA	32:f:543:MET:HE2	2.00	0.43
32:f:662:MET:O	32:f:781:TYR:OH	2.28	0.43
4:D:248:ARG:HG3	4:D:295:GLN:HE22	1.83	0.43
8:H:203:MET:HE3	8:H:230:LEU:HD11	2.00	0.43
16:P:203:ARG:NH2	16:P:205:ASP:OD2	2.47	0.43
21:U:637:VAL:HG13	21:U:652:ALA:HB1	2.00	0.43
22:V:315:LYS:HE2	25:Y:385:ARG:HD3	2.01	0.43
24:X:122:ARG:HB3	24:X:125:LEU:HB3	2.00	0.43
28:b:6:THR:HB	28:b:49:VAL:HG22	2.01	0.43
7:g:232:GLU:HA	7:g:235:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:m:163:CYS:SG	13:m:164:ALA:N	2.91	0.43
13:M:34:SER:OG	13:M:65:ARG:NH1	2.51	0.43
21:U:796:LYS:HG3	21:U:924:LEU:HD21	2.01	0.43
8:h:148:GLN:OE1	8:h:158:TRP:NE1	2.52	0.43
1:A:208:PRO:HA	1:A:209:PRO:HD3	1.87	0.42
1:A:364:VAL:HG12	1:A:404:ALA:HB3	1.99	0.42
3:C:336:MET:HE1	3:C:363:CYS:HB3	2.01	0.42
6:F:275:ALA:O	6:F:281:SER:OG	2.32	0.42
24:X:397:TYR:CE2	25:Y:365:GLN:HB3	2.54	0.42
24:X:397:TYR:HE1	26:Z:258:VAL:HG21	1.83	0.42
27:a:341:LEU:HD13	27:a:345:GLN:HB2	2.00	0.42
28:b:18:ASN:OD1	28:b:25:ARG:NH1	2.52	0.42
29:c:195:GLY:O	29:c:199:HIS:N	2.48	0.42
30:d:176:ASP:OD1	30:d:177:GLU:N	2.52	0.42
32:f:597:VAL:HG11	32:f:656:GLY:HA3	2.01	0.42
7:g:73:THR:HG22	7:g:76:ILE:HB	2.01	0.42
10:j:222:PRO:HA	10:j:225:ILE:HG22	2.00	0.42
13:m:215:TRP:CD1	13:m:227:VAL:HG22	2.54	0.42
5:E:19:HIS:HA	5:E:22:ILE:HG22	2.01	0.42
17:Q:31:ASP:OD1	17:Q:31:ASP:N	2.53	0.42
21:U:351:MET:O	21:U:355:ASN:N	2.49	0.42
21:U:623:GLY:HA3	21:U:658:ILE:HG13	2.00	0.42
25:Y:217:LYS:HZ2	25:Y:249:VAL:HB	1.83	0.42
30:d:208:ASP:HA	30:d:211:LYS:HG2	2.01	0.42
32:f:533:ASP:O	32:f:536:SER:OG	2.30	0.42
1:A:158:ASP:CG	1:A:256:MET:SD	3.02	0.42
5:E:186:ALA:O	5:E:190:GLN:OE1	2.36	0.42
6:F:172:VAL:HG12	6:F:274:LEU:HD13	2.01	0.42
11:K:146:VAL:HG11	11:K:222:PRO:HA	2.01	0.42
15:O:113:ILE:HG12	15:O:119:THR:HG22	2.00	0.42
26:Z:98:GLY:HA2	26:Z:99:PRO:HD3	1.90	0.42
29:c:139:ARG:HB2	29:c:161:ARG:NH1	2.35	0.42
9:i:136:TYR:HB2	9:i:148:TYR:HB2	2.00	0.42
18:r:106:LYS:HD2	18:r:107:ARG:HG3	2.00	0.42
1:A:39:SER:O	1:A:43:ARG:NH1	2.53	0.42
1:A:158:ASP:O	1:A:160:THR:N	2.53	0.42
1:A:397:ILE:HD13	2:B:211:TYR:HE1	1.84	0.42
2:B:86:LYS:HA	2:B:87:PRO:HD2	1.71	0.42
4:D:148:ASP:HB3	5:E:78:ARG:CZ	2.50	0.42
4:D:347:THR:HG22	24:X:226:LYS:HZ1	1.84	0.42
6:F:189:GLY:H	35:F:501:ADP:HN62	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:240:ASP:OD1	11:K:241:ILE:N	2.51	0.42
12:L:33:SER:HG	12:L:62:LYS:HZ2	1.64	0.42
17:Q:1:MET:HE3	17:Q:133:GLY:HA2	2.01	0.42
23:W:256:ILE:HG23	23:W:262:LYS:HB3	2.00	0.42
7:g:10:ASP:OD1	7:g:10:ASP:N	2.51	0.42
10:j:80:ALA:HA	10:j:129:ILE:HD13	2.02	0.42
1:A:172:VAL:HG21	1:A:227:ARG:HG2	2.02	0.42
1:A:369:ARG:HH21	1:A:372:LEU:HD13	1.85	0.42
2:B:71:TYR:HA	2:B:74:MET:HG2	2.02	0.42
3:C:164:VAL:HG13	3:C:165:ILE:HG13	2.02	0.42
5:E:128:GLY:HA3	5:E:185:ARG:HE	1.84	0.42
5:E:283:ASP:OD1	5:E:283:ASP:N	2.49	0.42
8:H:8:PHE:HB3	10:J:3:TYR:HE1	1.83	0.42
21:U:655:ALA:HA	21:U:658:ILE:HG12	2.01	0.42
22:V:103:SER:HA	22:V:106:ARG:HH12	1.84	0.42
26:Z:127:LYS:HB2	26:Z:127:LYS:HE2	1.87	0.42
30:d:190:LEU:HD22	30:d:192:THR:HG22	2.01	0.42
30:d:254:GLU:C	30:d:256:ILE:H	2.27	0.42
1:A:158:ASP:CB	1:A:160:THR:HG22	2.46	0.42
3:C:79:ALA:HB1	3:C:85:VAL:HA	2.02	0.42
3:C:347:ILE:HD11	3:C:380:GLN:HG3	2.01	0.42
19:S:83:MET:HE1	19:S:91:MET:HE3	2.01	0.42
20:T:54:SER:OG	20:T:55:GLY:N	2.53	0.42
21:U:447:GLY:HA3	21:U:480:GLY:HA2	2.01	0.42
25:Y:101:ARG:HA	25:Y:104:MET:HE2	2.02	0.42
28:b:2:VAL:O	28:b:44:ASN:ND2	2.42	0.42
30:d:12:LYS:NZ	30:d:14:PRO:HB3	2.34	0.42
32:f:266:LEU:HD11	32:f:278:VAL:HG13	2.01	0.42
11:k:189:MET:HE2	11:k:189:MET:HB3	1.86	0.42
1:A:114:ASN:HB3	1:A:120:LYS:HG2	2.00	0.42
5:E:247:THR:HG22	6:F:300:LYS:HD2	2.01	0.42
16:P:53:LEU:HG	16:P:107:PRO:HB3	2.01	0.42
18:R:133:VAL:HG21	17:q:137:PHE:HB3	2.01	0.42
19:S:31:GLU:CD	19:S:36:HIS:HE2	2.27	0.42
19:S:36:HIS:O	20:T:151:ARG:NH2	2.52	0.42
21:U:525:ASN:HD22	21:U:528:ALA:HB2	1.84	0.42
21:U:883:ARG:NH2	21:U:885:MET:SD	2.79	0.42
23:W:67:LEU:HD22	23:W:100:ALA:HB1	2.01	0.42
23:W:108:CYS:O	23:W:112:VAL:HG23	2.19	0.42
24:X:122:ARG:HD2	24:X:125:LEU:HB2	2.02	0.42
26:Z:73:ASP:H	28:b:63:THR:HG21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:189:LYS:HD2	32:f:189:LYS:HA	1.74	0.42
7:g:130:GLU:HG2	8:h:5:GLY:HA2	2.02	0.42
9:i:161:ALA:HB3	10:j:53:LEU:HD23	2.02	0.42
16:p:34:MET:HE3	16:p:34:MET:HB3	1.85	0.42
18:r:127:SER:HB3	18:r:136:TYR:CE1	2.55	0.42
3:C:49:ARG:HD2	21:U:639:LEU:HD21	2.01	0.42
6:F:224:LEU:HD13	6:F:348:LEU:HD21	2.01	0.42
17:Q:19:ARG:NH1	17:Q:179:SER:OG	2.43	0.42
21:U:229:VAL:HA	21:U:232:ILE:HG12	2.02	0.42
22:V:411:SER:CB	22:V:447:ILE:HG12	2.37	0.42
23:W:118:LEU:HD21	23:W:156:ASN:HD21	1.85	0.42
23:W:455:LEU:HB2	23:W:456:GLN:NE2	2.34	0.42
24:X:99:MET:SD	24:X:100:GLU:N	2.93	0.42
24:X:306:LEU:CD1	24:X:310:ARG:HH12	2.33	0.42
29:c:272:ILE:C	29:c:274:ASN:N	2.78	0.42
30:d:42:LYS:HA	30:d:45:LYS:HB2	2.01	0.42
30:d:217:LEU:HB2	30:d:222:TYR:HE1	1.85	0.42
32:f:478:ARG:O	32:f:482:ILE:HG12	2.20	0.42
13:m:73:VAL:HG22	13:m:139:SER:HB3	2.00	0.42
4:D:133:HIS:HB3	4:D:137:ASN:N	2.35	0.42
4:D:153:MET:SD	4:D:153:MET:N	2.93	0.42
5:E:153:LEU:HD12	5:E:154:THR:HG23	2.01	0.42
13:M:43:ASP:OD1	13:M:43:ASP:N	2.52	0.42
13:M:204:VAL:HG13	13:M:205:LYS:HD3	2.02	0.42
16:P:183:MET:HE3	16:P:183:MET:HB3	1.91	0.42
21:U:419:ALA:HA	21:U:422:LEU:HB3	2.02	0.42
24:X:103:THR:C	24:X:105:GLN:N	2.78	0.42
24:X:171:LEU:HD23	24:X:209:THR:HG22	2.02	0.42
13:m:215:TRP:CH2	13:m:219:LEU:HD11	2.55	0.42
1:A:284:ARG:NH1	1:A:289:ALA:H	2.18	0.42
2:B:118:ASP:N	2:B:118:ASP:OD1	2.50	0.42
15:O:122:LEU:HD12	15:O:125:VAL:HG12	2.01	0.42
23:W:380:GLN:HG3	23:W:381:LEU:HD12	2.01	0.42
24:X:286:ALA:HB1	24:X:313:LEU:HB3	2.02	0.42
24:X:402:GLU:HB2	29:c:249:LEU:HD11	2.01	0.42
32:f:384:ALA:HA	32:f:419:LEU:HB3	2.02	0.42
7:g:70:PHE:CD2	7:g:91:VAL:HG21	2.55	0.42
10:j:105:GLU:HA	10:j:145:TYR:HE2	1.85	0.42
17:q:85:ARG:HA	17:q:118:MET:HE1	2.02	0.42
20:t:63:LEU:HA	20:t:63:LEU:HD23	1.80	0.42
1:A:114:ASN:HA	1:A:120:LYS:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:106:PRO:HB2	8:H:109:GLN:HG2	2.02	0.41
23:W:330:LYS:HE3	23:W:330:LYS:HB3	1.93	0.41
27:a:247:ARG:HA	27:a:250:THR:HG22	2.02	0.41
31:e:58:ALA:HB1	31:e:62:LYS:HZ3	1.85	0.41
7:g:80:MET:HE1	7:g:90:GLN:HB2	2.01	0.41
17:q:140:LEU:HD23	17:q:140:LEU:HA	1.91	0.41
2:B:112:LEU:HD23	2:B:123:VAL:HG12	2.01	0.41
2:B:299:SER:OG	2:B:300:GLY:N	2.52	0.41
4:D:105:SER:OG	4:D:108:GLY:O	2.38	0.41
4:D:395:LEU:HD23	4:D:395:LEU:HA	1.91	0.41
6:F:410:ARG:HE	6:F:412:ALA:HB3	1.84	0.41
9:I:246:LYS:HG3	9:I:249:ARG:HH21	1.86	0.41
21:U:140:ARG:O	21:U:144:ASP:CB	2.62	0.41
27:a:150:SER:OG	27:a:154:ARG:NH1	2.53	0.41
32:f:526:ALA:O	32:f:565:ASN:OD1	2.38	0.41
32:f:564:LEU:HD23	32:f:564:LEU:HA	1.79	0.41
20:t:9:THR:OG1	20:t:10:SER:N	2.52	0.41
4:D:88:VAL:HG12	5:E:79:TYR:HE1	1.86	0.41
7:G:199:ILE:HG23	7:G:210:PHE:HZ	1.85	0.41
8:H:9:SER:OG	8:H:123:GLN:O	2.28	0.41
12:L:225:ASP:HB3	12:L:226:ASP:H	1.75	0.41
17:Q:102:LEU:HB2	17:Q:118:MET:HB2	2.02	0.41
21:U:148:LYS:HA	21:U:151:ILE:HG22	2.01	0.41
27:a:130:VAL:HA	27:a:133:GLU:OE2	2.20	0.41
32:f:45:LEU:HD23	32:f:50:LYS:HG2	2.01	0.41
7:g:165:ALA:HB3	8:h:56:LEU:HD22	2.01	0.41
12:l:7:ASP:OD1	12:l:7:ASP:N	2.49	0.41
18:r:105:ASP:OD1	18:r:105:ASP:N	2.52	0.41
2:B:412:MET:HA	2:B:412:MET:HE2	2.01	0.41
4:D:88:VAL:HG12	5:E:79:TYR:CE1	2.55	0.41
4:D:254:ALA:HB2	4:D:262:ILE:HD11	2.01	0.41
5:E:171:LEU:HD13	5:E:277:MET:HG3	2.01	0.41
20:T:50:MET:HE2	20:T:192:VAL:HG12	2.02	0.41
21:U:775:LEU:HD23	21:U:775:LEU:HA	1.92	0.41
23:W:357:ARG:HD3	23:W:357:ARG:HA	1.92	0.41
25:Y:141:VAL:HG11	25:Y:164:ALA:HB2	2.03	0.41
26:Z:15:VAL:HG23	26:Z:53:SER:HB2	2.03	0.41
29:c:46:ARG:HH12	29:c:147:PRO:C	2.25	0.41
30:d:255:MET:HB3	30:d:255:MET:HE3	1.64	0.41
32:f:795:GLY:HA3	32:f:823:ALA:HB3	2.03	0.41
10:j:212:ARG:H	10:j:215:GLN:NE2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:o:63:LEU:HD23	15:o:63:LEU:HA	1.91	0.41
3:C:44:ARG:HA	22:V:495:ARG:HG2	2.02	0.41
5:E:277:MET:HE1	5:E:289:LEU:HD21	2.01	0.41
10:J:220:LEU:HD22	10:J:220:LEU:HA	1.77	0.41
24:X:297:ARG:NH2	24:X:333:GLN:HB3	2.35	0.41
25:Y:14:ASN:HA	25:Y:15:PRO:HA	1.87	0.41
30:d:56:GLU:HG2	30:d:98:LEU:HD22	2.03	0.41
30:d:182:ILE:HG23	30:d:215:TRP:HZ2	1.86	0.41
9:i:53:HIS:HB3	9:i:56:LEU:HD23	2.02	0.41
33:u:27:LYS:HE2	33:u:43:LEU:HD23	2.03	0.41
3:C:190:GLY:HA2	3:C:191:PRO:HD3	1.80	0.41
4:D:45:LYS:HD3	4:D:45:LYS:HA	1.76	0.41
5:E:248:SER:HA	5:E:251:ARG:HD3	2.01	0.41
6:F:436:GLN:HG2	6:F:437:TYR:H	1.86	0.41
9:I:119:GLN:HE21	9:I:119:GLN:HB3	1.71	0.41
16:P:62:THR:O	16:P:66:ARG:HG3	2.21	0.41
21:U:170:SER:OG	21:U:172:ASP:OD1	2.32	0.41
25:Y:2:PRO:HG2	25:Y:5:ASN:HB2	2.01	0.41
26:Z:270:VAL:HG13	29:c:281:LYS:HE3	2.02	0.41
27:a:363:MET:HE2	29:c:307:VAL:HB	2.03	0.41
28:b:161:ASN:ND2	28:b:168:SER:H	2.12	0.41
32:f:56:LEU:HD23	32:f:56:LEU:HA	1.93	0.41
32:f:741:LEU:HA	32:f:744:MET:HB3	2.02	0.41
11:k:202:LEU:HA	11:k:205:VAL:HG22	2.02	0.41
21:U:490:ARG:HB2	21:U:493:VAL:HG12	2.03	0.41
23:W:234:ASP:HA	23:W:237:GLU:HB2	2.03	0.41
26:Z:116:CYS:O	26:Z:119:SER:OG	2.32	0.41
28:b:140:ILE:HD13	28:b:157:VAL:HG22	2.03	0.41
2:B:227:PRO:HD2	2:B:230:THR:HG21	2.03	0.41
4:D:415:GLU:OE2	8:H:57:TYR:OH	2.26	0.41
5:E:195:PHE:HD1	5:E:229:ILE:HG23	1.86	0.41
6:F:59:VAL:O	6:F:63:THR:OG1	2.32	0.41
6:F:410:ARG:HG3	6:F:412:ALA:H	1.86	0.41
10:J:67:ASP:OD1	10:J:67:ASP:N	2.52	0.41
11:K:195:ILE:HG23	11:K:217:LEU:HD21	2.01	0.41
9:i:216:LEU:HD12	9:i:225:ILE:HG12	2.03	0.41
1:A:158:ASP:HB2	1:A:160:THR:HG21	2.00	0.41
2:B:174:MET:N	2:B:174:MET:SD	2.94	0.41
2:B:181:GLN:HE21	2:B:237:LYS:HB2	1.86	0.41
4:D:103:VAL:HG21	4:D:132:LEU:HD21	2.02	0.41
4:D:238:LYS:HE3	4:D:239:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:169:ASP:HB3	6:F:172:VAL:HG23	2.03	0.41
7:G:13:ILE:HD12	7:G:13:ILE:HA	2.00	0.41
7:G:131:MET:SD	7:G:131:MET:N	2.93	0.41
9:I:17:ARG:NH2	9:I:22:GLU:OE1	2.54	0.41
9:I:41:ASP:OD1	9:I:41:ASP:N	2.53	0.41
15:O:112:SER:HB3	15:O:125:VAL:HG11	2.03	0.41
16:P:30:ILE:HG22	16:P:31:GLN:H	1.85	0.41
17:Q:52:ASP:OD1	18:R:88:TYR:OH	2.31	0.41
21:U:398:ASN:H	21:U:401:LYS:HZ3	1.66	0.41
21:U:521:LEU:HD13	21:U:554:LEU:HG	2.01	0.41
22:V:321:ALA:HB1	22:V:324:PHE:HB3	2.03	0.41
23:W:42:GLU:O	23:W:45:GLU:HG2	2.20	0.41
26:Z:35:VAL:H	26:Z:97:THR:HG22	1.86	0.41
26:Z:81:MET:HE2	26:Z:81:MET:HB3	1.98	0.41
28:b:86:PHE:CZ	28:b:90:ILE:HD11	2.55	0.41
29:c:56:LEU:HD23	29:c:111:TRP:HB3	2.01	0.41
30:d:84:ASP:HB3	30:d:87:GLU:HG3	2.02	0.41
7:g:5:SER:OG	7:g:11:ARG:NH2	2.54	0.41
12:l:71:GLY:HA3	12:l:221:PHE:CZ	2.55	0.41
13:m:15:SER:OG	13:m:19:ARG:N	2.45	0.41
1:A:141:GLY:N	1:A:151:ILE:O	2.52	0.41
1:A:284:ARG:NH2	1:A:286:ASP:HA	2.35	0.41
3:C:117:ARG:HH21	29:c:189:ILE:HG21	1.84	0.41
3:C:213:ARG:HD2	4:D:299:PHE:HD2	1.85	0.41
24:X:216:ILE:HD13	24:X:216:ILE:HA	1.94	0.41
25:Y:232:GLU:HG2	25:Y:233:ARG:HG2	2.02	0.41
29:c:122:LEU:HB2	29:c:200:TYR:CE1	2.56	0.41
29:c:198:ARG:HG3	29:c:199:HIS:CD2	2.57	0.41
29:c:208:ARG:HA	29:c:208:ARG:HD3	1.88	0.41
31:e:47:ASN:OD1	31:e:47:ASN:N	2.53	0.41
10:j:154:HIS:CG	11:k:59:MET:HE1	2.55	0.41
1:A:74:PRO:O	1:A:76:ALA:N	2.51	0.40
5:E:130:VAL:HG23	5:E:186:ALA:HA	2.03	0.40
17:Q:35:MET:HE3	17:Q:45:LEU:HD21	2.02	0.40
19:S:26:ASP:OD1	19:S:26:ASP:N	2.54	0.40
21:U:325:MET:HA	21:U:328:ILE:HG12	2.03	0.40
26:Z:14:LEU:HD12	29:c:39:LEU:HB3	2.03	0.40
29:c:132:SER:HB3	33:u:71:LEU:HD23	2.03	0.40
29:c:198:ARG:HD3	29:c:199:HIS:NE2	2.36	0.40
30:d:42:LYS:HD2	30:d:45:LYS:HB2	2.03	0.40
10:j:220:LEU:HD23	10:j:220:LEU:HA	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:168:GLY:HA2	4:D:347:THR:HG21	2.02	0.40
5:E:75:ASN:N	5:E:75:ASN:OD1	2.54	0.40
7:G:90:GLN:HE21	7:G:134:LEU:HD23	1.86	0.40
14:N:165:GLU:OE2	20:t:37:ARG:NH1	2.51	0.40
19:S:19:ASP:N	19:S:19:ASP:OD1	2.53	0.40
21:U:7:GLY:O	21:U:10:SER:OG	2.33	0.40
21:U:27:LEU:HD12	21:U:27:LEU:HA	1.92	0.40
23:W:115:ILE:HG13	23:W:124:LEU:HD21	2.03	0.40
30:d:179:ALA:HA	30:d:182:ILE:HG22	2.03	0.40
16:p:15:LYS:HE3	16:p:121:ILE:HG12	2.03	0.40
1:A:284:ARG:HH22	1:A:289:ALA:H	1.70	0.40
4:D:87:LEU:HD13	4:D:131:ALA:HB1	2.03	0.40
5:E:155:ASN:HD21	23:W:207:LYS:HD3	1.87	0.40
5:E:379:LYS:HA	5:E:379:LYS:HD3	1.99	0.40
17:Q:119:ASP:OD1	17:Q:119:ASP:N	2.55	0.40
22:V:315:LYS:HG2	25:Y:385:ARG:HD3	2.03	0.40
23:W:200:ILE:O	23:W:204:ILE:HG13	2.22	0.40
24:X:155:ARG:HH12	25:Y:1:MET:HA	1.87	0.40
24:X:316:ASP:HA	24:X:320:SER:H	1.85	0.40
24:X:397:TYR:CD2	25:Y:365:GLN:HB3	2.56	0.40
30:d:3:GLU:HB2	30:d:25:ARG:HD2	2.02	0.40
30:d:106:LEU:HD21	30:d:114:GLU:HB3	2.02	0.40
30:d:237:ILE:HG13	30:d:238:PRO:HD3	2.03	0.40
32:f:416:MET:HE3	32:f:416:MET:HB3	1.94	0.40
13:m:19:ARG:NH2	13:m:24:GLU:OE1	2.54	0.40
4:D:67:ASN:ND2	21:U:608:SER:HA	2.36	0.40
7:G:10:ASP:OD1	7:G:10:ASP:N	2.53	0.40
9:I:54:LYS:HB3	9:I:54:LYS:HE3	1.28	0.40
14:N:127:ILE:HD12	14:N:132:SER:HB2	2.04	0.40
19:S:45:LYS:HE3	19:S:203:ILE:HD12	2.04	0.40
21:U:210:LYS:HD2	21:U:210:LYS:HA	1.96	0.40
25:Y:315:THR:HA	25:Y:353:ILE:HD12	2.04	0.40
27:a:343:LEU:HA	27:a:346:ILE:HD12	2.04	0.40
29:c:75:MET:O	29:c:77:GLN:NE2	2.55	0.40
13:m:45:VAL:HG23	13:m:146:ALA:HB1	2.04	0.40
5:E:340:GLY:HA3	36:E:401:ATP:C4	2.56	0.40
6:F:219:PRO:HA	6:F:220:PRO:HD3	1.99	0.40
16:P:53:LEU:HB3	16:P:60:VAL:HG22	2.03	0.40
21:U:161:ASP:OD1	21:U:161:ASP:N	2.52	0.40
21:U:895:PRO:HB2	21:U:898:CYS:HB3	2.04	0.40
22:V:265:ASP:N	22:V:265:ASP:OD1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:297:ARG:HH22	24:X:333:GLN:HB3	1.86	0.40
29:c:162:LEU:HD12	29:c:162:LEU:HA	1.90	0.40
30:d:158:ILE:HG12	30:d:163:TYR:HB2	2.04	0.40
11:k:129:ASP:OD1	11:k:129:ASP:N	2.54	0.40
12:l:217:LYS:HE2	12:l:217:LYS:HB2	1.94	0.40
16:p:125:ASP:OD1	16:p:125:ASP:N	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	400/433 (92%)	351 (88%)	46 (12%)	3 (1%)	16	44
2	B	397/440 (90%)	359 (90%)	36 (9%)	2 (0%)	24	54
3	C	394/398 (99%)	339 (86%)	55 (14%)	0	100	100
4	D	378/418 (90%)	327 (86%)	49 (13%)	2 (0%)	24	54
5	E	387/403 (96%)	340 (88%)	43 (11%)	4 (1%)	12	40
6	F	391/439 (89%)	345 (88%)	44 (11%)	2 (0%)	24	54
7	G	242/246 (98%)	229 (95%)	13 (5%)	0	100	100
7	g	242/246 (98%)	225 (93%)	14 (6%)	3 (1%)	10	35
8	H	230/234 (98%)	221 (96%)	9 (4%)	0	100	100
8	h	230/234 (98%)	219 (95%)	9 (4%)	2 (1%)	14	42
9	I	249/261 (95%)	240 (96%)	7 (3%)	2 (1%)	16	44
9	i	248/261 (95%)	241 (97%)	7 (3%)	0	100	100
10	J	237/248 (96%)	225 (95%)	12 (5%)	0	100	100
10	j	237/248 (96%)	220 (93%)	17 (7%)	0	100	100
11	K	232/241 (96%)	219 (94%)	11 (5%)	2 (1%)	14	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	k	232/241 (96%)	225 (97%)	7 (3%)	0	100	100
12	L	236/263 (90%)	228 (97%)	8 (3%)	0	100	100
12	l	236/263 (90%)	227 (96%)	9 (4%)	0	100	100
13	M	238/255 (93%)	230 (97%)	8 (3%)	0	100	100
13	m	238/255 (93%)	231 (97%)	7 (3%)	0	100	100
14	N	200/239 (84%)	194 (97%)	6 (3%)	0	100	100
14	n	200/239 (84%)	192 (96%)	8 (4%)	0	100	100
15	O	218/277 (79%)	210 (96%)	8 (4%)	0	100	100
15	o	218/277 (79%)	211 (97%)	7 (3%)	0	100	100
16	P	202/205 (98%)	189 (94%)	13 (6%)	0	100	100
16	p	202/205 (98%)	192 (95%)	10 (5%)	0	100	100
17	Q	197/201 (98%)	189 (96%)	8 (4%)	0	100	100
17	q	197/201 (98%)	191 (97%)	6 (3%)	0	100	100
18	R	199/263 (76%)	194 (98%)	5 (2%)	0	100	100
18	r	199/263 (76%)	192 (96%)	7 (4%)	0	100	100
19	S	211/241 (88%)	202 (96%)	9 (4%)	0	100	100
19	s	211/241 (88%)	203 (96%)	8 (4%)	0	100	100
20	T	214/264 (81%)	208 (97%)	6 (3%)	0	100	100
20	t	214/264 (81%)	207 (97%)	7 (3%)	0	100	100
21	U	874/953 (92%)	800 (92%)	73 (8%)	1 (0%)	48	78
22	V	442/534 (83%)	419 (95%)	23 (5%)	0	100	100
23	W	439/456 (96%)	425 (97%)	14 (3%)	0	100	100
24	X	420/422 (100%)	393 (94%)	24 (6%)	3 (1%)	18	47
25	Y	387/389 (100%)	363 (94%)	24 (6%)	0	100	100
26	Z	284/324 (88%)	252 (89%)	32 (11%)	0	100	100
27	a	371/376 (99%)	335 (90%)	35 (9%)	1 (0%)	36	65
28	b	189/377 (50%)	169 (89%)	20 (11%)	0	100	100
29	c	285/310 (92%)	236 (83%)	47 (16%)	2 (1%)	18	47
30	d	255/350 (73%)	215 (84%)	40 (16%)	0	100	100
31	e	48/70 (69%)	42 (88%)	6 (12%)	0	100	100
32	f	840/908 (92%)	802 (96%)	38 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	u	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
All	All	13464/14952 (90%)	12535 (93%)	900 (7%)	29 (0%)	44	71

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	157	ILE
2	B	87	PRO
5	E	117	PRO
5	E	247	THR
5	E	248	SER
9	I	54	LYS
24	X	310	ARG
7	g	4	GLY
8	h	55	ILE
5	E	127	PRO
9	I	53	HIS
29	c	198	ARG
2	B	85	MET
11	K	128	ALA
27	a	69	HIS
29	c	270	LEU
8	h	54	SER
1	A	285	PHE
4	D	150	SER
24	X	312	GLU
1	A	158	ASP
4	D	146	GLU
6	F	300	LYS
7	g	5	SER
24	X	105	GLN
7	g	7	ALA
11	K	131	GLY
21	U	813	TYR
6	F	165	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	338/372 (91%)	335 (99%)	3 (1%)	70	76
2	B	349/385 (91%)	347 (99%)	2 (1%)	78	80
3	C	340/346 (98%)	340 (100%)	0	100	100
4	D	333/366 (91%)	331 (99%)	2 (1%)	78	80
5	E	341/353 (97%)	339 (99%)	2 (1%)	78	80
6	F	340/379 (90%)	336 (99%)	4 (1%)	63	72
7	G	205/210 (98%)	205 (100%)	0	100	100
7	g	202/210 (96%)	202 (100%)	0	100	100
8	H	188/191 (98%)	188 (100%)	0	100	100
8	h	188/191 (98%)	185 (98%)	3 (2%)	55	68
9	I	207/221 (94%)	204 (99%)	3 (1%)	59	70
9	i	206/221 (93%)	206 (100%)	0	100	100
10	J	201/211 (95%)	198 (98%)	3 (2%)	57	69
10	j	196/211 (93%)	196 (100%)	0	100	100
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%)	202 (100%)	0	100	100
12	l	201/224 (90%)	201 (100%)	0	100	100
13	M	196/212 (92%)	196 (100%)	0	100	100
13	m	198/212 (93%)	198 (100%)	0	100	100
14	N	157/181 (87%)	156 (99%)	1 (1%)	78	80
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%)	168 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	752/816 (92%)	751 (100%)	1 (0%)	88	89
22	V	390/460 (85%)	388 (100%)	2 (0%)	81	81
23	W	406/416 (98%)	405 (100%)	1 (0%)	87	85
24	X	362/362 (100%)	354 (98%)	8 (2%)	45	63
25	Y	344/344 (100%)	344 (100%)	0	100	100
26	Z	257/295 (87%)	256 (100%)	1 (0%)	84	83
27	a	333/336 (99%)	333 (100%)	0	100	100
28	b	167/312 (54%)	167 (100%)	0	100	100
29	c	252/268 (94%)	247 (98%)	5 (2%)	48	65
30	d	231/294 (79%)	227 (98%)	4 (2%)	53	67
31	e	44/63 (70%)	44 (100%)	0	100	100
32	f	711/763 (93%)	710 (100%)	1 (0%)	88	89
33	u	68/68 (100%)	68 (100%)	0	100	100
All	All	11512/12682 (91%)	11466 (100%)	46 (0%)	81	83

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	157	ILE
1	A	284	ARG
1	A	403	ILE
2	B	88	LEU
2	B	125	THR
4	D	146	GLU
4	D	148	ASP
5	E	118	LEU
5	E	248	SER
6	F	164	LEU
6	F	300	LYS
6	F	343	LEU
6	F	344	ARG
9	I	7[A]	SER

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Mol	Chain	Res	Type
9	I	7[B]	SER
9	I	54	LYS
10	J	219	ILE
10	J	220	LEU
10	J	221	ASN
14	N	148	THR
21	U	870	GLU
22	V	411	SER
22	V	412	LEU
23	W	455	LEU
24	X	105	GLN
24	X	107	VAL
24	X	108	GLU
24	X	142	ARG
24	X	313	LEU
24	X	314	ARG
24	X	318	ILE
24	X	320	SER
26	Z	144	VAL
29	c	196	LEU
29	c	197	ASN
29	c	198	ARG
29	c	270	LEU
29	c	272	ILE
30	d	199	PHE
30	d	255	MET
30	d	256	ILE
30	d	257	VAL
32	f	566	HIS
8	h	3	GLU
8	h	4	ARG
8	h	53	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	A	247	GLN
1	A	379	ASN
1	A	414	ASN
2	B	306	GLN
3	C	64	GLN

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Mol	Chain	Res	Type
3	C	124	HIS
3	C	206	HIS
3	C	332	HIS
4	D	48	GLN
4	D	67	ASN
4	D	278	GLN
5	E	39	GLN
5	E	155	ASN
5	E	316	HIS
6	F	92	ASN
6	F	325	GLN
7	G	33	ASN
7	G	75	ASN
7	G	90	GLN
8	H	88	HIS
8	H	102	GLN
9	I	102	GLN
9	I	142	HIS
11	K	97	GLN
11	K	204	GLN
12	L	60	GLN
12	L	86	ASN
14	N	66	HIS
15	O	66	HIS
15	O	165	ASN
15	O	172	ASN
16	P	7	ASN
16	P	145	GLN
17	Q	82	ASN
17	Q	101	ASN
17	Q	168	GLN
19	S	146	GLN
20	T	213	HIS
21	U	70	HIS
21	U	89	ASN
21	U	145	HIS
21	U	218	GLN
21	U	258	GLN
21	U	438	GLN
21	U	632	GLN
21	U	718	ASN
21	U	749	GLN

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Mol	Chain	Res	Type
22	V	146	GLN
22	V	199	ASN
22	V	281	ASN
22	V	282	ASN
22	V	452	ASN
23	W	96	GLN
23	W	453	HIS
24	X	36	GLN
24	X	44	GLN
24	X	292	GLN
24	X	322	HIS
24	X	406	ASN
25	Y	136	HIS
25	Y	160	ASN
26	Z	24	ASN
26	Z	77	ASN
26	Z	102	HIS
26	Z	145	HIS
26	Z	254	ASN
27	a	9	GLN
27	a	86	GLN
27	a	287	ASN
27	a	370	GLN
28	b	161	ASN
29	c	77	GLN
29	c	128	ASN
29	c	130	GLN
29	c	199	HIS
29	c	219	ASN
30	d	116	HIS
32	f	198	HIS
32	f	293	GLN
32	f	387	GLN
32	f	531	ASN
32	f	565	ASN
32	f	610	GLN
32	f	868	HIS
7	g	68	HIS
8	h	166	ASN
9	i	20	GLN
9	i	40	ASN
9	i	95	GLN

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Mol	Chain	Res	Type
10	j	175	ASN
12	l	8	ASN
12	l	69	HIS
12	l	143	HIS
12	l	175	HIS
14	n	66	HIS
14	n	158	ASN
16	p	93	ASN
17	q	101	ASN
17	q	110	HIS
17	q	132	HIS
18	r	89	GLN
18	r	162	GLN
18	r	196	HIS
19	s	58	HIS
33	u	41	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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
36	ATP	D	501	37	29,33,33	0.37	0	44,52,52	0.52	1 (2%)
35	ADP	A	501	-	27,29,29	1.35	4 (14%)	42,45,45	1.98	10 (23%)
36	ATP	E	401	-	29,33,33	0.36	0	44,52,52	0.60	0
35	ADP	F	501	-	27,29,29	1.39	4 (14%)	42,45,45	2.07	9 (21%)
36	ATP	C	501	37	29,33,33	0.34	0	44,52,52	0.47	0

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
36	ATP	D	501	37	-	5/22/38/38	0/3/3/3
35	ADP	A	501	-	-	2/16/32/32	0/3/3/3
36	ATP	E	401	-	-	9/22/38/38	0/3/3/3
35	ADP	F	501	-	-	5/16/32/32	0/3/3/3
36	ATP	C	501	37	-	3/22/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	A	501	ADP	C5-C4	4.54	1.47	1.39
35	F	501	ADP	C5-C4	4.53	1.47	1.39
35	F	501	ADP	C5-N7	-2.72	1.33	1.39
35	A	501	ADP	C5-C6	2.59	1.48	1.41
35	F	501	ADP	C5-C6	2.53	1.48	1.41
35	A	501	ADP	C8-N7	2.30	1.35	1.31
35	A	501	ADP	C5-N7	-2.20	1.34	1.39
35	F	501	ADP	C8-N7	2.20	1.35	1.31

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	F	501	ADP	C5-C4-N3	-7.02	117.59	126.75
35	A	501	ADP	C5-C4-N3	-6.06	118.85	126.75
35	F	501	ADP	N3-C4-N9	5.61	136.33	127.08
35	A	501	ADP	N3-C4-N9	4.80	134.99	127.08
35	F	501	ADP	C2-N3-C4	4.01	121.21	111.75
35	A	501	ADP	PA-O3A-PB	-3.83	119.69	132.83
35	A	501	ADP	C2-N3-C4	3.74	120.60	111.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	F	501	ADP	PA-O3A-PB	-3.53	120.72	132.83
35	A	501	ADP	C4-C5-N7	-3.17	106.75	110.62
35	F	501	ADP	C4-C5-N7	-3.09	106.86	110.62
35	A	501	ADP	N3-C2-N1	-3.06	123.82	128.60
35	F	501	ADP	N3-C2-N1	-2.93	124.02	128.60
35	F	501	ADP	C3'-C2'-C1'	2.90	106.93	101.43
35	A	501	ADP	C5-N7-C8	2.71	107.36	103.51
35	F	501	ADP	C5-N7-C8	2.62	107.23	103.51
35	A	501	ADP	C4-N9-C8	2.58	108.53	105.73
35	A	501	ADP	C3'-C2'-C1'	2.53	106.24	101.43
36	D	501	ATP	PB-O3B-PG	2.15	140.21	132.83
35	A	501	ADP	C6-C5-N7	2.06	135.85	132.02
35	F	501	ADP	C4-N9-C8	2.05	107.95	105.73

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	F	501	ADP	PA-O3A-PB-O3B
35	F	501	ADP	C5'-O5'-PA-O1A
35	F	501	ADP	C5'-O5'-PA-O2A
35	F	501	ADP	C5'-O5'-PA-O3A
36	C	501	ATP	PB-O3B-PG-O3G
36	D	501	ATP	C5'-O5'-PA-O3A
36	E	401	ATP	C5'-O5'-PA-O1A
36	E	401	ATP	C5'-O5'-PA-O2A
36	E	401	ATP	C3'-C4'-C5'-O5'
36	E	401	ATP	O4'-C4'-C5'-O5'
36	E	401	ATP	PB-O3B-PG-O1G
36	E	401	ATP	C4'-C5'-O5'-PA
36	D	501	ATP	C5'-O5'-PA-O1A
36	D	501	ATP	C4'-C5'-O5'-PA
36	D	501	ATP	PG-O3B-PB-O3A
35	A	501	ADP	O4'-C4'-C5'-O5'
35	F	501	ADP	PA-O3A-PB-O1B
36	C	501	ATP	PB-O3B-PG-O1G
36	C	501	ATP	PB-O3B-PG-O2G
36	E	401	ATP	PB-O3B-PG-O2G
36	E	401	ATP	PB-O3B-PG-O3G
35	A	501	ADP	C5'-O5'-PA-O3A
36	E	401	ATP	C5'-O5'-PA-O3A
36	D	501	ATP	PG-O3B-PB-O1B

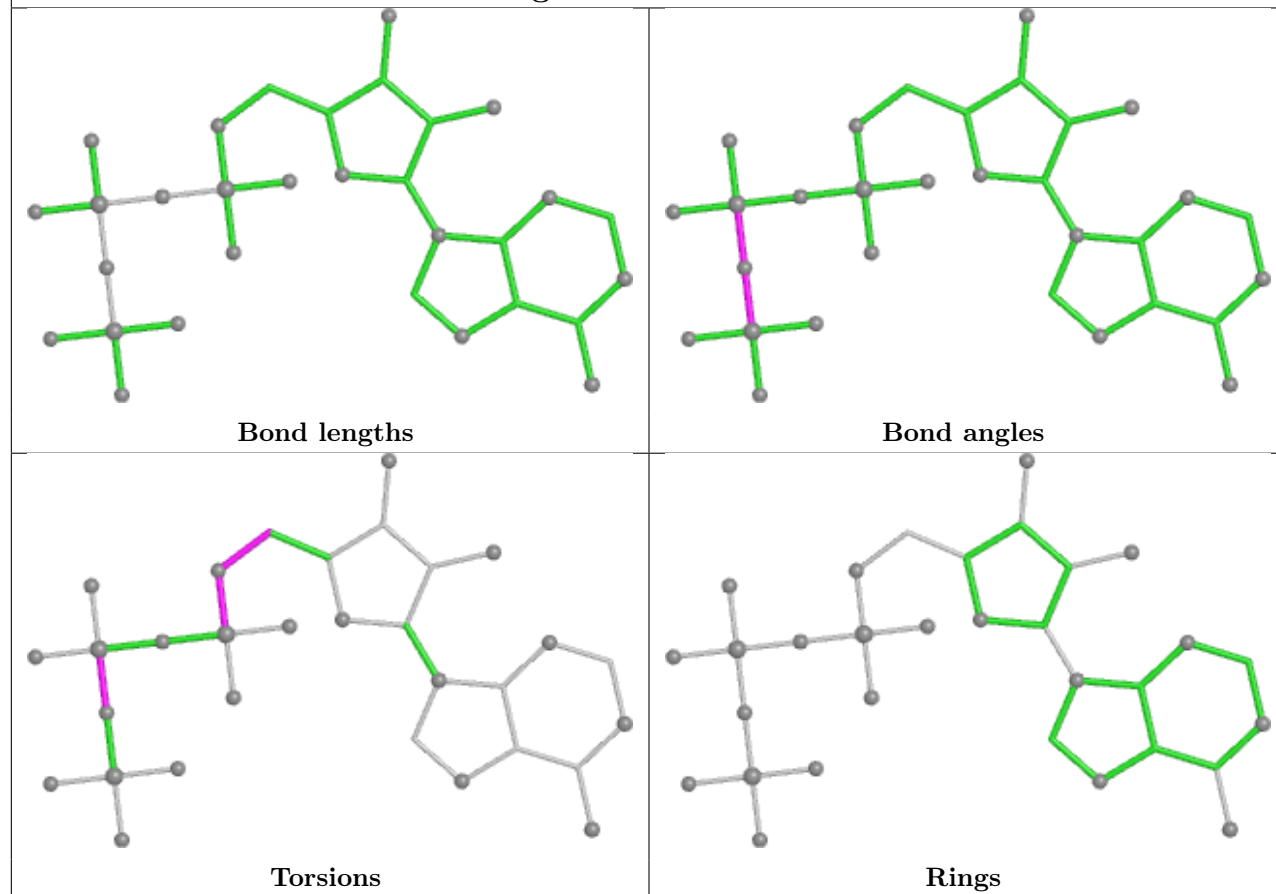
There are no ring outliers.

5 monomers are involved in 10 short contacts:

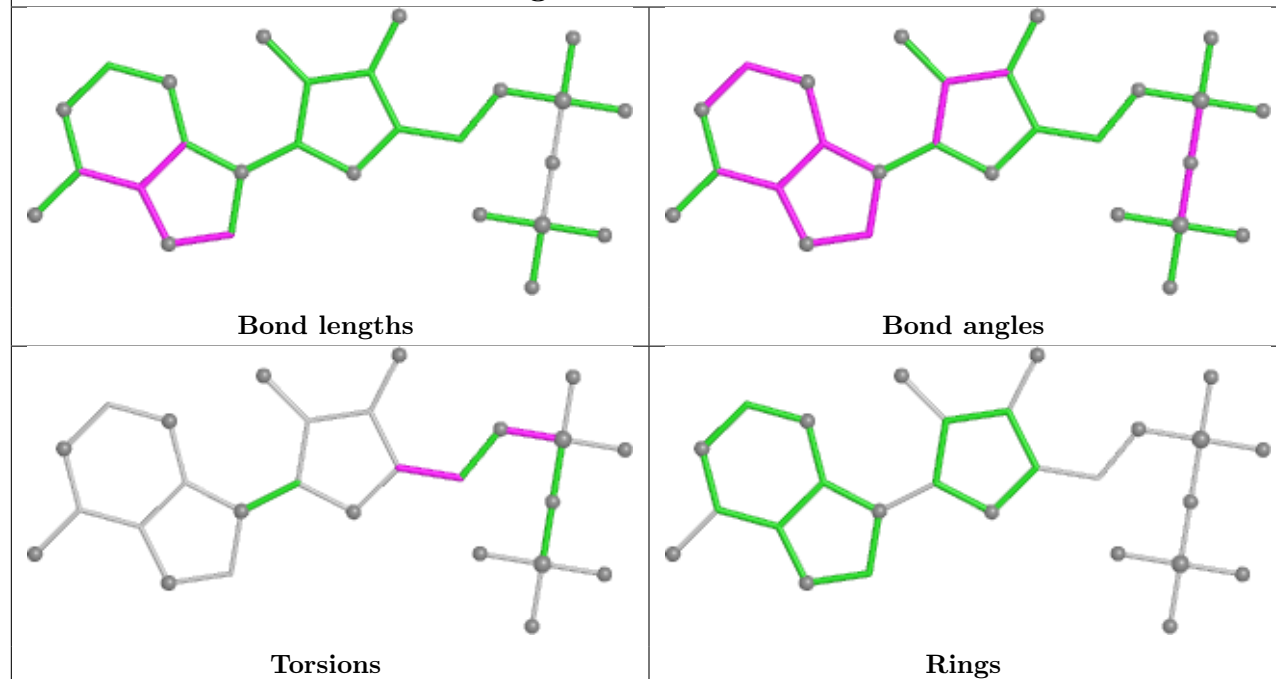
Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	D	501	ATP	1	0
35	A	501	ADP	2	0
36	E	401	ATP	3	0
35	F	501	ADP	1	0
36	C	501	ATP	3	0

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.

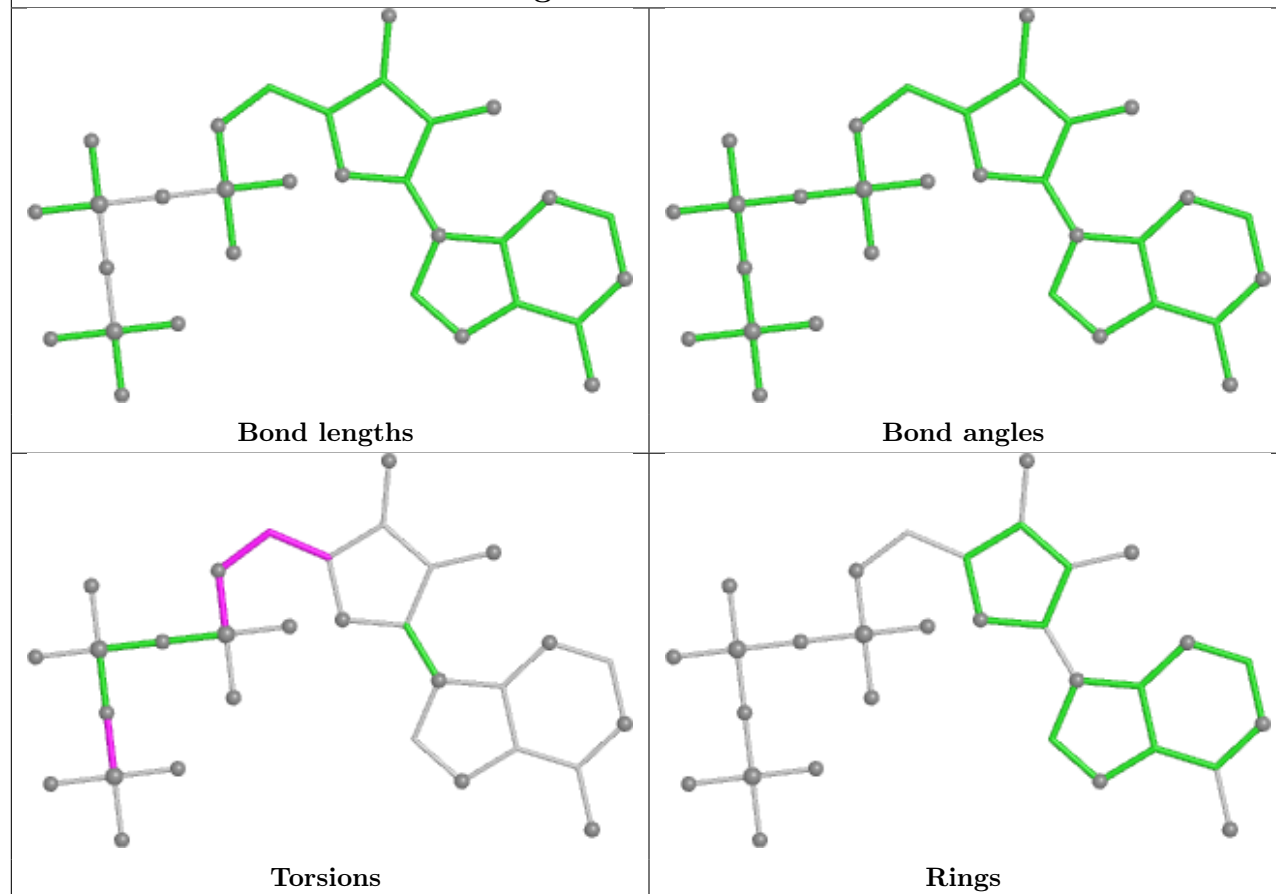
Ligand ATP D 501



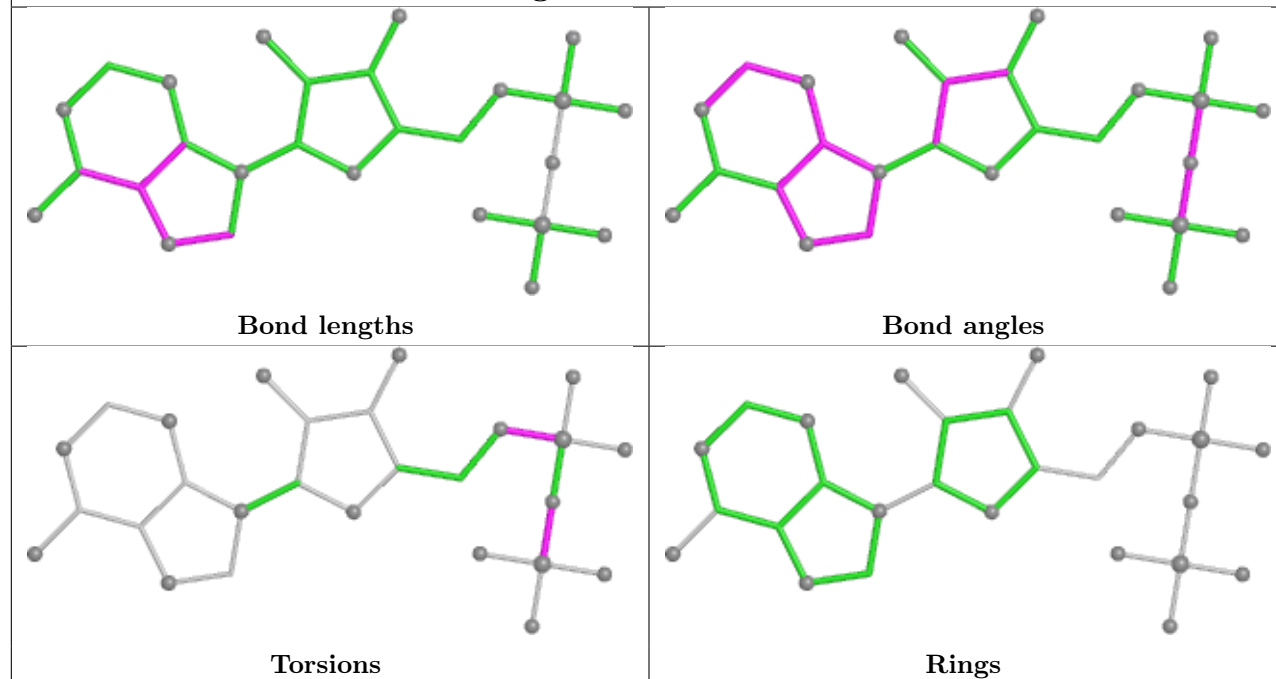
Ligand ADP A 501

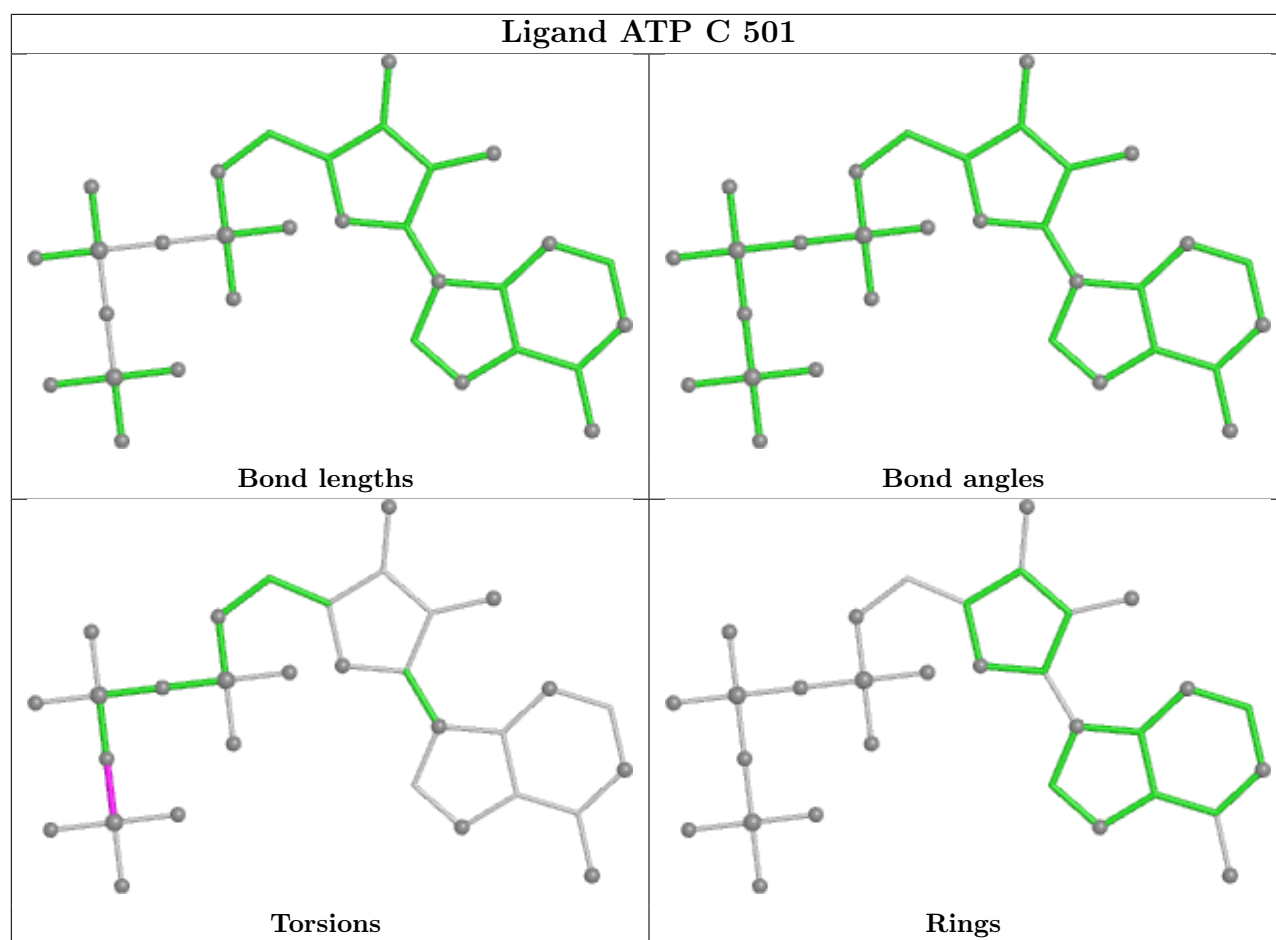


Ligand ATP E 401



Ligand ADP F 501





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.

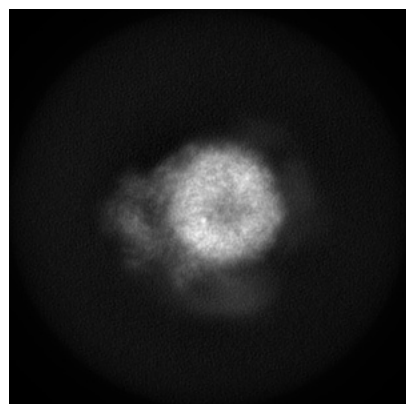
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62070. 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](#)

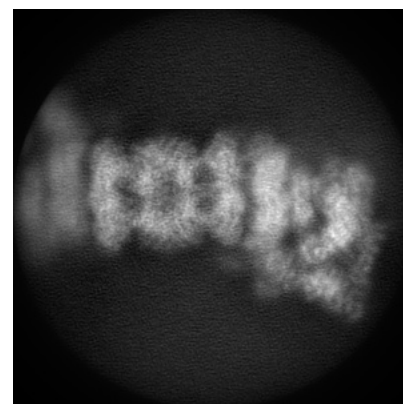
6.1.1 Primary map



X

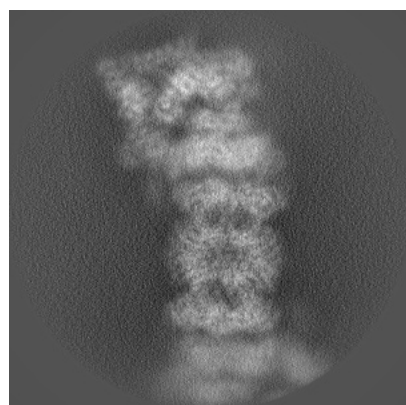


Y

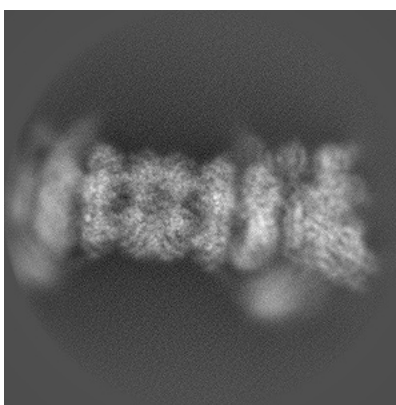


Z

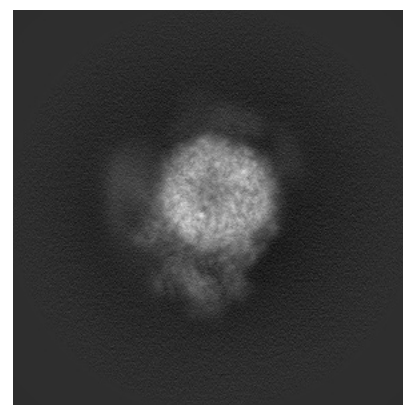
6.1.2 Raw map



X



Y

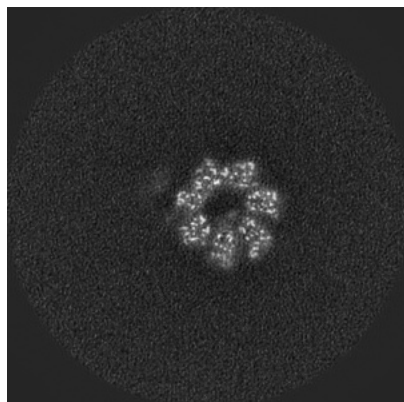


Z

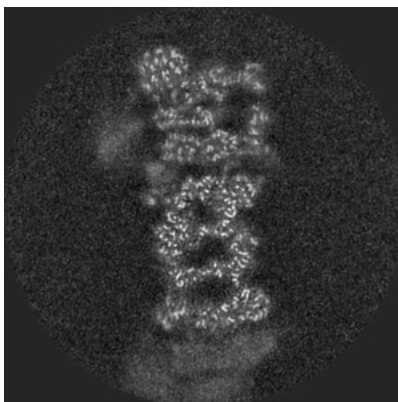
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

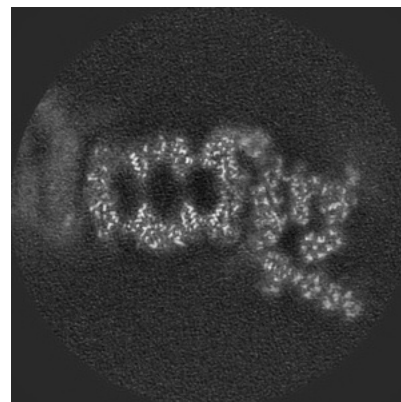
6.2.1 Primary map



X Index: 300

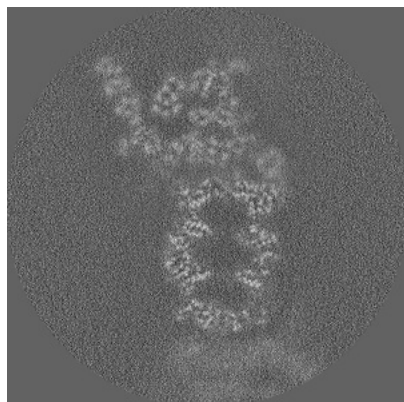


Y Index: 300

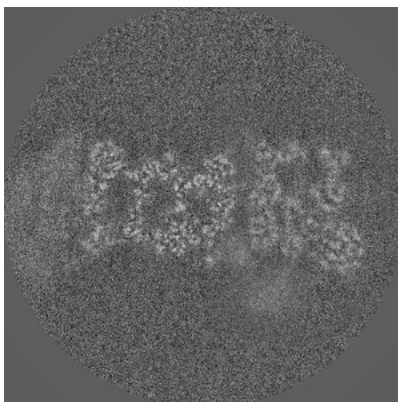


Z Index: 300

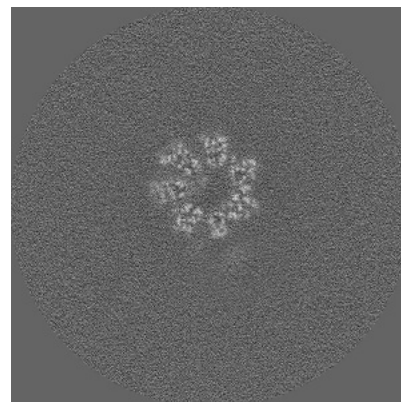
6.2.2 Raw map



X Index: 300



Y Index: 300

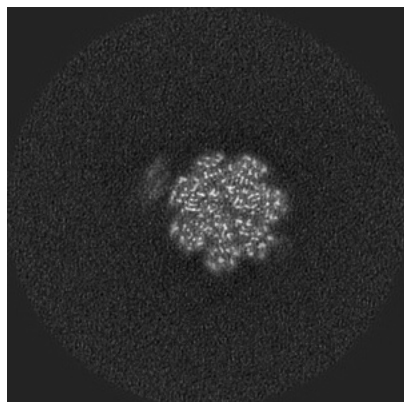


Z Index: 300

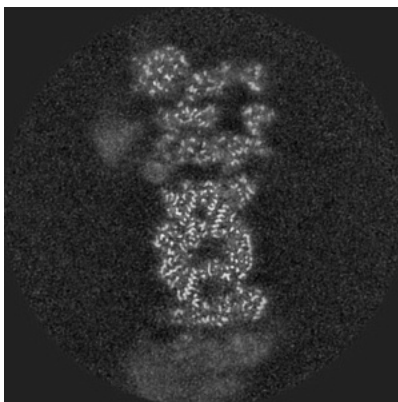
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

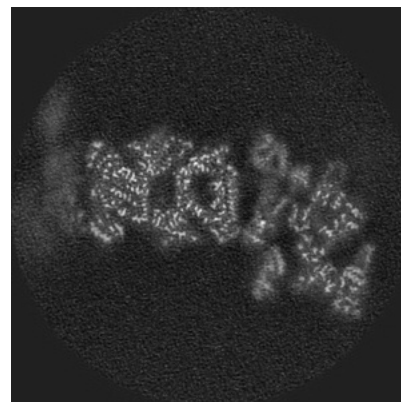
6.3.1 Primary map



X Index: 317

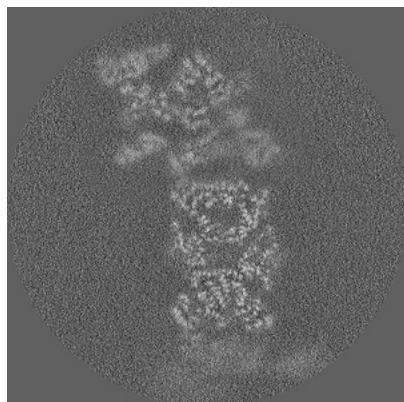


Y Index: 290

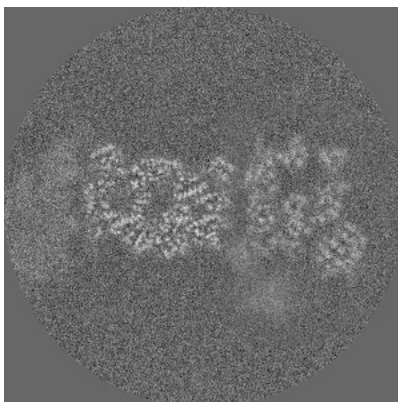


Z Index: 270

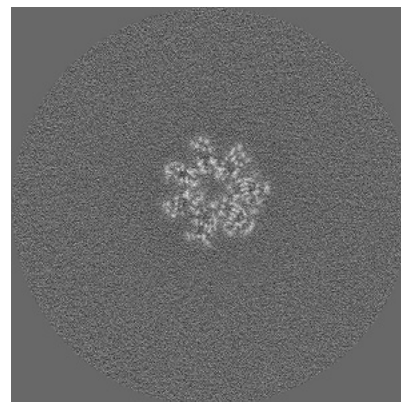
6.3.2 Raw map



X Index: 269



Y Index: 290

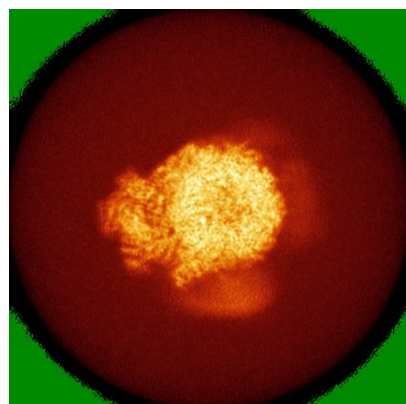


Z Index: 263

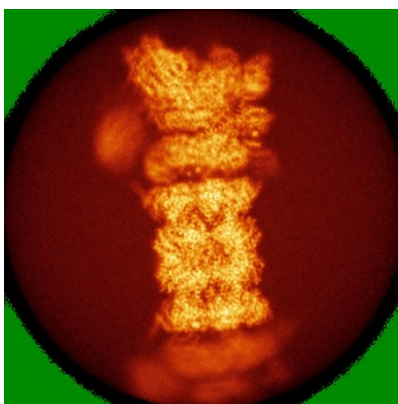
The images above show the largest variance slices of the map in three orthogonal directions.

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

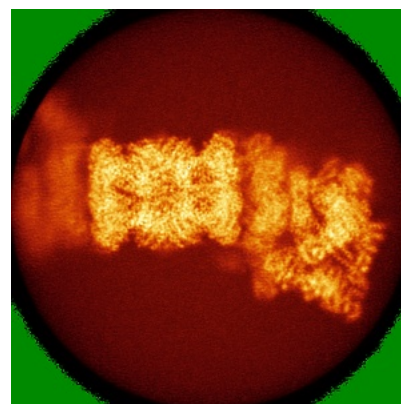
6.4.1 Primary map



X

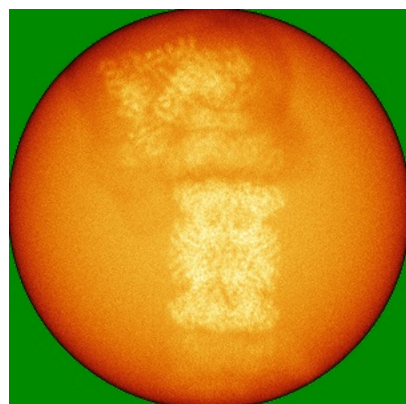


Y

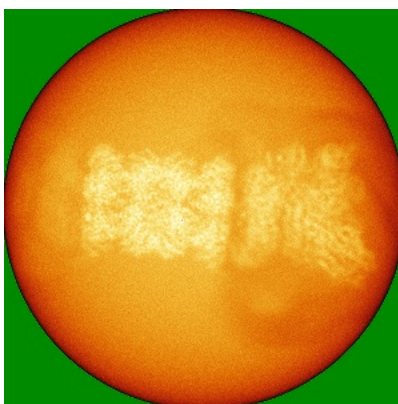


Z

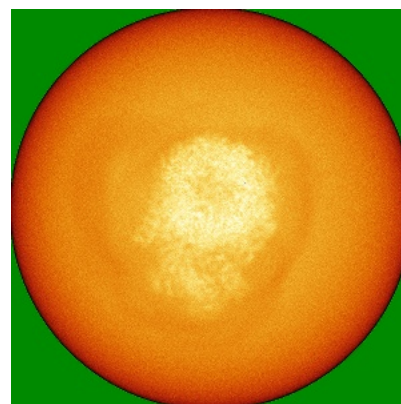
6.4.2 Raw map



X



Y

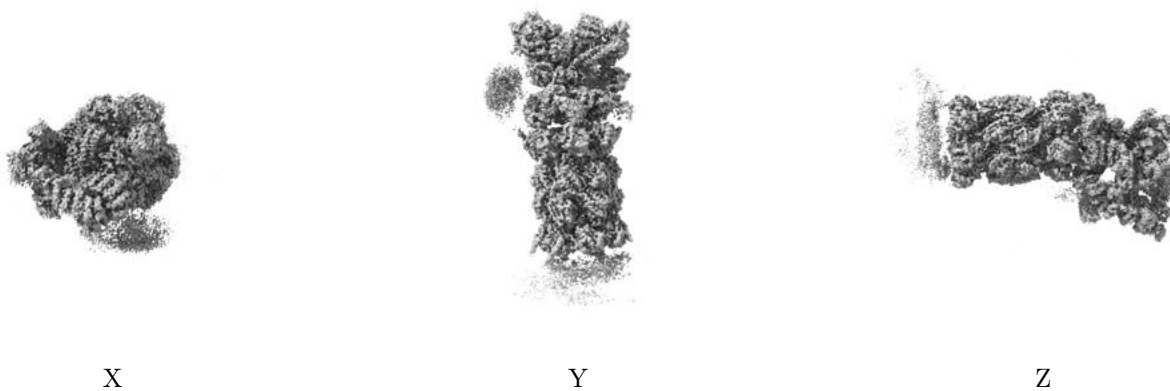


Z

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.

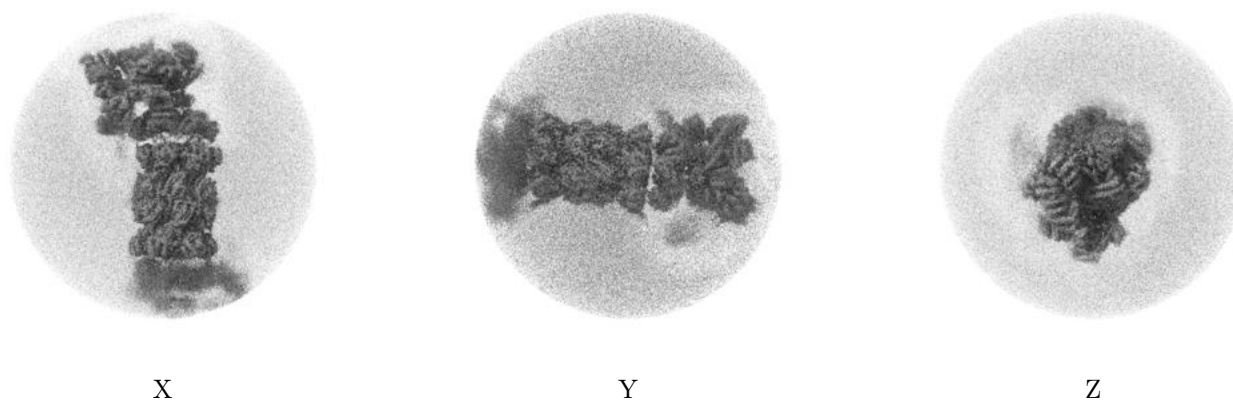
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00603. 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.

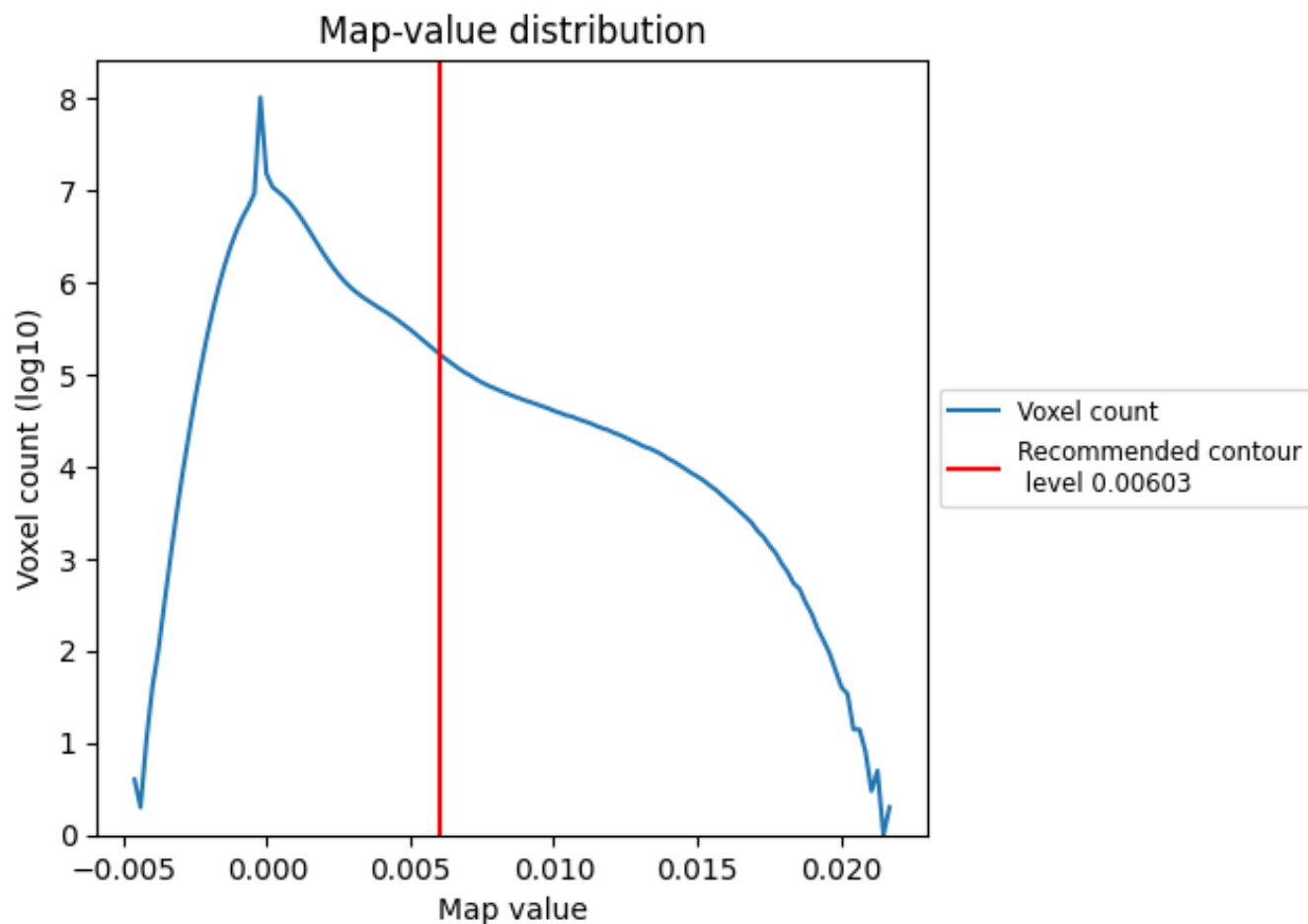
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

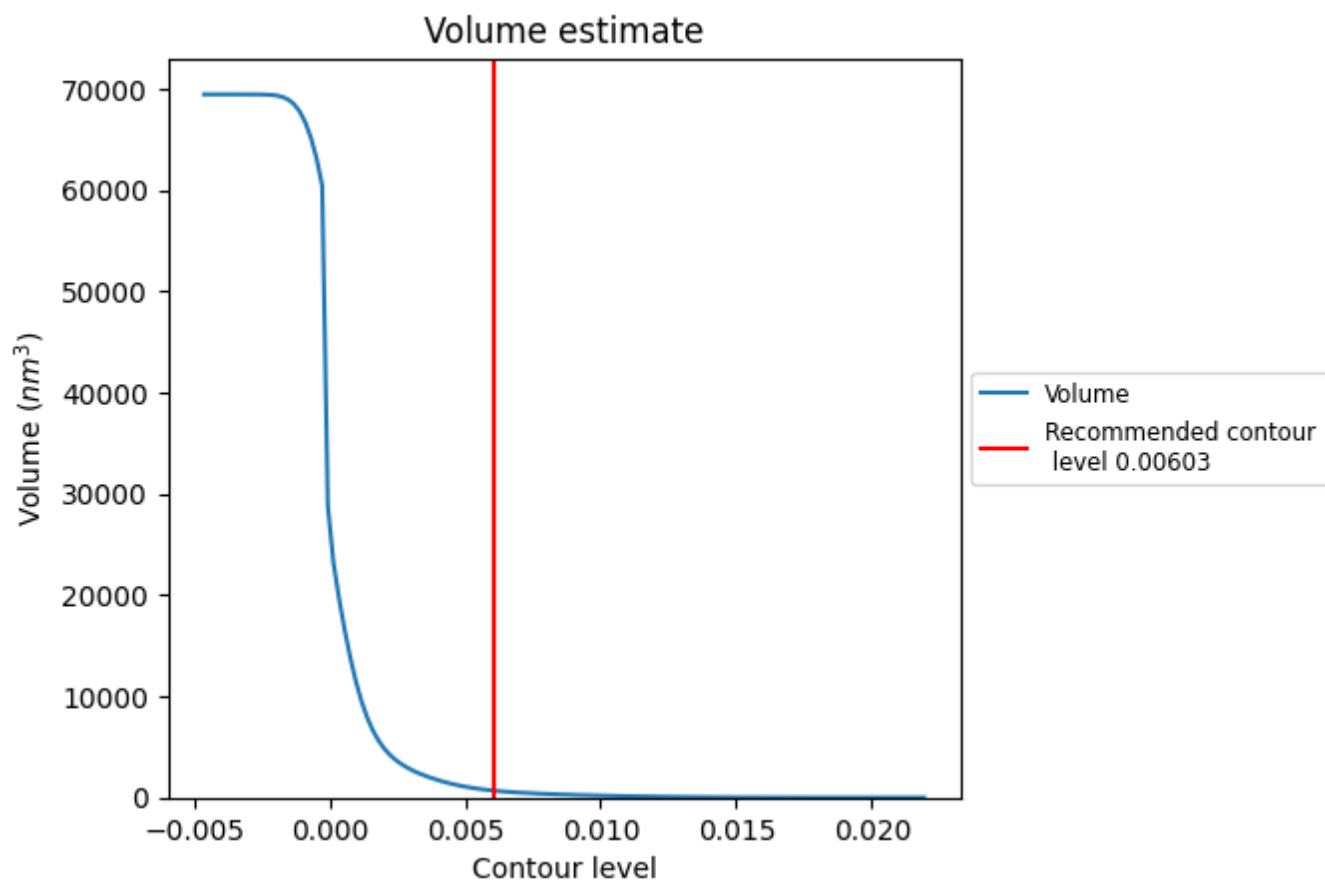
This section contains the results of statistical analysis of the map.

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.

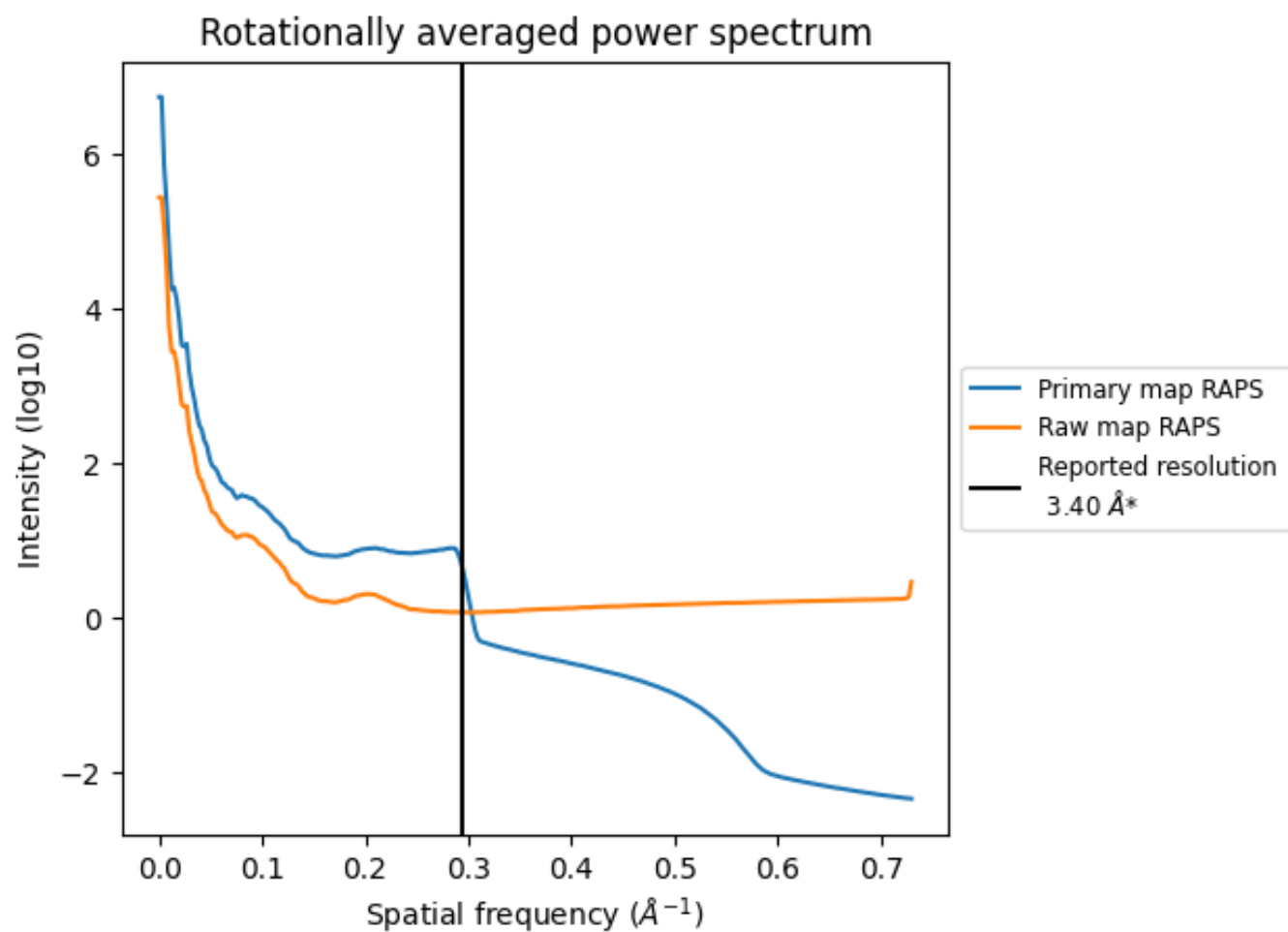
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 693 nm³; this corresponds to an approximate mass of 626 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 ⓘ

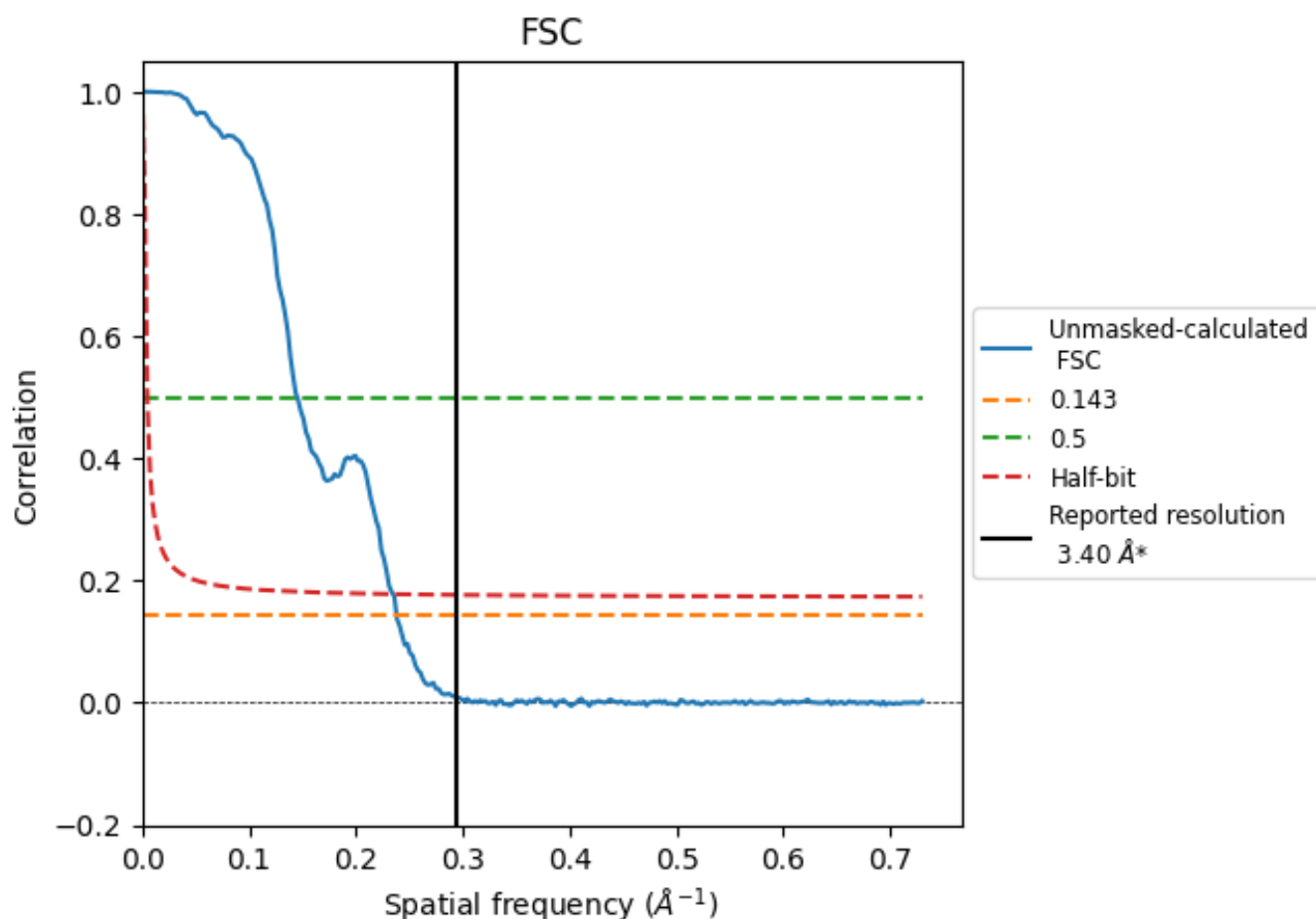


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 0.294 \AA^{-1}

8.2 Resolution estimates [i](#)

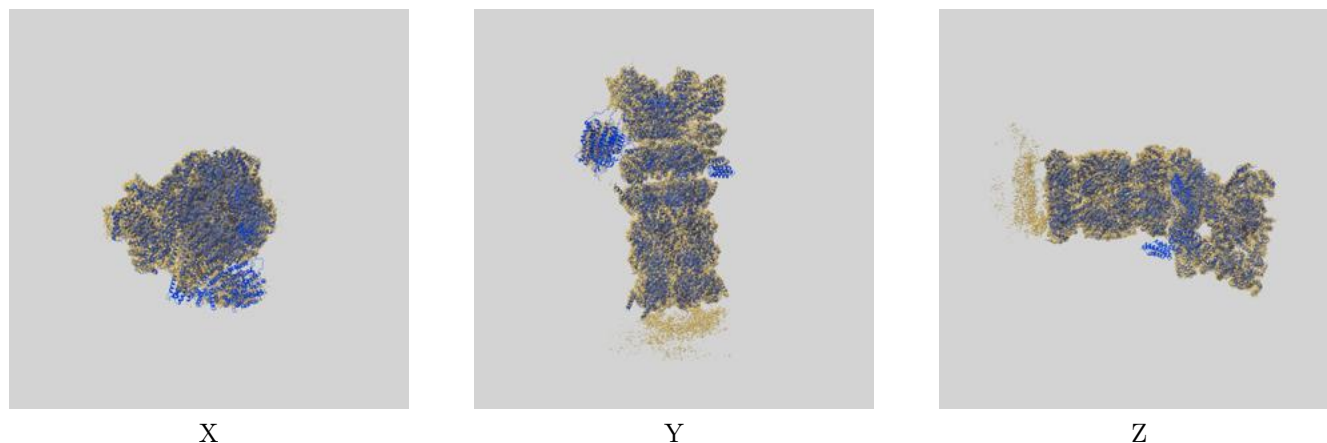
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.20	6.90	4.26

*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 4.20 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

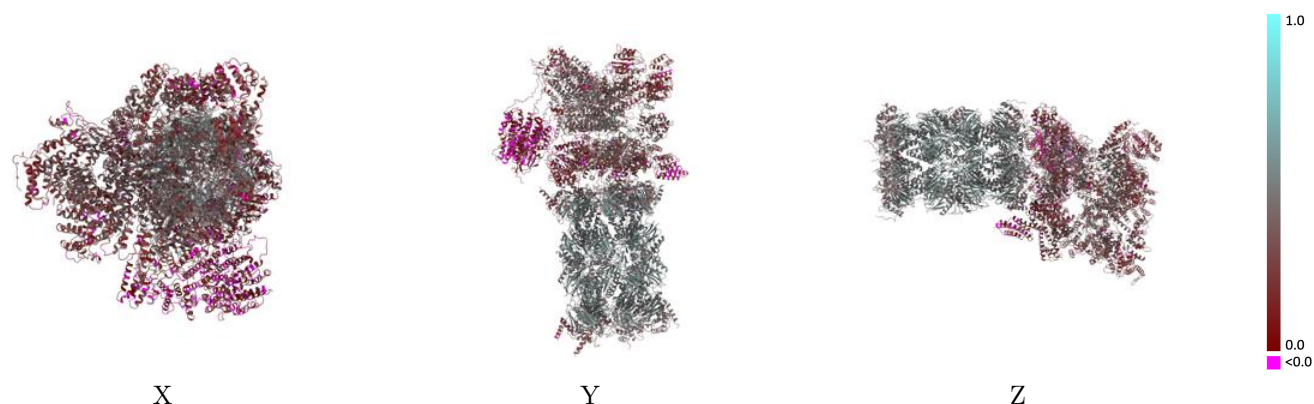
This section contains information regarding the fit between EMDB map EMD-62070 and PDB model 9K4U. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



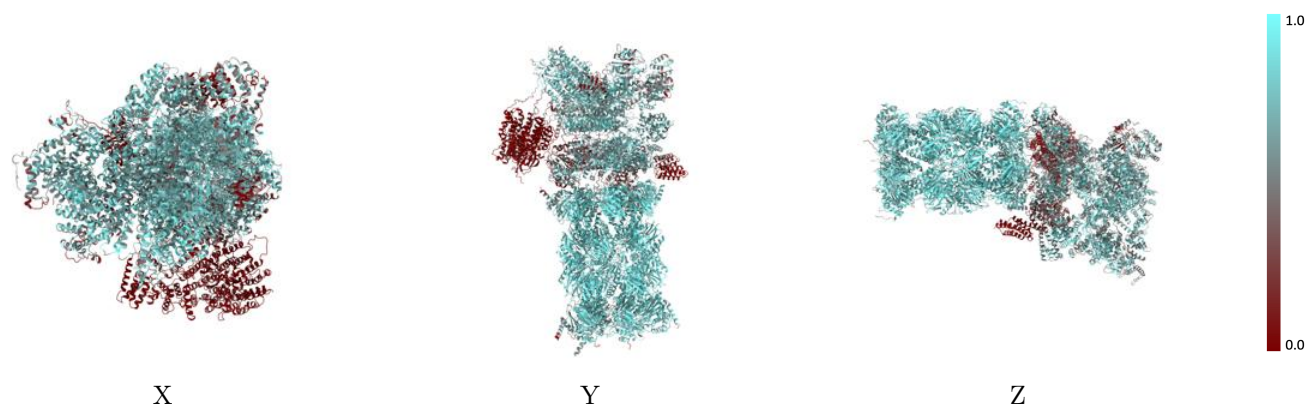
The images above show the 3D surface view of the map at the recommended contour level 0.00603 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



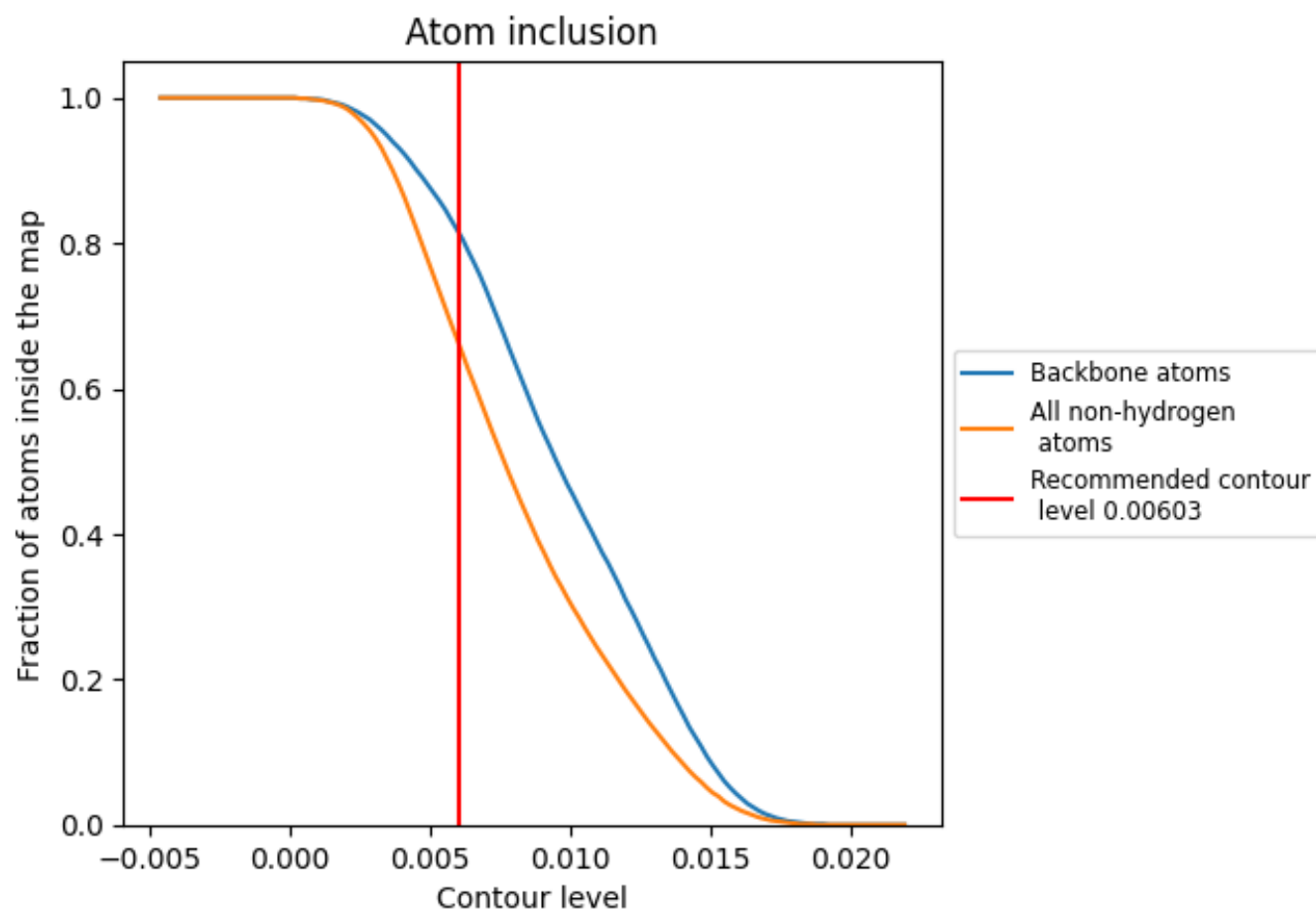
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00603).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 66% 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 (0.00603) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6610	 0.3680
A	 0.4530	 0.2370
B	 0.3200	 0.1890
C	 0.5850	 0.3170
D	 0.6790	 0.3630
E	 0.6900	 0.3620
F	 0.6220	 0.3120
G	 0.8240	 0.4720
H	 0.8410	 0.4740
I	 0.7760	 0.4470
J	 0.7390	 0.4160
K	 0.7890	 0.4580
L	 0.8620	 0.4800
M	 0.8500	 0.4750
N	 0.8830	 0.5120
O	 0.8730	 0.5010
P	 0.8840	 0.5030
Q	 0.8750	 0.5060
R	 0.8880	 0.5070
S	 0.8490	 0.5020
T	 0.8870	 0.5080
U	 0.6720	 0.3220
V	 0.6780	 0.3240
W	 0.4890	 0.2810
X	 0.3340	 0.2500
Y	 0.6800	 0.3100
Z	 0.6630	 0.3400
a	 0.6220	 0.2620
b	 0.5820	 0.2670
c	 0.6890	 0.3600
d	 0.5510	 0.2480
e	 0.5490	 0.3050
f	 0.0510	 0.0970
g	 0.7930	 0.4590
h	 0.8010	 0.4670



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Chain	Atom inclusion	Q-score
i	 0.7530	 0.4430
j	 0.6960	 0.4000
k	 0.7420	 0.4520
l	 0.8240	 0.4770
m	 0.8190	 0.4660
n	 0.8770	 0.5150
o	 0.8660	 0.4980
p	 0.8830	 0.5080
q	 0.8650	 0.4970
r	 0.8890	 0.5120
s	 0.8550	 0.5010
t	 0.8770	 0.5090
u	 0.1120	 0.2650
v	 0.2500	 0.3590