



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:00 AM UTC

PDB ID : 7DRW / pdb_00007drw
EMDB ID : EMD-30828
Title : Bovine 20S immunoproteasome in complex with two human PA28alpha-beta activators
Authors : Cong, Y.; Xu, C.
Deposited on : 2020-12-29
Resolution : 4.20 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:

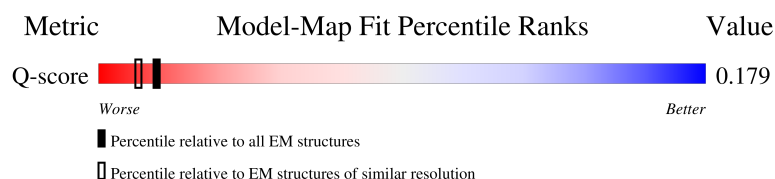
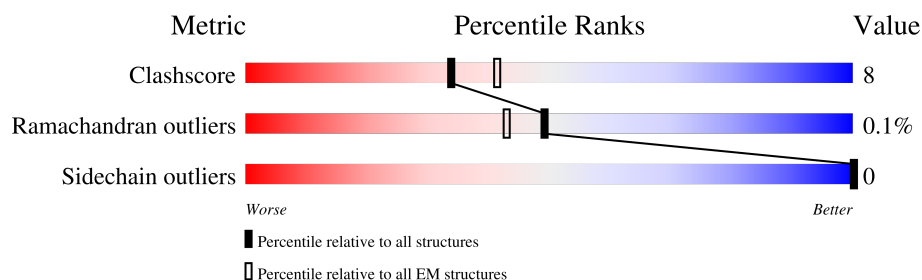
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.20 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	5410 (3.70 - 4.70)

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	246	41% 78% 17% .
1	f	246	33% 78% 19% .
2	B	234	44% 76% 20% .
2	h	234	31% 76% 21% .

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Mol	Chain	Length	Quality of chain
3	C	261	
3	j	261	
4	D	248	
4	P	248	
5	E	241	
5	R	241	
6	F	263	
6	b	263	
7	G	255	
7	d	255	
8	H	239	
8	K	239	
8	M	239	
8	O	239	
8	c	239	
8	g	239	
9	I	249	
9	J	249	
9	L	249	
9	N	249	
9	Q	249	
9	a	249	
9	e	249	
9	i	249	
10	S	205	

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Mol	Chain	Length	Quality of chain
10	k	205	
11	T	201	
11	l	201	
12	U	241	
12	m	241	
13	V	264	
13	n	264	
14	W	219	
14	Z	219	
15	1	273	
15	X	273	
16	2	276	
16	Y	276	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 71650 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	235	Total	C	N	O	S	0	0
			1841	1173	305	350	13		
1	f	237	Total	C	N	O	S	0	0
			1861	1184	310	354	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	226	Total	C	N	O	S	0	0
			1763	1127	298	332	6		
2	h	228	Total	C	N	O	S	0	0
			1777	1136	300	335	6		

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	245	Total	C	N	O	S	0	0
			1927	1219	329	368	11		
3	j	246	Total	C	N	O	S	0	0
			1936	1225	331	369	11		

- Molecule 4 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	232	Total	C	N	O	S	0	0
			1824	1149	322	348	5		
4	P	232	Total	C	N	O	S	0	0
			1824	1149	322	348	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	234	Total	C	N	O	S	0	0
			1790	1125	295	359	11		
5	R	234	Total	C	N	O	S	0	0
			1790	1125	295	359	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	235	Total	C	N	O	S	0	0
			1846	1156	330	349	11		
6	b	235	Total	C	N	O	S	0	0
			1846	1156	330	349	11		

- Molecule 7 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	240	Total	C	N	O	S	0	0
			1879	1191	321	356	11		
7	d	240	Total	C	N	O	S	0	0
			1879	1191	321	356	11		

- Molecule 8 is a protein called Proteasome activator complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	209	Total	C	N	O	S	0	0
			1684	1084	286	310	4		
8	K	207	Total	C	N	O	S	0	0
			1678	1080	283	311	4		
8	M	209	Total	C	N	O	S	0	0
			1689	1088	286	311	4		
8	O	209	Total	C	N	O	S	0	0
			1684	1084	286	310	4		
8	c	205	Total	C	N	O	S	0	0
			1658	1066	281	308	3		
8	g	209	Total	C	N	O	S	0	0
			1689	1088	286	311	4		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	89	PRO	HIS	variant	UNP Q9UL46
K	89	PRO	HIS	variant	UNP Q9UL46
M	89	PRO	HIS	variant	UNP Q9UL46

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Chain	Residue	Modelled	Actual	Comment	Reference
O	89	PRO	HIS	variant	UNP Q9UL46
c	89	PRO	HIS	variant	UNP Q9UL46
g	89	PRO	HIS	variant	UNP Q9UL46

- Molecule 9 is a protein called Proteasome activator complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	213	Total	C	N	O	S	0	0
			1721	1102	292	321	6		
9	J	206	Total	C	N	O	S	0	0
			1663	1063	284	310	6		
9	L	207	Total	C	N	O	S	0	0
			1672	1069	286	311	6		
9	N	205	Total	C	N	O	S	0	0
			1654	1057	283	306	8		
9	Q	213	Total	C	N	O	S	0	0
			1721	1102	292	321	6		
9	a	206	Total	C	N	O	S	0	0
			1663	1063	284	310	6		
9	e	207	Total	C	N	O	S	0	0
			1672	1069	286	311	6		
9	i	205	Total	C	N	O	S	0	0
			1654	1057	283	306	8		

- Molecule 10 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	204	Total	C	N	O	S	0	0
			1594	1015	265	295	19		
10	S	204	Total	C	N	O	S	0	0
			1594	1015	265	295	19		

- Molecule 11 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	198	Total	C	N	O	S	0	0
			1593	1023	270	292	8		
11	T	197	Total	C	N	O	S	0	0
			1584	1017	268	291	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	213	Total	C	N	O	S	0	0
			1645	1042	282	311	10		
12	U	213	Total	C	N	O	S	0	0
			1644	1042	282	310	10		

- Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	216	Total	C	N	O	S	0	0
			1685	1065	289	319	12		
13	V	216	Total	C	N	O	S	0	0
			1682	1063	289	318	12		

- Molecule 14 is a protein called Proteasome subunit beta type-9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	W	199	Total	C	N	O	S	0	0
			1500	942	257	291	10		
14	Z	199	Total	C	N	O	S	0	0
			1500	942	257	291	10		

- Molecule 15 is a protein called Proteasome subunit beta type-10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	X	219	Total	C	N	O	S	0	0
			1611	1010	281	309	11		
15	1	219	Total	C	N	O	S	0	0
			1611	1010	281	309	11		

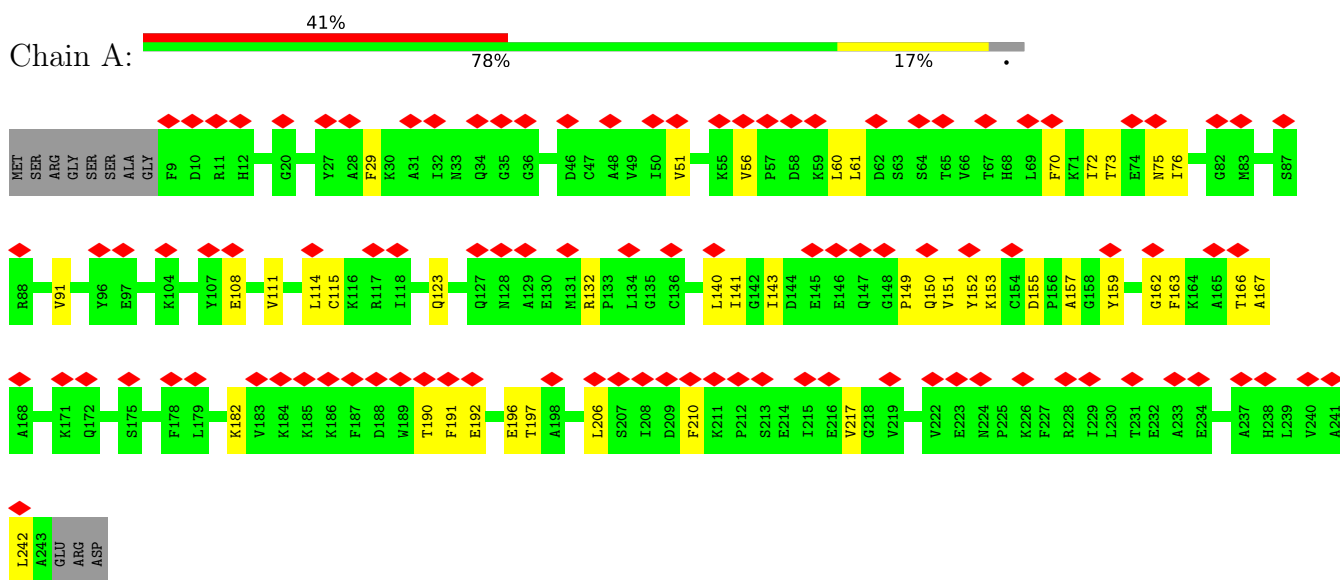
- Molecule 16 is a protein called Proteasome subunit beta type-8.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Y	201	Total	C	N	O	S	0	0
			1561	975	273	297	16		
16	2	201	Total	C	N	O	S	0	0
			1561	975	273	297	16		

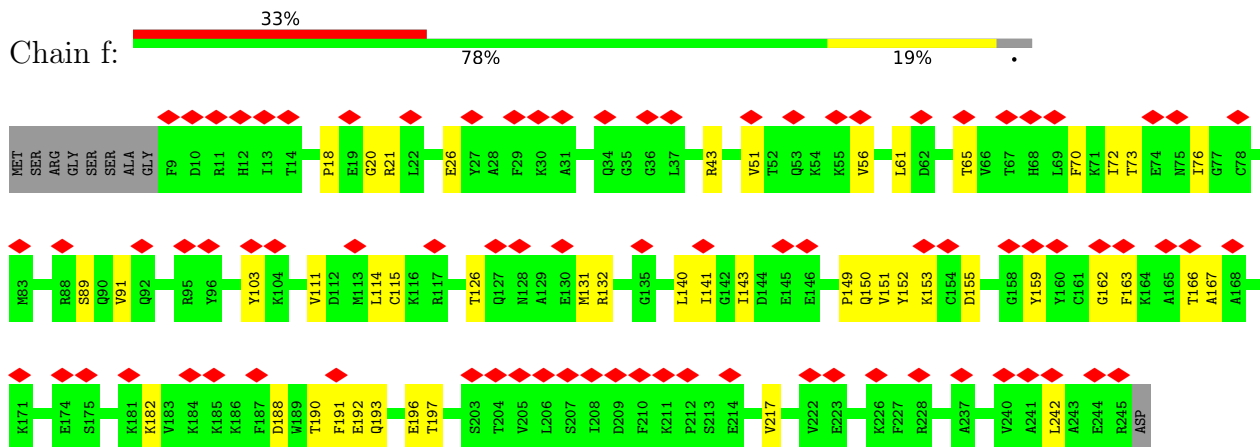
3 Residue-property plots [i](#)

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

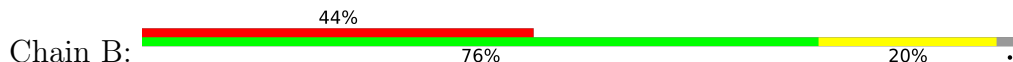
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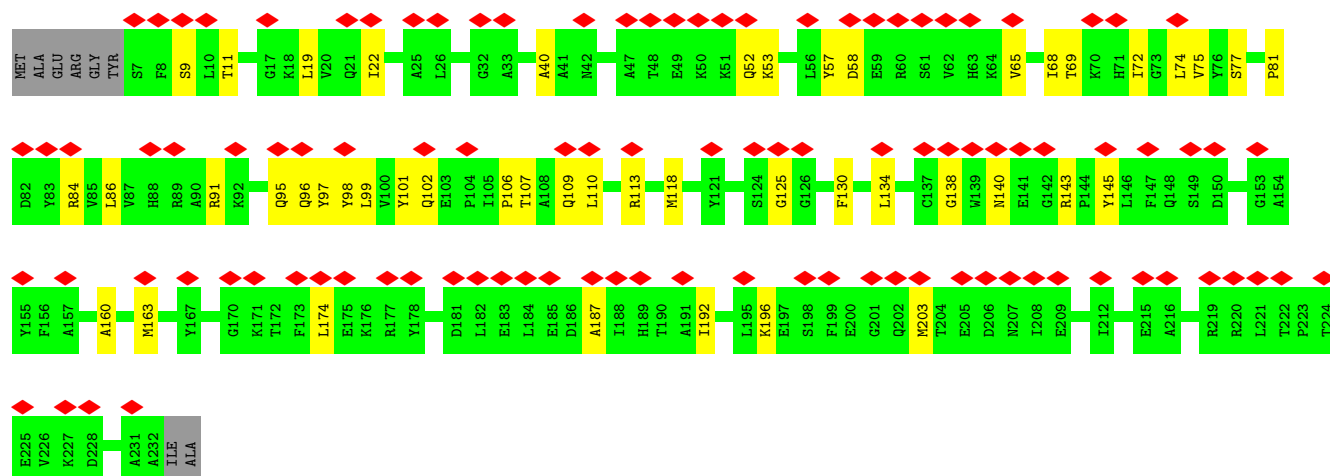


- Molecule 1: Proteasome subunit alpha type-6

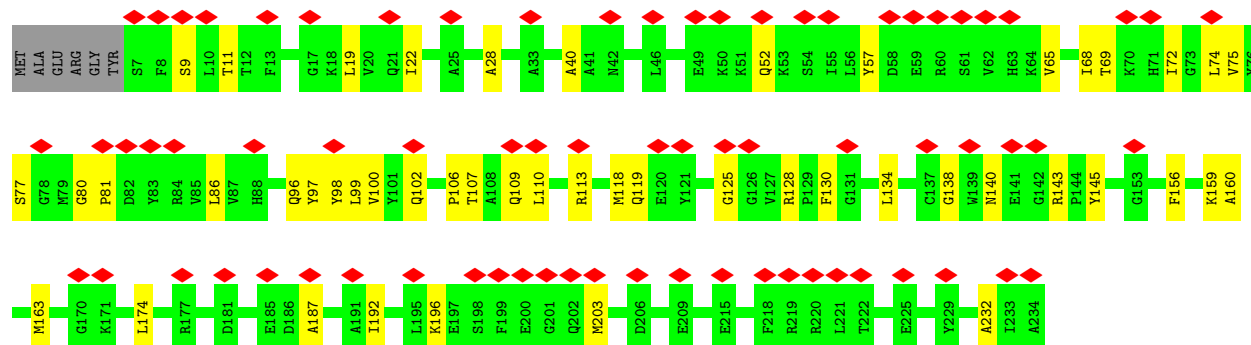
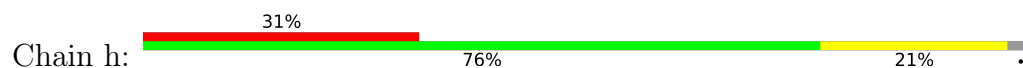


- Molecule 2: Proteasome subunit alpha type-2

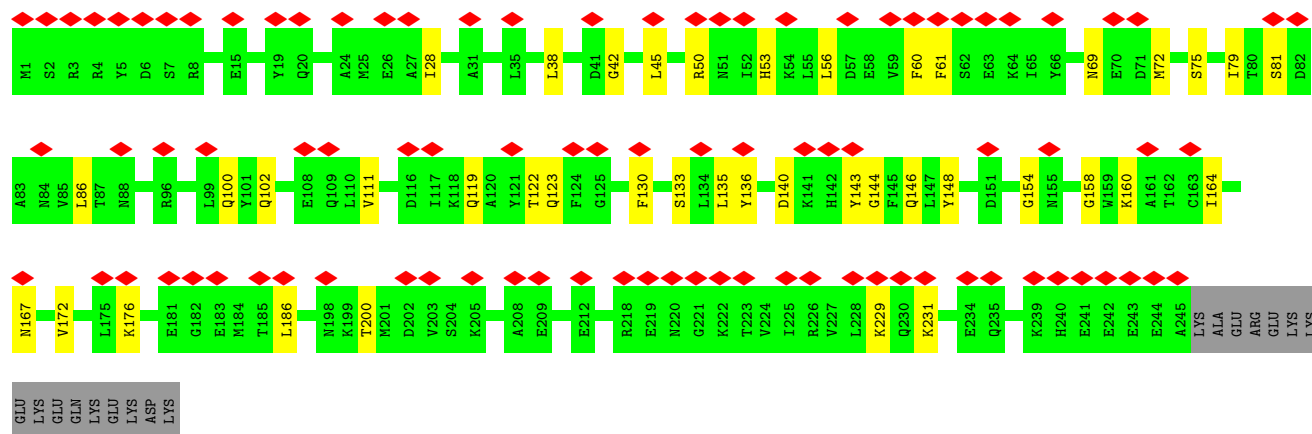
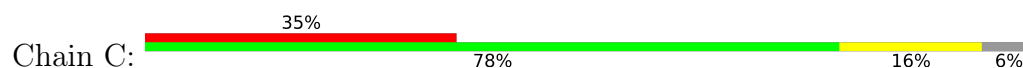




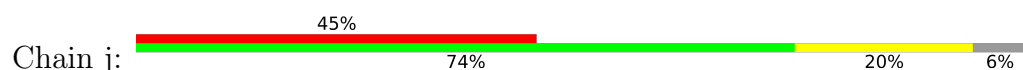
• Molecule 2: Proteasome subunit alpha type-2

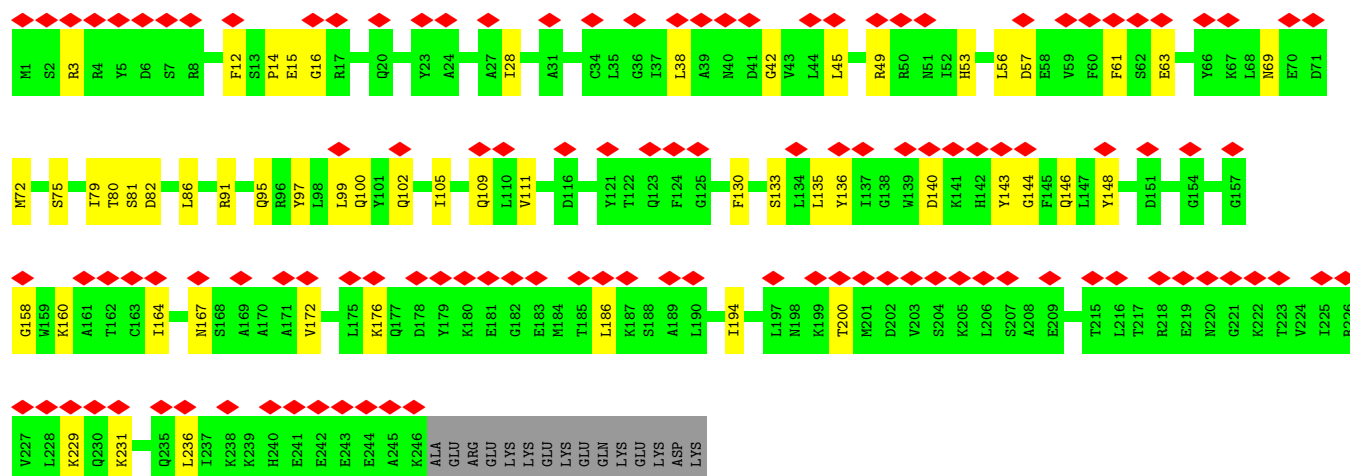


• Molecule 3: Proteasome subunit alpha type-4



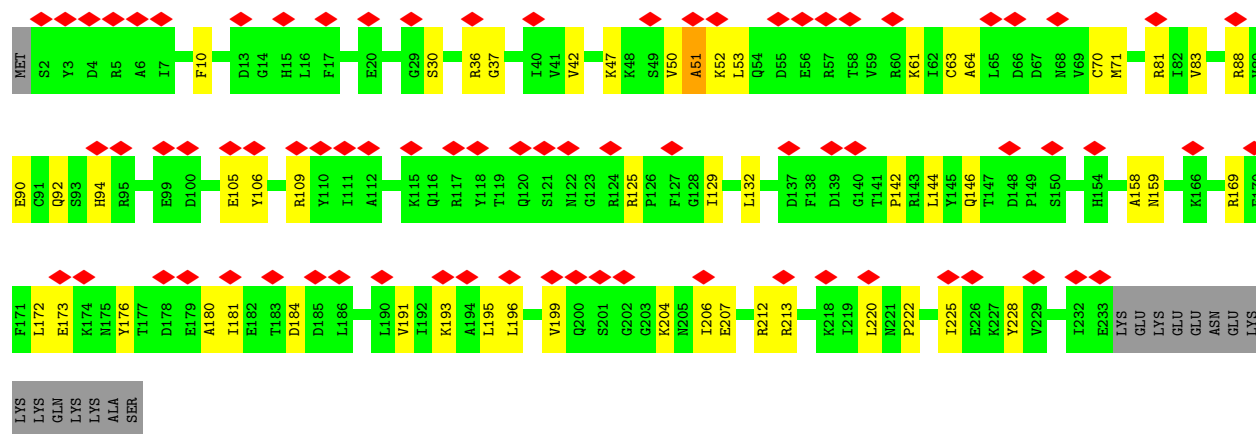
• Molecule 3: Proteasome subunit alpha type-4





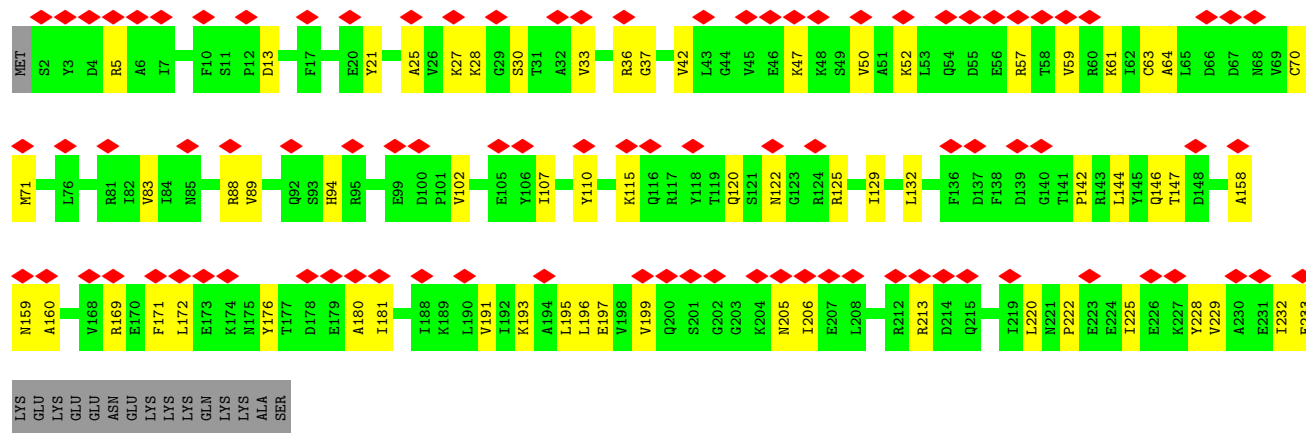
• Molecule 4: Proteasome subunit alpha type-7

Chain D: 31% 72% 21% 6%

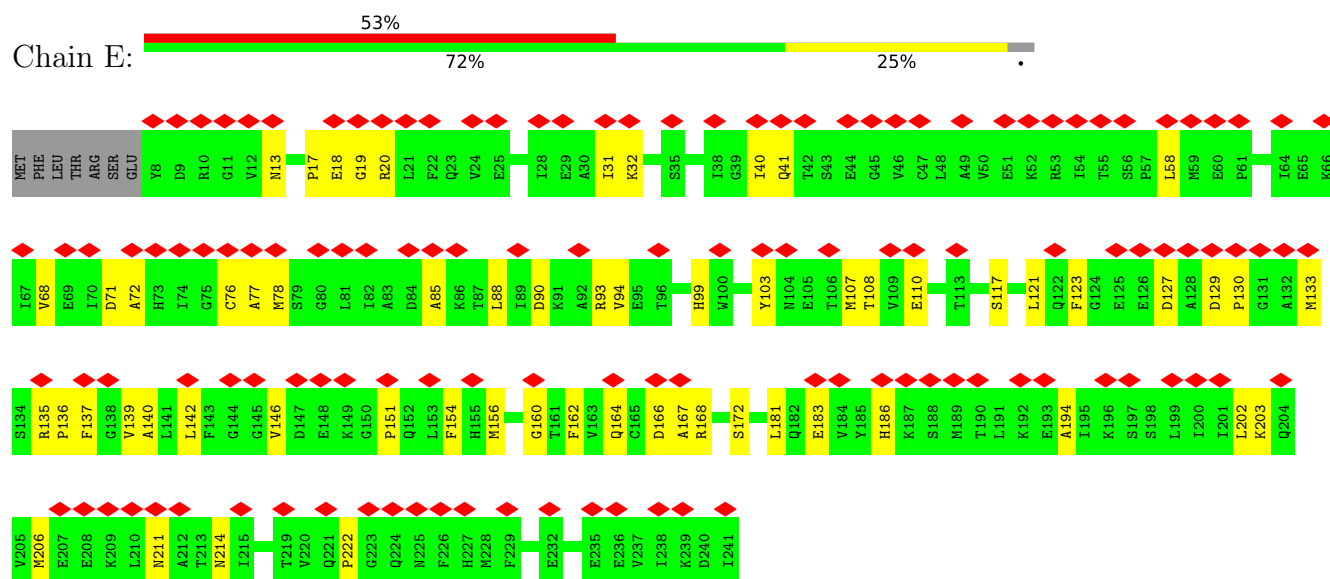


• Molecule 4: Proteasome subunit alpha type-7

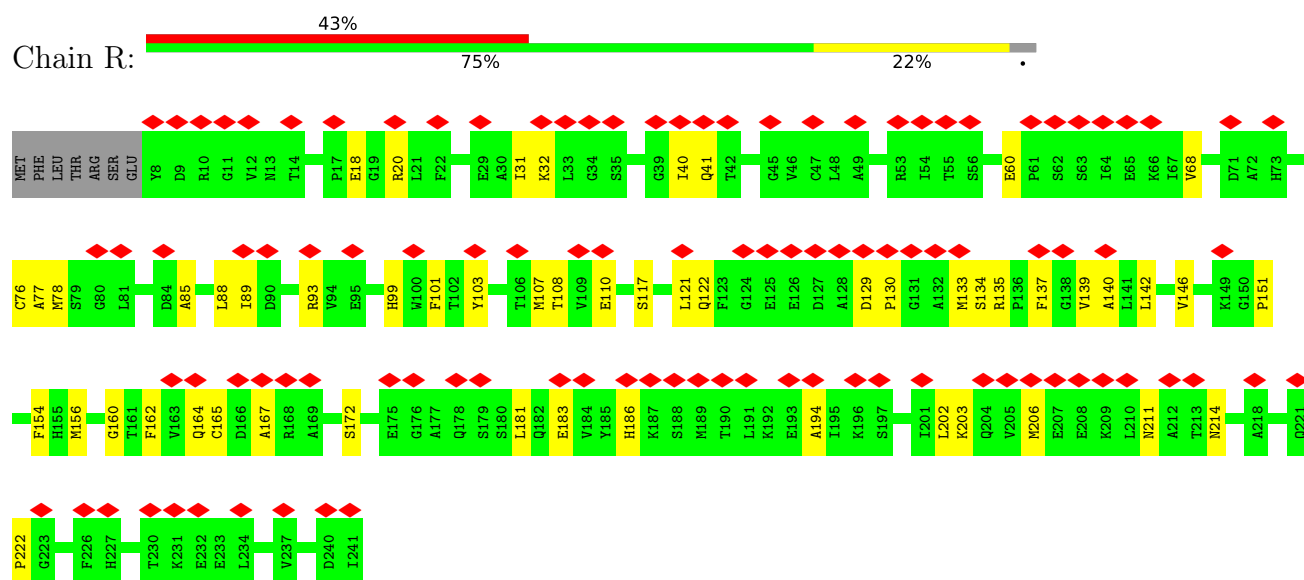
Chain P: 37% 68% 25% 6%



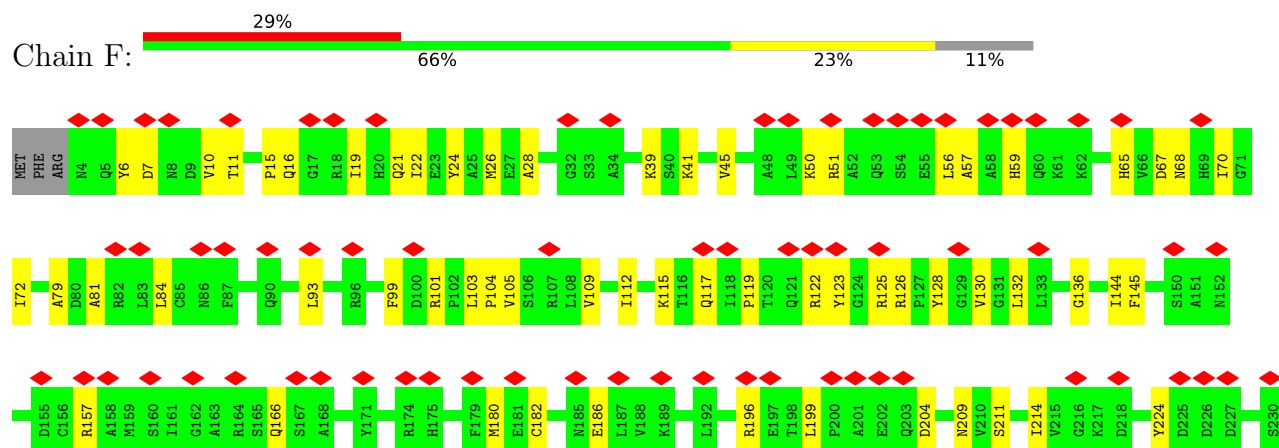
• Molecule 5: Proteasome subunit alpha type-5

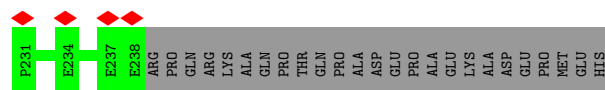


• Molecule 5: Proteasome subunit alpha type-5

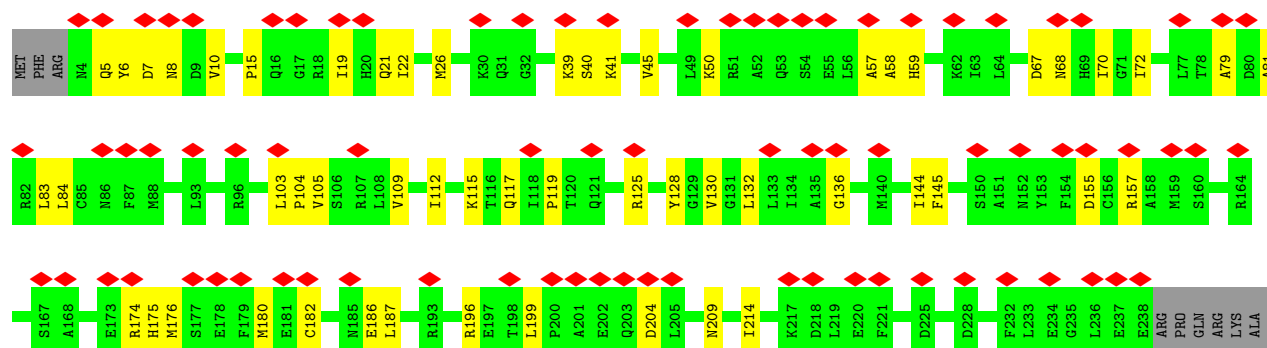


• Molecule 6: Proteasome subunit alpha type-1

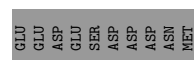
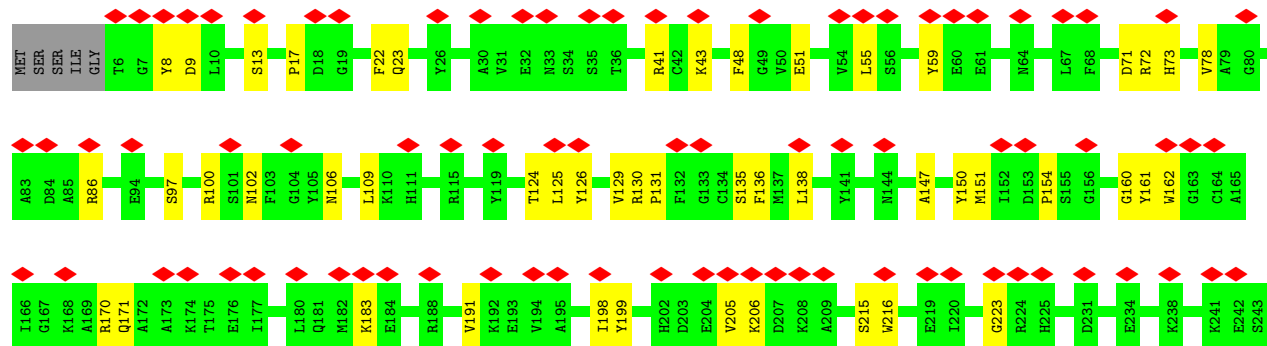
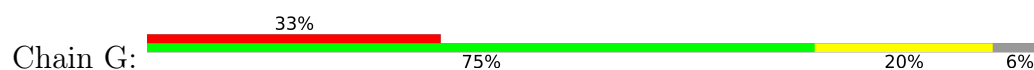




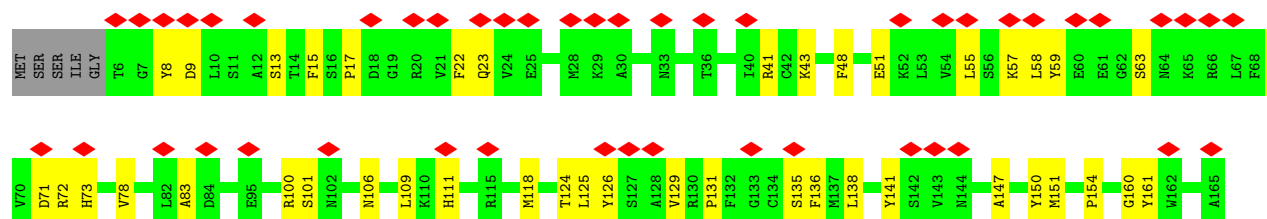
• Molecule 6: Proteasome subunit alpha type-1



• Molecule 7: Proteasome subunit alpha type-3

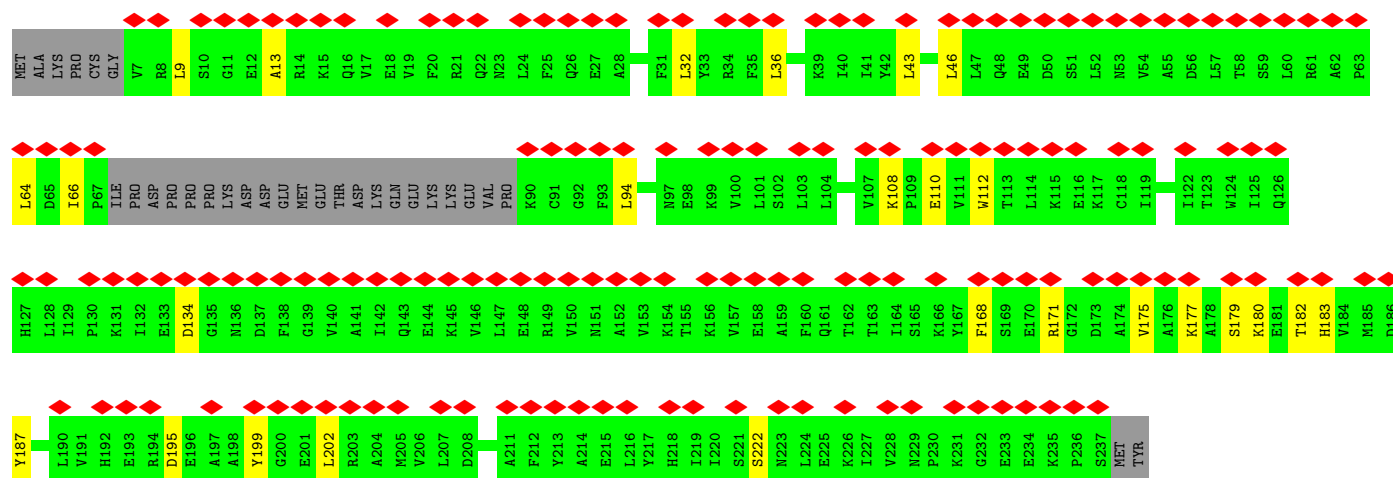
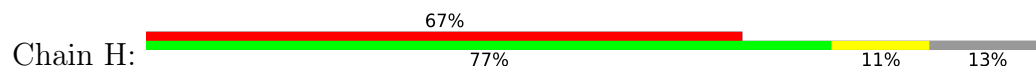


• Molecule 7: Proteasome subunit alpha type-3

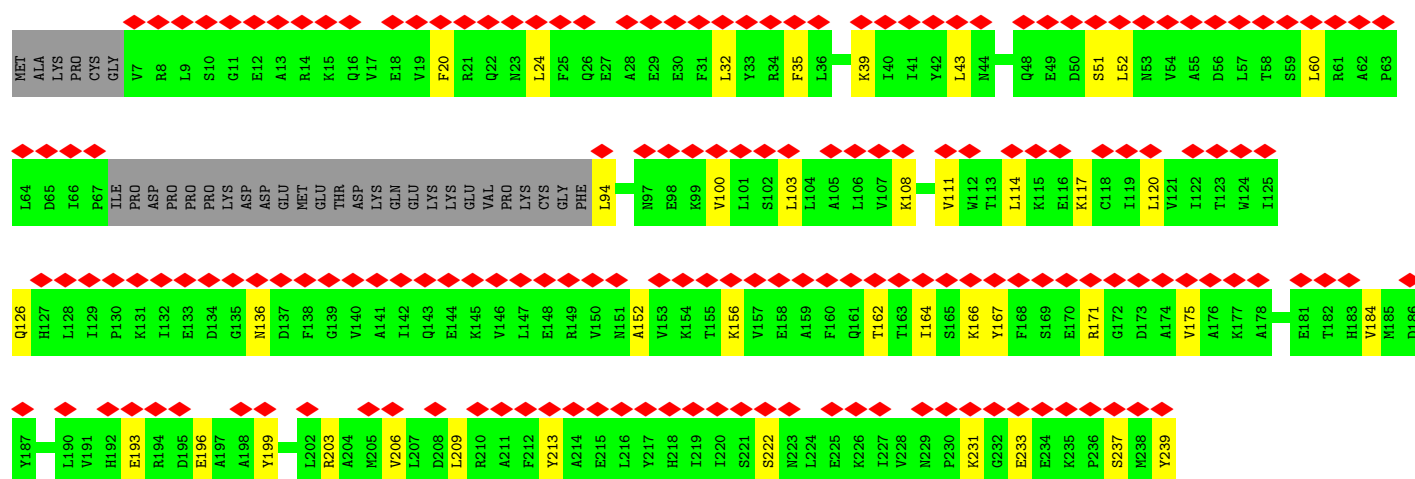




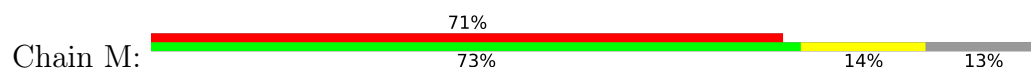
• Molecule 8: Proteasome activator complex subunit 2

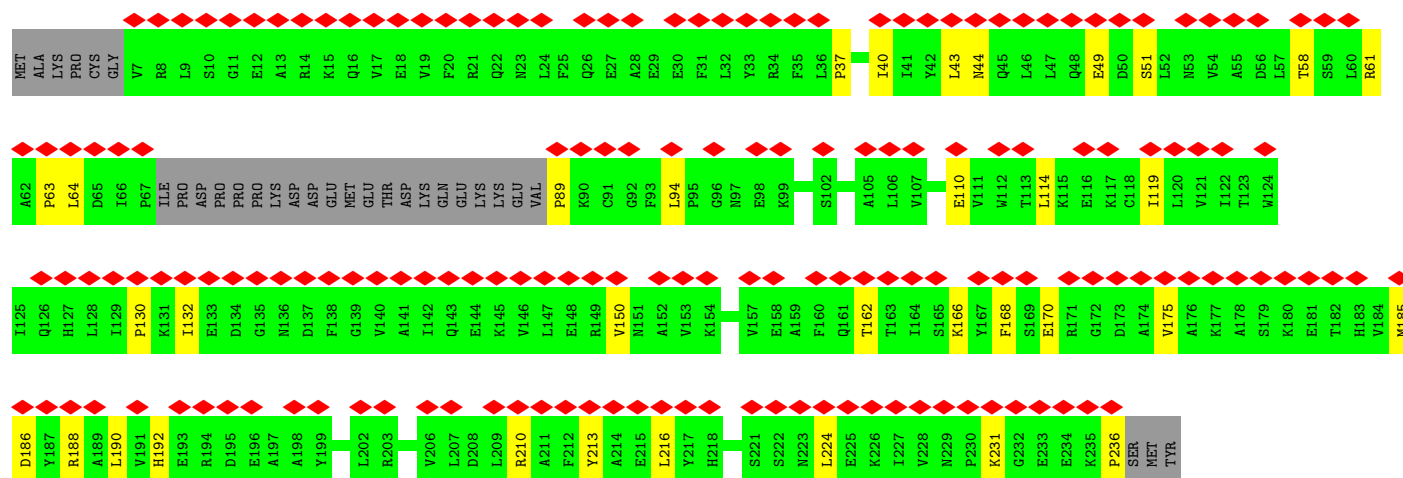


• Molecule 8: Proteasome activator complex subunit 2

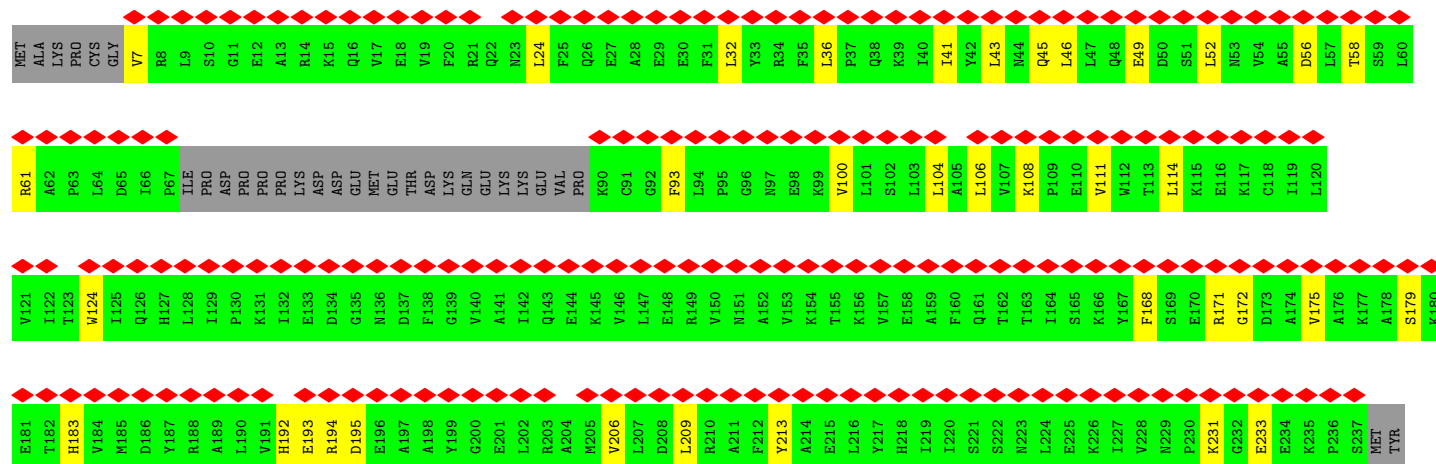
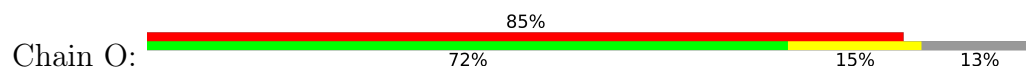


• Molecule 8: Proteasome activator complex subunit 2

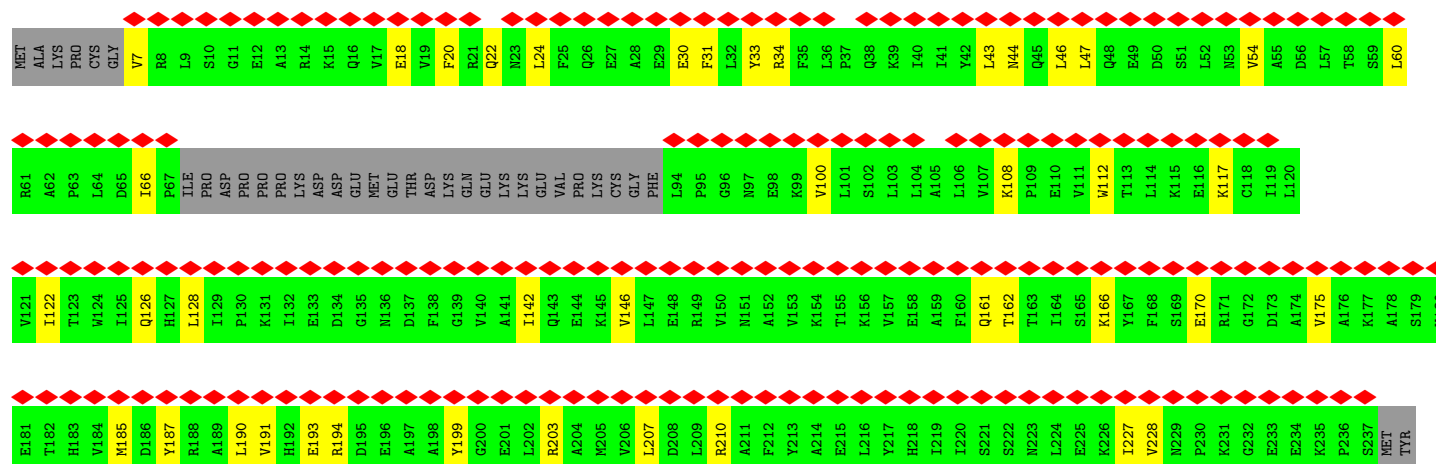
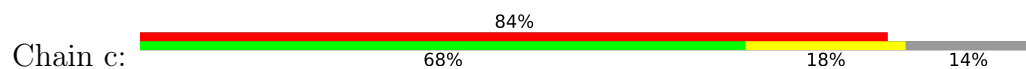


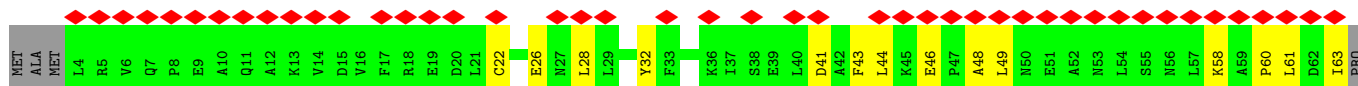


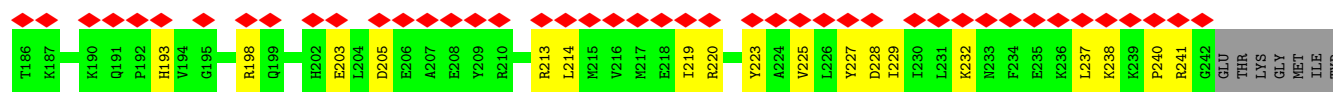
• Molecule 8: Proteasome activator complex subunit 2



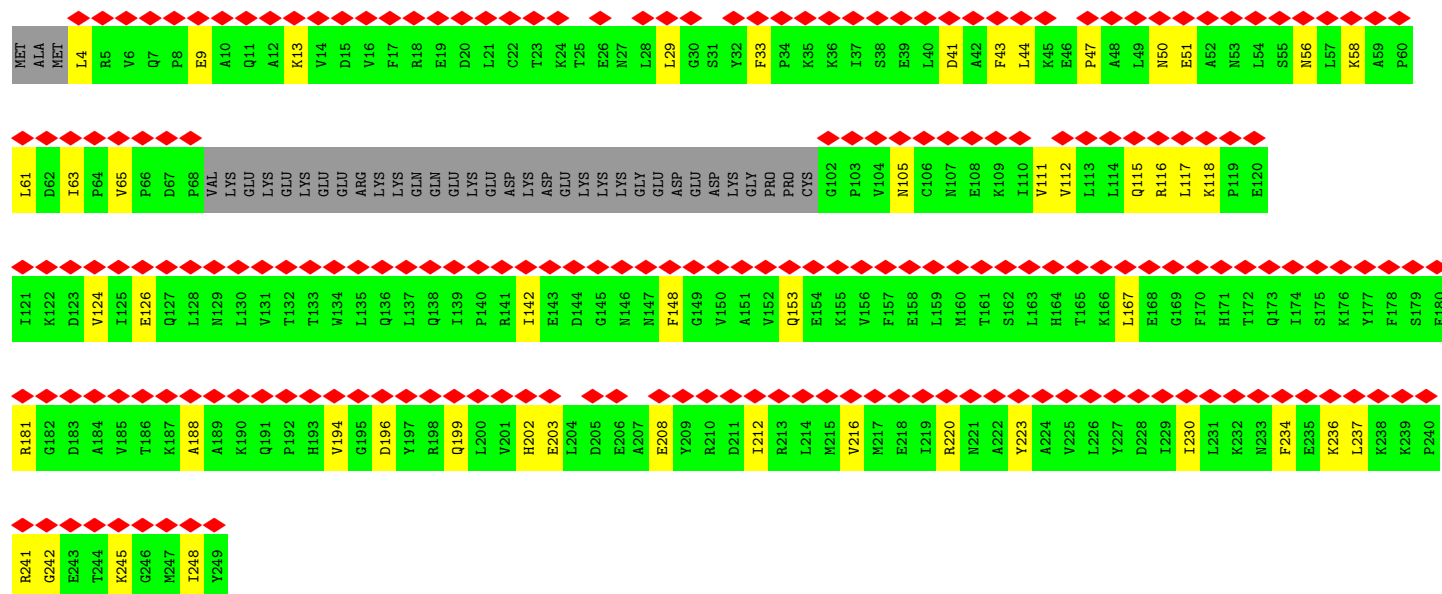
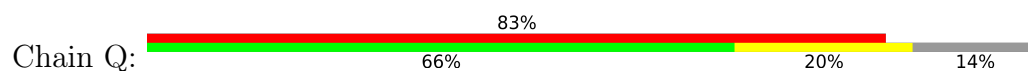
• Molecule 8: Proteasome activator complex subunit 2



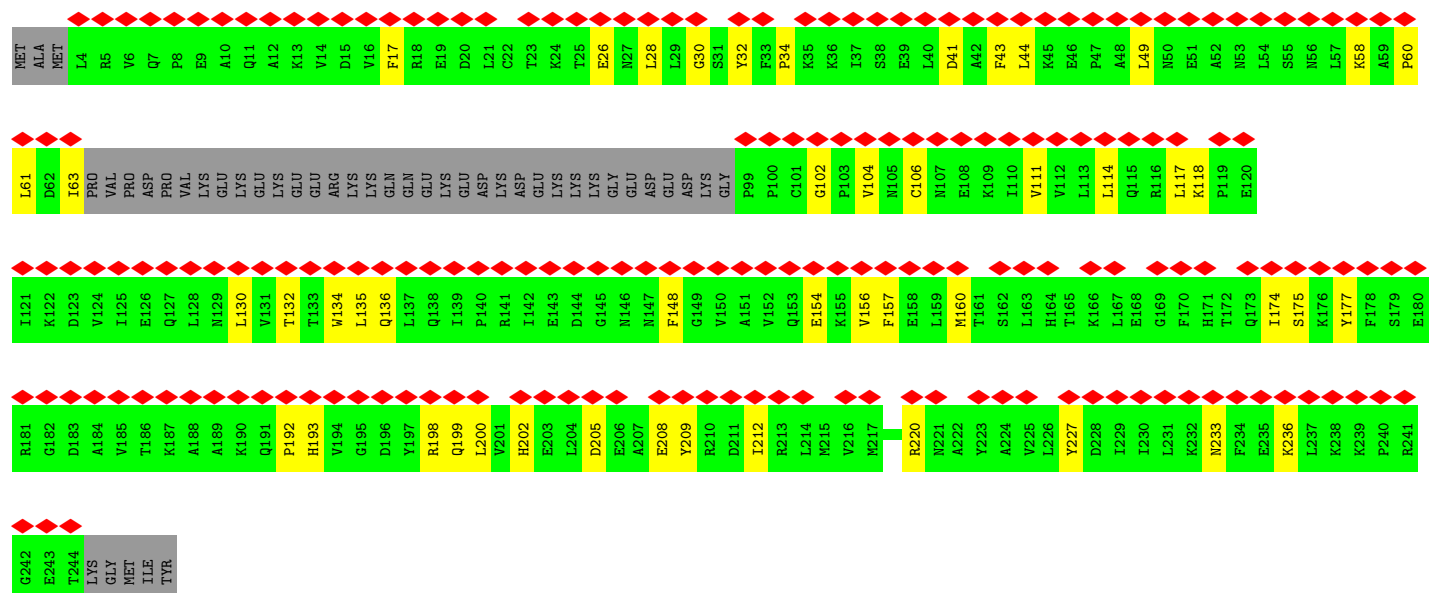
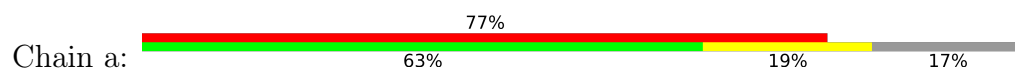




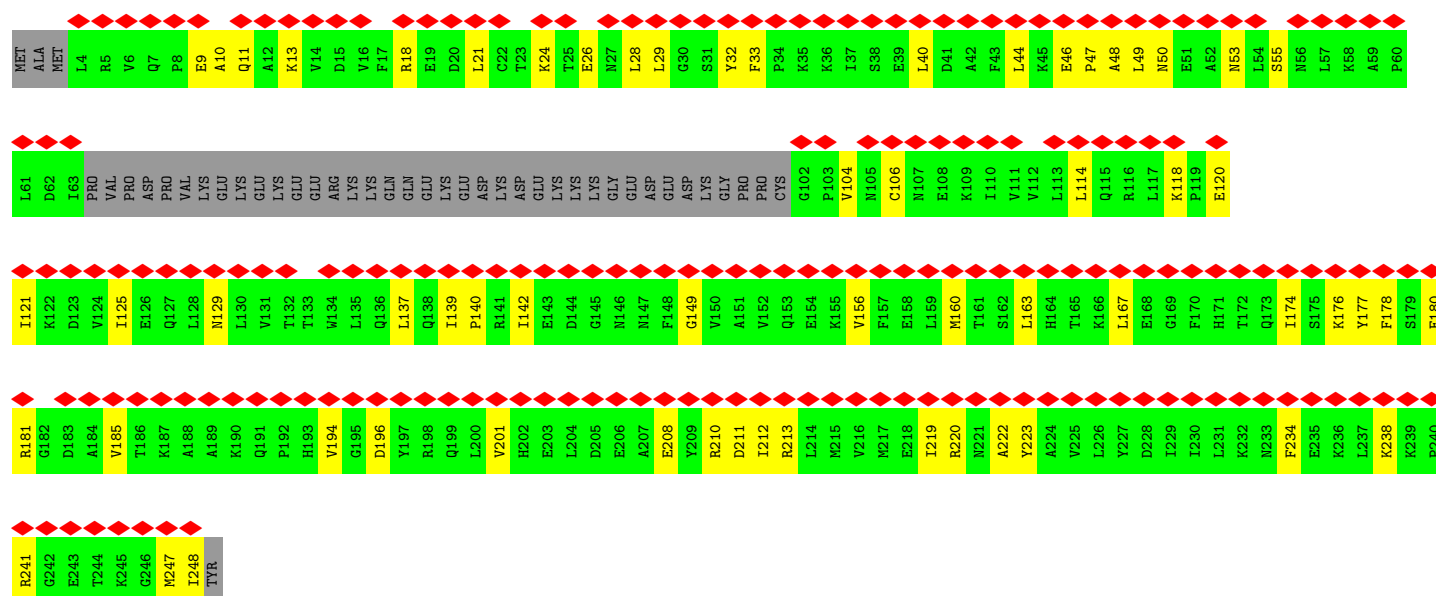
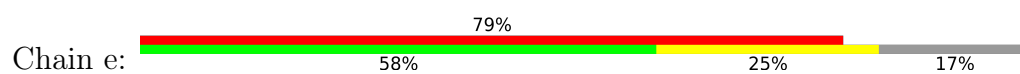
• Molecule 9: Proteasome activator complex subunit 1



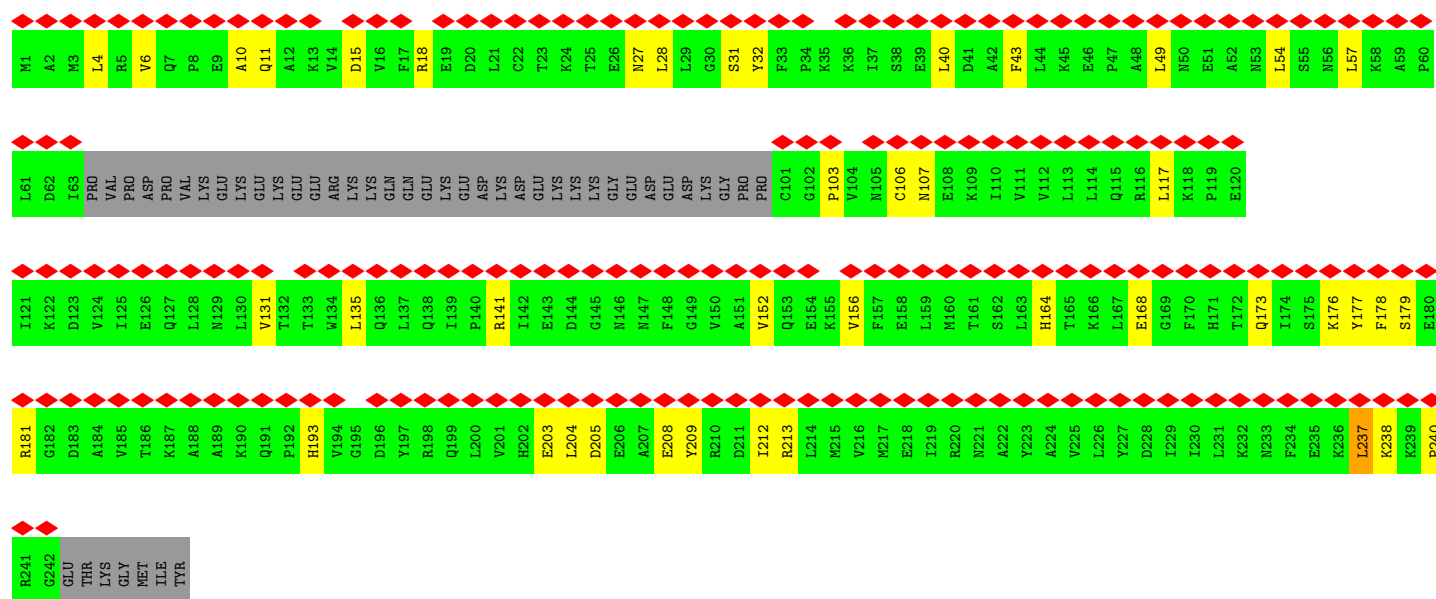
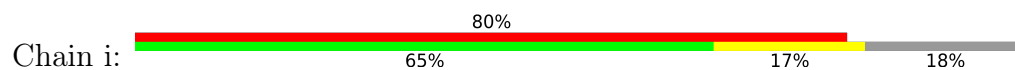
• Molecule 9: Proteasome activator complex subunit 1



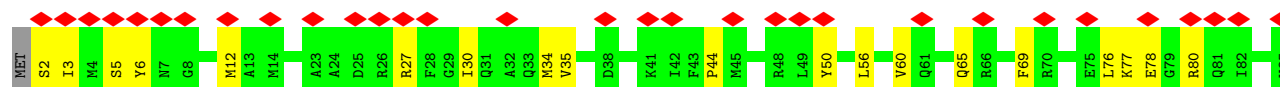
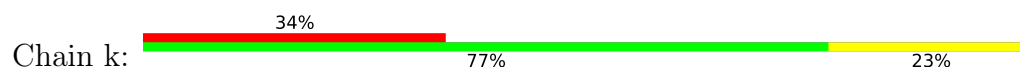
• Molecule 9: Proteasome activator complex subunit 1

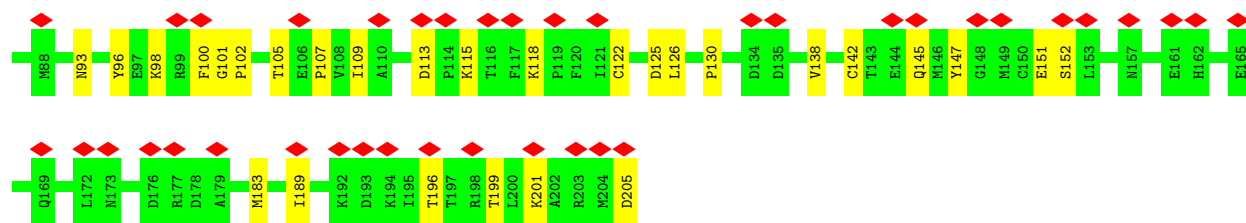


• Molecule 9: Proteasome activator complex subunit 1

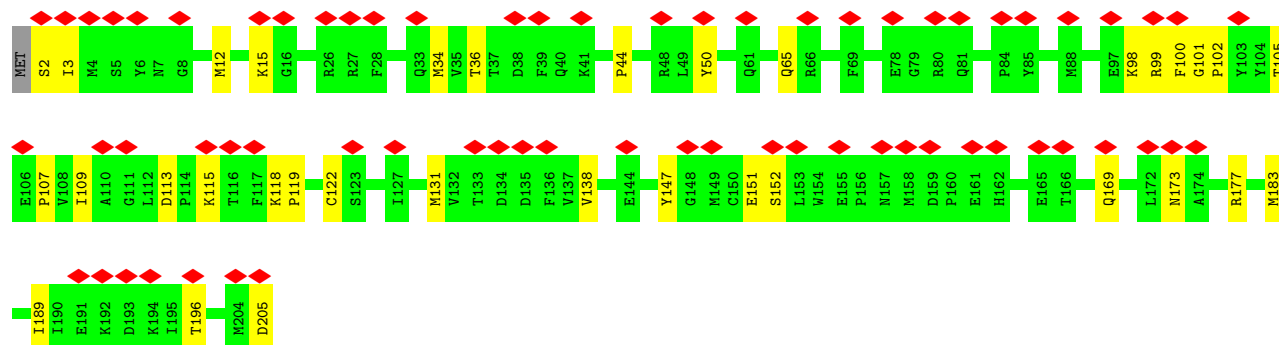
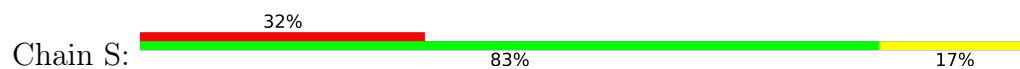


• Molecule 10: Proteasome subunit beta type-3

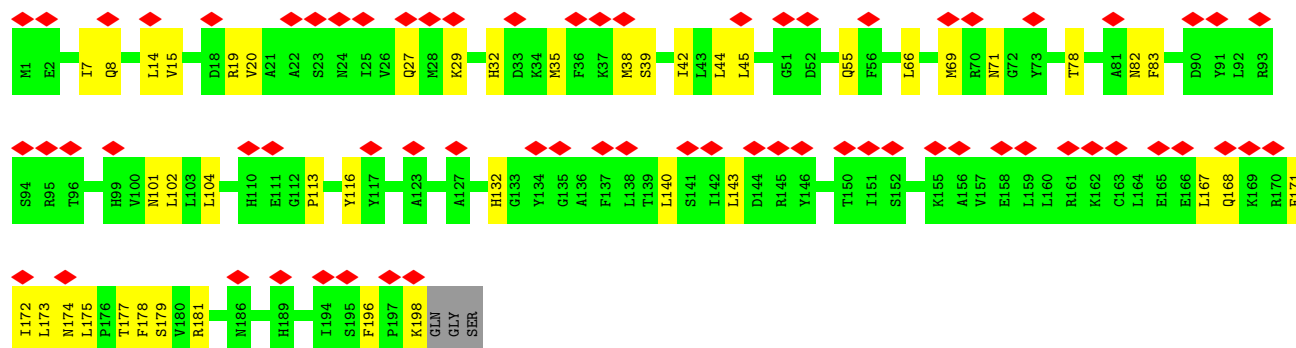
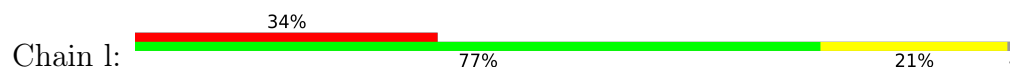




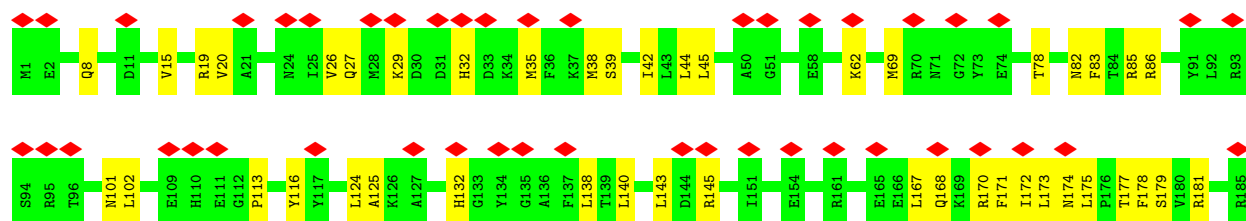
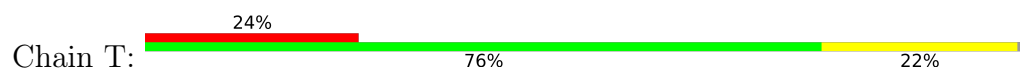
• Molecule 10: Proteasome subunit beta type-3

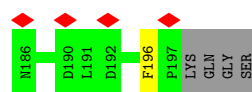


• Molecule 11: Proteasome subunit beta type-2

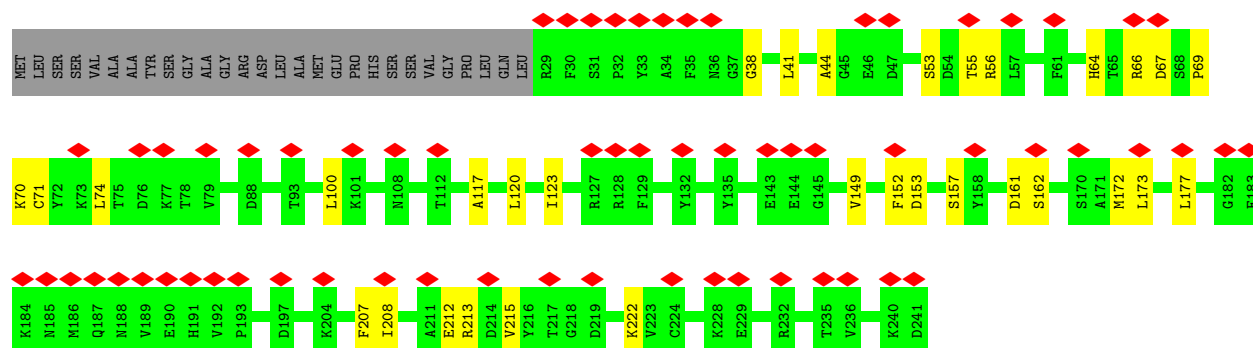
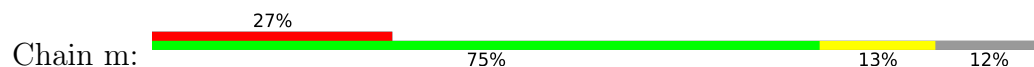


• Molecule 11: Proteasome subunit beta type-2

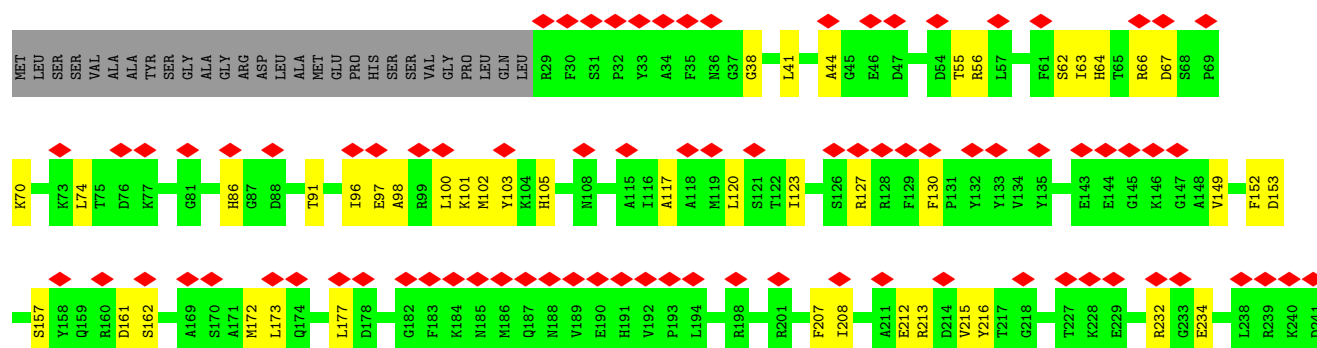




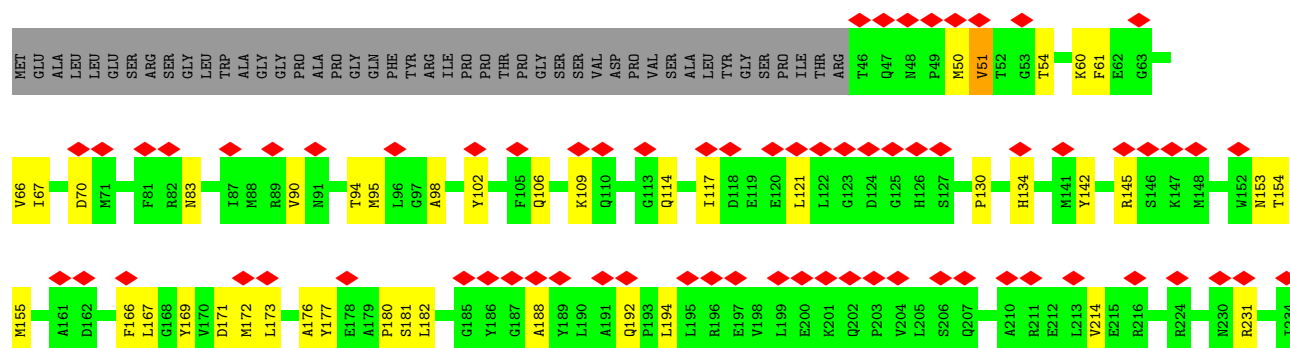
• Molecule 12: Proteasome subunit beta type-1



• Molecule 12: Proteasome subunit beta type-1

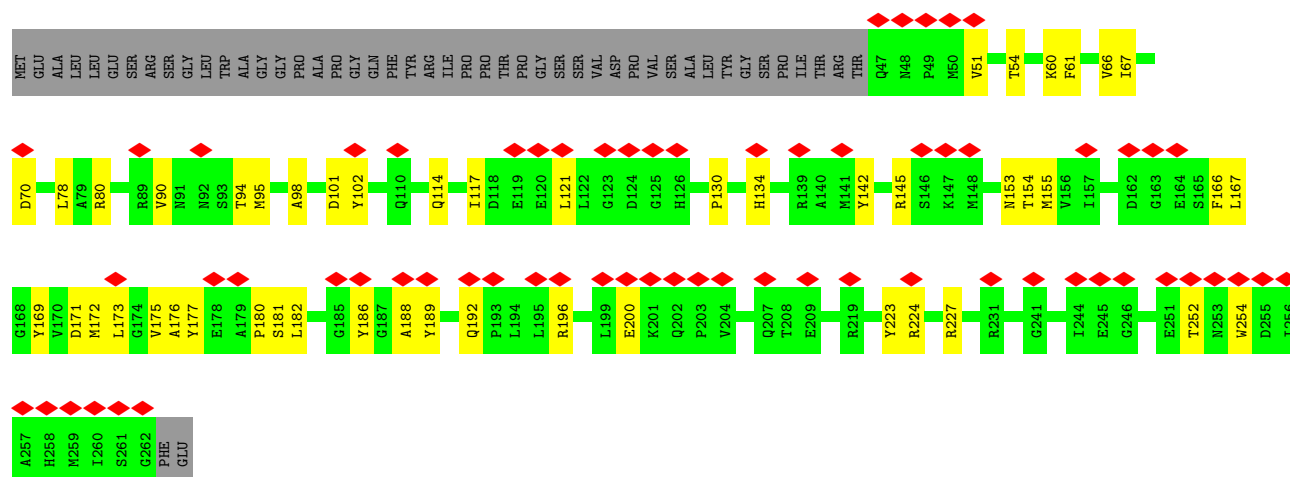


• Molecule 13: Proteasome subunit beta type-4

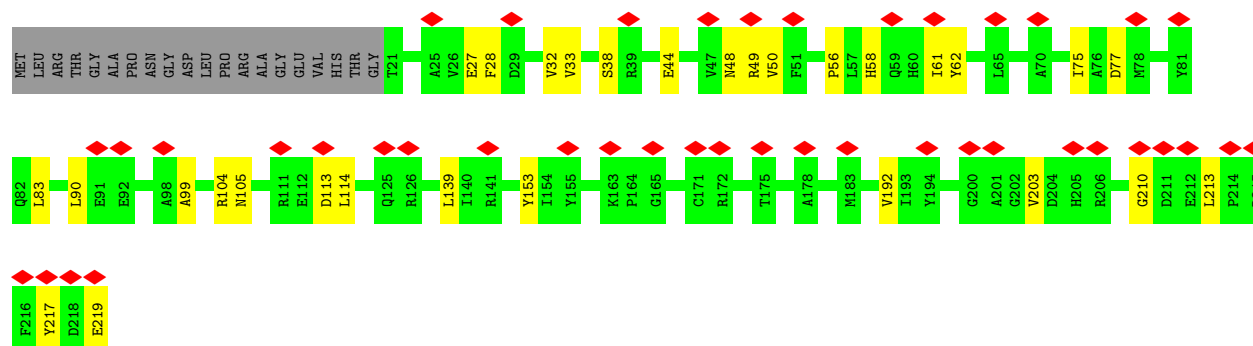
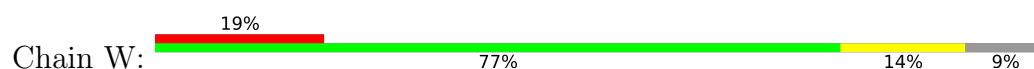




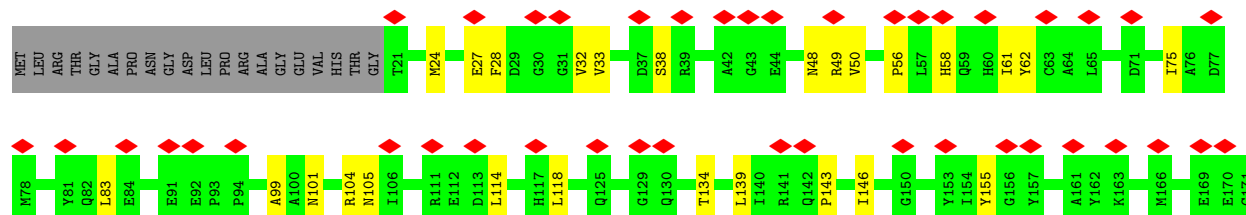
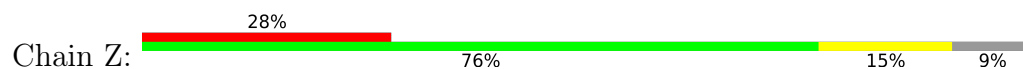
• Molecule 13: Proteasome subunit beta type-4

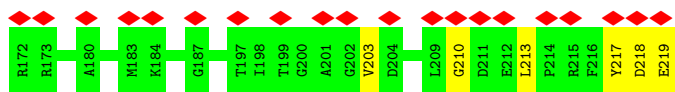


• Molecule 14: Proteasome subunit beta type-9

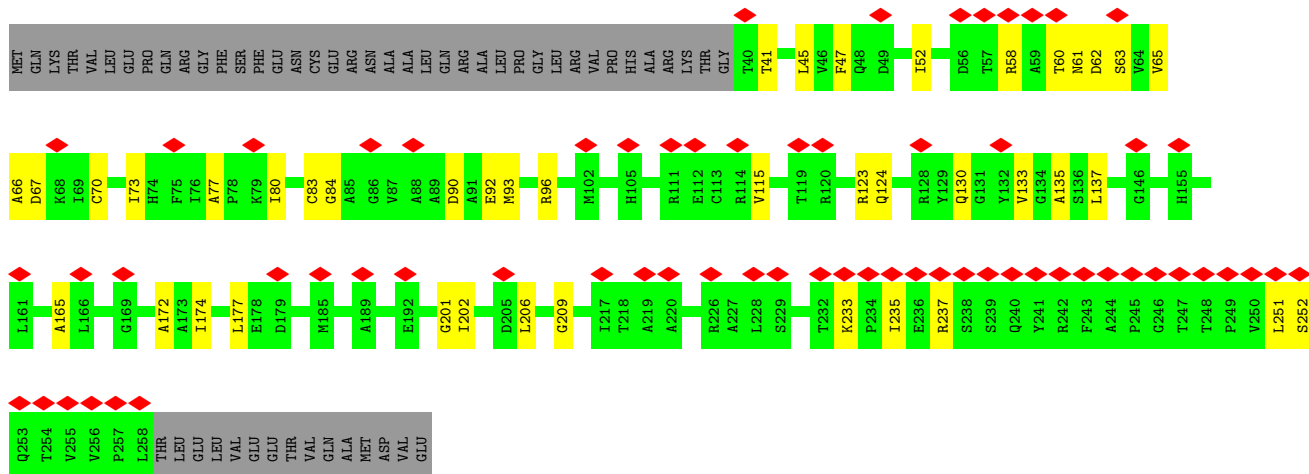


• Molecule 14: Proteasome subunit beta type-9

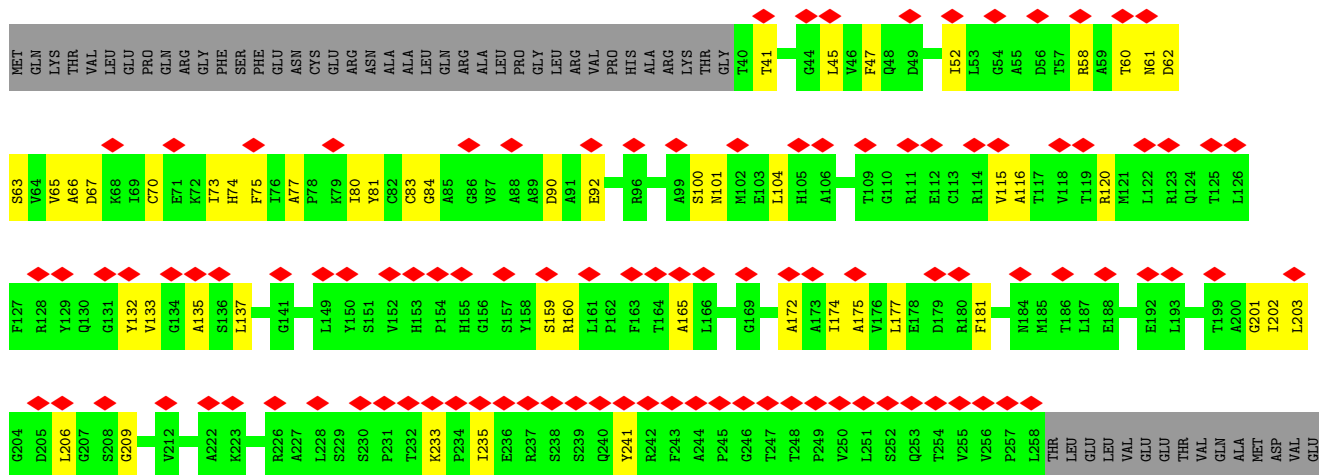




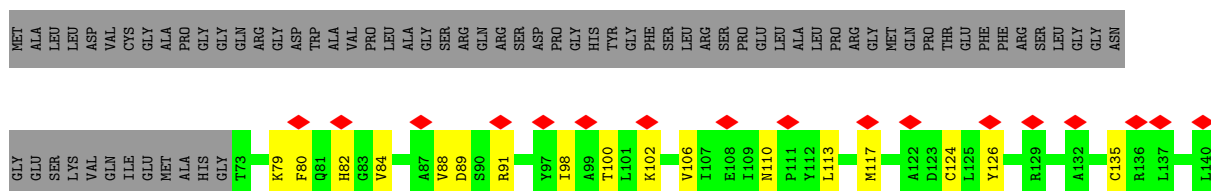
• Molecule 15: Proteasome subunit beta type-10

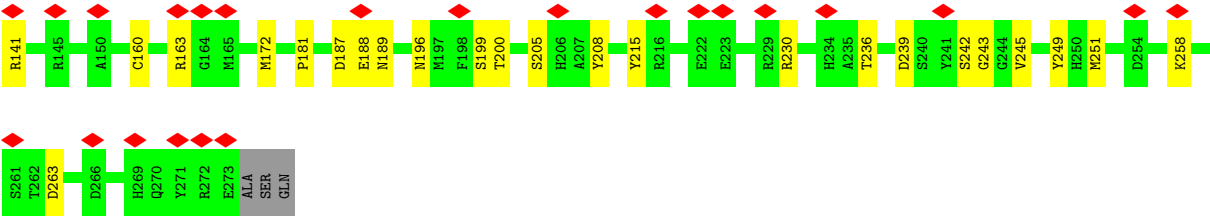


• Molecule 15: Proteasome subunit beta type-10

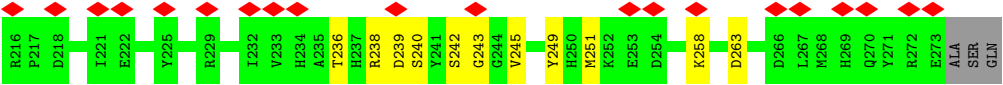
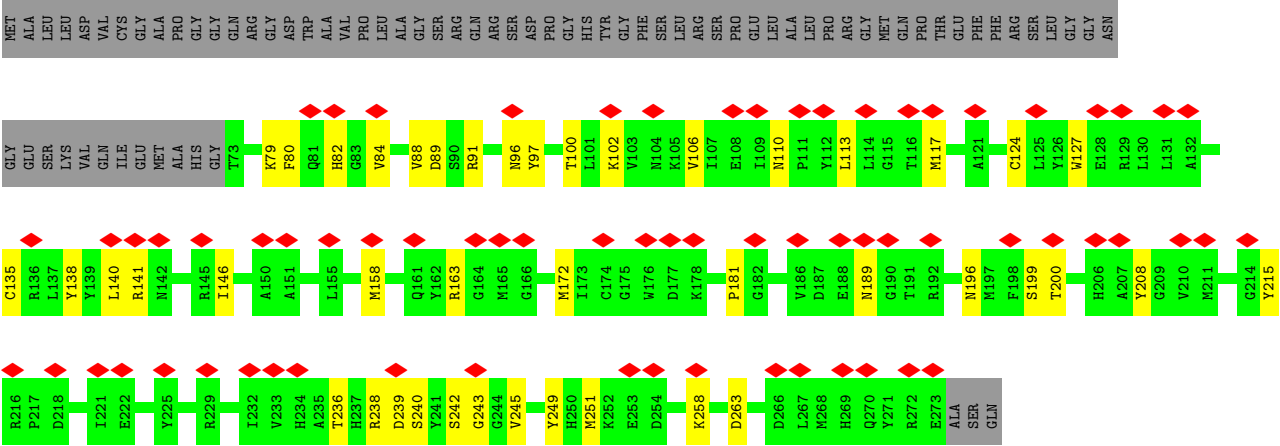


• Molecule 16: Proteasome subunit beta type-8





• Molecule 16: Proteasome subunit beta type-8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24657	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 ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.421	Depositor
Minimum map value	-1.431	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.666	Depositor
Map size (Å)	474.47998, 474.47998, 474.47998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.318, 1.318, 1.318	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.11	0/1875	0.34	0/2536
1	f	0.11	0/1895	0.34	0/2562
2	B	0.12	0/1801	0.35	0/2440
2	h	0.12	0/1815	0.36	1/2458 (0.0%)
3	C	0.22	1/1957 (0.1%)	0.36	0/2637
3	j	0.11	0/1966	0.34	0/2648
4	D	0.14	0/1851	0.44	3/2501 (0.1%)
4	P	0.14	0/1851	0.42	1/2501 (0.0%)
5	E	0.12	0/1818	0.35	0/2455
5	R	0.11	0/1818	0.33	0/2455
6	F	0.12	0/1880	0.36	0/2541
6	b	0.11	0/1880	0.36	0/2541
7	G	0.11	0/1914	0.33	0/2578
7	d	0.11	0/1914	0.33	0/2578
8	H	0.10	0/1714	0.27	0/2315
8	K	0.10	0/1708	0.30	0/2308
8	M	0.10	0/1720	0.31	0/2323
8	O	0.10	0/1714	0.31	0/2315
8	c	0.10	0/1687	0.30	0/2280
8	g	0.10	0/1720	0.32	0/2323
9	I	0.11	0/1752	0.32	0/2366
9	J	0.13	0/1692	0.32	0/2285
9	L	0.17	0/1699	0.32	0/2291
9	N	0.11	0/1681	0.34	0/2267
9	Q	0.14	0/1752	0.32	0/2366
9	a	0.12	0/1692	0.35	0/2285
9	e	0.15	0/1699	0.34	0/2291
9	i	0.17	0/1681	0.36	0/2267
10	S	0.11	0/1623	0.32	0/2188
10	k	0.11	0/1623	0.32	0/2188
11	T	0.10	0/1618	0.30	0/2190
11	l	0.11	0/1627	0.31	0/2201
12	U	0.13	0/1675	0.37	0/2257
12	m	0.11	0/1676	0.33	0/2258

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	V	0.11	0/1715	0.34	0/2319
13	n	0.13	0/1718	0.40	0/2324
14	W	0.11	0/1529	0.30	0/2071
14	Z	0.11	0/1529	0.30	0/2071
15	1	0.12	0/1637	0.37	0/2225
15	X	0.12	0/1637	0.37	0/2225
16	2	0.10	0/1592	0.32	0/2145
16	Y	0.11	0/1592	0.33	0/2145
All	All	0.12	1/72937 (0.0%)	0.34	5/98520 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	61	PHE	CA-C	7.42	1.56	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	h	232	ALA	CA-C-O	6.61	127.72	120.12
4	D	50	VAL	N-CA-C	5.64	116.25	108.12
4	P	213	ARG	CB-CA-C	-5.21	110.55	116.54
4	D	213	ARG	CB-CA-C	-5.19	110.57	116.54
4	D	51	ALA	N-CA-C	5.16	118.71	111.74

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1841	0	1853	35	0
1	f	1861	0	1872	38	0
2	B	1763	0	1759	34	0
2	h	1777	0	1775	33	0
3	C	1927	0	1948	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	j	1936	0	1961	43	0
4	D	1824	0	1851	37	0
4	P	1824	0	1851	51	0
5	E	1790	0	1773	51	0
5	R	1790	0	1773	43	0
6	F	1846	0	1832	48	0
6	b	1846	0	1832	39	0
7	G	1879	0	1864	43	0
7	d	1879	0	1864	50	0
8	H	1684	0	1721	21	0
8	K	1678	0	1713	26	0
8	M	1689	0	1728	21	0
8	O	1684	0	1721	27	0
8	c	1658	0	1695	27	0
8	g	1689	0	1728	31	0
9	I	1721	0	1759	22	0
9	J	1663	0	1700	28	0
9	L	1672	0	1716	21	0
9	N	1654	0	1698	36	0
9	Q	1721	0	1759	44	0
9	a	1663	0	1700	42	0
9	e	1672	0	1716	47	0
9	i	1654	0	1698	35	0
10	S	1594	0	1613	22	0
10	k	1594	0	1613	35	0
11	T	1584	0	1584	33	0
11	l	1593	0	1597	31	0
12	U	1644	0	1641	49	0
12	m	1645	0	1644	20	0
13	V	1682	0	1661	38	0
13	n	1685	0	1665	38	0
14	W	1500	0	1459	23	0
14	Z	1500	0	1459	26	0
15	1	1611	0	1624	34	0
15	X	1611	0	1624	31	0
16	2	1561	0	1516	36	0
16	Y	1561	0	1516	30	0
All	All	71650	0	72076	1178	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 8.

All (1178) 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)
9:a:63:ILE:HD12	9:a:192:PRO:O	1.40	1.18
6:F:93:LEU:HD13	12:U:102:MET:CE	1.92	1.00
5:E:90:ASP:O	5:E:94:VAL:HG23	1.64	0.97
6:F:93:LEU:CD1	12:U:102:MET:HE2	1.95	0.95
5:R:89:ILE:O	5:R:93:ARG:HG3	1.67	0.94
12:U:96:ILE:O	12:U:100:LEU:HG	1.69	0.92
5:E:93:ARG:HH22	16:2:141:ARG:HA	1.34	0.91
5:R:121:LEU:HD12	6:b:79:ALA:HB3	1.54	0.89
2:B:95:GLN:HG3	15:1:100:SER:HB3	1.54	0.89
6:F:93:LEU:HD13	12:U:102:MET:HE3	1.54	0.88
9:i:117:LEU:HD11	9:i:212:ILE:HG23	1.60	0.84
5:E:13:ASN:HB3	6:F:126:ARG:HB3	1.61	0.81
6:F:93:LEU:HD12	12:U:102:MET:HE2	1.63	0.79
9:a:63:ILE:CD1	9:a:192:PRO:O	2.29	0.78
2:B:91:ARG:HB3	15:1:104:LEU:HD22	1.66	0.78
9:e:40:LEU:HD22	9:e:223:TYR:HE2	1.49	0.76
12:U:74:LEU:HD22	12:U:100:LEU:HD11	1.68	0.75
1:A:132:ARG:HE	7:G:125:LEU:HA	1.51	0.74
6:F:81:ALA:HB2	6:F:130:VAL:HG21	1.70	0.74
9:a:61:LEU:O	9:a:198:ARG:NE	2.20	0.74
6:F:93:LEU:CD1	12:U:102:MET:CE	2.58	0.74
9:e:139:ILE:HG21	8:g:149:ARG:HH12	1.51	0.73
12:U:98:ALA:O	12:U:102:MET:HG3	1.88	0.73
6:b:81:ALA:HB2	6:b:130:VAL:HG21	1.70	0.73
9:a:26:GLU:HA	9:i:4:LEU:HD13	1.69	0.73
5:E:93:ARG:HH22	16:2:141:ARG:CA	2.02	0.73
3:C:123:GLN:HA	4:D:125:ARG:HE	1.53	0.73
4:P:36:ARG:NH1	5:R:60:GLU:OE2	2.22	0.72
4:P:88:ARG:NH1	11:l:69:MET:O	2.22	0.72
10:k:199:THR:HB	15:X:252:SER:HB2	1.72	0.72
9:e:40:LEU:HD21	9:e:120:GLU:HB3	1.72	0.71
9:i:237:LEU:C	9:i:237:LEU:HD12	2.16	0.71
9:e:125:ILE:O	9:e:129:ASN:ND2	2.25	0.70
2:B:74:LEU:HD21	2:B:134:LEU:HD22	1.74	0.70
5:E:77:ALA:HB3	5:E:142:LEU:HB2	1.72	0.70
8:H:183:HIS:ND1	9:J:102:GLY:O	2.25	0.70
9:L:18:ARG:HE	9:L:137:LEU:HB3	1.55	0.70
5:R:77:ALA:HB3	5:R:142:LEU:HB2	1.72	0.69
13:n:257:ALA:HA	14:Z:50:VAL:HG11	1.73	0.69
13:V:145:ARG:NH2	13:V:173:LEU:O	2.25	0.69
13:n:145:ARG:NH2	13:n:173:LEU:O	2.26	0.69
5:E:127:ASP:OD2	6:F:125:ARG:NE	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:ARG:HD3	7:G:13:SER:HA	1.75	0.68
7:d:13:SER:HA	1:f:132:ARG:HD3	1.74	0.68
4:P:94:HIS:HD2	4:P:102:VAL:HG22	1.59	0.68
5:R:89:ILE:CG2	5:R:93:ARG:HH21	2.06	0.68
2:h:74:LEU:HD21	2:h:134:LEU:HD22	1.74	0.68
6:F:122:ARG:HB3	6:F:125:ARG:HD2	1.74	0.68
8:g:116:GLU:OE2	9:i:213:ARG:NH2	2.24	0.68
3:C:154:GLY:O	4:D:81:ARG:NH2	2.27	0.68
6:F:7:ASP:O	6:F:21:GLN:NE2	2.27	0.68
7:G:55:LEU:HB2	7:G:59:TYR:HE2	1.59	0.68
1:f:150:GLN:NE2	1:f:152:TYR:OH	2.28	0.67
8:g:44:ASN:HA	8:g:210:ARG:HH11	1.60	0.67
1:A:150:GLN:NE2	1:A:152:TYR:OH	2.28	0.67
4:D:37:GLY:HA2	4:D:181:ILE:HB	1.77	0.67
6:b:7:ASP:O	6:b:21:GLN:NE2	2.27	0.67
4:P:37:GLY:HA2	4:P:181:ILE:HB	1.77	0.67
2:B:95:GLN:NE2	15:1:101:ASN:OD1	2.26	0.67
9:i:181:ARG:NH1	9:i:205:ASP:OD1	2.28	0.66
8:M:44:ASN:HA	8:M:210:ARG:HH11	1.60	0.66
16:Y:110:ASN:HB2	16:Y:113:LEU:HB3	1.78	0.66
8:O:171:ARG:NH1	8:O:195:ASP:OD1	2.28	0.66
9:N:57:LEU:HD21	9:N:109:LYS:HB2	1.77	0.65
9:N:238:LYS:HG3	9:N:240:PRO:HD3	1.77	0.65
7:d:55:LEU:HB2	7:d:59:TYR:HE2	1.59	0.65
14:W:77:ASP:OD2	15:X:123:ARG:NH1	2.30	0.65
3:C:45:LEU:HD21	3:C:75:SER:HB3	1.79	0.65
4:D:64:ALA:HA	4:D:70:CYS:HA	1.79	0.65
4:D:146:GLN:OE1	4:D:159:ASN:ND2	2.22	0.65
6:F:39:LYS:HE3	6:F:157:ARG:HA	1.79	0.65
11:T:78:THR:O	11:T:82:ASN:ND2	2.30	0.65
16:2:110:ASN:HB2	16:2:113:LEU:HB3	1.78	0.65
9:i:15:ASP:OD1	9:i:18:ARG:NH2	2.29	0.64
8:c:44:ASN:HA	8:c:210:ARG:HH11	1.61	0.64
12:U:232:ARG:NH1	12:U:234:GLU:OE2	2.29	0.64
4:P:64:ALA:HA	4:P:70:CYS:HA	1.79	0.64
3:j:45:LEU:HD21	3:j:75:SER:HB3	1.79	0.64
11:l:198:LYS:HB3	11:T:196:PHE:HB3	1.78	0.64
5:R:89:ILE:HG21	5:R:93:ARG:HH21	1.62	0.64
11:l:78:THR:O	11:l:82:ASN:ND2	2.30	0.64
5:E:103:TYR:CE2	12:U:103:TYR:CE1	2.86	0.64
4:P:88:ARG:HD3	11:l:69:MET:HB3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Y:236:THR:HG22	16:Y:242:SER:HB3	1.79	0.64
16:2:236:THR:HG22	16:2:242:SER:HB3	1.79	0.64
5:R:122:GLN:HE22	6:b:83:LEU:HD12	1.62	0.64
1:A:123:GLN:HE22	2:B:84:ARG:HB2	1.63	0.63
8:K:94:LEU:HD22	9:L:194:VAL:HA	1.79	0.63
6:b:39:LYS:HE3	6:b:157:ARG:HA	1.79	0.63
9:N:41:ASP:OD1	9:N:220:ARG:NH1	2.32	0.63
12:m:41:LEU:HD12	12:m:173:LEU:HD23	1.80	0.63
11:l:55:GLN:OE1	16:Y:163:ARG:NH1	2.29	0.63
9:a:63:ILE:HG13	9:a:63:ILE:O	1.98	0.63
12:U:41:LEU:HD12	12:U:173:LEU:HD23	1.80	0.62
7:G:206:LYS:HG2	9:N:1:MET:HE3	1.80	0.62
1:A:196:GLU:HG2	1:A:242:LEU:HG	1.79	0.62
2:B:97:TYR:HD1	2:B:113:ARG:HH22	1.47	0.62
12:U:74:LEU:HD22	12:U:100:LEU:CD1	2.29	0.62
14:Z:58:HIS:HB3	14:Z:61:ILE:HB	1.82	0.62
3:C:100:GLN:HB3	11:T:83:PHE:HD1	1.65	0.62
8:M:168:PHE:HE2	9:N:203:GLU:HG3	1.64	0.62
5:R:99:HIS:HB2	5:R:107:MET:HE3	1.82	0.62
5:E:99:HIS:HB2	5:E:107:MET:HE3	1.82	0.61
9:Q:181:ARG:NH1	9:Q:208:GLU:OE1	2.33	0.61
2:h:69:THR:HG22	2:h:72:ILE:HB	1.82	0.61
15:X:67:ASP:HB3	15:X:70:CYS:HB2	1.81	0.61
9:J:41:ASP:HA	9:J:220:ARG:HH11	1.65	0.61
2:h:97:TYR:HD1	2:h:113:ARG:HH22	1.47	0.61
15:1:60:THR:HG22	15:1:65:VAL:HA	1.83	0.61
14:W:58:HIS:HB3	14:W:61:ILE:HB	1.82	0.61
4:D:204:LYS:HG3	4:D:222:PRO:HB3	1.83	0.61
8:g:168:PHE:HE2	9:i:203:GLU:HG3	1.66	0.61
13:V:54:THR:HG21	13:V:70:ASP:HB2	1.83	0.61
9:a:41:ASP:HA	9:a:220:ARG:HH11	1.65	0.61
14:W:104:ARG:HD2	14:W:139:LEU:HB2	1.83	0.61
13:n:153:ASN:OD1	13:n:154:THR:N	2.34	0.61
4:P:47:LYS:HE2	4:P:59:VAL:O	2.00	0.61
2:B:118:MET:HG2	2:B:130:PHE:HD2	1.66	0.60
15:1:67:ASP:HB3	15:1:70:CYS:HB2	1.81	0.60
1:A:163:PHE:HD2	1:A:166:THR:HG22	1.66	0.60
9:J:44:LEU:HA	9:J:49:LEU:HD23	1.84	0.60
8:O:41:ILE:HB	9:a:17:PHE:HZ	1.65	0.60
2:h:118:MET:HG2	2:h:130:PHE:HD2	1.66	0.60
13:n:54:THR:HG21	13:n:70:ASP:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Z:104:ARG:HD2	14:Z:139:LEU:HB2	1.83	0.60
5:R:164:GLN:HB3	6:b:58:ALA:HB3	1.83	0.60
13:V:153:ASN:OD1	13:V:154:THR:N	2.34	0.60
15:X:60:THR:HG22	15:X:65:VAL:HA	1.83	0.60
4:D:105:GLU:OE2	4:D:109:ARG:NH2	2.34	0.60
9:a:148:PHE:HE2	6:b:5:GLN:HE22	1.50	0.60
6:b:117:GLN:NE2	7:d:83:ALA:O	2.33	0.60
11:l:29:LYS:HE2	11:l:32:HIS:HA	1.84	0.60
7:G:97:SER:O	13:V:114:GLN:NE2	2.35	0.60
8:H:108:LYS:NZ	9:I:203:GLU:OE1	2.30	0.60
2:B:69:THR:HG22	2:B:72:ILE:HB	1.82	0.60
1:f:163:PHE:HD2	1:f:166:THR:HG22	1.66	0.60
3:C:167:ASN:ND2	3:C:200:THR:O	2.35	0.60
12:U:62:SER:HB2	13:V:189:TYR:HE1	1.67	0.60
6:b:157:ARG:N	7:d:58:LEU:O	2.26	0.59
11:l:168:GLN:NE2	11:l:174:ASN:O	2.33	0.59
9:I:47:PRO:HA	9:I:50:ASN:HB3	1.83	0.59
9:a:44:LEU:HA	9:a:49:LEU:HD23	1.84	0.59
12:m:66:ARG:NH2	15:1:203:LEU:O	2.36	0.59
11:T:29:LYS:HE2	11:T:32:HIS:HA	1.84	0.59
6:F:65:HIS:HD2	12:U:105:HIS:NE2	2.00	0.59
9:I:118:LYS:NZ	8:K:193:GLU:OE1	2.33	0.59
9:N:57:LEU:HD22	9:N:107:ASN:HD21	1.68	0.59
9:a:30:GLY:HA3	9:i:6:VAL:HA	1.85	0.59
4:P:233:GLU:O	4:P:233:GLU:HG2	2.03	0.59
6:b:45:VAL:HG22	6:b:214:ILE:HG12	1.85	0.59
3:j:167:ASN:ND2	3:j:200:THR:O	2.35	0.59
3:C:50:ARG:HH21	9:I:248:ILE:HG23	1.68	0.59
1:A:143:ILE:HA	1:A:149:PRO:HA	1.85	0.58
9:I:242:GLY:HA3	9:I:245:LYS:HE3	1.85	0.58
4:P:5:ARG:HH12	3:j:3:ARG:HG2	1.67	0.58
4:P:120:GLN:HB3	5:R:135:ARG:HE	1.68	0.58
13:n:83:ASN:ND2	14:Z:219:GLU:OE1	2.31	0.58
11:T:168:GLN:NE2	11:T:174:ASN:O	2.33	0.58
4:D:146:GLN:HB3	9:L:247:MET:HE1	1.85	0.58
12:U:172:MET:HE1	12:U:213:ARG:HB2	1.85	0.58
13:V:167:LEU:HG	13:V:182:LEU:HD12	1.85	0.58
1:f:21:ARG:NH1	1:f:26:GLU:OE2	2.35	0.58
1:f:159:TYR:HE1	2:h:80:GLY:HA3	1.69	0.58
13:n:167:LEU:HG	13:n:182:LEU:HD12	1.85	0.58
5:E:18:GLU:OE1	5:E:20:ARG:NH2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:203:LYS:HA	5:E:206:MET:HE3	1.84	0.58
9:a:26:GLU:HG3	9:i:4:LEU:HB3	1.86	0.58
5:R:203:LYS:HA	5:R:206:MET:HE3	1.84	0.58
11:T:35:MET:HE1	11:T:181:ARG:HB2	1.85	0.58
4:D:220:LEU:HD11	4:D:228:TYR:HE2	1.69	0.58
5:E:103:TYR:CE2	12:U:103:TYR:HE1	2.22	0.58
8:g:185:MET:HA	8:g:188:ARG:HE	1.69	0.58
1:f:143:ILE:HA	1:f:149:PRO:HA	1.85	0.58
1:f:153:LYS:NZ	1:f:167:ALA:O	2.37	0.58
15:X:58:ARG:NH2	15:X:206:LEU:O	2.37	0.58
6:F:45:VAL:HG22	6:F:214:ILE:HG12	1.85	0.58
9:Q:220:ARG:HA	9:Q:223:TYR:HD2	1.69	0.58
10:k:35:VAL:O	16:2:238:ARG:NH1	2.37	0.58
14:W:217:TYR:CZ	14:W:219:GLU:HB3	2.39	0.58
9:a:28:LEU:HD12	9:a:32:TYR:HB2	1.86	0.58
9:i:173:GLN:HA	9:i:176:LYS:HB3	1.86	0.58
4:P:220:LEU:HD11	4:P:228:TYR:HE2	1.69	0.58
5:R:18:GLU:OE1	5:R:20:ARG:NH2	2.37	0.58
10:S:36:THR:HG21	11:T:125:ALA:HB1	1.85	0.58
9:Q:43:PHE:HE2	9:Q:216:VAL:HG21	1.69	0.57
9:e:149:GLY:HA3	9:e:241:ARG:HG2	1.86	0.57
14:W:27:GLU:HA	14:W:32:VAL:HG12	1.86	0.57
7:G:73:HIS:ND1	7:G:223:GLY:O	2.28	0.57
11:l:35:MET:HE1	11:l:181:ARG:HB2	1.85	0.57
12:m:172:MET:HE1	12:m:213:ARG:HB2	1.85	0.57
6:F:65:HIS:CD2	12:U:105:HIS:NE2	2.72	0.57
7:d:73:HIS:HD2	7:d:106:ASN:HD22	1.53	0.57
5:R:93:ARG:HH12	16:Y:141:ARG:HA	1.69	0.57
4:D:36:ARG:NH2	4:D:142:PRO:O	2.37	0.57
1:f:190:THR:HG22	1:f:191:PHE:H	1.70	0.57
1:A:153:LYS:NZ	1:A:167:ALA:O	2.37	0.57
8:M:185:MET:HA	8:M:188:ARG:HE	1.69	0.57
4:P:36:ARG:NH2	4:P:142:PRO:O	2.37	0.57
4:P:146:GLN:OE1	4:P:159:ASN:ND2	2.22	0.56
15:X:165:ALA:HB3	15:X:174:ILE:HG13	1.87	0.56
1:A:190:THR:HG22	1:A:191:PHE:H	1.70	0.56
9:e:118:LYS:NZ	8:g:193:GLU:OE1	2.33	0.56
9:e:247:MET:HB2	4:P:27:LYS:HE2	1.87	0.56
4:P:50:VAL:HG12	4:P:52:LYS:H	1.70	0.56
15:1:58:ARG:NH2	15:1:206:LEU:O	2.37	0.56
13:V:223:TYR:HB3	14:W:49:ARG:HD3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2:172:MET:HE2	16:2:200:THR:HG22	1.87	0.56
8:g:130:PRO:HB3	8:g:231:LYS:HB2	1.87	0.56
4:P:94:HIS:CD2	4:P:102:VAL:HG22	2.41	0.56
9:J:28:LEU:HD12	9:J:32:TYR:HB2	1.86	0.56
9:i:238:LYS:HG3	9:i:240:PRO:HD3	1.86	0.56
7:d:243:SER:C	7:d:245:LYS:H	2.13	0.56
12:m:69:PRO:HG3	12:m:222:LYS:HE3	1.88	0.56
8:K:43:LEU:HD22	8:K:206:VAL:HG13	1.86	0.56
9:e:177:TYR:OH	9:e:211:ASP:OD2	2.23	0.56
10:k:78:GLU:HG2	10:k:80:ARG:H	1.71	0.56
8:M:130:PRO:HB3	8:M:231:LYS:HB2	1.87	0.56
9:e:140:PRO:HG3	9:e:241:ARG:HB2	1.88	0.56
2:B:140:ASN:HB2	2:B:145:TYR:HE2	1.71	0.56
9:e:21:LEU:HD23	9:e:24:LYS:HD2	1.87	0.56
13:n:256:ILE:HD12	14:Z:49:ARG:NH2	2.21	0.56
4:D:173:GLU:HA	5:E:58:LEU:HD21	1.88	0.55
14:Z:27:GLU:HA	14:Z:32:VAL:HG12	1.86	0.55
12:m:74:LEU:HD22	12:m:100:LEU:HD11	1.87	0.55
12:m:173:LEU:HD21	12:m:207:PHE:HE1	1.72	0.55
1:A:61:LEU:HD12	7:G:160:GLY:O	2.06	0.55
4:P:5:ARG:NH1	3:j:3:ARG:HG2	2.21	0.55
9:a:134:TRP:HE3	9:a:135:LEU:HD12	1.71	0.55
9:e:248:ILE:HA	4:P:169:ARG:HH12	1.71	0.55
10:S:99:ARG:HG3	15:1:132:TYR:HE2	1.72	0.55
2:B:98:TYR:O	2:B:102:GLN:NE2	2.40	0.55
16:Y:172:MET:HE2	16:Y:200:THR:HG22	1.87	0.55
6:b:72:ILE:HD11	6:b:132:LEU:HB3	1.89	0.55
9:Q:194:VAL:HG12	9:Q:196:ASP:H	1.72	0.55
2:h:98:TYR:O	2:h:102:GLN:NE2	2.40	0.55
13:V:61:PHE:CE2	13:V:66:VAL:HG23	2.42	0.55
7:G:73:HIS:HD2	7:G:106:ASN:HD22	1.53	0.55
9:J:134:TRP:HE3	9:J:135:LEU:HD12	1.71	0.55
13:V:169:TYR:HB2	13:V:182:LEU:HD13	1.89	0.55
9:Q:4:LEU:HB3	8:c:33:TYR:HB3	1.89	0.54
4:P:180:ALA:O	4:P:181:ILE:HG13	2.07	0.54
13:n:169:TYR:HB2	13:n:182:LEU:HD13	1.88	0.54
8:O:32:LEU:HA	8:O:36:LEU:HD12	1.90	0.54
2:h:140:ASN:HB2	2:h:145:TYR:HE2	1.71	0.54
15:1:165:ALA:HB3	15:1:174:ILE:HG13	1.88	0.54
6:F:72:ILE:HD11	6:F:132:LEU:HB3	1.89	0.54
8:g:64:LEU:HD11	8:g:175:VAL:HG22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:173:LEU:HD21	12:U:207:PHE:HE1	1.72	0.54
13:V:90:VAL:HB	13:V:94:THR:HG23	1.89	0.54
4:D:180:ALA:O	4:D:181:ILE:HG13	2.07	0.54
9:J:58:LYS:HG2	9:J:60:PRO:HD3	1.90	0.54
8:O:43:LEU:HD23	8:O:46:LEU:HD22	1.89	0.54
3:j:49:ARG:HG3	3:j:63:GLU:OE1	2.07	0.54
15:X:60:THR:HA	15:X:66:ALA:H	1.73	0.54
15:1:60:THR:HA	15:1:66:ALA:H	1.73	0.54
8:H:112:TRP:HB3	9:I:210:ARG:HH21	1.72	0.54
8:c:128:LEU:HD13	8:c:228:VAL:HA	1.89	0.54
9:i:164:HIS:NE2	9:i:168:GLU:OE2	2.41	0.54
5:R:89:ILE:HG22	5:R:93:ARG:NE	2.23	0.54
5:R:99:HIS:CE1	5:R:103:TYR:HD2	2.26	0.54
12:U:153:ASP:OD1	12:U:157:SER:N	2.41	0.54
5:E:121:LEU:HD22	6:F:79:ALA:HB1	1.90	0.54
6:F:166:GLN:HG2	9:N:241:ARG:HH11	1.71	0.54
8:O:7:VAL:HG11	9:Q:29:LEU:HD12	1.89	0.54
9:e:118:LYS:NZ	8:g:196:GLU:OE1	2.36	0.54
3:j:109:GLN:OE1	11:l:71:ASN:ND2	2.33	0.54
12:m:153:ASP:OD1	12:m:157:SER:N	2.41	0.54
1:A:162:GLY:O	2:B:58:ASP:N	2.34	0.54
3:C:100:GLN:HG2	11:T:86:ARG:HD2	1.89	0.54
8:O:108:LYS:NZ	9:Q:203:GLU:OE1	2.40	0.54
1:f:103:TYR:O	15:X:124:GLN:NE2	2.40	0.54
13:n:90:VAL:HB	13:n:94:THR:HG23	1.89	0.54
7:G:48:PHE:HB2	7:G:215:SER:HB3	1.90	0.54
6:b:155:ASP:HB3	7:d:63:SER:HB2	1.89	0.54
13:n:61:PHE:CE2	13:n:66:VAL:HG23	2.42	0.54
4:D:222:PRO:HA	4:D:225:ILE:HD12	1.89	0.54
5:E:99:HIS:CE1	5:E:103:TYR:HD2	2.26	0.54
5:E:123:PHE:CE2	5:E:136:PRO:HA	2.42	0.54
9:J:164:HIS:NE2	9:J:168:GLU:OE2	2.41	0.54
11:T:171:PHE:CE2	11:T:173:LEU:HB2	2.43	0.54
12:U:56:ARG:NH1	12:U:215:VAL:O	2.41	0.54
12:U:213:ARG:HA	15:X:65:VAL:HB	1.90	0.54
9:Q:241:ARG:HH21	9:Q:245:LYS:HB2	1.73	0.53
14:W:210:GLY:HA2	14:W:213:LEU:HD13	1.90	0.53
2:h:160:ALA:HB1	2:h:174:LEU:HD13	1.90	0.53
15:1:41:THR:HG21	15:1:201:GLY:HA3	1.90	0.53
2:B:160:ALA:HB1	2:B:174:LEU:HD13	1.90	0.53
9:L:134:TRP:HZ2	9:L:238:LYS:HE3	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:d:48:PHE:HB2	7:d:215:SER:HB3	1.90	0.53
8:H:168:PHE:CE2	9:I:203:GLU:HG3	2.43	0.53
8:O:114:LEU:HD13	8:O:213:TYR:CE1	2.44	0.53
4:P:222:PRO:HA	4:P:225:ILE:HD12	1.89	0.53
11:l:171:PHE:CE2	11:l:173:LEU:HB2	2.43	0.53
10:S:189:ILE:HB	10:S:196:THR:HB	1.90	0.53
5:E:168:ARG:HH22	6:F:57:ALA:HB2	1.73	0.53
9:N:22:CYS:HA	9:N:134:TRP:HE1	1.73	0.53
8:c:162:THR:HG22	8:c:166:LYS:HE3	1.90	0.53
9:e:44:LEU:HD11	9:e:213:ARG:HG3	1.89	0.53
1:A:123:GLN:HG2	2:B:81:PRO:HB3	1.91	0.53
9:a:233:ASN:OD1	9:i:141:ARG:NH1	2.42	0.53
2:h:159:LYS:HG3	3:j:57:ASP:OD1	2.09	0.53
3:j:38:LEU:HD23	3:j:160:LYS:HD3	1.90	0.53
14:Z:210:GLY:HA2	14:Z:213:LEU:HD13	1.90	0.53
15:l:90:ASP:HB3	15:l:133:VAL:HG13	1.91	0.53
3:C:38:LEU:HD23	3:C:160:LYS:HD3	1.90	0.53
3:C:53:HIS:HB3	3:C:56:LEU:HG	1.91	0.53
5:E:123:PHE:CD2	5:E:136:PRO:HA	2.44	0.53
8:H:222:SER:HB3	9:J:141:ARG:HG2	1.91	0.53
8:M:64:LEU:HD11	8:M:175:VAL:HG22	1.90	0.53
8:c:43:LEU:HA	8:c:46:LEU:HB3	1.91	0.53
15:X:41:THR:HG21	15:X:201:GLY:HA3	1.90	0.53
10:k:189:ILE:HB	10:k:196:THR:HB	1.90	0.53
15:X:45:LEU:HD12	15:X:177:LEU:HD22	1.91	0.53
9:Q:181:ARG:HH21	8:c:190:LEU:HD11	1.74	0.53
3:j:99:LEU:HD11	10:k:69:PHE:HD1	1.73	0.53
5:E:88:LEU:HD21	5:E:137:PHE:CE2	2.44	0.53
8:H:183:HIS:NE2	9:J:63:ILE:HD11	2.24	0.53
10:k:100:PHE:C	10:k:102:PRO:HD3	2.34	0.53
7:G:150:TYR:HD1	7:G:160:GLY:HA2	1.75	0.52
7:d:141:TYR:OH	7:d:219:GLU:OE2	2.26	0.52
10:S:98:LYS:O	10:S:101:GLY:N	2.42	0.52
5:E:123:PHE:HE1	5:E:133:MET:HE3	1.74	0.52
5:R:211:ASN:HB2	5:R:214:ASN:HB2	1.90	0.52
2:h:52:GLN:HB3	2:h:57:TYR:HD2	1.74	0.52
15:l:77:ALA:HB3	15:l:80:ILE:HB	1.91	0.52
5:R:89:ILE:HG22	5:R:93:ARG:HE	1.74	0.52
12:m:56:ARG:NH1	12:m:215:VAL:O	2.41	0.52
12:U:64:HIS:HB3	13:V:177:TYR:CZ	2.45	0.52
13:n:260:ILE:O	15:l:160:ARG:NE	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S:100:PHE:C	10:S:102:PRO:HD3	2.34	0.52
4:D:176:TYR:HE1	4:D:181:ILE:HG12	1.75	0.52
3:j:53:HIS:HB3	3:j:56:LEU:HG	1.90	0.52
12:U:91:THR:HG21	13:V:142:TYR:CE2	2.45	0.52
5:E:90:ASP:O	5:E:94:VAL:CG2	2.49	0.52
9:e:29:LEU:HD23	9:e:33:PHE:HD2	1.75	0.52
1:A:132:ARG:NE	7:G:125:LEU:HA	2.23	0.52
8:K:100:VAL:HG11	8:K:171:ARG:HH12	1.75	0.52
9:Q:111:VAL:O	9:Q:115:GLN:N	2.40	0.52
1:f:159:TYR:CE1	2:h:81:PRO:HD3	2.44	0.52
15:1:45:LEU:HD12	15:1:177:LEU:HD22	1.91	0.52
8:H:171:ARG:NH1	8:H:195:ASP:OD1	2.42	0.52
3:j:140:ASP:OD1	3:j:144:GLY:N	2.42	0.52
10:k:98:LYS:O	10:k:101:GLY:N	2.42	0.52
1:A:162:GLY:HA3	2:B:58:ASP:HB3	1.92	0.52
5:E:211:ASN:HB2	5:E:214:ASN:HB2	1.90	0.52
6:F:41:LYS:HE3	6:F:180:MET:HB3	1.91	0.52
7:G:71:ASP:OD1	7:G:100:ARG:NH2	2.43	0.52
4:D:184:ASP:OD2	4:D:212:ARG:NH1	2.36	0.51
9:N:181:ARG:NH2	9:N:205:ASP:OD1	2.40	0.51
9:e:139:ILE:HG21	8:g:149:ARG:NH1	2.24	0.51
7:d:73:HIS:ND1	7:d:223:GLY:O	2.28	0.51
15:X:77:ALA:HB3	15:X:80:ILE:HB	1.91	0.51
15:X:90:ASP:HB3	15:X:133:VAL:HG13	1.91	0.51
8:K:60:LEU:HB3	8:K:199:TYR:CD2	2.44	0.51
9:Q:105:ASN:HA	8:c:185:MET:HB2	1.91	0.51
8:g:37:PRO:HA	8:g:40:ILE:HD12	1.93	0.51
8:g:138:PHE:CE1	4:P:13:ASP:HB3	2.46	0.51
7:d:150:TYR:HD1	7:d:160:GLY:HA2	1.75	0.51
10:k:201:LYS:HB2	15:X:251:LEU:HB2	1.93	0.51
6:b:41:LYS:HE3	6:b:180:MET:HB3	1.91	0.51
7:d:51:GLU:HG2	7:d:198:ILE:HG23	1.93	0.51
3:j:42:GLY:HA3	3:j:186:LEU:HD22	1.92	0.51
12:m:38:GLY:HA3	12:m:70:LYS:NZ	2.26	0.51
3:C:28:ILE:HD13	3:C:133:SER:HB2	1.93	0.51
4:D:184:ASP:CG	4:D:212:ARG:HH12	2.17	0.51
9:L:28:LEU:HA	9:L:32:TYR:HB2	1.93	0.51
1:A:132:ARG:HG2	7:G:125:LEU:HG	1.92	0.51
7:G:51:GLU:HG2	7:G:198:ILE:HG23	1.93	0.51
8:O:172:GLY:HA2	9:Q:194:VAL:HG11	1.92	0.51
9:a:61:LEU:H	9:a:198:ARG:HG3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:b:105:VAL:HG21	6:b:136:GLY:HA3	1.93	0.51
13:n:67:ILE:HB	13:n:95:MET:HE3	1.92	0.51
16:2:79:LYS:O	16:2:215:TYR:OH	2.28	0.51
3:C:140:ASP:OD1	3:C:144:GLY:N	2.42	0.51
9:Q:118:LYS:NZ	8:c:193:GLU:OE1	2.38	0.51
12:U:38:GLY:HA3	12:U:70:LYS:NZ	2.26	0.51
12:U:97:GLU:O	12:U:101:LYS:HG2	2.10	0.51
2:B:52:GLN:HB3	2:B:57:TYR:HD2	1.74	0.51
3:C:42:GLY:HA3	3:C:186:LEU:HD22	1.92	0.51
6:F:105:VAL:HG21	6:F:136:GLY:HA3	1.93	0.51
8:H:108:LYS:NZ	9:I:206:GLU:OE1	2.36	0.51
8:K:111:VAL:HG12	8:K:209:LEU:HD21	1.92	0.51
5:R:108:THR:HG22	5:R:110:GLU:H	1.76	0.51
13:V:67:ILE:HB	13:V:95:MET:HE3	1.92	0.51
14:W:38:SER:HB2	14:W:50:VAL:HA	1.93	0.51
6:F:122:ARG:NH1	6:F:123:TYR:O	2.43	0.51
8:g:93:PHE:HA	9:i:193:HIS:HB3	1.92	0.51
9:i:237:LEU:HD12	9:i:238:LYS:HB3	1.92	0.51
5:E:103:TYR:CD2	12:U:103:TYR:HE1	2.29	0.51
8:M:37:PRO:HA	8:M:40:ILE:HD12	1.92	0.51
9:e:9:GLU:O	9:e:13:LYS:HG2	2.11	0.51
1:f:196:GLU:HG2	1:f:242:LEU:HD13	1.92	0.51
6:F:196:ARG:HA	6:F:199:LEU:HD12	1.93	0.50
12:m:55:THR:HB	12:m:67:ASP:HA	1.92	0.50
16:Y:91:ARG:NH2	16:Y:242:SER:O	2.44	0.50
4:D:30:SER:OG	4:D:61:LYS:NZ	2.44	0.50
9:J:232:LYS:HB3	9:N:141:ARG:HG3	1.93	0.50
9:Q:51:GLU:OE2	9:Q:56:ASN:ND2	2.39	0.50
4:P:176:TYR:HE1	4:P:181:ILE:HG12	1.75	0.50
6:b:196:ARG:HA	6:b:199:LEU:HD12	1.93	0.50
1:f:182:LYS:HE3	1:f:197:THR:HG22	1.94	0.50
13:V:171:ASP:OD1	13:V:172:MET:N	2.45	0.50
16:Y:79:LYS:O	16:Y:215:TYR:OH	2.29	0.50
13:n:256:ILE:HD12	14:Z:49:ARG:HH21	1.75	0.50
13:V:181:SER:OG	13:V:192:GLN:NE2	2.43	0.50
5:E:93:ARG:HH21	16:2:140:LEU:C	2.19	0.50
9:Q:142:ILE:HD12	8:c:142:ILE:HG23	1.93	0.50
9:e:18:ARG:HG2	9:e:137:LEU:HD13	1.93	0.50
13:n:181:SER:OG	13:n:192:GLN:NE2	2.43	0.50
7:d:160:GLY:HA3	1:f:65:THR:HG21	1.92	0.50
9:J:43:PHE:CE1	9:J:116:ARG:HD3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Y:117:MET:HG2	16:Y:124:CYS:HB3	1.94	0.50
14:Z:38:SER:HB2	14:Z:50:VAL:HA	1.93	0.50
4:D:199:VAL:HG22	4:D:206:ILE:HD11	1.94	0.50
8:O:46:LEU:HD23	8:O:106:LEU:HB3	1.93	0.50
9:Q:58:LYS:HE3	9:Q:202:HIS:HB3	1.93	0.50
9:e:49:LEU:O	9:e:213:ARG:NH1	2.42	0.50
9:e:106:CYS:SG	9:e:181:ARG:HD3	2.52	0.50
7:G:43:LYS:HE3	7:G:183:LYS:HG2	1.94	0.50
9:N:124:VAL:HG21	9:N:219:ILE:HG23	1.93	0.50
8:O:52:LEU:HD13	8:O:206:VAL:HG21	1.93	0.50
9:e:121:ILE:HG23	9:e:167:LEU:HD22	1.94	0.50
12:U:55:THR:HB	12:U:67:ASP:HA	1.92	0.50
16:Y:249:TYR:HE1	16:Y:258:LYS:HG3	1.77	0.50
16:2:91:ARG:NH2	16:2:242:SER:O	2.44	0.50
5:E:108:THR:HG22	5:E:110:GLU:H	1.76	0.50
7:G:102:ASN:HA	14:Z:105:ASN:ND2	2.27	0.50
3:j:28:ILE:HD13	3:j:133:SER:HB2	1.93	0.50
11:T:19:ARG:HD3	11:T:177:THR:HG22	1.94	0.50
9:a:63:ILE:HD12	9:a:192:PRO:C	2.30	0.49
9:i:40:LEU:HD23	9:i:43:PHE:HD2	1.77	0.49
7:d:73:HIS:CD2	7:d:106:ASN:HD22	2.30	0.49
15:l:84:GLY:HA2	15:l:137:LEU:HD23	1.94	0.49
8:O:183:HIS:ND1	9:a:102:GLY:O	2.45	0.49
11:l:8:GLN:NE2	11:l:113:PRO:O	2.46	0.49
13:n:61:PHE:HE2	13:n:66:VAL:HG23	1.76	0.49
13:V:61:PHE:HE2	13:V:66:VAL:HG23	1.76	0.49
16:Y:117:MET:HE3	16:Y:124:CYS:HB2	1.94	0.49
16:2:117:MET:HE3	16:2:124:CYS:HB2	1.94	0.49
16:2:249:TYR:HE1	16:2:258:LYS:HG3	1.77	0.49
3:C:102:GLN:HE21	10:S:65:GLN:HG3	1.76	0.49
9:a:227:TYR:OH	9:i:11:GLN:OE1	2.29	0.49
8:c:100:VAL:HA	8:c:199:TYR:HE1	1.76	0.49
6:b:199:LEU:HD13	6:b:204:ASP:O	2.12	0.49
13:n:171:ASP:OD1	13:n:172:MET:N	2.45	0.49
10:S:177:ARG:NH2	16:Y:98:ILE:O	2.45	0.49
12:U:63:ILE:O	13:V:196:ARG:NH2	2.38	0.49
5:E:31:ILE:HD13	5:E:140:ALA:HB2	1.94	0.49
6:F:199:LEU:HD13	6:F:204:ASP:O	2.12	0.49
9:J:114:LEU:HD13	9:J:174:ILE:HG23	1.94	0.49
8:O:61:ARG:HD2	8:O:192:HIS:HB3	1.93	0.49
1:A:70:PHE:CD2	1:A:91:VAL:HG21	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:32:LYS:O	5:E:172:SER:OG	2.27	0.49
9:a:114:LEU:HD13	9:a:174:ILE:HG23	1.94	0.49
9:e:106:CYS:N	8:g:186:ASP:OD2	2.46	0.49
4:P:199:VAL:HG22	4:P:206:ILE:HD11	1.94	0.49
5:E:103:TYR:CE2	12:U:103:TYR:CD1	3.00	0.49
7:d:111:HIS:HB2	14:W:90:LEU:HD21	1.94	0.49
10:k:142:CYS:HA	16:2:97:TYR:HE1	1.78	0.49
13:n:142:TYR:O	13:n:145:ARG:HG2	2.13	0.49
1:A:153:LYS:HB3	1:A:163:PHE:CE2	2.48	0.49
8:H:32:LEU:HA	8:H:36:LEU:HD12	1.95	0.49
8:K:52:LEU:HB3	8:K:203:ARG:HB2	1.93	0.49
8:O:168:PHE:HE2	9:Q:203:GLU:HG3	1.77	0.49
9:Q:43:PHE:CE1	9:Q:116:ARG:HD3	2.47	0.49
9:a:236:LYS:HD2	9:i:141:ARG:HH22	1.78	0.49
5:R:101:PHE:HZ	16:Y:126:TYR:CE1	2.31	0.49
7:d:43:LYS:HE3	7:d:183:LYS:HG2	1.94	0.49
14:Z:48:ASN:HD22	15:1:159:SER:HB3	1.78	0.49
8:H:175:VAL:O	8:H:179:SER:N	2.46	0.49
7:d:78:VAL:HG22	7:d:136:PHE:HB3	1.95	0.49
14:Z:28:PHE:HE2	14:Z:33:VAL:HG23	1.78	0.49
7:G:73:HIS:CD2	7:G:106:ASN:HD22	2.30	0.49
8:H:43:LEU:HD23	8:H:46:LEU:HD12	1.94	0.49
8:K:20:PHE:HA	8:K:24:LEU:HB3	1.94	0.49
9:N:44:LEU:HA	9:N:49:LEU:HD12	1.95	0.49
1:f:70:PHE:CD2	1:f:91:VAL:HG21	2.48	0.49
11:T:8:GLN:NE2	11:T:113:PRO:O	2.46	0.49
4:D:63:CYS:O	4:D:71:MET:N	2.42	0.49
1:f:153:LYS:HB3	1:f:163:PHE:CE2	2.48	0.49
11:l:27:GLN:N	11:T:170:ARG:O	2.40	0.49
14:W:28:PHE:HE2	14:W:33:VAL:HG23	1.78	0.49
15:X:61:ASN:O	15:X:63:SER:N	2.41	0.49
15:X:84:GLY:HA2	15:X:137:LEU:HD23	1.94	0.49
2:B:19:LEU:HB2	2:B:22:ILE:HG22	1.95	0.48
5:E:166:ASP:HB2	6:F:56:LEU:HD11	1.95	0.48
7:G:199:TYR:CG	7:G:244:LEU:HD22	2.48	0.48
9:Q:126:GLU:OE2	8:c:203:ARG:NE	2.46	0.48
9:Q:248:ILE:HG21	3:j:80:THR:HG23	1.93	0.48
12:m:120:LEU:HD12	12:m:123:ILE:HB	1.95	0.48
1:A:182:LYS:HE3	1:A:197:THR:HG22	1.94	0.48
5:E:93:ARG:NH2	16:2:140:LEU:C	2.71	0.48
5:E:93:ARG:NH2	16:2:141:ARG:HA	2.15	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:182:CYS:HB3	6:F:186:GLU:HB2	1.95	0.48
9:N:28:LEU:HA	9:N:32:TYR:HB3	1.94	0.48
4:P:229:VAL:O	4:P:232:ILE:HG12	2.13	0.48
6:F:119:PRO:HA	6:F:125:ARG:HD3	1.96	0.48
8:O:41:ILE:HB	9:a:17:PHE:CZ	2.46	0.48
5:R:89:ILE:CG2	5:R:93:ARG:NH2	2.76	0.48
10:S:169:GLN:O	10:S:173:ASN:ND2	2.38	0.48
6:F:103:LEU:HD12	6:F:104:PRO:HD2	1.95	0.48
7:G:55:LEU:HB2	7:G:59:TYR:CE2	2.45	0.48
7:G:78:VAL:HG22	7:G:136:PHE:HB3	1.95	0.48
7:G:151:MET:HE2	7:G:161:TYR:HE2	1.78	0.48
8:H:43:LEU:HD21	8:H:110:GLU:HG3	1.96	0.48
9:L:128:LEU:HD11	9:L:160:MET:HB3	1.95	0.48
10:k:113:ASP:N	10:k:118:LYS:O	2.32	0.48
12:U:120:LEU:HD12	12:U:123:ILE:HB	1.95	0.48
12:U:161:ASP:OD1	12:U:162:SER:N	2.45	0.48
4:D:10:PHE:CE1	5:E:135:ARG:HD2	2.49	0.48
6:b:103:LEU:HD12	6:b:104:PRO:HD2	1.95	0.48
12:m:208:ILE:O	12:m:212:GLU:HG2	2.13	0.48
16:2:117:MET:HG2	16:2:124:CYS:HB3	1.93	0.48
2:B:192:ILE:HG22	2:B:196:LYS:HE3	1.96	0.48
6:F:10:VAL:HG13	6:F:19:ILE:HG21	1.96	0.48
6:F:51:ARG:NH2	8:M:236:PRO:O	2.46	0.48
9:I:247:MET:SD	9:I:249:TYR:OH	2.65	0.48
8:K:108:LYS:HB3	9:L:210:ARG:HH12	1.79	0.48
8:O:183:HIS:O	9:a:104:VAL:N	2.47	0.48
8:g:232:GLY:HA3	5:R:32:LYS:NZ	2.28	0.48
7:d:55:LEU:HB2	7:d:59:TYR:CE2	2.45	0.48
7:d:118:MET:HE1	1:f:89:SER:HA	1.95	0.48
3:j:111:VAL:HG22	3:j:136:TYR:CD2	2.49	0.48
11:T:145:ARG:HE	16:Y:230:ARG:HH11	1.61	0.48
12:U:44:ALA:HB2	12:U:149:VAL:HG23	1.96	0.48
13:V:142:TYR:O	13:V:145:ARG:HG2	2.13	0.48
4:D:51:ALA:C	4:D:53:LEU:H	2.21	0.48
9:e:26:GLU:OE2	9:e:238:LYS:NZ	2.45	0.48
8:g:64:LEU:HD22	8:g:94:LEU:HB3	1.95	0.48
5:R:31:ILE:HD13	5:R:140:ALA:HB2	1.94	0.48
16:Y:84:VAL:HG23	16:Y:181:PRO:HB2	1.96	0.48
9:I:54:LEU:HB3	9:I:206:GLU:HG2	1.95	0.48
9:L:18:ARG:HH21	9:L:137:LEU:HD22	1.78	0.48
9:L:29:LEU:HD11	9:L:230:ILE:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:d:151:MET:HE2	7:d:161:TYR:HE2	1.78	0.48
2:h:19:LEU:HB2	2:h:22:ILE:HG22	1.96	0.48
2:h:109:GLN:HE22	10:k:77:LYS:HB3	1.78	0.48
11:l:19:ARG:HD3	11:l:177:THR:HG22	1.94	0.48
13:n:231:ARG:NH2	14:Z:218:ASP:HB3	2.28	0.48
15:X:47:PHE:HE2	15:X:52:ILE:HG13	1.78	0.48
5:E:183:GLU:O	5:E:186:HIS:NE2	2.47	0.48
8:K:162:THR:HG22	8:K:166:LYS:HE3	1.94	0.48
8:O:43:LEU:HA	8:O:46:LEU:HB2	1.96	0.48
4:P:107:ILE:HD12	4:P:110:TYR:HB2	1.96	0.48
5:R:32:LYS:O	5:R:172:SER:OG	2.27	0.48
6:b:10:VAL:HG13	6:b:19:ILE:HG21	1.96	0.48
3:C:111:VAL:HG22	3:C:136:TYR:CD2	2.49	0.48
5:E:17:PRO:HA	6:F:24:TYR:CD1	2.49	0.48
9:I:186:THR:HG22	9:I:190:LYS:HE3	1.96	0.48
8:c:20:PHE:HA	8:c:24:LEU:HB3	1.96	0.48
9:e:28:LEU:HD23	9:e:32:TYR:HD2	1.78	0.48
5:R:183:GLU:O	5:R:186:HIS:NE2	2.47	0.48
6:b:182:CYS:HB3	6:b:186:GLU:HB2	1.95	0.48
1:f:20:GLY:HA3	2:h:28:ALA:HB2	1.94	0.48
11:l:175:LEU:HB3	11:l:178:PHE:HE1	1.78	0.48
8:H:177:LYS:HA	8:H:180:LYS:HE2	1.95	0.47
9:L:54:LEU:HG	9:L:57:LEU:HD12	1.95	0.47
13:V:130:PRO:HB2	13:V:166:PHE:CD2	2.49	0.47
15:1:47:PHE:HE2	15:1:52:ILE:HG13	1.78	0.47
3:C:100:GLN:HB3	11:T:83:PHE:CD1	2.47	0.47
8:M:132:ILE:HD11	9:N:229:ILE:HD12	1.95	0.47
9:N:124:VAL:HG12	9:N:167:LEU:HD11	1.96	0.47
8:g:113:THR:O	8:g:117:LYS:HG2	2.15	0.47
9:i:40:LEU:HD23	9:i:43:PHE:CD2	2.49	0.47
4:P:120:GLN:NE2	5:R:133:MET:HE1	2.29	0.47
7:d:124:THR:HG22	7:d:131:PRO:HB3	1.97	0.47
12:U:208:ILE:O	12:U:212:GLU:HG2	2.13	0.47
16:2:79:LYS:HE2	16:2:196:ASN:HA	1.96	0.47
16:2:80:PHE:CE1	16:2:82:HIS:HB2	2.50	0.47
7:G:41:ARG:NH2	7:G:147:ALA:O	2.44	0.47
8:M:49:GLU:HG2	8:M:51:SER:H	1.79	0.47
8:M:114:LEU:HD13	8:M:213:TYR:CE1	2.49	0.47
8:O:168:PHE:CE2	9:Q:203:GLU:HG3	2.49	0.47
3:j:99:LEU:HD11	10:k:69:PHE:CD1	2.49	0.47
13:n:98:ALA:HB2	13:n:155:MET:HG2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Z:62:TYR:HE2	14:Z:203:VAL:HG11	1.79	0.47
15:1:61:ASN:O	15:1:63:SER:N	2.41	0.47
6:b:109:VAL:HA	6:b:112:ILE:HD12	1.97	0.47
7:d:125:LEU:HA	1:f:132:ARG:HE	1.80	0.47
2:h:192:ILE:HG22	2:h:196:LYS:HE3	1.96	0.47
13:V:98:ALA:HB2	13:V:155:MET:HG2	1.97	0.47
16:Y:80:PHE:CE1	16:Y:82:HIS:HB2	2.50	0.47
7:G:124:THR:HG22	7:G:131:PRO:HB3	1.96	0.47
8:H:187:TYR:OH	9:J:186:THR:OG1	2.21	0.47
8:H:199:TYR:HA	8:H:202:LEU:HD12	1.96	0.47
8:M:64:LEU:HD22	8:M:94:LEU:HB3	1.95	0.47
8:O:175:VAL:O	8:O:179:SER:N	2.47	0.47
2:h:11:THR:HG22	2:h:19:LEU:HD22	1.96	0.47
13:n:130:PRO:HB2	13:n:166:PHE:CD2	2.49	0.47
9:e:156:VAL:HG22	9:e:160:MET:HE2	1.97	0.47
8:g:49:GLU:HG2	8:g:51:SER:H	1.80	0.47
4:P:63:CYS:O	4:P:71:MET:N	2.42	0.47
4:P:89:VAL:HG22	11:l:66:LEU:HD22	1.94	0.47
7:d:15:PHE:HE1	1:f:132:ARG:HD2	1.79	0.47
12:m:53:SER:HG	12:m:71:CYS:HG	1.57	0.47
10:S:113:ASP:N	10:S:118:LYS:O	2.32	0.47
9:L:40:LEU:HA	9:L:43:PHE:HB3	1.97	0.47
8:g:114:LEU:HD13	8:g:213:TYR:CE1	2.50	0.47
6:b:119:PRO:HB3	6:b:125:ARG:HG2	1.97	0.47
7:d:125:LEU:HD21	1:f:131:MET:HB3	1.97	0.47
11:T:101:ASN:HB3	11:T:132:HIS:ND1	2.29	0.47
3:C:119:GLN:OE1	3:C:122:THR:OG1	2.27	0.47
6:F:39:LYS:HD3	6:F:144:ILE:HG12	1.97	0.47
9:i:237:LEU:HD12	9:i:237:LEU:O	2.13	0.47
10:S:2:SER:OG	10:S:3:ILE:N	2.48	0.47
9:Q:43:PHE:CE2	9:Q:216:VAL:HG21	2.50	0.47
9:a:148:PHE:HD2	6:b:6:TYR:HE2	1.61	0.47
4:P:30:SER:OG	4:P:61:LYS:NZ	2.44	0.47
6:b:39:LYS:HD3	6:b:144:ILE:HG12	1.97	0.47
1:f:126:THR:HG22	2:h:128:ARG:HH21	1.80	0.47
15:1:80:ILE:HG12	15:1:115:VAL:HG22	1.97	0.47
15:1:172:ALA:HB3	15:1:201:GLY:HA2	1.96	0.47
5:E:41:GLN:NE2	5:E:151:PRO:O	2.48	0.47
6:F:109:VAL:HA	6:F:112:ILE:HD12	1.97	0.47
8:H:183:HIS:ND1	9:J:101:CYS:HB3	2.29	0.47
7:d:243:SER:O	7:d:245:LYS:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:44:LEU:HD11	11:l:102:LEU:HD23	1.97	0.47
14:Z:56:PRO:HA	14:Z:62:TYR:HD1	1.80	0.47
4:D:109:ARG:NH1	16:2:141:ARG:HG2	2.30	0.46
6:F:211:SER:OG	6:F:224:TYR:O	2.30	0.46
8:g:168:PHE:CE2	9:i:203:GLU:HG3	2.49	0.46
5:R:41:GLN:NE2	5:R:151:PRO:O	2.48	0.46
11:T:44:LEU:HD11	11:T:102:LEU:HD23	1.97	0.46
11:T:175:LEU:HB3	11:T:178:PHE:HE1	1.78	0.46
13:V:60:LYS:HD2	13:V:180:PRO:HA	1.96	0.46
14:W:56:PRO:HA	14:W:62:TYR:HD1	1.80	0.46
2:B:11:THR:HG22	2:B:19:LEU:HD22	1.97	0.46
9:L:117:LEU:HD13	9:L:216:VAL:HG22	1.96	0.46
9:e:178:PHE:CD1	8:g:190:LEU:HD13	2.50	0.46
2:h:100:VAL:HG22	10:k:93:ASN:ND2	2.29	0.46
12:m:161:ASP:OD1	12:m:162:SER:N	2.45	0.46
13:V:80:ARG:NH1	14:Z:155:TYR:OH	2.48	0.46
14:W:113:ASP:OD2	15:X:130:GLN:NE2	2.48	0.46
16:Y:79:LYS:HE2	16:Y:196:ASN:HA	1.96	0.46
5:E:78:MET:HE3	5:E:85:ALA:HB3	1.98	0.46
5:E:93:ARG:NH2	16:2:141:ARG:CA	2.76	0.46
2:h:119:GLN:HE22	3:j:82:ASP:HA	1.80	0.46
11:l:101:ASN:HB3	11:l:132:HIS:ND1	2.29	0.46
12:m:44:ALA:HB2	12:m:149:VAL:HG23	1.96	0.46
9:i:131:VAL:O	9:i:135:LEU:HG	2.16	0.46
7:d:109:LEU:HD11	7:d:138:LEU:HB3	1.98	0.46
12:U:66:ARG:NH1	13:V:200:GLU:OE2	2.46	0.46
14:W:75:ILE:HD11	14:W:114:LEU:HD13	1.98	0.46
3:C:135:LEU:HG	3:C:164:ILE:HD13	1.98	0.46
9:Q:61:LEU:O	9:Q:202:HIS:NE2	2.46	0.46
9:e:194:VAL:HG12	9:e:196:ASP:H	1.81	0.46
3:j:69:ASN:OD1	3:j:72:MET:N	2.49	0.46
13:n:60:LYS:HD2	13:n:180:PRO:HA	1.96	0.46
14:W:62:TYR:HE2	14:W:203:VAL:HG11	1.79	0.46
16:2:84:VAL:HG23	16:2:181:PRO:HB2	1.96	0.46
3:C:148:TYR:HD1	3:C:158:GLY:HA2	1.80	0.46
9:I:104:VAL:HG11	8:K:184:VAL:HG22	1.98	0.46
10:k:27:ARG:NH2	16:2:240:SER:HB3	2.30	0.46
12:m:120:LEU:HD23	12:m:152:PHE:CE2	2.51	0.46
13:n:194:LEU:HD11	15:1:175:ALA:HB1	1.98	0.46
15:X:80:ILE:HG12	15:X:115:VAL:HG22	1.97	0.46
14:Z:75:ILE:HD11	14:Z:114:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:69:ASN:OD1	3:C:72:MET:N	2.49	0.46
4:D:63:CYS:HB3	4:D:88:ARG:NH2	2.31	0.46
5:E:103:TYR:CZ	12:U:103:TYR:HD1	2.34	0.46
9:e:121:ILE:HG12	9:e:219:ILE:HG21	1.98	0.46
6:b:22:ILE:HG22	6:b:26:MET:HE2	1.98	0.46
1:A:111:VAL:HG12	1:A:152:TYR:HD2	1.80	0.46
5:E:19:GLY:HA3	6:F:28:ALA:HB2	1.98	0.46
7:G:109:LEU:HD11	7:G:138:LEU:HB3	1.98	0.46
7:G:150:TYR:CD1	7:G:160:GLY:HA2	2.51	0.46
8:K:136:ASN:ND2	8:K:231:LYS:HG3	2.31	0.46
8:c:54:VAL:O	8:c:60:LEU:HD11	2.15	0.46
7:d:71:ASP:OD1	7:d:72:ARG:N	2.47	0.46
3:j:148:TYR:HD1	3:j:158:GLY:HA2	1.80	0.46
11:l:39:SER:HB3	11:l:42:ILE:HB	1.97	0.46
11:T:39:SER:HB3	11:T:42:ILE:HB	1.97	0.46
13:V:227:ARG:HH11	14:W:44:GLU:CD	2.24	0.46
15:X:172:ALA:HB3	15:X:201:GLY:HA2	1.97	0.46
16:Y:89:ASP:HB2	16:Y:243:GLY:O	2.16	0.46
16:2:88:VAL:HG11	16:2:106:VAL:HG23	1.97	0.46
16:2:89:ASP:HB2	16:2:243:GLY:O	2.16	0.46
9:a:199:GLN:HG3	9:i:106:CYS:HB3	1.98	0.46
9:e:114:LEU:HD22	9:e:174:ILE:HG12	1.97	0.46
9:e:234:PHE:O	9:e:238:LYS:N	2.48	0.46
4:P:158:ALA:HB1	4:P:172:LEU:HD13	1.97	0.46
14:W:83:LEU:HD21	14:W:99:ALA:HA	1.97	0.46
9:Q:208:GLU:O	9:Q:212:ILE:HG13	2.16	0.46
3:j:135:LEU:HG	3:j:164:ILE:HD13	1.98	0.46
1:A:70:PHE:HD2	1:A:91:VAL:HG21	1.82	0.45
4:D:195:LEU:O	4:D:199:VAL:HG23	2.16	0.45
8:H:64:LEU:HD13	8:H:94:LEU:HB3	1.98	0.45
9:J:132:THR:O	9:J:136:GLN:HG2	2.15	0.45
6:b:155:ASP:HB3	7:d:63:SER:CB	2.45	0.45
7:d:243:SER:C	7:d:245:LYS:N	2.73	0.45
1:f:43:ARG:NE	1:f:149:PRO:O	2.38	0.45
3:j:102:GLN:NE2	10:k:65:GLN:HE21	2.14	0.45
14:Z:83:LEU:HD21	14:Z:99:ALA:HA	1.97	0.45
6:F:67:ASP:HB3	6:F:70:ILE:HB	1.98	0.45
7:G:205:VAL:HG13	9:N:1:MET:HA	1.99	0.45
4:P:47:LYS:O	4:P:205:ASN:HB3	2.16	0.45
1:f:70:PHE:HD2	1:f:91:VAL:HG21	1.82	0.45
1:f:192:GLU:O	1:f:196:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:41:LEU:HD11	12:m:177:LEU:HD11	1.99	0.45
16:Y:88:VAL:HG11	16:Y:106:VAL:HG23	1.97	0.45
15:1:73:ILE:HG12	15:1:83:CYS:HB2	1.97	0.45
5:E:156:MET:HG2	5:E:162:PHE:HB3	1.98	0.45
7:G:199:TYR:HB3	7:G:244:LEU:HD22	1.98	0.45
9:a:132:THR:O	9:a:136:GLN:HG2	2.15	0.45
4:P:195:LEU:O	4:P:199:VAL:HG23	2.16	0.45
1:f:111:VAL:HG12	1:f:152:TYR:HD2	1.80	0.45
12:U:41:LEU:HD11	12:U:177:LEU:HD11	1.99	0.45
5:E:123:PHE:HZ	5:E:137:PHE:CZ	2.35	0.45
6:F:67:ASP:OD1	6:F:68:ASN:N	2.46	0.45
9:L:28:LEU:HB3	9:L:33:PHE:CZ	2.52	0.45
9:L:194:VAL:HG12	9:L:196:ASP:H	1.81	0.45
9:Q:248:ILE:HD12	2:h:156:PHE:HZ	1.81	0.45
9:e:142:ILE:HD13	8:g:145:LYS:HB2	1.98	0.45
9:i:54:LEU:HD21	9:i:209:TYR:CD2	2.52	0.45
4:P:132:LEU:HD23	4:P:144:LEU:HD11	1.99	0.45
6:b:174:ARG:HE	6:b:175:HIS:CE1	2.34	0.45
10:k:152:SER:HA	15:X:237:ARG:NH1	2.32	0.45
7:G:71:ASP:OD1	7:G:72:ARG:N	2.47	0.45
8:H:134:ASP:OD2	9:I:148:PHE:HB2	2.17	0.45
9:N:34:PRO:HA	9:N:37:ILE:HD12	1.97	0.45
8:O:100:VAL:O	8:O:104:LEU:HG	2.15	0.45
8:c:122:ILE:O	8:c:126:GLN:HG2	2.16	0.45
9:i:57:LEU:HD22	9:i:107:ASN:HD21	1.81	0.45
7:d:69:ASN:HB3	13:n:121:LEU:O	2.17	0.45
3:j:61:PHE:CD2	3:j:61:PHE:N	2.84	0.45
11:T:20:VAL:HG21	11:T:175:LEU:HA	1.98	0.45
12:U:120:LEU:HD23	12:U:152:PHE:CE2	2.51	0.45
4:D:132:LEU:HD23	4:D:144:LEU:HD11	1.99	0.45
8:H:183:HIS:HD1	9:J:102:GLY:H	1.64	0.45
6:b:67:ASP:OD1	6:b:68:ASN:N	2.46	0.45
9:J:154:GLU:HA	9:J:157:PHE:CE2	2.52	0.45
9:e:10:ALA:HB1	8:g:37:PRO:HB2	1.99	0.45
9:e:40:LEU:HD22	9:e:223:TYR:CE2	2.40	0.45
5:R:78:MET:HE3	5:R:85:ALA:HB3	1.98	0.45
1:f:188:ASP:O	1:f:193:GLN:HG2	2.16	0.45
15:X:73:ILE:HG12	15:X:83:CYS:HB2	1.97	0.45
4:D:94:HIS:CG	4:D:106:TYR:HE2	2.35	0.45
4:D:158:ALA:HB1	4:D:172:LEU:HD13	1.98	0.45
9:I:4:LEU:HD21	8:K:32:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:146:ASN:HB2	9:I:241:ARG:HD3	1.99	0.45
9:J:177:TYR:OH	9:J:205:ASP:OD1	2.30	0.45
9:N:144:ASP:OD1	9:N:145:GLY:N	2.47	0.45
9:a:200:LEU:HD11	9:i:179:SER:HA	1.99	0.45
7:d:150:TYR:CD1	7:d:160:GLY:HA2	2.51	0.45
11:l:20:VAL:HG21	11:l:175:LEU:HA	1.98	0.45
10:S:105:THR:HG23	10:S:107:PRO:HD3	1.99	0.45
1:A:75:ASN:HB2	1:A:108:GLU:OE2	2.17	0.45
9:J:43:PHE:CE2	9:J:49:LEU:HD22	2.52	0.45
9:N:22:CYS:HA	9:N:134:TRP:NE1	2.32	0.45
9:a:43:PHE:CE2	9:a:49:LEU:HD22	2.52	0.45
9:a:154:GLU:HA	9:a:157:PHE:CE2	2.52	0.45
4:P:63:CYS:HB3	4:P:88:ARG:NH2	2.31	0.45
16:2:199:SER:HB3	16:2:208:TYR:CE1	2.52	0.45
7:G:126:TYR:HB2	7:G:129:VAL:HG22	1.98	0.45
9:a:106:CYS:SG	9:a:111:VAL:HG21	2.57	0.45
5:R:117:SER:OG	5:R:160:GLY:O	2.28	0.45
7:d:126:TYR:HB2	7:d:129:VAL:HG22	1.98	0.45
2:h:143:ARG:HE	2:h:145:TYR:HE1	1.65	0.45
10:k:205:ASP:OD1	16:2:243:GLY:HA3	2.16	0.45
16:Y:187:ASP:OD1	16:Y:188:GLU:N	2.44	0.45
3:C:102:GLN:HE22	11:T:85:ARG:NH2	2.16	0.44
9:J:106:CYS:SG	9:J:111:VAL:HG21	2.57	0.44
8:O:194:ARG:HH12	9:a:175:SER:HB3	1.82	0.44
9:Q:148:PHE:HD2	1:f:18:PRO:HB3	1.82	0.44
15:1:116:ALA:HB1	15:1:120:ARG:HH12	1.81	0.44
8:M:89:PRO:O	9:N:193:HIS:NE2	2.50	0.44
5:R:156:MET:HG2	5:R:162:PHE:HB3	1.97	0.44
2:B:53:LYS:HB2	2:B:57:TYR:HE2	1.82	0.44
6:F:22:ILE:HG22	6:F:26:MET:HE2	1.98	0.44
7:G:170:ARG:HG3	7:G:171:GLN:N	2.33	0.44
9:J:61:LEU:H	9:J:198:ARG:HG3	1.81	0.44
9:N:27:ASN:O	9:N:31:SER:HB2	2.17	0.44
9:Q:124:VAL:HG13	9:Q:167:LEU:HD13	1.99	0.44
9:Q:230:ILE:O	9:Q:234:PHE:N	2.50	0.44
7:d:15:PHE:CE1	1:f:132:ARG:HD2	2.53	0.44
7:d:69:ASN:OD1	13:n:121:LEU:HD22	2.18	0.44
1:f:56:VAL:HG13	1:f:61:LEU:HD23	1.99	0.44
3:j:172:VAL:HG12	3:j:176:LYS:HE3	1.99	0.44
11:l:167:LEU:HA	11:l:171:PHE:HB3	1.98	0.44
1:A:192:GLU:O	1:A:196:GLU:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:GLU:HA	1:A:242:LEU:HD23	1.99	0.44
9:e:44:LEU:HA	9:e:49:LEU:HD12	1.99	0.44
16:2:138:TYR:CD2	16:2:146:ILE:HB	2.52	0.44
3:C:79:ILE:HG22	3:C:81:SER:H	1.83	0.44
4:D:92:GLN:HB3	11:T:62:LYS:HD2	2.00	0.44
9:a:58:LYS:HG2	9:a:60:PRO:HD3	1.98	0.44
8:c:187:TYR:O	8:c:191:VAL:HG23	2.18	0.44
9:e:177:TYR:CG	9:e:208:GLU:HG2	2.52	0.44
9:i:204:LEU:O	9:i:208:GLU:HG3	2.17	0.44
4:P:25:ALA:HB2	3:j:16:GLY:HA3	1.98	0.44
5:R:89:ILE:HG22	5:R:93:ARG:NH2	2.32	0.44
6:b:67:ASP:HB3	6:b:70:ILE:HB	1.98	0.44
12:m:117:ALA:HA	12:m:152:PHE:HZ	1.83	0.44
11:T:167:LEU:HA	11:T:171:PHE:HB3	1.98	0.44
12:U:215:VAL:O	15:X:206:LEU:HD22	2.17	0.44
9:e:47:PRO:HA	9:e:50:ASN:HB2	1.98	0.44
7:d:170:ARG:HG3	7:d:171:GLN:N	2.33	0.44
12:m:64:HIS:HB3	13:n:177:TYR:CZ	2.53	0.44
10:S:34:MET:HE1	10:S:183:MET:HG3	2.00	0.44
16:Y:100:THR:HG22	16:Y:102:LYS:H	1.82	0.44
4:D:169:ARG:NH2	9:L:247:MET:SD	2.91	0.44
6:F:93:LEU:HD11	12:U:102:MET:HG2	2.00	0.44
6:F:117:GLN:HE22	7:G:86:ARG:HB2	1.81	0.44
8:K:60:LEU:HD12	8:K:196:GLU:HG3	2.00	0.44
4:P:125:ARG:HD2	3:j:12:PHE:CE1	2.53	0.44
5:R:88:LEU:HD21	5:R:137:PHE:CE2	2.53	0.44
10:k:34:MET:HE1	10:k:183:MET:HG3	2.00	0.44
12:U:38:GLY:HA3	12:U:70:LYS:HZ2	1.82	0.44
9:I:141:ARG:HB3	8:K:222:SER:HB3	2.00	0.44
5:R:129:ASP:HB2	5:R:130:PRO:HD2	2.00	0.44
5:R:154:PHE:HE1	5:R:164:GLN:HG3	1.83	0.44
3:C:229:LYS:HE3	3:C:231:LYS:HB3	2.00	0.44
4:D:90:GLU:HG3	4:D:94:HIS:NE2	2.33	0.44
7:G:9:ASP:HB3	7:G:22:PHE:HD2	1.83	0.44
2:h:65:VAL:HG22	2:h:75:VAL:HG12	2.00	0.44
10:S:152:SER:HB3	15:1:241:TYR:HE2	1.83	0.44
12:U:213:ARG:HH11	15:X:65:VAL:HG12	1.83	0.44
1:A:72:ILE:HG21	1:A:114:LEU:HD21	1.99	0.43
2:B:96:GLN:HA	2:B:99:LEU:HD12	2.00	0.43
8:O:93:PHE:HD1	9:Q:65:VAL:HB	1.82	0.43
9:a:209:TYR:HA	9:a:212:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:72:ILE:HG21	1:f:114:LEU:HD21	1.99	0.43
13:n:50:MET:O	13:n:51:VAL:C	2.60	0.43
12:U:62:SER:HB2	13:V:189:TYR:CE1	2.50	0.43
14:W:217:TYR:OH	14:Z:143:PRO:HG3	2.18	0.43
16:Y:199:SER:HB3	16:Y:208:TYR:CE1	2.52	0.43
3:C:172:VAL:HG12	3:C:176:LYS:HE3	1.99	0.43
4:D:88:ARG:NH1	11:T:69:MET:O	2.51	0.43
9:Q:153:GLN:HG2	9:Q:237:LEU:HA	2.00	0.43
8:c:47:LEU:HD21	8:c:207:LEU:HD12	2.00	0.43
4:P:229:VAL:O	4:P:232:ILE:HD11	2.17	0.43
10:k:105:THR:HG23	10:k:107:PRO:HD3	1.99	0.43
7:G:135:SER:HB2	7:G:154:PRO:HD3	2.01	0.43
9:I:117:LEU:HD13	9:I:216:VAL:HG22	1.99	0.43
9:a:117:LEU:HD22	9:a:212:ILE:HG23	2.01	0.43
9:i:28:LEU:HA	9:i:32:TYR:HB3	2.00	0.43
13:n:106:GLN:HA	13:n:109:LYS:HD2	1.99	0.43
13:n:252:THR:OG1	13:n:254:TRP:NE1	2.51	0.43
1:A:56:VAL:HG13	1:A:61:LEU:HD23	1.99	0.43
2:B:68:ILE:HG21	2:B:110:LEU:HD21	2.00	0.43
4:D:83:VAL:HG21	4:D:129:ILE:HD11	2.00	0.43
5:E:154:PHE:HE1	5:E:164:GLN:HG3	1.83	0.43
8:O:231:LYS:HG2	8:O:233:GLU:H	1.83	0.43
7:d:9:ASP:HB3	7:d:22:PHE:HD2	1.83	0.43
7:d:125:LEU:HG	1:f:132:ARG:HG2	2.00	0.43
7:d:151:MET:HE2	7:d:161:TYR:CE2	2.53	0.43
12:U:216:TYR:CE1	15:X:206:LEU:HD13	2.53	0.43
15:1:202:ILE:HG23	15:1:209:GLY:HA2	2.01	0.43
5:E:202:LEU:HG	5:E:206:MET:HE2	2.01	0.43
8:c:18:GLU:O	8:c:22:GLN:HB2	2.19	0.43
9:e:181:ARG:NH1	9:e:201:VAL:HB	2.32	0.43
5:R:165:CYS:HA	6:b:57:ALA:HA	2.00	0.43
10:k:12:MET:HA	10:k:138:VAL:HG12	2.00	0.43
12:U:117:ALA:HA	12:U:152:PHE:HZ	1.83	0.43
16:2:100:THR:HG22	16:2:102:LYS:H	1.83	0.43
1:A:29:PHE:CZ	1:A:157:ALA:HB2	2.54	0.43
9:I:28:LEU:HB3	9:I:33:PHE:CZ	2.54	0.43
9:J:209:TYR:HA	9:J:212:ILE:HD12	1.99	0.43
9:N:171:HIS:HA	9:N:174:ILE:HD12	1.99	0.43
9:N:225:VAL:O	9:N:229:ILE:HG12	2.19	0.43
9:Q:117:LEU:HD13	9:Q:216:VAL:HG22	2.00	0.43
7:d:135:SER:HB2	7:d:154:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:113:ASP:HB3	10:k:118:LYS:HB3	2.00	0.43
14:Z:217:TYR:CZ	14:Z:219:GLU:HB2	2.54	0.43
9:J:117:LEU:HD22	9:J:212:ILE:HG23	2.00	0.43
8:M:119:ILE:HD12	9:N:214:LEU:HD22	2.00	0.43
5:R:85:ALA:HB2	5:R:139:VAL:HG21	2.01	0.43
6:b:174:ARG:HH21	6:b:175:HIS:HE1	1.66	0.43
13:V:186:TYR:OH	14:W:44:GLU:HB2	2.18	0.43
14:W:62:TYR:CE2	14:W:203:VAL:HG11	2.54	0.43
16:Y:163:ARG:NH2	16:Y:189:ASN:O	2.50	0.43
16:Y:245:VAL:HG12	16:Y:263:ASP:HA	2.01	0.43
2:B:40:ALA:HB3	2:B:187:ALA:HB2	2.01	0.43
5:R:68:VAL:HG23	5:R:76:CYS:HB3	2.01	0.43
5:R:167:ALA:HB1	5:R:181:LEU:HD13	2.01	0.43
7:d:41:ARG:NH2	7:d:147:ALA:O	2.44	0.43
10:k:2:SER:OG	10:k:3:ILE:N	2.47	0.43
11:l:27:GLN:HG3	11:T:172:ILE:HG12	2.01	0.43
11:l:173:LEU:HD22	11:T:172:ILE:HG22	2.01	0.43
10:S:113:ASP:HB3	10:S:118:LYS:HB3	2.00	0.43
13:V:252:THR:OG1	13:V:254:TRP:NE1	2.51	0.43
16:Y:110:ASN:HD21	16:Y:135:CYS:HB3	1.84	0.43
16:Y:160:CYS:SG	16:Y:163:ARG:NH2	2.83	0.43
2:B:65:VAL:HG22	2:B:75:VAL:HG12	2.00	0.43
3:C:75:SER:OG	3:C:135:LEU:HB2	2.19	0.43
9:L:4:LEU:HB2	8:M:224:LEU:HD13	1.99	0.43
9:L:28:LEU:HD23	9:L:32:TYR:HD2	1.84	0.43
1:f:141:ILE:HG22	1:f:151:VAL:HG22	2.01	0.43
3:j:79:ILE:HG22	3:j:81:SER:H	1.83	0.43
3:j:229:LYS:HE3	3:j:231:LYS:HB3	2.00	0.43
15:X:202:ILE:HG23	15:X:209:GLY:HA2	2.01	0.43
15:X:233:LYS:O	15:X:235:ILE:N	2.52	0.43
16:2:245:VAL:HG12	16:2:263:ASP:HA	2.01	0.43
5:E:146:VAL:HG11	5:E:222:PRO:HA	2.01	0.43
9:N:32:TYR:O	9:N:36:LYS:HG2	2.19	0.43
9:e:11:GLN:OE1	8:g:217:TYR:OH	2.34	0.43
13:n:231:ARG:HH22	14:Z:218:ASP:HB3	1.84	0.43
2:B:107:THR:OG1	2:B:138:GLY:HA3	2.19	0.42
5:E:167:ALA:HB1	5:E:181:LEU:HD13	2.01	0.42
6:F:11:THR:HA	7:G:130:ARG:HD3	2.00	0.42
9:I:21:LEU:HD23	9:I:24:LYS:HD2	1.99	0.42
9:N:114:LEU:O	9:N:118:LYS:HG3	2.18	0.42
9:Q:41:ASP:HA	9:Q:220:ARG:HH11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:83:VAL:HG21	4:P:129:ILE:HD11	2.00	0.42
3:j:75:SER:OG	3:j:135:LEU:HB2	2.19	0.42
14:Z:62:TYR:CE2	14:Z:203:VAL:HG11	2.54	0.42
15:1:233:LYS:O	15:1:235:ILE:N	2.52	0.42
16:2:163:ARG:NH2	16:2:189:ASN:O	2.50	0.42
5:E:85:ALA:HB2	5:E:139:VAL:HG21	2.01	0.42
6:F:84:LEU:HD22	6:F:132:LEU:HD11	2.01	0.42
6:F:115:LYS:HG3	6:F:128:TYR:HE2	1.84	0.42
9:J:156:VAL:HG12	9:J:160:MET:HE2	2.01	0.42
8:c:66:ILE:HD11	8:c:175:VAL:HG13	2.01	0.42
8:c:146:VAL:HG21	8:c:227:ILE:HD11	1.99	0.42
7:d:191:VAL:HG11	7:d:216:TRP:HZ2	1.85	0.42
1:f:155:ASP:OD1	1:f:159:TYR:N	2.52	0.42
2:h:68:ILE:HG21	2:h:110:LEU:HD21	2.00	0.42
2:h:96:GLN:HA	2:h:99:LEU:HD12	2.00	0.42
10:k:44:PRO:HA	10:k:50:TYR:HD1	1.85	0.42
13:n:51:VAL:HG12	13:n:102:TYR:HB3	2.01	0.42
10:S:12:MET:HA	10:S:138:VAL:HG12	2.00	0.42
1:A:152:TYR:CD1	1:A:162:GLY:HA2	2.54	0.42
2:B:9:SER:HA	2:B:125:GLY:HA2	2.01	0.42
2:B:140:ASN:HB2	2:B:145:TYR:CE2	2.52	0.42
5:E:68:VAL:HG23	5:E:76:CYS:HB3	2.01	0.42
8:K:126:GLN:HG2	9:L:225:VAL:HG22	2.00	0.42
9:L:233:ASN:OD1	9:L:237:LEU:HD13	2.19	0.42
2:h:107:THR:OG1	2:h:138:GLY:HA3	2.19	0.42
11:T:19:ARG:HD2	11:T:179:SER:HB2	2.02	0.42
1:A:190:THR:HG22	1:A:191:PHE:N	2.35	0.42
7:G:9:ASP:O	7:G:23:GLN:NE2	2.31	0.42
9:I:54:LEU:HD23	9:I:206:GLU:HB3	2.01	0.42
9:N:30:GLY:HA2	9:N:227:TYR:HE1	1.83	0.42
9:Q:220:ARG:HA	9:Q:223:TYR:CD2	2.52	0.42
8:c:30:GLU:O	8:c:34:ARG:HB3	2.19	0.42
8:c:112:TRP:HB2	8:c:161:GLN:NE2	2.34	0.42
8:g:150:VAL:HG22	8:g:216:LEU:HD22	2.01	0.42
5:R:202:LEU:HG	5:R:206:MET:HE2	2.01	0.42
6:b:105:VAL:HG12	6:b:145:PHE:CD2	2.55	0.42
6:b:115:LYS:HG3	6:b:128:TYR:HE2	1.84	0.42
3:j:91:ARG:HD3	10:k:76:LEU:HB3	2.01	0.42
11:l:196:PHE:O	11:l:198:LYS:N	2.51	0.42
16:2:84:VAL:O	16:2:251:MET:N	2.51	0.42
2:B:143:ARG:HE	2:B:145:TYR:HE1	1.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:28:LEU:HD22	9:J:130:LEU:HD22	2.02	0.42
8:K:35:PHE:CE2	8:K:117:LYS:HG3	2.55	0.42
13:V:51:VAL:HG12	13:V:102:TYR:HB3	2.01	0.42
13:V:78:LEU:HD13	14:W:153:TYR:CE2	2.55	0.42
16:2:110:ASN:HD21	16:2:135:CYS:HB3	1.84	0.42
5:E:88:LEU:HD21	5:E:137:PHE:CZ	2.55	0.42
8:O:45:GLN:O	8:O:49:GLU:N	2.52	0.42
9:Q:153:GLN:NE2	9:Q:236:LYS:O	2.52	0.42
4:P:122:ASN:OD1	5:R:134:SER:HB3	2.19	0.42
4:P:171:PHE:HE2	4:P:197:GLU:HG2	1.83	0.42
10:k:125:ASP:OD1	10:k:126:LEU:N	2.47	0.42
16:Y:239:ASP:HB3	16:Y:242:SER:HB2	2.01	0.42
3:C:86:LEU:HD21	3:C:130:PHE:CD2	2.55	0.42
5:E:129:ASP:HB2	5:E:130:PRO:HD2	2.00	0.42
9:I:43:PHE:HE2	9:I:216:VAL:HG21	1.85	0.42
8:c:20:PHE:CZ	9:e:220:ARG:HD2	2.55	0.42
9:i:43:PHE:O	9:i:49:LEU:HB2	2.20	0.42
5:R:146:VAL:HG11	5:R:222:PRO:HA	2.01	0.42
6:b:84:LEU:HD22	6:b:132:LEU:HD11	2.01	0.42
1:f:73:THR:HG22	1:f:76:ILE:HB	2.01	0.42
1:f:152:TYR:CD1	1:f:162:GLY:HA2	2.53	0.42
13:n:259:MET:HE1	15:l:181:PHE:HE2	1.85	0.42
11:T:26:VAL:HG21	16:2:208:TYR:CE2	2.54	0.42
2:B:77:SER:HB3	2:B:163:MET:HG2	2.02	0.42
4:D:42:VAL:HB	4:D:191:VAL:HG21	2.02	0.42
4:D:180:ALA:C	4:D:181:ILE:HG13	2.44	0.42
6:F:105:VAL:HG12	6:F:145:PHE:CD2	2.55	0.42
9:Q:63:ILE:HG13	9:Q:188:ALA:HB1	2.01	0.42
9:a:28:LEU:HD22	9:a:130:LEU:HD22	2.02	0.42
3:j:102:GLN:HE21	10:k:65:GLN:HG2	1.84	0.42
10:k:109:ILE:HB	10:k:122:CYS:SG	2.60	0.42
10:S:109:ILE:HB	10:S:122:CYS:SG	2.60	0.42
12:U:86:HIS:CD2	13:V:175:VAL:HG13	2.54	0.42
13:V:134:HIS:HE1	13:V:176:ALA:HB1	1.85	0.42
1:A:141:ILE:HG22	1:A:151:VAL:HG22	2.01	0.42
1:A:155:ASP:OD1	1:A:159:TYR:N	2.51	0.42
7:G:191:VAL:HG11	7:G:216:TRP:HZ2	1.85	0.42
8:K:164:ILE:HA	8:K:167:TYR:CD2	2.55	0.42
8:c:31:PHE:CE2	8:c:117:LYS:HE3	2.55	0.42
6:b:8:ASN:HB3	3:j:3:ARG:HH22	1.85	0.42
2:h:77:SER:HB3	2:h:163:MET:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:38:MET:HB2	11:l:42:ILE:HG22	2.01	0.42
13:n:134:HIS:HE1	13:n:176:ALA:HB1	1.85	0.42
2:B:86:LEU:HD13	2:B:134:LEU:HD11	2.02	0.42
8:M:63:PRO:HA	8:M:192:HIS:CD2	2.55	0.42
9:N:153:GLN:HE21	9:N:237:LEU:HA	1.85	0.42
9:e:28:LEU:HA	9:e:32:TYR:HB2	2.00	0.42
9:i:27:ASN:O	9:i:31:SER:HB2	2.20	0.42
7:d:9:ASP:O	7:d:23:GLN:NE2	2.31	0.42
7:d:100:ARG:HB3	13:n:114:GLN:HE21	1.84	0.42
3:j:86:LEU:HD21	3:j:130:PHE:CD2	2.55	0.42
12:U:103:TYR:C	12:U:103:TYR:CD2	2.96	0.42
13:V:188:ALA:HA	13:V:192:GLN:HB2	2.02	0.42
1:A:206:LEU:HD12	1:A:210:PHE:HZ	1.85	0.41
2:B:95:GLN:CG	15:1:100:SER:HB3	2.38	0.41
7:G:151:MET:HE2	7:G:161:TYR:CE2	2.53	0.41
9:I:22:CYS:SG	9:I:134:TRP:NE1	2.69	0.41
9:N:57:LEU:HD22	9:N:107:ASN:ND2	2.34	0.41
9:a:177:TYR:OH	9:a:205:ASP:OD1	2.30	0.41
4:P:180:ALA:C	4:P:181:ILE:HG13	2.44	0.41
2:h:40:ALA:HB3	2:h:187:ALA:HB2	2.01	0.41
3:j:100:GLN:HB3	11:l:83:PHE:HD1	1.85	0.41
10:k:5:SER:HB2	16:2:96:ASN:HD21	1.85	0.41
11:l:19:ARG:HD2	11:l:179:SER:HB2	2.02	0.41
1:A:115:CYS:SG	1:A:140:LEU:HD12	2.60	0.41
3:C:143:TYR:HB3	3:C:146:GLN:NE2	2.35	0.41
4:D:47:LYS:HD3	4:D:207:GLU:OE2	2.20	0.41
6:F:16:GLN:HG2	9:N:144:ASP:HB3	2.03	0.41
8:K:114:LEU:HD13	8:K:213:TYR:CE1	2.55	0.41
9:N:124:VAL:HG22	9:N:223:TYR:CZ	2.56	0.41
6:b:176:MET:HE1	7:d:57:LYS:HB3	2.03	0.41
2:h:9:SER:HA	2:h:125:GLY:HA2	2.01	0.41
2:h:119:GLN:NE2	3:j:82:ASP:HA	2.34	0.41
3:j:143:TYR:HB3	3:j:146:GLN:NE2	2.36	0.41
13:n:188:ALA:HA	13:n:192:GLN:HB2	2.02	0.41
10:S:205:ASP:OD1	16:Y:91:ARG:NH1	2.53	0.41
1:A:73:THR:HG22	1:A:76:ILE:HB	2.01	0.41
4:D:193:LYS:HA	4:D:196:LEU:HD12	2.02	0.41
7:G:102:ASN:O	14:Z:101:ASN:HB3	2.20	0.41
8:K:51:SER:HB2	8:K:103:LEU:HD21	2.02	0.41
9:N:61:LEU:HB3	9:N:198:ARG:HE	1.85	0.41
8:O:56:ASP:OD1	8:O:58:THR:OG1	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Q:181:ARG:HH21	8:c:190:LEU:HD21	1.84	0.41
9:a:156:VAL:HG12	9:a:160:MET:HE2	2.01	0.41
8:g:138:PHE:CD1	4:P:13:ASP:HB3	2.55	0.41
9:i:152:VAL:O	9:i:156:VAL:HG23	2.19	0.41
4:P:21:TYR:CD1	3:j:14:PRO:HA	2.55	0.41
4:P:42:VAL:HB	4:P:191:VAL:HG21	2.02	0.41
11:l:15:VAL:HB	11:l:45:LEU:HD11	2.02	0.41
10:S:15:LYS:HG3	10:S:119:PRO:HB2	2.02	0.41
4:D:90:GLU:HG3	4:D:94:HIS:CE1	2.55	0.41
8:M:150:VAL:HG22	8:M:216:LEU:HD22	2.01	0.41
8:O:111:VAL:HG22	8:O:209:LEU:HD11	2.01	0.41
9:Q:44:LEU:HD12	9:Q:220:ARG:NH1	2.36	0.41
9:a:199:GLN:HB3	9:i:178:PHE:CD2	2.54	0.41
2:h:86:LEU:HD13	2:h:134:LEU:HD11	2.03	0.41
10:k:130:PRO:HG3	15:X:96:ARG:HH22	1.86	0.41
12:m:120:LEU:HA	12:m:123:ILE:HD12	2.02	0.41
13:V:224:ARG:HH12	14:W:48:ASN:HA	1.85	0.41
6:F:50:LYS:HB3	6:F:59:HIS:HB3	2.02	0.41
6:F:59:HIS:CE1	6:F:209:ASN:HB3	2.55	0.41
7:G:8:TYR:CD2	7:G:17:PRO:HD3	2.56	0.41
8:H:9:LEU:HD13	8:H:13:ALA:HB3	2.01	0.41
8:M:186:ASP:O	8:M:190:LEU:N	2.53	0.41
9:N:44:LEU:HD11	9:N:213:ARG:HE	1.83	0.41
9:Q:199:GLN:NE2	9:Q:203:GLU:OE2	2.54	0.41
8:c:7:VAL:HB	9:e:234:PHE:HE2	1.86	0.41
8:g:58:THR:O	8:g:61:ARG:HG2	2.20	0.41
8:g:63:PRO:HA	8:g:192:HIS:CD2	2.56	0.41
8:g:186:ASP:O	8:g:190:LEU:N	2.53	0.41
9:i:177:TYR:CD1	9:i:208:GLU:HG2	2.55	0.41
4:P:57:ARG:NH2	3:j:148:TYR:OH	2.53	0.41
11:l:7:ILE:N	11:l:14:LEU:O	2.50	0.41
13:n:117:ILE:O	13:n:121:LEU:HG	2.21	0.41
16:Y:249:TYR:HD1	16:Y:258:LYS:HA	1.86	0.41
16:2:239:ASP:HB3	16:2:242:SER:HB2	2.02	0.41
1:A:51:VAL:HG22	1:A:217:VAL:HG22	2.02	0.41
7:G:100:ARG:HH12	13:V:117:ILE:HG21	1.84	0.41
9:J:208:GLU:O	9:J:212:ILE:HG13	2.21	0.41
9:L:208:GLU:O	9:L:212:ILE:HG13	2.20	0.41
9:N:61:LEU:HD23	9:N:198:ARG:HB2	2.03	0.41
9:N:228:ASP:O	9:N:232:LYS:HG3	2.20	0.41
9:Q:9:GLU:O	9:Q:13:LYS:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:b:59:HIS:CE1	6:b:209:ASN:HB3	2.56	0.41
7:d:203:ASP:OD1	7:d:204:GLU:N	2.51	0.41
1:f:115:CYS:SG	1:f:140:LEU:HD12	2.60	0.41
10:k:96:TYR:CD1	15:X:93:MET:HG3	2.55	0.41
11:T:38:MET:HB2	11:T:42:ILE:HG22	2.02	0.41
6:F:99:PHE:HB3	6:F:101:ARG:HG2	2.01	0.41
8:K:35:PHE:O	8:K:39:LYS:HG2	2.21	0.41
9:a:34:PRO:HB2	9:i:10:ALA:HB1	2.02	0.41
1:f:51:VAL:HG22	1:f:217:VAL:HG22	2.02	0.41
16:Y:84:VAL:O	16:Y:251:MET:N	2.51	0.41
5:E:117:SER:OG	5:E:160:GLY:O	2.28	0.41
9:N:141:ARG:NH2	9:N:143:GLU:OE2	2.54	0.41
9:Q:47:PRO:HA	9:Q:50:ASN:HB3	2.03	0.41
9:e:53:ASN:ND2	9:e:55:SER:OG	2.54	0.41
10:k:56:LEU:O	10:k:60:VAL:HG23	2.21	0.41
10:k:142:CYS:O	10:k:145:GLN:N	2.49	0.41
11:T:140:LEU:HD23	11:T:143:LEU:HD12	2.02	0.41
14:Z:118:LEU:O	14:Z:134:THR:OG1	2.33	0.41
15:l:75:PHE:CD1	15:l:81:TYR:HE1	2.38	0.41
2:B:196:LYS:HA	2:B:203:MET:HE1	2.03	0.41
7:G:102:ASN:O	14:Z:105:ASN:ND2	2.53	0.41
8:K:152:ALA:O	8:K:156:LYS:HG2	2.20	0.41
8:K:171:ARG:O	8:K:175:VAL:HG22	2.21	0.41
8:K:231:LYS:HE2	8:K:233:GLU:HG2	2.02	0.41
8:M:43:LEU:HD21	8:M:110:GLU:HG3	2.03	0.41
8:M:58:THR:O	8:M:61:ARG:HG2	2.20	0.41
8:O:24:LEU:HD21	8:O:124:TRP:HA	2.02	0.41
8:c:108:LYS:HB3	9:e:210:ARG:HH22	1.85	0.41
8:c:170:GLU:OE1	8:c:194:ARG:NH2	2.54	0.41
9:e:46:GLU:HG2	9:e:48:ALA:H	1.86	0.41
9:e:176:LYS:O	9:e:180:GLU:HG2	2.21	0.41
8:g:221:SER:HA	8:g:224:LEU:HG	2.03	0.41
4:P:33:VAL:HG23	4:P:160:ALA:HB2	2.03	0.41
4:P:115:LYS:NZ	4:P:147:THR:OG1	2.49	0.41
2:h:106:PRO:HG2	2:h:109:GLN:HB2	2.02	0.41
2:h:140:ASN:HB2	2:h:145:TYR:CE2	2.52	0.41
3:j:194:ILE:HD11	3:j:236:LEU:HD13	2.03	0.41
13:n:106:GLN:O	13:n:109:LYS:HB2	2.21	0.41
12:U:86:HIS:HB3	13:V:175:VAL:HG22	2.03	0.41
13:V:117:ILE:O	13:V:121:LEU:HG	2.21	0.41
15:X:133:VAL:HG12	15:X:135:ALA:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1:74:HIS:NE2	15:1:92:GLU:OE1	2.41	0.41
15:1:133:VAL:HG12	15:1:135:ALA:H	1.86	0.41
2:B:52:GLN:HB3	2:B:57:TYR:CD2	2.55	0.41
2:B:97:TYR:CE1	2:B:101:TYR:HD2	2.39	0.41
8:K:237:SER:HB3	8:K:239:TYR:CD2	2.56	0.41
8:O:193:GLU:OE2	9:a:118:LYS:NZ	2.49	0.41
9:Q:112:VAL:HA	9:Q:115:GLN:HB3	2.03	0.41
4:P:120:GLN:CD	5:R:133:MET:HE1	2.46	0.41
5:R:89:ILE:HG22	5:R:93:ARG:CZ	2.51	0.41
6:b:50:LYS:HB3	6:b:59:HIS:HB3	2.02	0.41
7:d:126:TYR:HE1	1:f:131:MET:HG2	1.86	0.41
7:d:151:MET:HB3	7:d:161:TYR:HE2	1.85	0.41
13:n:66:VAL:HG11	13:n:214:VAL:HG21	2.03	0.41
13:n:98:ALA:HB1	13:n:153:ASN:OD1	2.21	0.41
7:G:151:MET:HB3	7:G:161:TYR:HE2	1.85	0.40
8:M:162:THR:O	8:M:166:LYS:N	2.54	0.40
9:Q:242:GLY:HA3	9:Q:245:LYS:HE3	2.03	0.40
9:a:208:GLU:O	9:a:212:ILE:HG13	2.21	0.40
8:g:162:THR:O	8:g:166:LYS:N	2.54	0.40
4:P:193:LYS:HA	4:P:196:LEU:HD12	2.02	0.40
6:b:6:TYR:CE2	6:b:15:PRO:HD3	2.56	0.40
10:k:147:TYR:O	10:k:151:GLU:HG2	2.21	0.40
11:l:104:LEU:HD23	11:l:116:TYR:HD2	1.86	0.40
10:S:44:PRO:HA	10:S:50:TYR:HD1	1.85	0.40
10:S:131:MET:SD	15:1:66:ALA:HB1	2.60	0.40
10:S:147:TYR:O	10:S:151:GLU:HG2	2.22	0.40
11:T:15:VAL:HB	11:T:45:LEU:HD11	2.02	0.40
14:Z:24:MET:HG3	14:Z:146:ILE:HG22	2.03	0.40
6:F:6:TYR:CE2	6:F:15:PRO:HD3	2.56	0.40
9:J:46:GLU:HG2	9:J:48:ALA:H	1.86	0.40
8:K:24:LEU:HD11	8:K:120:LEU:HD22	2.03	0.40
9:Q:199:GLN:HE21	9:Q:203:GLU:HG2	1.86	0.40
9:e:104:VAL:HG11	9:e:185:VAL:HG11	2.03	0.40
4:P:28:LYS:HE3	3:j:15:GLU:HB3	2.02	0.40
4:P:125:ARG:HD2	3:j:12:PHE:HE1	1.85	0.40
11:T:116:TYR:HB3	11:T:124:LEU:HD11	2.03	0.40
13:V:254:TRP:CE3	14:W:192:VAL:HG13	2.56	0.40
16:2:127:TRP:CZ3	16:2:158:MET:HB3	2.56	0.40
9:J:22:CYS:O	9:J:26:GLU:HG3	2.21	0.40
7:d:8:TYR:CD2	7:d:17:PRO:HD3	2.56	0.40
2:h:196:LYS:HA	2:h:203:MET:HE1	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:j:91:ARG:O	3:j:95:GLN:HG2	2.21	0.40
12:U:127:ARG:O	12:U:130:PHE:N	2.54	0.40
5:E:40:ILE:HG21	5:E:194:ALA:HB1	2.04	0.40
5:E:71:ASP:OD1	5:E:72:ALA:N	2.48	0.40
9:e:163:LEU:HD21	9:e:222:ALA:HB1	2.03	0.40
9:e:208:GLU:O	9:e:212:ILE:HG13	2.21	0.40
5:R:40:ILE:HG21	5:R:194:ALA:HB1	2.04	0.40
6:b:40:SER:HB3	6:b:187:LEU:HD11	2.03	0.40
7:d:101:SER:O	14:W:105:ASN:ND2	2.54	0.40
7:d:170:ARG:HG3	7:d:171:GLN:H	1.86	0.40
3:j:97:TYR:CE2	3:j:105:ILE:HA	2.57	0.40
10:S:131:MET:SD	15:l:67:ASP:HB2	2.62	0.40
12:U:120:LEU:HA	12:U:123:ILE:HD12	2.02	0.40
13:V:51:VAL:O	13:V:101:ASP:HA	2.22	0.40
16:2:80:PHE:HE1	16:2:82:HIS:HB2	1.86	0.40
1:A:60:LEU:O	7:G:162:TRP:N	2.39	0.40
2:B:106:PRO:HG2	2:B:109:GLN:HB2	2.03	0.40
8:H:66:ILE:HG22	8:H:182:THR:HG22	2.02	0.40
9:L:227:TYR:CZ	9:L:231:LEU:HD22	2.56	0.40
8:M:166:LYS:HG2	8:M:170:GLU:HG3	2.04	0.40
9:Q:29:LEU:HD23	9:Q:33:PHE:CE2	2.56	0.40
9:a:58:LYS:HA	9:a:202:HIS:CE1	2.57	0.40
9:a:193:HIS:O	9:i:103:PRO:HA	2.21	0.40
3:j:91:ARG:NH1	10:k:76:LEU:O	2.55	0.40
10:k:6:TYR:CZ	10:k:30:ILE:HG23	2.57	0.40
11:l:140:LEU:HD23	11:l:143:LEU:HD12	2.02	0.40
11:l:172:ILE:HG12	11:T:27:GLN:HG3	2.04	0.40
11:T:138:LEU:HD23	16:Y:205:SER:O	2.21	0.40
15:X:92:GLU:O	15:X:96:ARG:HG3	2.21	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	233/246 (95%)	222 (95%)	11 (5%)	0	100	100
1	f	235/246 (96%)	224 (95%)	11 (5%)	0	100	100
2	B	224/234 (96%)	221 (99%)	3 (1%)	0	100	100
2	h	226/234 (97%)	224 (99%)	2 (1%)	0	100	100
3	C	243/261 (93%)	231 (95%)	11 (4%)	1 (0%)	30	66
3	j	244/261 (94%)	232 (95%)	12 (5%)	0	100	100
4	D	230/248 (93%)	224 (97%)	5 (2%)	1 (0%)	30	66
4	P	230/248 (93%)	221 (96%)	9 (4%)	0	100	100
5	E	232/241 (96%)	226 (97%)	6 (3%)	0	100	100
5	R	232/241 (96%)	226 (97%)	6 (3%)	0	100	100
6	F	233/263 (89%)	223 (96%)	10 (4%)	0	100	100
6	b	233/263 (89%)	223 (96%)	10 (4%)	0	100	100
7	G	238/255 (93%)	230 (97%)	8 (3%)	0	100	100
7	d	238/255 (93%)	228 (96%)	9 (4%)	1 (0%)	30	66
8	H	205/239 (86%)	202 (98%)	3 (2%)	0	100	100
8	K	203/239 (85%)	196 (97%)	7 (3%)	0	100	100
8	M	205/239 (86%)	202 (98%)	3 (2%)	0	100	100
8	O	205/239 (86%)	201 (98%)	4 (2%)	0	100	100
8	c	201/239 (84%)	196 (98%)	5 (2%)	0	100	100
8	g	205/239 (86%)	202 (98%)	3 (2%)	0	100	100
9	I	209/249 (84%)	204 (98%)	4 (2%)	1 (0%)	24	62
9	J	202/249 (81%)	197 (98%)	5 (2%)	0	100	100
9	L	203/249 (82%)	195 (96%)	8 (4%)	0	100	100
9	N	201/249 (81%)	193 (96%)	8 (4%)	0	100	100
9	Q	209/249 (84%)	204 (98%)	5 (2%)	0	100	100
9	a	202/249 (81%)	197 (98%)	5 (2%)	0	100	100
9	e	203/249 (82%)	195 (96%)	8 (4%)	0	100	100
9	i	201/249 (81%)	195 (97%)	5 (2%)	1 (0%)	24	62
10	S	202/205 (98%)	194 (96%)	7 (4%)	1 (0%)	24	62
10	k	202/205 (98%)	194 (96%)	7 (4%)	1 (0%)	24	62
11	T	195/201 (97%)	190 (97%)	5 (3%)	0	100	100
11	l	196/201 (98%)	190 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	U	211/241 (88%)	206 (98%)	5 (2%)	0	100	100
12	m	211/241 (88%)	205 (97%)	6 (3%)	0	100	100
13	V	214/264 (81%)	208 (97%)	6 (3%)	0	100	100
13	n	214/264 (81%)	207 (97%)	6 (3%)	1 (0%)	24	62
14	W	197/219 (90%)	194 (98%)	3 (2%)	0	100	100
14	Z	197/219 (90%)	194 (98%)	3 (2%)	0	100	100
15	1	217/273 (80%)	207 (95%)	9 (4%)	1 (0%)	24	62
15	X	217/273 (80%)	207 (95%)	9 (4%)	1 (0%)	24	62
16	2	199/276 (72%)	194 (98%)	5 (2%)	0	100	100
16	Y	199/276 (72%)	194 (98%)	5 (2%)	0	100	100
All	All	8996/10280 (88%)	8718 (97%)	268 (3%)	10 (0%)	49	82

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	52	LYS
3	C	60	PHE
9	i	237	LEU
7	d	244	LEU
13	n	51	VAL
15	X	62	ASP
15	1	62	ASP
10	k	115	LYS
10	S	115	LYS
9	I	248	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	202/210 (96%)	202 (100%)	0	100	100
1	f	204/210 (97%)	204 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	186/191 (97%)	186 (100%)	0	100	100
2	h	187/191 (98%)	187 (100%)	0	100	100
3	C	206/221 (93%)	206 (100%)	0	100	100
3	j	207/221 (94%)	207 (100%)	0	100	100
4	D	196/211 (93%)	196 (100%)	0	100	100
4	P	196/211 (93%)	196 (100%)	0	100	100
5	E	196/203 (97%)	196 (100%)	0	100	100
5	R	196/203 (97%)	196 (100%)	0	100	100
6	F	201/225 (89%)	201 (100%)	0	100	100
6	b	201/225 (89%)	201 (100%)	0	100	100
7	G	198/212 (93%)	198 (100%)	0	100	100
7	d	198/212 (93%)	198 (100%)	0	100	100
8	H	183/212 (86%)	183 (100%)	0	100	100
8	K	183/212 (86%)	183 (100%)	0	100	100
8	M	184/212 (87%)	184 (100%)	0	100	100
8	O	183/212 (86%)	183 (100%)	0	100	100
8	c	181/212 (85%)	181 (100%)	0	100	100
8	g	184/212 (87%)	184 (100%)	0	100	100
9	I	191/224 (85%)	191 (100%)	0	100	100
9	J	185/224 (83%)	185 (100%)	0	100	100
9	L	185/224 (83%)	185 (100%)	0	100	100
9	N	183/224 (82%)	183 (100%)	0	100	100
9	Q	191/224 (85%)	191 (100%)	0	100	100
9	a	185/224 (83%)	185 (100%)	0	100	100
9	e	185/224 (83%)	185 (100%)	0	100	100
9	i	183/224 (82%)	183 (100%)	0	100	100
10	S	174/175 (99%)	174 (100%)	0	100	100
10	k	174/175 (99%)	174 (100%)	0	100	100
11	T	168/171 (98%)	168 (100%)	0	100	100
11	l	169/171 (99%)	169 (100%)	0	100	100
12	U	176/198 (89%)	176 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	m	177/198 (89%)	177 (100%)	0	100	100
13	V	177/215 (82%)	177 (100%)	0	100	100
13	n	178/215 (83%)	178 (100%)	0	100	100
14	W	153/167 (92%)	153 (100%)	0	100	100
14	Z	153/167 (92%)	153 (100%)	0	100	100
15	1	170/216 (79%)	170 (100%)	0	100	100
15	X	170/216 (79%)	170 (100%)	0	100	100
16	2	166/222 (75%)	166 (100%)	0	100	100
16	Y	166/222 (75%)	166 (100%)	0	100	100
All	All	7731/8738 (88%)	7731 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (109) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	123	GLN
1	A	150	GLN
2	B	71	HIS
2	B	102	GLN
2	B	109	GLN
2	B	112	GLN
2	B	140	ASN
3	C	142	HIS
3	C	146	GLN
3	C	198	ASN
3	C	240	HIS
4	D	15	HIS
4	D	215	GLN
5	E	41	GLN
5	E	99	HIS
6	F	20	HIS
6	F	59	HIS
6	F	65	HIS
6	F	117	GLN
6	F	143	HIS
6	F	166	GLN
6	F	175	HIS

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Mol	Chain	Res	Type
7	G	111	HIS
7	G	225	HIS
8	H	161	GLN
9	I	164	HIS
9	I	173	GLN
9	I	193	HIS
9	J	7	GLN
8	K	126	GLN
9	L	7	GLN
9	L	193	HIS
8	M	218	HIS
9	N	7	GLN
9	N	153	GLN
9	N	221	ASN
9	Q	173	GLN
9	Q	193	HIS
9	Q	199	GLN
9	a	7	GLN
9	a	199	GLN
9	e	7	GLN
9	e	53	ASN
9	e	136	GLN
9	e	173	GLN
8	g	38	GLN
8	g	218	HIS
9	i	202	HIS
4	P	15	HIS
4	P	18	GLN
4	P	94	HIS
4	P	120	GLN
4	P	154	HIS
4	P	215	GLN
5	R	41	GLN
5	R	122	GLN
6	b	20	HIS
6	b	59	HIS
6	b	65	HIS
6	b	117	GLN
6	b	143	HIS
6	b	166	GLN
6	b	175	HIS
7	d	225	HIS

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Mol	Chain	Res	Type
1	f	24	GLN
1	f	92	GLN
1	f	150	GLN
1	f	193	GLN
2	h	71	HIS
2	h	95	GLN
2	h	102	GLN
2	h	109	GLN
2	h	112	GLN
2	h	189	HIS
3	j	102	GLN
3	j	146	GLN
3	j	198	ASN
3	j	240	HIS
10	k	93	ASN
10	k	169	GLN
11	l	65	GLN
11	l	99	HIS
11	l	101	ASN
12	m	108	ASN
13	n	91	ASN
13	n	192	GLN
10	S	61	GLN
10	S	162	HIS
10	S	169	GLN
11	T	65	GLN
11	T	101	ASN
11	T	168	GLN
12	U	108	ASN
13	V	91	ASN
13	V	114	GLN
13	V	126	HIS
13	V	192	GLN
14	W	60	HIS
16	Y	96	ASN
16	Y	110	ASN
16	Y	234	HIS
16	Y	247	ASN
14	Z	60	HIS
14	Z	86	HIS
16	2	96	ASN
16	2	110	ASN

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Mol	Chain	Res	Type
16	2	234	HIS
16	2	247	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

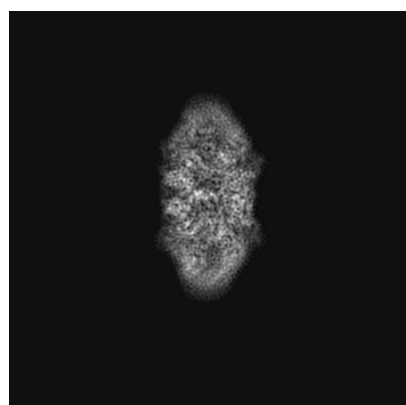
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30828. These allow visual inspection of the internal detail of the map and identification of artifacts.

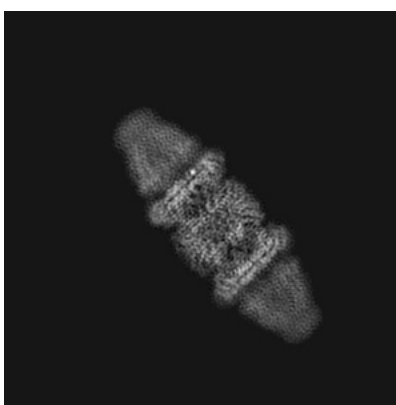
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

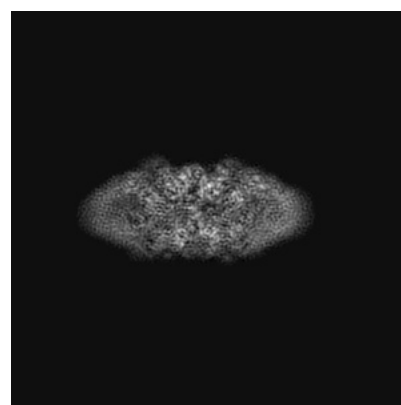
6.1.1 Primary map



X



Y

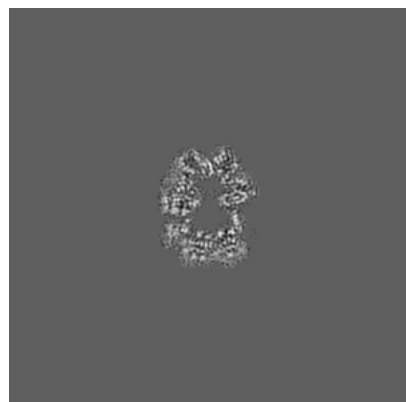


Z

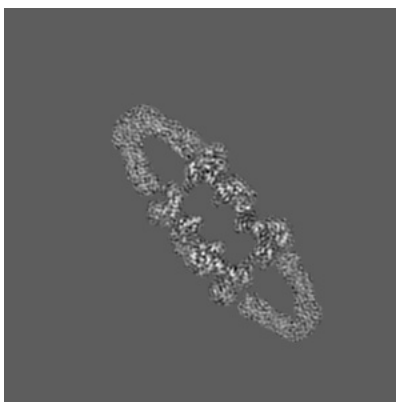
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

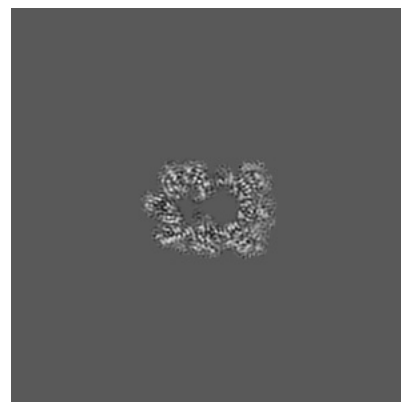
6.2.1 Primary map



X Index: 180



Y Index: 180

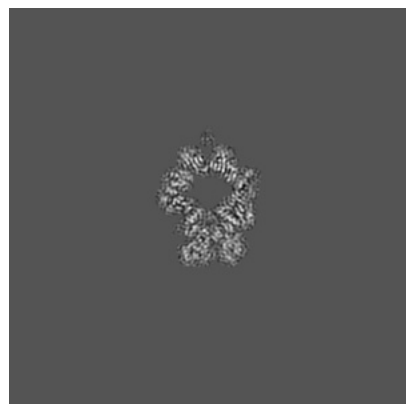


Z Index: 180

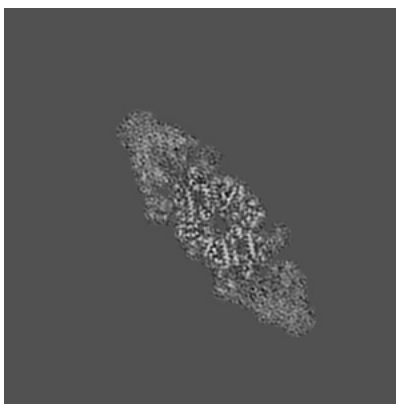
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 171



Y Index: 161

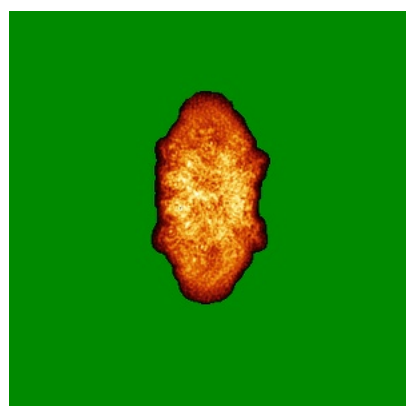


Z Index: 194

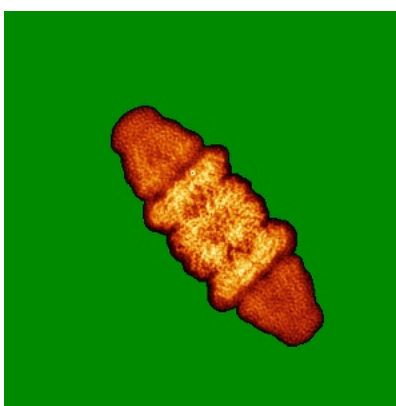
The images above show the largest variance slices of the map in three orthogonal directions.

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

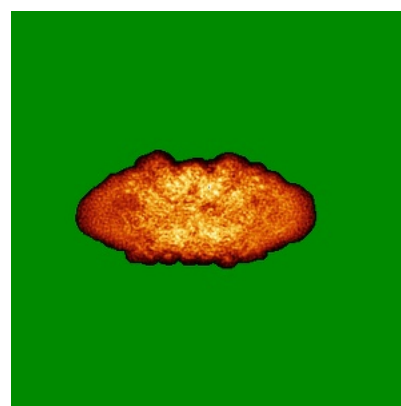
6.4.1 Primary map



X



Y

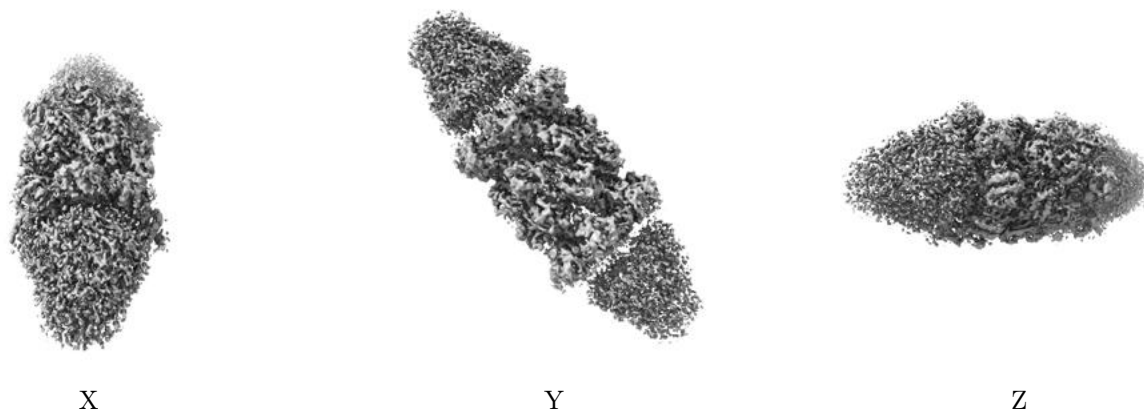


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.666. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

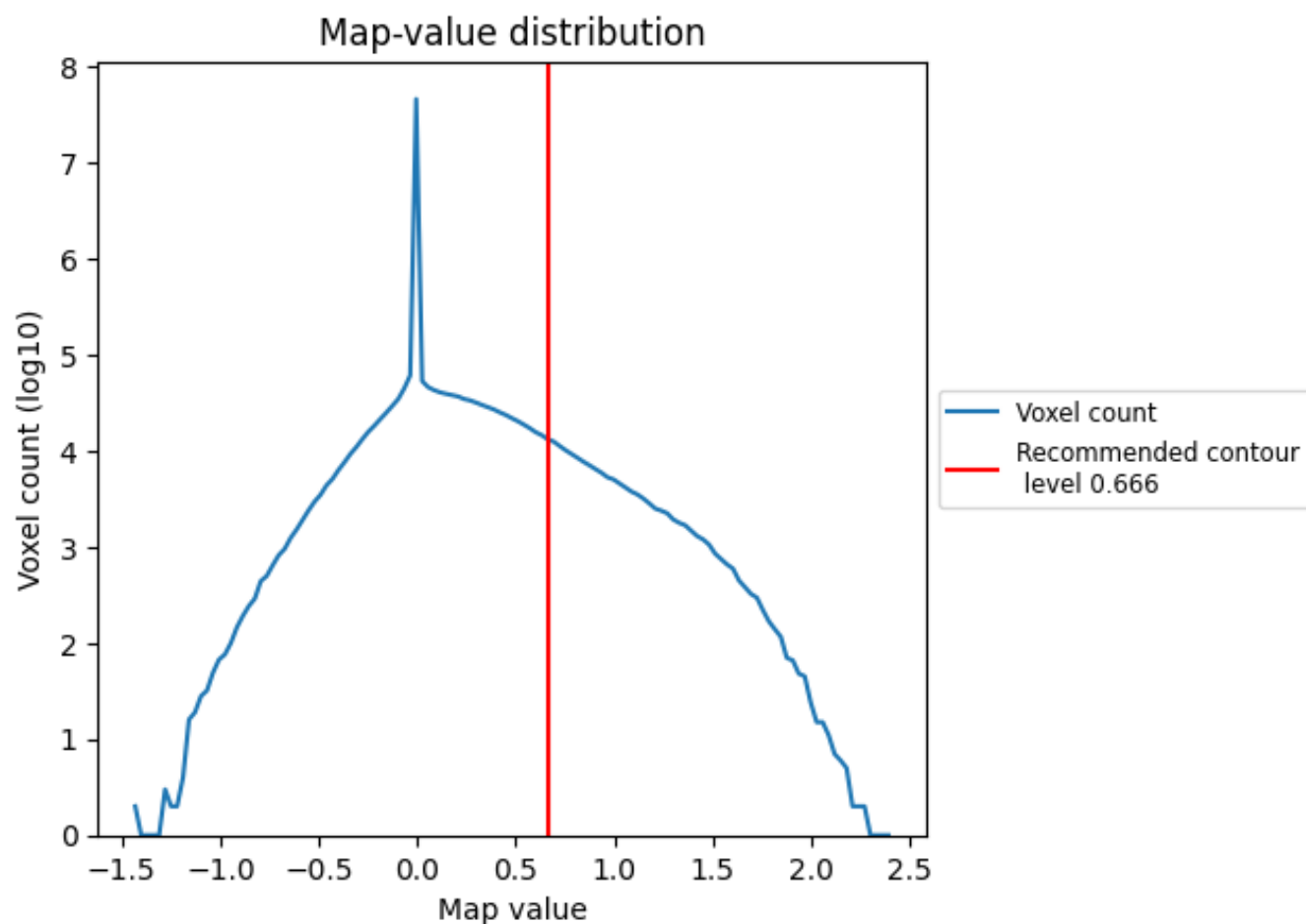
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

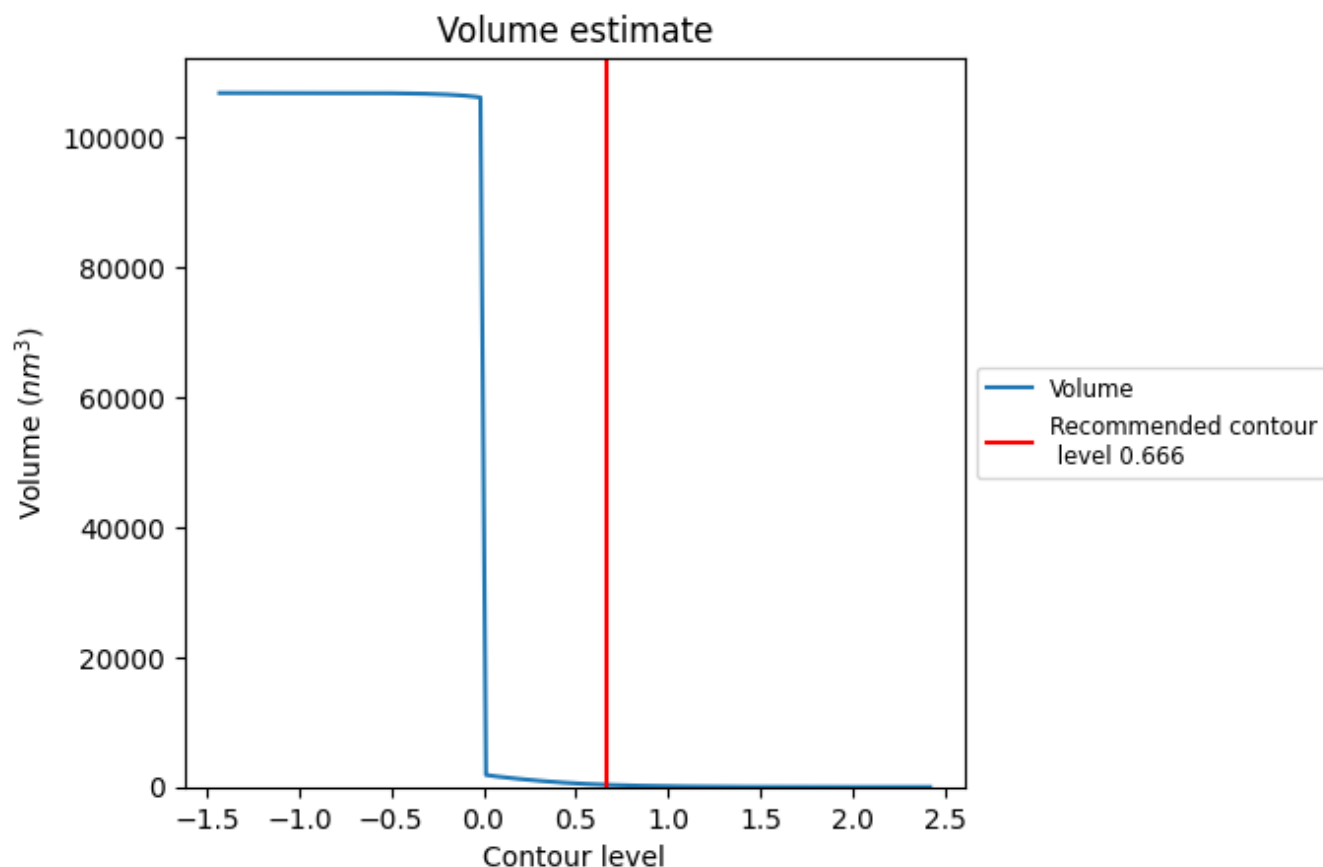
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

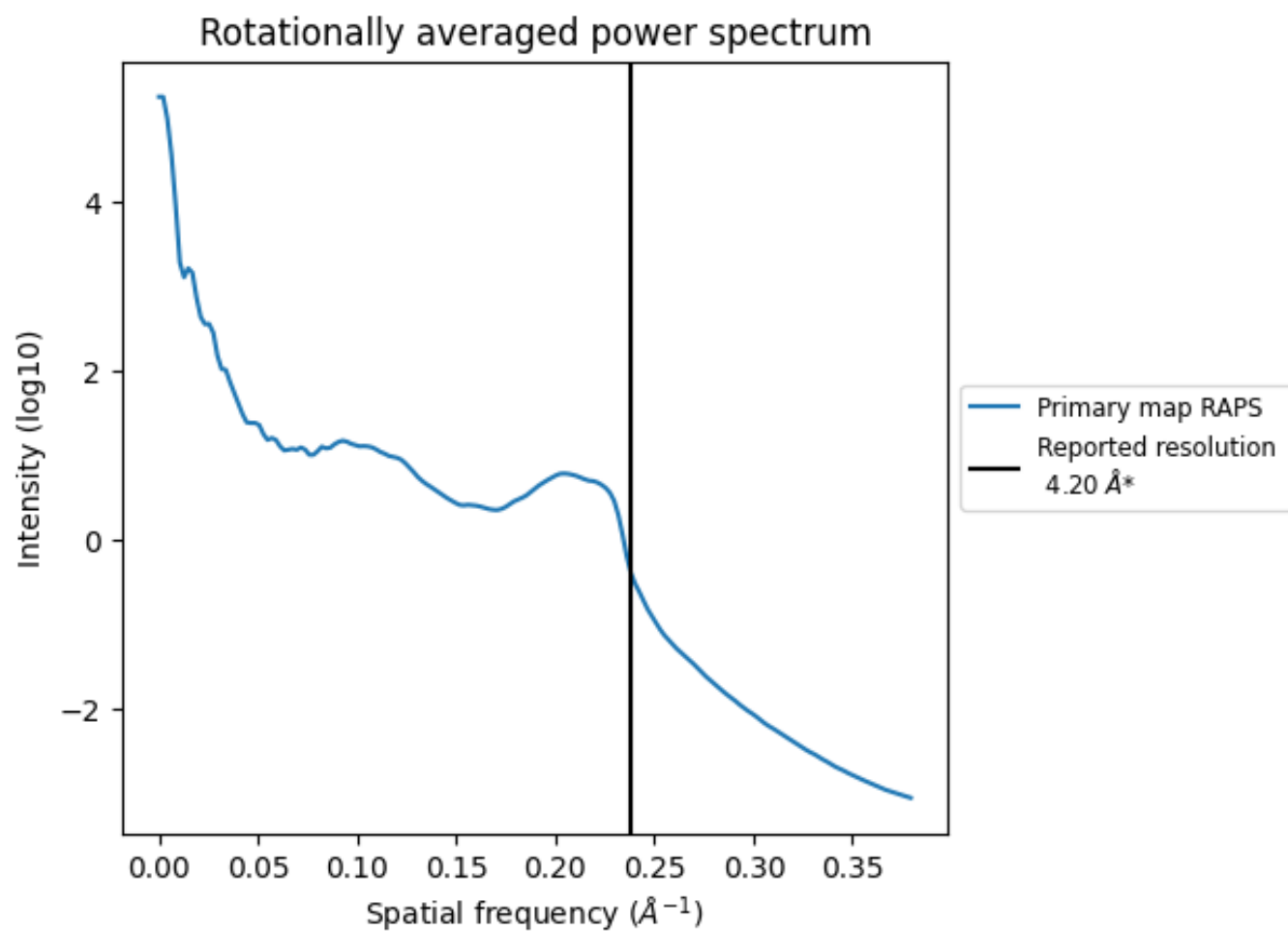
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332 nm^3 ; this corresponds to an approximate mass of 300 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 0.238 Å⁻¹

8 Fourier-Shell correlation

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

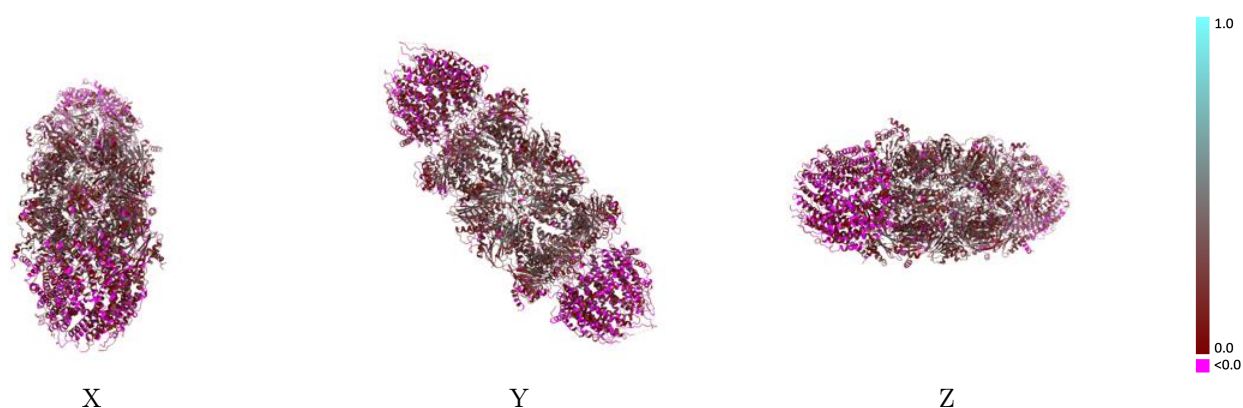
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30828 and PDB model 7DRW. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)

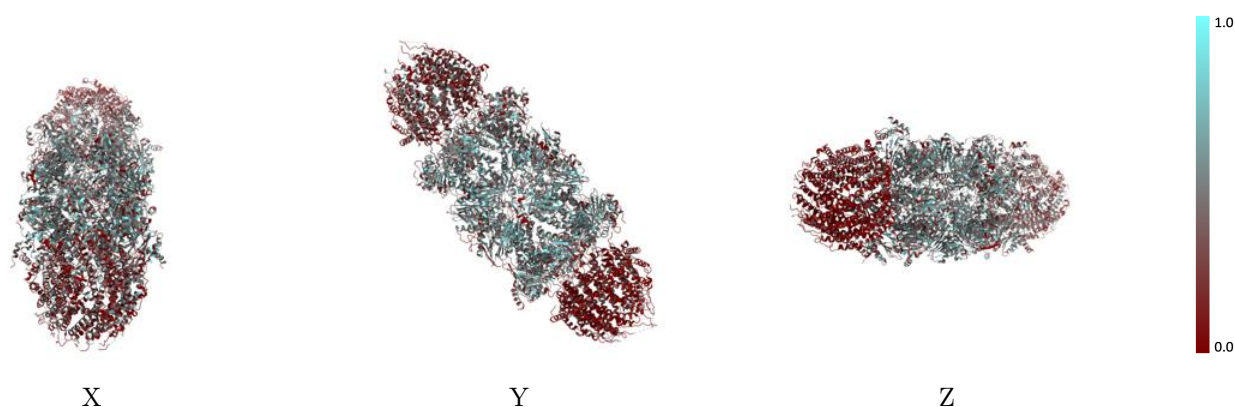
This section was not generated.

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



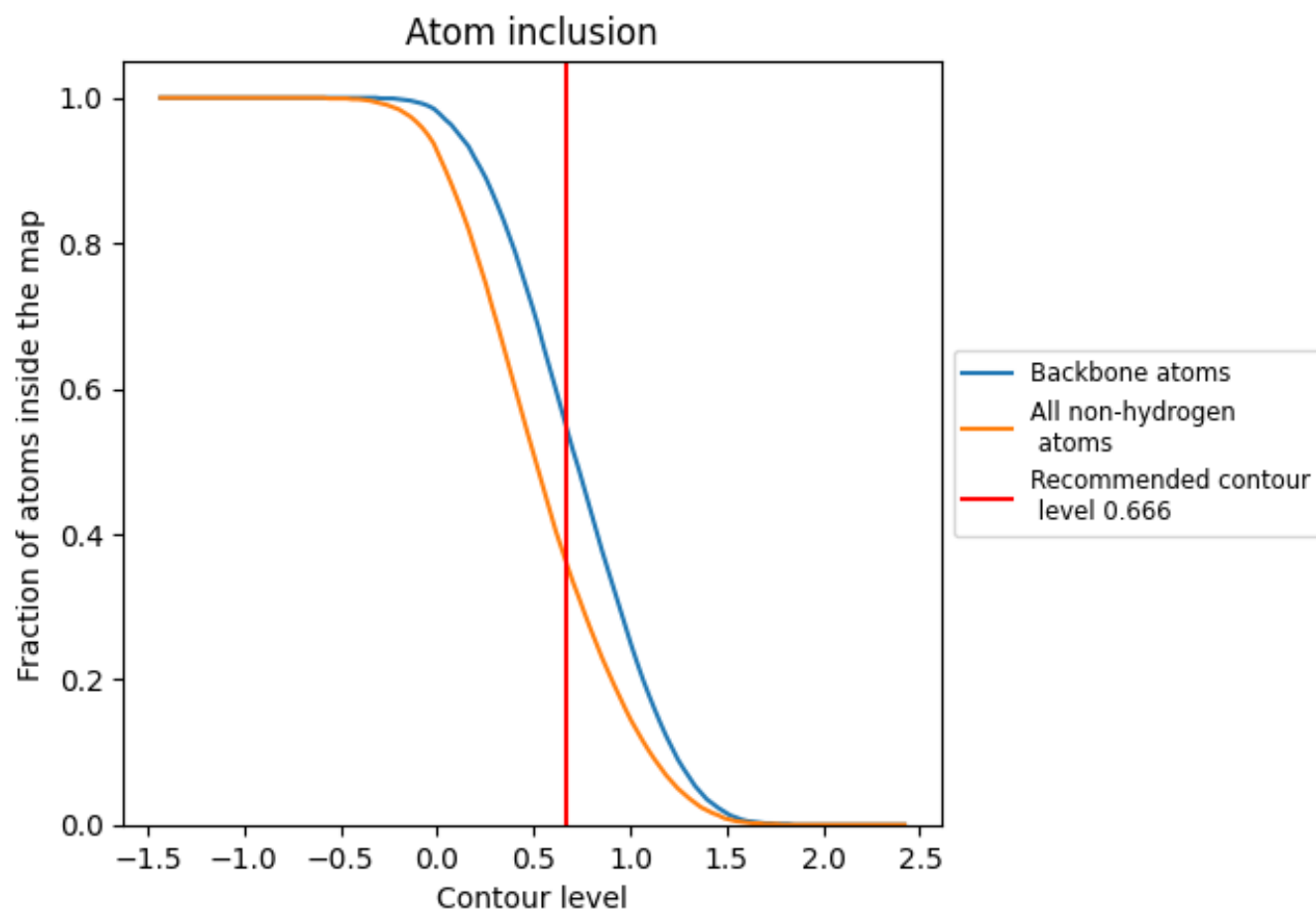
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.666).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 36% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.666) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3630	 0.1790
1	 0.4270	 0.2090
2	 0.4760	 0.2200
A	 0.4220	 0.1910
B	 0.4330	 0.2110
C	 0.4560	 0.2310
D	 0.4700	 0.2440
E	 0.3670	 0.1370
F	 0.4940	 0.2540
G	 0.4600	 0.2430
H	 0.2260	 0.1050
I	 0.2080	 0.0870
J	 0.2900	 0.1150
K	 0.2010	 0.0790
L	 0.2100	 0.0550
M	 0.2160	 0.0740
N	 0.2390	 0.0860
O	 0.1050	 0.0680
P	 0.4580	 0.2280
Q	 0.0770	 0.0610
R	 0.4190	 0.1980
S	 0.4810	 0.2600
T	 0.5160	 0.2870
U	 0.4550	 0.2350
V	 0.4830	 0.2620
W	 0.5370	 0.2840
X	 0.4810	 0.2500
Y	 0.5270	 0.2870
Z	 0.4950	 0.2440
a	 0.1090	 0.0170
b	 0.4630	 0.2360
c	 0.0840	 0.0390
d	 0.4550	 0.2380
e	 0.0900	 0.0420
f	 0.4620	 0.2370



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Chain	Atom inclusion	Q-score
g	 0.0850	 0.0390
h	 0.4760	 0.2320
i	 0.0830	 0.0350
j	 0.3980	 0.1940
k	 0.4870	 0.2480
l	 0.4850	 0.2480
m	 0.4680	 0.2560
n	 0.4430	 0.2390