



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 07:31 AM UTC

PDB ID : 4HRD / pdb_00004hrd
Title : Crystal structure of yeast 20S proteasome in complex with the natural product carmaphycin A
Authors : Trivella, D.B.B.; Stein, M.; Groll, M.
Deposited on : 2012-10-27
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

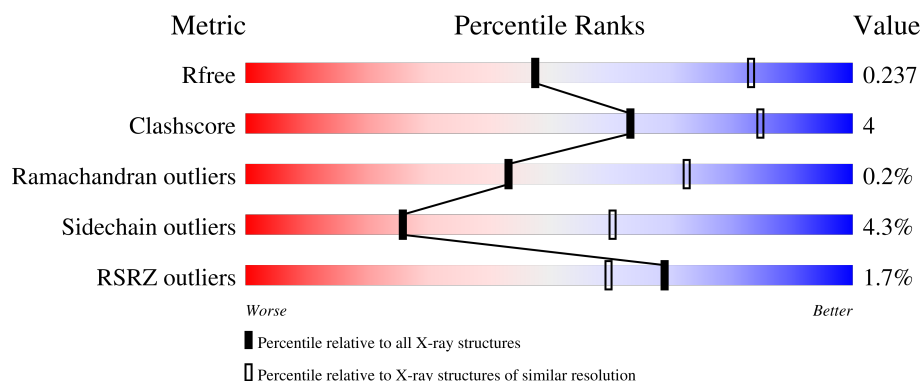
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	250	2% 91% 8%
1	O	250	2% 88% 11%
2	B	244	2% 86% 13%
2	P	244	4% 86% 13%
3	C	241	4% 85% 13%

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Mol	Chain	Length	Quality of chain
3	Q	241	 6% 85% 12% .
4	D	242	 5% 88% 12% .
4	R	242	 4% 89% 11% .
5	E	233	 2% 88% 12% .
5	S	233	 3% 82% 17% .
6	F	244	 0% 87% 11% .
6	T	244	 2% 87% 11% .
7	G	243	 0% 88% 11% .
7	U	243	 0% 88% 12% .
8	H	222	 0% 87% 11% .
8	V	222	 0% 88% 12% .
9	I	204	 0% 85% 15% .
9	W	204	 0% 89% 11% .
10	J	198	 2% 86% 14% .
10	X	198	 2% 86% 13% .
11	K	212	 0% 82% 16% .
11	Y	212	 0% 83% 16% .
12	L	222	 0% 89% 9% .
12	Z	222	 0% 93% 5% .
13	M	233	 0% 87% 12% .
13	a	233	 0% 87% 12% .
14	N	196	 0% 87% 10% ..
14	b	196	 0% 89% 9% .

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 50744 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 component Y7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome component Y13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome component PRE6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			
3	Q	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			

- Molecule 4 is a protein called Proteasome component PUP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			
4	R	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			

- Molecule 5 is a protein called Proteasome component PRE5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			
5	S	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			

- Molecule 6 is a protein called Proteasome component C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			
6	T	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			

- Molecule 7 is a protein called Proteasome component C7-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			
7	U	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			

- Molecule 8 is a protein called Proteasome component PUP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	1	0
			1691	1065	294	325	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			

- Molecule 9 is a protein called Proteasome component PUP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome component C11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

- Molecule 11 is a protein called Proteasome component PRE2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			

- Molecule 12 is a protein called Proteasome component C5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

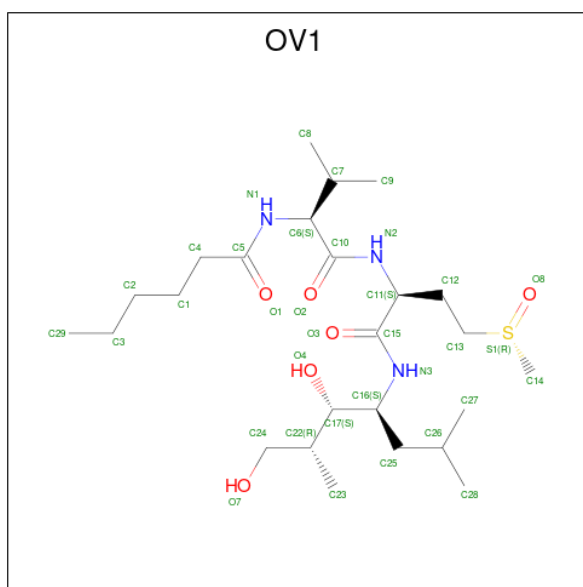
- Molecule 13 is a protein called Proteasome component PRE4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	a	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 14 is a protein called Proteasome component PRE3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is N-[(2S)-1-({(2S)-1-[(2R,3S,4S)-1,3-dihydroxy-2,6-dimethylheptan-4-yl]amino}-4-[(R)-methylsulfinyl]-1-oxobutan-2-yl]amino)-3-methyl-1-oxobutan-2-yl]hexanamide (CCD ID: OV1) (formula: C₂₅H₄₉N₃O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	H	1	Total	C	N	O	S	0	1
			70	50	6	12	2		
15	K	1	Total	C	N	O	S	0	0
			35	25	3	6	1		
15	N	1	Total	C	N	O	S	0	0
			35	25	3	6	1		
15	V	1	Total	C	N	O	S	0	0
			35	25	3	6	1		
15	Y	1	Total	C	N	O	S	0	0
			35	25	3	6	1		
15	b	1	Total	C	N	O	S	0	0
			35	25	3	6	1		

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	39	Total	O	0	0
			39	39		
16	B	33	Total	O	0	0
			33	33		
16	C	35	Total	O	0	0
			35	35		
16	D	40	Total	O	0	0
			40	40		
16	E	28	Total	O	0	0
			28	28		
16	F	29	Total	O	0	0
			29	29		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	37	Total O 37 37	0	0
16	H	32	Total O 32 32	0	0
16	I	27	Total O 27 27	0	0
16	J	32	Total O 32 32	0	0
16	K	36	Total O 36 36	0	0
16	L	43	Total O 43 43	0	0
16	M	27	Total O 27 27	0	0
16	N	34	Total O 34 34	0	0
16	O	27	Total O 27 27	0	0
16	P	32	Total O 32 32	0	0
16	Q	41	Total O 41 41	0	0
16	R	40	Total O 40 40	0	0
16	S	22	Total O 22 22	0	0
16	T	43	Total O 43 43	0	0
16	U	33	Total O 33 33	0	0
16	V	41	Total O 41 41	0	0
16	W	17	Total O 17 17	0	0
16	X	35	Total O 35 35	0	0
16	Y	30	Total O 30 30	0	0
16	Z	37	Total O 37 37	0	0
16	a	45	Total O 45 45	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	b	39	Total	O	0	0
			39	39		

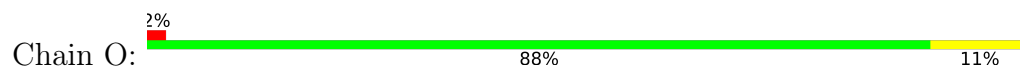
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

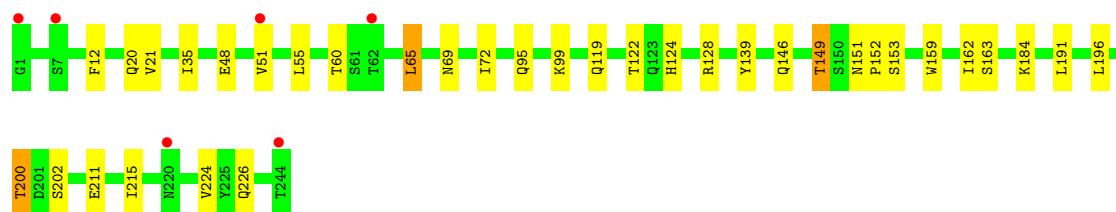
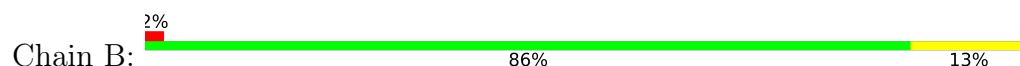
- Molecule 1: Proteasome component Y7



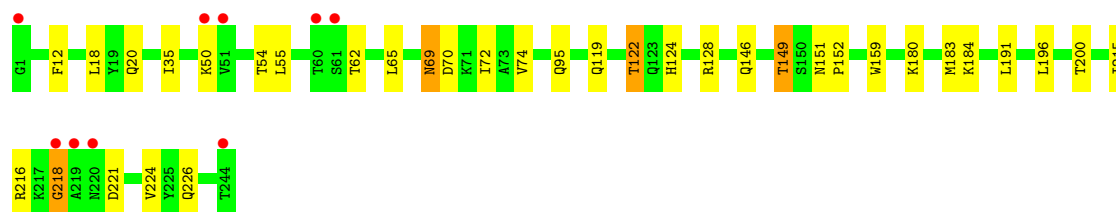
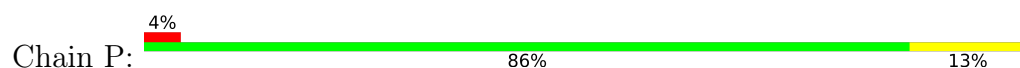
- Molecule 1: Proteasome component Y7



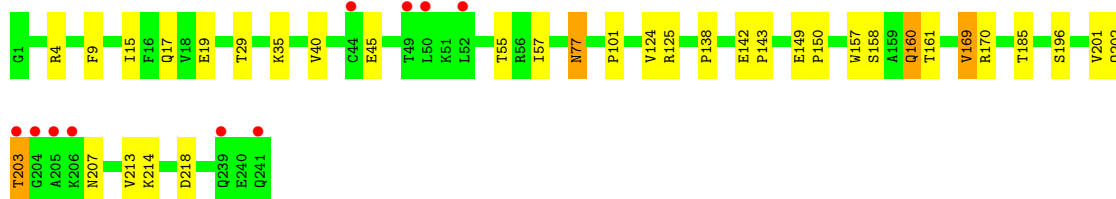
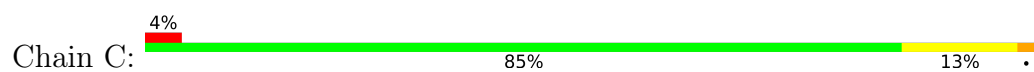
- Molecule 2: Proteasome component Y13



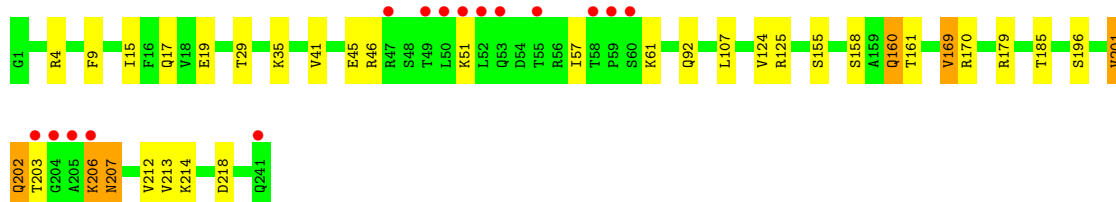
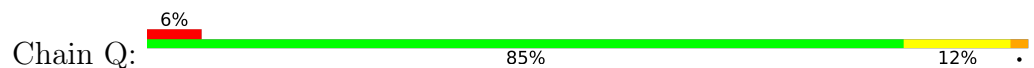
- Molecule 2: Proteasome component Y13



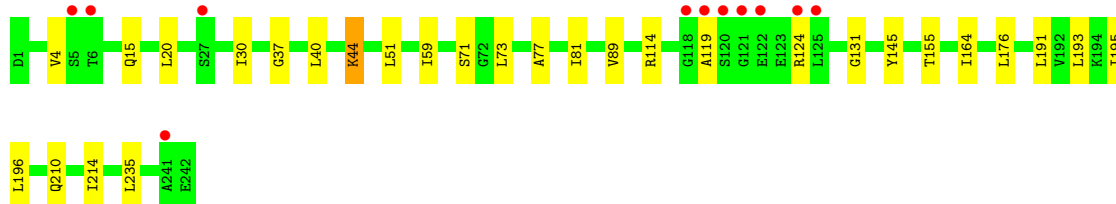
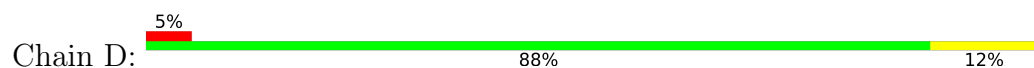
- Molecule 3: Proteasome component PRE6



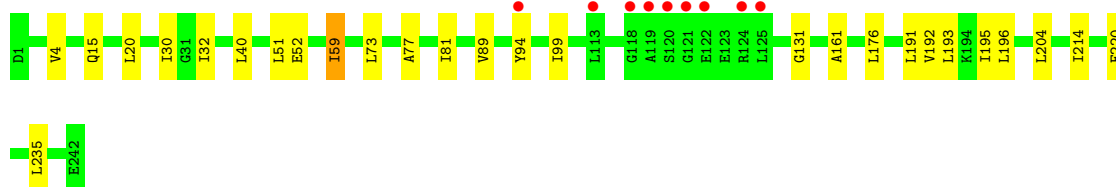
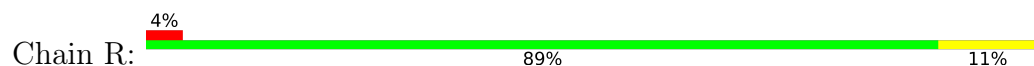
- Molecule 3: Proteasome component PRE6



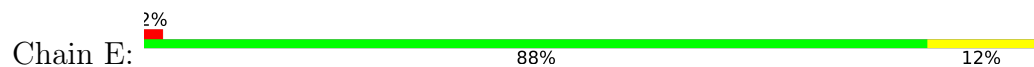
- Molecule 4: Proteasome component PUP2



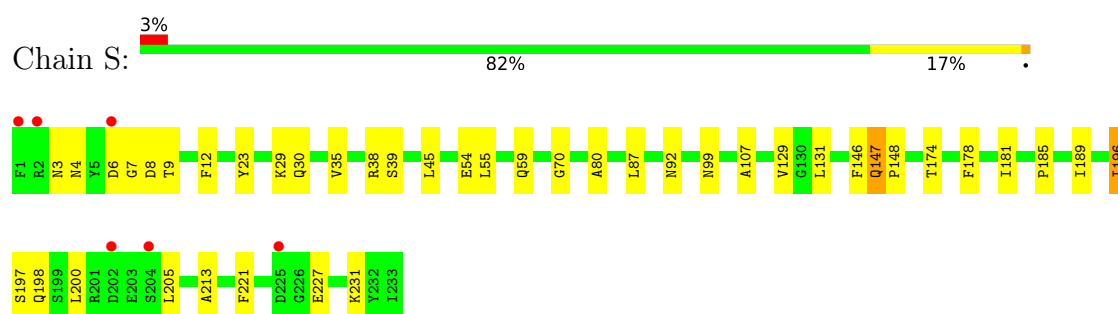
- Molecule 4: Proteasome component PUP2



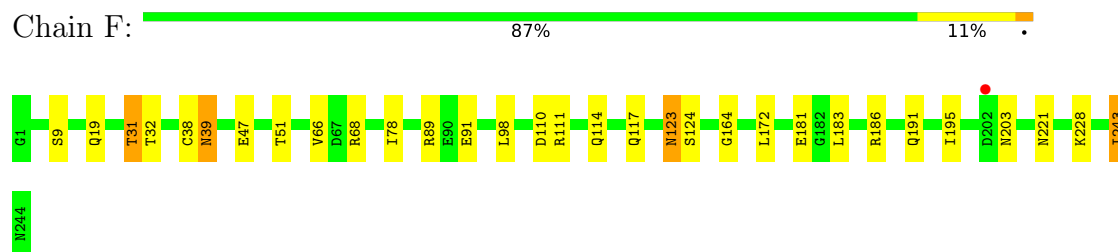
- Molecule 5: Proteasome component PRE5



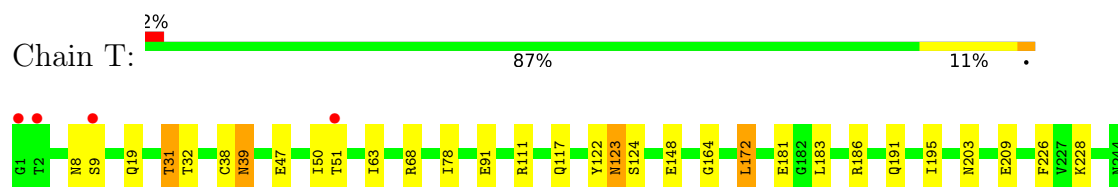
- Molecule 5: Proteasome component PRE5



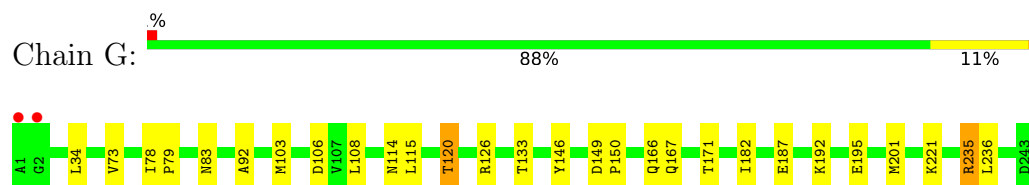
- Molecule 6: Proteasome component C1



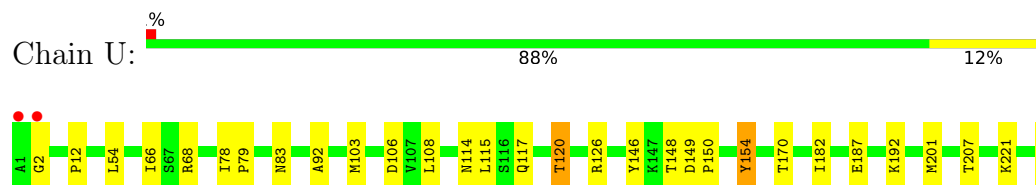
- Molecule 6: Proteasome component C1



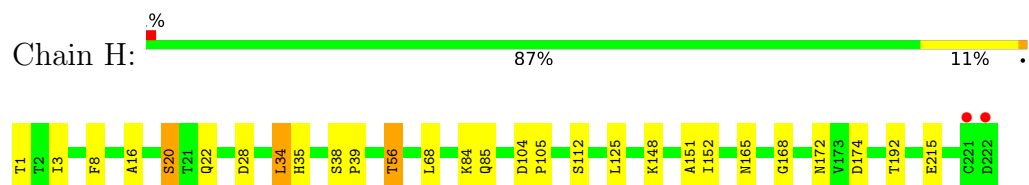
- Molecule 7: Proteasome component C7-alpha



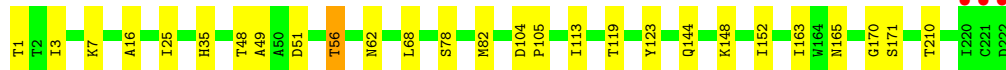
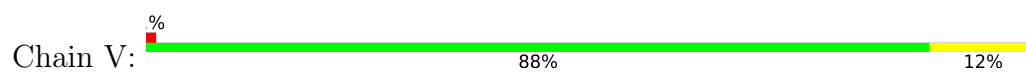
- Molecule 7: Proteasome component C7-alpha



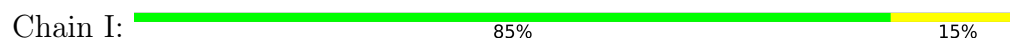
- Molecule 8: Proteasome component PUP1



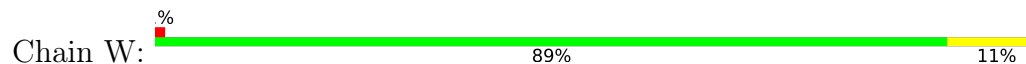
- Molecule 8: Proteasome component PUP1



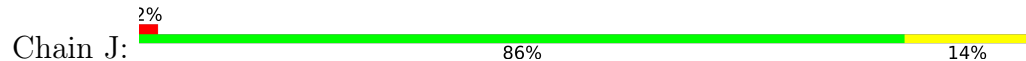
- Molecule 9: Proteasome component PUP3



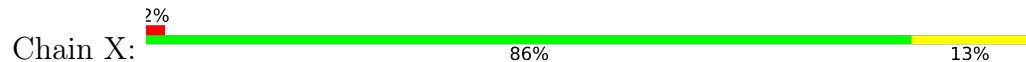
- Molecule 9: Proteasome component PUP3



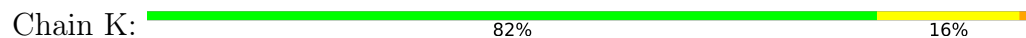
- Molecule 10: Proteasome component C11



- Molecule 10: Proteasome component C11

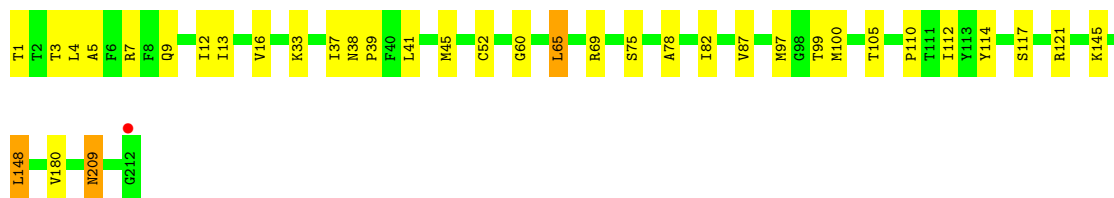


- Molecule 11: Proteasome component PRE2



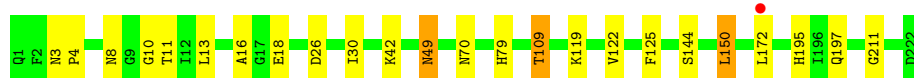
- Molecule 11: Proteasome component PRE2

Chain Y:  83% 16% .



- Molecule 12: Proteasome component C5

Chain L:  89% 9% .



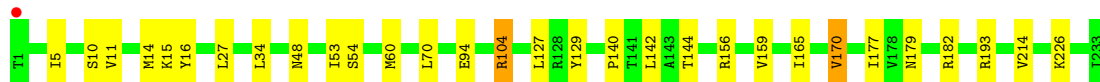
- Molecule 12: Proteasome component C5

Chain Z:  93% 5% .



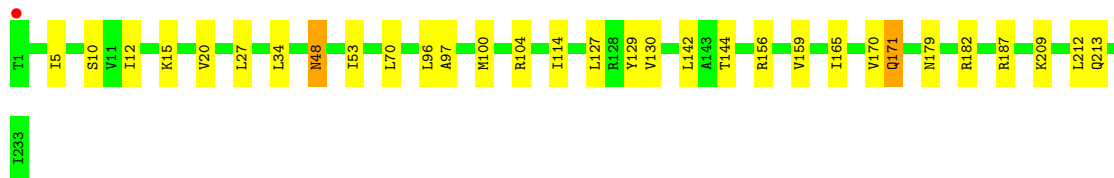
- Molecule 13: Proteasome component PRE4

Chain M:  87% 12% .



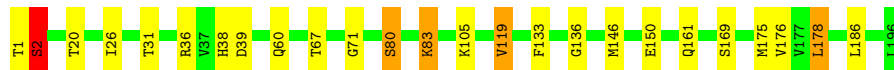
- Molecule 13: Proteasome component PRE4

Chain a:  87% 12% .

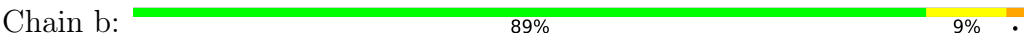


- Molecule 14: Proteasome component PRE3

Chain N:  87% 10% ..



- Molecule 14: Proteasome component PRE3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	134.62Å 300.28Å 144.57Å 90.00° 112.49° 90.00°	Depositor
Resolution (Å)	49.59 – 2.80 49.59 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.1 (49.59-2.80) 98.1 (49.59-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.10 (at 2.81Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.204 , 0.239 0.205 , 0.237	Depositor DCC
R_{free} test set	12672 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	59.0	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	50744	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: OV1

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	0.43	0/1952	0.77	0/2642
1	O	0.42	0/1952	0.77	0/2642
2	B	0.43	0/1934	0.76	0/2618
2	P	0.44	0/1934	0.77	0/2618
3	C	0.43	0/1919	0.79	0/2598
3	Q	0.45	0/1919	0.78	1/2598 (0.0%)
4	D	0.42	0/1886	0.78	0/2541
4	R	0.43	0/1886	0.75	0/2541
5	E	0.44	0/1823	0.79	0/2463
5	S	0.49	0/1823	0.82	4/2463 (0.2%)
6	F	0.46	1/1936 (0.1%)	0.80	0/2614
6	T	0.46	1/1936 (0.1%)	0.82	1/2614 (0.0%)
7	G	0.44	0/1959	0.76	0/2652
7	U	0.43	0/1959	0.76	0/2652
8	H	0.45	0/1722	0.78	0/2336
8	V	0.45	0/1715	0.76	0/2326
9	I	0.43	0/1611	0.76	0/2174
9	W	0.44	0/1611	0.75	0/2174
10	J	0.43	0/1613	0.76	0/2173
10	X	0.43	0/1613	0.76	0/2173
11	K	0.40	0/1681	0.78	1/2274 (0.0%)
11	Y	0.41	0/1681	0.76	0/2274
12	L	0.41	0/1795	0.75	0/2420
12	Z	0.43	0/1795	0.78	0/2420
13	M	0.43	0/1855	0.75	1/2514 (0.0%)
13	a	0.45	0/1855	0.75	0/2514
14	N	0.49	1/1541 (0.1%)	0.77	3/2087 (0.1%)
14	b	0.74	3/1541 (0.2%)	0.79	3/2087 (0.1%)
All	All	0.45	6/50447 (0.0%)	0.77	14/68202 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
8	H	0	2
8	V	0	1
11	K	0	1
11	Y	0	1
14	N	0	1
14	b	0	2
All	All	0	8

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	b	1	THR	C-N	19.66	1.58	1.33
14	N	2	SER	C-N	9.37	1.47	1.33
6	F	78	ILE	CA-CB	5.75	1.57	1.54
6	T	78	ILE	CA-CB	5.74	1.57	1.54
14	b	53	GLN	C-O	-5.19	1.18	1.24
14	b	49	ALA	C-O	-5.17	1.18	1.24

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	S	4	ASN	N-CA-C	8.70	120.84	111.36
5	S	7	GLY	N-CA-C	8.00	122.33	112.73
14	N	2	SER	O-C-N	-6.56	115.60	123.27
14	b	1	THR	CA-C-N	6.45	131.87	122.77
14	b	1	THR	C-N-CA	6.45	131.87	122.77
14	N	2	SER	CA-C-N	5.99	132.22	122.69
14	N	2	SER	C-N-CA	5.99	132.22	122.69
3	Q	201	VAL	N-CA-C	5.79	116.44	110.82
5	S	147	GLN	CA-C-N	5.71	125.38	119.56
5	S	147	GLN	C-N-CA	5.71	125.38	119.56
14	b	1	THR	O-C-N	-5.67	113.93	123.00
6	T	8	ASN	N-CA-C	5.36	116.93	111.14
13	M	10	SER	N-CA-C	5.28	117.73	110.35
11	K	189	GLY	N-CA-C	5.22	118.65	112.33

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	1[A]	THR	Peptide
8	H	1[B]	THR	Peptide
11	K	1	THR	Peptide
14	N	1	THR	Mainchain
8	V	1	THR	Peptide
11	Y	1	THR	Peptide
14	b	1	THR	Peptide,Mainchain

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	1915	0	1929	14	0
1	O	1915	0	1929	19	0
2	B	1904	0	1904	23	0
2	P	1904	0	1904	20	0
3	C	1890	0	1903	22	0
3	Q	1890	0	1903	23	0
4	D	1861	0	1839	12	0
4	R	1861	0	1839	11	0
5	E	1795	0	1800	15	0
5	S	1795	0	1800	19	0
6	F	1896	0	1889	16	0
6	T	1896	0	1889	16	0
7	G	1921	0	1913	16	0
7	U	1921	0	1913	19	0
8	H	1691	0	1690	17	0
8	V	1684	0	1685	14	0
9	I	1581	0	1574	18	0
9	W	1581	0	1574	14	0
10	J	1585	0	1590	14	0
10	X	1585	0	1590	13	0
11	K	1644	0	1592	24	0
11	Y	1644	0	1592	19	0
12	L	1757	0	1711	16	0
12	Z	1757	0	1711	7	0
13	M	1824	0	1832	15	0
13	a	1824	0	1832	16	0
14	N	1512	0	1478	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	b	1512	0	1478	12	0
15	H	70	0	94	3	0
15	K	35	0	47	2	0
15	N	35	0	47	0	0
15	V	35	0	47	2	0
15	Y	35	0	47	1	0
15	b	35	0	47	4	0
16	A	39	0	0	0	0
16	B	33	0	0	0	0
16	C	35	0	0	0	0
16	D	40	0	0	2	0
16	E	28	0	0	0	0
16	F	29	0	0	0	0
16	G	37	0	0	0	0
16	H	32	0	0	0	0
16	I	27	0	0	0	0
16	J	32	0	0	0	0
16	K	36	0	0	1	0
16	L	43	0	0	0	0
16	M	27	0	0	0	0
16	N	34	0	0	0	0
16	O	27	0	0	0	0
16	P	32	0	0	1	0
16	Q	41	0	0	0	0
16	R	40	0	0	0	0
16	S	22	0	0	0	0
16	T	43	0	0	0	0
16	U	33	0	0	0	0
16	V	41	0	0	0	0
16	W	17	0	0	0	0
16	X	35	0	0	0	0
16	Y	30	0	0	0	0
16	Z	37	0	0	0	0
16	a	45	0	0	0	0
16	b	39	0	0	0	0
All	All	50744	0	49612	395	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 4.

All (395) 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)
7:G:92:ALA:HA	7:G:103:MET:HE2	1.59	0.83
7:U:92:ALA:HA	7:U:103:MET:HE2	1.62	0.81
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.48	0.79
1:A:12:PHE:H	2:B:20:GLN:HE22	1.34	0.76
11:K:33:LYS:HE2	15:K:301:OV1:H14	1.67	0.76
1:O:12:PHE:H	2:P:20:GLN:HE22	1.33	0.76
3:Q:206:LYS:O	3:Q:207:ASN:HB2	1.84	0.74
11:Y:33:LYS:HE2	15:Y:301:OV1:H14	1.68	0.74
3:Q:201:VAL:O	3:Q:202:GLN:HB2	1.86	0.74
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.70	0.74
2:B:122:THR:HG22	3:C:125:ARG:HH21	1.53	0.73
14:N:161:GLN:HE21	14:b:136:GLY:HA2	1.55	0.72
6:F:91:GLU:HG2	6:F:111:ARG:HB3	1.72	0.72
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.35	0.71
1:O:128:ARG:HH21	7:U:120:THR:HG22	1.55	0.71
2:B:12:PHE:H	3:C:17:GLN:HE22	1.38	0.70
10:J:147:HIS:HB3	10:J:160:LEU:HD11	1.74	0.70
3:C:9:PHE:H	4:D:15:GLN:HE22	1.38	0.69
4:D:30:ILE:HD12	4:D:196:LEU:HG	1.75	0.68
5:S:6:ASP:OD1	5:S:23:TYR:OH	2.08	0.68
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.41	0.67
6:F:31:THR:HG21	6:F:47:GLU:O	1.94	0.67
8:H:35:HIS:HB3	8:H:56:THR:HG21	1.76	0.67
7:G:34:LEU:HD23	7:G:201:MET:HE3	1.78	0.66
3:Q:160:GLN:HE22	3:Q:170:ARG:HE	1.42	0.66
3:C:160:GLN:HE22	3:C:170:ARG:HE	1.43	0.66
6:T:31:THR:HG21	6:T:47:GLU:O	1.95	0.66
11:Y:209:ASN:HD22	11:Y:209:ASN:H	1.45	0.65
13:a:27:LEU:HD21	13:a:34:LEU:HD22	1.79	0.65
1:O:119:GLN:O	1:O:122:THR:HB	1.95	0.65
13:a:209:LYS:HB3	13:a:212:LEU:HD11	1.79	0.65
10:J:1:MET:HG2	10:J:2:ASP:H	1.62	0.65
14:b:175:MET:HB2	14:b:186:LEU:HB2	1.78	0.64
12:L:13:LEU:HD11	12:L:150:LEU:HD21	1.78	0.64
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.80	0.64
7:U:187:GLU:HG2	7:U:192:LYS:HB2	1.80	0.64
6:T:91:GLU:HG2	6:T:111:ARG:HB3	1.78	0.63
14:N:36:ARG:HH21	14:N:60:GLN:HE21	1.47	0.63
10:J:152:MET:HE2	10:J:156:GLU:HB3	1.80	0.63
2:P:122:THR:HG22	3:Q:125:ARG:HH21	1.62	0.63
1:A:128:ARG:HH21	7:G:120:THR:CG2	2.13	0.62
1:O:83:ARG:HE	7:U:114:ASN:HD21	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:109:THR:HG23	12:L:125:PHE:HB2	1.81	0.62
7:G:103:MET:HE3	7:G:108:LEU:HD13	1.82	0.61
13:M:14:MET:HG2	13:M:177:ILE:HD11	1.82	0.61
1:A:83:ARG:HE	7:G:114:ASN:HD21	1.48	0.61
3:C:29:THR:HB	3:C:45:GLU:HG3	1.82	0.61
12:L:195:HIS:HD2	12:L:197:GLN:H	1.49	0.60
1:O:187:ASP:O	1:O:191:ILE:HD12	2.02	0.60
11:K:37:ILE:HB	11:K:41:LEU:HB3	1.83	0.60
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.67	0.60
14:N:67:THR:HA	14:N:71:GLY:O	2.01	0.60
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.67	0.60
14:N:146:MET:HE2	14:N:150:GLU:HB3	1.83	0.60
6:F:32:THR:HB	6:F:164:GLY:H	1.65	0.60
14:N:136:GLY:HA2	14:b:161:GLN:HE21	1.67	0.59
12:Z:109:THR:HG23	12:Z:125:PHE:HB2	1.84	0.59
8:V:78:SER:O	8:V:82:MET:HG3	2.03	0.59
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.84	0.59
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.33	0.59
12:L:49:ASN:HD21	12:L:211:GLY:HA2	1.67	0.58
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.86	0.58
4:D:114:ARG:HD3	16:D:303:HOH:O	2.03	0.58
1:O:128:ARG:HH21	7:U:120:THR:CG2	2.17	0.57
6:T:91:GLU:HG3	6:T:111:ARG:HH11	1.68	0.57
1:A:187:ASP:O	1:A:191:ILE:HD12	2.04	0.57
14:b:49:ALA:HB2	15:b:301:OV1:H17	1.86	0.57
5:S:12:PHE:H	6:T:19:GLN:HE22	1.53	0.57
2:P:146:GLN:HG2	3:Q:57:ILE:HG21	1.85	0.57
6:T:123:ASN:HD22	6:T:124:SER:N	2.02	0.56
6:F:123:ASN:C	6:F:123:ASN:HD22	2.13	0.56
11:Y:97:MET:HG2	11:Y:117:SER:HB3	1.87	0.56
6:F:38:CYS:HB2	6:F:183:LEU:O	2.05	0.56
6:T:50:ILE:HD11	6:T:209:GLU:HB2	1.87	0.56
13:M:27:LEU:HD21	13:M:34:LEU:HD22	1.86	0.56
1:A:128:ARG:HH21	7:G:120:THR:HG22	1.70	0.56
5:S:87:LEU:HD11	5:S:107:ALA:HB1	1.89	0.55
7:G:167:GLN:HE21	7:G:171:THR:HG23	1.71	0.55
10:J:3:ILE:H	10:J:18:SER:HB2	1.72	0.55
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.55	0.55
9:I:120:ILE:HD12	9:I:136:ILE:HG12	1.87	0.55
7:U:148:THR:HG22	7:U:154:TYR:HB2	1.89	0.55
8:V:48:THR:HB	8:V:51:ASP:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:b:48:SER:O	14:b:52:THR:HG23	2.07	0.55
10:J:33:ASP:OD2	10:J:35:THR:HG22	2.06	0.55
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.89	0.55
8:H:165:ASN:HD22	13:a:156:ARG:HH11	1.53	0.55
13:M:15:LYS:HG3	13:M:165:ILE:HD12	1.89	0.55
2:B:146:GLN:HG2	3:C:57:ILE:HG21	1.89	0.54
10:X:152:MET:HE2	10:X:156:GLU:HB3	1.90	0.54
8:H:112:SER:HB3	8:H:125:LEU:HD13	1.90	0.54
5:S:45:LEU:HB2	5:S:213:ALA:HB3	1.89	0.54
6:T:31:THR:HG23	6:T:47:GLU:HB3	1.88	0.54
3:C:157:TRP:CE2	4:D:51:LEU:HD23	2.43	0.54
11:K:37:ILE:HG23	11:K:60:GLY:HA2	1.90	0.54
11:K:38:ASN:HB2	11:K:39:PRO:HD2	1.90	0.54
2:P:215:ILE:HG12	2:P:226:GLN:HG2	1.90	0.54
5:E:9:THR:HG21	5:E:119:THR:HA	1.90	0.53
10:J:22:THR:HG21	10:X:173:PRO:HB3	1.90	0.53
8:H:148:LYS:O	8:H:152:ILE:HG12	2.09	0.53
5:S:6:ASP:OD1	5:S:23:TYR:CE2	2.61	0.53
7:U:103:MET:HE3	7:U:108:LEU:HD13	1.90	0.53
3:C:160:GLN:HE21	3:C:161:THR:H	1.57	0.53
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.90	0.53
3:Q:29:THR:HB	3:Q:45:GLU:HG3	1.91	0.53
3:Q:160:GLN:HE21	3:Q:160:GLN:CA	2.21	0.53
4:R:73:LEU:HD12	4:R:131:GLY:HA3	1.91	0.53
9:W:106:PRO:HD2	9:W:123:PHE:HB2	1.90	0.53
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.91	0.52
3:Q:206:LYS:O	3:Q:207:ASN:CB	2.54	0.52
2:B:200:THR:HG22	2:B:202:SER:H	1.75	0.52
9:I:106:PRO:HD2	9:I:123:PHE:HB2	1.91	0.52
2:B:99:LYS:HG3	9:I:64:GLU:HB3	1.91	0.52
6:T:123:ASN:HD22	6:T:123:ASN:C	2.16	0.52
3:Q:214:LYS:HB2	3:Q:218:ASP:HB3	1.91	0.52
5:S:35:VAL:HG23	5:S:196:ILE:HD12	1.91	0.52
11:K:99:THR:HG22	11:K:115:VAL:HB	1.92	0.52
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.92	0.52
11:Y:3:THR:HG22	11:Y:16:VAL:HG12	1.92	0.51
14:N:175:MET:HB2	14:N:186:LEU:HB2	1.92	0.51
8:V:35:HIS:HB3	8:V:56:THR:HG21	1.92	0.51
2:B:122:THR:CG2	3:C:125:ARG:HH21	2.21	0.51
4:R:77:ALA:O	4:R:81:ILE:HG12	2.11	0.51
2:P:12:PHE:H	3:Q:17:GLN:HE22	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:16:ALA:HB2	12:L:122:VAL:HG23	1.93	0.51
6:F:191:GLN:O	6:F:195:ILE:HG12	2.11	0.51
12:L:3:ASN:HD22	12:L:4:PRO:HD2	1.75	0.51
6:T:38:CYS:HB2	6:T:183:LEU:O	2.11	0.51
11:K:3:THR:HG22	11:K:16:VAL:HG12	1.93	0.50
9:W:20:VAL:HG23	9:W:189:ILE:HB	1.93	0.50
2:B:215:ILE:HG12	2:B:226:GLN:HG2	1.92	0.50
7:G:106:ASP:HB3	7:G:146:TYR:CZ	2.46	0.50
5:E:205:LEU:HA	5:E:209:ASN:HD22	1.76	0.50
2:B:35:ILE:HD12	2:B:196:LEU:HG	1.94	0.50
5:E:49:LYS:HB3	5:E:58:TYR:HB3	1.94	0.50
6:F:31:THR:HG23	6:F:47:GLU:HB3	1.92	0.50
8:V:148:LYS:O	8:V:152:ILE:HG12	2.12	0.50
13:a:53:ILE:HG12	13:a:114:ILE:HG12	1.93	0.50
4:D:71:SER:HB3	4:D:164:ILE:HD12	1.94	0.50
12:L:18:GLU:O	12:L:119:LYS:HA	2.12	0.50
11:Y:209:ASN:H	11:Y:209:ASN:ND2	2.08	0.50
9:I:141:ALA:HB2	9:I:177:ASP:HB2	1.94	0.50
1:O:115:ALA:HB1	1:O:154:GLY:O	2.11	0.49
1:O:83:ARG:HE	7:U:114:ASN:ND2	2.10	0.49
9:W:94:LEU:HD11	9:W:106:PRO:HG2	1.93	0.49
5:E:12:PHE:H	6:F:19:GLN:HE22	1.61	0.49
10:J:92:ILE:HG13	10:J:122:LEU:HD23	1.95	0.49
11:K:107:LYS:H	11:K:107:LYS:HD2	1.77	0.49
5:S:185:PRO:O	5:S:189:ILE:HG12	2.13	0.49
10:X:147:HIS:HB3	10:X:160:LEU:HD11	1.94	0.49
9:W:120:ILE:HD12	9:W:136:ILE:HG12	1.95	0.49
4:D:119:ALA:HB3	4:D:124:ARG:HD3	1.95	0.49
8:H:20:SER:HB3	8:H:28:ASP:HB3	1.95	0.49
11:K:209:ASN:H	11:K:209:ASN:HD22	1.61	0.49
11:Y:37:ILE:HB	11:Y:41:LEU:HB3	1.95	0.49
13:a:96:LEU:O	13:a:100:MET:HG2	2.12	0.49
8:H:38:SER:HB2	8:H:39:PRO:HD2	1.94	0.49
1:A:83:ARG:HH21	7:G:114:ASN:HD22	1.61	0.49
5:S:200:LEU:HD11	5:S:205:LEU:HD22	1.94	0.48
6:T:172:LEU:HB3	7:U:54:LEU:HD21	1.95	0.48
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.43	0.48
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.94	0.48
10:X:195:PHE:HA	10:X:198:GLN:HB2	1.96	0.48
9:I:11:VAL:HG23	9:I:53:THR:HG23	1.95	0.48
11:K:33:LYS:HA	11:K:45:MET:HE2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.43	0.48
13:a:179:ASN:HD22	13:a:182:ARG:HH11	1.60	0.48
14:b:146:MET:HE2	14:b:150:GLU:HB3	1.94	0.48
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.57	0.48
6:T:9:SER:HB2	7:U:126:ARG:HB3	1.95	0.48
9:W:141:ALA:HB2	9:W:177:ASP:HB2	1.94	0.48
11:K:209:ASN:H	11:K:209:ASN:ND2	2.11	0.48
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.44	0.48
14:b:47:GLY:O	15:b:301:OV1:H13	2.13	0.47
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.96	0.47
3:Q:161:THR:HG21	3:Q:169:VAL:HG13	1.96	0.47
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.94	0.47
7:G:195:GLU:HG3	7:G:235:ARG:HG3	1.96	0.47
2:B:119:GLN:O	2:B:122:THR:HB	2.15	0.47
11:K:1:THR:HG23	11:K:33:LYS:HD3	1.95	0.47
7:G:187:GLU:HG2	7:G:192:LYS:HB2	1.96	0.47
11:K:4:LEU:HA	11:K:100:MET:HE1	1.95	0.47
1:A:227:ILE:HG22	1:A:230:ASP:H	1.80	0.47
4:D:89:VAL:HG21	11:K:65:LEU:HD13	1.96	0.47
10:J:92:ILE:HA	10:J:97:PRO:HB3	1.96	0.47
2:B:65:LEU:HD22	2:B:211:GLU:HB3	1.96	0.47
2:P:35:ILE:HD12	2:P:196:LEU:HG	1.96	0.47
9:W:15:THR:HG22	9:W:20:VAL:HG12	1.96	0.47
11:Y:12:ILE:HB	11:Y:180:VAL:HB	1.95	0.47
13:a:129:TYR:HE1	13:a:144:THR:HG22	1.79	0.47
2:P:69:ASN:HB3	2:P:72:ILE:H	1.80	0.47
9:W:185:VAL:HG21	9:W:196:LYS:HE3	1.96	0.47
13:a:15:LYS:HG3	13:a:165:ILE:HD12	1.97	0.47
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.44	0.47
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.97	0.47
12:L:4:PRO:O	13:M:104:ARG:NH1	2.45	0.46
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.43	0.46
2:P:149:THR:CG2	2:P:159:TRP:HE1	2.28	0.46
6:T:191:GLN:O	6:T:195:ILE:HG12	2.15	0.46
2:B:69:ASN:HB3	2:B:72:ILE:H	1.80	0.46
9:I:65:MET:O	9:I:68:TYR:HB3	2.16	0.46
2:P:95:GLN:HE22	9:W:71:ASN:HD22	1.63	0.46
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	1.97	0.46
14:b:20:THR:HG22	15:b:301:OV1:C28	2.45	0.46
5:S:70:GLY:HA3	5:S:221:PHE:CE2	2.50	0.46
8:V:3:ILE:HG22	8:V:16:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Y:38:ASN:HB2	11:Y:39:PRO:CD	2.46	0.46
13:a:15:LYS:HB3	13:a:20:VAL:HG12	1.97	0.46
7:U:149:ASP:HB2	7:U:150:PRO:HD2	1.96	0.46
5:E:185:PRO:O	5:E:189:ILE:HG12	2.16	0.46
6:F:110:ASP:O	6:F:114:GLN:HG2	2.16	0.46
3:Q:41:VAL:HG22	3:Q:212:VAL:HG22	1.98	0.46
4:R:89:VAL:HG21	11:Y:65:LEU:HD13	1.98	0.46
10:X:25:ILE:HG22	10:X:25:ILE:O	2.16	0.46
8:H:35:HIS:CB	8:H:56:THR:HG21	2.43	0.46
13:M:179:ASN:HD22	13:M:182:ARG:HH11	1.63	0.46
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.46	0.46
3:C:77:ASN:N	3:C:77:ASN:HD22	2.14	0.46
10:J:195:PHE:HA	10:J:198:GLN:HB2	1.98	0.46
14:b:20:THR:HG22	15:b:301:OV1:H15	1.98	0.46
3:C:214:LYS:HB2	3:C:218:ASP:HB3	1.97	0.45
8:H:168:GLY:O	15:H:301[A]:OV1:H23	2.16	0.45
13:M:11:VAL:HG23	13:M:54:SER:HB3	1.98	0.45
5:E:231:LYS:H	5:E:231:LYS:HD2	1.81	0.45
5:S:80:ALA:HB2	5:S:129:VAL:HG21	1.98	0.45
7:U:106:ASP:HB3	7:U:146:TYR:CZ	2.51	0.45
10:X:19:LYS:HD3	10:X:180:ILE:HG13	1.98	0.45
13:a:179:ASN:HD22	13:a:182:ARG:NH1	2.14	0.45
1:O:1:MET:HG3	6:T:122:TYR:CZ	2.51	0.45
14:b:38:HIS:O	14:b:39:ASP:C	2.58	0.45
1:A:83:ARG:HE	7:G:114:ASN:ND2	2.11	0.45
4:D:73:LEU:HD12	4:D:131:GLY:HA3	1.99	0.45
11:Y:38:ASN:HB2	11:Y:39:PRO:HD2	1.98	0.45
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.64	0.45
1:O:66:LEU:HD12	1:O:235:PHE:CD2	2.52	0.45
1:O:83:ARG:HH21	7:U:114:ASN:HD22	1.63	0.45
1:A:222:LEU:HD13	1:A:232:GLY:HA2	1.98	0.45
5:E:178:PHE:HA	5:E:181:ILE:HG12	1.99	0.45
12:L:8:ASN:HA	12:L:30:ILE:O	2.16	0.45
14:N:133:PHE:HA	14:b:132:THR:O	2.16	0.45
13:a:171:GLN:H	13:a:171:GLN:NE2	2.15	0.45
2:B:139:TYR:CD1	2:B:224:VAL:HG21	2.52	0.45
8:V:49:ALA:HB2	15:V:301:OV1:H17	1.98	0.45
2:B:48:GLU:OE2	2:B:200:THR:HG23	2.17	0.45
6:F:66:VAL:HG22	6:F:89:ARG:HG3	1.99	0.45
11:K:75:SER:HA	11:K:105:THR:HG21	1.99	0.45
1:O:26:THR:O	1:O:30:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:6:ASP:OD1	5:S:23:TYR:CZ	2.70	0.45
13:a:48:ASN:H	13:a:48:ASN:HD22	1.65	0.45
3:Q:92:GLN:HG3	10:X:66:LEU:HB2	1.99	0.44
1:O:64:VAL:HG11	1:O:212:ALA:HB3	1.99	0.44
9:W:15:THR:HG23	9:W:120:ILE:HG12	1.99	0.44
4:D:77:ALA:O	4:D:81:ILE:HG12	2.16	0.44
1:O:110:LEU:O	1:O:114:VAL:HG23	2.18	0.44
4:R:30:ILE:HD12	4:R:196:LEU:HG	1.98	0.44
2:B:21:VAL:HG11	2:B:153:SER:HB3	1.99	0.44
12:Z:49:ASN:HD21	12:Z:211:GLY:HA2	1.83	0.44
5:E:206:THR:H	5:E:209:ASN:HB3	1.82	0.44
10:J:173:PRO:HB3	10:X:22:THR:HG21	2.00	0.44
11:K:89:GLN:HG3	16:K:416:HOH:O	2.18	0.44
5:S:70:GLY:HA3	5:S:221:PHE:CZ	2.53	0.44
3:C:35:LYS:HG2	3:C:158:SER:O	2.18	0.44
9:I:20:VAL:HG23	9:I:189:ILE:HB	2.00	0.44
2:P:18:LEU:HD13	2:P:122:THR:HG23	2.00	0.44
4:R:59:ILE:HG22	4:R:220:PHE:HZ	1.82	0.44
6:F:98:LEU:O	14:N:80:SER:HB3	2.18	0.43
13:M:53:ILE:HB	13:M:60:MET:HG3	2.00	0.43
4:D:44:LYS:HE3	4:D:210:GLN:HB2	2.00	0.43
12:L:42:LYS:HB3	12:L:42:LYS:HE2	1.86	0.43
6:T:39:ASN:HD22	6:T:39:ASN:C	2.26	0.43
7:U:78:ILE:N	7:U:79:PRO:HD2	2.33	0.43
10:X:119:ILE:HA	10:X:124:THR:O	2.18	0.43
11:Y:5:ALA:HA	11:Y:13:ILE:O	2.18	0.43
5:E:131:LEU:HB2	5:E:146:PHE:HB3	2.00	0.43
6:F:91:GLU:HG3	6:F:111:ARG:HH11	1.84	0.43
2:P:119:GLN:O	2:P:122:THR:HB	2.18	0.43
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.49	0.43
13:M:140:PRO:HB3	13:M:165:ILE:HD11	2.00	0.43
14:N:20:THR:HG23	14:N:31:THR:OG1	2.19	0.43
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.54	0.43
10:X:39:SER:HB2	10:X:40:PRO:HD2	2.01	0.43
11:Y:78:ALA:O	11:Y:82:ILE:HG12	2.18	0.43
9:I:189:ILE:HD13	9:I:194:VAL:HG13	2.00	0.43
13:M:16:TYR:CE2	13:M:170:VAL:HG22	2.53	0.43
14:N:176:VAL:HG12	14:N:178:LEU:HD13	2.01	0.43
2:P:149:THR:HG22	2:P:159:TRP:HE1	1.83	0.43
8:V:210:THR:HG21	9:W:167:SER:HB3	2.00	0.43
3:C:160:GLN:NE2	3:C:161:THR:H	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:168:GLY:O	15:H:301[B]:OV1:H23	2.18	0.43
11:K:158:LYS:HB2	11:K:177:LEU:HD11	1.99	0.43
6:T:32:THR:HB	6:T:164:GLY:H	1.84	0.43
13:a:27:LEU:HD11	13:a:34:LEU:HB3	2.01	0.43
5:E:99:ASN:HB2	13:M:94:GLU:HG2	2.01	0.43
13:M:156:ARG:HH11	8:V:165:ASN:HD22	1.67	0.43
1:O:21:ILE:HD11	1:O:122:THR:HG23	2.01	0.43
3:C:101:PRO:HB2	3:C:138:PRO:HG3	2.00	0.43
9:I:87:THR:HG23	9:I:123:PHE:CZ	2.53	0.43
13:a:127:LEU:HG	13:a:142:LEU:HD12	2.00	0.43
3:C:149:GLU:HB2	3:C:150:PRO:HD2	2.01	0.43
6:F:9:SER:HB2	7:G:126:ARG:HB3	2.01	0.43
5:S:38:ARG:NH1	5:S:39:SER:O	2.52	0.43
3:C:202:GLN:O	3:C:203:THR:C	2.62	0.43
4:R:191:LEU:O	4:R:195:ILE:HD12	2.18	0.43
5:S:178:PHE:HA	5:S:181:ILE:HG12	2.01	0.43
10:X:15:LEU:HD12	10:X:43:LEU:HD23	2.01	0.43
4:D:191:LEU:O	4:D:195:ILE:HD12	2.18	0.42
10:J:152:MET:SD	10:J:160:LEU:HD22	2.59	0.42
2:P:218:GLY:HA3	2:P:221:ASP:HB3	2.01	0.42
5:S:131:LEU:HB2	5:S:146:PHE:HB3	2.01	0.42
5:S:197:SER:HA	5:S:200:LEU:HG	2.01	0.42
8:H:34:LEU:HD22	8:H:174:ASP:HB3	2.01	0.42
9:I:94:LEU:HD11	9:I:106:PRO:HG2	2.01	0.42
14:b:176:VAL:HG12	14:b:178:LEU:HD13	2.00	0.42
13:M:27:LEU:HD11	13:M:34:LEU:HB3	2.01	0.42
14:N:26:ILE:HB	13:a:187:ARG:HA	2.01	0.42
8:V:62:ASN:HB3	8:V:82:MET:HE1	2.02	0.42
6:F:39:ASN:C	6:F:39:ASN:HD22	2.28	0.42
9:I:7:ASN:HA	9:I:29:GLY:O	2.19	0.42
11:Y:114:TYR:O	11:Y:121:ARG:HA	2.20	0.42
12:Z:100:LYS:O	12:Z:104:PRO:HA	2.19	0.42
10:J:158:LEU:HD21	10:J:183:ILE:HD11	2.02	0.42
11:K:197:PHE:HZ	11:K:210:VAL:HG21	1.84	0.42
1:O:68:THR:HB	1:O:69:PRO:HD2	2.01	0.42
6:T:63:ILE:HB	6:T:226:PHE:HE2	1.84	0.42
7:U:66:ILE:HG21	7:U:108:LEU:HD21	2.00	0.42
8:V:7:LYS:HG3	8:V:123:TYR:HA	2.00	0.42
11:Y:7:ARG:HD2	11:Y:110:PRO:O	2.19	0.42
11:K:163:ALA:HB1	10:X:142:SER:HB2	2.02	0.42
11:Y:75:SER:HA	11:Y:105:THR:HG21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:99:ASN:HD22	5:E:99:ASN:HA	1.70	0.42
8:V:113:ILE:HG12	8:V:119:THR:HG22	2.02	0.42
3:C:142:GLU:HA	3:C:143:PRO:HD3	1.84	0.42
2:P:70:ASP:HB2	16:P:321:HOH:O	2.19	0.42
7:G:73:VAL:HG12	7:G:133:THR:HB	2.02	0.42
11:K:12:ILE:HB	11:K:180:VAL:HB	2.02	0.42
3:Q:46:ARG:HB2	3:Q:207:ASN:HA	2.00	0.42
16:D:323:HOH:O	12:L:79:HIS:HE1	2.02	0.42
7:G:78:ILE:N	7:G:79:PRO:HD2	2.35	0.42
1:A:115:ALA:HB1	1:A:154:GLY:O	2.20	0.41
4:D:37:GLY:HA2	4:D:145:TYR:CE1	2.54	0.41
11:K:25:TRP:CH2	12:L:144:SER:HA	2.55	0.41
1:O:55:LEU:HD12	7:U:170:THR:HG23	2.00	0.41
4:R:32:ILE:HD12	4:R:192:VAL:HG23	2.01	0.41
4:R:161:ALA:HB3	5:S:55:LEU:HD23	2.01	0.41
8:V:163:ILE:HG23	8:V:170:GLY:HA2	2.02	0.41
8:H:8:PHE:HB3	8:H:151:ALA:HB2	2.01	0.41
1:A:122:THR:HG22	2:B:128:ARG:HE	1.86	0.41
2:B:149:THR:HG22	2:B:159:TRP:HE1	1.85	0.41
2:B:162:ILE:HG13	2:B:163:SER:N	2.35	0.41
9:I:58:ASP:OD1	10:J:93:ARG:NH2	2.54	0.41
11:K:49:ALA:HB2	15:K:301:OV1:H17	2.03	0.41
11:K:114:TYR:O	11:K:121:ARG:HA	2.20	0.41
11:Y:33:LYS:HA	11:Y:45:MET:HE2	2.02	0.41
5:E:68:HIS:HE1	5:E:102:LEU:O	2.03	0.41
13:M:127:LEU:HG	13:M:142:LEU:HD12	2.02	0.41
13:M:129:TYR:HE1	13:M:144:THR:HG22	1.86	0.41
14:N:38:HIS:O	14:N:39:ASP:C	2.64	0.41
2:P:69:ASN:HD22	2:P:69:ASN:HA	1.65	0.41
5:S:6:ASP:OD1	5:S:23:TYR:HE2	2.03	0.41
11:Y:45:MET:HB3	11:Y:52:CYS:HB3	2.02	0.41
1:A:10:THR:O	2:B:128:ARG:HD3	2.20	0.41
6:F:117:GLN:HE21	6:F:117:GLN:HB3	1.73	0.41
6:F:123:ASN:HD22	6:F:124:SER:N	2.19	0.41
9:I:148:MET:SD	12:Z:148:PRO:HB2	2.60	0.41
3:Q:35:LYS:HD3	3:Q:158:SER:HA	2.03	0.41
3:Q:179:ARG:HH22	4:R:52:GLU:HA	1.84	0.41
7:U:117:GLN:O	7:U:120:THR:HB	2.20	0.41
5:E:92:ASN:ND2	12:L:70:ASN:HD21	2.18	0.41
10:X:1:MET:HE1	10:X:135:TYR:H	1.86	0.41
1:A:149:GLN:O	1:A:156:TYR:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:211:ILE:HD11	9:W:38:LYS:HG2	2.03	0.41
13:M:193:ARG:HG3	13:M:214:VAL:HB	2.01	0.41
3:Q:160:GLN:NE2	3:Q:170:ARG:HE	2.14	0.41
13:a:97:ALA:HA	13:a:130:VAL:HG21	2.03	0.41
1:A:28:VAL:HG11	1:A:133:SER:HB2	2.03	0.41
5:E:95:SER:O	5:E:99:ASN:HA	2.21	0.41
12:L:10:GLY:HA2	12:L:26:ASP:OD1	2.21	0.41
3:Q:155:SER:HB2	4:R:51:LEU:HD21	2.02	0.41
9:W:22:ILE:HG12	9:W:42:ILE:HD12	2.03	0.41
3:C:201:VAL:HG11	3:C:207:ASN:HB3	2.03	0.40
14:N:2:SER:OG	14:N:169:SER:HB3	2.21	0.40
5:S:147:GLN:HA	5:S:148:PRO:HD3	1.92	0.40
3:C:160:GLN:HA	3:C:160:GLN:NE2	2.35	0.40
8:H:172:ASN:HD22	8:H:192:THR:HA	1.86	0.40
8:H:84:LYS:HG3	8:H:85:GLN:N	2.36	0.40
10:J:172:MET:HA	10:J:173:PRO:HD3	1.85	0.40
2:P:180:LYS:O	2:P:183:MET:HG3	2.21	0.40
15:V:301:OV1:H37	9:W:124:ASP:HB3	2.02	0.40
8:H:215:GLU:HG3	9:I:197:ARG:HG2	2.04	0.40
9:I:22:ILE:HG12	9:I:42:ILE:HD12	2.02	0.40
8:H:3:ILE:HG22	8:H:16:ALA:HB2	2.04	0.40
15:H:301[A]:OV1:H25	15:H:301[A]:OV1:H11	1.90	0.40
11:K:128:CYS:HB2	11:K:137:TYR:CE1	2.56	0.40
9:W:10:ILE:HG21	9:W:141:ALA:HB3	2.02	0.40
12:Z:207:VAL:HG22	12:Z:212:VAL:HG22	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	248/250 (99%)	242 (98%)	5 (2%)	1 (0%)	30 60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	248/250 (99%)	242 (98%)	6 (2%)	0	100	100
2	B	242/244 (99%)	234 (97%)	8 (3%)	0	100	100
2	P	242/244 (99%)	233 (96%)	7 (3%)	2 (1%)	16	44
3	C	239/241 (99%)	233 (98%)	5 (2%)	1 (0%)	30	60
3	Q	239/241 (99%)	231 (97%)	5 (2%)	3 (1%)	9	31
4	D	240/242 (99%)	234 (98%)	6 (2%)	0	100	100
4	R	240/242 (99%)	231 (96%)	9 (4%)	0	100	100
5	E	231/233 (99%)	223 (96%)	7 (3%)	1 (0%)	30	60
5	S	231/233 (99%)	223 (96%)	7 (3%)	1 (0%)	30	60
6	F	242/244 (99%)	230 (95%)	11 (4%)	1 (0%)	30	60
6	T	242/244 (99%)	232 (96%)	10 (4%)	0	100	100
7	G	241/243 (99%)	235 (98%)	6 (2%)	0	100	100
7	U	241/243 (99%)	236 (98%)	4 (2%)	1 (0%)	30	60
8	H	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
8	V	220/222 (99%)	210 (96%)	9 (4%)	1 (0%)	24	55
9	I	202/204 (99%)	196 (97%)	6 (3%)	0	100	100
9	W	202/204 (99%)	196 (97%)	6 (3%)	0	100	100
10	J	196/198 (99%)	190 (97%)	5 (3%)	1 (0%)	24	55
10	X	196/198 (99%)	190 (97%)	6 (3%)	0	100	100
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	205 (98%)	5 (2%)	0	100	100
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	212 (96%)	8 (4%)	0	100	100
13	M	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
13	a	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
14	N	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
14	b	194/196 (99%)	187 (96%)	6 (3%)	1 (0%)	24	55
All	All	6312/6368 (99%)	6112 (97%)	186 (3%)	14 (0%)	43	72

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	218	GLY

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Mol	Chain	Res	Type
3	Q	207	ASN
5	E	3	ASN
3	Q	202	GLN
7	U	2	GLY
14	b	39	ASP
3	C	203	THR
2	P	50	LYS
3	Q	203	THR
8	V	171	SER
1	A	2	THR
5	S	3	ASN
6	F	243	ILE
10	J	9	VAL

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 X-ray entries followed by that with respect to entries of similar resolution.

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	209/209 (100%)	204 (98%)	5 (2%)	43	77
1	O	209/209 (100%)	202 (97%)	7 (3%)	33	69
2	B	203/203 (100%)	195 (96%)	8 (4%)	28	64
2	P	203/203 (100%)	190 (94%)	13 (6%)	16	44
3	C	213/213 (100%)	203 (95%)	10 (5%)	23	57
3	Q	213/213 (100%)	202 (95%)	11 (5%)	21	53
4	D	198/198 (100%)	188 (95%)	10 (5%)	21	54
4	R	198/198 (100%)	187 (94%)	11 (6%)	19	50
5	E	192/192 (100%)	182 (95%)	10 (5%)	21	53
5	S	192/192 (100%)	179 (93%)	13 (7%)	14	42
6	F	201/201 (100%)	189 (94%)	12 (6%)	17	47
6	T	201/201 (100%)	189 (94%)	12 (6%)	17	47
7	G	207/207 (100%)	199 (96%)	8 (4%)	28	64
7	U	207/207 (100%)	197 (95%)	10 (5%)	23	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	182/181 (101%)	177 (97%)	5 (3%)	39	74
8	V	181/181 (100%)	177 (98%)	4 (2%)	45	78
9	I	172/172 (100%)	168 (98%)	4 (2%)	44	78
9	W	172/172 (100%)	167 (97%)	5 (3%)	37	73
10	J	175/175 (100%)	168 (96%)	7 (4%)	28	63
10	X	175/175 (100%)	166 (95%)	9 (5%)	21	54
11	K	169/169 (100%)	160 (95%)	9 (5%)	20	52
11	Y	169/169 (100%)	159 (94%)	10 (6%)	18	48
12	L	185/185 (100%)	180 (97%)	5 (3%)	39	74
12	Z	185/185 (100%)	180 (97%)	5 (3%)	39	74
13	M	199/199 (100%)	192 (96%)	7 (4%)	32	67
13	a	199/199 (100%)	189 (95%)	10 (5%)	22	54
14	N	162/162 (100%)	156 (96%)	6 (4%)	30	65
14	b	162/162 (100%)	157 (97%)	5 (3%)	35	70
All	All	5333/5332 (100%)	5102 (96%)	231 (4%)	26	60

All (231) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	62	SER
1	A	133	SER
1	A	184	GLU
1	A	209	ILE
2	B	51	VAL
2	B	55	LEU
2	B	60	THR
2	B	65	LEU
2	B	149	THR
2	B	184	LYS
2	B	191	LEU
2	B	200	THR
3	C	4	ARG
3	C	15	ILE
3	C	19	GLU
3	C	40	VAL
3	C	55	THR

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Mol	Chain	Res	Type
3	C	77	ASN
3	C	160	GLN
3	C	169	VAL
3	C	185	THR
3	C	213	VAL
4	D	4	VAL
4	D	20	LEU
4	D	40	LEU
4	D	44	LYS
4	D	59	ILE
4	D	155	THR
4	D	176	LEU
4	D	193	LEU
4	D	214	ILE
4	D	235	LEU
5	E	9	THR
5	E	15	THR
5	E	29	LYS
5	E	59	GLN
5	E	71	LEU
5	E	92	ASN
5	E	188	LEU
5	E	198	GLN
5	E	207	VAL
5	E	227	GLU
6	F	31	THR
6	F	39	ASN
6	F	51	THR
6	F	68	ARG
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	186	ARG
6	F	203	ASN
6	F	221	ASN
6	F	228	LYS
6	F	243	ILE
7	G	83	ASN
7	G	115	LEU
7	G	120	THR
7	G	166	GLN
7	G	182	ILE

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Mol	Chain	Res	Type
7	G	221	LYS
7	G	235	ARG
7	G	236	LEU
8	H	20	SER
8	H	22	GLN
8	H	34	LEU
8	H	56	THR
8	H	68	LEU
9	I	37	ASN
9	I	81	ILE
9	I	171	LEU
9	I	182	TRP
10	J	25	ILE
10	J	36	ARG
10	J	71	GLU
10	J	92	ILE
10	J	110	LYS
10	J	136	SER
10	J	196	GLN
11	K	4	LEU
11	K	41	LEU
11	K	65	LEU
11	K	69	ARG
11	K	73	ARG
11	K	87	VAL
11	K	99	THR
11	K	148	LEU
11	K	209	ASN
12	L	11	THR
12	L	49	ASN
12	L	109	THR
12	L	150	LEU
12	L	172	LEU
13	M	5	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	159	VAL
13	M	170	VAL
13	M	226	LYS
14	N	2	SER
14	N	80	SER

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Mol	Chain	Res	Type
14	N	83	LYS
14	N	105	LYS
14	N	119	VAL
14	N	178	LEU
1	O	2	THR
1	O	30	GLN
1	O	62	SER
1	O	133	SER
1	O	157	PHE
1	O	184	GLU
1	O	209	ILE
2	P	54	THR
2	P	55	LEU
2	P	62	THR
2	P	65	LEU
2	P	69	ASN
2	P	74	VAL
2	P	122	THR
2	P	149	THR
2	P	184	LYS
2	P	191	LEU
2	P	200	THR
2	P	216	ARG
2	P	224	VAL
3	Q	4	ARG
3	Q	15	ILE
3	Q	19	GLU
3	Q	51	LYS
3	Q	61	LYS
3	Q	107	LEU
3	Q	160	GLN
3	Q	169	VAL
3	Q	185	THR
3	Q	206	LYS
3	Q	213	VAL
4	R	4	VAL
4	R	20	LEU
4	R	40	LEU
4	R	59	ILE
4	R	94	TYR
4	R	99	ILE
4	R	176	LEU

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Mol	Chain	Res	Type
4	R	193	LEU
4	R	204	LEU
4	R	214	ILE
4	R	235	LEU
5	S	8	ASP
5	S	9	THR
5	S	29	LYS
5	S	30	GLN
5	S	54	GLU
5	S	59	GLN
5	S	92	ASN
5	S	99	ASN
5	S	174	THR
5	S	196	ILE
5	S	198	GLN
5	S	227	GLU
5	S	231	LYS
6	T	31	THR
6	T	39	ASN
6	T	51	THR
6	T	68	ARG
6	T	117	GLN
6	T	123	ASN
6	T	148	GLU
6	T	172	LEU
6	T	181	GLU
6	T	186	ARG
6	T	203	ASN
6	T	228	LYS
7	U	68	ARG
7	U	83	ASN
7	U	115	LEU
7	U	120	THR
7	U	154	TYR
7	U	182	ILE
7	U	201	MET
7	U	207	THR
7	U	221	LYS
7	U	235	ARG
8	V	25	ILE
8	V	56	THR
8	V	68	LEU

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Mol	Chain	Res	Type
8	V	144	GLN
9	W	37	ASN
9	W	52	ILE
9	W	81	ILE
9	W	171	LEU
9	W	185	VAL
10	X	1	MET
10	X	22	THR
10	X	35	THR
10	X	71	GLU
10	X	92	ILE
10	X	110	LYS
10	X	127	GLU
10	X	174	MET
10	X	183	ILE
11	Y	4	LEU
11	Y	9	GLN
11	Y	65	LEU
11	Y	69	ARG
11	Y	87	VAL
11	Y	99	THR
11	Y	100	MET
11	Y	112	ILE
11	Y	148	LEU
11	Y	209	ASN
12	Z	13	LEU
12	Z	23	LEU
12	Z	108	HIS
12	Z	109	THR
12	Z	150	LEU
13	a	5	ILE
13	a	10	SER
13	a	12	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	159	VAL
13	a	170	VAL
13	a	171	GLN
13	a	213	GLN
14	b	83	LYS
14	b	115	LEU

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Mol	Chain	Res	Type
14	b	119	VAL
14	b	149	GLU
14	b	178	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (198) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	94	HIS
1	A	143	ASN
1	A	149	GLN
2	B	20	GLN
2	B	69	ASN
2	B	93	HIS
2	B	95	GLN
2	B	102	ASN
2	B	119	GLN
2	B	123	GLN
2	B	146	GLN
2	B	155	ASN
2	B	220	ASN
3	C	17	GLN
3	C	77	ASN
3	C	115	GLN
3	C	147	GLN
3	C	160	GLN
3	C	241	GLN
4	D	15	GLN
4	D	91	HIS
4	D	100	ASN
4	D	106	GLN
4	D	146	GLN
4	D	160	ASN
4	D	198	GLN
4	D	217	GLN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	147	GLN

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Mol	Chain	Res	Type
5	E	184	ASN
5	E	198	GLN
5	E	209	ASN
6	F	19	GLN
6	F	39	ASN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	224	HIS
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	167	GLN
7	G	175	ASN
7	G	176	HIS
7	G	186	ASN
8	H	30	ASN
8	H	66	HIS
8	H	144	GLN
8	H	165	ASN
8	H	172	ASN
8	H	189	ASN
8	H	200	GLN
9	I	37	ASN
9	I	88	GLN
9	I	156	ASN
9	I	168	GLN
10	J	37	GLN
10	J	55	GLN
10	J	63	ASN
10	J	78	GLN
10	J	86	GLN
10	J	146	HIS
10	J	191	GLN
11	K	9	GLN
11	K	29	GLN
11	K	85	ASN
11	K	143	ASN
11	K	176	ASN

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Mol	Chain	Res	Type
11	K	208	ASN
12	L	3	ASN
12	L	36	ASN
12	L	49	ASN
12	L	70	ASN
12	L	76	HIS
12	L	79	HIS
12	L	108	HIS
12	L	153	GLN
12	L	158	ASN
12	L	159	GLN
12	L	197	GLN
13	M	2	GLN
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
13	M	171	GLN
13	M	179	ASN
13	M	213	GLN
14	N	60	GLN
14	N	141	ASN
14	N	161	GLN
1	O	30	GLN
1	O	94	HIS
1	O	143	ASN
2	P	20	GLN
2	P	69	ASN
2	P	93	HIS
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	124	HIS
2	P	155	ASN
3	Q	17	GLN
3	Q	77	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
3	Q	165	ASN
3	Q	236	GLN

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Mol	Chain	Res	Type
3	Q	241	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	146	GLN
4	R	160	ASN
4	R	198	GLN
4	R	225	ASN
5	S	30	GLN
5	S	68	HIS
5	S	90	GLN
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	151	ASN
5	S	184	ASN
5	S	198	GLN
6	T	19	GLN
6	T	39	ASN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	140	ASN
6	T	143	HIS
6	T	178	HIS
7	U	6	HIS
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	172	ASN
7	U	175	ASN
7	U	186	ASN
8	V	30	ASN
8	V	66	HIS
8	V	165	ASN
8	V	172	ASN
8	V	189	ASN
8	V	194	ASN
9	W	37	ASN

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Mol	Chain	Res	Type
9	W	44	HIS
9	W	88	GLN
10	X	55	GLN
10	X	63	ASN
10	X	118	GLN
10	X	146	HIS
10	X	147	HIS
10	X	191	GLN
10	X	198	GLN
11	Y	9	GLN
11	Y	24	ASN
11	Y	85	ASN
11	Y	133	GLN
11	Y	143	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	79	HIS
12	Z	80	ASN
12	Z	152	ASN
12	Z	153	GLN
12	Z	158	ASN
12	Z	195	HIS
13	a	2	GLN
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	171	GLN
13	a	179	ASN
13	a	213	GLN
14	b	38	HIS
14	b	69	GLN
14	b	141	ASN
14	b	157	HIS
14	b	161	GLN

5.3.3 RNA ⓘ

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](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	OV1	H	301[A]	8	33,34,34	1.44	7 (21%)	39,44,44	2.08	5 (12%)
15	OV1	Y	301	11	33,34,34	0.63	1 (3%)	39,44,44	1.47	3 (7%)
15	OV1	V	301	8	33,34,34	0.55	0	39,44,44	1.48	2 (5%)
15	OV1	H	301[B]	8	33,34,34	1.56	9 (27%)	39,44,44	1.97	6 (15%)
15	OV1	b	301	14	33,34,34	0.60	1 (3%)	39,44,44	1.18	4 (10%)
15	OV1	N	301	14	33,34,34	0.87	1 (3%)	39,44,44	2.09	5 (12%)
15	OV1	K	301	11	33,34,34	0.64	1 (3%)	39,44,44	1.55	3 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	OV1	H	301[A]	8	-	9/48/48/48	-
15	OV1	Y	301	11	-	16/48/48/48	-
15	OV1	V	301	8	-	11/48/48/48	-
15	OV1	H	301[B]	8	-	10/48/48/48	-
15	OV1	b	301	14	-	17/48/48/48	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	OV1	N	301	14	-	17/48/48/48	-
15	OV1	K	301	11	-	12/48/48/48	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	N	301	OV1	C16-N3	3.55	1.52	1.46
15	H	301[B]	OV1	C6-C10	-2.70	1.46	1.52
15	H	301[A]	OV1	O1-C5	-2.68	1.17	1.23
15	H	301[B]	OV1	O1-C5	-2.68	1.17	1.23
15	H	301[A]	OV1	C24-C22	-2.65	1.50	1.52
15	H	301[A]	OV1	C6-C10	-2.64	1.46	1.52
15	H	301[B]	OV1	C24-C22	-2.55	1.50	1.52
15	H	301[B]	OV1	O2-C10	-2.52	1.18	1.23
15	H	301[A]	OV1	O2-C10	-2.48	1.18	1.23
15	H	301[A]	OV1	C6-N1	-2.44	1.40	1.45
15	H	301[B]	OV1	C6-N1	-2.44	1.40	1.45
15	H	301[B]	OV1	C5-N1	-2.43	1.28	1.34
15	H	301[A]	OV1	C5-N1	-2.37	1.29	1.34
15	H	301[B]	OV1	C13-S1	-2.29	1.70	1.80
15	Y	301	OV1	C13-S1	-2.23	1.70	1.80
15	K	301	OV1	C13-S1	-2.22	1.70	1.80
15	H	301[A]	OV1	O3-C15	-2.20	1.19	1.23
15	H	301[B]	OV1	O3-C15	-2.19	1.19	1.23
15	b	301	OV1	C13-S1	-2.15	1.70	1.80
15	H	301[B]	OV1	O8-S1	-2.08	1.44	1.50

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	N	301	OV1	C25-C16-N3	-9.83	97.58	110.20
15	H	301[A]	OV1	C25-C16-C17	-7.16	100.72	112.18
15	H	301[A]	OV1	C14-S1-C13	6.78	114.41	97.45
15	H	301[B]	OV1	C25-C16-C17	-6.24	102.21	112.18
15	N	301	OV1	C14-S1-C13	6.18	112.91	97.45
15	K	301	OV1	C25-C16-N3	-6.13	102.33	110.20
15	V	301	OV1	C25-C16-N3	-5.94	102.57	110.20
15	H	301[B]	OV1	C14-S1-C13	5.83	112.03	97.45
15	V	301	OV1	C14-S1-C13	5.64	111.56	97.45
15	Y	301	OV1	C25-C16-N3	-5.60	103.01	110.20
15	H	301[A]	OV1	C7-C6-N1	-5.52	98.10	111.44
15	H	301[B]	OV1	C7-C6-N1	-5.36	98.47	111.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	b	301	OV1	C14-S1-C13	4.96	109.86	97.45
15	Y	301	OV1	C14-S1-C13	4.91	109.72	97.45
15	K	301	OV1	C14-S1-C13	4.77	109.38	97.45
15	b	301	OV1	C6-N1-C5	2.79	127.31	121.80
15	H	301[B]	OV1	C25-C16-N3	-2.76	106.66	110.20
15	N	301	OV1	O4-C17-C16	-2.65	102.92	109.28
15	H	301[A]	OV1	O2-C10-C6	-2.50	115.68	120.75
15	N	301	OV1	O4-C17-C22	2.45	114.46	109.79
15	H	301[B]	OV1	O2-C10-C6	-2.32	116.03	120.75
15	K	301	OV1	C23-C22-C24	-2.27	106.86	109.76
15	b	301	OV1	C7-C6-N1	-2.25	106.00	111.44
15	N	301	OV1	C16-N3-C15	2.16	127.01	123.25
15	H	301[A]	OV1	C1-C4-C5	-2.14	107.25	113.19
15	H	301[B]	OV1	C1-C4-C5	-2.12	107.30	113.19
15	b	301	OV1	C25-C16-N3	-2.11	107.48	110.20
15	Y	301	OV1	C25-C16-C17	-2.03	108.93	112.18

There are no chirality outliers.

All (92) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	H	301[A]	OV1	C12-C13-S1-C14
15	H	301[A]	OV1	C17-C22-C24-O7
15	H	301[A]	OV1	C23-C22-C24-O7
15	H	301[B]	OV1	C12-C13-S1-C14
15	H	301[B]	OV1	C16-C17-C22-C24
15	H	301[B]	OV1	C16-C17-C22-C23
15	H	301[B]	OV1	C17-C22-C24-O7
15	H	301[B]	OV1	C23-C22-C24-O7
15	K	301	OV1	C10-C6-C7-C9
15	K	301	OV1	C12-C13-S1-C14
15	K	301	OV1	N3-C16-C25-C26
15	K	301	OV1	C17-C16-C25-C26
15	K	301	OV1	C16-C17-C22-C24
15	K	301	OV1	C16-C17-C22-C23
15	N	301	OV1	C12-C13-S1-C14
15	N	301	OV1	C17-C16-C25-C26
15	N	301	OV1	C16-C17-C22-C24
15	N	301	OV1	C16-C17-C22-C23
15	V	301	OV1	C17-C16-C25-C26
15	V	301	OV1	C16-C17-C22-C24
15	V	301	OV1	C16-C17-C22-C23

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Mol	Chain	Res	Type	Atoms
15	V	301	OV1	C17-C22-C24-O7
15	V	301	OV1	C23-C22-C24-O7
15	Y	301	OV1	N3-C16-C25-C26
15	Y	301	OV1	C17-C16-C25-C26
15	Y	301	OV1	C16-C17-C22-C24
15	Y	301	OV1	C16-C17-C22-C23
15	b	301	OV1	C10-C6-C7-C9
15	b	301	OV1	C12-C13-S1-C14
15	b	301	OV1	C17-C16-C25-C26
15	b	301	OV1	C16-C17-C22-C24
15	b	301	OV1	C16-C17-C22-C23
15	K	301	OV1	N1-C6-C7-C9
15	b	301	OV1	N1-C6-C7-C9
15	N	301	OV1	C10-C6-C7-C9
15	Y	301	OV1	C2-C1-C4-C5
15	N	301	OV1	N1-C6-C7-C9
15	K	301	OV1	C10-C6-C7-C8
15	N	301	OV1	C10-C6-C7-C8
15	b	301	OV1	C10-C6-C7-C8
15	K	301	OV1	N1-C6-C7-C8
15	N	301	OV1	N1-C6-C7-C8
15	b	301	OV1	N1-C6-C7-C8
15	Y	301	OV1	C10-C6-C7-C9
15	H	301[A]	OV1	N2-C11-C12-C13
15	b	301	OV1	O4-C17-C22-C24
15	Y	301	OV1	C4-C1-C2-C3
15	H	301[A]	OV1	C16-C17-C22-C23
15	Y	301	OV1	C10-C6-C7-C8
15	H	301[A]	OV1	O4-C17-C22-C23
15	H	301[B]	OV1	O4-C17-C22-C23
15	K	301	OV1	O4-C17-C22-C24
15	K	301	OV1	O4-C17-C22-C23
15	N	301	OV1	O4-C17-C22-C24
15	N	301	OV1	O4-C17-C22-C23
15	Y	301	OV1	O4-C17-C22-C24
15	Y	301	OV1	O4-C17-C22-C23
15	b	301	OV1	O4-C17-C22-C23
15	H	301[A]	OV1	C12-C13-S1-O8
15	H	301[B]	OV1	C12-C13-S1-O8
15	K	301	OV1	C12-C13-S1-O8
15	N	301	OV1	C12-C13-S1-O8
15	b	301	OV1	C12-C13-S1-O8

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Mol	Chain	Res	Type	Atoms
15	Y	301	OV1	N1-C6-C7-C9
15	N	301	OV1	N3-C16-C25-C26
15	V	301	OV1	N3-C16-C25-C26
15	b	301	OV1	N3-C16-C25-C26
15	V	301	OV1	O4-C17-C22-C23
15	N	301	OV1	C1-C4-C5-O1
15	b	301	OV1	O3-C15-N3-C16
15	N	301	OV1	C1-C2-C3-C29
15	H	301[A]	OV1	C16-C17-C22-C24
15	N	301	OV1	C1-C4-C5-N1
15	H	301[A]	OV1	C11-C12-C13-S1
15	H	301[B]	OV1	C11-C12-C13-S1
15	V	301	OV1	C11-C12-C13-S1
15	Y	301	OV1	N1-C6-C7-C8
15	H	301[B]	OV1	N2-C11-C12-C13
15	H	301[B]	OV1	O4-C17-C22-C24
15	V	301	OV1	C12-C13-S1-C14
15	Y	301	OV1	C1-C2-C3-C29
15	b	301	OV1	N2-C11-C15-O3
15	Y	301	OV1	C15-C11-C12-C13
15	V	301	OV1	O4-C17-C22-C24
15	b	301	OV1	C4-C1-C2-C3
15	b	301	OV1	N2-C11-C15-N3
15	N	301	OV1	N2-C11-C15-O3
15	Y	301	OV1	C12-C13-S1-C14
15	V	301	OV1	N2-C11-C15-O3
15	Y	301	OV1	C16-C25-C26-C28
15	N	301	OV1	N2-C11-C15-N3
15	b	301	OV1	C11-C15-N3-C16

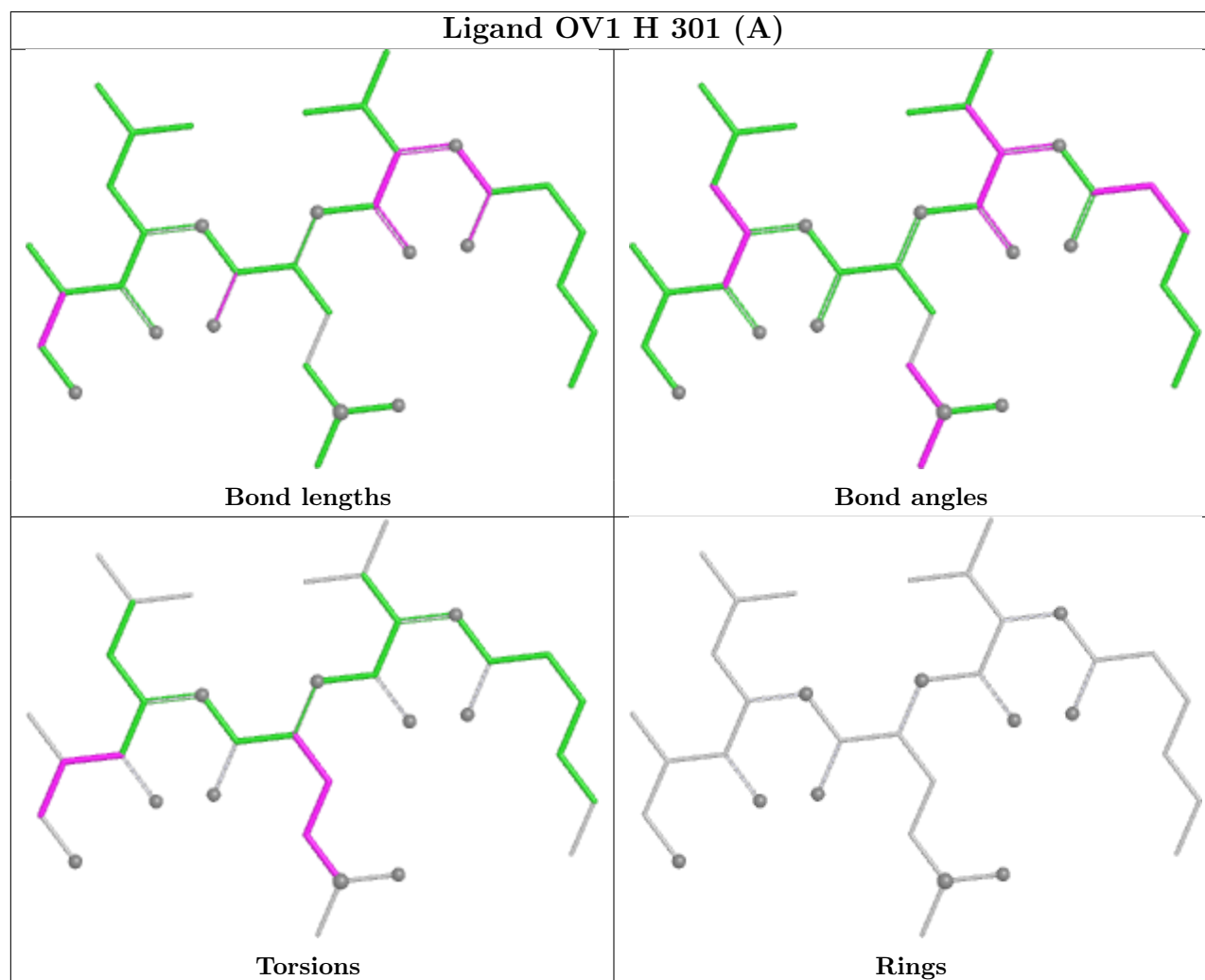
There are no ring outliers.

6 monomers are involved in 12 short contacts:

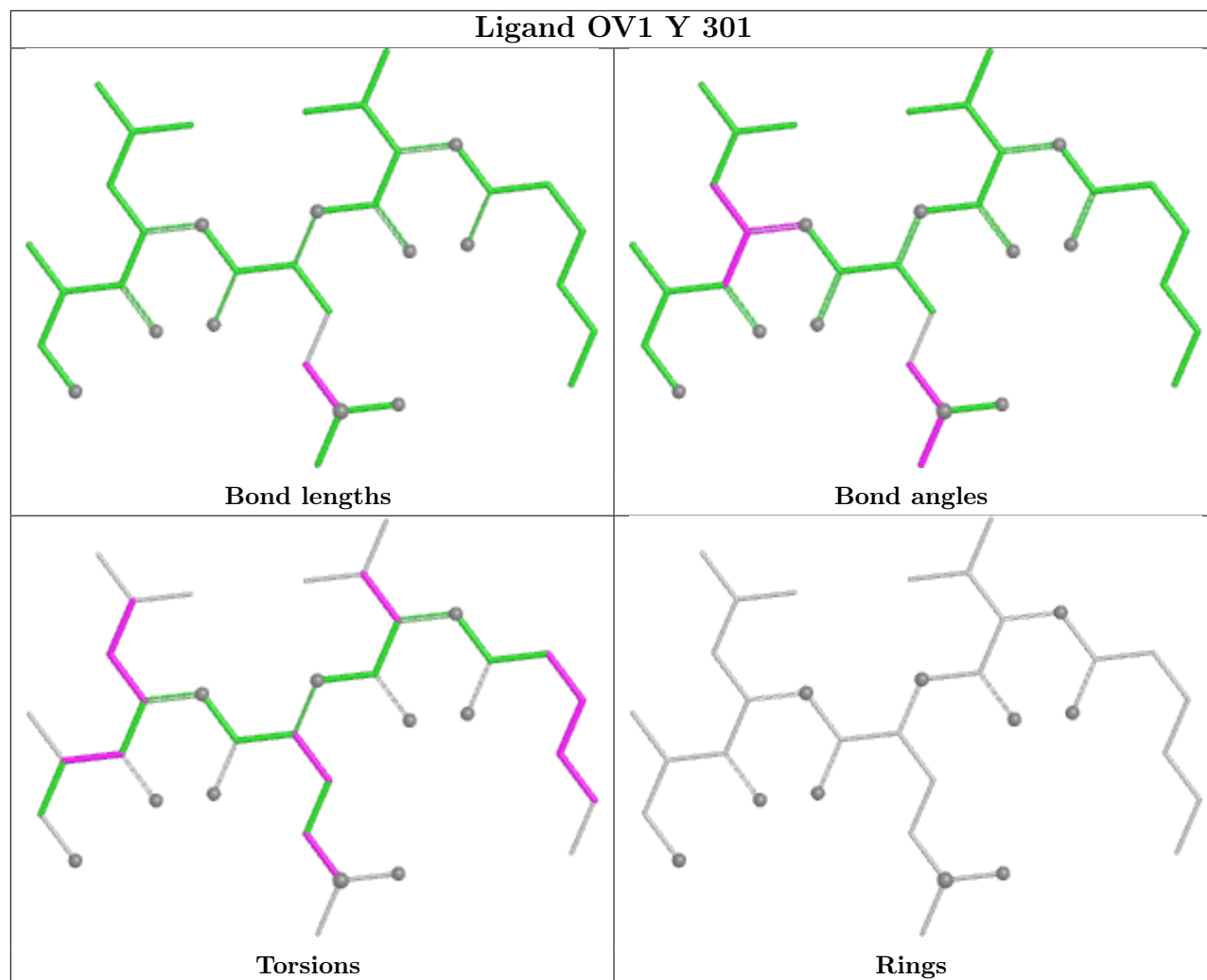
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	H	301[A]	OV1	2	0
15	Y	301	OV1	1	0
15	V	301	OV1	2	0
15	H	301[B]	OV1	1	0
15	b	301	OV1	4	0
15	K	301	OV1	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

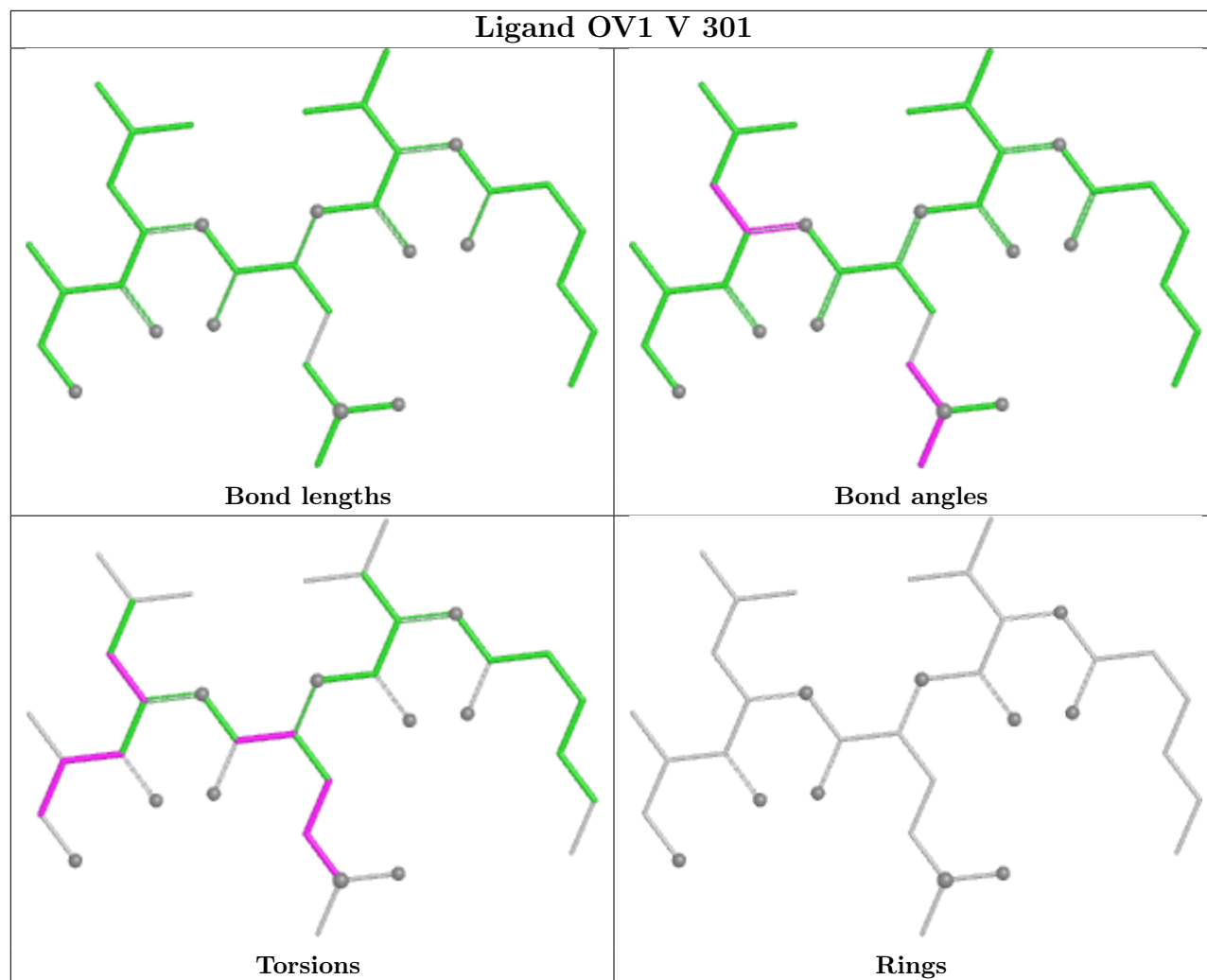
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within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



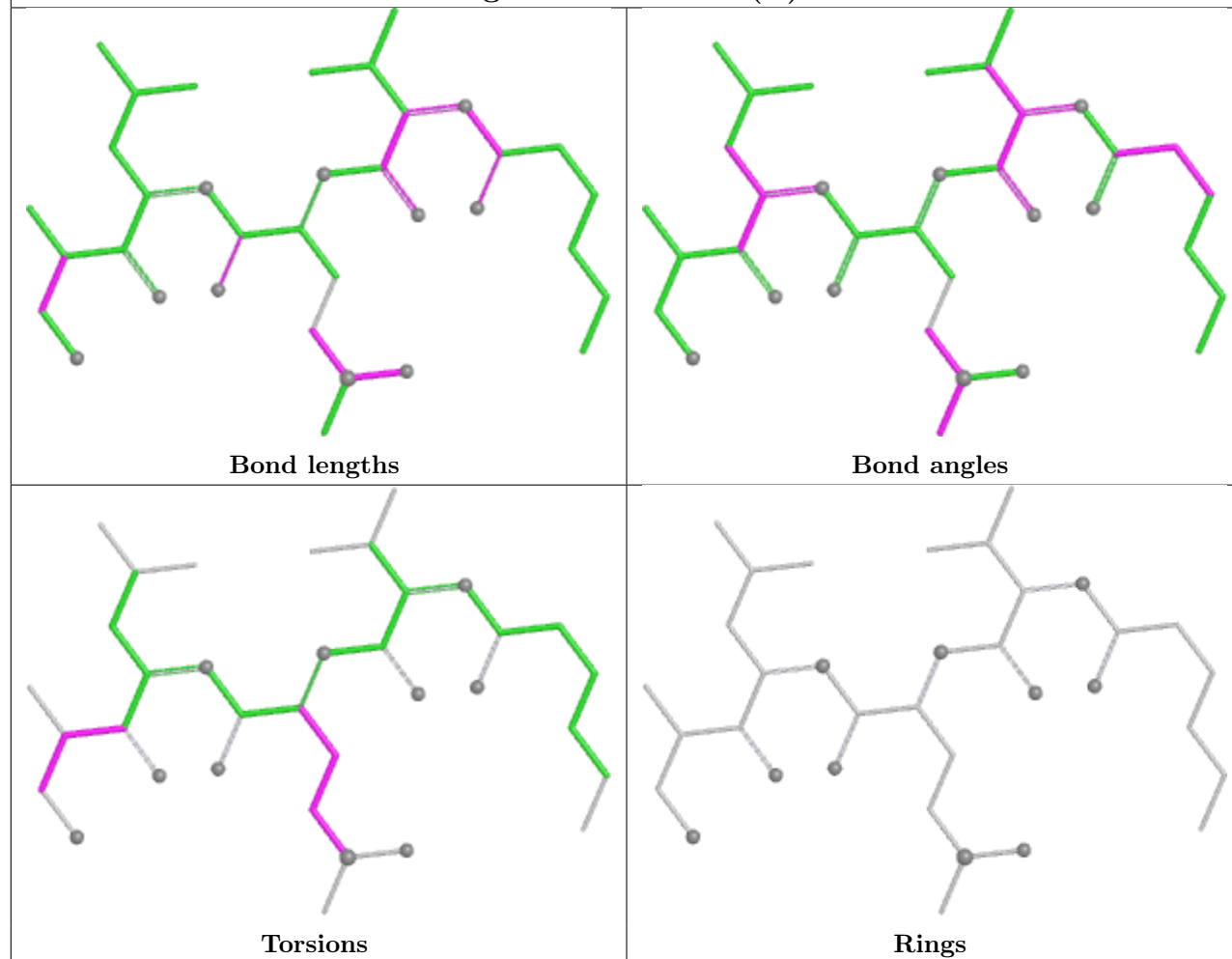
Ligand OV1 Y 301



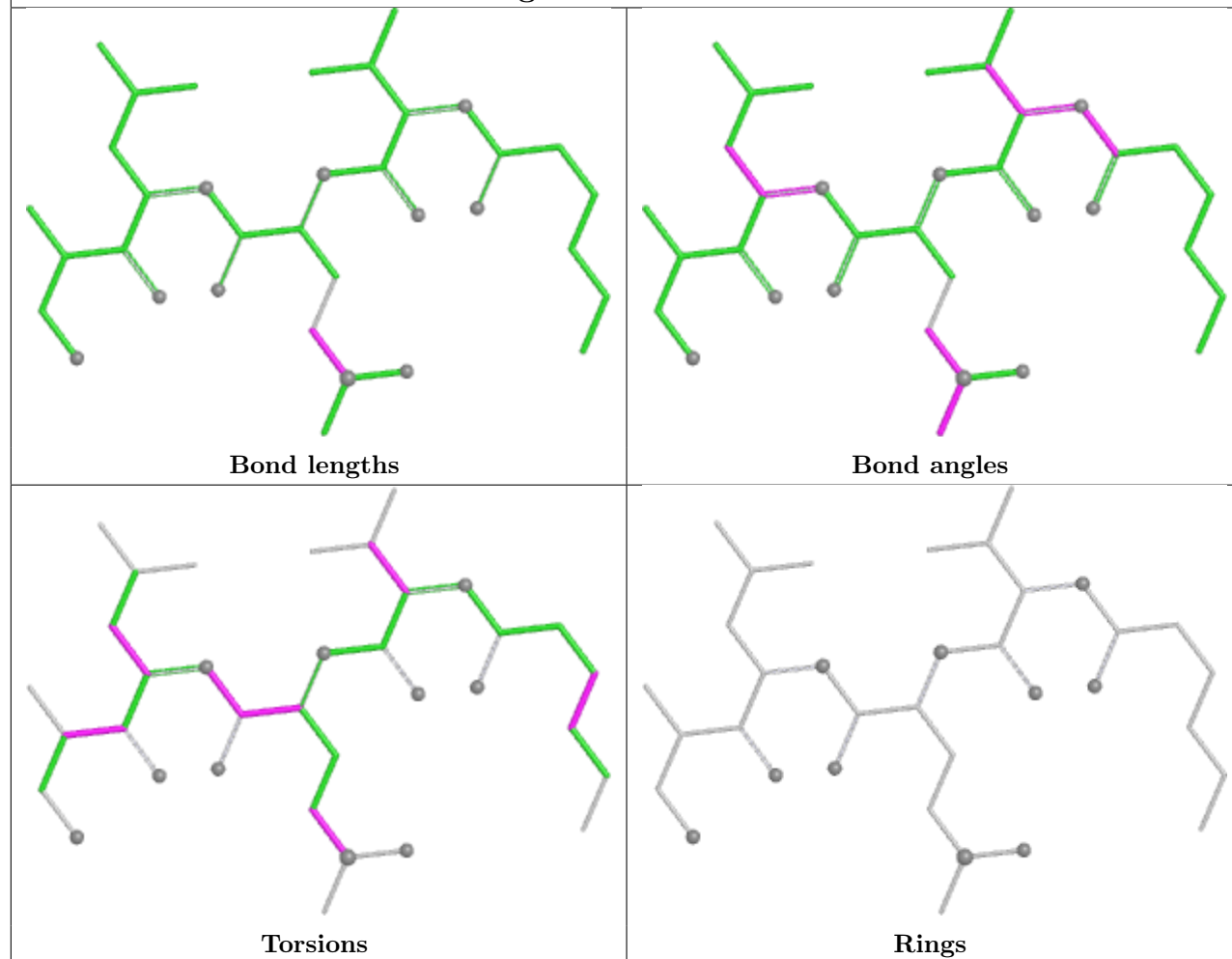
Ligand OV1 V 301



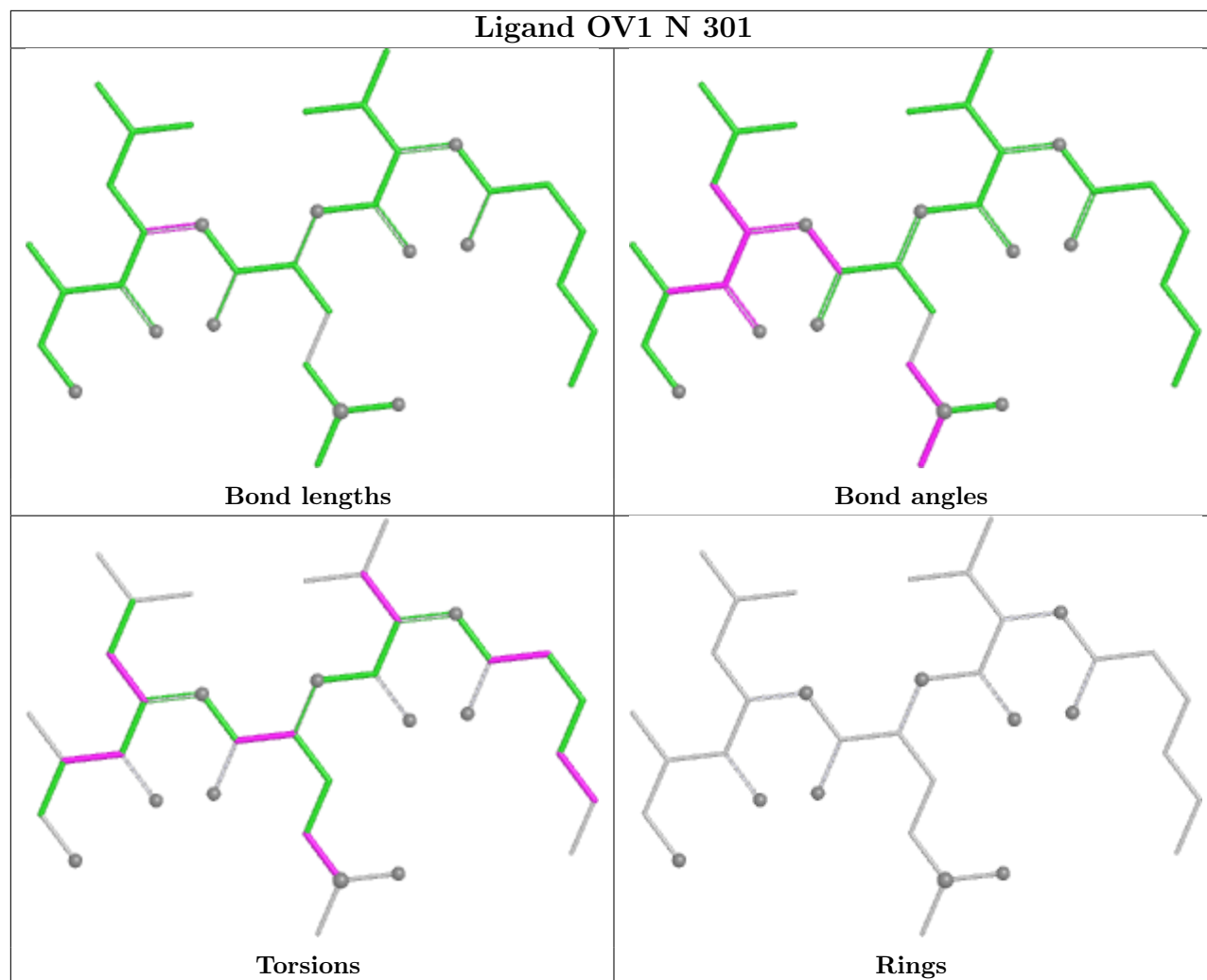
Ligand OV1 H 301 (B)

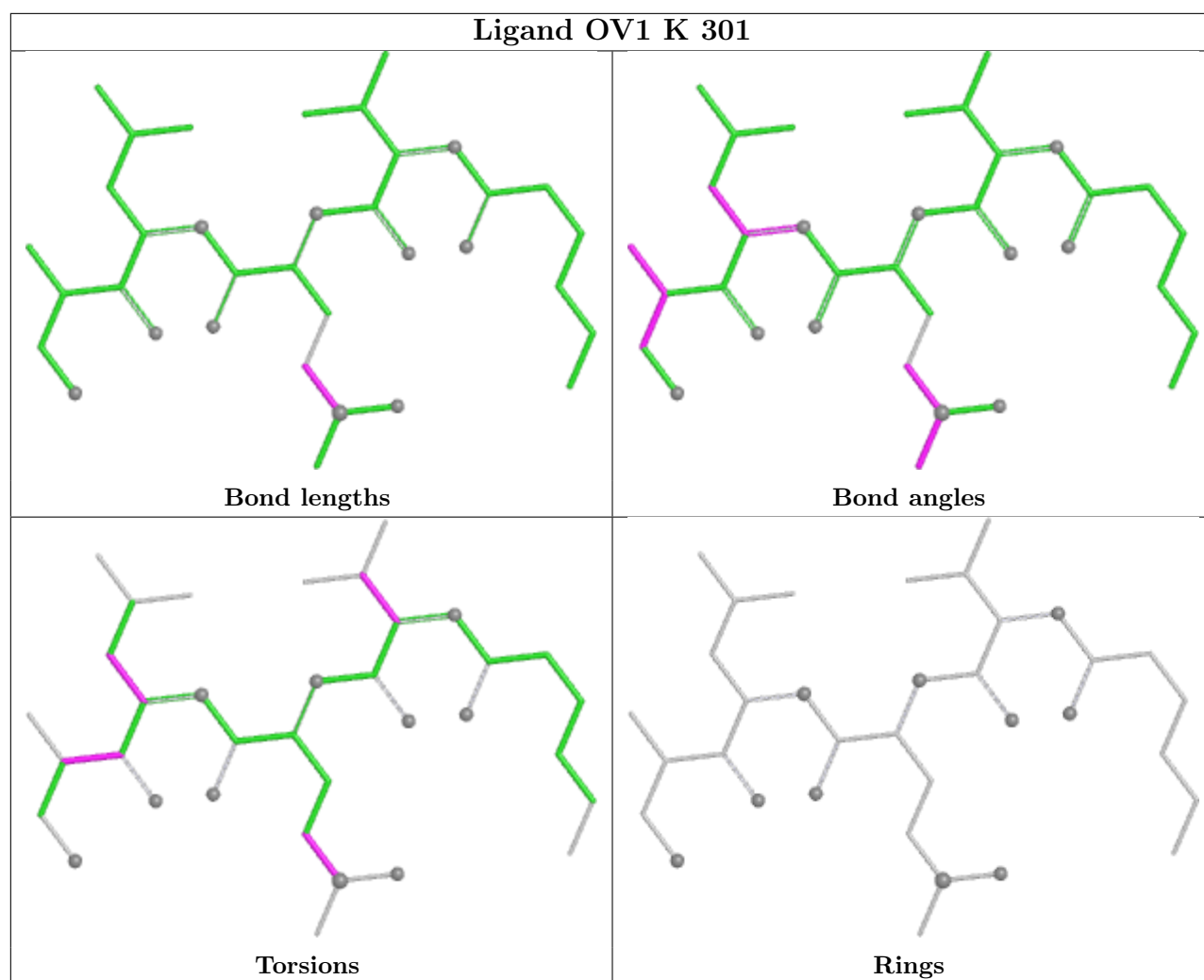


Ligand OV1 b 301



Ligand OV1 N 301





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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	250/250 (100%)	-0.03	6 (2%) 59 49	44, 60, 86, 101	0
1	O	250/250 (100%)	0.01	4 (1%) 70 61	48, 64, 91, 106	0
2	B	244/244 (100%)	0.08	6 (2%) 58 48	45, 60, 90, 99	0
2	P	244/244 (100%)	0.19	9 (3%) 45 36	51, 65, 89, 104	0
3	C	241/241 (100%)	0.20	10 (4%) 41 33	45, 64, 102, 132	0
3	Q	241/241 (100%)	0.38	15 (6%) 26 20	52, 77, 116, 148	0
4	D	242/242 (100%)	0.11	11 (4%) 38 30	49, 64, 87, 110	0
4	R	242/242 (100%)	0.24	9 (3%) 45 36	54, 69, 94, 116	0
5	E	233/233 (100%)	0.11	4 (1%) 69 60	52, 69, 96, 104	0
5	S	233/233 (100%)	0.32	6 (2%) 57 47	48, 74, 101, 108	0
6	F	244/244 (100%)	0.06	1 (0%) 88 84	47, 66, 94, 116	0
6	T	244/244 (100%)	0.06	4 (1%) 70 61	49, 66, 93, 114	0
7	G	243/243 (100%)	-0.01	2 (0%) 82 75	45, 62, 88, 108	0
7	U	243/243 (100%)	-0.04	3 (1%) 76 68	48, 62, 83, 102	0
8	H	222/222 (100%)	-0.15	2 (0%) 81 74	25, 54, 72, 92	1 (0%)
8	V	222/222 (100%)	-0.18	3 (1%) 73 64	41, 54, 72, 96	0
9	I	204/204 (100%)	-0.17	1 (0%) 87 82	41, 52, 72, 77	0
9	W	204/204 (100%)	-0.20	2 (0%) 79 72	43, 53, 72, 77	0
10	J	198/198 (100%)	-0.06	3 (1%) 72 63	40, 53, 72, 89	0
10	X	198/198 (100%)	-0.12	3 (1%) 72 63	45, 57, 74, 90	0
11	K	212/212 (100%)	-0.27	1 (0%) 87 82	39, 51, 71, 78	0
11	Y	212/212 (100%)	-0.21	1 (0%) 87 82	44, 54, 75, 83	0
12	L	222/222 (100%)	-0.25	1 (0%) 87 82	40, 54, 70, 80	0
12	Z	222/222 (100%)	-0.26	1 (0%) 87 82	41, 56, 74, 85	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/233 (100%)	-0.22	1 (0%) 88 84	42, 56, 71, 77	0
13	a	233/233 (100%)	-0.28	1 (0%) 88 84	40, 54, 68, 73	0
14	N	196/196 (100%)	-0.28	0 100 100	42, 52, 71, 80	0
14	b	196/196 (100%)	-0.24	0 100 100	42, 51, 71, 77	0
All	All	6368/6368 (100%)	-0.03	110 (1%) 69 60	25, 59, 91, 148	1 (0%)

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	Q	50	LEU	6.6
4	R	119	ALA	5.8
4	R	120	SER	5.4
2	B	51	VAL	5.2
4	R	125	LEU	5.0
2	B	1	GLY	5.0
4	D	125	LEU	4.8
4	D	119	ALA	4.8
10	J	197	ALA	4.7
3	C	50	LEU	4.6
4	R	121	GLY	4.5
4	D	120	SER	4.4
1	A	1	MET	4.3
1	O	1	MET	4.2
4	D	124	ARG	4.2
2	P	50	LYS	4.2
13	a	1	THR	4.1
2	P	219	ALA	4.0
2	P	1	GLY	3.9
3	Q	205	ALA	3.9
10	X	197	ALA	3.8
3	Q	52	LEU	3.8
4	D	118	GLY	3.8
10	J	1	MET	3.8
3	C	206	LYS	3.7
5	S	6	ASP	3.6
3	C	205	ALA	3.6
5	S	202	ASP	3.5
8	H	222	ASP	3.4
7	U	1	ALA	3.3
5	E	202	ASP	3.3
2	P	51	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
10	J	198	GLN	3.1
2	P	220	ASN	3.1
2	B	244	THR	3.1
3	Q	49	THR	3.0
3	Q	55	THR	3.0
12	Z	108	HIS	3.0
4	R	118	GLY	3.0
3	Q	204	GLY	3.0
5	E	1	PHE	2.9
3	Q	51	LYS	2.9
3	C	203	THR	2.9
6	F	202	ASP	2.8
3	Q	59	PRO	2.8
7	U	243	ASP	2.8
4	D	121	GLY	2.8
3	C	241	GLN	2.8
3	Q	47	ARG	2.8
3	Q	53	GLN	2.8
8	V	220	ILE	2.8
3	Q	60	SER	2.8
8	V	221	CYS	2.7
7	G	1	ALA	2.7
3	C	52	LEU	2.7
2	P	244	THR	2.7
6	T	2	THR	2.7
2	P	61	SER	2.7
1	O	52	SER	2.7
4	D	27	SER	2.7
8	H	221	CYS	2.7
8	V	222	ASP	2.7
4	D	122	GLU	2.6
12	L	172	LEU	2.6
1	O	2	THR	2.6
1	A	249	ALA	2.6
5	S	1	PHE	2.6
3	C	49	THR	2.6
6	T	1	GLY	2.6
4	R	124	ARG	2.5
1	O	62	SER	2.5
11	K	212	GLY	2.5
3	Q	241	GLN	2.5
4	D	6	THR	2.5

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Mol	Chain	Res	Type	RSRZ
5	S	225	ASP	2.4
3	C	239	GLN	2.4
11	Y	212	GLY	2.4
9	I	192	ASP	2.4
4	D	5	SER	2.4
4	R	94	TYR	2.4
3	Q	58	THR	2.4
10	X	196	GLN	2.3
7	G	2	GLY	2.3
1	A	201	GLU	2.3
1	A	29	LYS	2.3
3	C	44	CYS	2.2
2	B	62	THR	2.2
2	B	7	SER	2.2
4	R	113	LEU	2.2
10	X	198	GLN	2.2
4	D	241	ALA	2.2
2	P	60	THR	2.2
5	S	2	ARG	2.1
2	B	220	ASN	2.1
5	E	209	ASN	2.1
1	A	2	THR	2.1
2	P	218	GLY	2.1
3	C	204	GLY	2.1
7	U	2	GLY	2.1
13	M	1	THR	2.1
5	S	204	SER	2.1
3	Q	203	THR	2.1
9	W	130	ASP	2.1
5	E	233	ILE	2.1
9	W	131	GLU	2.1
3	Q	206	LYS	2.0
1	A	52	SER	2.0
6	T	9	SER	2.0
6	T	51	THR	2.0
4	R	122	GLU	2.0

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

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

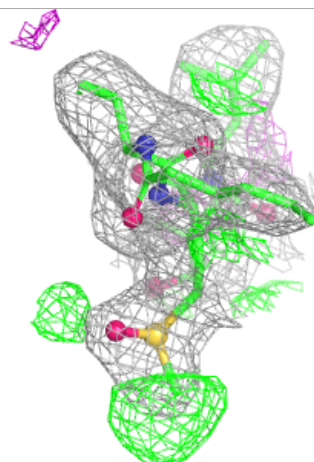
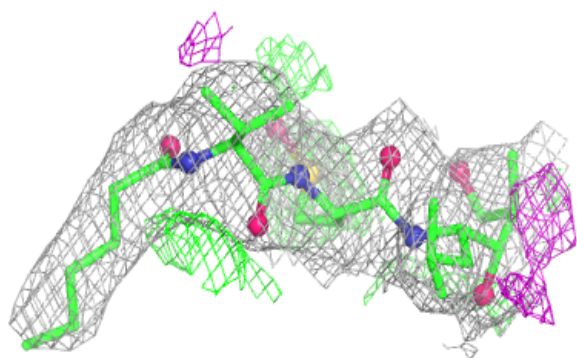
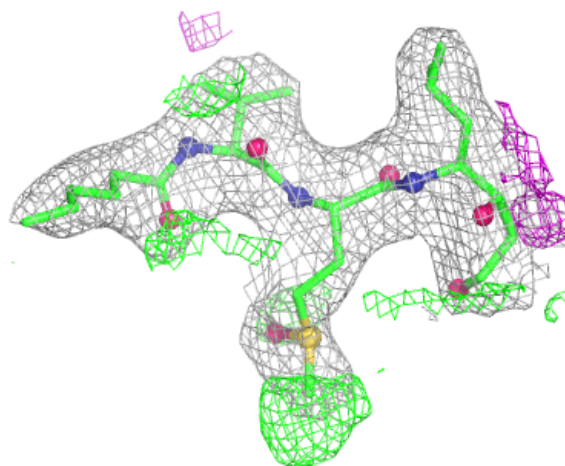
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	OV1	H	301[A]	35/35	0.84	0.15	49,50,54,55	35
15	OV1	H	301[B]	35/35	0.84	0.15	41,44,48,49	35
15	OV1	N	301	35/35	0.88	0.15	46,52,61,62	0
15	OV1	b	301	35/35	0.90	0.13	46,51,60,62	0
15	OV1	V	301	35/35	0.91	0.14	51,53,63,64	0
15	OV1	K	301	35/35	0.92	0.11	42,47,56,58	0
15	OV1	Y	301	35/35	0.94	0.10	45,49,59,59	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

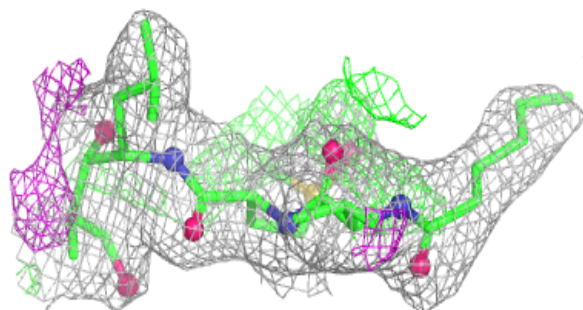
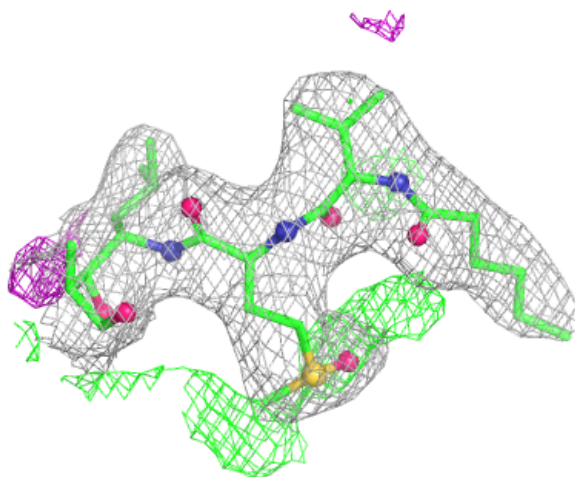
Electron density around OV1 H 301 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



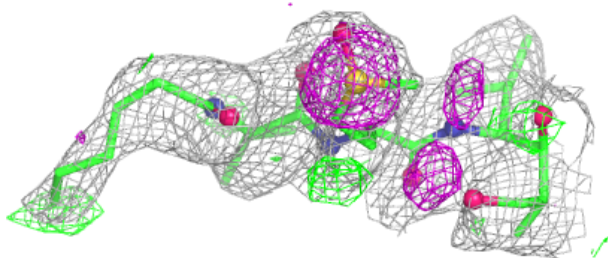
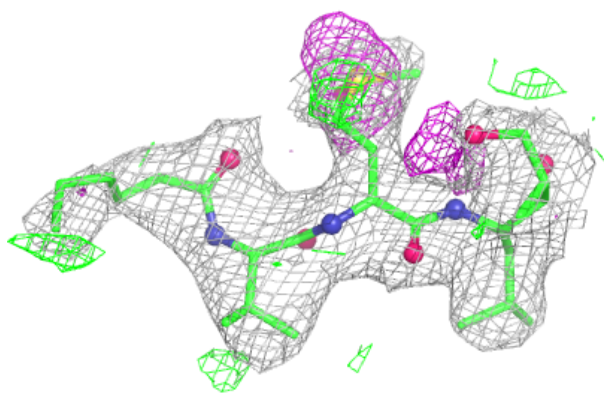
Electron density around OV1 H 301 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

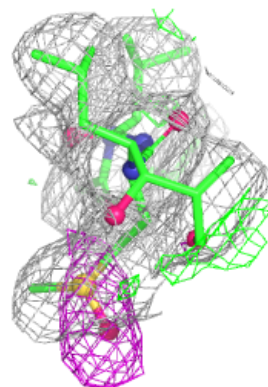
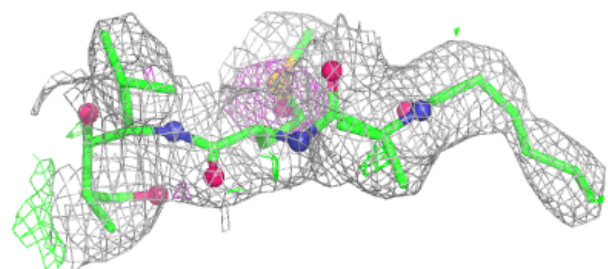
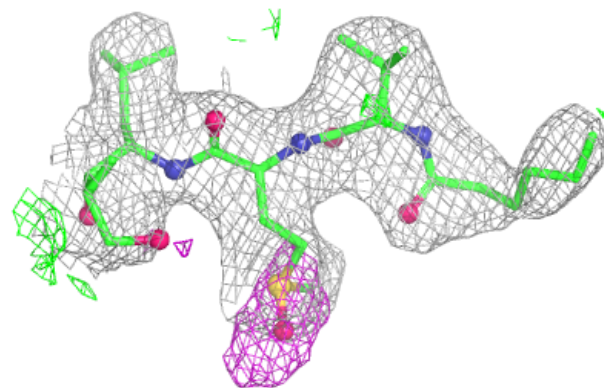


Electron density around OV1 N 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

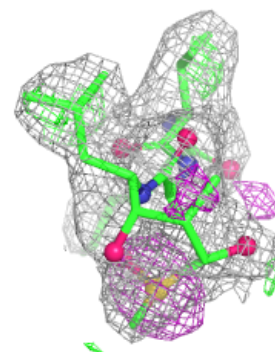
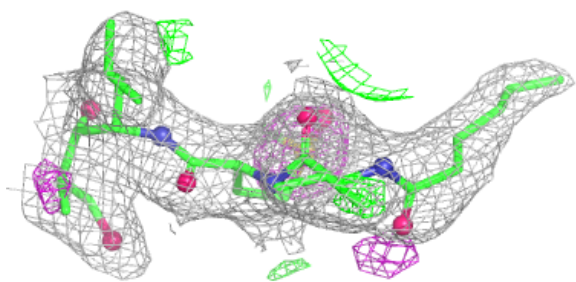
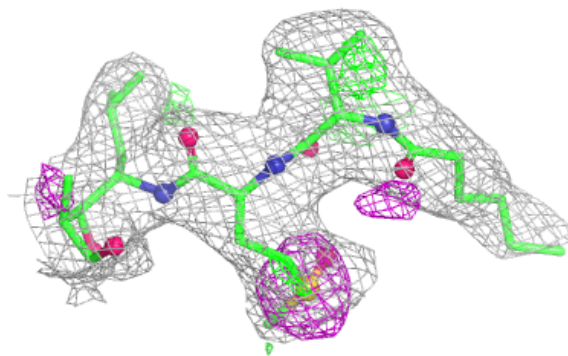
**Electron density around OV1 b 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

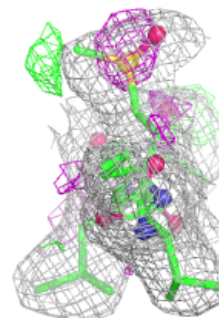
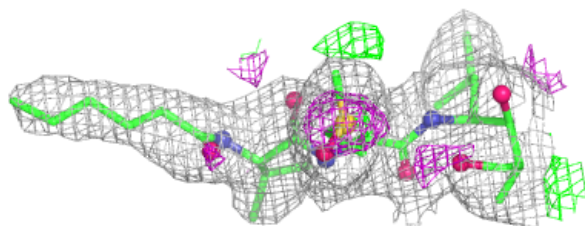
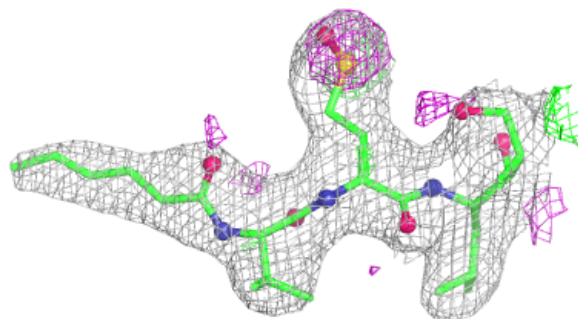


Electron density around OV1 V 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

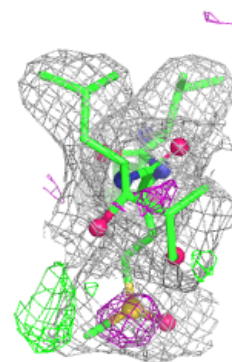
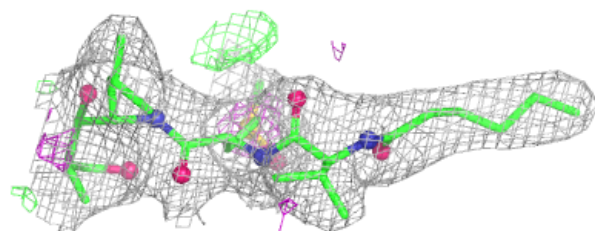
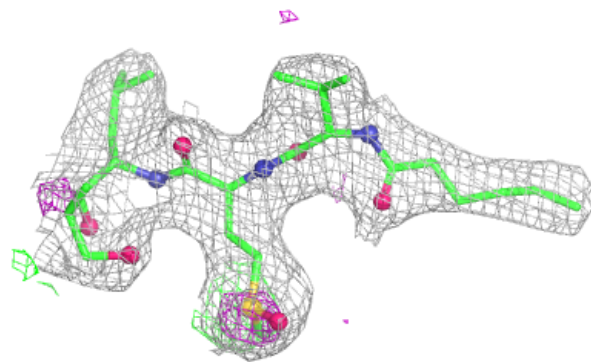
**Electron density around OV1 K 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around OV1 Y 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.