



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:21 AM UTC

PDB ID : 1J2Q / pdb_00001j2q
Title : 20S proteasome in complex with calpain-Inhibitor I from archaeoglobus fulgidus
Authors : Groll, M.; Brandstetter, H.; Bartunik, H.; Bourenkow, G.; Huber, R.
Deposited on : 2003-01-08
Resolution : 2.83 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

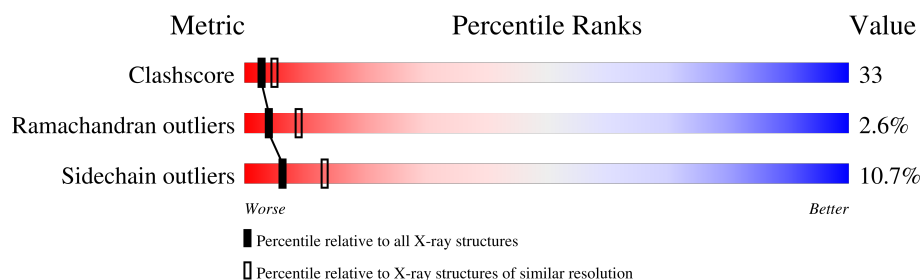
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.83 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))
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)

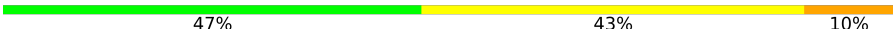
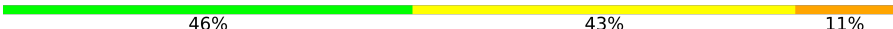
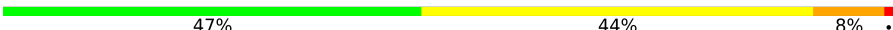
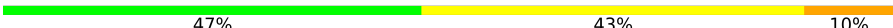
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	237	43% 50% 7%
1	B	237	42% 50% 7%
1	C	237	45% 48% 7%
1	D	237	46% 46% 8%
1	E	237	45% 47% 8%
1	F	237	44% 47% 8%
1	G	237	43% 49% 8%
2	H	202	42% 48% 10%

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Mol	Chain	Length	Quality of chain
2	I	202	 44% 45% 11%
2	J	202	 47% 43% 10%
2	K	202	 46% 43% 11%
2	L	202	 49% 42% 8% .
2	M	202	 47% 44% 8% .
2	N	202	 47% 43% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 24227 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.

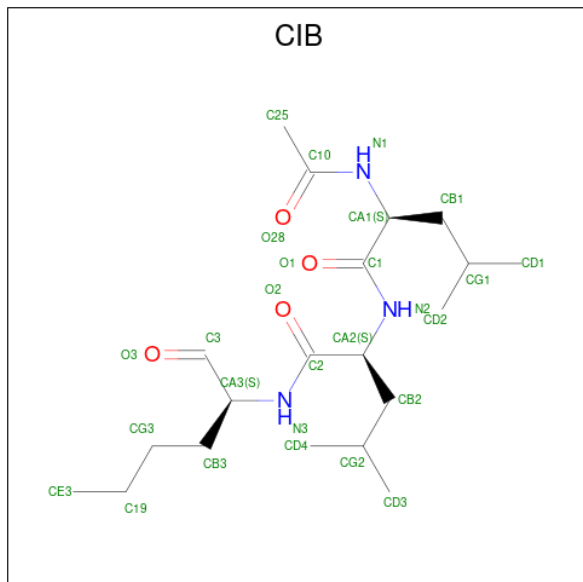
- Molecule 1 is a protein called Proteasome alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	B	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	C	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	D	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	E	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	F	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			
1	G	237	Total	C	N	O	S	45	0	0
			1866	1186	315	359	6			

- Molecule 2 is a protein called Proteasome beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	I	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	J	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	K	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	L	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	M	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			
2	N	202	Total	C	N	O	S	19	0	0
			1553	982	260	305	6			

- Molecule 3 is 2-ACETYLAMINO-4-METHYL-PENTANOIC ACID [1-(1-FORMYL-PENTYL CARBAMOYL)-3-METHYL-BUTYL]-AMIDE (CCD ID: CIB) (formula: $C_{20}H_{37}N_3O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total	C	N	O	0	0
			27	20	3	4		
3	I	1	Total	C	N	O	0	0
			27	20	3	4		
3	J	1	Total	C	N	O	0	0
			27	20	3	4		
3	K	1	Total	C	N	O	0	0
			27	20	3	4		
3	L	1	Total	C	N	O	0	0
			27	20	3	4		
3	M	1	Total	C	N	O	0	0
			27	20	3	4		
3	N	1	Total	C	N	O	0	0
			27	20	3	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	O	0	0
			4	4		
4	B	7	Total	O	0	0
			7	7		
4	C	9	Total	O	0	0
			9	9		

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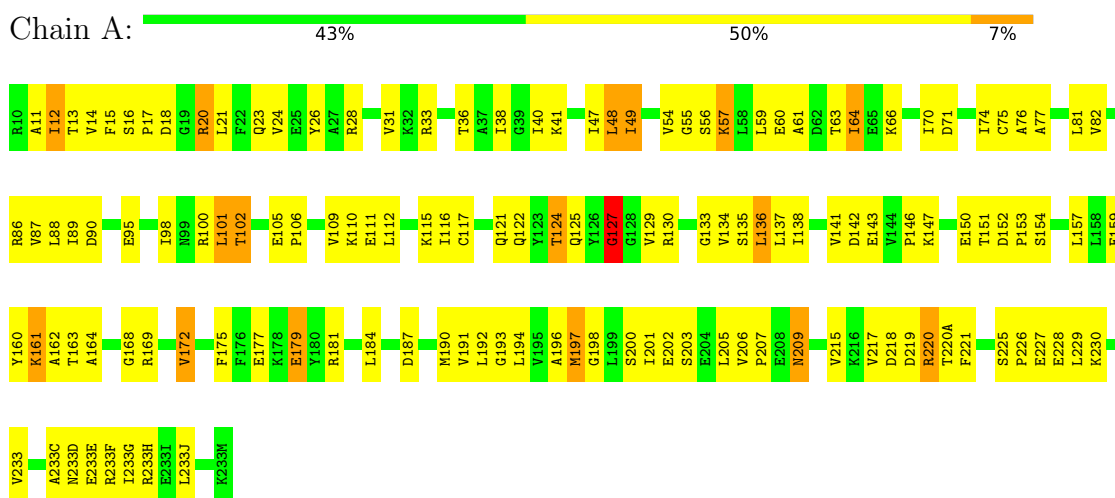
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	4	Total 4	O 4	0	0
4	E	7	Total 7	O 7	0	0
4	F	5	Total 5	O 5	0	0
4	G	5	Total 5	O 5	0	0
4	H	13	Total 13	O 13	0	0
4	I	14	Total 14	O 14	0	0
4	J	5	Total 5	O 5	0	0
4	K	7	Total 7	O 7	0	0
4	L	6	Total 6	O 6	0	0
4	M	12	Total 12	O 12	0	0
4	N	7	Total 7	O 7	0	0

3 Residue-property plots [i](#)

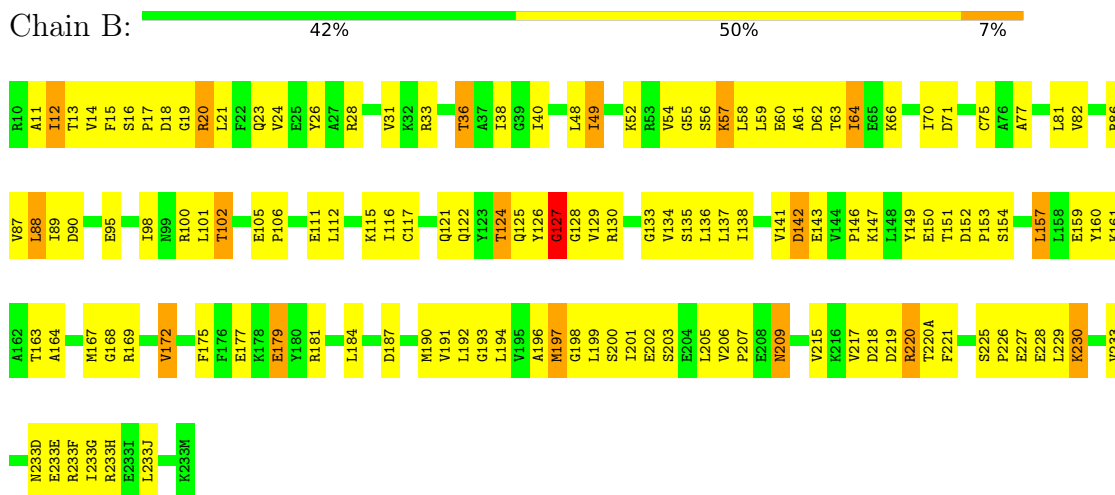
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

- Molecule 1: Proteasome alpha subunit

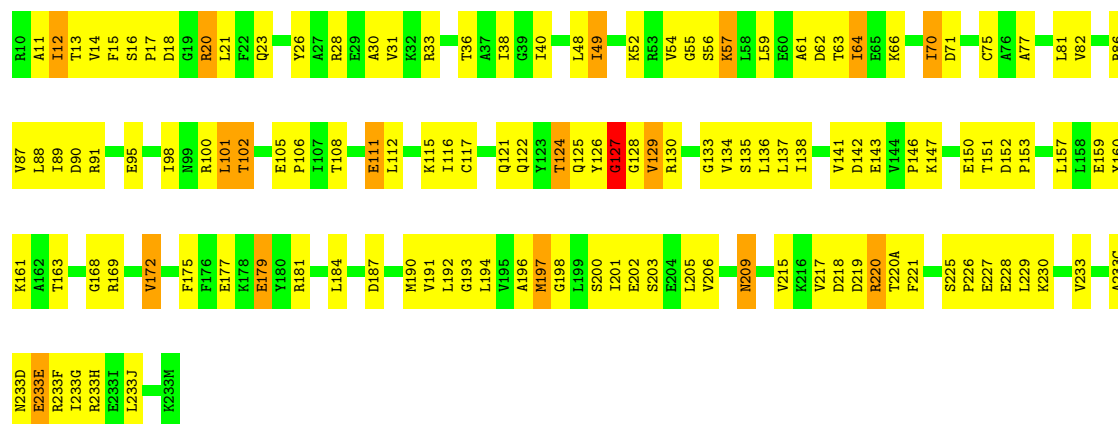


- Molecule 1: Proteasome alpha subunit



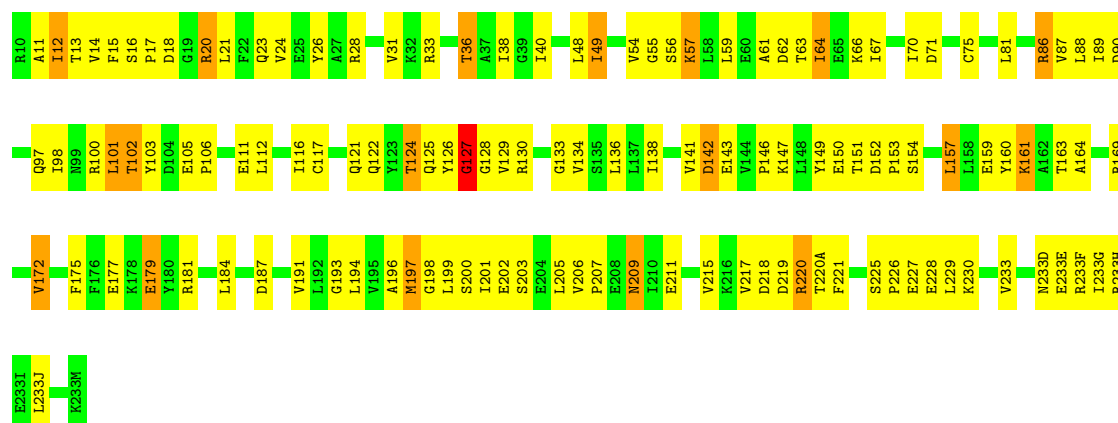
- Molecule 1: Proteasome alpha subunit





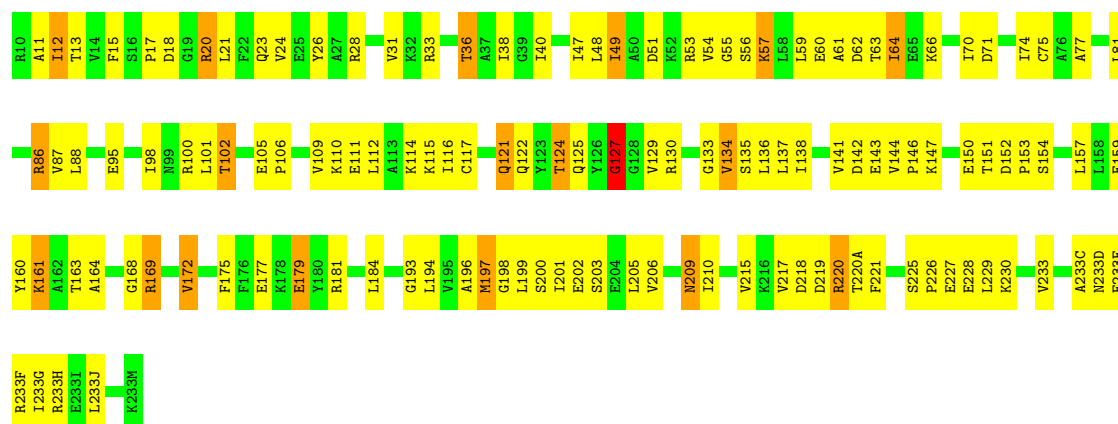
• Molecule 1: Proteasome subunit

Chain D: 46% 46% 8%



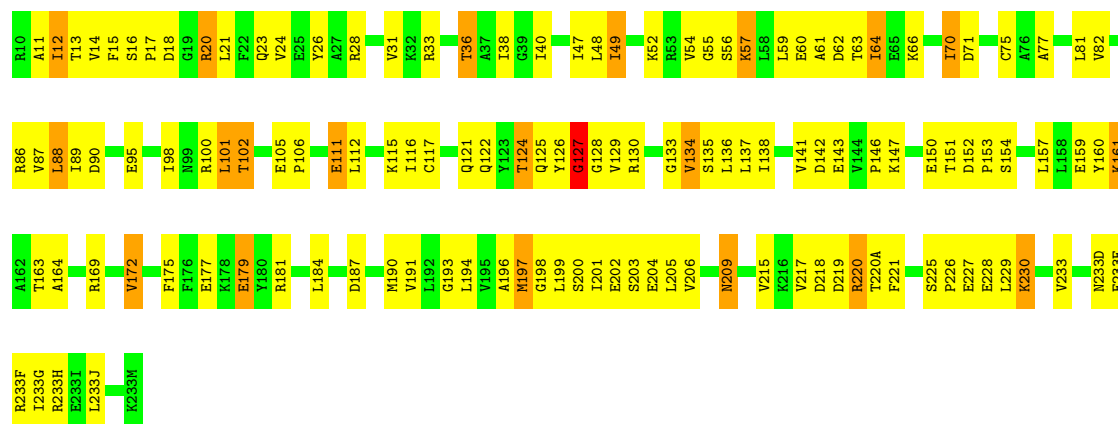
• Molecule 1: Proteasome subunit

Chain E: 45% 47% 8%



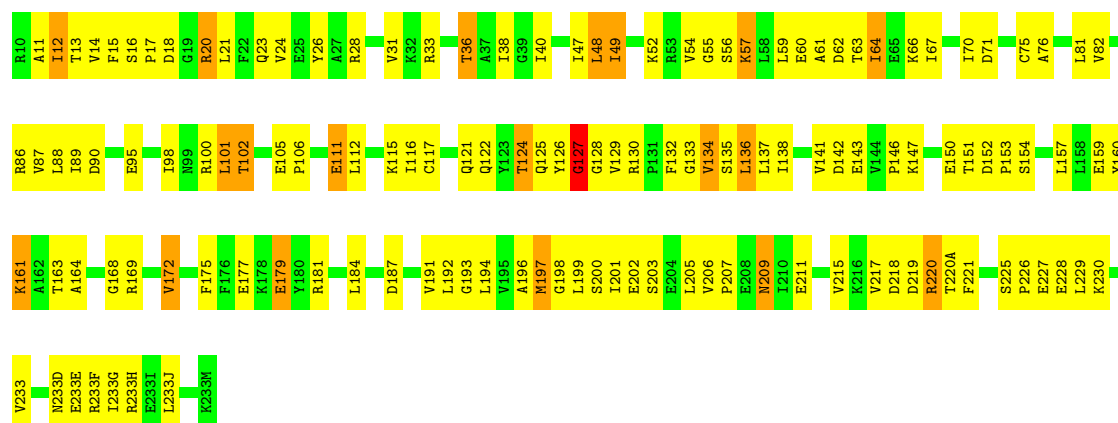
• Molecule 1: Proteasome subunit

Chain F: 44% 47% 8%



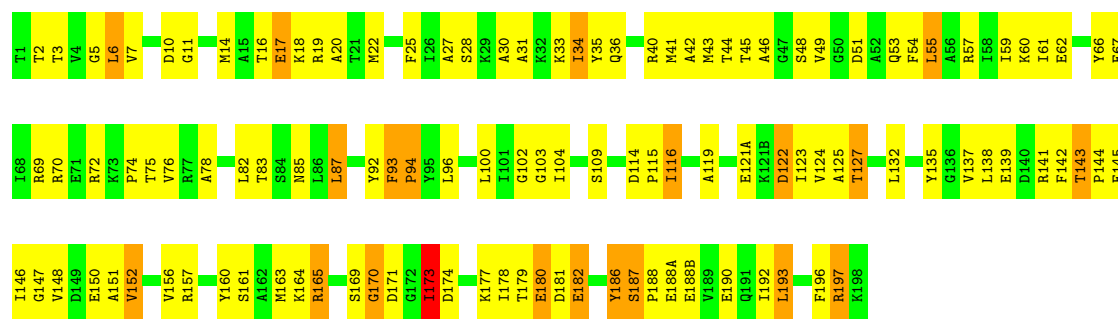
• Molecule 1: Proteasome alpha subunit

Chain G: 43% 49% 8%



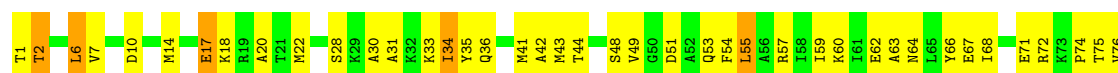
• Molecule 2: Proteasome beta subunit

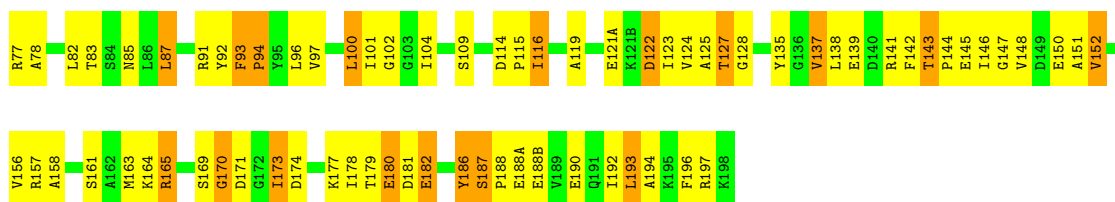
Chain H: 42% 48% 10%



• Molecule 2: Proteasome beta subunit

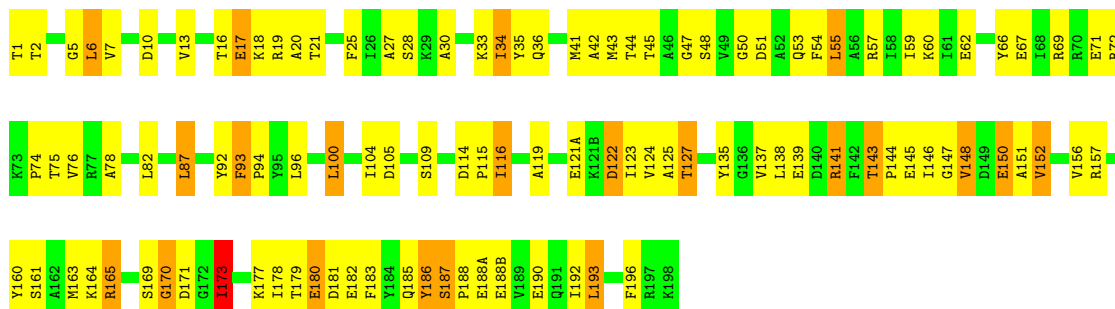
Chain I: 44% 45% 11%





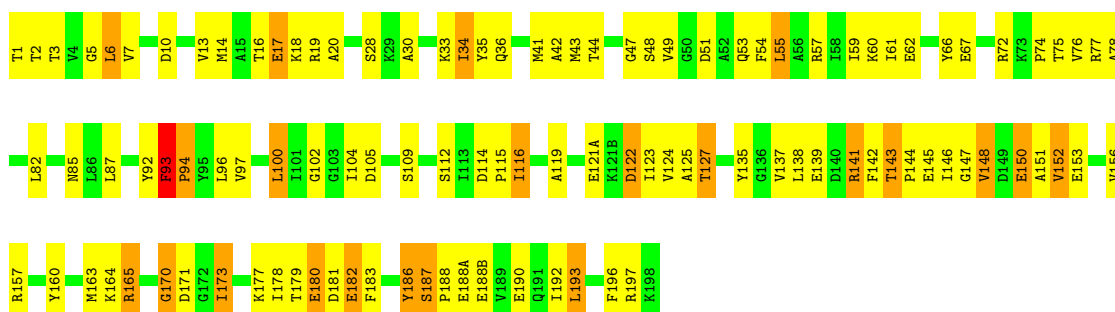
• Molecule 2: Proteasome beta subunit

Chain J: 47% 43% 10%



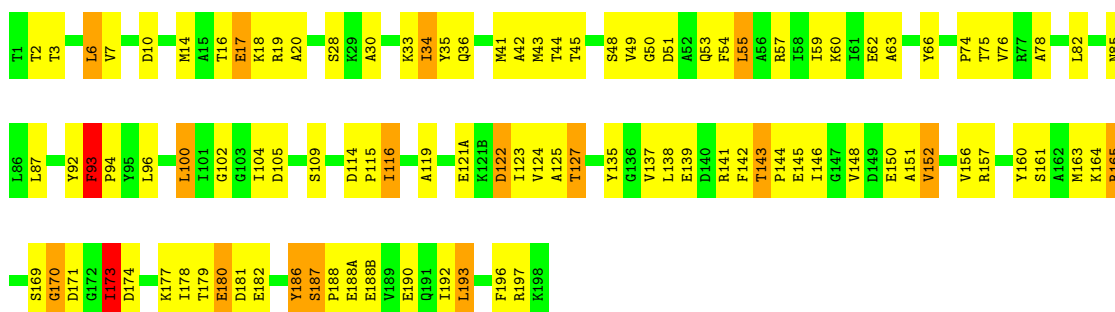
• Molecule 2: Proteasome beta subunit

Chain K: 46% 43% 11%

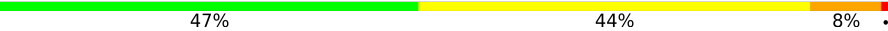


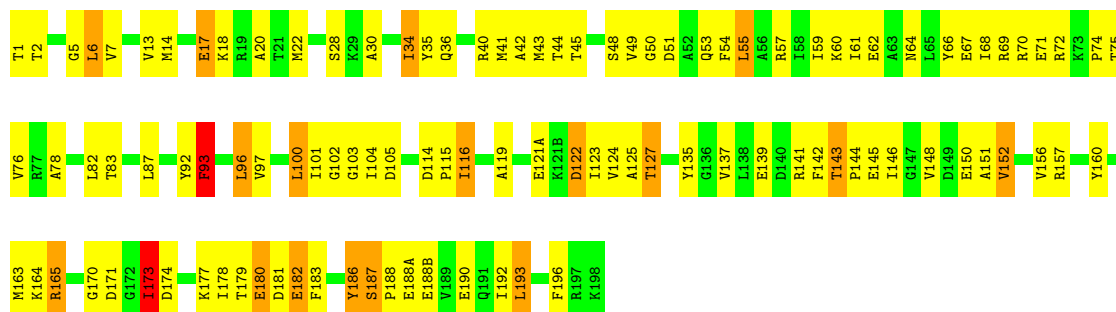
• Molecule 2: Proteasome beta subunit

Chain L: 49% 42% 8%



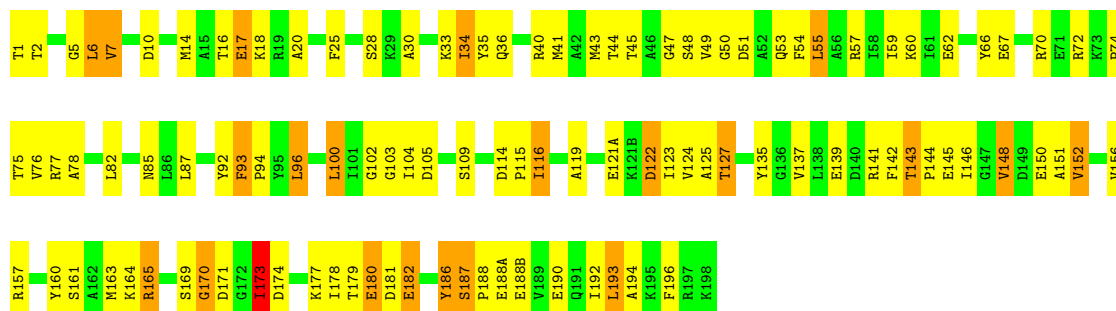
• Molecule 2: Proteasome beta subunit

Chain M:  47% 44% 8%



• Molecule 2: Proteasome beta subunit

Chain N:  47% 43% 10%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	148.10Å 148.10Å 303.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	16.99 – 2.83	Depositor
% Data completeness (in resolution range)	94.6 (16.99-2.83)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.241 , 0.279	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	24227	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.48	0/1892	0.93	6/2549 (0.2%)
1	B	0.51	1/1892 (0.1%)	0.94	6/2549 (0.2%)
1	C	0.50	0/1892	0.94	6/2549 (0.2%)
1	D	0.48	0/1892	0.93	6/2549 (0.2%)
1	E	0.51	0/1892	0.94	6/2549 (0.2%)
1	F	0.50	0/1892	0.93	8/2549 (0.3%)
1	G	0.49	0/1892	0.95	6/2549 (0.2%)
2	H	0.57	0/1573	1.06	7/2121 (0.3%)
2	I	0.57	0/1573	1.06	7/2121 (0.3%)
2	J	0.58	0/1573	1.07	8/2121 (0.4%)
2	K	0.60	0/1573	1.06	11/2121 (0.5%)
2	L	0.56	0/1573	1.08	7/2121 (0.3%)
2	M	0.58	0/1573	1.04	7/2121 (0.3%)
2	N	0.57	0/1573	1.06	5/2121 (0.2%)
All	All	0.53	1/24255 (0.0%)	1.00	96/32690 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	167	MET	SD-CE	5.38	1.93	1.79

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	186	TYR	N-CA-C	11.74	127.60	112.34
2	N	186	TYR	N-CA-C	11.63	127.46	112.34
2	I	186	TYR	N-CA-C	11.57	127.38	112.34
2	M	186	TYR	N-CA-C	11.53	127.33	112.34
2	K	186	TYR	N-CA-C	11.40	127.16	112.34

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1866	0	1908	142	0
1	B	1866	0	1908	145	0
1	C	1866	0	1908	137	0
1	D	1866	0	1908	127	0
1	E	1866	0	1908	130	0
1	F	1866	0	1908	127	0
1	G	1866	0	1908	137	0
2	H	1553	0	1582	119	0
2	I	1553	0	1582	109	0
2	J	1553	0	1582	108	0
2	K	1553	0	1582	105	0
2	L	1553	0	1582	99	0
2	M	1553	0	1582	110	0
2	N	1553	0	1582	112	0
3	H	27	0	36	5	0
3	I	27	0	36	4	0
3	J	27	0	36	2	0
3	K	27	0	36	2	0
3	L	27	0	36	2	0
3	M	27	0	36	2	0
3	N	27	0	36	4	0
4	A	4	0	0	1	0
4	B	7	0	0	2	0
4	C	9	0	0	2	0
4	D	4	0	0	0	0
4	E	7	0	0	1	0
4	F	5	0	0	1	0
4	G	5	0	0	1	0
4	H	13	0	0	0	0
4	I	14	0	0	3	0
4	J	5	0	0	1	0
4	K	7	0	0	0	0
4	L	6	0	0	0	0
4	M	12	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	N	7	0	0	0	0
All	All	24227	0	24682	1559	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 33.

The worst 5 of 1559 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:12:ILE:HG21	1:G:127:GLY:HA2	1.21	1.14
1:F:12:ILE:HG21	1:F:127:GLY:HA2	1.23	1.12
1:E:12:ILE:HG21	1:E:127:GLY:HA2	1.18	1.11
2:M:121(A):GLU:HG2	2:M:124:VAL:HB	1.34	1.10
1:B:12:ILE:HG21	1:B:127:GLY:HA2	1.16	1.09

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 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	235/237 (99%)	217 (92%)	10 (4%)	8 (3%)	3	6
1	B	235/237 (99%)	215 (92%)	11 (5%)	9 (4%)	2	4
1	C	235/237 (99%)	213 (91%)	14 (6%)	8 (3%)	3	6
1	D	235/237 (99%)	215 (92%)	12 (5%)	8 (3%)	3	6
1	E	235/237 (99%)	213 (91%)	16 (7%)	6 (3%)	4	9
1	F	235/237 (99%)	217 (92%)	10 (4%)	8 (3%)	3	6
1	G	235/237 (99%)	215 (92%)	12 (5%)	8 (3%)	3	6
2	H	200/202 (99%)	184 (92%)	12 (6%)	4 (2%)	6	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	200/202 (99%)	188 (94%)	9 (4%)	3 (2%)	8	17
2	J	200/202 (99%)	186 (93%)	11 (6%)	3 (2%)	8	17
2	K	200/202 (99%)	187 (94%)	9 (4%)	4 (2%)	6	12
2	L	200/202 (99%)	188 (94%)	9 (4%)	3 (2%)	8	17
2	M	200/202 (99%)	188 (94%)	9 (4%)	3 (2%)	8	17
2	N	200/202 (99%)	188 (94%)	8 (4%)	4 (2%)	6	12
All	All	3045/3073 (99%)	2814 (92%)	152 (5%)	79 (3%)	4	9

5 of 79 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	ILE
1	A	127	GLY
1	A	220	ARG
1	B	12	ILE
1	B	127	GLY

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	199/199 (100%)	179 (90%)	20 (10%)	7	15
1	B	199/199 (100%)	178 (89%)	21 (11%)	6	13
1	C	199/199 (100%)	179 (90%)	20 (10%)	7	15
1	D	199/199 (100%)	179 (90%)	20 (10%)	7	15
1	E	199/199 (100%)	178 (89%)	21 (11%)	6	13
1	F	199/199 (100%)	178 (89%)	21 (11%)	6	13
1	G	199/199 (100%)	178 (89%)	21 (11%)	6	13
2	H	164/164 (100%)	148 (90%)	16 (10%)	7	17
2	I	164/164 (100%)	145 (88%)	19 (12%)	5	11
2	J	164/164 (100%)	145 (88%)	19 (12%)	5	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	K	164/164 (100%)	145 (88%)	19 (12%)	5	11
2	L	164/164 (100%)	147 (90%)	17 (10%)	7	14
2	M	164/164 (100%)	146 (89%)	18 (11%)	6	12
2	N	164/164 (100%)	144 (88%)	20 (12%)	5	10
All	All	2541/2541 (100%)	2269 (89%)	272 (11%)	6	13

5 of 272 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	165	ARG
2	M	87	LEU
2	N	96	LEU
1	E	134	VAL
1	E	121	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	85	ASN
2	K	85	ASN
2	I	185	GLN
2	J	98	GLN
2	L	24	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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
3	CIB	H	1001	-	25,26,26	1.02	1 (4%)	31,33,33	1.12	2 (6%)
3	CIB	I	1101	-	25,26,26	1.20	3 (12%)	31,33,33	1.56	7 (22%)
3	CIB	K	1301	-	25,26,26	0.93	0	31,33,33	1.21	3 (9%)
3	CIB	L	1401	-	25,26,26	1.09	2 (8%)	31,33,33	1.41	5 (16%)
3	CIB	J	1201	-	25,26,26	1.01	1 (4%)	31,33,33	1.33	6 (19%)
3	CIB	M	1501	-	25,26,26	0.95	0	31,33,33	1.11	3 (9%)
3	CIB	N	1601	-	25,26,26	0.90	0	31,33,33	0.91	1 (3%)

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
3	CIB	H	1001	-	-	2/33/34/34	-
3	CIB	I	1101	-	-	5/33/34/34	-
3	CIB	K	1301	-	-	1/33/34/34	-
3	CIB	L	1401	-	-	0/33/34/34	-
3	CIB	J	1201	-	-	0/33/34/34	-
3	CIB	M	1501	-	-	1/33/34/34	-
3	CIB	N	1601	-	-	2/33/34/34	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	1101	CIB	CA2-N2	-2.53	1.40	1.45
3	L	1401	CIB	C10-N1	2.33	1.41	1.34
3	H	1001	CIB	CB2-CA2	2.31	1.60	1.53
3	I	1101	CIB	CA1-C1	-2.23	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	1401	CIB	CA1-N1	2.02	1.50	1.45

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1101	CIB	CB1-CA1-N1	4.42	120.56	110.58
3	K	1301	CIB	C3-CA3-N3	-3.60	102.55	109.50
3	L	1401	CIB	C3-CA3-N3	-3.47	102.81	109.50
3	L	1401	CIB	O28-C10-C25	-3.42	115.96	122.05
3	L	1401	CIB	CB1-CA1-C1	-3.16	103.09	110.59

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	I	1101	CIB	CA3-CB3-CG3-C19
3	H	1001	CIB	CA3-CB3-CG3-C19
3	I	1101	CIB	CE3-C19-CG3-CB3
3	N	1601	CIB	CE3-C19-CG3-CB3
3	M	1501	CIB	CE3-C19-CG3-CB3

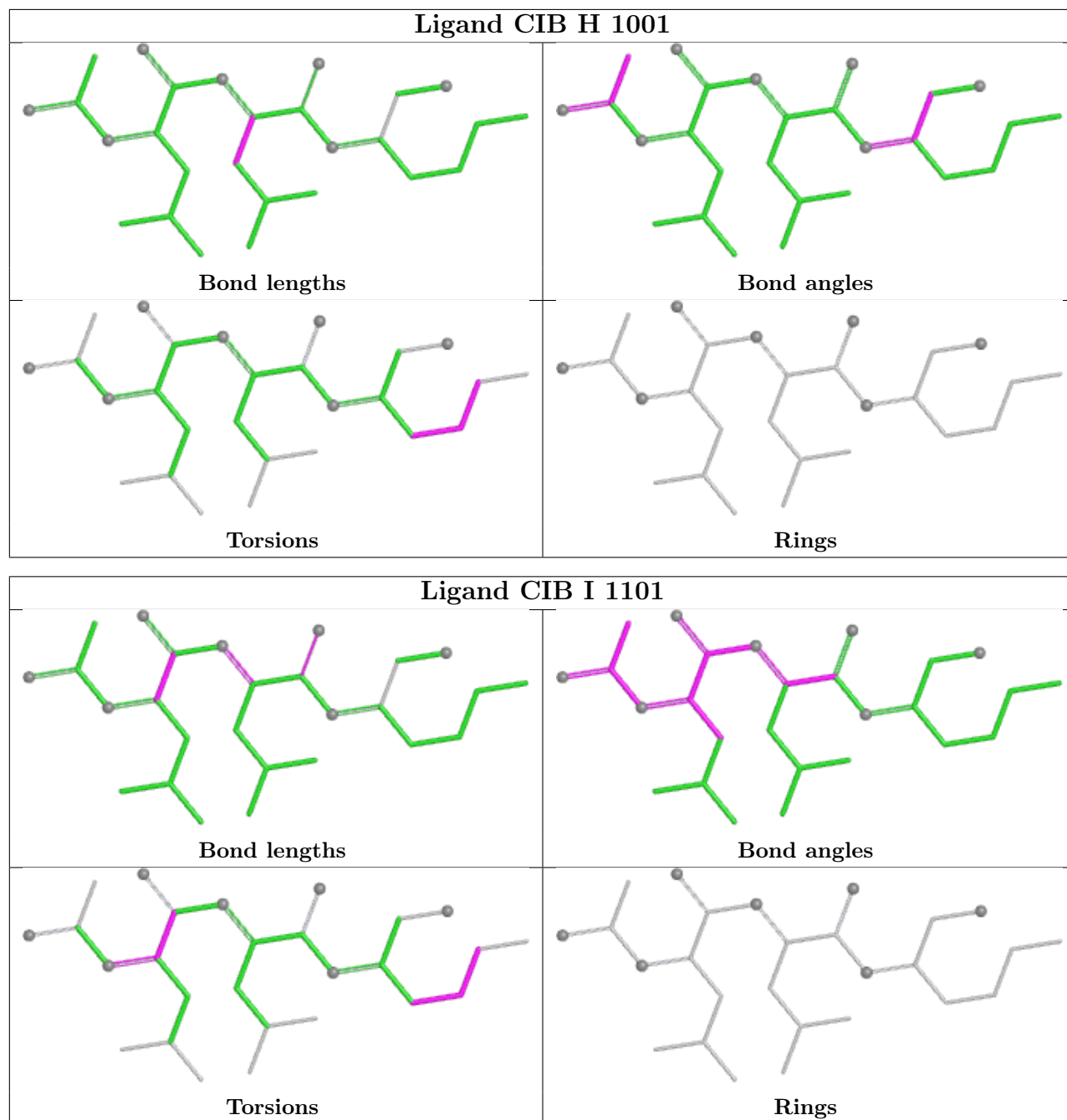
There are no ring outliers.

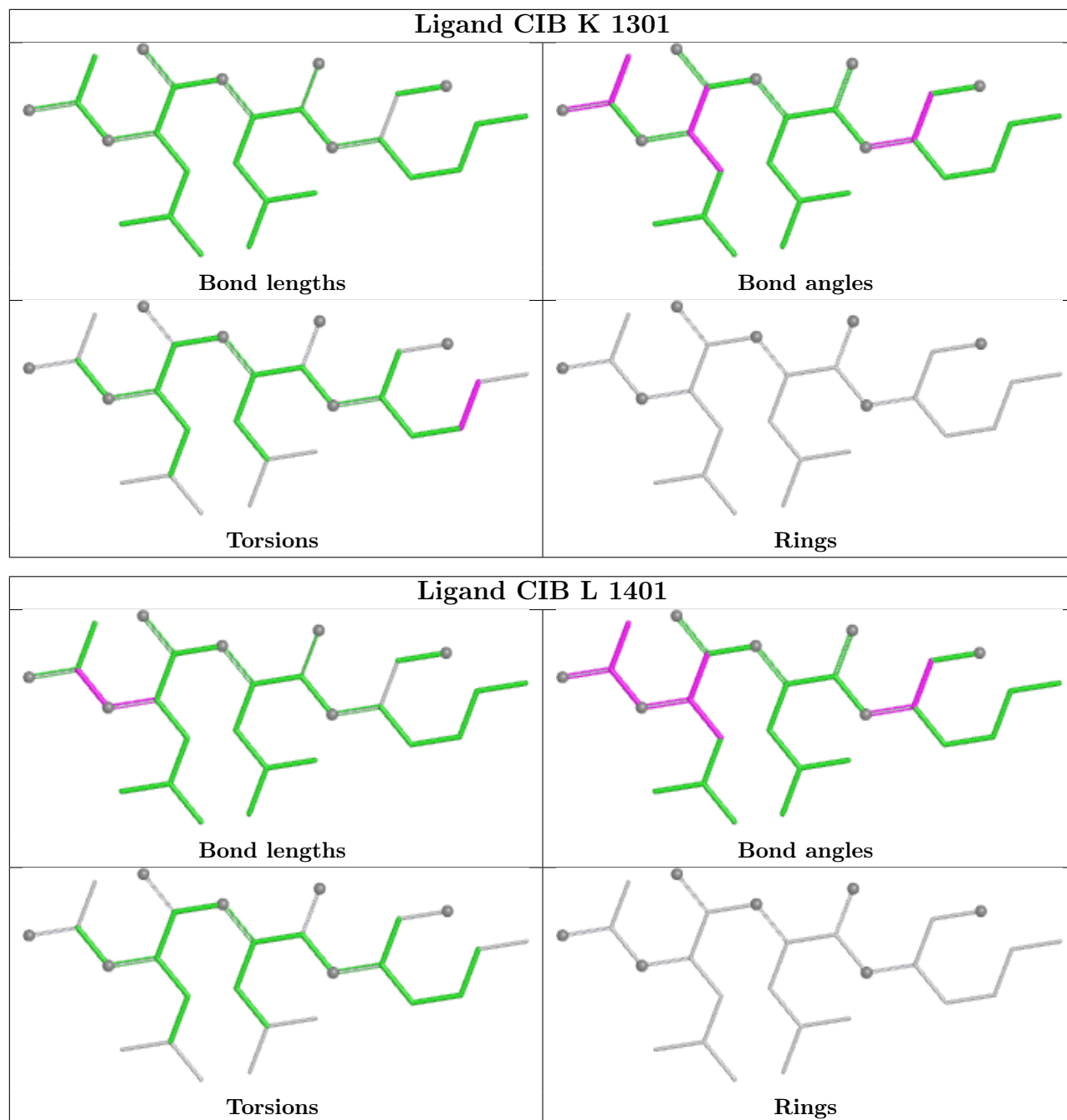
7 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1001	CIB	5	0
3	I	1101	CIB	4	0
3	K	1301	CIB	2	0
3	L	1401	CIB	2	0
3	J	1201	CIB	2	0
3	M	1501	CIB	2	0
3	N	1601	CIB	4	0

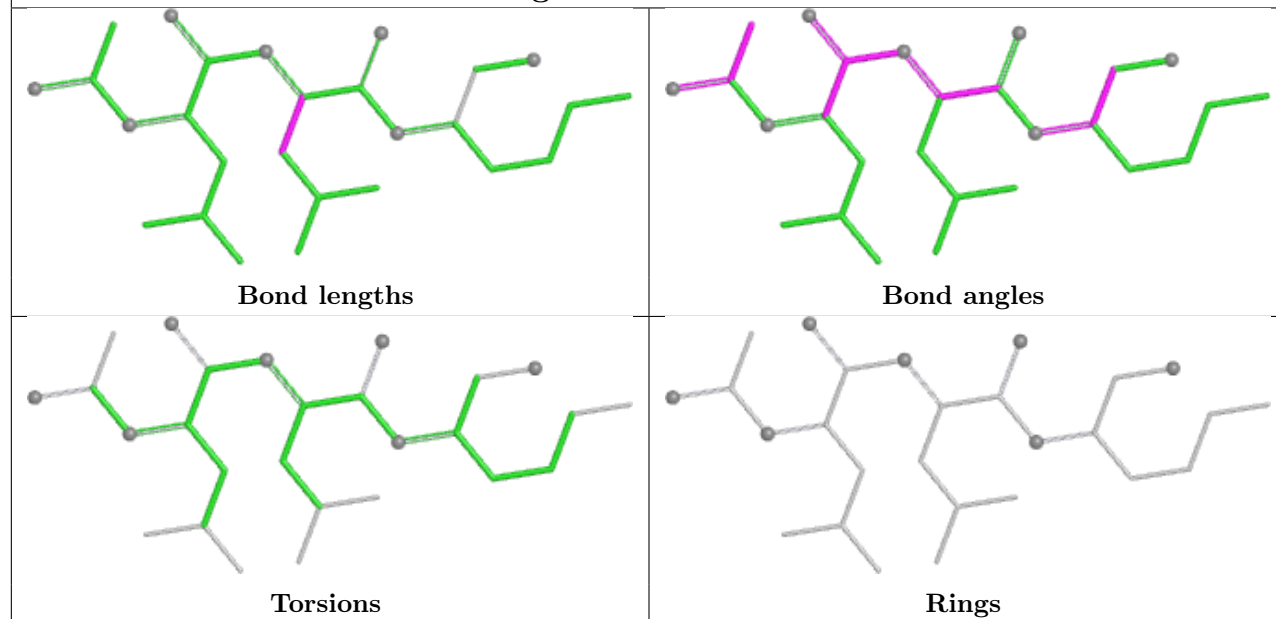
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

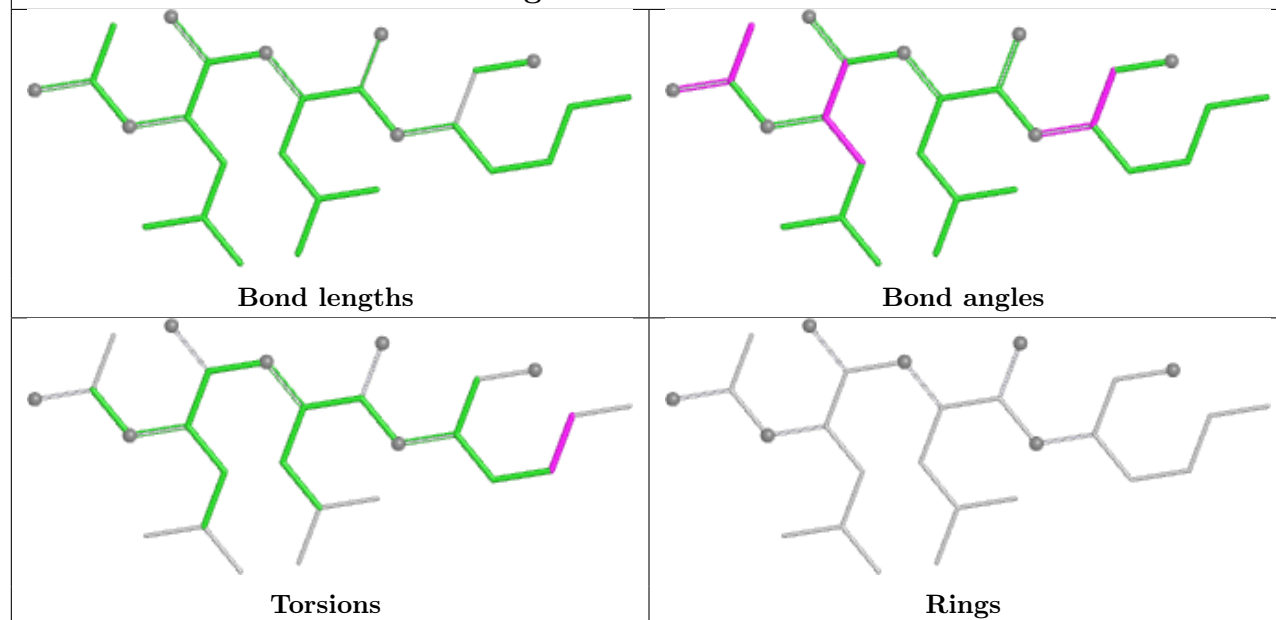


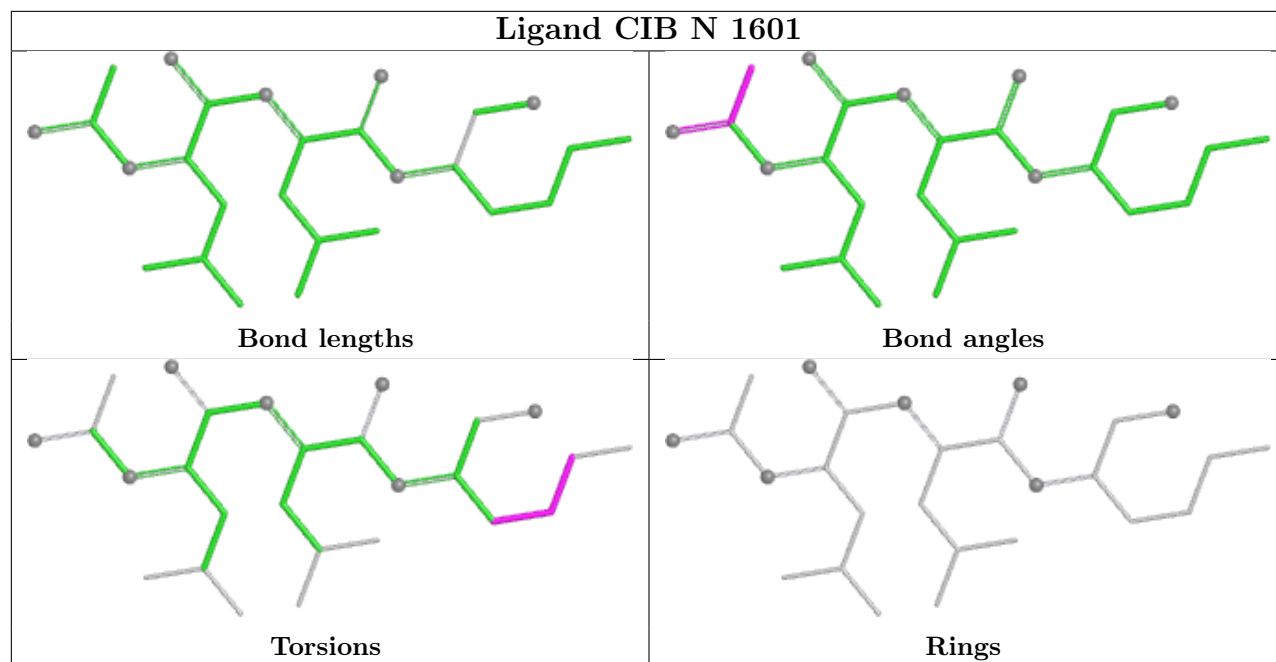


Ligand CIB J 1201



Ligand CIB M 1501





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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.