wwPDB X-ray Structure Validation Summary Report (i)

Jan 4, 2024 – 09:54 am GMT

PDB ID	:	5L5V
Title	:	'Yeast 20S proteasome with human beta5i (1-138; V31M) and human beta6 (97-111; 118-133) in complex with epoxyketone inhibitor 18
Authors	:	Groll, M.; Huber, E.M.
Deposited on	:	2016-05-28
Resolution	:	2.70 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 (i) 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 (i)) were used in the production of this report:

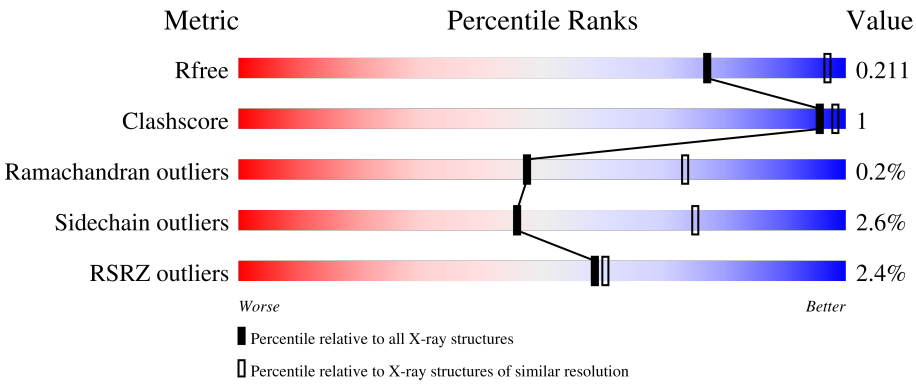
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 <=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%, 99%, •
1	O	250	2%, 98%, •
2	B	258	3%, 90%, • 5%
2	P	258	4%, 91%, • 5%
3	C	254	6%, 88%, 6% • 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	9% 88% 6% 6%
4	D	260	87% 10%
4	R	260	2% 87% 10%
5	E	234	3% 97%
5	S	234	2% 96%
6	F	288	2% 82% 16%
6	T	288	3% 82% 16%
7	G	252	2% 91% 5%
7	U	252	2% 90% 6%
8	H	232	2% 90% 7%
8	V	232	2% 91% 6%
9	I	205	.% 95% 5%
9	W	205	.% 94% 6%
10	J	198	3% 92% 5%
10	X	198	2% 92% 5%
11	K	211	2% 91% 8%
11	Y	211	.% 93% 6%
12	L	222	2% 95% 5%
12	Z	222	.% 95% 5%
13	M	246	.% 90% 5%
13	a	246	.% 92% 5%
14	N	196	.% 95%
14	b	196	.% 98%

2 Entry composition (i)

There are 18 unique types of molecules in this entry. The entry contains 49839 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 subunit alpha type-2.

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

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	240	1881	1176	329	372	4	0	0	0
3	Q	240	1881	1176	329	372	4	0	0	0

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	235	1813	1136	304	366	7	0	0	0
4	R	235	1813	1136	304	366	7	0	0	0

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	231	1773	1114	307	348	4	0	0	0
5	S	231	1773	1114	307	348	4	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	243	1892	1203	329	356	4	0	0	0
6	T	243	1892	1203	329	356	4	0	0	0

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	G	241	1907	1214	320	365	8	0	0	0
7	U	241	1907	1214	320	365	8	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	226	1729	1088	301	333	7	0	1	0
8	V	226	1719	1082	298	332	7	0	0	0

- Molecule 9 is a protein called Proteasome subunit beta type-3.

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

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	J	195	1561	992	264	299	6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	X	195	1561	992	264	299	6	0	0	0

- Molecule 11 is a protein called Proteasome subunit beta type-8,Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	K	211	1641	1035	282	311	13	0	0	0
			Total	C	N	O	S			
11	Y	211	1641	1035	282	311	13	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	31	MET	VAL	conflict	UNP P28062
Y	31	MET	VAL	conflict	UNP P28062

- Molecule 12 is a protein called Proteasome subunit beta type-6,Proteasome subunit beta type-1,Proteasome subunit beta type-6,Proteasome subunit beta type-1,Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	222	1764	1119	305	336	4	0	0	0
			Total	C	N	O	S			
12	Z	222	1764	1119	305	336	4	0	0	0

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	M	233	1832	1159	315	351	7	0	1	0
			Total	C	N	O	S			
13	a	233	1824	1154	312	351	7	0	0	0

- Molecule 14 is a protein called Proteasome subunit beta type-1.

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

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

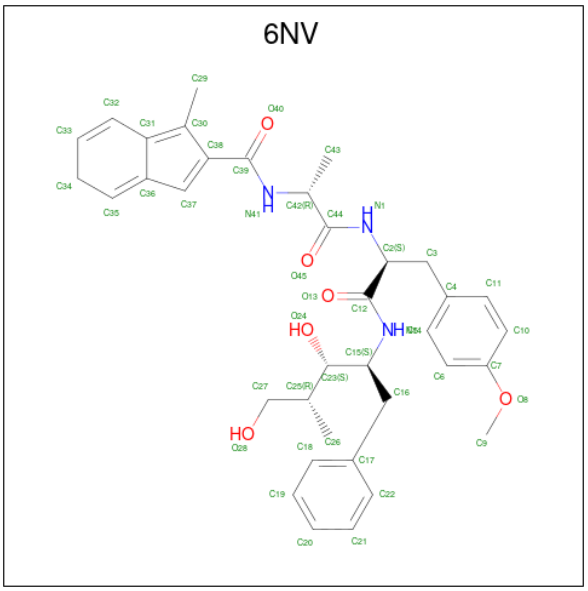
- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
15	G	1	1	1	0	0
15	I	2	2	2	0	0
15	J	1	1	1	0	0
15	K	1	1	1	0	0
15	L	1	1	1	0	0
15	N	1	1	1	0	0
15	Z	1	1	1	0	0
15	b	1	1	1	0	0

- Molecule 16 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
16	G	1	1	1	0	0
16	U	1	1	1	0	0

- Molecule 17 is {N}-[(2 {R})-1-[[(2 {S})-3-(4-methoxyphenyl)-1-[[(2 {S},3 {S},4 {R})-4-methyl-3,5-bis(oxidanyl)-1-phenyl-pentan-2-yl]amino]-1-oxidanylidene-propan-2-yl]amino]-1-oxidanylidene-propan-2-yl]-1-methyl-5 {H}-indene-2-carboxamide (three-letter code: 6NV) (formula: $C_{36}H_{43}N_3O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
17	K	1	45	36	3	6	0	0
17	Y	1	45	36	3	6	0	0

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
18	A	16	16	16	0	0
18	B	13	13	13	0	0
18	C	12	12	12	0	0
18	D	9	9	9	0	0
18	E	9	9	9	0	0
18	F	13	13	13	0	0
18	G	10	10	10	0	0
18	H	13	13	13	0	0
18	I	9	9	9	0	0
18	J	11	11	11	0	0

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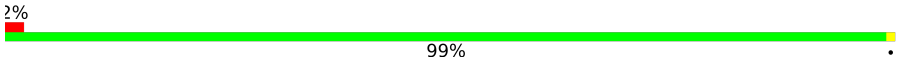
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
18	K	7	7	7	0	0
			Total	O		
18	L	19	19	19	0	0
			Total	O		
18	M	21	21	21	0	0
			Total	O		
18	N	16	16	16	0	0
			Total	O		
18	O	17	17	17	0	0
			Total	O		
18	P	12	12	12	0	0
			Total	O		
18	Q	5	5	5	0	0
			Total	O		
18	R	9	9	9	0	0
			Total	O		
18	S	8	8	8	0	0
			Total	O		
18	T	12	12	12	0	0
			Total	O		
18	U	15	15	15	0	0
			Total	O		
18	V	17	17	17	0	0
			Total	O		
18	W	7	7	7	0	0
			Total	O		
18	X	13	13	13	0	0
			Total	O		
18	Y	12	12	12	0	0
			Total	O		
18	Z	5	5	5	0	0
			Total	O		
18	a	19	19	19	0	0
			Total	O		
18	b	17	17	17	0	0

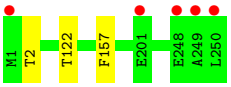
3 Residue-property plots (i)

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 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 subunit alpha type-2

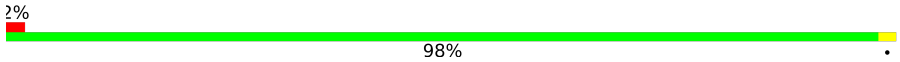
Chain A:





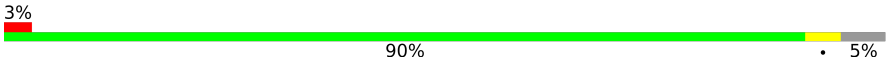
• Molecule 1: Proteasome subunit alpha type-2

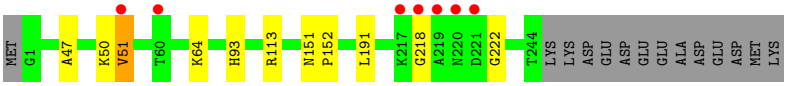
Chain O:



• Molecule 2: Proteasome subunit alpha type-3

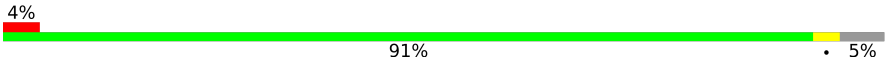
Chain B:

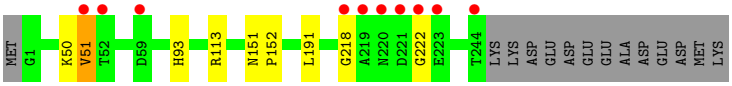




• Molecule 2: Proteasome subunit alpha type-3

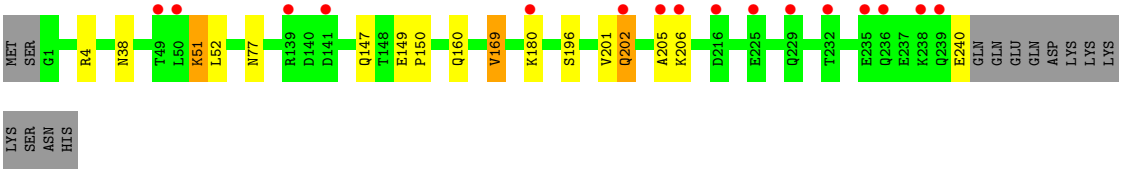
Chain P:





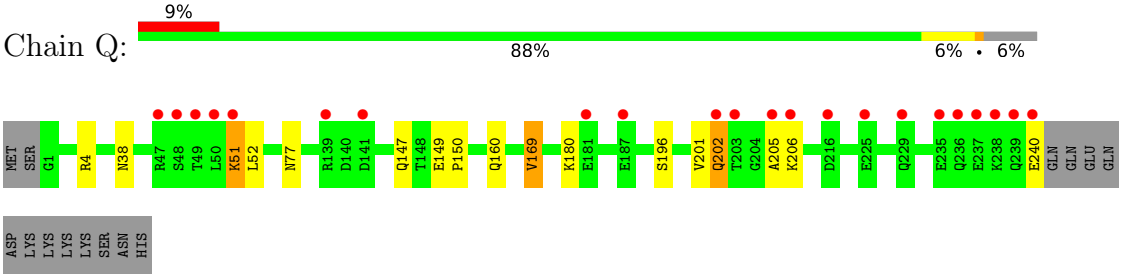
• Molecule 3: Proteasome subunit alpha type-4

Chain C:



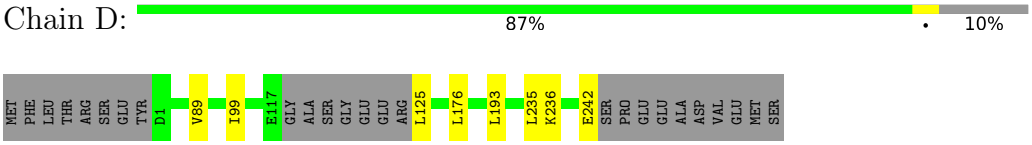
• Molecule 3: Proteasome subunit alpha type-4

Chain Q:



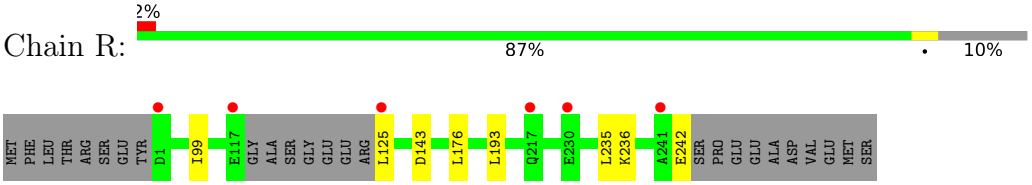
• Molecule 4: Proteasome subunit alpha type-5

Chain D:



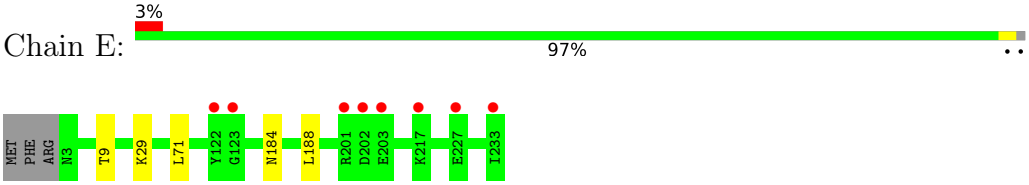
• Molecule 4: Proteasome subunit alpha type-5

Chain R:



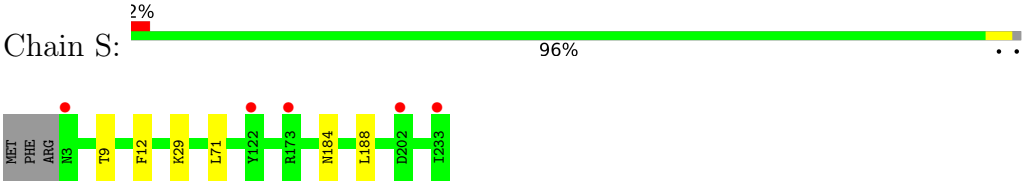
• Molecule 5: Proteasome subunit alpha type-6

Chain E:



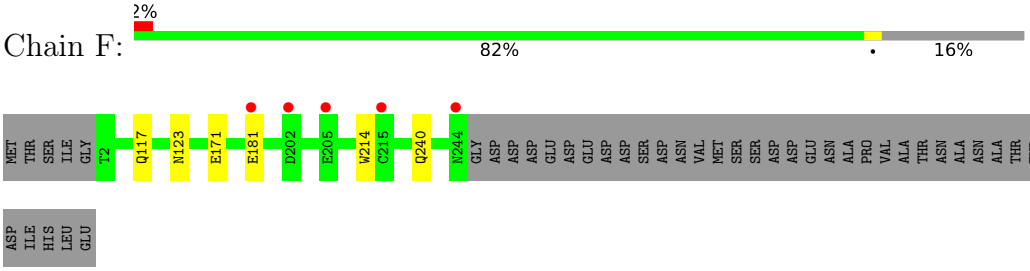
• Molecule 5: Proteasome subunit alpha type-6

Chain S:



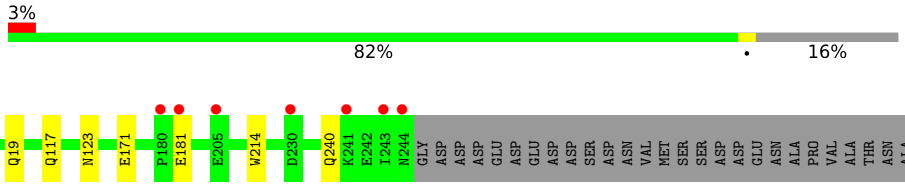
• Molecule 6: Probable proteasome subunit alpha type-7

Chain F:



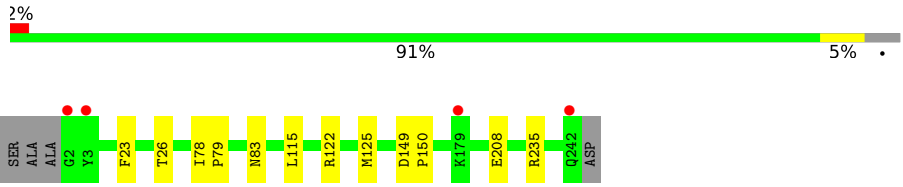
• Molecule 6: Probable proteasome subunit alpha type-7

Chain T:



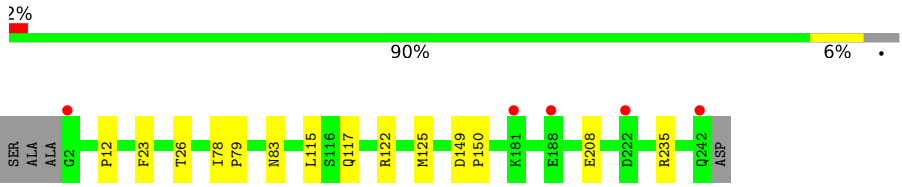
• Molecule 7: Proteasome subunit alpha type-1

Chain G:



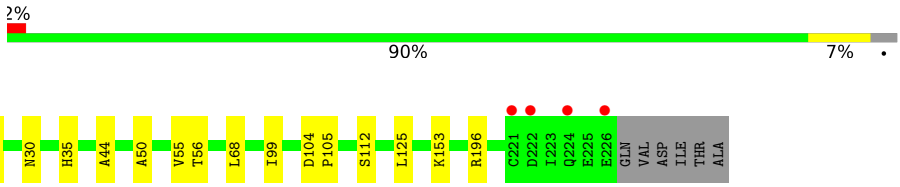
• Molecule 7: Proteasome subunit alpha type-1

Chain U:



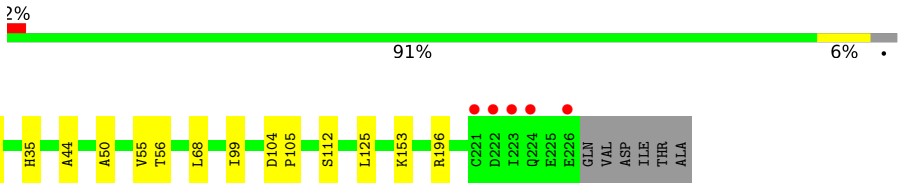
• Molecule 8: Proteasome subunit beta type-2

Chain H:



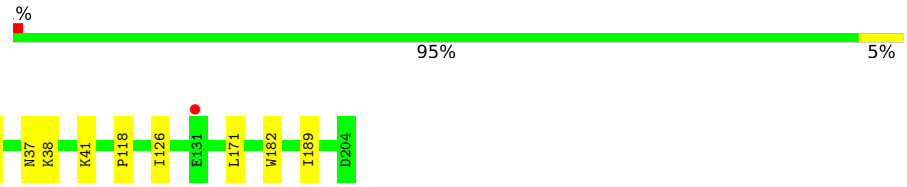
• Molecule 8: Proteasome subunit beta type-2

Chain V:



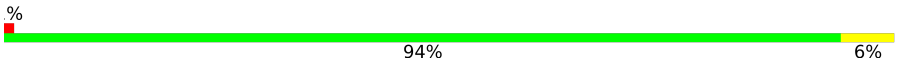
• Molecule 9: Proteasome subunit beta type-3

Chain I:



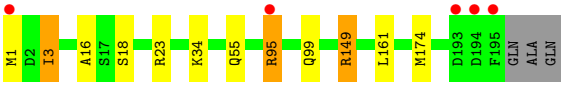
• Molecule 9: Proteasome subunit beta type-3

Chain W:



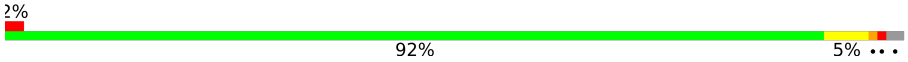
• Molecule 10: Proteasome subunit beta type-4

Chain J:



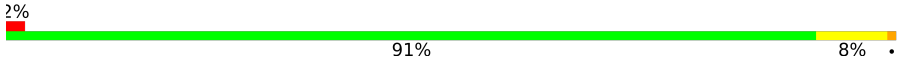
• Molecule 10: Proteasome subunit beta type-4

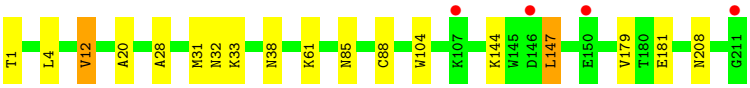
Chain X:



• Molecule 11: Proteasome subunit beta type-8,Proteasome subunit beta type-5

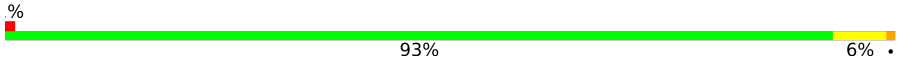
Chain K:





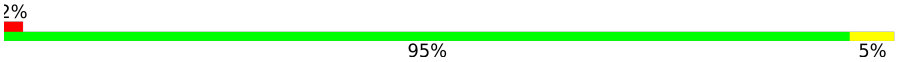
• Molecule 11: Proteasome subunit beta type-8,Proteasome subunit beta type-5

Chain Y:



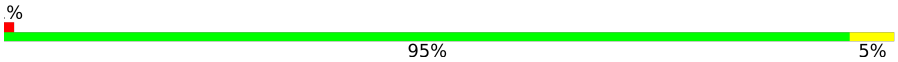
• Molecule 12: Proteasome subunit beta type-6,Proteasome subunit beta type-1,Proteasome subunit beta type-6,Proteasome subunit beta type-1,Proteasome subunit beta type-6

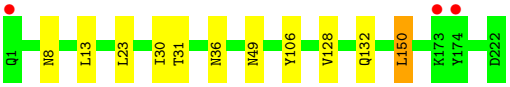
Chain L:



• Molecule 12: Proteasome subunit beta type-6,Proteasome subunit beta type-1,Proteasome subunit beta type-6,Proteasome subunit beta type-1,Proteasome subunit beta type-6

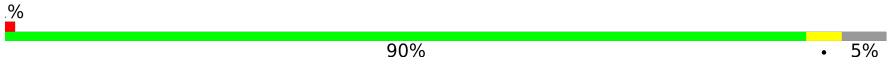
Chain Z:

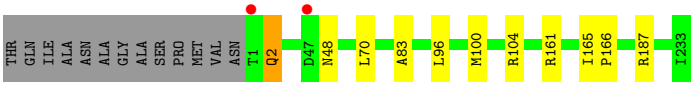




• Molecule 13: Proteasome subunit beta type-7

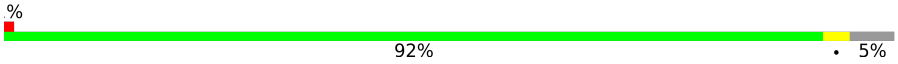
Chain M:

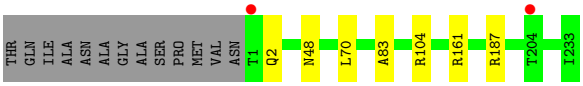




• Molecule 13: Proteasome subunit beta type-7

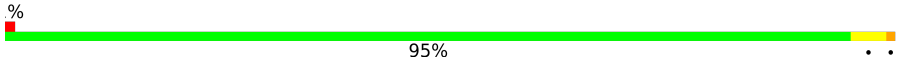
Chain a:





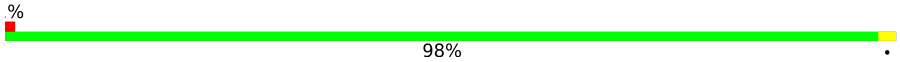
• Molecule 14: Proteasome subunit beta type-1

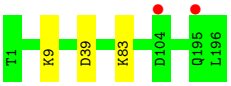
Chain N:



• Molecule 14: Proteasome subunit beta type-1

Chain b:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	136.24Å 300.97Å 145.64Å 90.00° 112.84° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (15.00-2.70) 98.8 (15.00-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.65 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.186 , 0.208 0.191 , 0.211	Depositor DCC
R_{free} test set	14474 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	53.7	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 37.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	49839	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.49% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 6NV, CL, MG

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	0.27	0/1952	0.46	0/2642
1	O	0.27	0/1952	0.46	0/2642
2	B	0.27	0/1934	0.48	0/2618
2	P	0.27	0/1934	0.48	0/2618
3	C	0.28	0/1910	0.49	0/2586
3	Q	0.27	0/1910	0.49	0/2586
4	D	0.27	0/1837	0.46	0/2475
4	R	0.27	0/1837	0.46	0/2475
5	E	0.27	0/1800	0.46	0/2433
5	S	0.27	0/1800	0.46	0/2433
6	F	0.27	0/1932	0.44	0/2609
6	T	0.27	0/1932	0.44	0/2609
7	G	0.27	0/1945	0.46	0/2634
7	U	0.27	0/1945	0.46	0/2634
8	H	0.26	0/1761	0.51	1/2388 (0.0%)
8	V	0.26	0/1750	0.52	1/2373 (0.0%)
9	I	0.27	0/1611	0.50	0/2174
9	W	0.27	0/1611	0.50	0/2174
10	J	0.28	0/1589	0.96	6/2142 (0.3%)
10	X	0.27	0/1589	0.95	6/2142 (0.3%)
11	K	0.36	2/1678 (0.1%)	0.53	1/2263 (0.0%)
11	Y	0.36	1/1678 (0.1%)	0.54	1/2263 (0.0%)
12	L	0.27	0/1802	0.48	0/2430
12	Z	0.27	0/1802	0.48	0/2430
13	M	0.27	0/1866	0.51	0/2528
13	a	0.27	0/1855	0.52	0/2514
14	N	0.25	0/1541	0.48	0/2087
14	b	0.25	0/1541	0.48	0/2087
All	All	0.28	3/50294 (0.0%)	0.53	16/67989 (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
10	J	0	2
10	X	0	2
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	K	32	ASN	CG-ND2	-5.53	1.19	1.32
11	K	85	ASN	CG-ND2	-5.52	1.19	1.32
11	Y	85	ASN	CG-ND2	-5.06	1.20	1.32

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	X	149	ARG	NE-CZ-NH2	-20.57	110.02	120.30
10	J	95	ARG	NE-CZ-NH2	-20.55	110.03	120.30
10	J	149	ARG	NE-CZ-NH1	-19.68	110.46	120.30
10	X	95	ARG	NE-CZ-NH1	-19.23	110.68	120.30
10	J	149	ARG	NE-CZ-NH2	16.27	128.44	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	J	149	ARG	Sidechain
10	J	95	ARG	Sidechain
10	X	149	ARG	Sidechain
10	X	95	ARG	Sidechain

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	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	1915	0	1929	1	0
2	B	1904	0	1904	5	0
2	P	1904	0	1904	3	0
3	C	1881	0	1895	5	0
3	Q	1881	0	1895	5	0
4	D	1813	0	1797	1	0
4	R	1813	0	1797	0	0
5	E	1773	0	1775	0	0
5	S	1773	0	1775	1	0
6	F	1892	0	1883	0	0
6	T	1892	0	1883	1	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	4	0
8	H	1729	0	1725	12	0
8	V	1719	0	1719	11	0
9	I	1581	0	1574	5	0
9	W	1581	0	1574	6	0
10	J	1561	0	1569	5	0
10	X	1561	0	1569	5	0
11	K	1641	0	1578	10	0
11	Y	1641	0	1578	7	0
12	L	1764	0	1716	3	0
12	Z	1764	0	1716	3	0
13	M	1832	0	1845	3	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	4	0
14	b	1512	0	1481	0	0
15	G	1	0	0	0	0
15	I	2	0	0	0	0
15	J	1	0	0	0	0
15	K	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
15	Z	1	0	0	0	0
15	b	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	K	45	0	0	3	0
17	Y	45	0	0	2	0
18	A	16	0	0	0	0
18	B	13	0	0	1	0
18	C	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	D	9	0	0	0	0
18	E	9	0	0	0	0
18	F	13	0	0	0	0
18	G	10	0	0	0	0
18	H	13	0	0	0	0
18	I	9	0	0	0	0
18	J	11	0	0	2	0
18	K	7	0	0	0	0
18	L	19	0	0	0	0
18	M	21	0	0	1	0
18	N	16	0	0	0	0
18	O	17	0	0	0	0
18	P	12	0	0	1	0
18	Q	5	0	0	0	0
18	R	9	0	0	0	0
18	S	8	0	0	0	0
18	T	12	0	0	0	0
18	U	15	0	0	0	0
18	V	17	0	0	0	0
18	W	7	0	0	0	0
18	X	13	0	0	0	0
18	Y	12	0	0	0	0
18	Z	5	0	0	0	0
18	a	19	0	0	0	0
18	b	17	0	0	0	0
All	All	49839	0	49125	97	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 1.

The worst 5 of 97 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)
8:V:3:ILE:HD11	8:V:44:ALA:CB	1.58	1.34
8:H:3:ILE:HD11	8:H:44:ALA:CB	1.68	1.23
8:H:3:ILE:HD11	8:H:44:ALA:HB1	1.09	1.08
8:V:3:ILE:HD11	8:V:44:ALA:HB1	1.20	1.08
8:V:3:ILE:HD11	8:V:44:ALA:HB3	1.40	1.03

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	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	34	60
1	O	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	34	60
2	B	242/258 (94%)	233 (96%)	6 (2%)	3 (1%)	13	32
2	P	242/258 (94%)	233 (96%)	6 (2%)	3 (1%)	13	32
3	C	238/254 (94%)	233 (98%)	3 (1%)	2 (1%)	19	43
3	Q	238/254 (94%)	233 (98%)	3 (1%)	2 (1%)	19	43
4	D	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
4	R	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
5	E	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
5	S	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
6	F	241/288 (84%)	239 (99%)	2 (1%)	0	100	100
6	T	241/288 (84%)	239 (99%)	2 (1%)	0	100	100
7	G	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
7	U	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
8	H	225/232 (97%)	218 (97%)	7 (3%)	0	100	100
8	V	224/232 (97%)	217 (97%)	7 (3%)	0	100	100
9	I	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
10	J	193/198 (98%)	190 (98%)	3 (2%)	0	100	100
10	X	193/198 (98%)	190 (98%)	3 (2%)	0	100	100
11	K	209/211 (99%)	200 (96%)	9 (4%)	0	100	100
11	Y	209/211 (99%)	201 (96%)	8 (4%)	0	100	100
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	232/246 (94%)	222 (96%)	9 (4%)	1 (0%)	34	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	a	231/246 (94%)	221 (96%)	9 (4%)	1 (0%)	34	60
14	N	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
14	b	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
All	All	6284/6612 (95%)	6109 (97%)	161 (3%)	14 (0%)	47	73

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
2	P	51	VAL
3	Q	202	GLN
1	A	2	THR

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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%)	207 (99%)	2 (1%)	76	91
1	O	209/209 (100%)	207 (99%)	2 (1%)	76	91
2	B	203/216 (94%)	201 (99%)	2 (1%)	76	91
2	P	203/216 (94%)	201 (99%)	2 (1%)	76	91
3	C	212/226 (94%)	202 (95%)	10 (5%)	26	54
3	Q	212/226 (94%)	202 (95%)	10 (5%)	26	54
4	D	194/215 (90%)	187 (96%)	7 (4%)	35	64
4	R	194/215 (90%)	186 (96%)	8 (4%)	30	59
5	E	190/193 (98%)	185 (97%)	5 (3%)	46	75
5	S	190/193 (98%)	185 (97%)	5 (3%)	46	75
6	F	201/239 (84%)	195 (97%)	6 (3%)	41	70
6	T	201/239 (84%)	195 (97%)	6 (3%)	41	70
7	G	206/210 (98%)	200 (97%)	6 (3%)	42	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	U	206/210 (98%)	199 (97%)	7 (3%)	37	66
8	H	186/190 (98%)	180 (97%)	6 (3%)	39	68
8	V	185/190 (97%)	179 (97%)	6 (3%)	39	68
9	I	172/173 (99%)	169 (98%)	3 (2%)	60	84
9	W	172/173 (99%)	169 (98%)	3 (2%)	60	84
10	J	173/175 (99%)	170 (98%)	3 (2%)	60	84
10	X	173/175 (99%)	170 (98%)	3 (2%)	60	84
11	K	170/170 (100%)	166 (98%)	4 (2%)	49	77
11	Y	170/170 (100%)	166 (98%)	4 (2%)	49	77
12	L	186/186 (100%)	180 (97%)	6 (3%)	39	68
12	Z	186/186 (100%)	180 (97%)	6 (3%)	39	68
13	M	200/208 (96%)	194 (97%)	6 (3%)	41	70
13	a	199/208 (96%)	193 (97%)	6 (3%)	41	70
14	N	162/162 (100%)	159 (98%)	3 (2%)	57	82
14	b	162/162 (100%)	159 (98%)	3 (2%)	57	82
All	All	5326/5544 (96%)	5186 (97%)	140 (3%)	46	75

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	W	37	ASN
10	X	23	ARG
12	Z	150	LEU
10	J	23	ARG
10	J	3	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
5	S	116	GLN
9	W	37	ASN
5	S	120	GLN
6	T	123	ASN
12	Z	3	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 11 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
17	6NV	Y	301	11	48,48,48	1.97	12 (25%)	54,66,66	1.57	10 (18%)
17	6NV	K	301	11	48,48,48	1.95	11 (22%)	54,66,66	1.60	11 (20%)

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
17	6NV	Y	301	11	-	16/44/67/67	0/4/4/4
17	6NV	K	301	11	-	16/44/67/67	0/4/4/4

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	K	301	6NV	C3-C4	-5.99	1.36	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Y	301	6NV	C3-C4	-5.53	1.38	1.51
17	K	301	6NV	C38-C39	-5.29	1.33	1.49
17	Y	301	6NV	C38-C39	-5.03	1.33	1.49
17	Y	301	6NV	C31-C36	-4.80	1.32	1.47

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	Y	301	6NV	C16-C15-N14	-5.40	102.20	110.07
17	K	301	6NV	C16-C15-N14	-5.05	102.71	110.07
17	K	301	6NV	C38-C37-C36	-4.13	104.60	109.47
17	Y	301	6NV	C43-C42-N41	-3.68	103.47	110.38
17	Y	301	6NV	C38-C37-C36	-3.56	105.27	109.47

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	K	301	6NV	C15-C23-C25-C26
17	K	301	6NV	C15-C23-C25-C27
17	K	301	6NV	C26-C25-C27-O28
17	K	301	6NV	C23-C25-C27-O28
17	Y	301	6NV	C15-C23-C25-C26

There are no ring outliers.

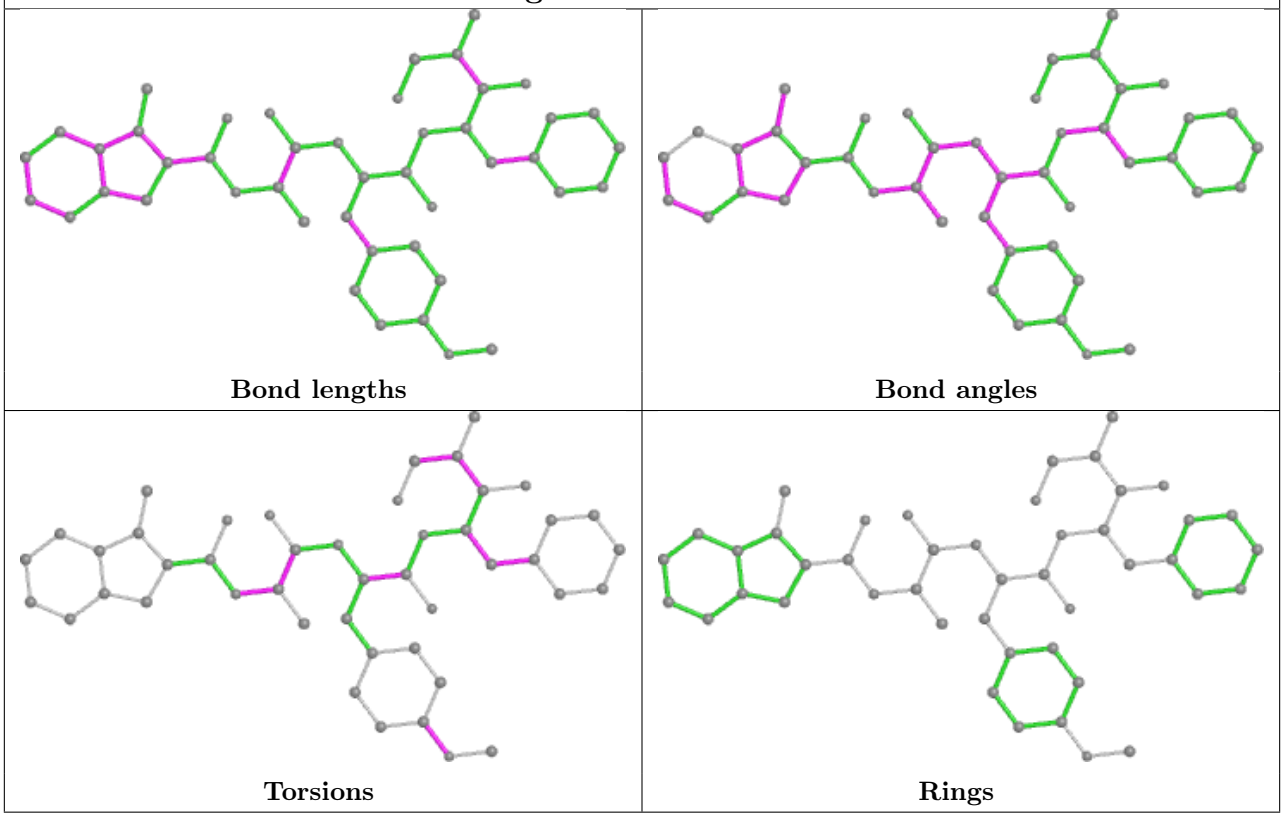
2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	Y	301	6NV	2	0
17	K	301	6NV	3	0

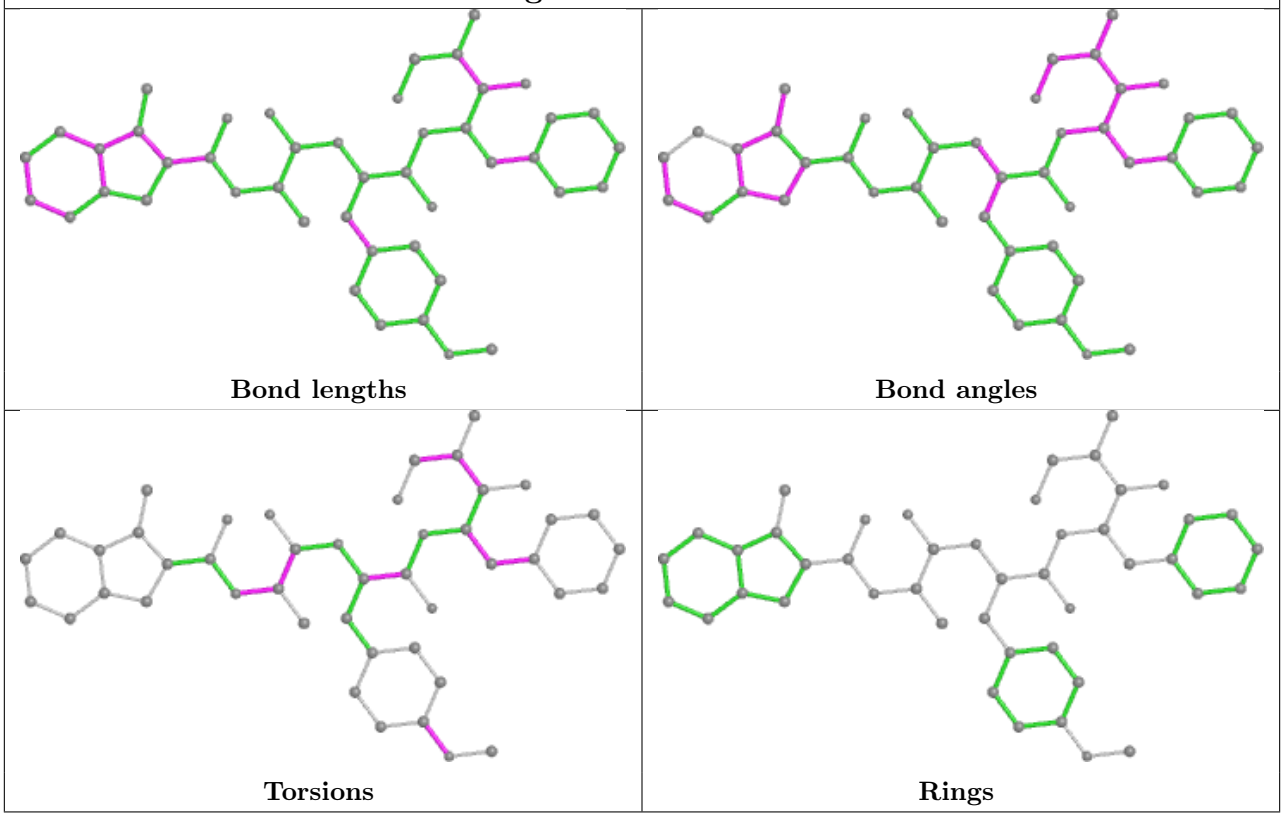
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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 6NV Y 301



Ligand 6NV K 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 (i)

6.1 Protein, DNA and RNA chains (i)

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%)	-0.39	5 (2%)	65	67	29, 49, 85, 124	0
1	O	250/250 (100%)	-0.35	6 (2%)	59	60	36, 55, 98, 132	0
2	B	244/258 (94%)	-0.24	7 (2%)	51	52	36, 56, 101, 158	0
2	P	244/258 (94%)	-0.24	10 (4%)	37	36	35, 58, 101, 158	0
3	C	240/254 (94%)	-0.04	16 (6%)	17	16	36, 62, 130, 162	0
3	Q	240/254 (94%)	0.05	22 (9%)	9	7	41, 70, 149, 182	0
4	D	235/260 (90%)	-0.30	0	100	100	39, 59, 90, 126	0
4	R	235/260 (90%)	-0.19	6 (2%)	56	57	50, 68, 108, 139	0
5	E	231/234 (98%)	-0.25	8 (3%)	44	44	42, 60, 97, 137	0
5	S	231/234 (98%)	-0.23	5 (2%)	62	63	43, 63, 100, 127	0
6	F	243/288 (84%)	-0.45	5 (2%)	63	65	33, 54, 101, 129	0
6	T	243/288 (84%)	-0.34	8 (3%)	46	46	34, 59, 109, 142	0
7	G	241/252 (95%)	-0.44	4 (1%)	70	72	33, 52, 88, 148	0
7	U	241/252 (95%)	-0.43	5 (2%)	63	65	36, 50, 86, 125	0
8	H	226/232 (97%)	-0.33	4 (1%)	68	70	38, 50, 82, 144	0
8	V	226/232 (97%)	-0.32	5 (2%)	62	63	37, 51, 86, 165	0
9	I	204/205 (99%)	-0.56	2 (0%)	82	83	35, 49, 81, 101	0
9	W	204/205 (99%)	-0.55	2 (0%)	82	83	34, 51, 81, 100	0
10	J	195/198 (98%)	-0.42	5 (2%)	56	57	34, 52, 79, 119	0
10	X	195/198 (98%)	-0.41	4 (2%)	63	65	37, 54, 80, 133	0
11	K	211/211 (100%)	-0.27	4 (1%)	66	69	38, 62, 91, 115	0
11	Y	211/211 (100%)	-0.28	3 (1%)	75	77	38, 63, 93, 119	0
12	L	222/222 (100%)	-0.40	4 (1%)	68	70	34, 55, 93, 123	0
12	Z	222/222 (100%)	-0.39	3 (1%)	75	77	40, 58, 94, 125	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
13	M	233/246 (94%)	-0.62	2 (0%)	84	85	32, 49, 74, 92	0
13	a	233/246 (94%)	-0.53	2 (0%)	84	85	35, 52, 77, 96	0
14	N	196/196 (100%)	-0.58	2 (1%)	82	83	33, 46, 76, 102	0
14	b	196/196 (100%)	-0.61	2 (1%)	82	83	34, 46, 77, 105	0
All	All	6342/6612 (95%)	-0.36	151 (2%)	59	60	29, 56, 98, 182	0

The worst 5 of 151 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	221	ASP	7.1
10	J	1	MET	6.7
10	X	1	MET	6.5
3	Q	50	LEU	6.3
2	P	51	VAL	6.2

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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
17	6NV	Y	301	45/45	0.86	0.29	38,56,75,79	0
17	6NV	K	301	45/45	0.88	0.24	38,54,76,77	0
15	MG	G	301	1/1	0.90	0.11	49,49,49,49	0
15	MG	I	301	1/1	0.92	0.17	61,61,61,61	0
15	MG	Z	301	1/1	0.94	0.23	63,63,63,63	0
15	MG	b	201	1/1	0.97	0.09	42,42,42,42	0
15	MG	N	201	1/1	0.97	0.14	47,47,47,47	0

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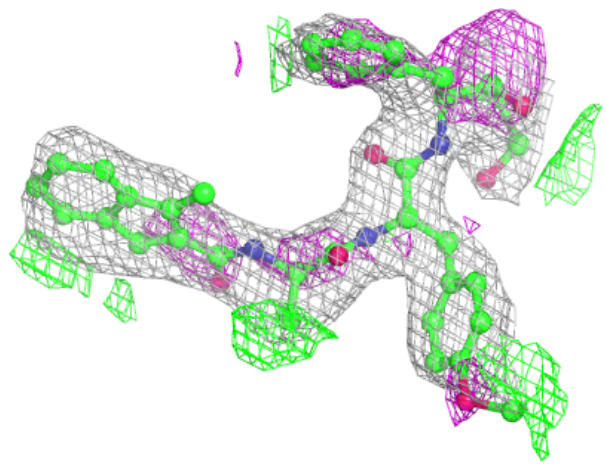
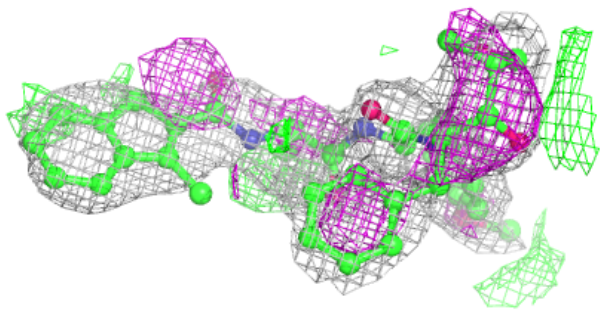
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
15	MG	I	302	1/1	0.97	0.11	59,59,59,59	0
15	MG	L	301	1/1	0.98	0.05	58,58,58,58	0
15	MG	J	201	1/1	0.98	0.10	53,53,53,53	0
16	CL	U	301	1/1	0.99	0.14	38,38,38,38	0
15	MG	K	302	1/1	0.99	0.05	62,62,62,62	0
16	CL	G	302	1/1	0.99	0.09	40,40,40,40	0

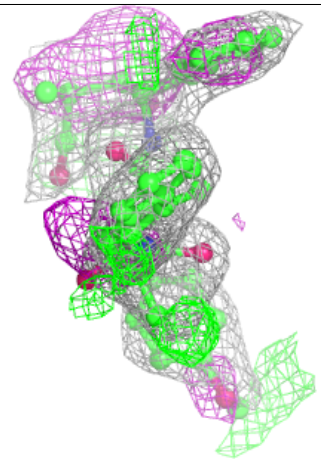
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 6NV 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)

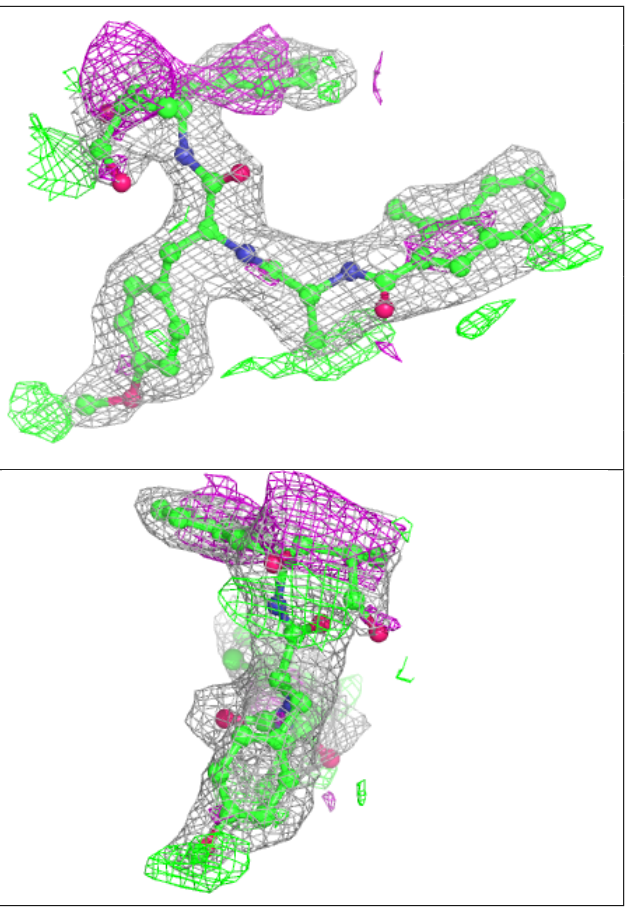


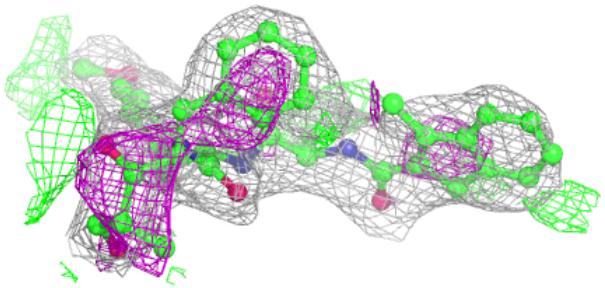




Electron density around 6NV K 301:

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





6.5 Other polymers (i)

There are no such residues in this entry.