wwPDB X-ray Structure Validation Summary Report (i)

Sep 14, 2023 – 07:16 AM EDT

PDB ID	:	3GPW
Title	:	Crystal structure of the yeast 20S proteasome in complex with Salinosporamide derivatives: irreversible inhibitor ligand
Authors	:	Groll, M.; Macherla, V.R.; Manam, R.R.; Arthur, K.A.M.; Potts, C.B.
Deposited on	:	2009-03-23
Resolution	:	2.50 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:

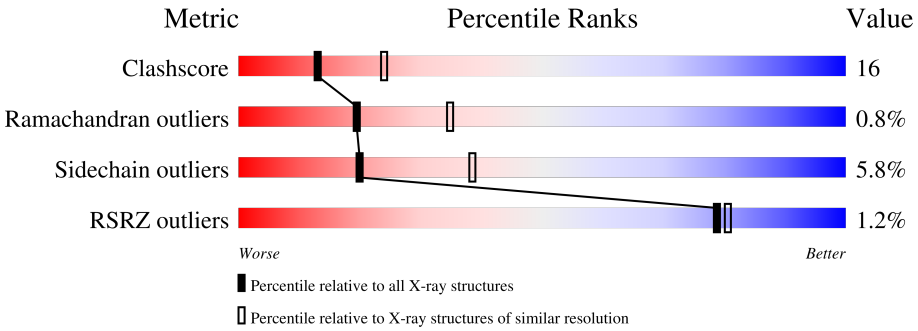
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.50 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	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	77% 21% •
1	O	250	% 76% 22% •
2	B	244	2% 61% 33% 6%
2	P	244	2% 61% 32% 7%
3	C	241	% 59% 36% 5%
3	Q	241	7% 59% 36% 5%

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Mol	Chain	Length	Quality of chain
4	D	242	3% 73% 24%
4	R	242	2% 71% 26%
5	E	233	2% 61% 33% 6%
5	S	233	4% 59% 35% 6%
6	F	244	66% 30%
6	T	244	64% 32%
7	G	243	% 68% 29%
7	U	243	% 67% 30%
8	H	222	65% 32%
8	V	222	63% 35%
9	I	204	74% 25%
9	W	204	74% 25%
10	J	198	2% 72% 25%
10	X	198	% 70% 28%
11	K	212	74% 24%
11	Y	212	72% 25%
12	L	222	72% 25%
12	Z	222	% 72% 26%
13	1	233	69% 29%
13	M	233	70% 28%
14	2	196	65% 32%
14	N	196	69% 28%

2 Entry composition (i)

There are 16 unique types of molecules in this entry. The entry contains 51001 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
			1905	1201	321	380	3			
2	P	244	Total	C	N	O	S	0	0	0
			1905	1201	321	380	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
			1891	1181	331	375	4			
3	Q	241	Total	C	N	O	S	0	0	0
			1891	1181	331	375	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
			1862	1162	314	379	7			
4	R	242	Total	C	N	O	S	0	0	0
			1862	1162	314	379	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
			1897	1205	330	358	4			
6	T	244	Total	C	N	O	S	0	0	0
			1897	1205	330	358	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	0	0
			1685	1061	293	324	7			
8	V	222	Total	C	N	O	S	0	0	0
			1685	1061	293	324	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			

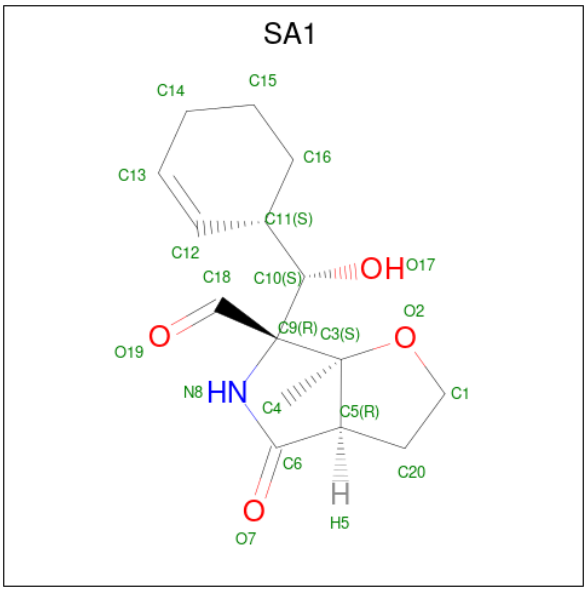
- Molecule 13 is a protein called Proteasome component PRE4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	1	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	2	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is (3AR,6R,6AS)-6-((S)-((S)-CYCLOHEX-2-ENYL)(HYDROXY)METHYL)-6A-METHYL-4-OXO-HEXAHYDRO-2H-FURO[3,2-C]PYRROLE-6-CARBALDEHYDE (three-letter code: SA1) (formula: $C_{15}H_{21}NO_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	H	1	Total C N O 20 15 1 4	0	0
15	K	1	Total C N O 20 15 1 4	0	0
15	N	1	Total C N O 20 15 1 4	0	0
15	V	1	Total C N O 20 15 1 4	0	0
15	Y	1	Total C N O 20 15 1 4	0	0
15	2	1	Total C N O 20 15 1 4	0	0

- Molecule 16 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	A	57	Total O 57 57	0	0
16	B	37	Total O 37 37	0	0
16	C	42	Total O 42 42	0	0
16	D	40	Total O 40 40	0	0
16	E	23	Total O 23 23	0	0
16	F	48	Total O 48 48	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	63	Total O 63 63	0	0
16	H	50	Total O 50 50	0	0
16	I	68	Total O 68 68	0	0
16	J	50	Total O 50 50	0	0
16	K	47	Total O 47 47	0	0
16	L	55	Total O 55 55	0	0
16	M	70	Total O 70 70	0	0
16	N	57	Total O 57 57	0	0
16	O	34	Total O 34 34	0	0
16	P	28	Total O 28 28	0	0
16	Q	28	Total O 28 28	0	0
16	R	30	Total O 30 30	0	0
16	S	20	Total O 20 20	0	0
16	T	40	Total O 40 40	0	0
16	U	60	Total O 60 60	0	0
16	V	49	Total O 49 49	0	0
16	W	60	Total O 60 60	0	0
16	X	47	Total O 47 47	0	0
16	Y	49	Total O 49 49	0	0
16	Z	53	Total O 53 53	0	0
16	1	72	Total O 72 72	0	0

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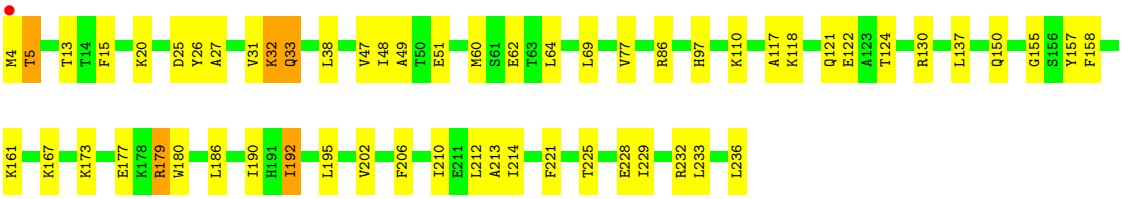
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	2	56	Total	O	0	0
			56	56		

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.

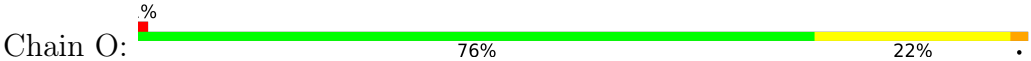
• Molecule 1: Proteasome component Y7

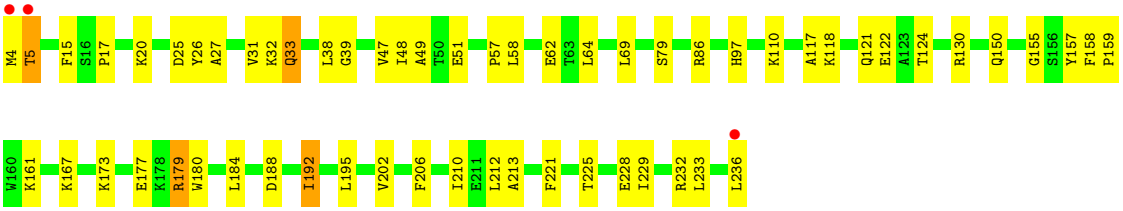
Chain A:



• Molecule 1: Proteasome component Y7

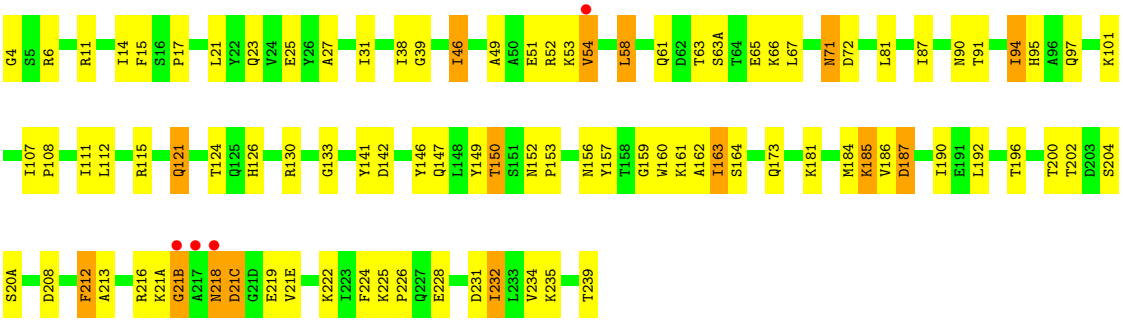
Chain O:





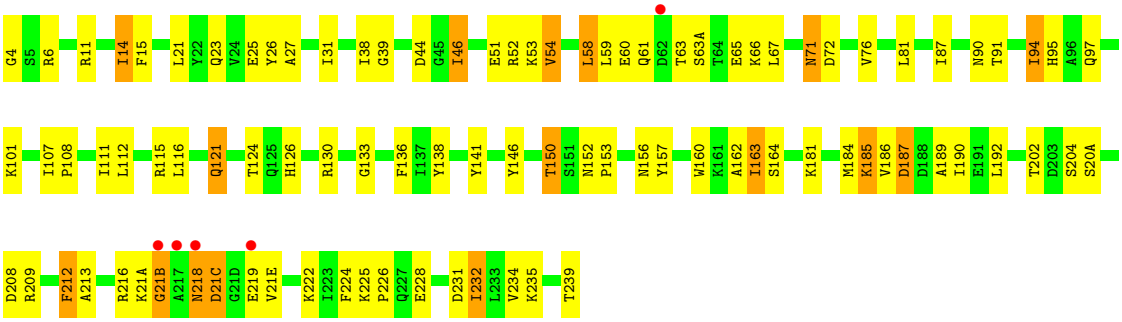
• Molecule 2: Proteasome component Y13

Chain B:

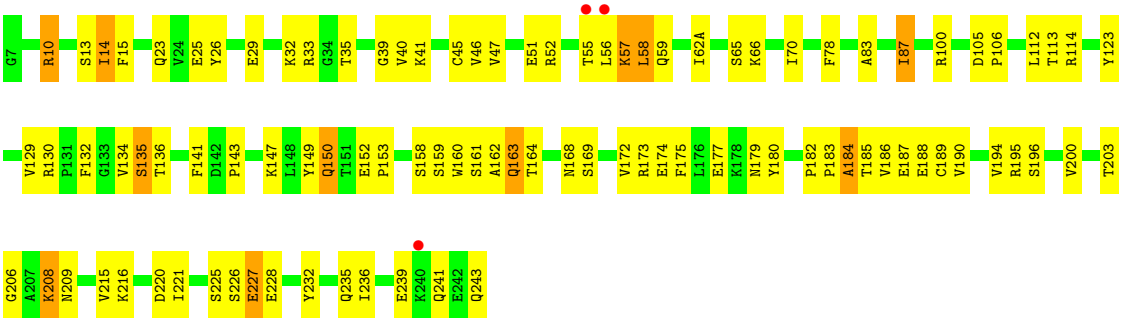


• Molecule 2: Proteasome component Y13

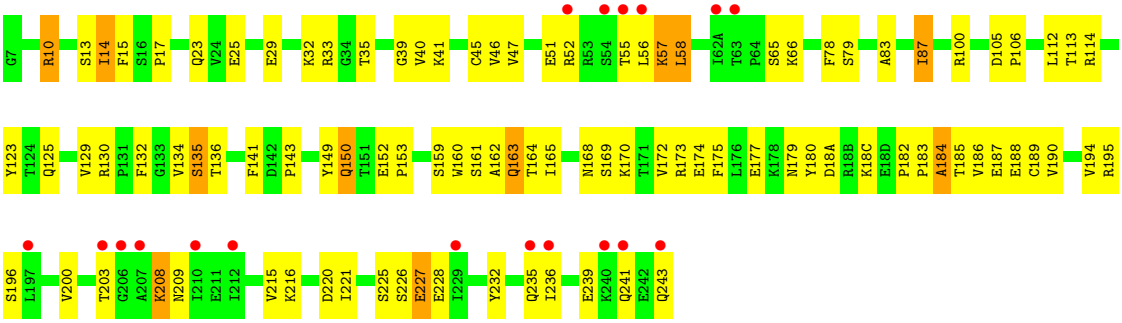
Chain P:



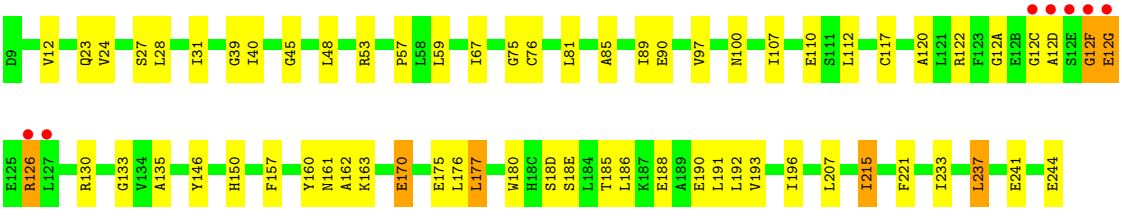
• Molecule 3: Proteasome component PRE6



• Molecule 3: Proteasome component PRE6

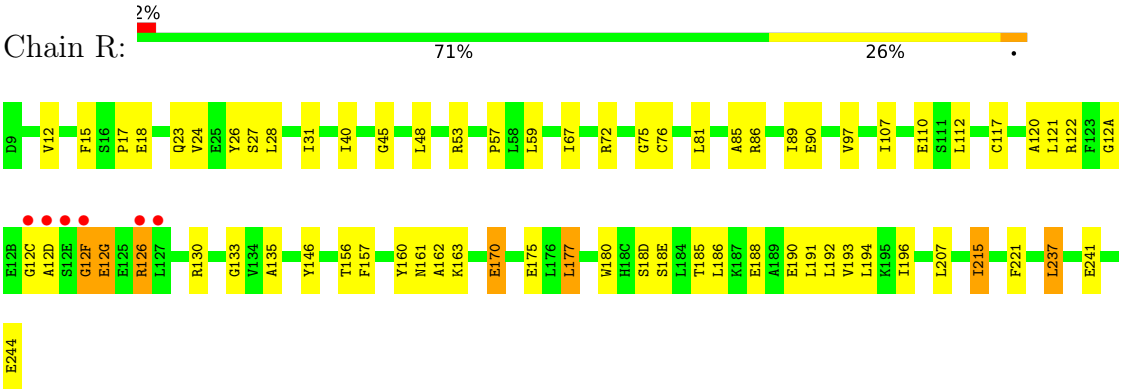


• Molecule 4: Proteasome component PUP2



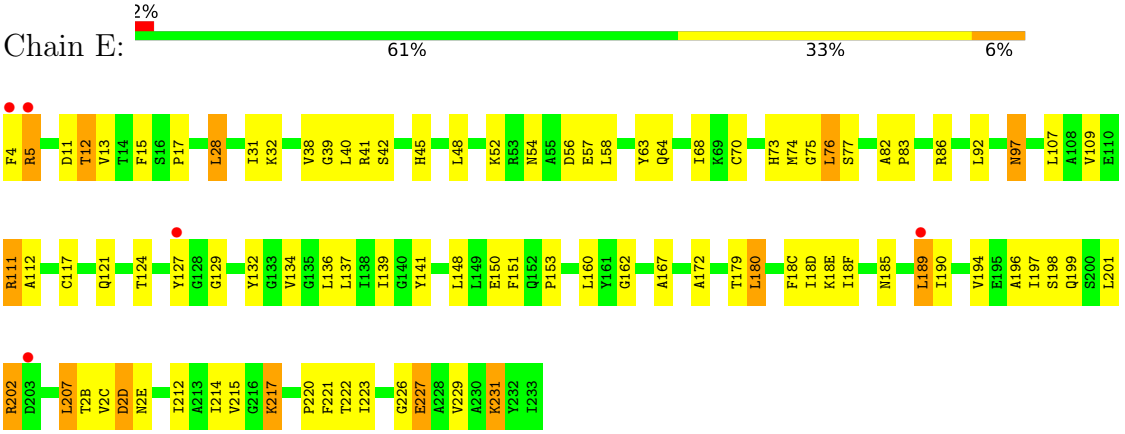
• Molecule 4: Proteasome component PUP2

Chain R:



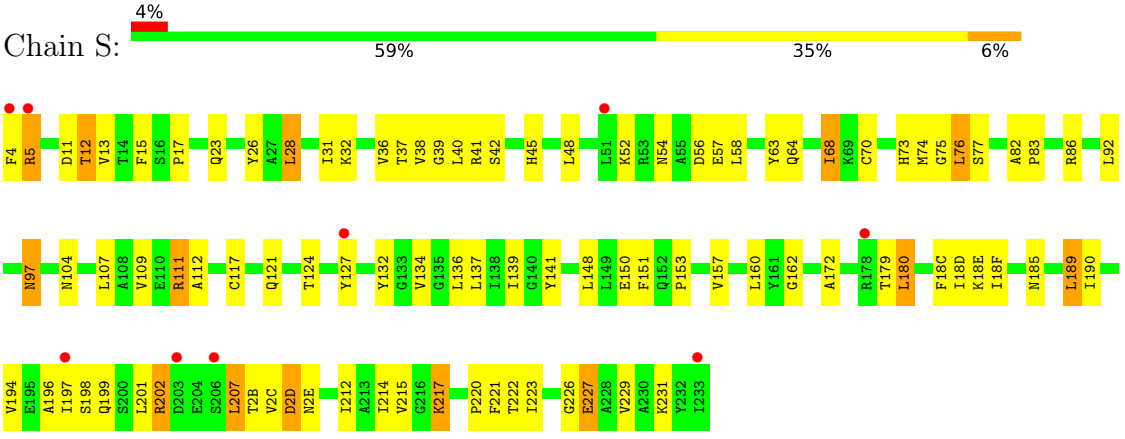
• Molecule 5: Proteasome component PRE5

Chain E:



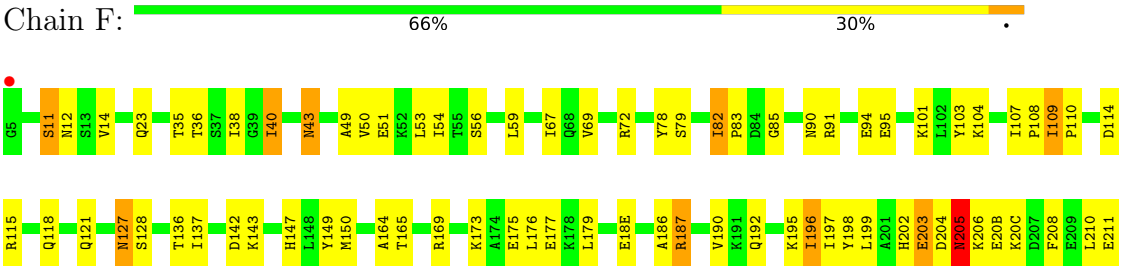
• Molecule 5: Proteasome component PRE5

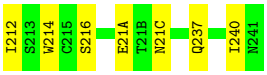
Chain S:



• Molecule 6: Proteasome component C1

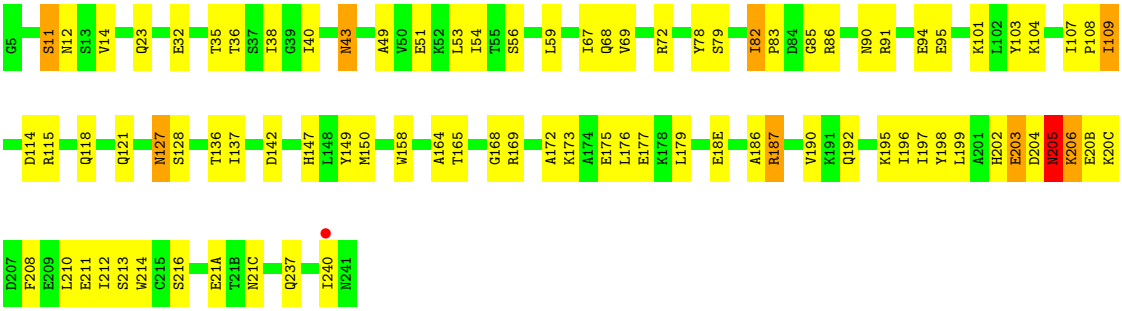
Chain F:





• Molecule 6: Proteasome component C1

Chain T:

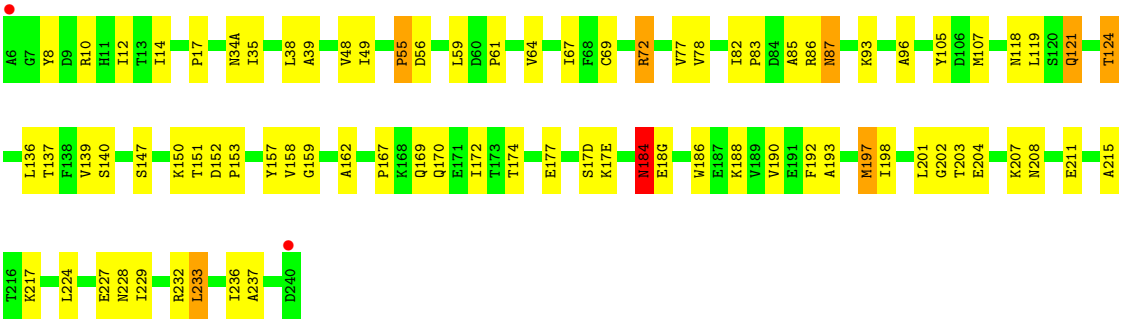


• Molecule 7: Proteasome component C7-alpha

Chain G:

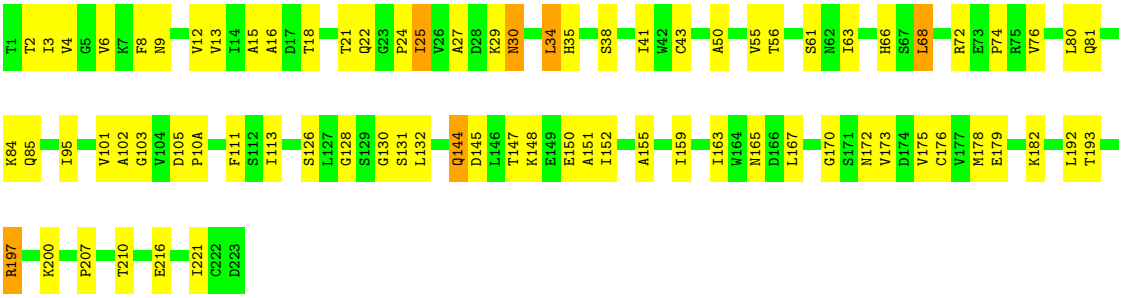
• Molecule 7: Proteasome component C7-alpha

Chain U:



• Molecule 8: Proteasome component PUP1

Chain H:

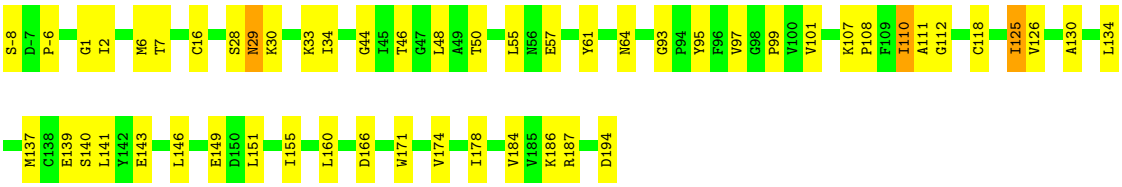


• Molecule 8: Proteasome component PUP1

Chain V:

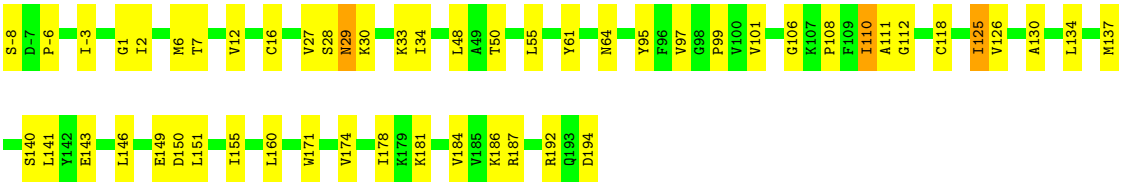
• Molecule 9: Proteasome component PUP3

Chain I:



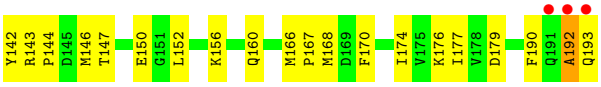
• Molecule 9: Proteasome component PUP3

Chain W:

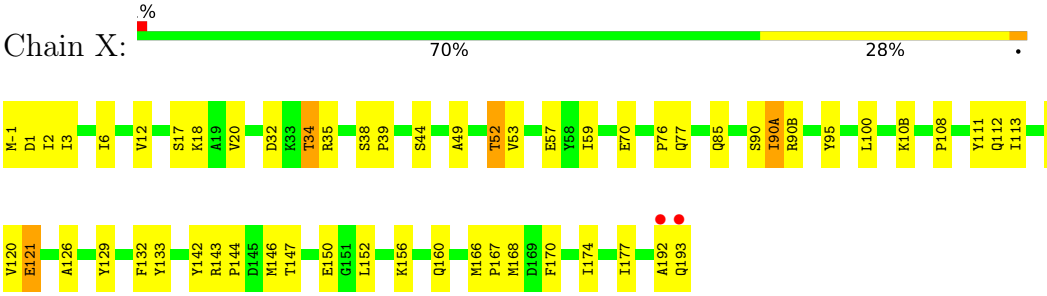


• Molecule 10: Proteasome component C11

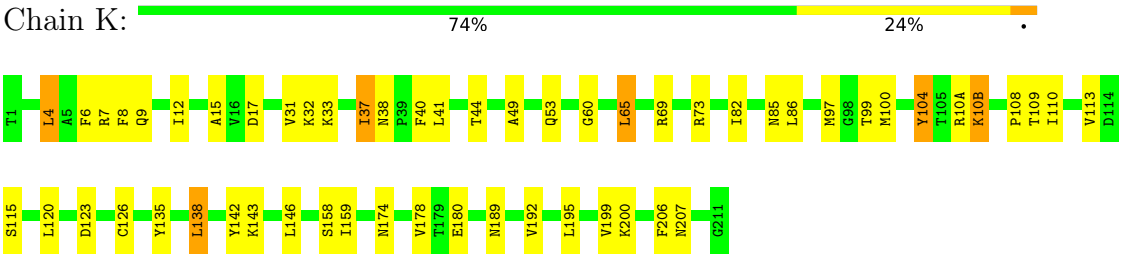
Chain J:



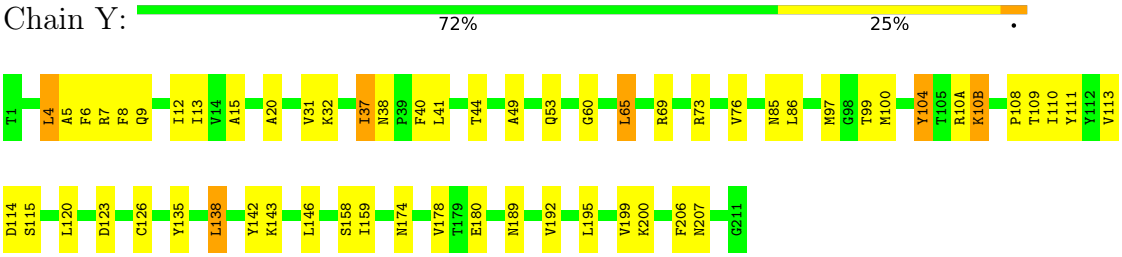
• Molecule 10: Proteasome component C11



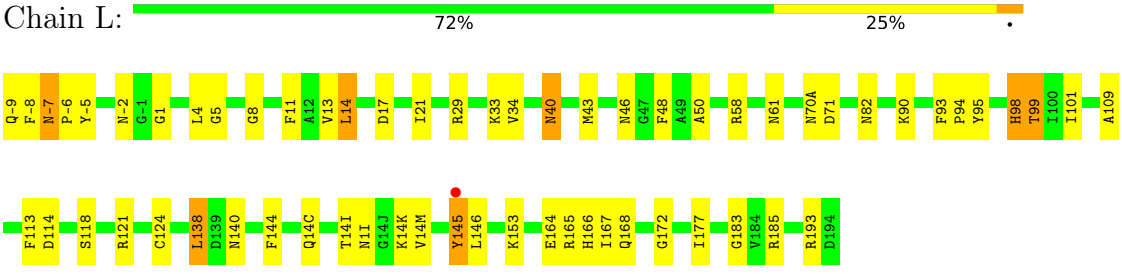
• Molecule 11: Proteasome component PRE2



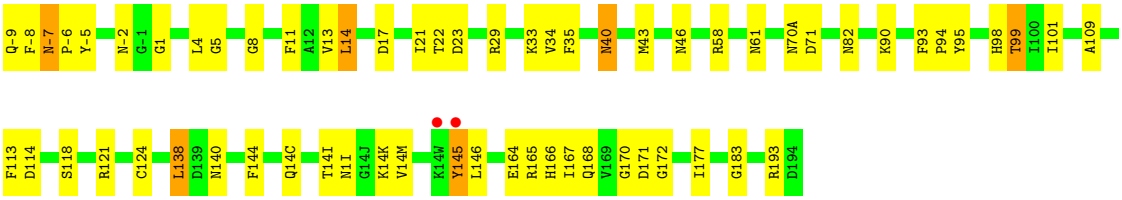
• Molecule 11: Proteasome component PRE2



• Molecule 12: Proteasome component C5

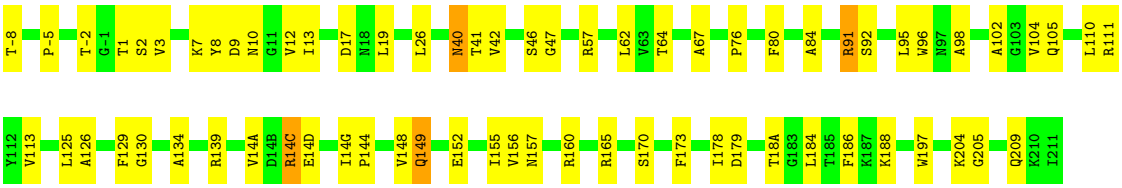


• Molecule 12: Proteasome component C5



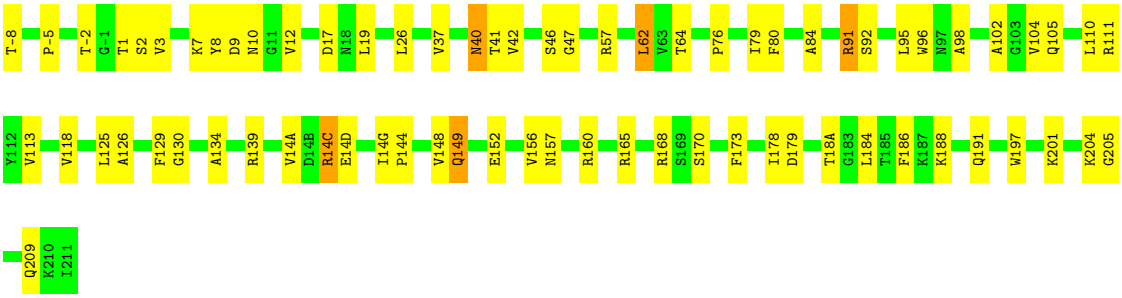
• Molecule 13: Proteasome component PRE4

Chain M:



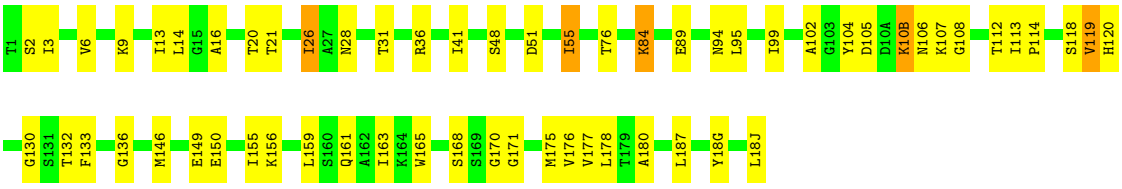
• Molecule 13: Proteasome component PRE4

Chain 1:



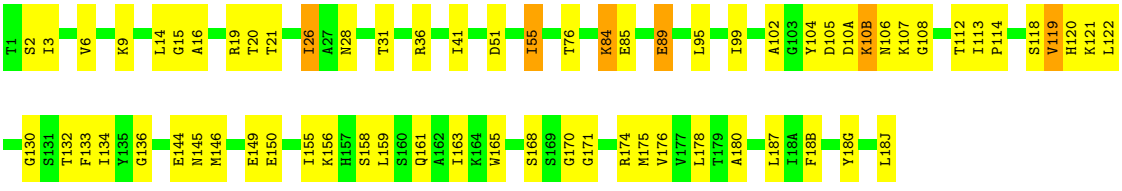
• Molecule 14: Proteasome component PRE3

Chain N:



• Molecule 14: Proteasome component PRE3

Chain 2:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	135.24Å 301.45Å 144.42Å 90.00° 112.94° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 49.48 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.7 (15.00-2.50) 99.2 (49.48-2.21)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.90 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.230 , 0.255 0.220 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	25.4	Xtriage
Anisotropy	0.792	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 30.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	51001	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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: SA1

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	0.36	0/1952	0.65	0/2642
1	O	0.38	0/1952	0.64	0/2642
2	B	0.37	0/1935	0.62	0/2618
2	P	0.38	0/1935	0.63	0/2618
3	C	0.35	0/1920	0.61	0/2598
3	Q	0.35	0/1920	0.61	0/2598
4	D	0.35	0/1887	0.61	0/2541
4	R	0.36	0/1887	0.61	0/2541
5	E	0.35	0/1823	0.61	0/2463
5	S	0.36	0/1823	0.60	0/2463
6	F	0.37	0/1937	0.61	0/2614
6	T	0.38	0/1937	0.62	0/2614
7	G	0.39	0/1959	0.62	0/2652
7	U	0.41	0/1959	0.62	0/2652
8	H	0.39	0/1716	0.68	0/2326
8	V	0.37	0/1716	0.68	0/2326
9	I	0.39	0/1611	0.66	0/2174
9	W	0.41	0/1611	0.67	0/2174
10	J	0.37	0/1613	0.65	0/2173
10	X	0.38	0/1613	0.65	0/2173
11	K	0.40	0/1681	0.65	0/2274
11	Y	0.38	0/1681	0.64	0/2274
12	L	0.38	0/1795	0.66	0/2420
12	Z	0.38	0/1795	0.66	0/2420
13	1	0.41	0/1855	0.69	1/2514 (0.0%)
13	M	0.39	0/1855	0.68	1/2514 (0.0%)
14	2	0.40	0/1541	0.66	0/2087
14	N	0.41	0/1541	0.66	0/2087
All	All	0.38	0/50450	0.64	2/68192 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	1	95	LEU	N-CA-C	-5.39	96.45	111.00
13	M	95	LEU	N-CA-C	-5.20	96.96	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1926	51	0
1	O	1915	0	1926	59	0
2	B	1905	0	1901	93	0
2	P	1905	0	1901	93	0
3	C	1891	0	1900	105	0
3	Q	1891	0	1900	97	0
4	D	1862	0	1836	47	0
4	R	1862	0	1836	49	0
5	E	1795	0	1797	83	0
5	S	1795	0	1797	92	0
6	F	1897	0	1886	71	0
6	T	1897	0	1886	74	0
7	G	1921	0	1910	69	0
7	U	1921	0	1910	74	0
8	H	1685	0	1687	65	0
8	V	1685	0	1687	64	0
9	I	1581	0	1574	41	0
9	W	1581	0	1574	43	0
10	J	1585	0	1590	52	0
10	X	1585	0	1590	59	0
11	K	1644	0	1594	52	0
11	Y	1644	0	1594	54	0
12	L	1757	0	1711	51	0
12	Z	1757	0	1711	50	0
13	1	1824	0	1832	63	0
13	M	1824	0	1832	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	2	1512	0	1480	61	0
14	N	1512	0	1480	57	0
15	2	20	0	20	4	0
15	H	20	0	20	1	0
15	K	20	0	20	1	0
15	N	20	0	20	4	0
15	V	20	0	20	1	0
15	Y	20	0	20	1	0
16	1	72	0	0	4	0
16	2	56	0	0	1	0
16	A	57	0	0	2	0
16	B	37	0	0	2	0
16	C	42	0	0	3	0
16	D	40	0	0	1	0
16	E	23	0	0	2	0
16	F	48	0	0	4	0
16	G	63	0	0	3	0
16	H	50	0	0	2	0
16	I	68	0	0	1	0
16	J	50	0	0	2	0
16	K	47	0	0	2	0
16	L	55	0	0	3	0
16	M	70	0	0	1	0
16	N	57	0	0	2	0
16	O	34	0	0	2	0
16	P	28	0	0	2	0
16	Q	28	0	0	3	0
16	R	30	0	0	3	0
16	S	20	0	0	0	0
16	T	40	0	0	2	0
16	U	60	0	0	3	0
16	V	49	0	0	4	0
16	W	60	0	0	2	0
16	X	47	0	0	3	0
16	Y	49	0	0	2	0
16	Z	53	0	0	2	0
All	All	51001	0	49368	1624	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 16.

The worst 5 of 1624 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)
11:Y:10(B):LYS:H	11:Y:10(B):LYS:HD2	1.06	1.19
11:K:10(B):LYS:H	11:K:10(B):LYS:HD2	1.05	1.13
7:U:96:ALA:HA	7:U:107:MET:HE2	1.32	1.10
14:N:161:GLN:HE21	14:2:136:GLY:HA2	1.16	1.10
14:N:136:GLY:HA2	14:2:161:GLN:HE21	1.17	1.06

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%)	233 (94%)	13 (5%)	2 (1%)	19	35
1	O	248/250 (99%)	232 (94%)	14 (6%)	2 (1%)	19	35
2	B	242/244 (99%)	221 (91%)	17 (7%)	4 (2%)	9	16
2	P	242/244 (99%)	220 (91%)	18 (7%)	4 (2%)	9	16
3	C	239/241 (99%)	220 (92%)	15 (6%)	4 (2%)	9	16
3	Q	239/241 (99%)	221 (92%)	14 (6%)	4 (2%)	9	16
4	D	240/242 (99%)	227 (95%)	8 (3%)	5 (2%)	7	11
4	R	240/242 (99%)	226 (94%)	9 (4%)	5 (2%)	7	11
5	E	231/233 (99%)	211 (91%)	16 (7%)	4 (2%)	9	16
5	S	231/233 (99%)	211 (91%)	16 (7%)	4 (2%)	9	16
6	F	242/244 (99%)	229 (95%)	12 (5%)	1 (0%)	34	54
6	T	242/244 (99%)	230 (95%)	10 (4%)	2 (1%)	19	35
7	G	241/243 (99%)	230 (95%)	10 (4%)	1 (0%)	34	54
7	U	241/243 (99%)	226 (94%)	13 (5%)	2 (1%)	19	35
8	H	220/222 (99%)	211 (96%)	8 (4%)	1 (0%)	29	48
8	V	220/222 (99%)	211 (96%)	8 (4%)	1 (0%)	29	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
9	I	202/204 (99%)	196 (97%)	5 (2%)	1 (0%)	29 48
9	W	202/204 (99%)	195 (96%)	7 (4%)	0	100 100
10	J	196/198 (99%)	187 (95%)	7 (4%)	2 (1%)	15 28
10	X	196/198 (99%)	187 (95%)	7 (4%)	2 (1%)	15 28
11	K	210/212 (99%)	204 (97%)	6 (3%)	0	100 100
11	Y	210/212 (99%)	205 (98%)	5 (2%)	0	100 100
12	L	220/222 (99%)	210 (96%)	9 (4%)	1 (0%)	29 48
12	Z	220/222 (99%)	211 (96%)	8 (4%)	1 (0%)	29 48
13	1	231/233 (99%)	220 (95%)	11 (5%)	0	100 100
13	M	231/233 (99%)	221 (96%)	10 (4%)	0	100 100
14	2	194/196 (99%)	187 (96%)	7 (4%)	0	100 100
14	N	194/196 (99%)	188 (97%)	6 (3%)	0	100 100
All	All	6312/6368 (99%)	5970 (95%)	289 (5%)	53 (1%)	19 35

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	58	LEU
4	D	12(G)	GLU
3	Q	58	LEU
4	R	12(G)	GLU
1	A	5	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%)	202 (97%)	7 (3%)	38 64
1	O	209/209 (100%)	203 (97%)	6 (3%)	42 69
2	B	203/203 (100%)	187 (92%)	16 (8%)	12 24
2	P	203/203 (100%)	186 (92%)	17 (8%)	11 21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	213/213 (100%)	201 (94%)	12 (6%)	21	40
3	Q	213/213 (100%)	201 (94%)	12 (6%)	21	40
4	D	198/198 (100%)	185 (93%)	13 (7%)	16	32
4	R	198/198 (100%)	185 (93%)	13 (7%)	16	32
5	E	192/192 (100%)	174 (91%)	18 (9%)	8	17
5	S	192/192 (100%)	173 (90%)	19 (10%)	8	15
6	F	201/201 (100%)	185 (92%)	16 (8%)	12	23
6	T	201/201 (100%)	186 (92%)	15 (8%)	13	26
7	G	207/207 (100%)	195 (94%)	12 (6%)	20	38
7	U	207/207 (100%)	195 (94%)	12 (6%)	20	38
8	H	181/181 (100%)	172 (95%)	9 (5%)	24	46
8	V	181/181 (100%)	171 (94%)	10 (6%)	21	41
9	I	172/172 (100%)	166 (96%)	6 (4%)	36	62
9	W	172/172 (100%)	165 (96%)	7 (4%)	30	55
10	J	175/175 (100%)	167 (95%)	8 (5%)	27	50
10	X	175/175 (100%)	167 (95%)	8 (5%)	27	50
11	K	169/169 (100%)	161 (95%)	8 (5%)	26	49
11	Y	169/169 (100%)	161 (95%)	8 (5%)	26	49
12	L	185/185 (100%)	174 (94%)	11 (6%)	19	37
12	Z	185/185 (100%)	174 (94%)	11 (6%)	19	37
13	1	199/199 (100%)	192 (96%)	7 (4%)	36	62
13	M	199/199 (100%)	192 (96%)	7 (4%)	36	62
14	2	162/162 (100%)	152 (94%)	10 (6%)	18	35
14	N	162/162 (100%)	153 (94%)	9 (6%)	21	40
All	All	5332/5332 (100%)	5025 (94%)	307 (6%)	20	38

5 of 307 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	T	205	ASN
12	Z	99	THR
7	U	121	GLN
9	W	125	ILE
14	2	84	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 195 such sidechains are listed below:

Mol	Chain	Res	Type
3	Q	163	GLN
7	U	34(A)	ASN
4	R	108	ASN
5	S	121	GLN
7	U	178	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)

6 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	SA1	K	0	11	18,22,22	1.30	1 (5%)	24,34,34	1.89	2 (8%)
15	SA1	H	0	8	18,22,22	1.51	3 (16%)	24,34,34	1.75	2 (8%)
15	SA1	V	0	8	18,22,22	1.37	2 (11%)	24,34,34	1.78	2 (8%)
15	SA1	2	0	14	18,22,22	1.28	1 (5%)	24,34,34	1.92	3 (12%)
15	SA1	Y	0	11	18,22,22	1.23	1 (5%)	24,34,34	1.87	2 (8%)
15	SA1	N	0	14	18,22,22	1.30	2 (11%)	24,34,34	1.95	2 (8%)

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	SA1	K	0	11	-	0/4/52/52	0/3/3/3
15	SA1	H	0	8	-	0/4/52/52	0/3/3/3
15	SA1	V	0	8	-	0/4/52/52	0/3/3/3
15	SA1	2	0	14	-	0/4/52/52	0/3/3/3
15	SA1	Y	0	11	-	0/4/52/52	0/3/3/3
15	SA1	N	0	14	-	0/4/52/52	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	K	0	SA1	C4-C3	3.58	1.57	1.51
15	V	0	SA1	C4-C3	3.47	1.57	1.51
15	H	0	SA1	C4-C3	3.36	1.57	1.51
15	Y	0	SA1	C4-C3	3.26	1.57	1.51
15	2	0	SA1	C4-C3	3.11	1.57	1.51

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	N	0	SA1	C9-C10-C11	7.24	123.18	114.09
15	2	0	SA1	C9-C10-C11	6.99	122.87	114.09
15	Y	0	SA1	C9-C10-C11	6.75	122.57	114.09
15	K	0	SA1	C9-C10-C11	6.71	122.52	114.09
15	V	0	SA1	C9-C10-C11	6.55	122.31	114.09

There are no chirality outliers.

There are no torsion outliers.

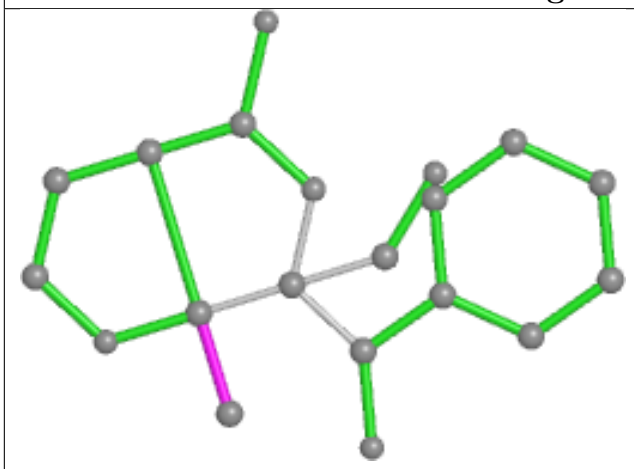
There are no ring outliers.

6 monomers are involved in 12 short contacts:

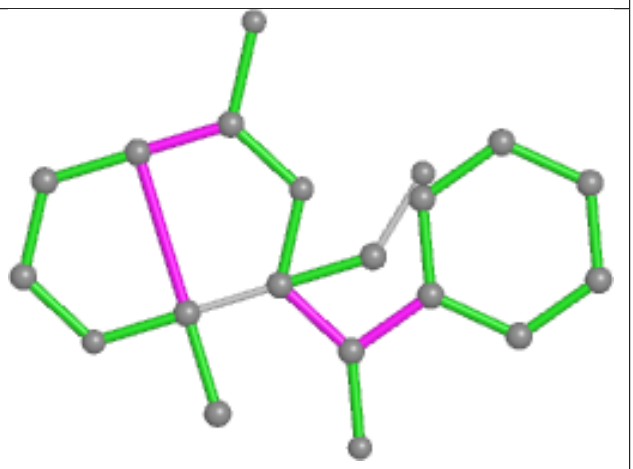
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	K	0	SA1	1	0
15	H	0	SA1	1	0
15	V	0	SA1	1	0
15	2	0	SA1	4	0
15	Y	0	SA1	1	0
15	N	0	SA1	4	0

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 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.

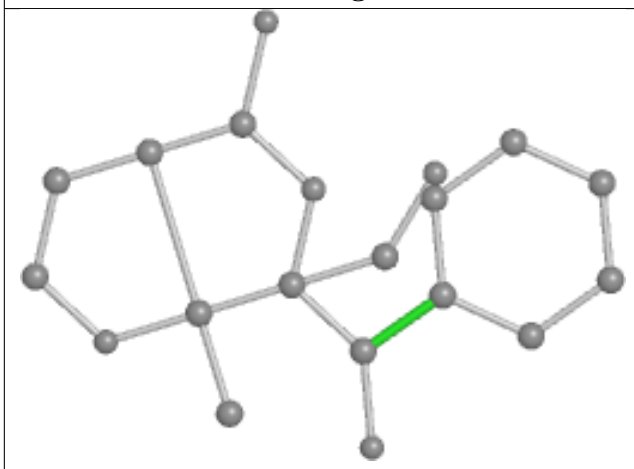
Ligand SA1 K 0



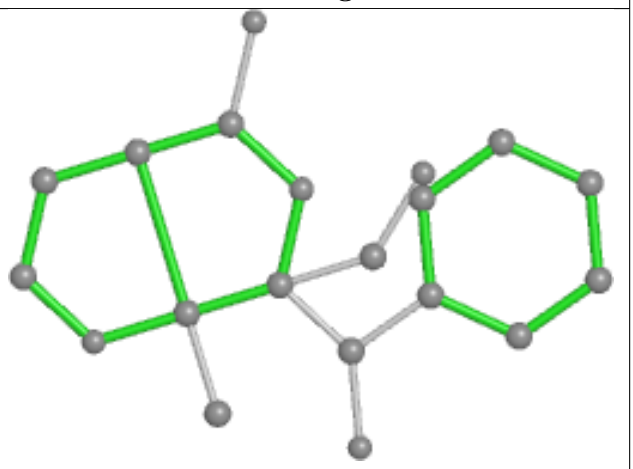
Bond lengths



Bond angles

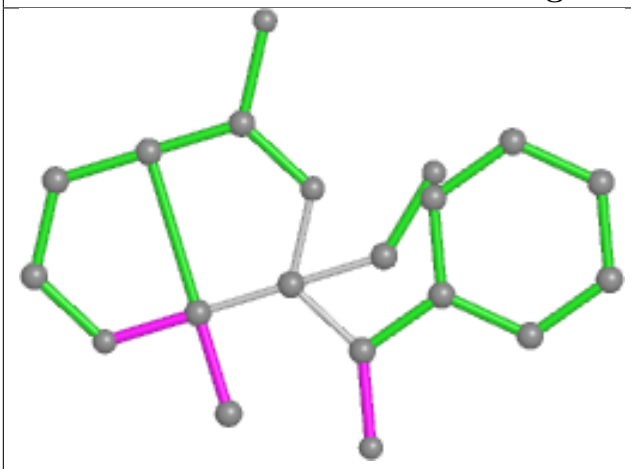


Torsions

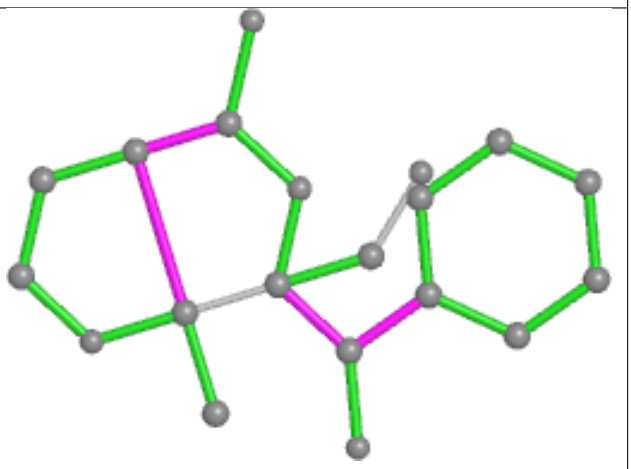


Rings

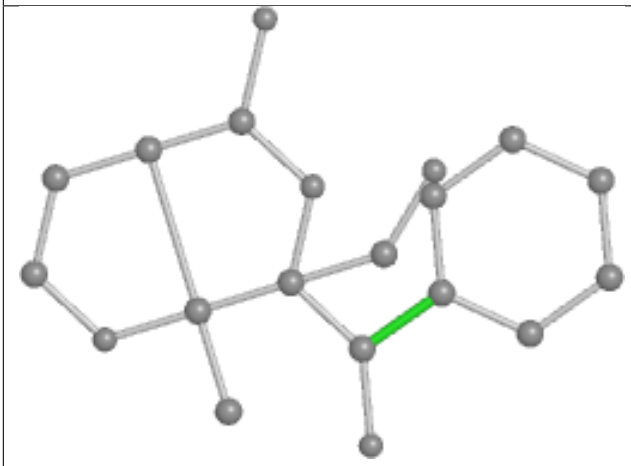
Ligand SA1 H 0



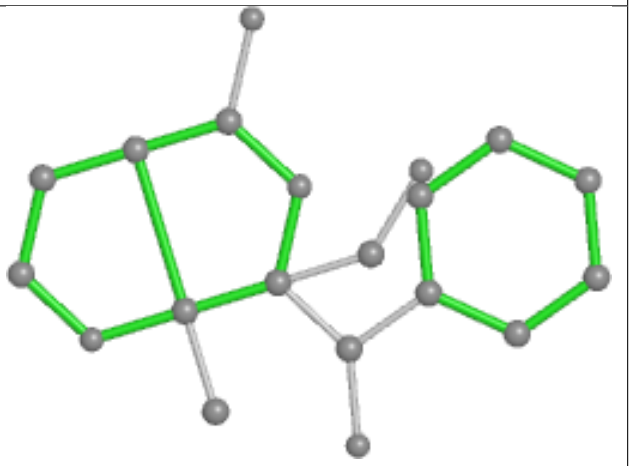
Bond lengths



Bond angles

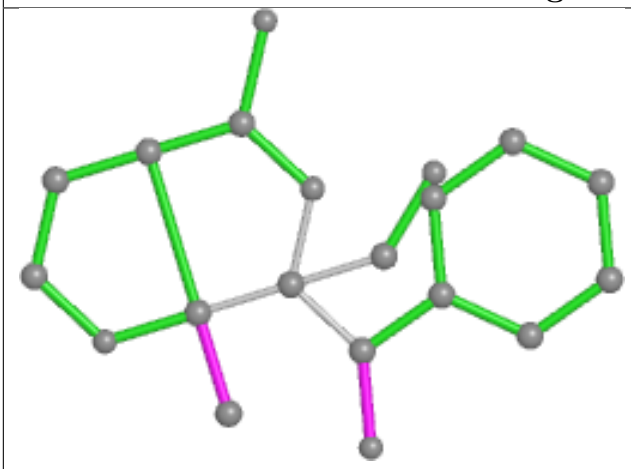


Torsions

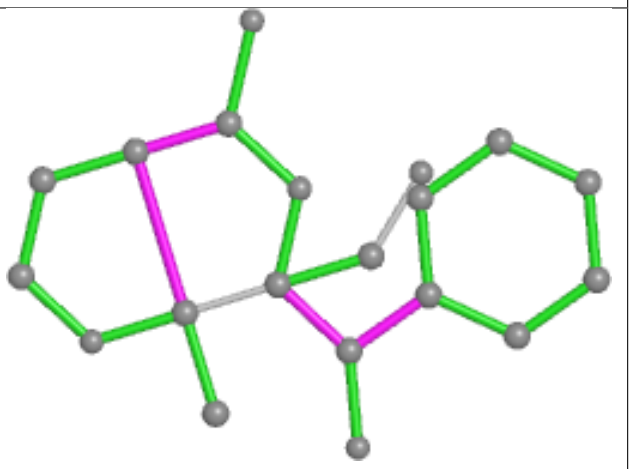


Rings

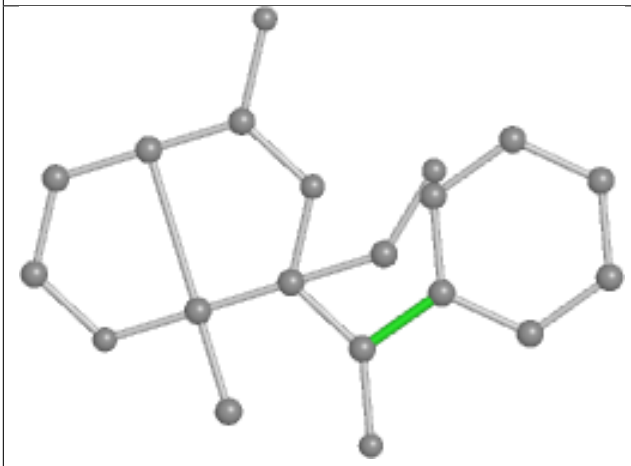
Ligand SA1 V 0



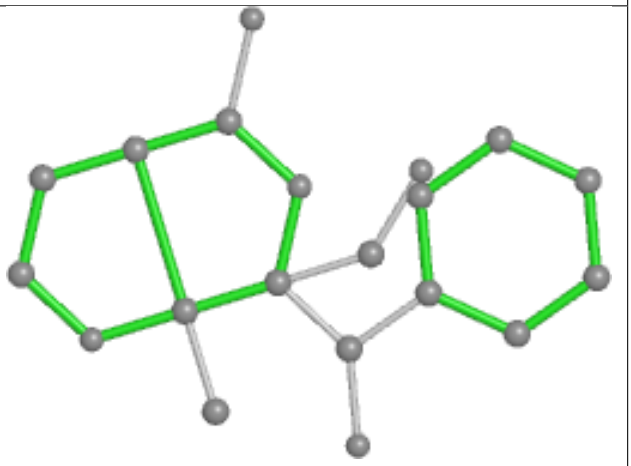
Bond lengths



Bond angles

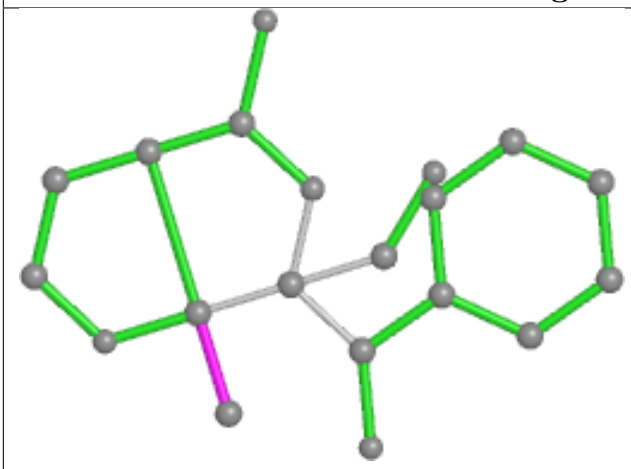


Torsions

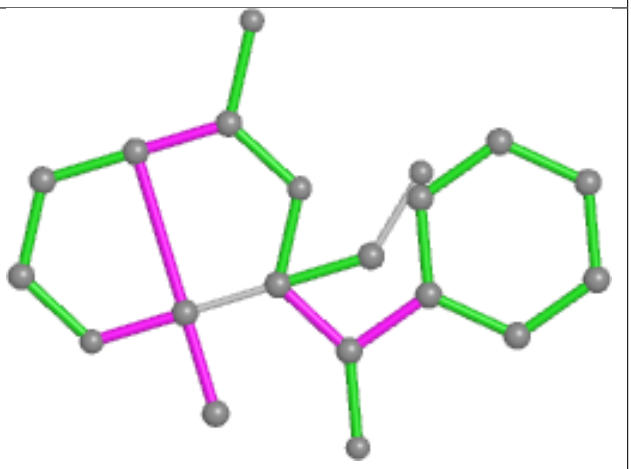


Rings

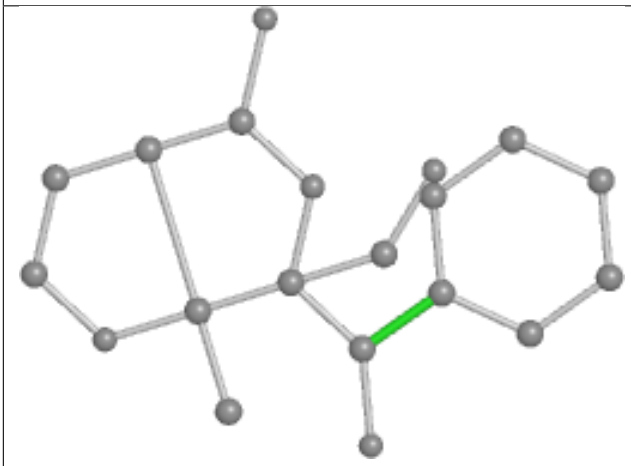
Ligand SA1 2 0



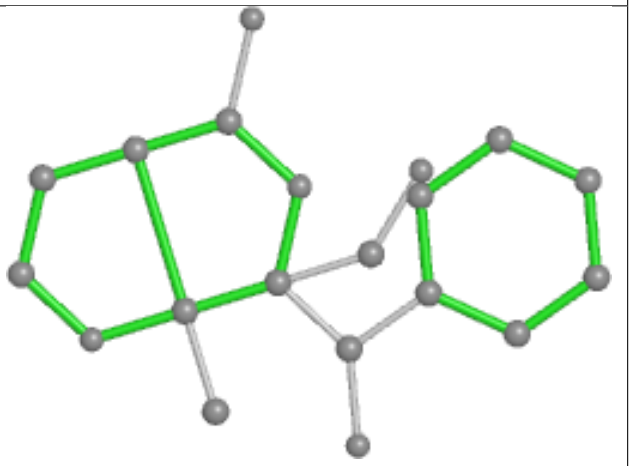
Bond lengths



Bond angles

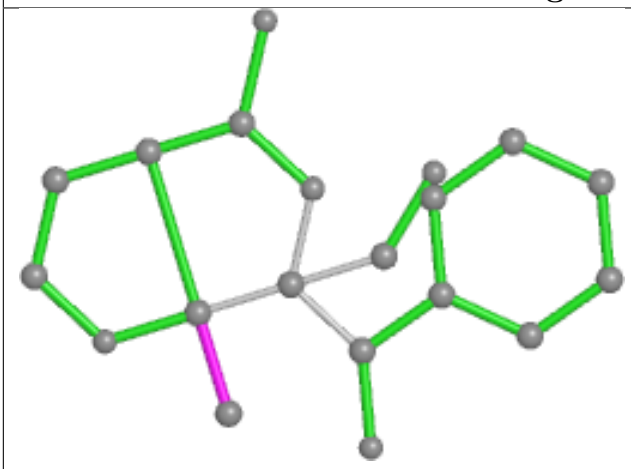


Torsions

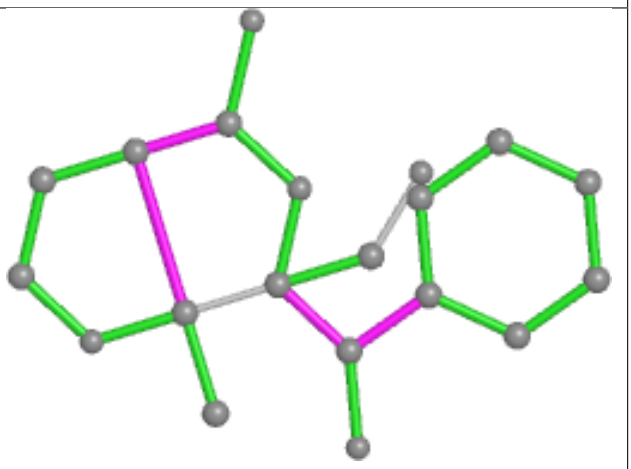


Rings

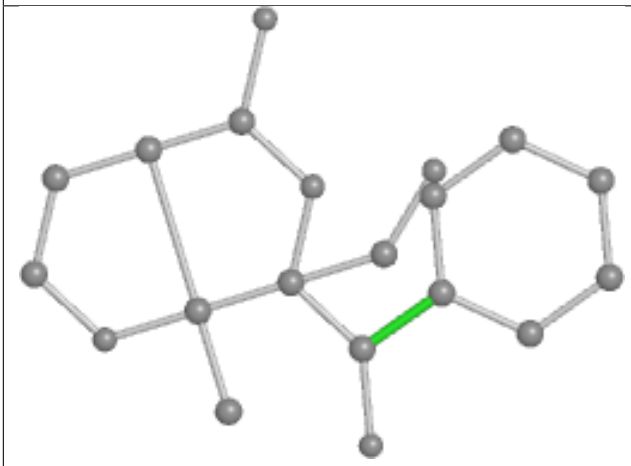
Ligand SA1 Y 0



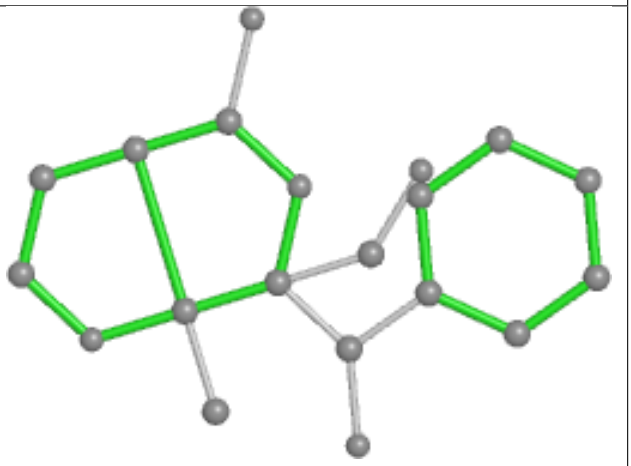
Bond lengths



Bond angles

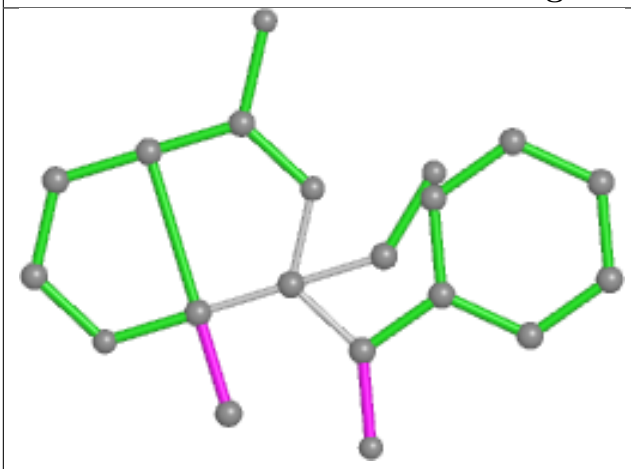


Torsions

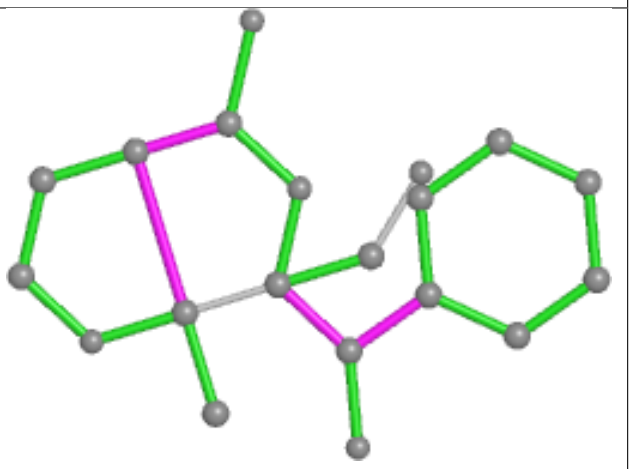


Rings

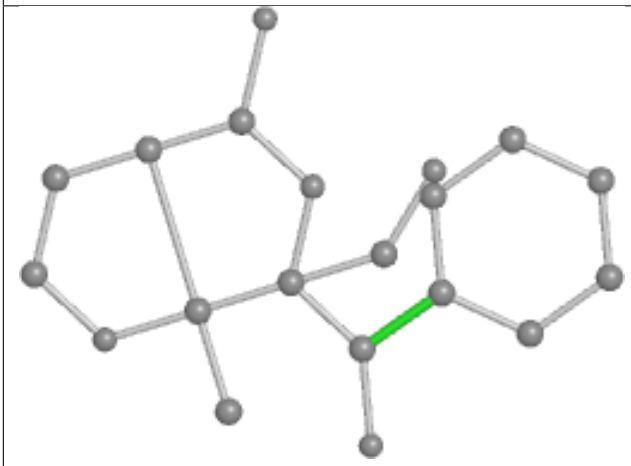
Ligand SA1 N 0



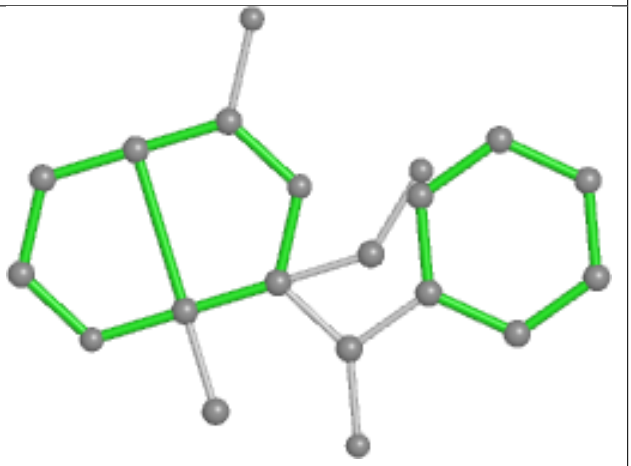
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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%)	-0.45	1 (0%)	92	93	21, 34, 63, 92	0
1	O	250/250 (100%)	-0.40	3 (1%)	79	80	24, 41, 69, 93	0
2	B	244/244 (100%)	-0.24	4 (1%)	72	74	19, 42, 77, 105	0
2	P	244/244 (100%)	-0.20	5 (2%)	65	68	23, 43, 78, 105	0
3	C	241/241 (100%)	-0.25	3 (1%)	79	80	22, 43, 96, 110	0
3	Q	241/241 (100%)	0.06	18 (7%)	14	14	28, 49, 98, 109	0
4	D	242/242 (100%)	-0.28	7 (2%)	51	55	23, 43, 77, 108	0
4	R	242/242 (100%)	-0.18	6 (2%)	57	61	27, 48, 79, 109	0
5	E	233/233 (100%)	-0.24	5 (2%)	63	66	30, 47, 72, 98	0
5	S	233/233 (100%)	-0.07	9 (3%)	39	42	29, 51, 77, 95	0
6	F	244/244 (100%)	-0.43	1 (0%)	92	93	20, 41, 76, 93	0
6	T	244/244 (100%)	-0.27	1 (0%)	92	93	22, 43, 78, 95	0
7	G	243/243 (100%)	-0.47	2 (0%)	86	87	19, 36, 62, 101	0
7	U	243/243 (100%)	-0.37	2 (0%)	86	87	19, 38, 62, 102	0
8	H	222/222 (100%)	-0.52	0	100	100	16, 31, 52, 81	0
8	V	222/222 (100%)	-0.52	0	100	100	22, 35, 54, 83	0
9	I	204/204 (100%)	-0.61	0	100	100	18, 32, 48, 65	0
9	W	204/204 (100%)	-0.56	0	100	100	16, 31, 51, 66	0
10	J	198/198 (100%)	-0.49	3 (1%)	73	75	19, 35, 52, 106	0
10	X	198/198 (100%)	-0.48	2 (1%)	82	84	21, 35, 51, 108	0
11	K	212/212 (100%)	-0.60	0	100	100	16, 32, 50, 58	0
11	Y	212/212 (100%)	-0.57	0	100	100	19, 35, 53, 62	0
12	L	222/222 (100%)	-0.57	1 (0%)	91	91	17, 33, 55, 75	0
12	Z	222/222 (100%)	-0.55	2 (0%)	84	86	19, 34, 55, 75	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
13	1	233/233 (100%)	-0.60	0	100	100	18, 33, 47, 50	0
13	M	233/233 (100%)	-0.59	0	100	100	19, 34, 48, 55	0
14	2	196/196 (100%)	-0.57	0	100	100	18, 31, 51, 63	0
14	N	196/196 (100%)	-0.58	0	100	100	16, 29, 50, 65	0
All	All	6368/6368 (100%)	-0.41	75 (1%)	79	80	16, 38, 70, 110	0

The worst 5 of 75 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	12(D)	ALA	9.3
4	R	12(E)	SER	9.0
7	U	240	ASP	8.9
4	R	12(D)	ALA	8.1
7	U	6	ALA	7.9

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.

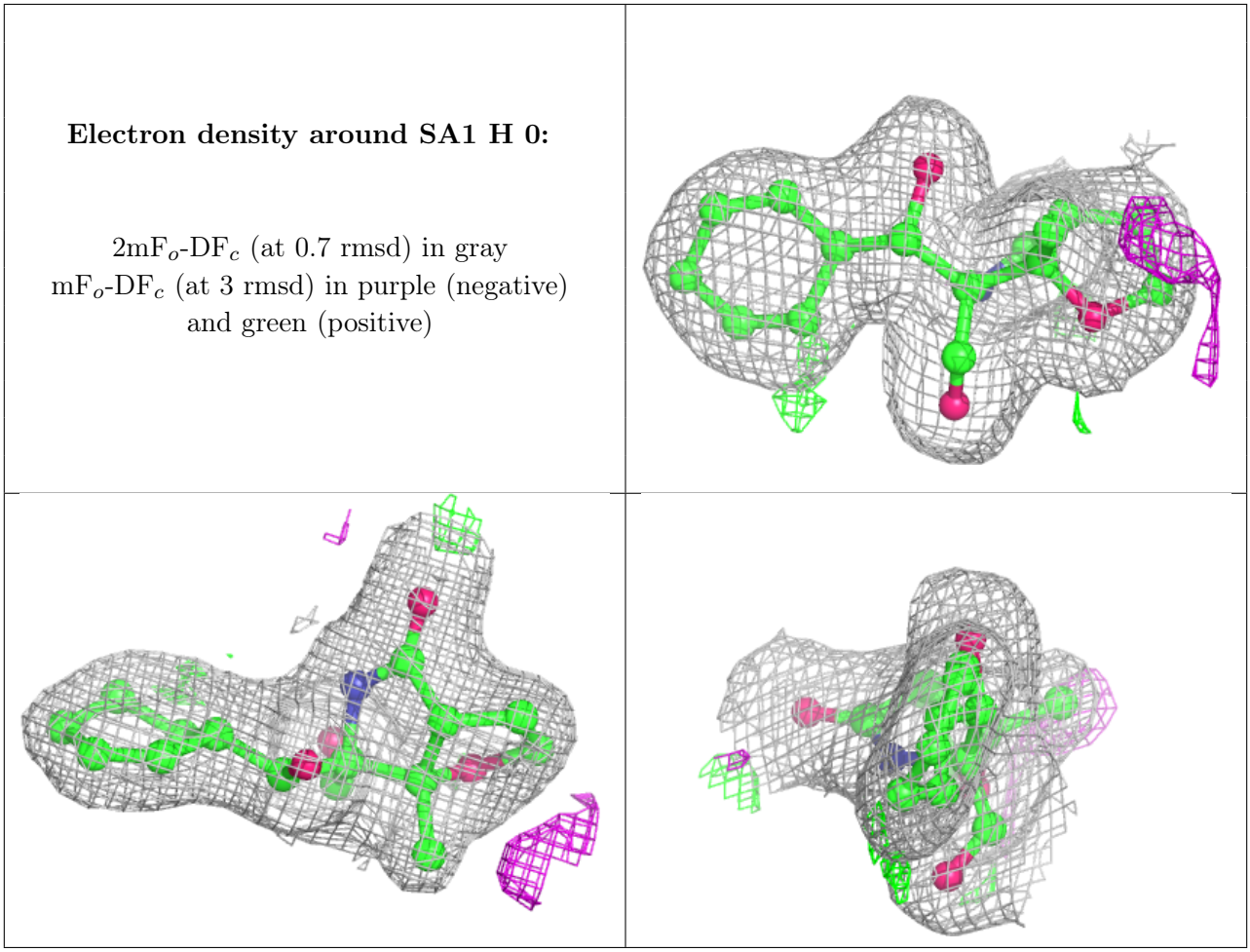
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
15	SA1	H	0	20/20	0.95	0.10	30,34,36,36	0
15	SA1	K	0	20/20	0.95	0.11	19,30,33,33	0
15	SA1	N	0	20/20	0.95	0.12	19,26,29,30	0
15	SA1	Y	0	20/20	0.95	0.11	27,30,32,33	0
15	SA1	2	0	20/20	0.95	0.13	27,30,32,32	0
15	SA1	V	0	20/20	0.96	0.12	32,34,40,41	0

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.

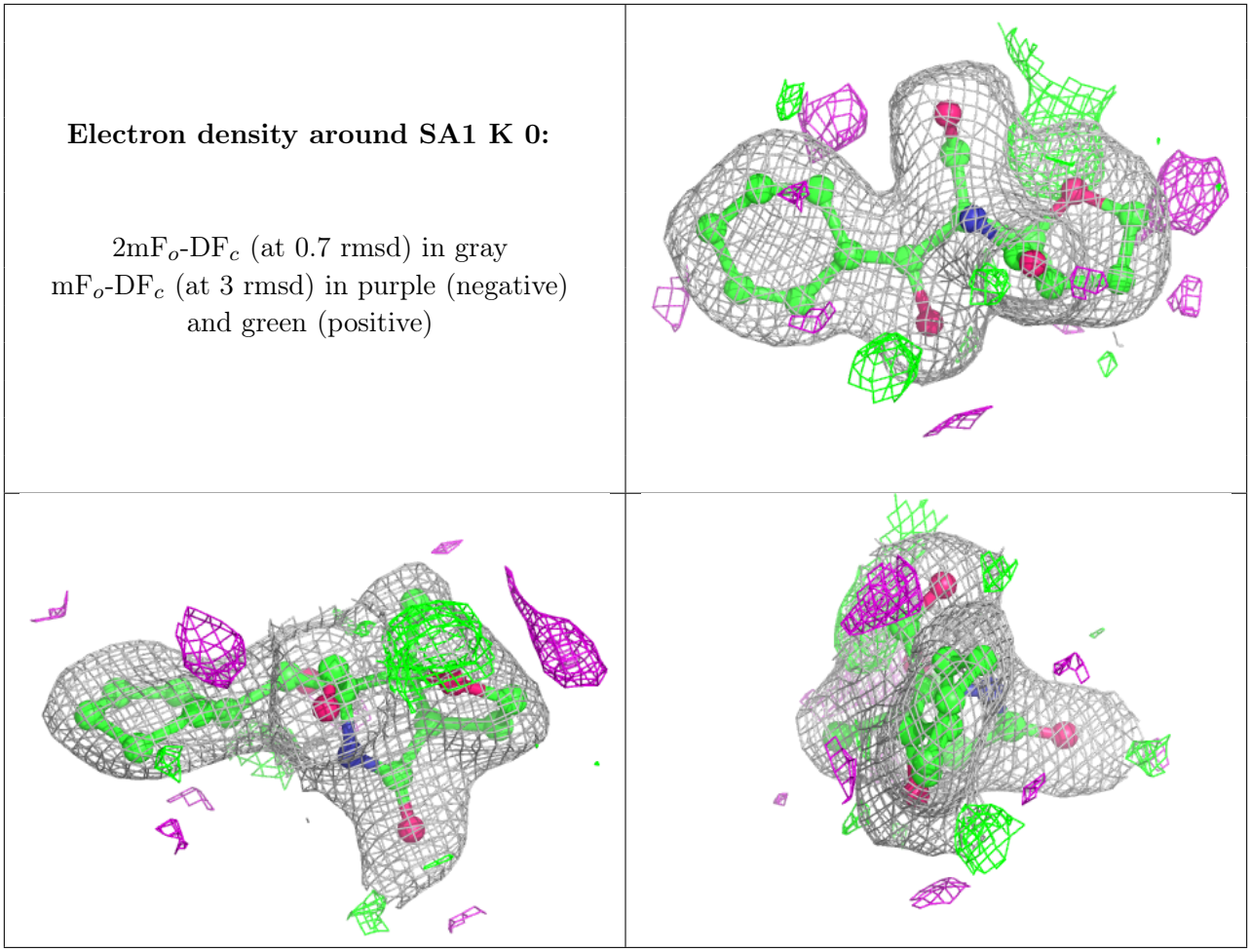
Electron density around SA1 H 0:

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



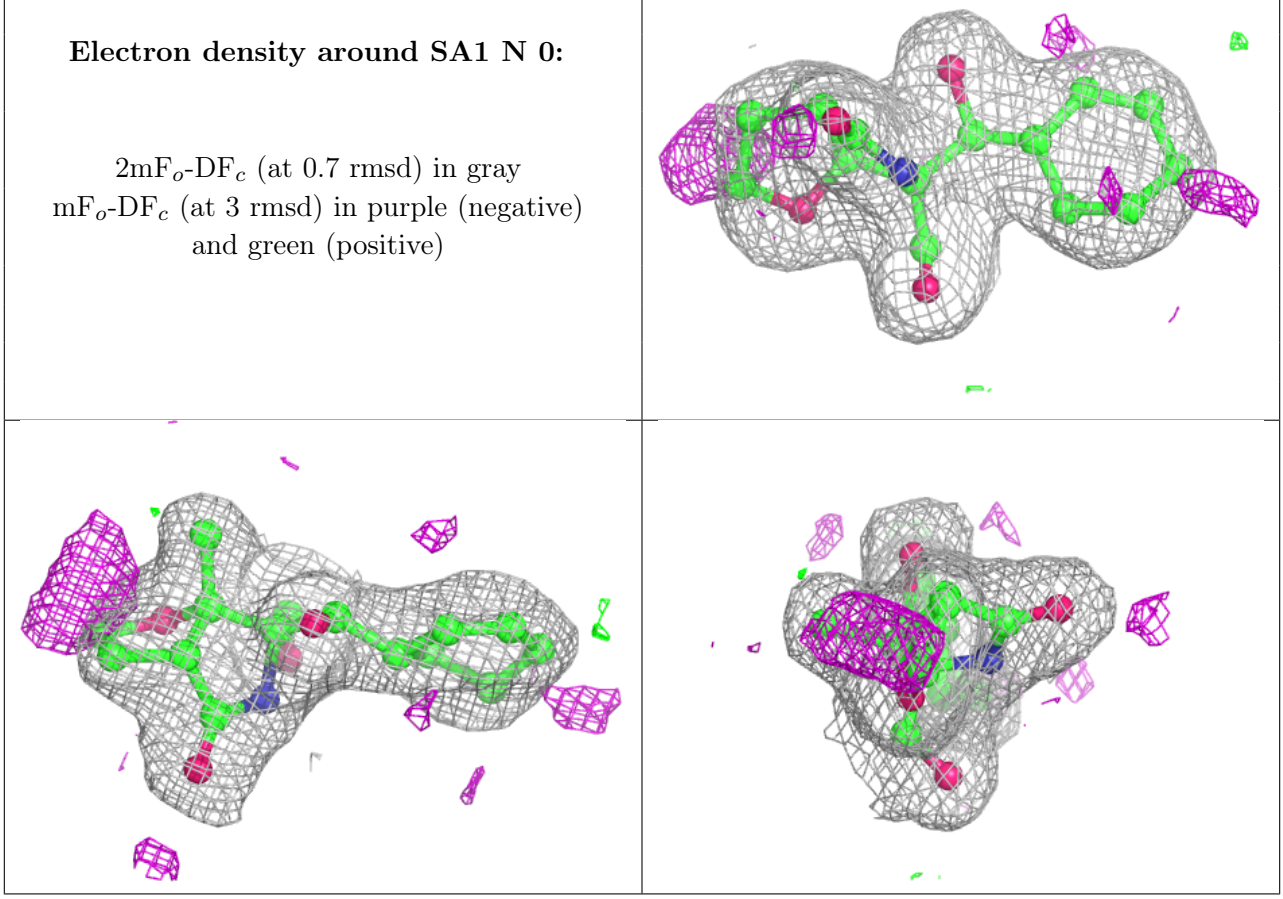
Electron density around SA1 K 0:

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



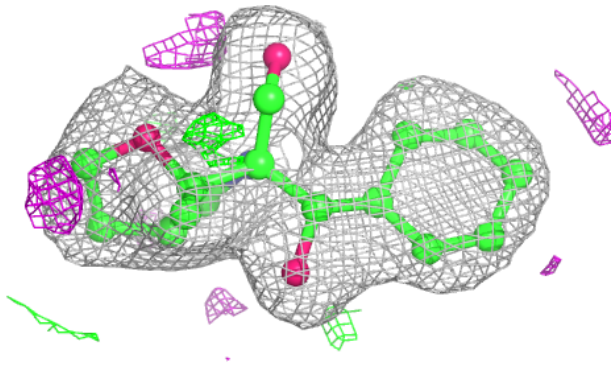
Electron density around SA1 N 0:

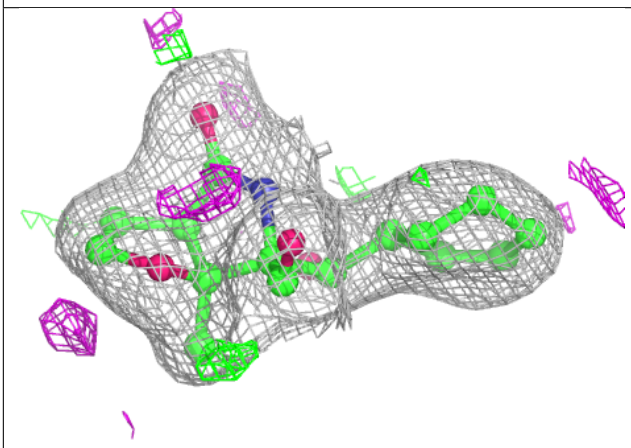
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

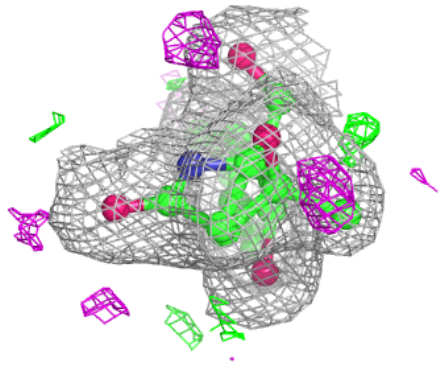


Electron density around SA1 Y 0:

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

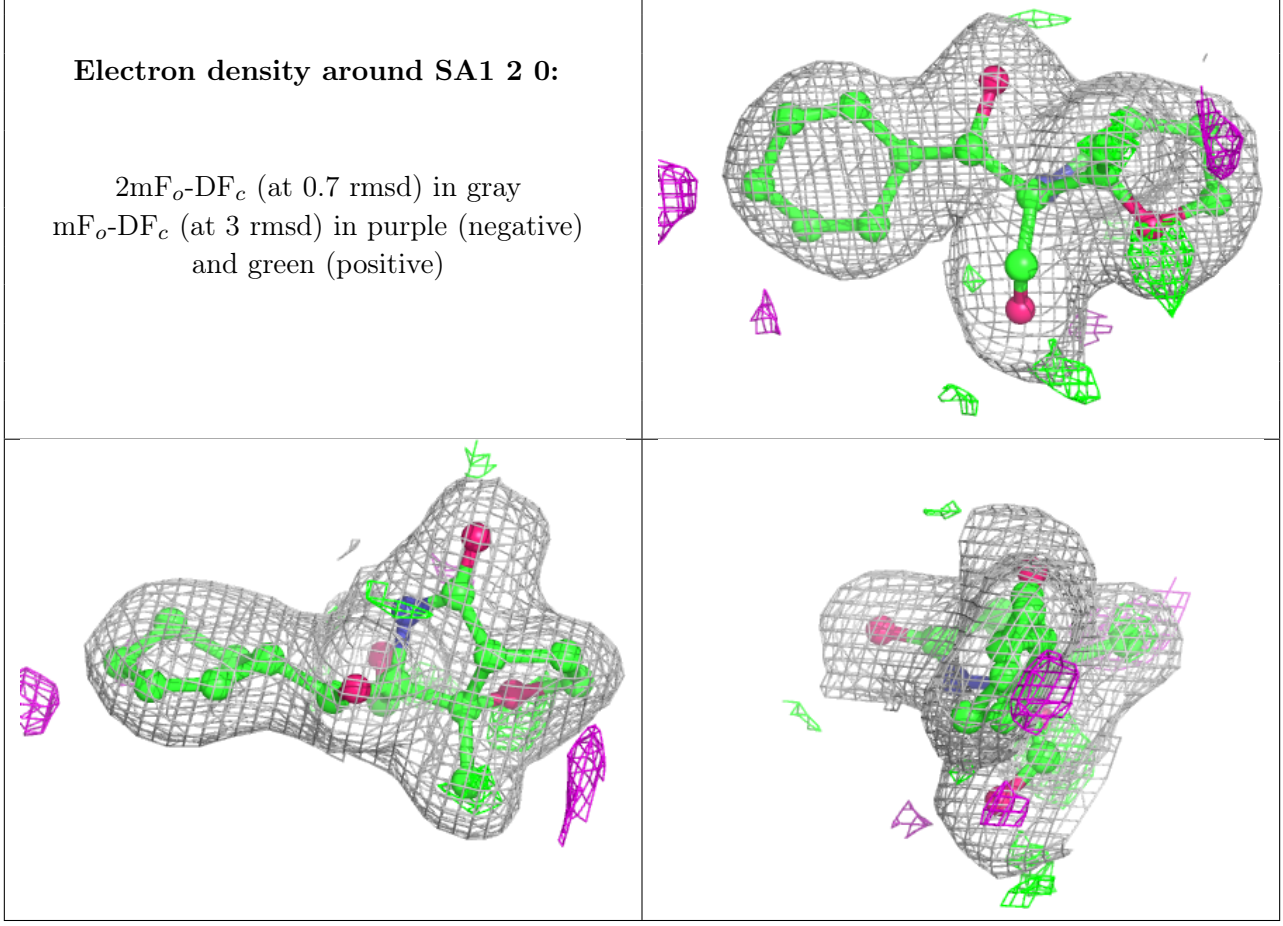






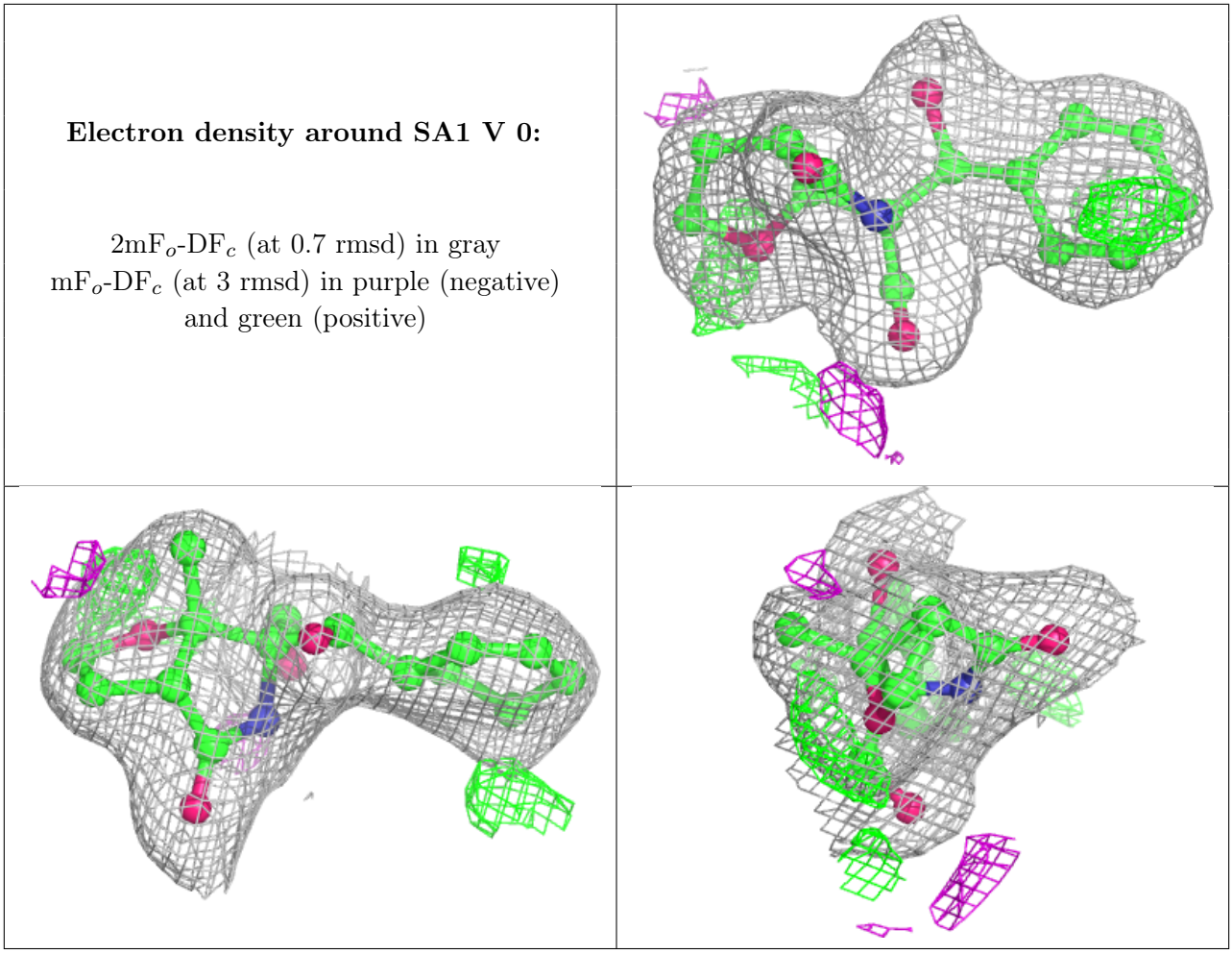
Electron density around SA1 2 0:

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



Electron density around SA1 V 0:

$2mF_o$-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.