wwPDB X-ray Structure Validation Summary Report (i)

Mar 12, 2026 – 12:29 PM UTC

PDB ID	:	6HV4 / pdb_00006hv4
Title	:	Yeast 20S proteasome with human beta2i (1-53) in complex with ONX 0914
Authors	:	Huber, E.M.; Groll, M.
Deposited on	:	2018-10-10
Resolution	:	3.00 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:

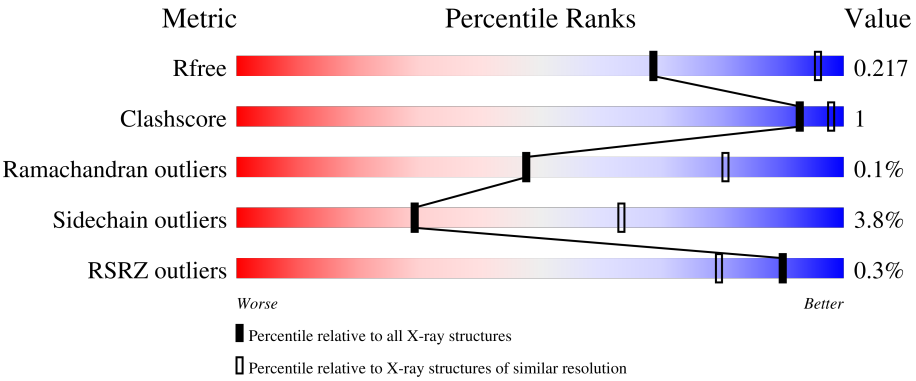
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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% 97% .
1	O	250	98% .
2	B	258	% 88% 6% • 5%
2	P	258	88% 6% 5%
3	C	254	87% 6% • 6%

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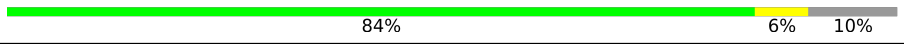
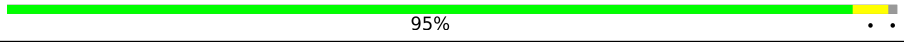
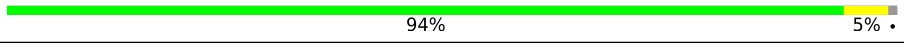
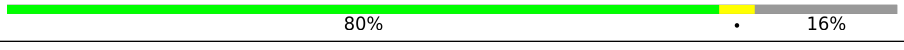
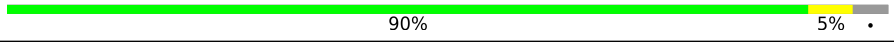
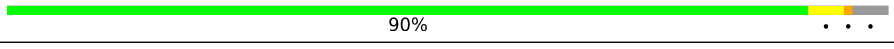
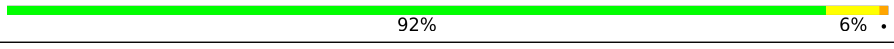
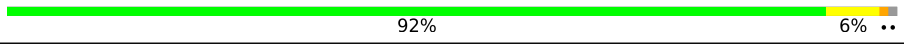
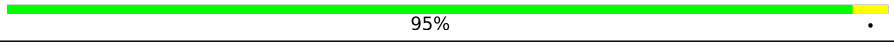
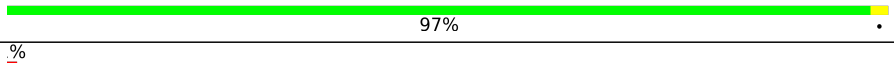
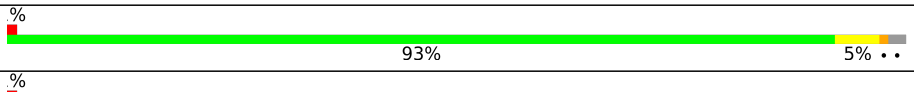
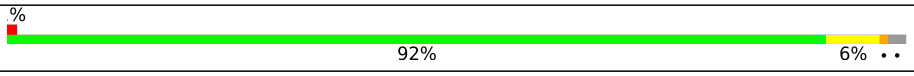
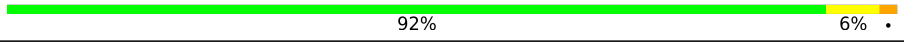
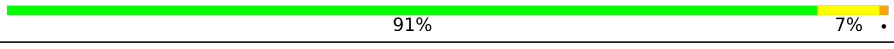
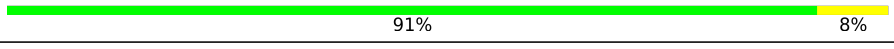
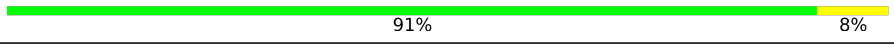
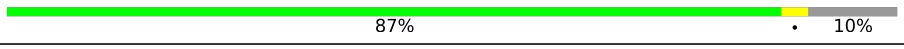
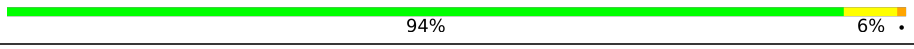
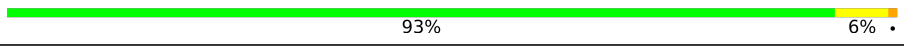
Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	226	
8	V	226	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
19	SO4	b	202	-	-	X	-

2 Entry composition (i)

There are 20 unique types of molecules in this entry. The entry contains 49728 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
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 subunit alpha type-3.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 8 is a protein called Proteasome subunit beta type-10,Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	226	Total	C	N	O	S	0	0	0
			1716	1081	291	336	8			
8	V	223	Total	C	N	O	S	0	0	0
			1688	1066	287	327	8			

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

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 subunit beta type-4.

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

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

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

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 subunit beta type-6.

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 subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	222	Total	C	N	O	S	0	0	0
			1736	1098	297	334	7			
13	a	222	Total	C	N	O	S	0	0	0
			1736	1098	297	334	7			

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

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

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	I	1	Total	Mg	0	0
			1	1		

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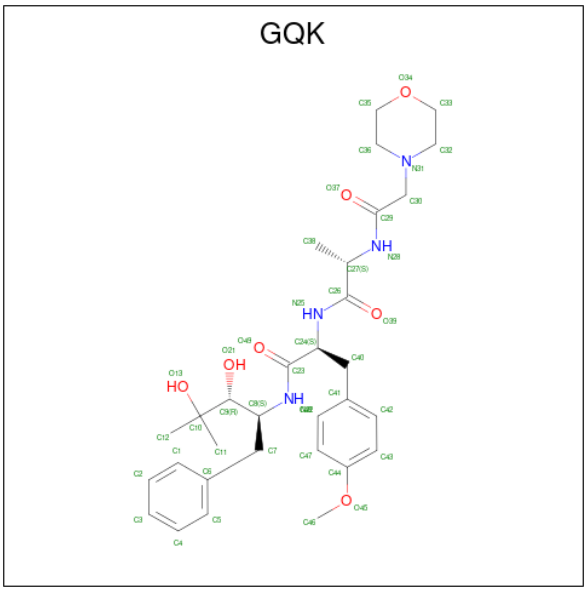
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	K	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	V	1	Total Mg 1 1	0	0
15	W	1	Total Mg 1 1	0	0
15	Y	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

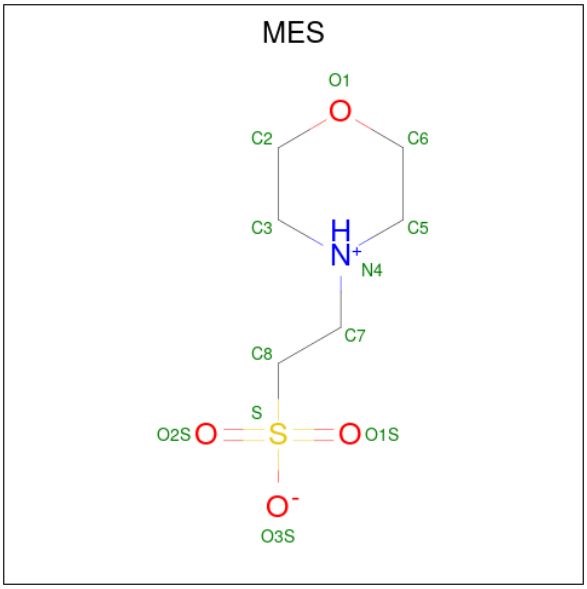
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is (2 {S})-3-(4-methoxyphenyl)- {N}-[(2 {S},3 {R})-4-methyl-3,4-bis(oxidanyl) -1-phenyl-pentan-2-yl]-2-[[(2 {S})-2-(2-morpholin-4-ylethanoylamino)propanoyl]amino]prop anamide (CCD ID: GQK) (formula: $C_{31}H_{44}N_4O_7$).



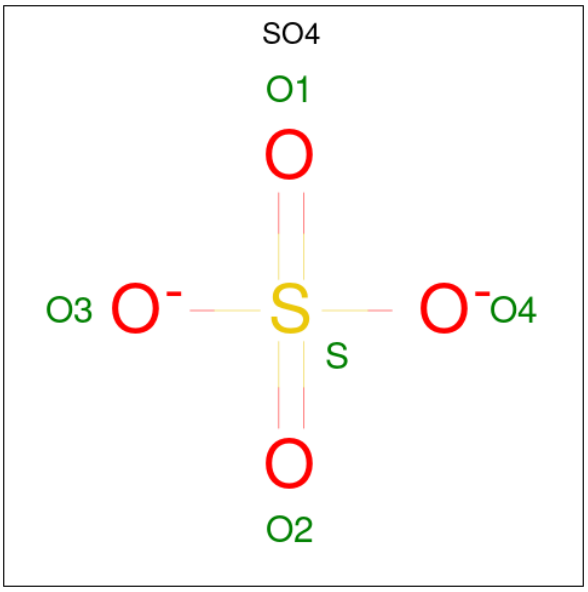
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	H	1	Total	C	N	O		0	0
			42	31	4	7			
17	K	1	Total	C	N	O		0	0
			42	31	4	7			
17	N	1	Total	C	N	O		0	0
			42	31	4	7			
17	V	1	Total	C	N	O		0	0
			42	31	4	7			
17	Y	1	Total	C	N	O		0	0
			42	31	4	7			
17	b	1	Total	C	N	O		0	0
			42	31	4	7			

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
18	H	1	Total	C	N	O	S		0	0
			12	6	1	4	1			
18	K	1	Total	C	N	O	S		0	0
			12	6	1	4	1			
18	V	1	Total	C	N	O	S		0	0
			12	6	1	4	1			
18	Y	1	Total	C	N	O	S		0	0
			12	6	1	4	1			

- Molecule 19 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	N	1	Total O S 5 4 1	0	0
19	b	1	Total O S 5 4 1	0	0

- Molecule 20 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
20	A	6	Total O 6 6	0	0
20	B	12	Total O 12 12	0	0
20	C	7	Total O 7 7	0	0
20	D	11	Total O 11 11	0	0
20	E	7	Total O 7 7	0	0
20	F	6	Total O 6 6	0	0
20	G	11	Total O 11 11	0	0
20	H	12	Total O 12 12	0	0
20	I	6	Total O 6 6	0	0
20	J	14	Total O 14 14	0	0

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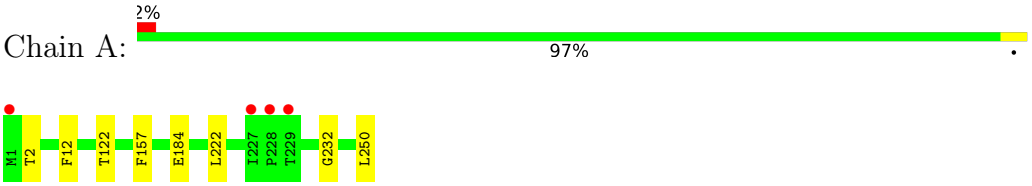
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
20	K	16	Total O 16 16	0	0
20	L	13	Total O 13 13	0	0
20	M	15	Total O 15 15	0	0
20	N	4	Total O 4 4	0	0
20	O	3	Total O 3 3	0	0
20	P	6	Total O 6 6	0	0
20	Q	2	Total O 2 2	0	0
20	R	3	Total O 3 3	0	0
20	S	8	Total O 8 8	0	0
20	T	9	Total O 9 9	0	0
20	U	9	Total O 9 9	0	0
20	V	9	Total O 9 9	0	0
20	W	5	Total O 5 5	0	0
20	X	10	Total O 10 10	0	0
20	Y	19	Total O 19 19	0	0
20	Z	11	Total O 11 11	0	0
20	a	13	Total O 13 13	0	0
20	b	5	Total O 5 5	0	0

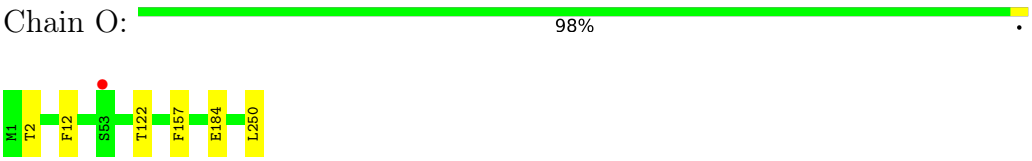
3 Residue-property plots (i)

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.

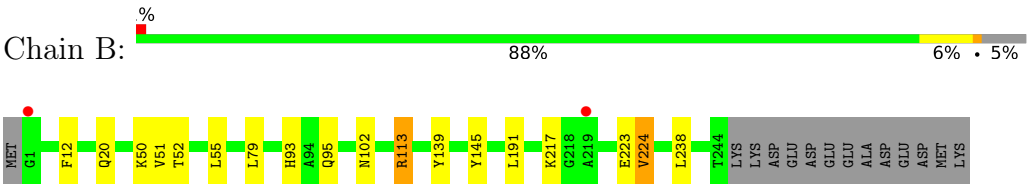
• Molecule 1: Proteasome subunit alpha type-2



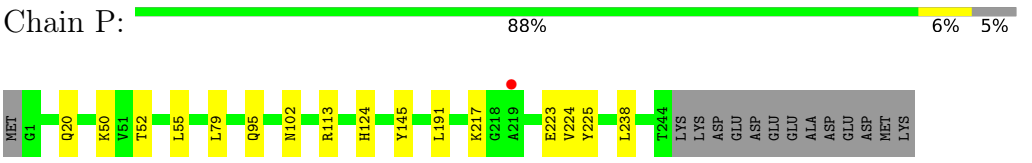
• Molecule 1: Proteasome subunit alpha type-2



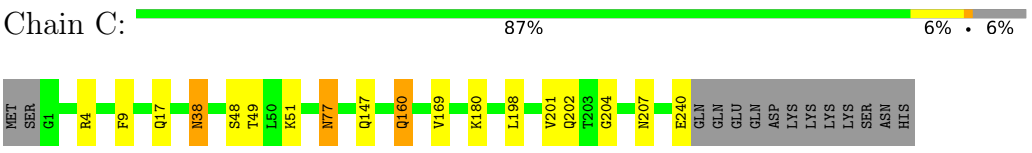
• Molecule 2: Proteasome subunit alpha type-3



• Molecule 2: Proteasome subunit alpha type-3

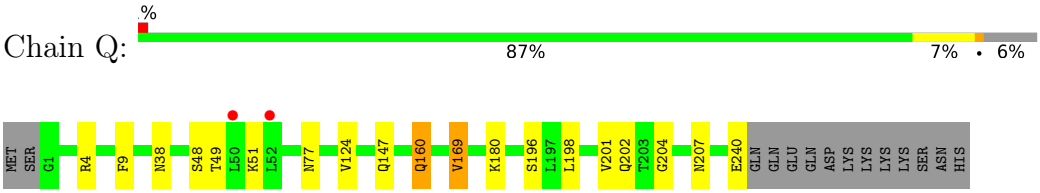


• Molecule 3: Proteasome subunit alpha type-4



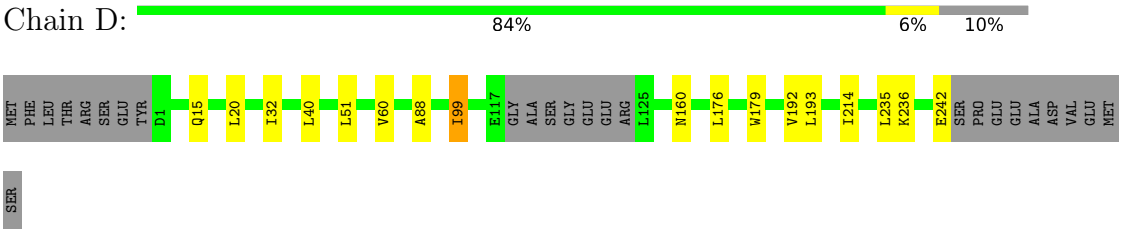
• Molecule 3: Proteasome subunit alpha type-4

Chain Q:



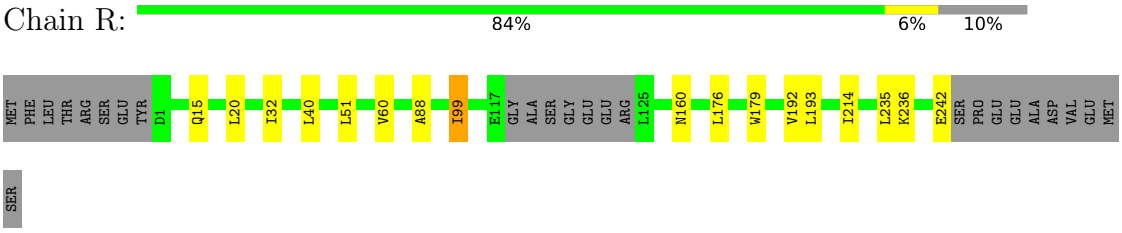
• Molecule 4: Proteasome subunit alpha type-5

Chain D:



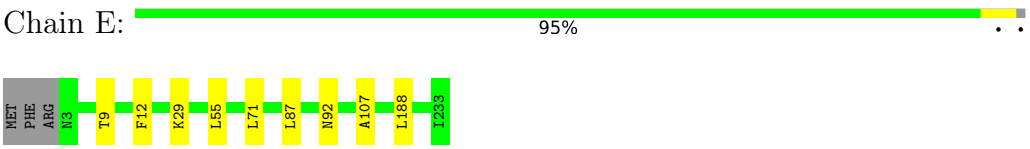
• Molecule 4: Proteasome subunit alpha type-5

Chain R:



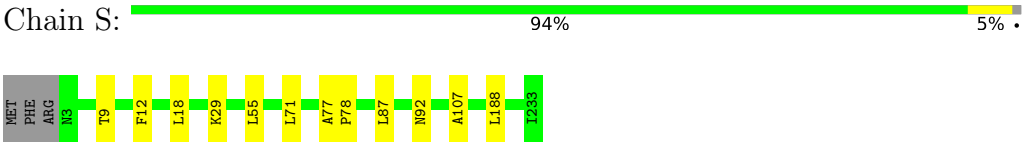
• Molecule 5: Proteasome subunit alpha type-6

Chain E:



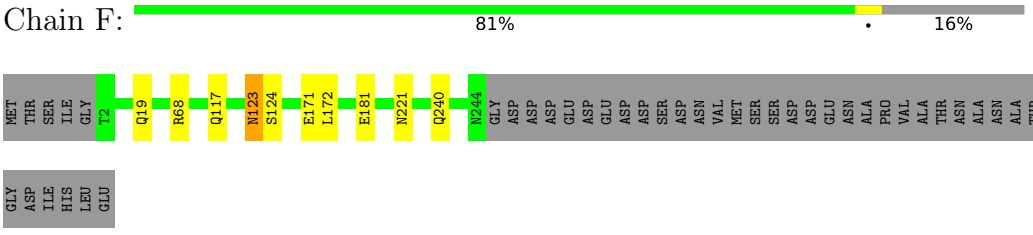
• Molecule 5: Proteasome subunit alpha type-6

Chain S:



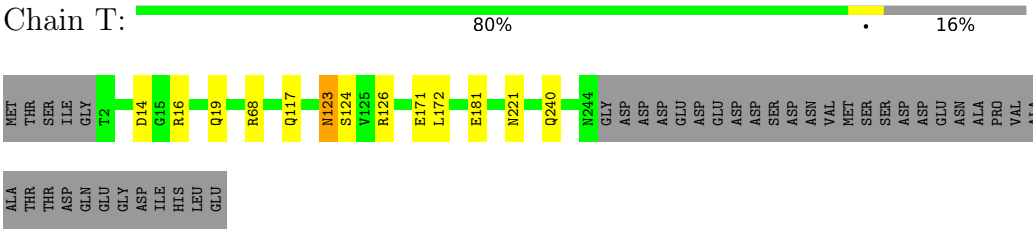
• Molecule 6: Probable proteasome subunit alpha type-7

Chain F:



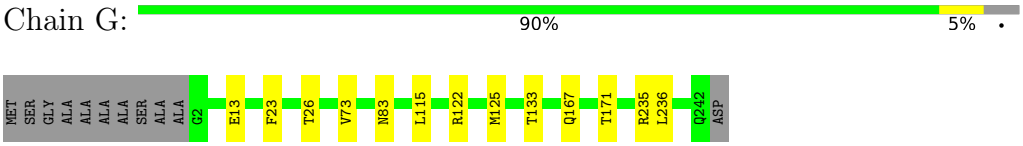
• Molecule 6: Probable proteasome subunit alpha type-7

Chain T:



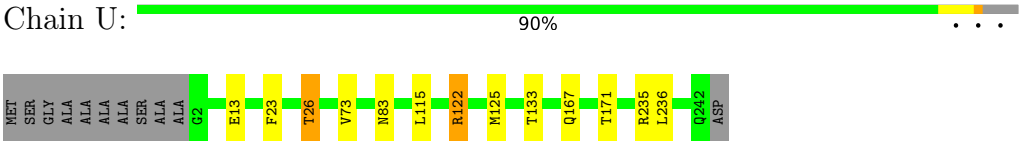
• Molecule 7: Proteasome subunit alpha type-1

Chain G:



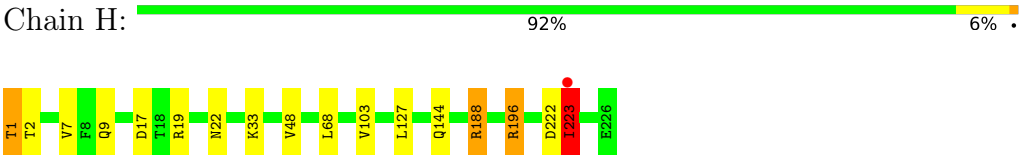
• Molecule 7: Proteasome subunit alpha type-1

Chain U:



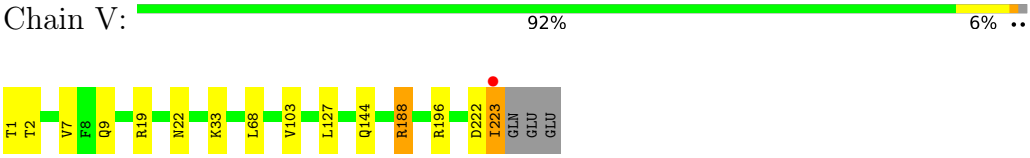
• Molecule 8: Proteasome subunit beta type-10,Proteasome subunit beta type-2

Chain H:



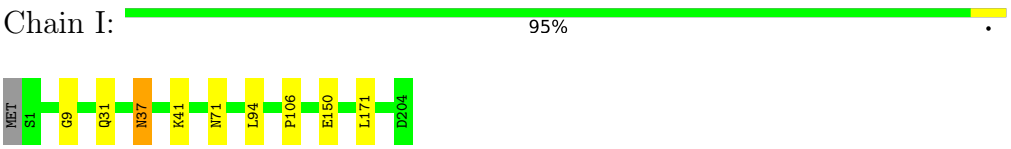
• Molecule 8: Proteasome subunit beta type-10,Proteasome subunit beta type-2

Chain V:



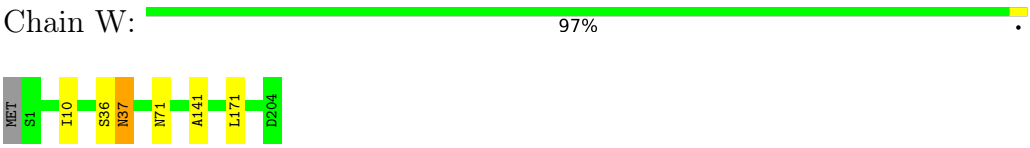
• Molecule 9: Proteasome subunit beta type-3

Chain I:



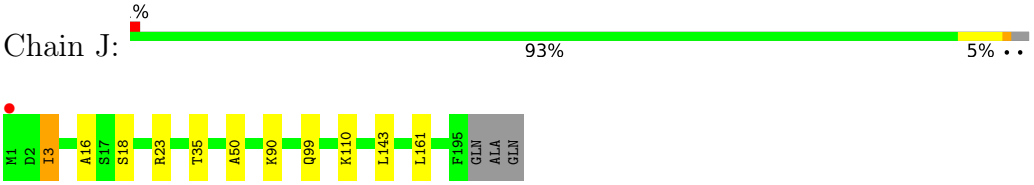
• Molecule 9: Proteasome subunit beta type-3

Chain W:



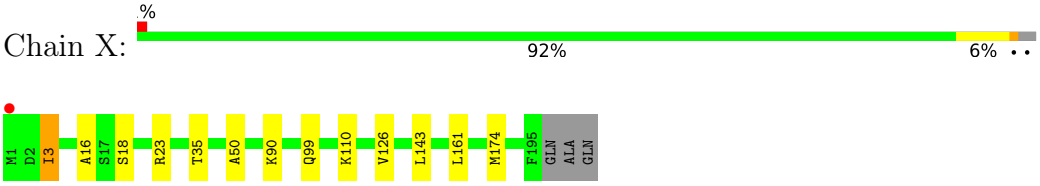
• Molecule 10: Proteasome subunit beta type-4

Chain J:



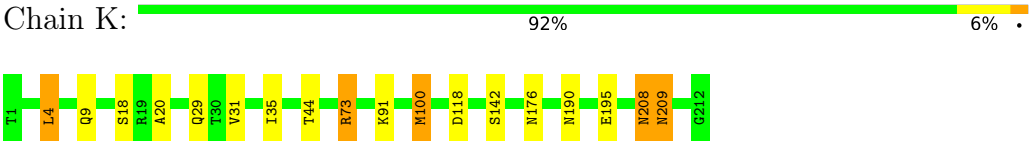
• Molecule 10: Proteasome subunit beta type-4

Chain X:



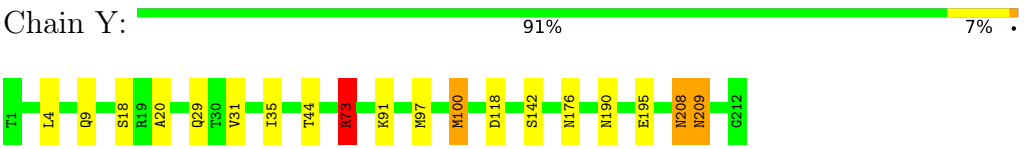
• Molecule 11: Proteasome subunit beta type-5

Chain K:



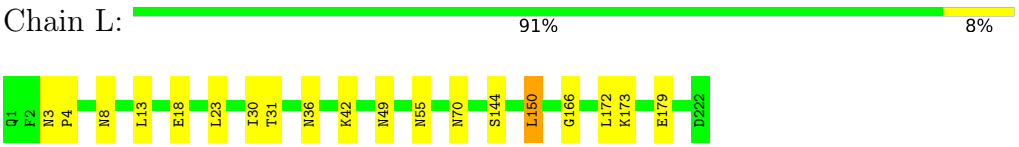
• Molecule 11: Proteasome subunit beta type-5

Chain Y:



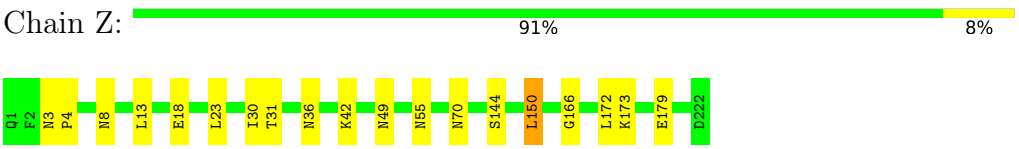
• Molecule 12: Proteasome subunit beta type-6

Chain L:



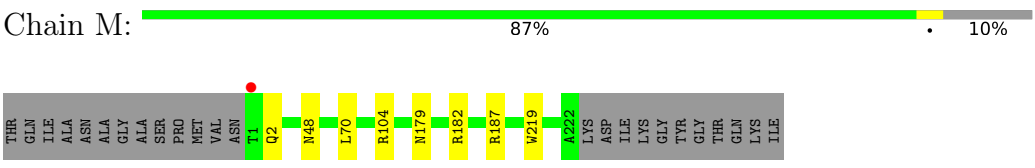
• Molecule 12: Proteasome subunit beta type-6

Chain Z:



• Molecule 13: Proteasome subunit beta type-7

Chain M:

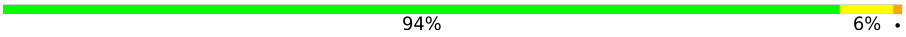


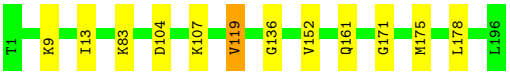
• Molecule 13: Proteasome subunit beta type-7

Chain a:

• Molecule 14: Proteasome subunit beta type-1

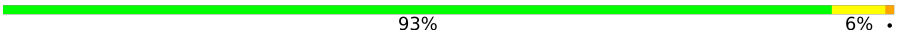
Chain N:

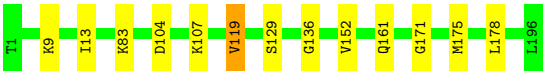




• Molecule 14: Proteasome subunit beta type-1

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	134.99Å 298.78Å 143.44Å 90.00° 112.52° 90.00°	Depositor
Resolution (Å)	15.00 – 3.00 15.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.6 (15.00-3.00) 96.6 (15.00-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.45 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.184 , 0.214 0.191 , 0.217	Depositor DCC
R_{free} test set	10084 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	64.9	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 53.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	49728	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GQK, SO4, MG, CL, MES

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	0.52	0/1952	0.78	0/2642
1	O	0.52	0/1952	0.79	0/2642
2	B	0.54	0/1934	0.81	0/2618
2	P	0.53	0/1934	0.81	0/2618
3	C	0.52	0/1910	0.81	0/2586
3	Q	0.52	0/1910	0.82	0/2586
4	D	0.50	0/1837	0.80	0/2475
4	R	0.50	0/1837	0.79	0/2475
5	E	0.51	0/1800	0.77	0/2433
5	S	0.51	0/1800	0.78	0/2433
6	F	0.51	0/1932	0.80	0/2609
6	T	0.51	0/1932	0.80	0/2609
7	G	0.51	0/1945	0.77	0/2634
7	U	0.51	0/1945	0.77	0/2634
8	H	0.52	0/1746	0.94	5/2365 (0.2%)
8	V	0.49	0/1718	0.87	3/2329 (0.1%)
9	I	0.49	0/1611	0.76	0/2174
9	W	0.48	0/1611	0.75	0/2174
10	J	0.51	0/1589	0.79	0/2142
10	X	0.51	0/1589	0.79	0/2142
11	K	0.49	0/1681	0.94	5/2274 (0.2%)
11	Y	0.48	0/1681	0.95	5/2274 (0.2%)
12	L	0.49	0/1795	0.79	0/2420
12	Z	0.48	0/1795	0.78	0/2420
13	M	0.52	0/1766	0.80	0/2398
13	a	0.53	0/1766	0.80	0/2398
14	N	0.50	0/1541	0.77	0/2087
14	b	0.49	0/1541	0.78	0/2087
All	All	0.51	0/50050	0.81	18/67678 (0.0%)

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

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

Mol	Chain	#Chirality outliers	#Planarity outliers
8	H	0	1
8	V	0	1
11	K	0	1
11	Y	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	Y	4	LEU	CD1-CG-CD2	-16.84	73.75	110.80
11	K	4	LEU	CD1-CG-CD2	-16.52	74.46	110.80
8	H	1	THR	CA-CB-OG1	13.23	129.45	109.60
11	Y	73	ARG	NE-CZ-NH1	-11.08	110.42	121.50
8	V	188	ARG	NE-CZ-NH2	-10.54	109.71	119.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	188	ARG	Sidechain
11	K	73	ARG	Sidechain
8	V	188	ARG	Sidechain
11	Y	73	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	2	0
1	O	1915	0	1929	1	0
2	B	1904	0	1904	8	0
2	P	1904	0	1904	9	0
3	C	1881	0	1895	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Q	1881	0	1895	7	0
4	D	1813	0	1797	4	0
4	R	1813	0	1797	4	0
5	E	1773	0	1775	5	0
5	S	1773	0	1775	7	0
6	F	1892	0	1883	3	0
6	T	1892	0	1883	5	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	4	0
8	H	1716	0	1701	13	0
8	V	1688	0	1681	8	0
9	I	1581	0	1574	6	0
9	W	1581	0	1574	5	0
10	J	1561	0	1569	5	0
10	X	1561	0	1569	7	0
11	K	1644	0	1593	13	0
11	Y	1644	0	1593	12	0
12	L	1757	0	1711	10	0
12	Z	1757	0	1711	10	0
13	M	1736	0	1737	2	0
13	a	1736	0	1737	1	0
14	N	1512	0	1479	6	0
14	b	1512	0	1479	7	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	W	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	H	42	0	0	2	0
17	K	42	0	0	2	0
17	N	42	0	0	1	0
17	V	42	0	0	0	0
17	Y	42	0	0	1	0
17	b	42	0	0	1	0
18	H	12	0	13	1	0
18	K	12	0	13	1	0
18	V	12	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Y	12	0	13	0	0
19	N	5	0	0	1	0
19	b	5	0	0	2	0
20	A	6	0	0	0	0
20	B	12	0	0	2	0
20	C	7	0	0	0	0
20	D	11	0	0	0	0
20	E	7	0	0	0	0
20	F	6	0	0	0	0
20	G	11	0	0	0	0
20	H	12	0	0	0	0
20	I	6	0	0	1	0
20	J	14	0	0	0	0
20	K	16	0	0	0	0
20	L	13	0	0	0	0
20	M	15	0	0	0	0
20	N	4	0	0	0	0
20	O	3	0	0	0	0
20	P	6	0	0	0	0
20	Q	2	0	0	0	0
20	R	3	0	0	0	0
20	S	8	0	0	0	0
20	T	9	0	0	0	0
20	U	9	0	0	1	0
20	V	9	0	0	0	0
20	W	5	0	0	0	0
20	X	10	0	0	1	0
20	Y	19	0	0	0	0
20	Z	11	0	0	0	0
20	a	13	0	0	0	0
20	b	5	0	0	0	0
All	All	49728	0	48928	145	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 145 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:H:1:THR:HG23	8:H:33:LYS:NZ	1.86	0.90
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.48	0.78
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.32	0.76
8:H:1:THR:HG23	8:H:33:LYS:HZ2	1.50	0.76

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%)	241 (97%)	7 (3%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
2	B	242/258 (94%)	233 (96%)	9 (4%)	0	100	100
2	P	242/258 (94%)	232 (96%)	10 (4%)	0	100	100
3	C	238/254 (94%)	235 (99%)	2 (1%)	1 (0%)	30	65
3	Q	238/254 (94%)	235 (99%)	2 (1%)	1 (0%)	30	65
4	D	231/260 (89%)	224 (97%)	7 (3%)	0	100	100
4	R	231/260 (89%)	224 (97%)	7 (3%)	0	100	100
5	E	229/234 (98%)	221 (96%)	8 (4%)	0	100	100
5	S	229/234 (98%)	221 (96%)	8 (4%)	0	100	100
6	F	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
6	T	241/288 (84%)	239 (99%)	2 (1%)	0	100	100
7	G	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
7	U	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
8	H	224/226 (99%)	218 (97%)	5 (2%)	1 (0%)	30	65
8	V	221/226 (98%)	216 (98%)	5 (2%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
10	X	193/198 (98%)	190 (98%)	3 (2%)	0	100	100
11	K	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
11	Y	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
12	L	220/222 (99%)	213 (97%)	6 (3%)	1 (0%)	24	60
12	Z	220/222 (99%)	213 (97%)	6 (3%)	1 (0%)	24	60
13	M	220/246 (89%)	210 (96%)	10 (4%)	0	100	100
13	a	220/246 (89%)	212 (96%)	8 (4%)	0	100	100
14	N	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
14	b	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
All	All	6259/6602 (95%)	6099 (97%)	155 (2%)	5 (0%)	48	80

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	223	ILE
3	C	204	GLY
3	Q	204	GLY
12	L	166	GLY
12	Z	166	GLY

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%)	204 (98%)	5 (2%)	43	73
1	O	209/209 (100%)	204 (98%)	5 (2%)	43	73
2	B	203/216 (94%)	192 (95%)	11 (5%)	20	53
2	P	203/216 (94%)	193 (95%)	10 (5%)	22	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	212/226 (94%)	202 (95%)	10 (5%)	23	58
3	Q	212/226 (94%)	202 (95%)	10 (5%)	23	58
4	D	194/215 (90%)	183 (94%)	11 (6%)	18	52
4	R	194/215 (90%)	183 (94%)	11 (6%)	18	52
5	E	190/193 (98%)	185 (97%)	5 (3%)	40	72
5	S	190/193 (98%)	185 (97%)	5 (3%)	40	72
6	F	201/239 (84%)	193 (96%)	8 (4%)	28	62
6	T	201/239 (84%)	193 (96%)	8 (4%)	28	62
7	G	206/210 (98%)	199 (97%)	7 (3%)	32	66
7	U	206/210 (98%)	198 (96%)	8 (4%)	28	62
8	H	184/184 (100%)	174 (95%)	10 (5%)	20	53
8	V	181/184 (98%)	171 (94%)	10 (6%)	19	53
9	I	172/173 (99%)	170 (99%)	2 (1%)	63	82
9	W	172/173 (99%)	170 (99%)	2 (1%)	63	82
10	J	173/175 (99%)	168 (97%)	5 (3%)	37	70
10	X	173/175 (99%)	168 (97%)	5 (3%)	37	70
11	K	169/169 (100%)	162 (96%)	7 (4%)	27	61
11	Y	169/169 (100%)	161 (95%)	8 (5%)	23	58
12	L	185/185 (100%)	177 (96%)	8 (4%)	26	60
12	Z	185/185 (100%)	177 (96%)	8 (4%)	26	60
13	M	190/208 (91%)	185 (97%)	5 (3%)	40	72
13	a	190/208 (91%)	184 (97%)	6 (3%)	34	67
14	N	162/162 (100%)	157 (97%)	5 (3%)	35	68
14	b	162/162 (100%)	157 (97%)	5 (3%)	35	68
All	All	5297/5528 (96%)	5097 (96%)	200 (4%)	29	63

5 of 200 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	Q	38	ASN
6	T	171	GLU
14	b	178	LEU
3	Q	147	GLN
4	R	193	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 163 such sidechains are listed below:

Mol	Chain	Res	Type
6	T	240	GLN
12	Z	29	ASN
7	U	121	GLN
9	W	168	GLN
12	Z	153	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 22 ligands modelled in this entry, 10 are monoatomic - leaving 12 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	GQK	H	301	8	44,44,44	1.76	6 (13%)	60,60,60	2.46	14 (23%)
17	GQK	Y	301	11	44,44,44	1.32	5 (11%)	60,60,60	1.65	8 (13%)
18	MES	Y	303	-	12,12,12	2.27	1 (8%)	15,16,16	1.36	2 (13%)
18	MES	K	303	-	12,12,12	2.23	1 (8%)	15,16,16	1.47	2 (13%)
19	SO4	b	202	-	4,4,4	0.56	0	6,6,6	0.16	0
18	MES	V	303	-	12,12,12	2.33	1 (8%)	15,16,16	1.49	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
19	SO4	N	203	-	4,4,4	0.55	0	6,6,6	0.26	0
17	GQK	N	201	14	44,44,44	1.38	4 (9%)	60,60,60	1.30	9 (15%)
18	MES	H	302	-	12,12,12	2.30	1 (8%)	15,16,16	1.23	1 (6%)
17	GQK	b	201	14	44,44,44	1.39	4 (9%)	60,60,60	1.29	8 (13%)
17	GQK	K	301	11	44,44,44	1.28	3 (6%)	60,60,60	1.64	7 (11%)
17	GQK	V	301	8	44,44,44	1.39	4 (9%)	60,60,60	1.35	9 (15%)

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	GQK	H	301	8	-	8/44/52/52	0/3/3/3
17	GQK	Y	301	11	-	9/44/52/52	0/3/3/3
18	MES	Y	303	-	-	3/6/14/14	0/1/1/1
18	MES	K	303	-	-	0/6/14/14	0/1/1/1
18	MES	V	303	-	-	5/6/14/14	0/1/1/1
17	GQK	N	201	14	-	8/44/52/52	0/3/3/3
18	MES	H	302	-	-	0/6/14/14	0/1/1/1
17	GQK	b	201	14	-	8/44/52/52	0/3/3/3
17	GQK	K	301	11	-	9/44/52/52	0/3/3/3
17	GQK	V	301	8	-	4/44/52/52	0/3/3/3

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	V	303	MES	C8-S	-7.90	1.66	1.77
18	H	302	MES	C8-S	-7.79	1.66	1.77
18	Y	303	MES	C8-S	-7.44	1.67	1.77
18	K	303	MES	C8-S	-7.39	1.67	1.77
17	H	301	GQK	C40-C41	-5.61	1.38	1.51

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	H	301	GQK	O13-C10-C9	10.33	131.73	107.71
17	H	301	GQK	O13-C10-C12	-8.36	89.56	107.90
17	K	301	GQK	C12-C10-C11	-7.32	99.84	110.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	Y	301	GQK	C12-C10-C11	-7.19	100.02	110.52
17	H	301	GQK	C12-C10-C11	-7.18	100.04	110.52

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	K	301	GQK	C11-C10-C9-C8
17	K	301	GQK	C11-C10-C9-O21
17	K	301	GQK	C12-C10-C9-C8
17	K	301	GQK	C12-C10-C9-O21
17	K	301	GQK	O13-C10-C9-C8

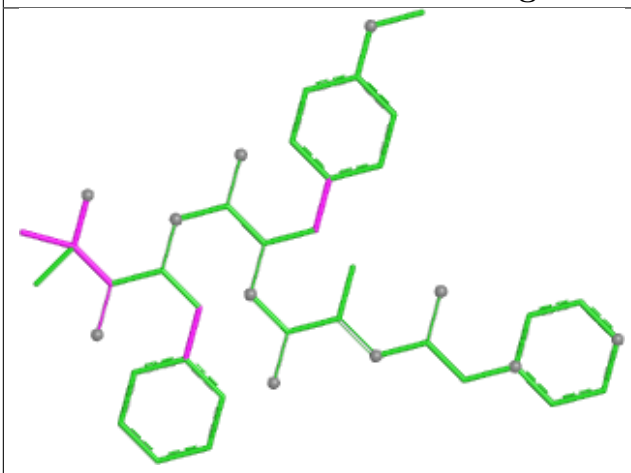
There are no ring outliers.

9 monomers are involved in 8 short contacts:

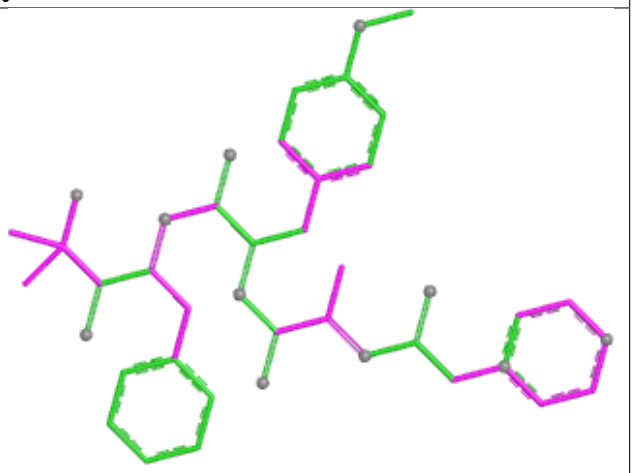
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	H	301	GQK	2	0
17	Y	301	GQK	1	0
18	K	303	MES	1	0
19	b	202	SO4	2	0
19	N	203	SO4	1	0
17	N	201	GQK	1	0
18	H	302	MES	1	0
17	b	201	GQK	1	0
17	K	301	GQK	2	0

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

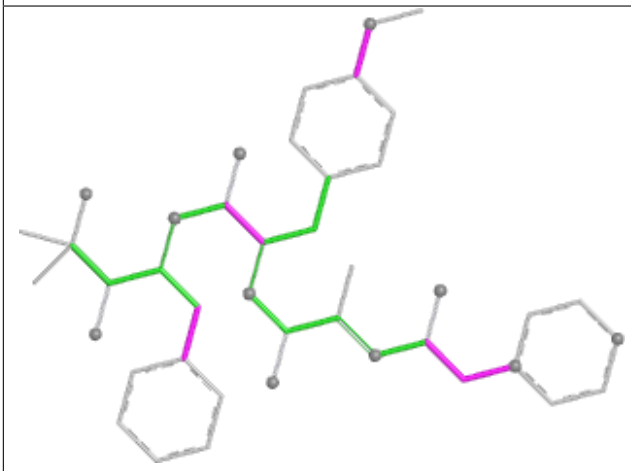
Ligand GQK H 301



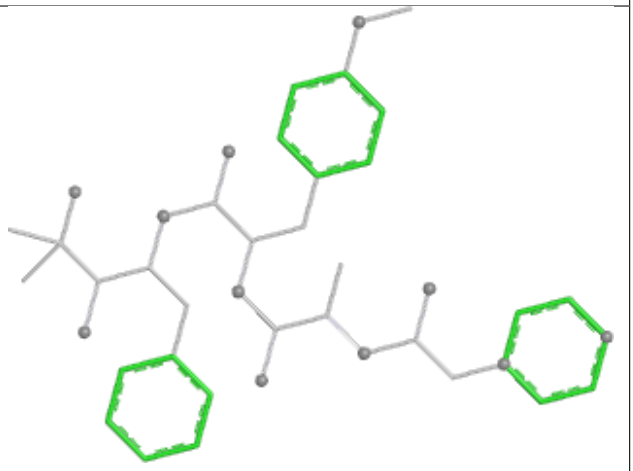
Bond lengths



Bond angles

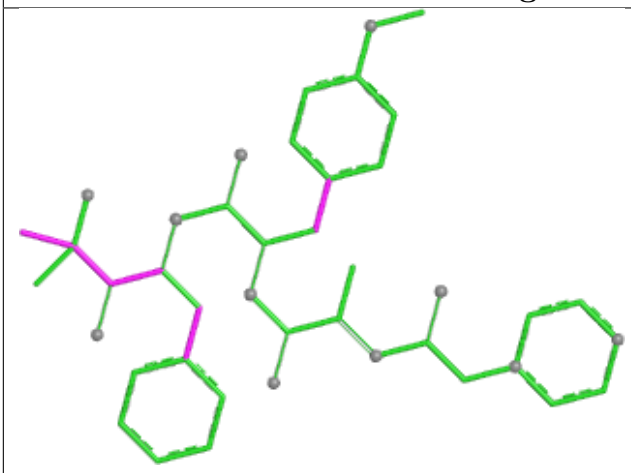


Torsions



Rings

Ligand GQK Y 301



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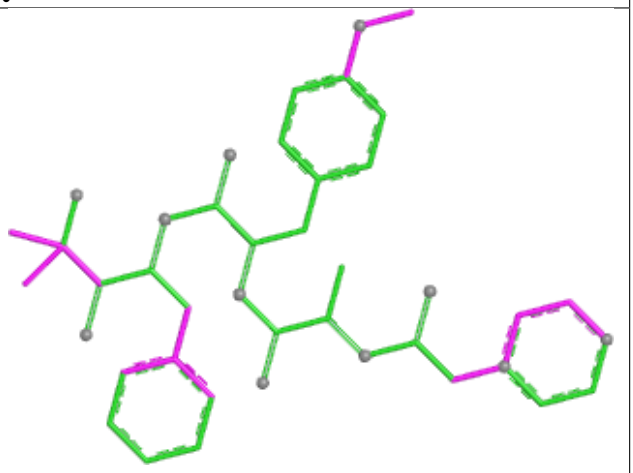

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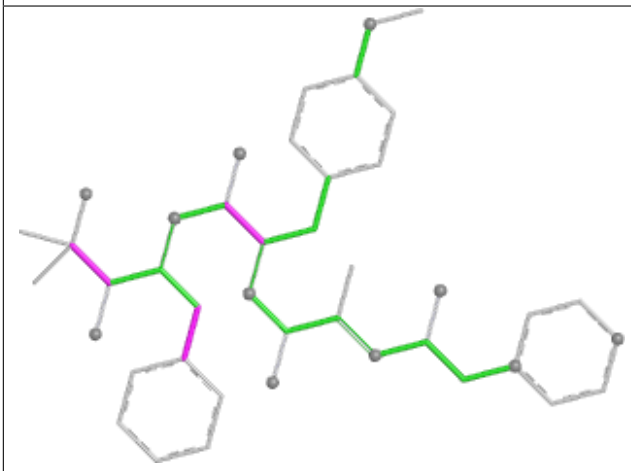
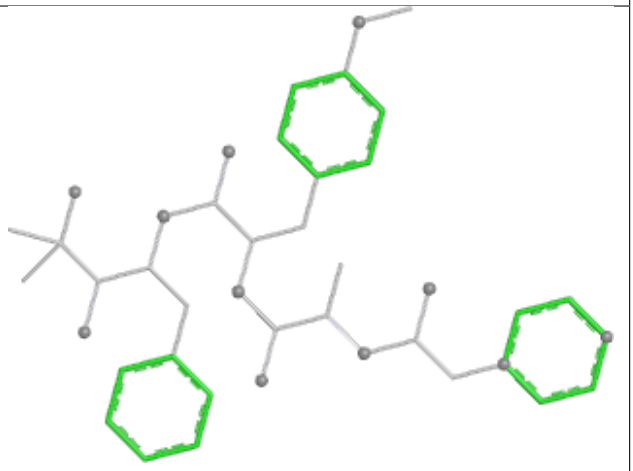
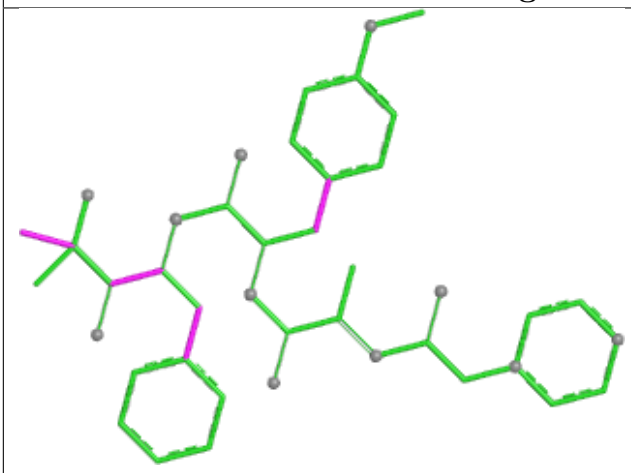


Torsions

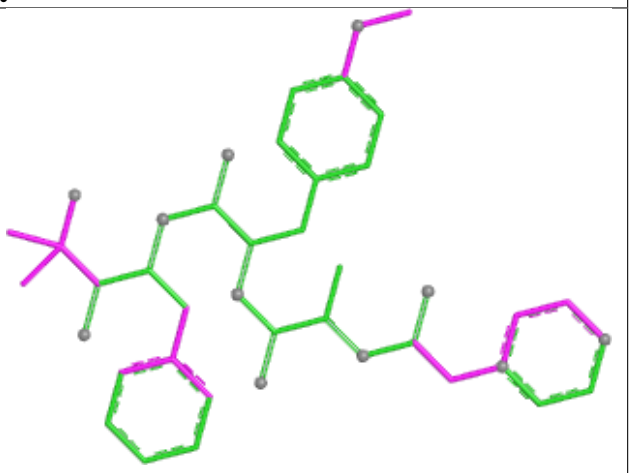


Rings

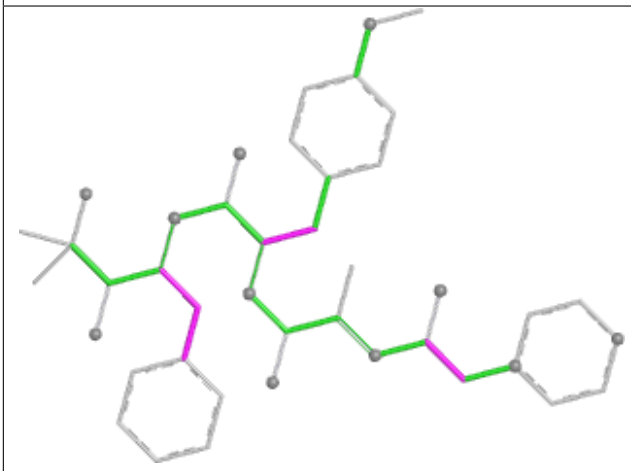
Ligand GQK N 201



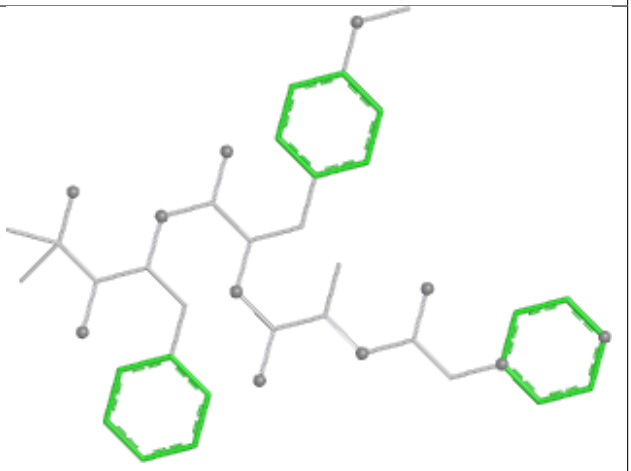
Bond lengths



Bond angles

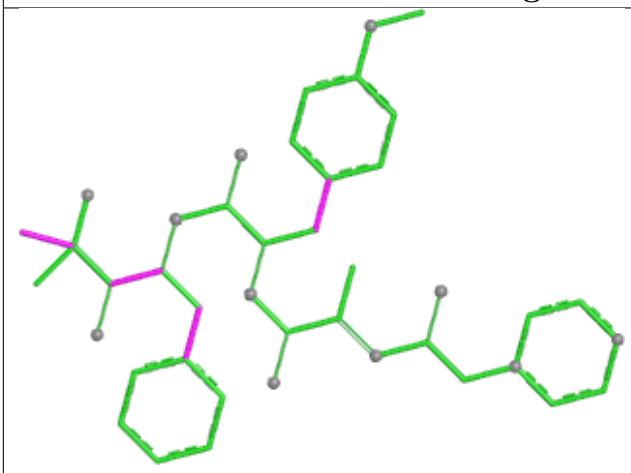


Torsions



Rings

Ligand GQK b 201



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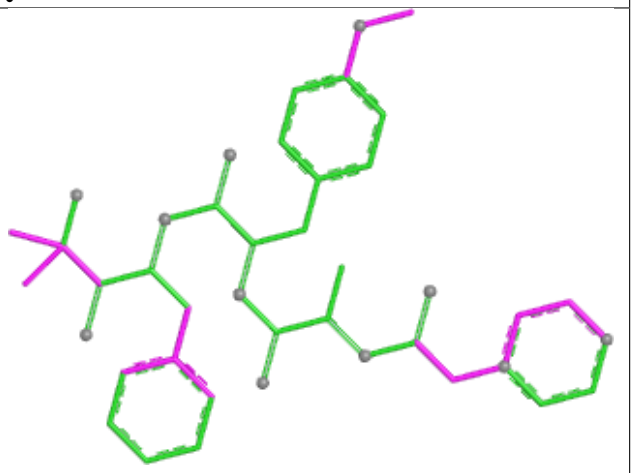
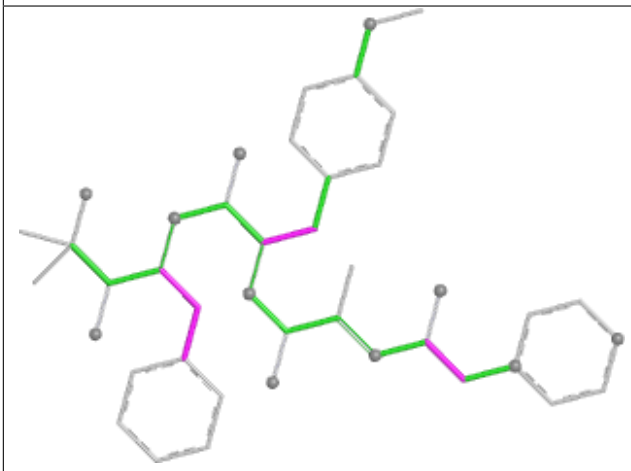
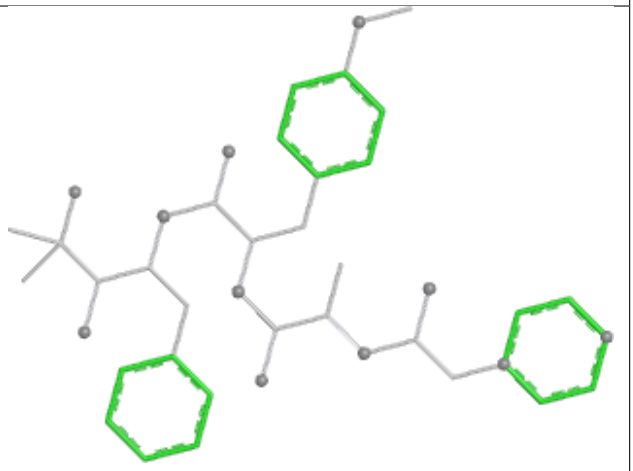


Bond angles

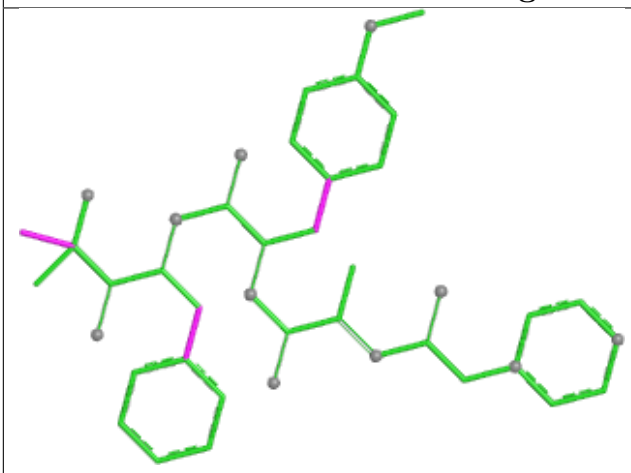


Torsions

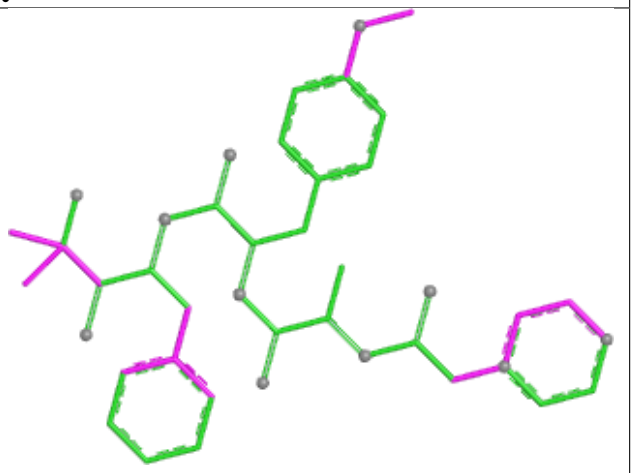


Rings

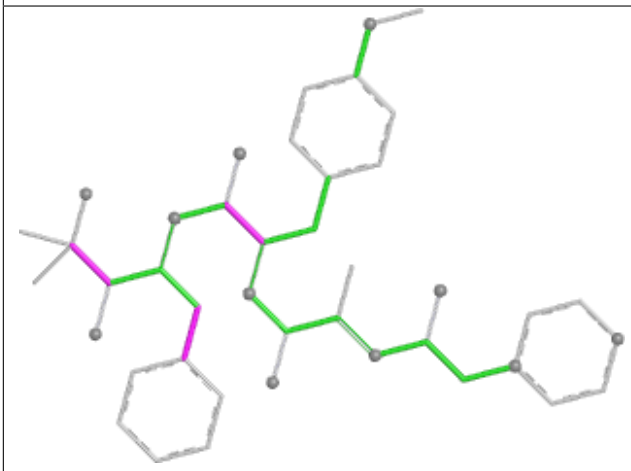
Ligand GQK K 301



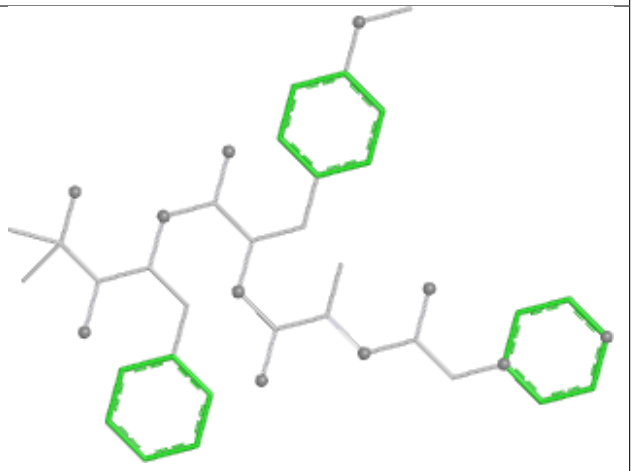
Bond lengths



Bond angles

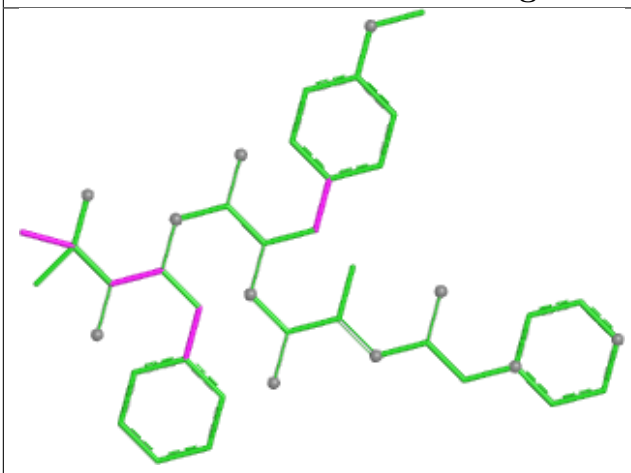


Torsions

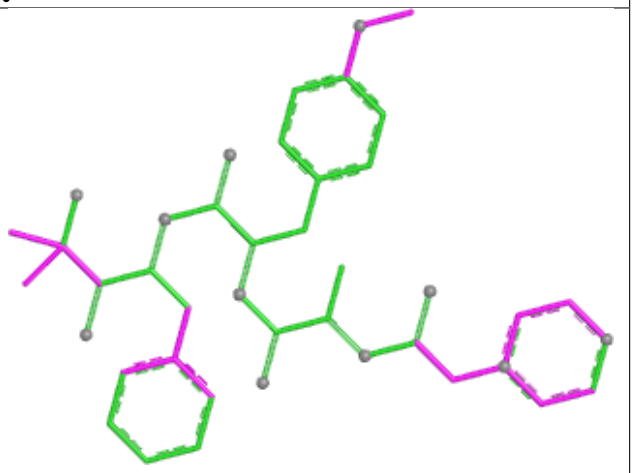


Rings

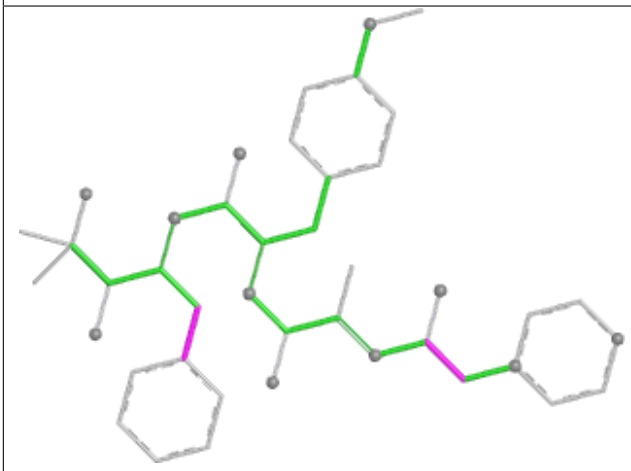
Ligand GQK V 301



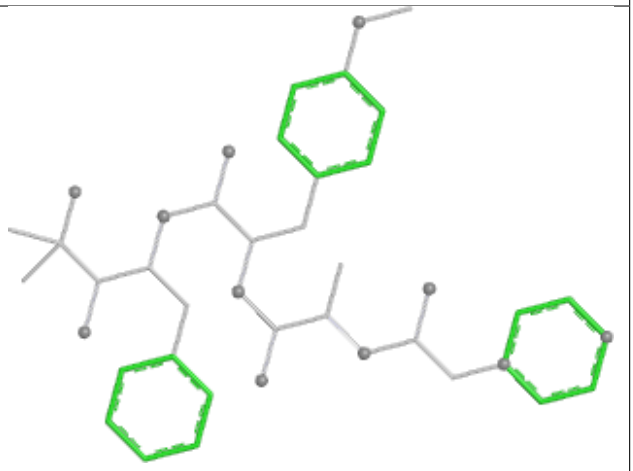
Bond lengths



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%)	-0.55	4 (1%) 70 47	52, 69, 109, 133	0
1	O	250/250 (100%)	-0.50	1 (0%) 88 76	56, 77, 119, 145	0
2	B	244/258 (94%)	-0.51	2 (0%) 82 64	52, 72, 112, 132	0
2	P	244/258 (94%)	-0.49	1 (0%) 88 76	56, 76, 114, 141	0
3	C	240/254 (94%)	-0.53	0 100 100	49, 77, 129, 167	0
3	Q	240/254 (94%)	-0.34	2 (0%) 82 64	59, 93, 163, 209	0
4	D	235/260 (90%)	-0.55	0 100 100	55, 75, 105, 146	0
4	R	235/260 (90%)	-0.39	0 100 100	67, 86, 119, 155	0
5	E	231/234 (98%)	-0.50	0 100 100	59, 79, 118, 138	0
5	S	231/234 (98%)	-0.33	0 100 100	64, 89, 131, 153	0
6	F	243/288 (84%)	-0.60	0 100 100	51, 74, 116, 135	0
6	T	243/288 (84%)	-0.45	0 100 100	51, 82, 126, 152	0
7	G	241/252 (95%)	-0.61	0 100 100	52, 70, 104, 148	0
7	U	241/252 (95%)	-0.56	0 100 100	56, 71, 102, 138	0
8	H	226/226 (100%)	-0.62	1 (0%) 88 76	51, 65, 96, 153	0
8	V	223/226 (98%)	-0.56	1 (0%) 88 76	50, 67, 94, 131	0
9	I	204/205 (99%)	-0.74	0 100 100	44, 60, 86, 104	0
9	W	204/205 (99%)	-0.74	0 100 100	46, 63, 86, 104	0
10	J	195/198 (98%)	-0.62	1 (0%) 87 72	47, 64, 89, 109	0
10	X	195/198 (98%)	-0.60	1 (0%) 87 72	51, 67, 92, 119	0
11	K	212/212 (100%)	-0.67	0 100 100	38, 63, 87, 100	0
11	Y	212/212 (100%)	-0.70	0 100 100	39, 65, 90, 104	0
12	L	222/222 (100%)	-0.64	0 100 100	50, 64, 93, 111	0
12	Z	222/222 (100%)	-0.65	0 100 100	51, 65, 95, 111	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	M	222/246 (90%)	-0.73	1 (0%) 87 72	44, 63, 87, 109	0
13	a	222/246 (90%)	-0.71	1 (0%) 87 72	46, 63, 85, 101	0
14	N	196/196 (100%)	-0.69	0 100 100	46, 62, 90, 104	0
14	b	196/196 (100%)	-0.69	0 100 100	45, 64, 93, 105	0
All	All	6319/6602 (95%)	-0.58	16 (0%) 90 79	38, 70, 115, 209	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	H	223	ILE	4.3
10	J	1	MET	3.7
10	X	1	MET	3.5
1	A	229	THR	3.3
1	A	1	MET	3.2

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 oligosaccharides 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
18	MES	V	303	12/12	0.92	0.19	47,73,78,78	12
17	GQK	N	201	42/42	0.93	0.09	48,66,85,91	0
17	GQK	H	301	42/42	0.93	0.09	51,61,87,90	0
17	GQK	K	301	42/42	0.94	0.08	36,52,69,71	0
17	GQK	Y	301	42/42	0.95	0.08	37,53,72,73	0
18	MES	H	302	12/12	0.95	0.17	45,68,76,77	12
17	GQK	V	301	42/42	0.95	0.08	47,56,89,92	0

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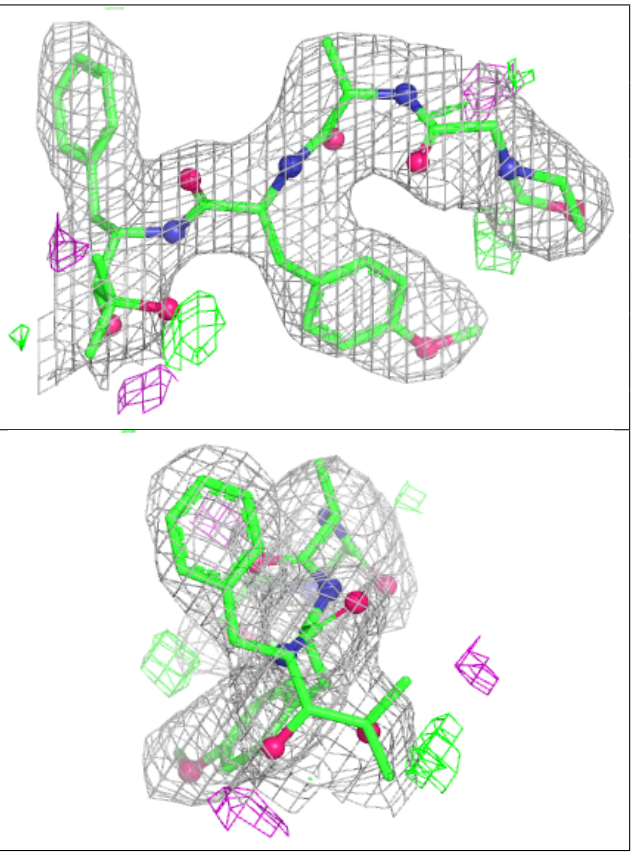
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
19	SO4	N	203	5/5	0.95	0.14	44,47,52,55	5
19	SO4	b	202	5/5	0.95	0.16	42,47,50,50	5
15	MG	V	302	1/1	0.96	0.07	88,88,88,88	0
17	GQK	b	201	42/42	0.96	0.08	47,64,89,93	0
15	MG	Z	301	1/1	0.97	0.05	76,76,76,76	0
16	CL	U	301	1/1	0.97	0.09	57,57,57,57	0
15	MG	I	301	1/1	0.97	0.19	78,78,78,78	0
15	MG	W	301	1/1	0.97	0.19	83,83,83,83	0
15	MG	Y	302	1/1	0.98	0.04	69,69,69,69	0
18	MES	Y	303	12/12	0.98	0.07	28,29,32,35	12
15	MG	K	302	1/1	0.98	0.07	67,67,67,67	0
18	MES	K	303	12/12	0.98	0.09	29,29,37,40	12
15	MG	N	202	1/1	0.99	0.03	53,53,53,53	0
16	CL	G	302	1/1	0.99	0.10	48,48,48,48	0
15	MG	G	301	1/1	0.99	0.02	59,59,59,59	0

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

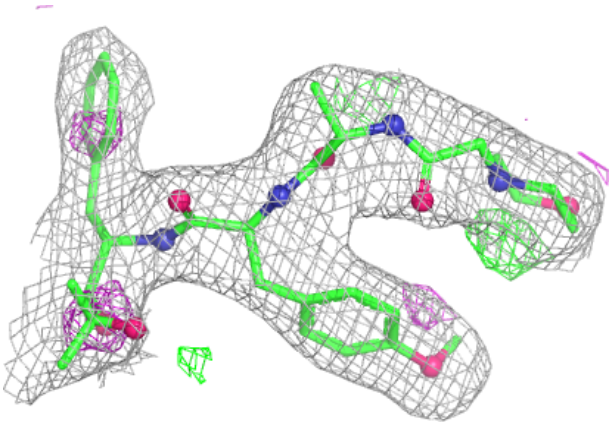
Electron density around GQK N 201:

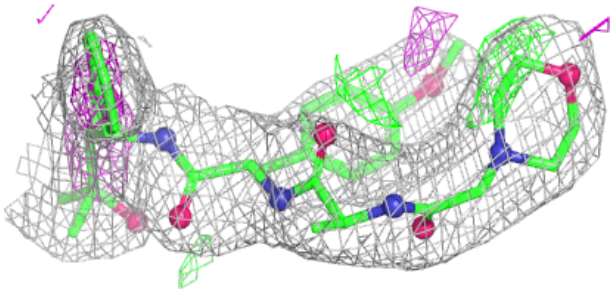
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around GQK H 301:

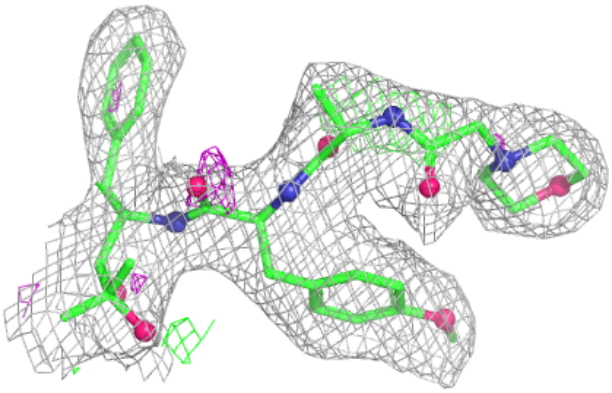
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

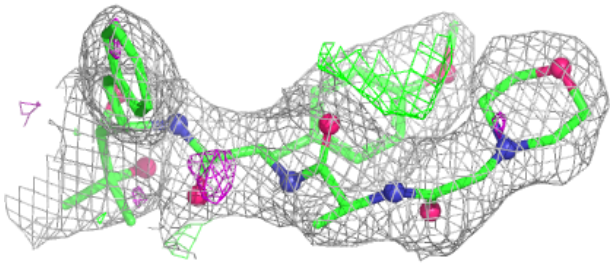


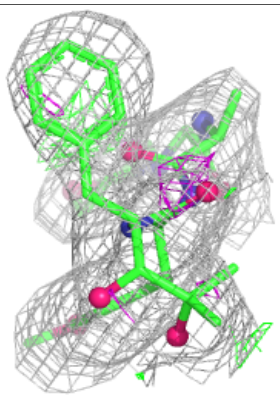


Electron density around GQK K 301:

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

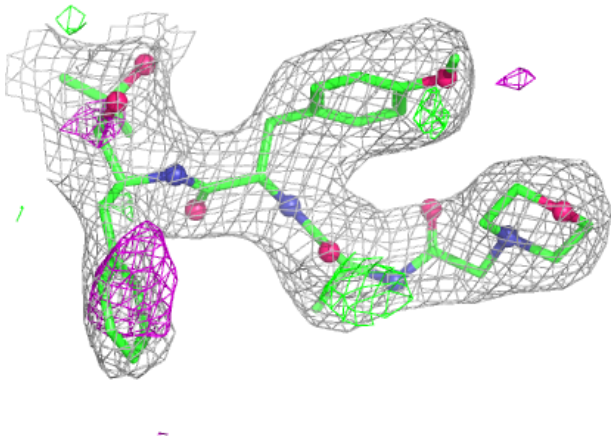


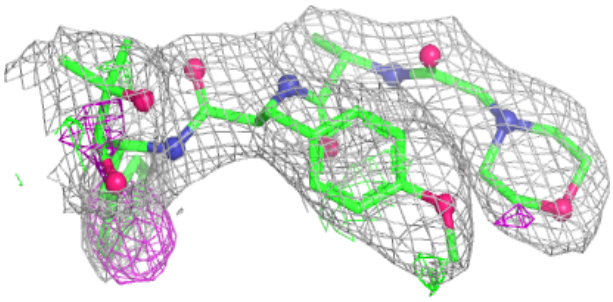


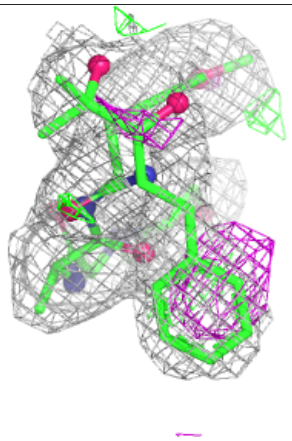


Electron density around GQK Y 301:

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

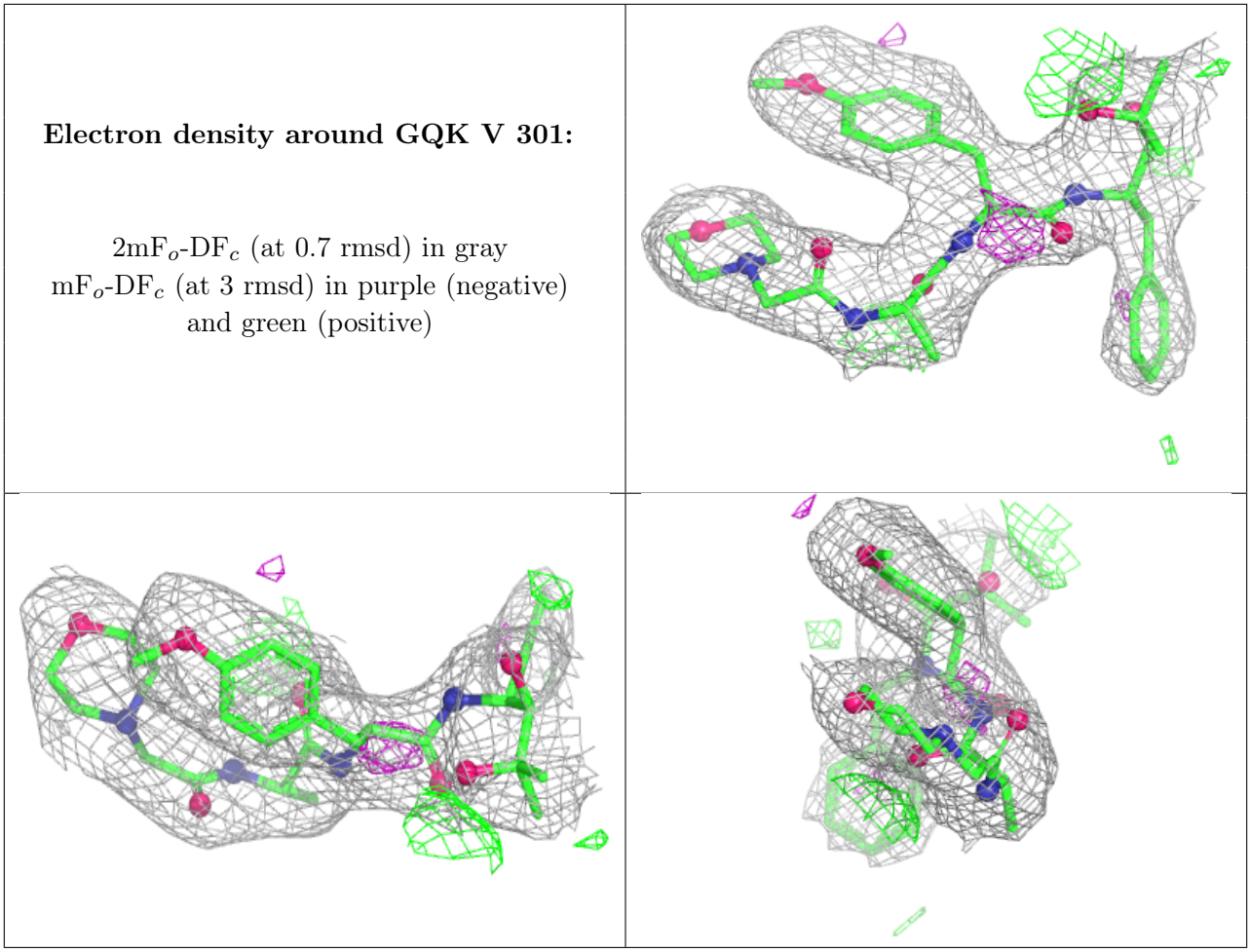






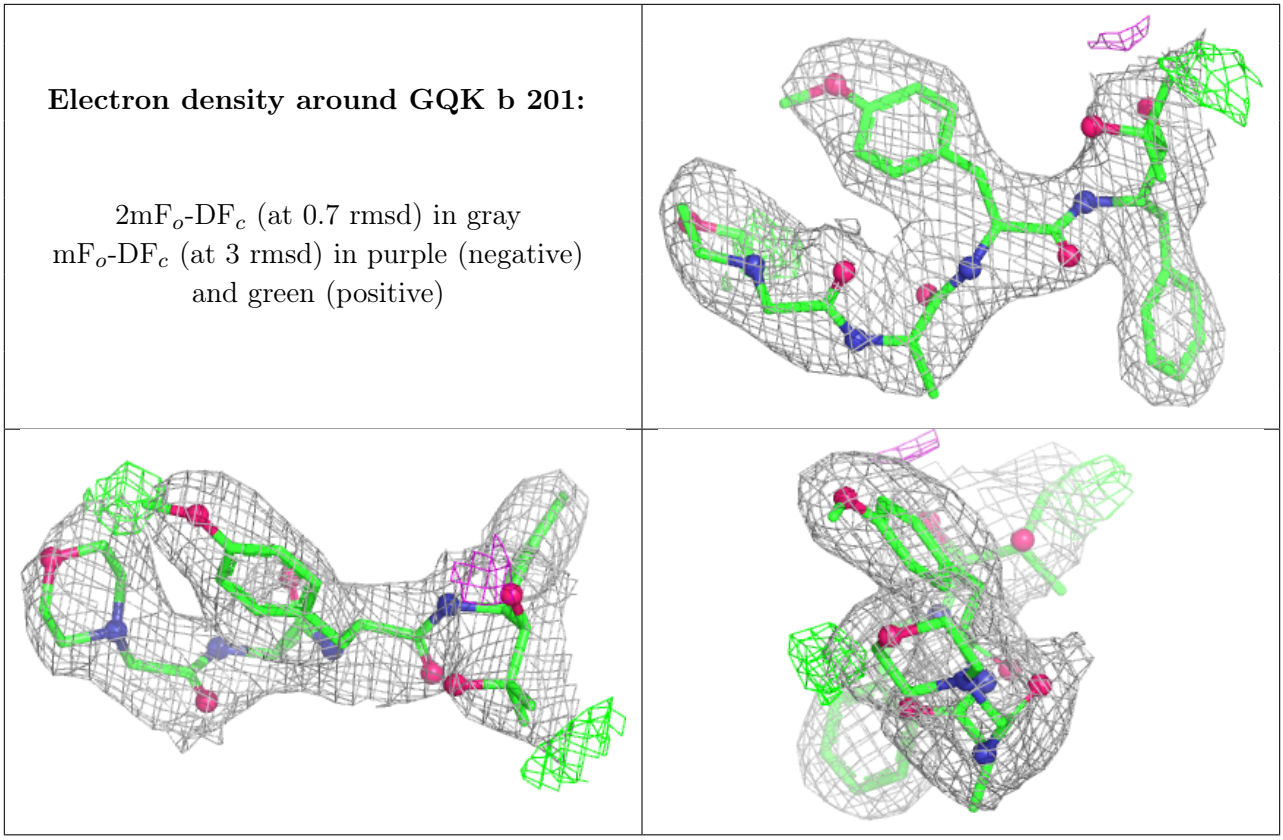
Electron density around GQK V 301:

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



Electron density around GQK b 201:

$2mF_o$-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.