Full wwPDB X-ray Structure Validation Report (i)

Jun 15, 2024 – 05:24 PM EDT

PDB ID	:	4QLS
Title	:	yCP in complex with tripeptidic epoxyketone inhibitor 11
Authors	:	De Bruin, G.; Huber, E.; Xin, B.; Van Rooden, E.; Al-Ayed, K.; Kim, K.; Kisselev, A.; Driessen, C.; Van der Marel, G.; Groll, M.; Overkleeft, H.
Deposited on	:	2014-06-13
Resolution	:	2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (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:

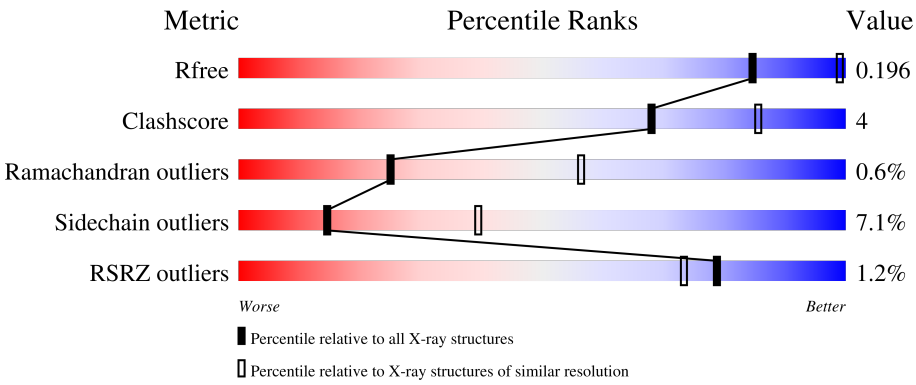
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	%, 90%, 8%, •
1	O	250	%, 90%, 9%, •
2	B	258	3%, 77%, 16%, • 5%
2	P	258	4%, 78%, 15%, • 5%
3	C	254	4%, 77%, 14%, • 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	5% 78% 13% • 6%
4	D	260	% 75% 14% • 10%
4	R	260	% 74% 15% • 10%
5	E	234	% 79% 19% ••
5	S	234	% 79% 19% ••
6	F	288	% 73% 10% • 16%
6	T	288	73% 10% • 16%
7	G	252	83% 11% • •
7	U	252	81% 13% • •
8	H	232	% 87% 8% • •
8	V	232	% 88% 7% • •
9	I	205	90% 9% •
9	W	205	89% 10%
10	J	198	% 83% 14% • •
10	X	198	% 83% 14% • •
11	K	212	88% 9% •
11	Y	212	87% 9% •
12	L	222	85% 14% •
12	Z	222	84% 15% •
13	M	246	85% 8% • 5%
13	a	246	89% 5% 5%
14	N	196	92% 7% •
14	b	196	96% •

2 Entry composition (i)

There are 18 unique types of molecules in this entry. The entry contains 49601 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Proteasome subunit alpha type-2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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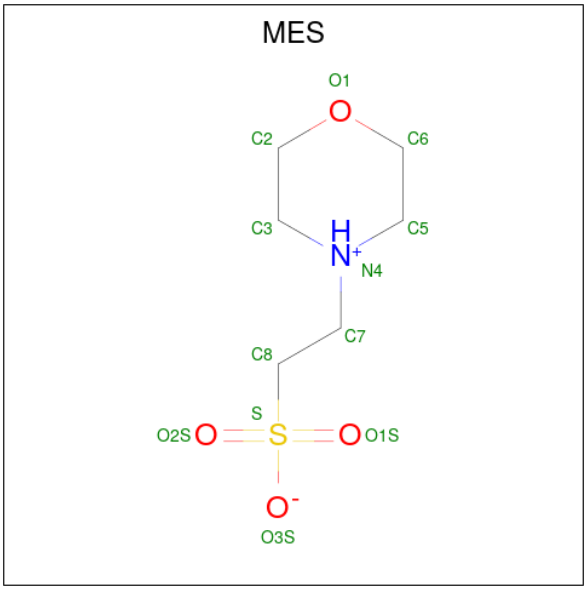
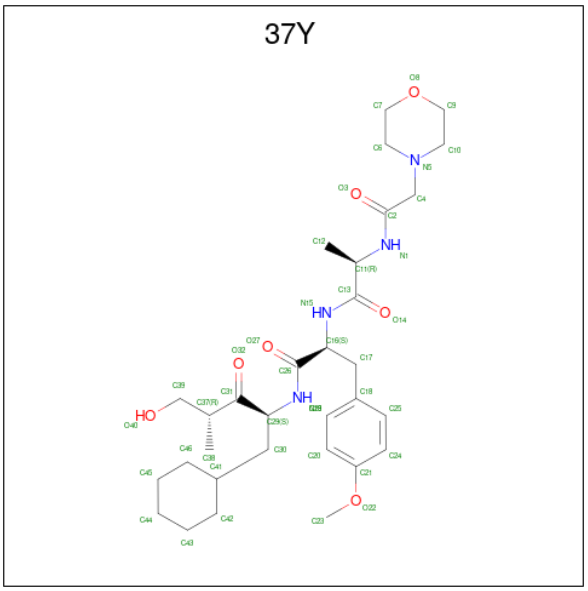
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
15	K	1	1	1	0	0
			Total	Mg		
15	N	2	2	2	0	0
			Total	Mg		
15	V	1	1	1	0	0
			Total	Mg		
15	Y	1	1	1	0	0
			Total	Mg		
15	Z	1	1	1	0	0

- Molecule 16 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



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

- Molecule 17 is N-(morpholin-4-ylacetyl)-D-alanyl-N-[(2S,4R)-1-cyclohexyl-5-hydroxy-4-methyl-3-oxopentan-2-yl]-O-methyl-L-tyrosinamide (three-letter code: 37Y) (formula: $C_{31}H_{48}N_4O_7$).



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

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
18	A	1	1	1	0	0
			Total	O		
18	B	7	7	7	0	0
			Total	O		
18	C	9	9	9	0	0
			Total	O		
18	D	4	4	4	0	0
			Total	O		
18	E	3	3	3	0	0
			Total	O		
18	F	4	4	4	0	0
			Total	O		
18	G	8	8	8	0	0
			Total	O		
18	H	14	14	14	0	0
			Total	O		
18	I	6	6	6	0	0
			Total	O		
18	J	6	6	6	0	0

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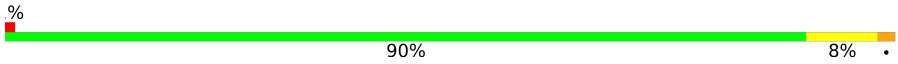
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
18	K	9	Total O 9 9	0	0
18	L	9	Total O 9 9	0	0
18	M	9	Total O 9 9	0	0
18	N	7	Total O 7 7	0	0
18	O	2	Total O 2 2	0	0
18	P	7	Total O 7 7	0	0
18	Q	6	Total O 6 6	0	0
18	R	5	Total O 5 5	0	0
18	S	3	Total O 3 3	0	0
18	T	5	Total O 5 5	0	0
18	U	7	Total O 7 7	0	0
18	V	5	Total O 5 5	0	0
18	W	5	Total O 5 5	0	0
18	X	9	Total O 9 9	0	0
18	Y	13	Total O 13 13	0	0
18	Z	10	Total O 10 10	0	0
18	a	10	Total O 10 10	0	0
18	b	6	Total O 6 6	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

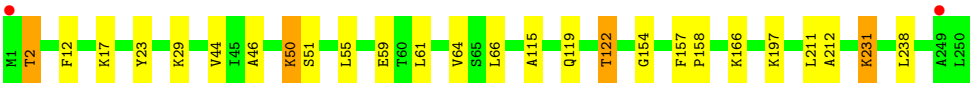
• Molecule 1: Proteasome subunit alpha type-2

Chain A:



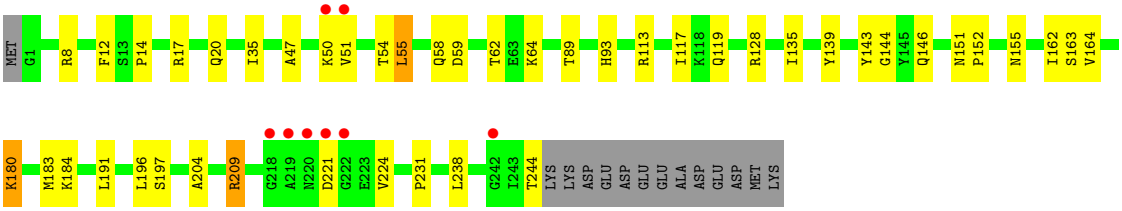
• Molecule 1: Proteasome subunit alpha type-2

Chain O:



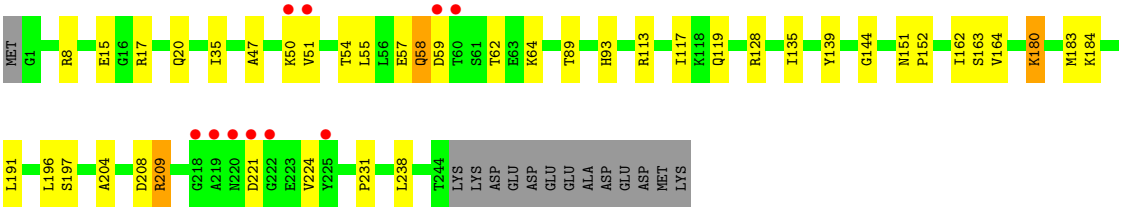
• Molecule 2: Proteasome subunit alpha type-3

Chain B:



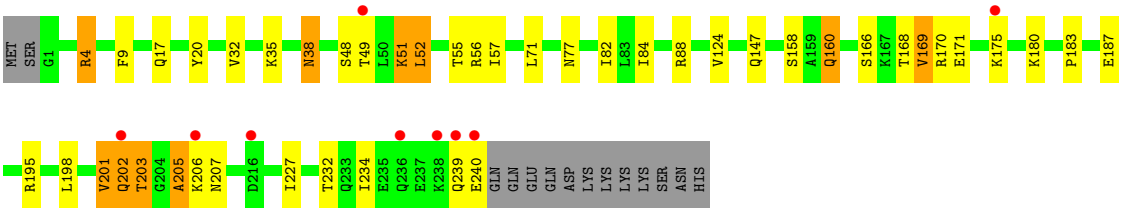
• Molecule 2: Proteasome subunit alpha type-3

Chain P:



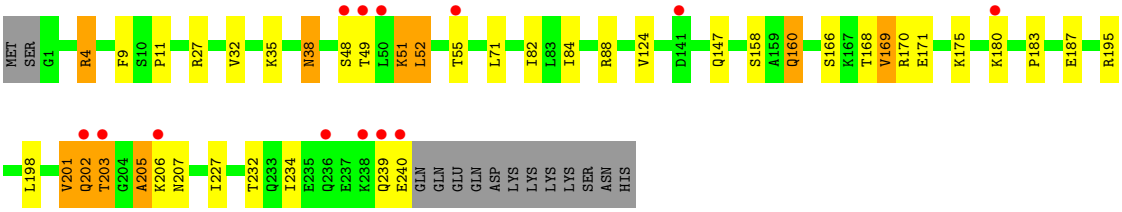
• Molecule 3: Proteasome subunit alpha type-4

Chain C:



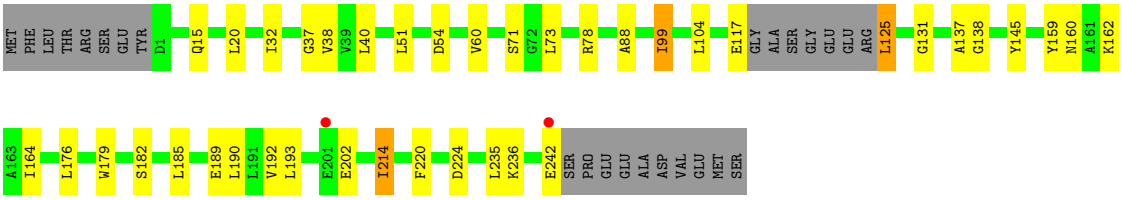
- Molecule 3: Proteasome subunit alpha type-4

Chain Q:



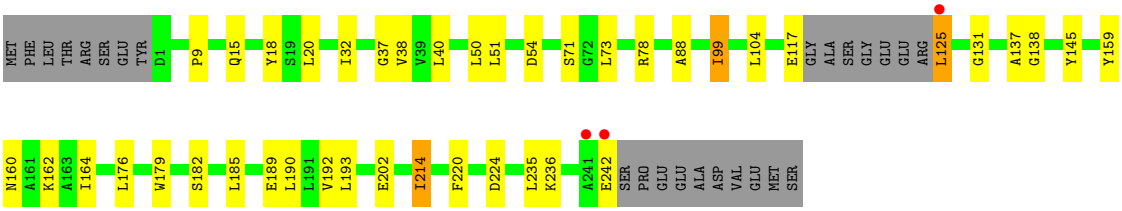
- Molecule 4: Proteasome subunit alpha type-5

Chain D:



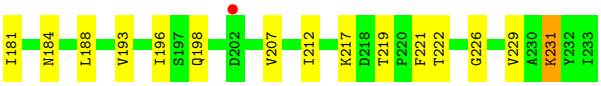
- Molecule 4: Proteasome subunit alpha type-5

Chain R:



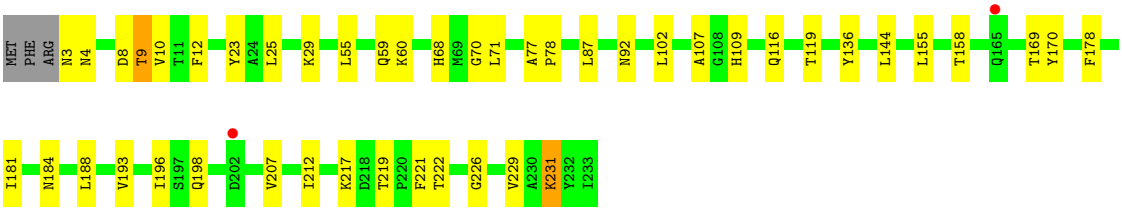
- Molecule 5: Proteasome subunit alpha type-6

Chain E:



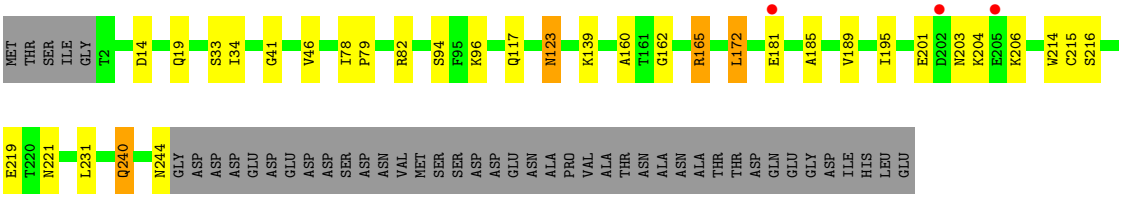
• Molecule 5: Proteasome subunit alpha type-6

Chain S:



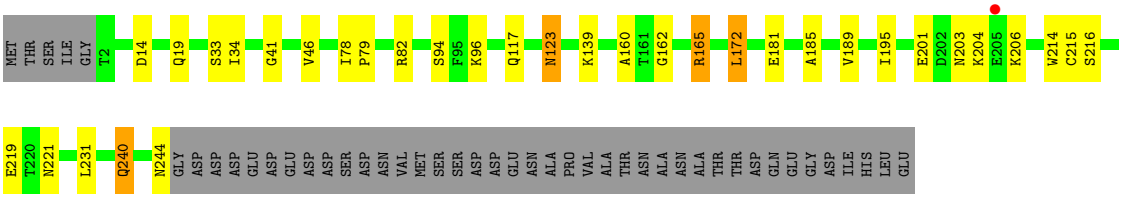
• Molecule 6: Probable proteasome subunit alpha type-7

Chain F:



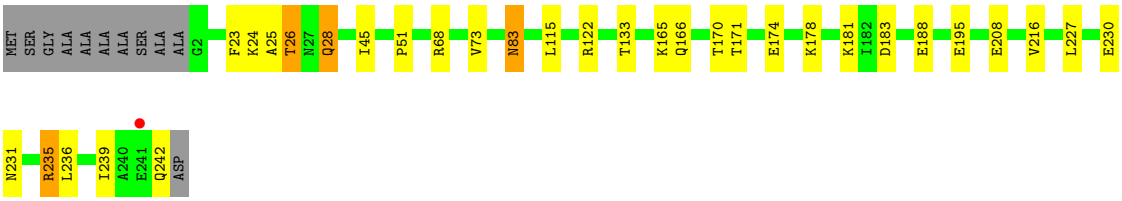
• Molecule 6: Probable proteasome subunit alpha type-7

Chain T:



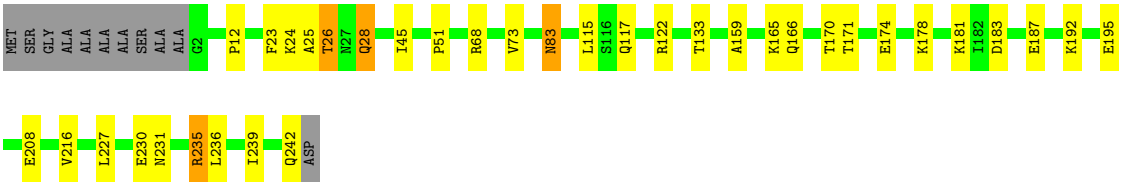
• Molecule 7: Proteasome subunit alpha type-1

Chain G:



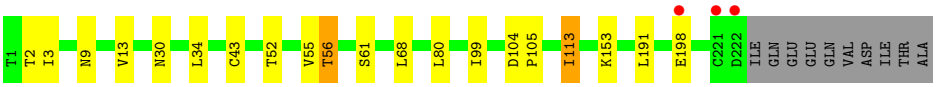
• Molecule 7: Proteasome subunit alpha type-1

Chain U:



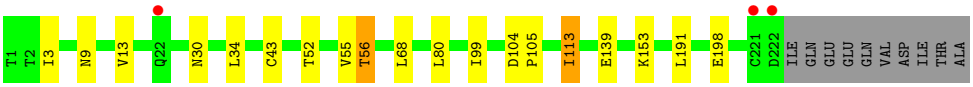
• Molecule 8: Proteasome subunit beta type-2

Chain H:



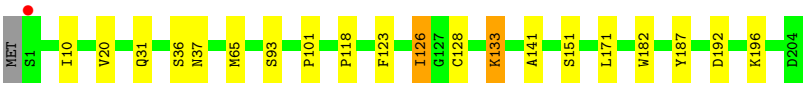
• Molecule 8: Proteasome subunit beta type-2

Chain V:



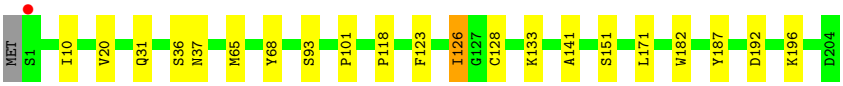
• Molecule 9: Proteasome subunit beta type-3

Chain I:



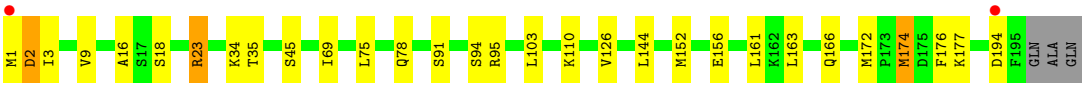
• Molecule 9: Proteasome subunit beta type-3

Chain W:



• Molecule 10: Proteasome subunit beta type-4

Chain J:

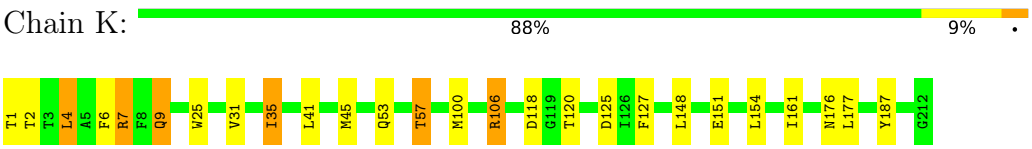


• Molecule 10: Proteasome subunit beta type-4

Chain X:

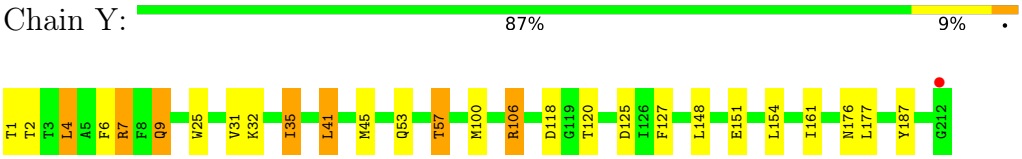
• Molecule 11: Proteasome subunit beta type-5

Chain K:



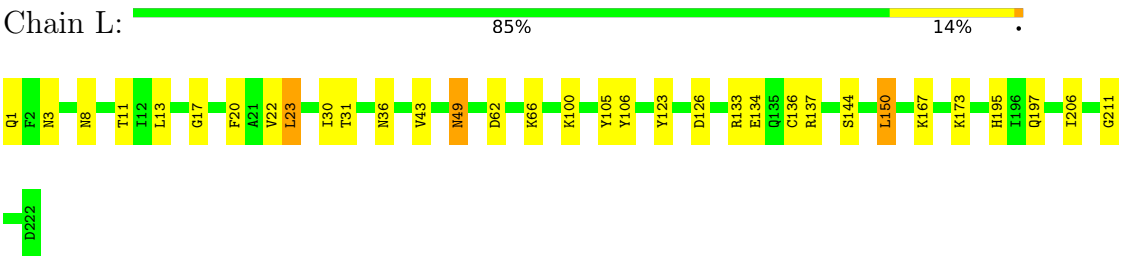
• Molecule 11: Proteasome subunit beta type-5

Chain Y:



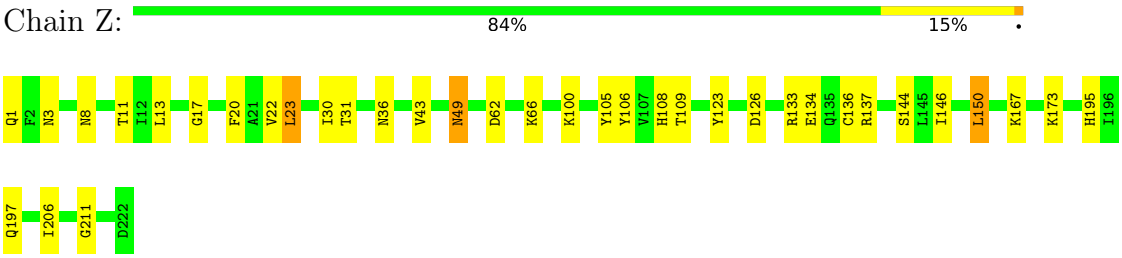
• Molecule 12: Proteasome subunit beta type-6

Chain L:



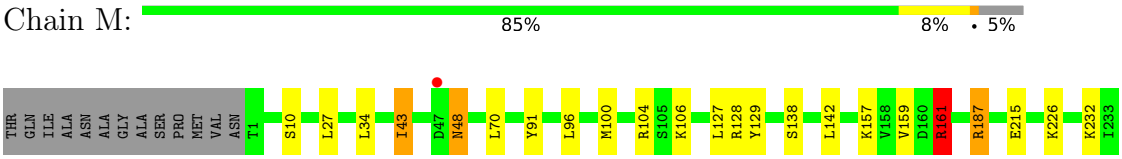
• Molecule 12: Proteasome subunit beta type-6

Chain Z:



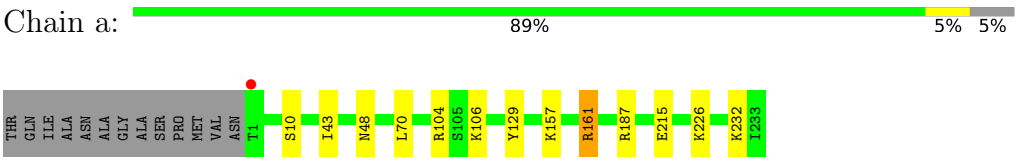
• Molecule 13: Proteasome subunit beta type-7

Chain M:



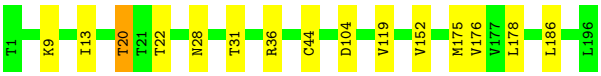
• Molecule 13: Proteasome subunit beta type-7

Chain a:



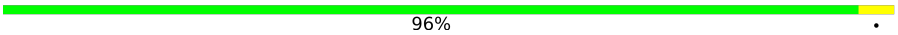
• Molecule 14: Proteasome subunit beta type-1

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	136.42Å 299.95Å 145.96Å 90.00° 113.18° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.4 (15.00-2.80) 96.4 (15.00-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 2.81Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.179 , 0.199 0.181 , 0.196	Depositor DCC
R_{free} test set	12637 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	60.2	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 46.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	49601	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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: MG, MES, 37Y

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	0.29	0/1952	0.56	0/2642
1	O	0.29	0/1952	0.56	0/2642
2	B	0.29	0/1934	0.60	0/2618
2	P	0.29	0/1934	0.60	0/2618
3	C	0.30	0/1910	0.61	0/2586
3	Q	0.30	0/1910	0.61	0/2586
4	D	0.29	0/1837	0.59	0/2475
4	R	0.28	0/1837	0.59	0/2475
5	E	0.28	0/1800	0.57	0/2433
5	S	0.29	0/1800	0.57	0/2433
6	F	0.29	0/1932	0.55	0/2609
6	T	0.29	0/1932	0.55	0/2609
7	G	0.29	0/1945	0.57	0/2634
7	U	0.29	0/1945	0.57	0/2634
8	H	0.27	0/1715	0.57	1/2326 (0.0%)
8	V	0.27	0/1715	0.54	0/2326
9	I	0.29	0/1611	0.56	0/2174
9	W	0.29	0/1611	0.56	0/2174
10	J	0.28	0/1589	0.55	0/2142
10	X	0.28	0/1589	0.55	0/2142
11	K	0.29	0/1681	0.57	0/2274
11	Y	0.29	0/1681	0.57	0/2274
12	L	0.28	0/1795	0.54	0/2420
12	Z	0.29	0/1795	0.54	0/2420
13	M	0.29	0/1855	0.60	1/2514 (0.0%)
13	a	0.30	0/1855	0.60	1/2514 (0.0%)
14	N	0.26	0/1541	0.53	0/2087
14	b	0.26	0/1541	0.52	0/2087
All	All	0.29	0/50194	0.57	3/67868 (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
9	I	0	1
9	W	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	H	2	THR	N-CA-CB	6.54	122.72	110.30
13	M	161	ARG	NE-CZ-NH1	5.32	122.96	120.30
13	a	161	ARG	NE-CZ-NH1	5.29	122.95	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	I	192	ASP	Peptide
9	W	192	ASP	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	14	0
1	O	1915	0	1929	15	0
2	B	1904	0	1904	24	0
2	P	1904	0	1904	21	0
3	C	1881	0	1895	27	0
3	Q	1881	0	1895	22	0
4	D	1813	0	1797	15	0
4	R	1813	0	1797	19	0
5	E	1773	0	1775	15	0
5	S	1773	0	1775	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1892	0	1883	16	0
6	T	1892	0	1883	17	0
7	G	1907	0	1901	12	0
7	U	1907	0	1901	14	0
8	H	1684	0	1688	5	0
8	V	1684	0	1688	6	0
9	I	1581	0	1574	11	0
9	W	1581	0	1574	11	0
10	J	1561	0	1569	16	0
10	X	1561	0	1569	15	0
11	K	1644	0	1593	15	0
11	Y	1644	0	1592	16	0
12	L	1757	0	1711	16	0
12	Z	1757	0	1711	20	0
13	M	1824	0	1832	10	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	9	0
14	b	1512	0	1481	0	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	2	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	K	12	0	13	0	0
16	Y	12	0	13	0	0
17	K	42	0	47	1	0
17	Y	42	0	47	1	0
18	A	1	0	0	0	0
18	B	7	0	0	0	0
18	C	9	0	0	0	0
18	D	4	0	0	0	0
18	E	3	0	0	0	0
18	F	4	0	0	0	0
18	G	8	0	0	0	0
18	H	14	0	0	0	0
18	I	6	0	0	0	0
18	J	6	0	0	0	0
18	K	9	0	0	0	0
18	L	9	0	0	0	0
18	M	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	N	7	0	0	0	0
18	O	2	0	0	0	0
18	P	7	0	0	0	0
18	Q	6	0	0	0	0
18	R	5	0	0	0	0
18	S	3	0	0	0	0
18	T	5	0	0	0	0
18	U	7	0	0	0	0
18	V	5	0	0	0	0
18	W	5	0	0	0	0
18	X	9	0	0	0	0
18	Y	13	0	0	0	0
18	Z	10	0	0	0	0
18	a	10	0	0	0	0
18	b	6	0	0	0	0
All	All	49601	0	49183	354	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (354) 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)
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.31	0.94
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.31	0.93
6:F:240:GLN:HE21	6:F:240:GLN:HA	1.39	0.87
6:T:240:GLN:HE21	6:T:240:GLN:HA	1.39	0.87
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.57	0.86
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.59	0.84
11:Y:100:MET:CE	11:Y:127:PHE:HB2	2.08	0.83
11:K:100:MET:CE	11:K:127:PHE:HB2	2.09	0.82
3:C:202:GLN:HG3	3:C:203:THR:H	1.44	0.81
1:A:176:GLU:HG3	2:B:55:LEU:HD22	1.62	0.80
3:Q:202:GLN:HG3	3:Q:203:THR:H	1.45	0.79
11:Y:53:GLN:O	11:Y:57:THR:HG23	1.82	0.79
5:E:9:THR:HG21	5:E:119:THR:HA	1.65	0.79
11:K:53:GLN:O	11:K:57:THR:HG23	1.82	0.79
5:S:9:THR:HG21	5:S:119:THR:HA	1.65	0.78
11:K:100:MET:HE3	11:K:127:PHE:CB	2.18	0.74
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.53	0.73
14:N:20:THR:HG22	14:N:31:THR:OG1	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.53	0.73
11:Y:100:MET:HE3	11:Y:127:PHE:CB	2.18	0.73
3:Q:51:LYS:O	3:Q:52:LEU:HB2	1.91	0.70
17:Y:303:37Y:H2	12:Z:126:ASP:HB3	1.73	0.69
3:C:51:LYS:O	3:C:52:LEU:HB2	1.90	0.69
10:X:23:ARG:NH2	11:Y:120:THR:OG1	2.26	0.69
17:K:303:37Y:H2	12:L:126:ASP:HB3	1.74	0.69
8:H:80:LEU:HD12	8:H:113:ILE:HD11	1.76	0.68
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.58	0.68
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.59	0.68
4:D:32:ILE:HD12	4:D:192:VAL:HG23	1.74	0.68
6:T:34:ILE:HG22	6:T:160:ALA:HB2	1.76	0.67
4:R:32:ILE:HD12	4:R:192:VAL:HG23	1.75	0.67
7:G:23:PHE:O	7:G:26:THR:HB	1.95	0.67
10:J:23:ARG:NH2	11:K:120:THR:OG1	2.27	0.67
6:T:201:GLU:O	6:T:204:LYS:HD2	1.95	0.66
6:F:34:ILE:HG22	6:F:160:ALA:HB2	1.77	0.66
6:F:201:GLU:O	6:F:204:LYS:HD2	1.95	0.66
8:V:80:LEU:HD12	8:V:113:ILE:HD11	1.76	0.66
2:B:180:LYS:O	2:B:183:MET:HB2	1.97	0.65
7:U:23:PHE:O	7:U:26:THR:HB	1.95	0.65
2:P:180:LYS:O	2:P:183:MET:HB2	1.98	0.64
13:M:161:ARG:HG3	13:M:161:ARG:HH11	1.63	0.63
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.82	0.62
3:C:160:GLN:HE22	3:C:170:ARG:HE	1.49	0.60
3:C:35:LYS:HG2	3:C:158:SER:O	2.01	0.60
6:T:172:LEU:HD13	6:T:195:ILE:HD13	1.83	0.60
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.82	0.60
6:F:172:LEU:HD13	6:F:195:ILE:HD13	1.84	0.60
9:W:101:PRO:HB3	9:W:126:ILE:HD12	1.84	0.59
12:Z:49:ASN:HD21	12:Z:211:GLY:HA2	1.67	0.59
9:I:101:PRO:HB3	9:I:126:ILE:HD12	1.83	0.59
1:O:122:THR:CG2	2:P:128:ARG:HH21	2.15	0.59
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.85	0.59
12:L:8:ASN:HA	12:L:30:ILE:O	2.03	0.59
12:L:49:ASN:HD21	12:L:211:GLY:HA2	1.66	0.58
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.03	0.58
3:Q:160:GLN:HE22	3:Q:170:ARG:HE	1.49	0.58
6:T:240:GLN:HA	6:T:240:GLN:NE2	2.15	0.58
2:B:8:ARG:HD2	3:C:4:ARG:NH2	2.18	0.58
12:L:23:LEU:HD13	12:L:43:VAL:HG13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:202:GLN:CG	3:C:203:THR:H	2.16	0.58
2:P:89:THR:HG21	2:P:117:ILE:CD1	2.34	0.58
7:U:73:VAL:HG12	7:U:133:THR:HB	1.86	0.58
2:B:89:THR:HG21	2:B:117:ILE:CD1	2.34	0.58
6:F:240:GLN:HA	6:F:240:GLN:NE2	2.15	0.58
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.85	0.57
12:Z:23:LEU:HD13	12:Z:43:VAL:HG13	1.85	0.57
7:G:73:VAL:HG12	7:G:133:THR:HB	1.87	0.57
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.03	0.57
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.86	0.57
2:P:47:ALA:HB1	2:P:64:LYS:HD2	1.86	0.57
3:Q:202:GLN:CG	3:Q:203:THR:H	2.16	0.56
5:S:136:TYR:CE1	5:S:217:LYS:HA	2.41	0.56
5:E:136:TYR:CE1	5:E:217:LYS:HA	2.40	0.56
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.70	0.56
8:H:52:THR:O	8:H:56:THR:HB	2.06	0.55
1:A:122:THR:CG2	2:B:128:ARG:HH21	2.20	0.55
8:V:52:THR:O	8:V:56:THR:HB	2.07	0.55
10:J:3:ILE:HB	10:J:18:SER:HB3	1.89	0.55
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.55	0.54
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.56	0.54
12:Z:108:HIS:HD2	12:Z:109:THR:N	2.06	0.54
10:X:3:ILE:HB	10:X:18:SER:HB3	1.89	0.54
12:L:17:GLY:HA3	12:L:20:PHE:CE1	2.42	0.54
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.06	0.54
12:Z:17:GLY:HA3	12:Z:20:PHE:CE1	2.42	0.54
4:R:185:LEU:O	4:R:189:GLU:HG3	2.08	0.54
2:B:146:GLN:HG2	3:C:57:ILE:HG21	1.90	0.54
12:L:195:HIS:HD2	12:L:197:GLN:H	1.55	0.54
3:C:201:VAL:O	3:C:202:GLN:HB2	2.07	0.54
7:G:239:ILE:O	7:G:242:GLN:HB3	2.08	0.54
3:Q:195:ARG:HG3	3:Q:234:ILE:HD13	1.89	0.53
11:Y:176:ASN:ND2	11:Y:187:TYR:OH	2.40	0.53
4:D:185:LEU:O	4:D:189:GLU:HG3	2.08	0.53
3:C:195:ARG:HG3	3:C:234:ILE:HD13	1.89	0.53
11:K:176:ASN:ND2	11:K:187:TYR:OH	2.42	0.53
8:H:3:ILE:HG22	8:H:99:ILE:HD12	1.91	0.53
3:C:201:VAL:HG13	3:C:202:GLN:N	2.25	0.52
8:V:3:ILE:HG22	8:V:99:ILE:HD12	1.91	0.52
12:Z:100:LYS:HD3	12:Z:105:TYR:CE2	2.45	0.52
12:L:100:LYS:HD3	12:L:105:TYR:CE2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:239:ILE:O	7:U:242:GLN:HB3	2.09	0.52
14:N:20:THR:CG2	14:N:31:THR:OG1	2.55	0.52
5:S:109:HIS:HB3	6:T:82:ARG:NH2	2.25	0.52
7:U:227:LEU:HB3	7:U:231:ASN:HB2	1.91	0.52
2:B:12:PHE:H	3:C:17:GLN:HE22	1.58	0.52
5:S:155:LEU:HD13	5:S:158:THR:HB	1.91	0.52
10:J:3:ILE:HD12	10:J:176:PHE:CD2	2.45	0.52
13:M:159:VAL:HG23	13:M:159:VAL:O	2.09	0.52
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.92	0.52
7:G:227:LEU:HB3	7:G:231:ASN:HB2	1.90	0.52
13:M:48:ASN:H	13:M:48:ASN:HD22	1.58	0.52
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.25	0.52
9:W:101:PRO:HB3	9:W:126:ILE:CD1	2.40	0.52
7:U:83:ASN:C	7:U:83:ASN:HD22	2.13	0.51
10:X:3:ILE:HD12	10:X:176:PHE:CD2	2.45	0.51
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.92	0.51
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.92	0.51
6:T:185:ALA:O	6:T:189:VAL:HG23	2.10	0.51
4:R:88:ALA:HA	4:R:99:ILE:HG21	1.92	0.51
9:I:101:PRO:HB3	9:I:126:ILE:CD1	2.40	0.51
11:K:35:ILE:HB	11:K:45:MET:CE	2.40	0.51
7:G:83:ASN:C	7:G:83:ASN:HD22	2.14	0.51
5:E:155:LEU:HD13	5:E:158:THR:HB	1.91	0.51
1:O:158:PRO:HB2	2:P:57:GLU:HB3	1.92	0.51
10:J:174:MET:HA	10:X:174:MET:HA	1.92	0.51
10:X:1:MET:HA	10:X:34:LYS:CE	2.41	0.50
11:Y:35:ILE:HB	11:Y:45:MET:CE	2.41	0.50
6:F:185:ALA:O	6:F:189:VAL:HG23	2.10	0.50
2:B:93:HIS:HB3	2:B:113:ARG:NH2	2.15	0.50
2:B:14:PRO:HA	3:C:20:TYR:CD1	2.47	0.50
3:C:38:ASN:N	3:C:38:ASN:HD22	2.10	0.50
10:J:1:MET:HA	10:J:34:LYS:CE	2.42	0.50
4:D:99:ILE:HD13	4:D:104:LEU:HB2	1.94	0.49
4:R:9:PRO:HA	5:S:23:TYR:CG	2.47	0.49
5:E:68:HIS:HE1	5:E:102:LEU:O	1.95	0.49
3:C:9:PHE:H	4:D:15:GLN:HE22	1.60	0.49
4:R:99:ILE:HD13	4:R:104:LEU:HB2	1.94	0.49
3:C:205:ALA:C	3:C:207:ASN:H	2.16	0.49
5:S:68:HIS:HE1	5:S:102:LEU:O	1.95	0.49
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.48	0.49
11:K:7:ARG:HG2	11:K:7:ARG:HH11	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:20:THR:HG22	14:N:31:THR:HG1	1.78	0.49
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.48	0.49
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.43	0.48
3:Q:38:ASN:N	3:Q:38:ASN:HD22	2.10	0.48
2:B:155:ASN:ND2	3:C:77:ASN:HB2	2.29	0.48
5:S:12:PHE:H	6:T:19:GLN:HE22	1.62	0.48
4:D:71:SER:HB3	4:D:164:ILE:HD12	1.95	0.48
6:T:123:ASN:C	6:T:123:ASN:HD22	2.17	0.48
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.43	0.48
5:E:12:PHE:H	6:F:19:GLN:HE22	1.62	0.48
5:E:109:HIS:HB3	6:F:82:ARG:NH2	2.28	0.48
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.96	0.48
3:Q:205:ALA:C	3:Q:207:ASN:H	2.16	0.48
1:O:12:PHE:H	2:P:20:GLN:HE22	1.60	0.48
6:T:240:GLN:HE21	6:T:240:GLN:CA	2.17	0.48
1:O:50:LYS:HG3	1:O:50:LYS:O	2.14	0.47
9:W:65:MET:CE	9:W:93:SER:HB3	2.44	0.47
11:Y:7:ARG:HH11	11:Y:7:ARG:HG2	1.78	0.47
6:F:123:ASN:C	6:F:123:ASN:HD22	2.17	0.47
1:A:50:LYS:O	1:A:50:LYS:HG3	2.14	0.47
2:P:59:ASP:HB3	2:P:231:PRO:HG2	1.96	0.47
4:R:71:SER:HB3	4:R:164:ILE:HD12	1.96	0.47
14:N:20:THR:HG23	14:N:28:ASN:HB3	1.96	0.47
7:U:83:ASN:C	7:U:83:ASN:ND2	2.68	0.47
9:I:65:MET:CE	9:I:93:SER:HB3	2.44	0.47
10:J:1:MET:HA	10:J:34:LYS:HE3	1.96	0.47
2:P:8:ARG:HD2	3:Q:4:ARG:NH2	2.30	0.47
4:R:73:LEU:HD12	4:R:131:GLY:HA3	1.97	0.47
2:B:59:ASP:HB3	2:B:231:PRO:HG2	1.96	0.47
4:R:38:VAL:HG11	4:R:137:ALA:HB1	1.97	0.47
12:Z:22:VAL:HG12	12:Z:206:ILE:HG13	1.97	0.47
10:X:1:MET:HA	10:X:34:LYS:HE3	1.96	0.47
10:X:3:ILE:HD12	10:X:176:PHE:CG	2.50	0.47
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.45	0.47
4:D:73:LEU:HD12	4:D:131:GLY:HA3	1.97	0.46
7:G:45:ILE:HG22	7:G:216:VAL:HG22	1.97	0.46
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.49	0.46
1:O:211:LEU:HD22	1:O:238:LEU:HD12	1.98	0.46
7:U:45:ILE:HG22	7:U:216:VAL:HG22	1.97	0.46
12:Z:108:HIS:C	12:Z:108:HIS:CD2	2.88	0.46
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:83:ASN:C	7:G:83:ASN:ND2	2.69	0.46
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.98	0.46
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.97	0.46
10:X:91:SER:HA	10:X:94:SER:OG	2.16	0.46
7:G:25:ALA:O	7:G:28:GLN:HB2	2.15	0.46
7:U:25:ALA:O	7:U:28:GLN:HB2	2.16	0.46
1:A:211:LEU:HD22	1:A:238:LEU:HD12	1.98	0.46
3:Q:88:ARG:HG2	10:X:69:ILE:HG21	1.98	0.46
4:R:99:ILE:CD1	4:R:104:LEU:HB2	2.46	0.46
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.81	0.45
12:L:22:VAL:HG12	12:L:206:ILE:HG13	1.97	0.45
13:M:187:ARG:NH1	8:V:139:GLU:OE1	2.48	0.45
3:C:201:VAL:O	3:C:202:GLN:CB	2.64	0.45
4:D:38:VAL:HG11	4:D:137:ALA:HB1	1.98	0.45
5:S:226:GLY:O	5:S:229:VAL:HG22	2.16	0.45
5:E:226:GLY:O	5:E:229:VAL:HG22	2.16	0.45
10:J:3:ILE:HD12	10:J:176:PHE:CG	2.50	0.45
1:A:66:LEU:C	1:A:66:LEU:HD23	2.37	0.45
4:R:138:GLY:HA2	4:R:214:ILE:HG12	1.99	0.45
1:A:12:PHE:H	2:B:20:GLN:HE22	1.65	0.45
6:F:172:LEU:CD1	6:F:195:ILE:HD13	2.47	0.45
2:P:15:GLU:O	3:Q:27:ARG:NH1	2.47	0.45
4:D:37:GLY:HA2	4:D:145:TYR:CE1	2.52	0.45
10:J:91:SER:HA	10:J:94:SER:OG	2.17	0.45
5:S:70:GLY:HA3	5:S:221:PHE:CE2	2.52	0.45
1:A:44:VAL:HG23	1:A:211:LEU:HD21	1.99	0.45
2:B:162:ILE:HG13	2:B:163:SER:N	2.32	0.45
3:C:198:LEU:HA	3:C:201:VAL:HG12	1.99	0.45
4:D:99:ILE:CD1	4:D:104:LEU:HB2	2.46	0.45
9:I:65:MET:HE1	9:I:93:SER:HB3	1.99	0.45
1:O:46:ALA:HB2	1:O:211:LEU:HG	1.99	0.45
2:P:162:ILE:HG13	2:P:163:SER:N	2.31	0.45
7:U:73:VAL:CG1	7:U:133:THR:HB	2.46	0.45
4:D:125:LEU:HD12	4:D:125:LEU:O	2.17	0.44
3:Q:160:GLN:HE21	3:Q:160:GLN:CA	2.28	0.44
11:Y:25:TRP:CH2	12:Z:144:SER:HA	2.52	0.44
5:E:170:TYR:HB2	5:E:198:GLN:HG3	2.00	0.44
4:R:37:GLY:HA2	4:R:145:TYR:CE1	2.52	0.44
12:Z:123:TYR:CE2	12:Z:133:ARG:HB2	2.52	0.44
6:F:33:SER:HB3	6:F:46:VAL:HG23	1.99	0.44
5:E:70:GLY:HA3	5:E:221:PHE:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:98:PHE:O	13:M:91:TYR:HA	2.17	0.44
7:G:170:THR:O	7:G:174:GLU:HG3	2.18	0.44
1:O:44:VAL:HG23	1:O:211:LEU:HD21	1.98	0.44
9:W:36:SER:CB	10:X:126:VAL:HG11	2.48	0.44
11:Y:6:PHE:HA	11:Y:125:ASP:O	2.18	0.44
3:C:160:GLN:HE21	3:C:160:GLN:CA	2.27	0.44
11:K:6:PHE:HA	11:K:125:ASP:O	2.18	0.44
1:O:115:ALA:HB1	1:O:154:GLY:O	2.17	0.44
4:R:125:LEU:HD12	4:R:125:LEU:O	2.16	0.44
6:T:33:SER:HB3	6:T:46:VAL:HG23	1.99	0.44
9:I:20:VAL:HG13	9:I:118:PRO:HB3	2.00	0.44
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	1.99	0.44
9:W:65:MET:HE1	9:W:93:SER:HB3	1.99	0.44
7:U:170:THR:O	7:U:174:GLU:HG3	2.18	0.44
7:G:73:VAL:CG1	7:G:133:THR:HB	2.47	0.43
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.45	0.43
1:A:115:ALA:HB1	1:A:154:GLY:O	2.18	0.43
11:Y:106:ARG:HH11	11:Y:106:ARG:HB3	1.83	0.43
1:A:46:ALA:HB2	1:A:211:LEU:HG	1.99	0.43
14:N:13:ILE:HG21	14:N:175:MET:HE3	2.00	0.43
1:O:66:LEU:HD23	1:O:66:LEU:C	2.39	0.43
1:A:119:GLN:O	1:A:122:THR:HB	2.18	0.43
2:B:135:ILE:HD11	2:B:164:VAL:HG22	2.01	0.43
6:F:240:GLN:HE21	6:F:240:GLN:CA	2.17	0.43
11:K:35:ILE:HB	11:K:45:MET:HE2	2.00	0.43
11:K:154:LEU:HD22	11:K:177:LEU:HD13	2.01	0.43
12:L:62:ASP:O	12:L:66:LYS:HB2	2.19	0.43
12:L:123:TYR:CE2	12:L:133:ARG:HB2	2.53	0.43
5:S:170:TYR:HB2	5:S:198:GLN:HG3	1.99	0.43
8:V:104:ASP:HB2	8:V:105:PRO:HD2	2.01	0.43
2:B:139:TYR:CD1	2:B:224:VAL:HG21	2.53	0.43
4:D:138:GLY:HA2	4:D:214:ILE:HG12	1.99	0.43
14:N:152:VAL:HA	14:N:175:MET:HE1	2.00	0.43
1:O:231:LYS:HB2	1:O:231:LYS:HE3	1.80	0.43
3:C:88:ARG:HG2	10:J:69:ILE:HG21	2.01	0.43
2:P:139:TYR:CD1	2:P:224:VAL:HG21	2.54	0.43
2:B:139:TYR:CE2	2:B:144:GLY:HA2	2.53	0.43
4:R:159:TYR:CZ	4:R:162:LYS:HD3	2.54	0.43
6:T:172:LEU:CD1	6:T:195:ILE:HD13	2.46	0.43
11:K:4:LEU:HD13	11:K:161:ILE:HD11	2.00	0.43
2:P:139:TYR:CE2	2:P:144:GLY:HA2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:20:VAL:HG13	9:W:118:PRO:HB3	2.00	0.43
4:D:159:TYR:CZ	4:D:162:LYS:HD3	2.54	0.43
11:K:106:ARG:HH11	11:K:106:ARG:HB3	1.83	0.43
4:R:50:LEU:HD23	4:R:50:LEU:HA	1.92	0.43
13:M:128:ARG:HH11	13:M:138:SER:HB2	1.84	0.42
2:P:135:ILE:HD11	2:P:164:VAL:HG22	2.01	0.42
12:Z:62:ASP:O	12:Z:66:LYS:HB2	2.19	0.42
13:M:127:LEU:HG	13:M:142:LEU:HD12	2.01	0.42
5:S:77:ALA:HB3	5:S:78:PRO:HD3	2.01	0.42
11:Y:4:LEU:HD13	11:Y:161:ILE:HD11	2.00	0.42
1:A:99:ARG:HE	8:H:61:SER:HG	1.68	0.42
7:G:195:GLU:HG3	7:G:235:ARG:HG3	2.02	0.42
8:H:104:ASP:HB2	8:H:105:PRO:HD2	2.00	0.42
5:S:212:ILE:HD12	5:S:229:VAL:HG12	2.00	0.42
6:T:162:GLY:O	6:T:165:ARG:HB3	2.19	0.42
7:U:195:GLU:HG3	7:U:235:ARG:HG3	2.02	0.42
12:Z:108:HIS:CD2	12:Z:109:THR:N	2.86	0.42
10:J:152:MET:CE	10:J:156:GLU:HB3	2.50	0.42
2:B:14:PRO:HA	3:C:20:TYR:CG	2.54	0.42
6:F:162:GLY:O	6:F:165:ARG:HB3	2.20	0.42
9:I:187:TYR:OH	9:I:196:LYS:HE3	2.19	0.42
11:K:1:THR:HG22	11:K:2:THR:N	2.35	0.42
3:Q:166:SER:HA	3:Q:169:VAL:HG13	2.01	0.42
12:Z:206:ILE:HD12	12:Z:206:ILE:N	2.35	0.42
2:B:204:ALA:O	2:B:209:ARG:NH2	2.53	0.42
11:K:25:TRP:CH2	12:L:144:SER:HA	2.55	0.42
5:E:77:ALA:HB3	5:E:78:PRO:HD3	2.02	0.42
5:E:212:ILE:HD12	5:E:229:VAL:HG12	2.00	0.42
13:M:43:ILE:HG12	13:M:43:ILE:O	2.20	0.42
3:Q:71:LEU:HD22	3:Q:84:ILE:HG12	2.02	0.42
3:C:168:THR:O	3:C:171:GLU:HB3	2.20	0.42
1:O:119:GLN:O	1:O:122:THR:HB	2.20	0.42
5:E:178:PHE:HA	5:E:181:ILE:HG13	2.02	0.41
2:B:143:TYR:O	3:C:56:ARG:NH1	2.44	0.41
9:I:123:PHE:HA	9:I:128:CYS:O	2.20	0.41
13:M:96:LEU:O	13:M:100:MET:HG2	2.21	0.41
2:P:93:HIS:HB3	2:P:113:ARG:NH2	2.14	0.41
3:Q:11:PRO:HA	4:R:18:TYR:CD1	2.54	0.41
3:C:166:SER:HA	3:C:169:VAL:HG13	2.01	0.41
13:M:27:LEU:HD21	13:M:34:LEU:HD22	2.02	0.41
2:P:204:ALA:O	2:P:209:ARG:NH2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:193:VAL:O	5:S:196:ILE:HG22	2.20	0.41
12:Z:146:ILE:HG22	12:Z:150:LEU:HD22	2.02	0.41
12:L:134:GLU:OE1	12:L:137:ARG:NH2	2.54	0.41
14:N:175:MET:HB2	14:N:186:LEU:HB2	2.02	0.41
1:O:64:VAL:HG11	1:O:212:ALA:HB3	2.02	0.41
5:E:193:VAL:O	5:E:196:ILE:HG22	2.20	0.41
6:T:41:GLY:HA3	6:T:215:CYS:O	2.21	0.41
11:Y:154:LEU:HD22	11:Y:177:LEU:HD13	2.01	0.41
6:T:34:ILE:HG22	6:T:160:ALA:CB	2.49	0.41
9:W:187:TYR:OH	9:W:196:LYS:HE3	2.19	0.41
11:Y:32:LYS:HE2	11:Y:32:LYS:HB3	1.96	0.41
2:B:35:ILE:HD12	2:B:196:LEU:HG	2.02	0.41
3:C:71:LEU:HD22	3:C:84:ILE:HG12	2.03	0.41
12:L:206:ILE:N	12:L:206:ILE:HD12	2.36	0.41
2:P:35:ILE:HD12	2:P:196:LEU:HG	2.02	0.41
6:T:78:ILE:HB	6:T:79:PRO:HD3	2.03	0.41
9:W:123:PHE:HA	9:W:128:CYS:O	2.20	0.41
10:X:152:MET:CE	10:X:156:GLU:HB3	2.51	0.41
1:A:231:LYS:HE3	1:A:231:LYS:HB2	1.80	0.41
10:J:152:MET:HE3	10:J:156:GLU:HB3	2.03	0.41
10:J:177:LYS:NZ	10:X:169:GLU:O	2.54	0.41
14:N:13:ILE:HG21	14:N:175:MET:CE	2.50	0.41
2:P:93:HIS:CG	2:P:113:ARG:HE	2.39	0.41
5:S:87:LEU:HD21	5:S:107:ALA:HB1	2.03	0.41
11:Y:1:THR:HG22	11:Y:2:THR:N	2.35	0.41
5:E:87:LEU:HD21	5:E:107:ALA:HB1	2.03	0.41
1:O:55:LEU:HB3	7:U:159:ALA:O	2.21	0.41
3:Q:168:THR:O	3:Q:171:GLU:HB3	2.20	0.41
1:A:64:VAL:HG11	1:A:212:ALA:HB3	2.03	0.40
4:D:214:ILE:HG22	4:D:220:PHE:HD1	1.86	0.40
5:S:178:PHE:HA	5:S:181:ILE:HG13	2.02	0.40
3:C:202:GLN:CG	3:C:203:THR:N	2.83	0.40
6:F:78:ILE:HB	6:F:79:PRO:HD3	2.03	0.40
9:I:36:SER:CB	10:J:126:VAL:HG11	2.51	0.40
4:R:214:ILE:HG22	4:R:220:PHE:HD1	1.86	0.40
4:R:214:ILE:O	4:R:214:ILE:HG13	2.21	0.40
8:V:80:LEU:HD12	8:V:113:ILE:CD1	2.49	0.40
12:Z:134:GLU:OE1	12:Z:137:ARG:NH2	2.54	0.40
6:F:41:GLY:HA3	6:F:215:CYS:O	2.21	0.40
6:F:216:SER:HB3	6:F:219:GLU:HB2	2.04	0.40
10:J:45:SER:OG	10:J:103:LEU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:216:SER:HB3	6:T:219:GLU:HB2	2.03	0.40
9:W:65:MET:O	9:W:68:TYR:HB3	2.21	0.40
7:G:188:GLU:HA	7:G:188:GLU:OE2	2.21	0.40
7:U:187:GLU:HG2	7:U:192:LYS:CB	2.52	0.40
10:X:45:SER:OG	10:X:103:LEU:HB2	2.22	0.40
9:I:133:LYS:H	9:I:133:LYS:HG2	1.70	0.40
2:P:58:GLN:NE2	2:P:208:ASP:HA	2.37	0.40
11:Y:41:LEU:HD23	11:Y:41:LEU:HA	1.99	0.40

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%)	238 (96%)	8 (3%)	2 (1%)	19	49
1	O	248/250 (99%)	238 (96%)	8 (3%)	2 (1%)	19	49
2	B	242/258 (94%)	231 (96%)	9 (4%)	2 (1%)	19	49
2	P	242/258 (94%)	230 (95%)	10 (4%)	2 (1%)	19	49
3	C	238/254 (94%)	227 (95%)	4 (2%)	7 (3%)	4	15
3	Q	238/254 (94%)	227 (95%)	4 (2%)	7 (3%)	4	15
4	D	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
4	R	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
5	E	229/234 (98%)	214 (93%)	13 (6%)	2 (1%)	17	46
5	S	229/234 (98%)	214 (93%)	13 (6%)	2 (1%)	17	46
6	F	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	235 (98%)	3 (1%)	1 (0%)	34	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	U	239/252 (95%)	235 (98%)	3 (1%)	1 (0%)	34	66
8	H	220/232 (95%)	211 (96%)	8 (4%)	1 (0%)	29	61
8	V	220/232 (95%)	211 (96%)	8 (4%)	1 (0%)	29	61
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
9	W	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	2 (1%)	2 (1%)	15	44
10	X	193/198 (98%)	188 (97%)	3 (2%)	2 (1%)	15	44
11	K	210/212 (99%)	202 (96%)	7 (3%)	1 (0%)	29	61
11	Y	210/212 (99%)	203 (97%)	6 (3%)	1 (0%)	29	61
12	L	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
12	Z	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
13	M	231/246 (94%)	224 (97%)	7 (3%)	0	100	100
13	a	231/246 (94%)	224 (97%)	7 (3%)	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	6276/6614 (95%)	6057 (96%)	183 (3%)	36 (1%)	25	56

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
2	B	51	VAL
3	C	202	GLN
11	K	9	GLN
1	O	2	THR
2	P	51	VAL
3	Q	202	GLN
11	Y	9	GLN
3	C	205	ALA
5	E	231	LYS
8	H	9	ASN
3	Q	205	ALA
5	S	231	LYS
8	V	9	ASN
3	C	183	PRO
5	E	59	GLN
10	J	2	ASP

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Mol	Chain	Res	Type
3	Q	183	PRO
5	S	59	GLN
10	X	2	ASP
3	C	52	LEU
3	C	206	LYS
3	Q	52	LEU
3	Q	206	LYS
1	A	166	LYS
2	B	221	ASP
1	O	166	LYS
2	P	221	ASP
3	Q	239	GLN
3	C	239	GLN
3	C	201	VAL
7	G	51	PRO
10	J	9	VAL
7	U	51	PRO
10	X	9	VAL
3	Q	201	VAL

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%)	198 (95%)	11 (5%)	22	54
1	O	209/209 (100%)	198 (95%)	11 (5%)	22	54
2	B	203/216 (94%)	189 (93%)	14 (7%)	15	41
2	P	203/216 (94%)	190 (94%)	13 (6%)	17	45
3	C	212/226 (94%)	193 (91%)	19 (9%)	9	28
3	Q	212/226 (94%)	193 (91%)	19 (9%)	9	28
4	D	194/215 (90%)	175 (90%)	19 (10%)	8	24
4	R	194/215 (90%)	176 (91%)	18 (9%)	9	26
5	E	190/193 (98%)	170 (90%)	20 (10%)	7	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	S	190/193 (98%)	170 (90%)	20 (10%)	7	20
6	F	201/239 (84%)	185 (92%)	16 (8%)	12	34
6	T	201/239 (84%)	185 (92%)	16 (8%)	12	34
7	G	206/210 (98%)	189 (92%)	17 (8%)	11	32
7	U	206/210 (98%)	188 (91%)	18 (9%)	10	30
8	H	181/190 (95%)	170 (94%)	11 (6%)	18	48
8	V	181/190 (95%)	170 (94%)	11 (6%)	18	48
9	I	172/173 (99%)	165 (96%)	7 (4%)	30	64
9	W	172/173 (99%)	165 (96%)	7 (4%)	30	64
10	J	173/175 (99%)	160 (92%)	13 (8%)	13	37
10	X	173/175 (99%)	160 (92%)	13 (8%)	13	37
11	K	169/169 (100%)	158 (94%)	11 (6%)	17	44
11	Y	169/169 (100%)	158 (94%)	11 (6%)	17	44
12	L	185/185 (100%)	175 (95%)	10 (5%)	22	53
12	Z	185/185 (100%)	175 (95%)	10 (5%)	22	53
13	M	199/208 (96%)	186 (94%)	13 (6%)	17	44
13	a	199/208 (96%)	186 (94%)	13 (6%)	17	44
14	N	162/162 (100%)	155 (96%)	7 (4%)	29	62
14	b	162/162 (100%)	155 (96%)	7 (4%)	29	62
All	All	5312/5540 (96%)	4937 (93%)	375 (7%)	14	39

All (375) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	17	LYS
1	A	29	LYS
1	A	50	LYS
1	A	51	SER
1	A	59	GLU
1	A	61	LEU
1	A	122	THR
1	A	157	PHE
1	A	197	LYS
1	A	231	LYS

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Mol	Chain	Res	Type
2	B	17	ARG
2	B	50	LYS
2	B	54	THR
2	B	55	LEU
2	B	58	GLN
2	B	62	THR
2	B	119	GLN
2	B	180	LYS
2	B	184	LYS
2	B	191	LEU
2	B	197	SER
2	B	209	ARG
2	B	238	LEU
2	B	244	THR
3	C	4	ARG
3	C	32	VAL
3	C	38	ASN
3	C	48	SER
3	C	49	THR
3	C	51	LYS
3	C	55	THR
3	C	82	ILE
3	C	124	VAL
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	175	LYS
3	C	180	LYS
3	C	187	GLU
3	C	203	THR
3	C	227	ILE
3	C	232	THR
3	C	240	GLU
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	54	ASP
4	D	60	VAL
4	D	78	ARG
4	D	99	ILE
4	D	117	GLU
4	D	125	LEU

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Mol	Chain	Res	Type
4	D	176	LEU
4	D	182	SER
4	D	190	LEU
4	D	193	LEU
4	D	202	GLU
4	D	214	ILE
4	D	224	ASP
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	3	ASN
5	E	4	ASN
5	E	8	ASP
5	E	9	THR
5	E	10	VAL
5	E	25	LEU
5	E	29	LYS
5	E	55	LEU
5	E	60	LYS
5	E	71	LEU
5	E	92	ASN
5	E	116	GLN
5	E	144	LEU
5	E	169	THR
5	E	184	ASN
5	E	188	LEU
5	E	207	VAL
5	E	219	THR
5	E	222	THR
5	E	231	LYS
6	F	14	ASP
6	F	94	SER
6	F	96	LYS
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	165	ARG
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN
6	F	206	LYS
6	F	214	TRP

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Mol	Chain	Res	Type
6	F	221	ASN
6	F	231	LEU
6	F	240	GLN
6	F	244	ASN
7	G	24	LYS
7	G	26	THR
7	G	28	GLN
7	G	68	ARG
7	G	83	ASN
7	G	115	LEU
7	G	122	ARG
7	G	165	LYS
7	G	166	GLN
7	G	171	THR
7	G	178	LYS
7	G	181	LYS
7	G	183	ASP
7	G	208	GLU
7	G	230	GLU
7	G	235	ARG
7	G	236	LEU
8	H	13	VAL
8	H	30	ASN
8	H	34	LEU
8	H	43	CYS
8	H	55	VAL
8	H	56	THR
8	H	68	LEU
8	H	113	ILE
8	H	153	LYS
8	H	191	LEU
8	H	198	GLU
9	I	31	GLN
9	I	37	ASN
9	I	126	ILE
9	I	133	LYS
9	I	151	SER
9	I	171	LEU
9	I	182	TRP
10	J	2	ASP
10	J	23	ARG
10	J	35	THR

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Mol	Chain	Res	Type
10	J	75	LEU
10	J	78	GLN
10	J	95	ARG
10	J	110	LYS
10	J	144	LEU
10	J	163	LEU
10	J	166	GLN
10	J	172	MET
10	J	174	MET
10	J	194	ASP
11	K	4	LEU
11	K	7	ARG
11	K	9	GLN
11	K	31	VAL
11	K	35	ILE
11	K	41	LEU
11	K	57	THR
11	K	106	ARG
11	K	118	ASP
11	K	148	LEU
11	K	151	GLU
12	L	1	GLN
12	L	3	ASN
12	L	11	THR
12	L	23	LEU
12	L	49	ASN
12	L	106	TYR
12	L	136	CYS
12	L	150	LEU
12	L	167	LYS
12	L	173	LYS
13	M	10	SER
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	106	LYS
13	M	129	TYR
13	M	157	LYS
13	M	161	ARG
13	M	187	ARG
13	M	215	GLU

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Mol	Chain	Res	Type
13	M	226	LYS
13	M	232	LYS
14	N	9	LYS
14	N	20	THR
14	N	22	THR
14	N	36	ARG
14	N	44	CYS
14	N	104	ASP
14	N	119	VAL
1	O	2	THR
1	O	17	LYS
1	O	29	LYS
1	O	50	LYS
1	O	51	SER
1	O	59	GLU
1	O	61	LEU
1	O	122	THR
1	O	157	PHE
1	O	197	LYS
1	O	231	LYS
2	P	17	ARG
2	P	50	LYS
2	P	54	THR
2	P	55	LEU
2	P	58	GLN
2	P	62	THR
2	P	119	GLN
2	P	180	LYS
2	P	184	LYS
2	P	191	LEU
2	P	197	SER
2	P	209	ARG
2	P	238	LEU
3	Q	4	ARG
3	Q	32	VAL
3	Q	38	ASN
3	Q	48	SER
3	Q	49	THR
3	Q	51	LYS
3	Q	55	THR
3	Q	82	ILE
3	Q	124	VAL

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Mol	Chain	Res	Type
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	175	LYS
3	Q	180	LYS
3	Q	187	GLU
3	Q	203	THR
3	Q	227	ILE
3	Q	232	THR
3	Q	240	GLU
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	54	ASP
4	R	78	ARG
4	R	99	ILE
4	R	117	GLU
4	R	125	LEU
4	R	176	LEU
4	R	182	SER
4	R	190	LEU
4	R	193	LEU
4	R	202	GLU
4	R	214	ILE
4	R	224	ASP
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	3	ASN
5	S	4	ASN
5	S	8	ASP
5	S	9	THR
5	S	10	VAL
5	S	25	LEU
5	S	29	LYS
5	S	55	LEU
5	S	60	LYS
5	S	71	LEU
5	S	92	ASN
5	S	116	GLN
5	S	144	LEU
5	S	169	THR

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Mol	Chain	Res	Type
5	S	184	ASN
5	S	188	LEU
5	S	207	VAL
5	S	219	THR
5	S	222	THR
5	S	231	LYS
6	T	14	ASP
6	T	94	SER
6	T	96	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	165	ARG
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	214	TRP
6	T	221	ASN
6	T	231	LEU
6	T	240	GLN
6	T	244	ASN
7	U	24	LYS
7	U	26	THR
7	U	28	GLN
7	U	68	ARG
7	U	83	ASN
7	U	115	LEU
7	U	117	GLN
7	U	122	ARG
7	U	165	LYS
7	U	166	GLN
7	U	171	THR
7	U	178	LYS
7	U	181	LYS
7	U	183	ASP
7	U	208	GLU
7	U	230	GLU
7	U	235	ARG
7	U	236	LEU
8	V	13	VAL
8	V	30	ASN

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Mol	Chain	Res	Type
8	V	34	LEU
8	V	43	CYS
8	V	55	VAL
8	V	56	THR
8	V	68	LEU
8	V	113	ILE
8	V	153	LYS
8	V	191	LEU
8	V	198	GLU
9	W	31	GLN
9	W	37	ASN
9	W	126	ILE
9	W	133	LYS
9	W	151	SER
9	W	171	LEU
9	W	182	TRP
10	X	2	ASP
10	X	23	ARG
10	X	35	THR
10	X	75	LEU
10	X	78	GLN
10	X	95	ARG
10	X	110	LYS
10	X	144	LEU
10	X	163	LEU
10	X	166	GLN
10	X	172	MET
10	X	174	MET
10	X	194	ASP
11	Y	4	LEU
11	Y	7	ARG
11	Y	9	GLN
11	Y	31	VAL
11	Y	35	ILE
11	Y	41	LEU
11	Y	57	THR
11	Y	106	ARG
11	Y	118	ASP
11	Y	148	LEU
11	Y	151	GLU
12	Z	1	GLN
12	Z	3	ASN

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Mol	Chain	Res	Type
12	Z	11	THR
12	Z	23	LEU
12	Z	49	ASN
12	Z	106	TYR
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
12	Z	173	LYS
13	a	10	SER
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	106	LYS
13	a	129	TYR
13	a	157	LYS
13	a	161	ARG
13	a	187	ARG
13	a	215	GLU
13	a	226	LYS
13	a	232	LYS
14	b	9	LYS
14	b	20	THR
14	b	22	THR
14	b	36	ARG
14	b	44	CYS
14	b	104	ASP
14	b	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (139) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	94	HIS
2	B	20	GLN
2	B	58	GLN
2	B	95	GLN
2	B	102	ASN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN

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Mol	Chain	Res	Type
3	C	17	GLN
3	C	38	ASN
3	C	77	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	100	ASN
4	D	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	191	GLN
6	F	240	GLN
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN
7	G	175	ASN
8	H	30	ASN
8	H	66	HIS
8	H	144	GLN
8	H	172	ASN
8	H	189	ASN
9	I	31	GLN
9	I	37	ASN
10	J	55	GLN
10	J	118	GLN
10	J	191	GLN
11	K	85	ASN
11	K	176	ASN

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Mol	Chain	Res	Type
12	L	1	GLN
12	L	3	ASN
12	L	36	ASN
12	L	49	ASN
12	L	70	ASN
12	L	76	HIS
12	L	80	ASN
12	L	195	HIS
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	69	GLN
14	N	161	GLN
1	O	30	GLN
1	O	94	HIS
2	P	20	GLN
2	P	58	GLN
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	155	ASN
2	P	176	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	100	ASN
4	R	146	GLN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN

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Mol	Chain	Res	Type
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
6	T	240	GLN
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	167	GLN
7	U	175	ASN
8	V	30	ASN
8	V	66	HIS
8	V	144	GLN
8	V	172	ASN
8	V	189	ASN
9	W	31	GLN
9	W	37	ASN
10	X	55	GLN
10	X	86	GLN
10	X	118	GLN
10	X	191	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	1	GLN
12	Z	3	ASN
12	Z	36	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	76	HIS
12	Z	80	ASN
12	Z	108	HIS
12	Z	195	HIS
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	179	ASN
13	a	194	ASN

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Mol	Chain	Res	Type
13	a	213	GLN
14	b	69	GLN
14	b	161	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
16	MES	Y	302	-	12,12,12	2.23	1 (8%)	14,16,16	1.27	2 (14%)
17	37Y	Y	303	-	43,44,44	2.38	4 (9%)	51,58,58	1.69	9 (17%)
17	37Y	K	303	-	43,44,44	2.37	4 (9%)	51,58,58	1.69	8 (15%)
16	MES	K	302	-	12,12,12	2.24	1 (8%)	14,16,16	1.29	2 (14%)

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
16	MES	Y	302	-	-	0/6/14/14	0/1/1/1
17	37Y	Y	303	-	-	9/44/60/60	0/3/3/3
17	37Y	K	303	-	-	9/44/60/60	0/3/3/3
16	MES	K	302	-	-	0/6/14/14	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Y	303	37Y	O32-C31	14.24	1.44	1.21
17	K	303	37Y	O32-C31	14.10	1.44	1.21
16	K	302	MES	C8-S	-7.47	1.66	1.77
16	Y	302	MES	C8-S	-7.46	1.66	1.77
17	K	303	37Y	C17-C18	-3.87	1.42	1.51
17	Y	303	37Y	C17-C18	-3.83	1.42	1.51
17	Y	303	37Y	C37-C31	2.71	1.60	1.52
17	K	303	37Y	C37-C31	2.70	1.60	1.52
17	Y	303	37Y	C29-C31	2.06	1.55	1.52
17	K	303	37Y	C29-C31	2.05	1.55	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	K	303	37Y	O32-C31-C37	-6.21	109.75	121.26
17	Y	303	37Y	O32-C31-C37	-6.13	109.89	121.26
17	Y	303	37Y	C9-C10-N5	-4.91	102.67	110.10
17	K	303	37Y	C9-C10-N5	-4.85	102.74	110.10
17	K	303	37Y	C4-N5-C10	4.21	117.62	111.09
17	Y	303	37Y	C4-N5-C10	4.17	117.57	111.09
17	K	303	37Y	C30-C41-C42	-3.37	104.41	111.73
17	Y	303	37Y	C30-C41-C42	-3.32	104.53	111.73
16	Y	302	MES	O3S-S-C8	2.83	110.34	105.77
16	K	302	MES	O3S-S-C8	2.74	110.20	105.77
17	K	303	37Y	O8-C7-C6	-2.54	106.20	111.80
17	Y	303	37Y	O8-C7-C6	-2.53	106.22	111.80
17	K	303	37Y	C4-N5-C6	2.36	114.76	111.09
16	K	302	MES	O2S-S-C8	2.35	109.74	106.92
17	Y	303	37Y	C4-N5-C6	2.29	114.65	111.09
17	K	303	37Y	C43-C42-C41	-2.22	107.96	112.15
17	Y	303	37Y	C43-C42-C41	-2.17	108.06	112.15
17	Y	303	37Y	C18-C17-C16	-2.06	107.69	113.39
16	Y	302	MES	O2S-S-C8	2.06	109.39	106.92
17	K	303	37Y	C18-C17-C16	-2.03	107.80	113.39
17	Y	303	37Y	C4-C2-N1	-2.02	110.76	115.31

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	K	303	37Y	O32-C31-C37-C38
17	K	303	37Y	C31-C37-C39-O40
17	K	303	37Y	C38-C37-C39-O40
17	Y	303	37Y	O32-C31-C37-C38
17	Y	303	37Y	C31-C37-C39-O40
17	Y	303	37Y	C38-C37-C39-O40
17	Y	303	37Y	C20-C21-O22-C23
17	K	303	37Y	C20-C21-O22-C23
17	Y	303	37Y	C24-C21-O22-C23
17	K	303	37Y	C24-C21-O22-C23
17	K	303	37Y	C29-C31-C37-C38
17	Y	303	37Y	C29-C31-C37-C38
17	K	303	37Y	N15-C16-C26-O27
17	Y	303	37Y	N15-C16-C26-O27
17	K	303	37Y	C30-C29-C31-O32
17	Y	303	37Y	C30-C29-C31-O32
17	K	303	37Y	N28-C29-C31-C37
17	Y	303	37Y	N28-C29-C31-C37

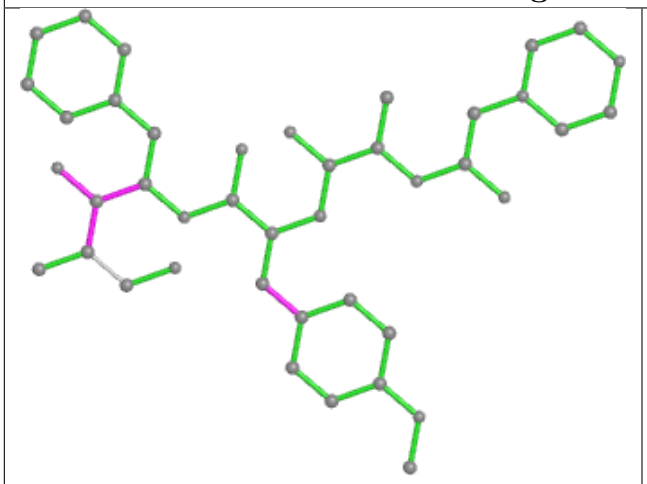
There are no ring outliers.

2 monomers are involved in 2 short contacts:

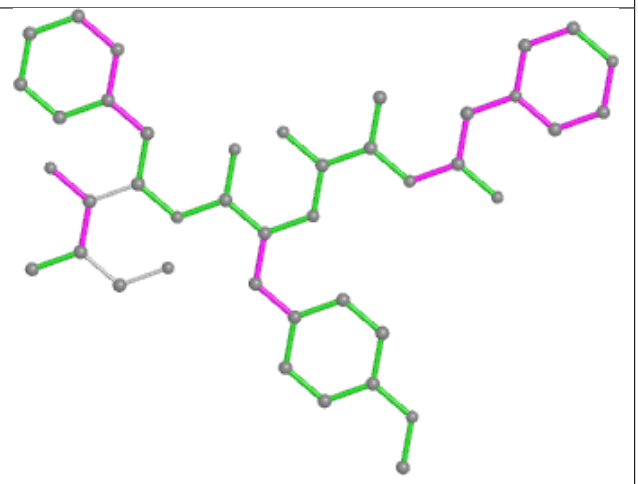
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	Y	303	37Y	1	0
17	K	303	37Y	1	0

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.

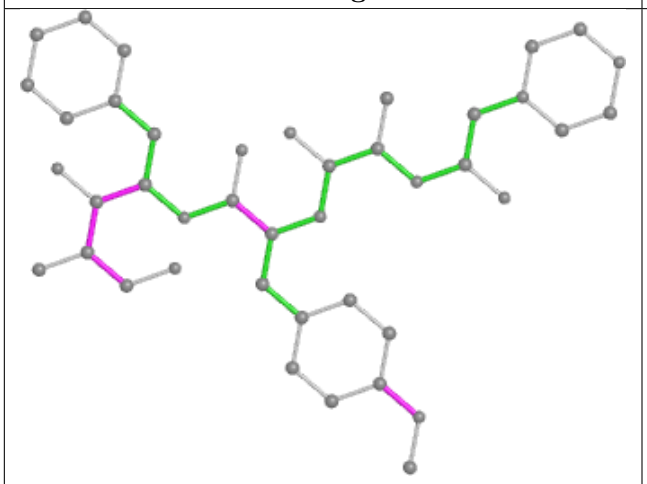
Ligand 37Y Y 303



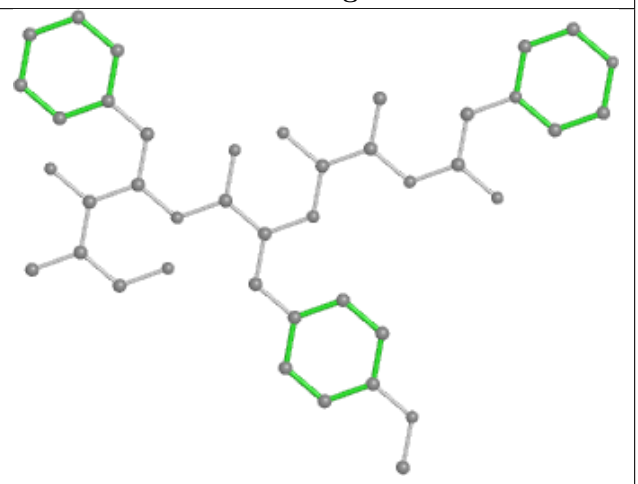
Bond lengths



Bond angles

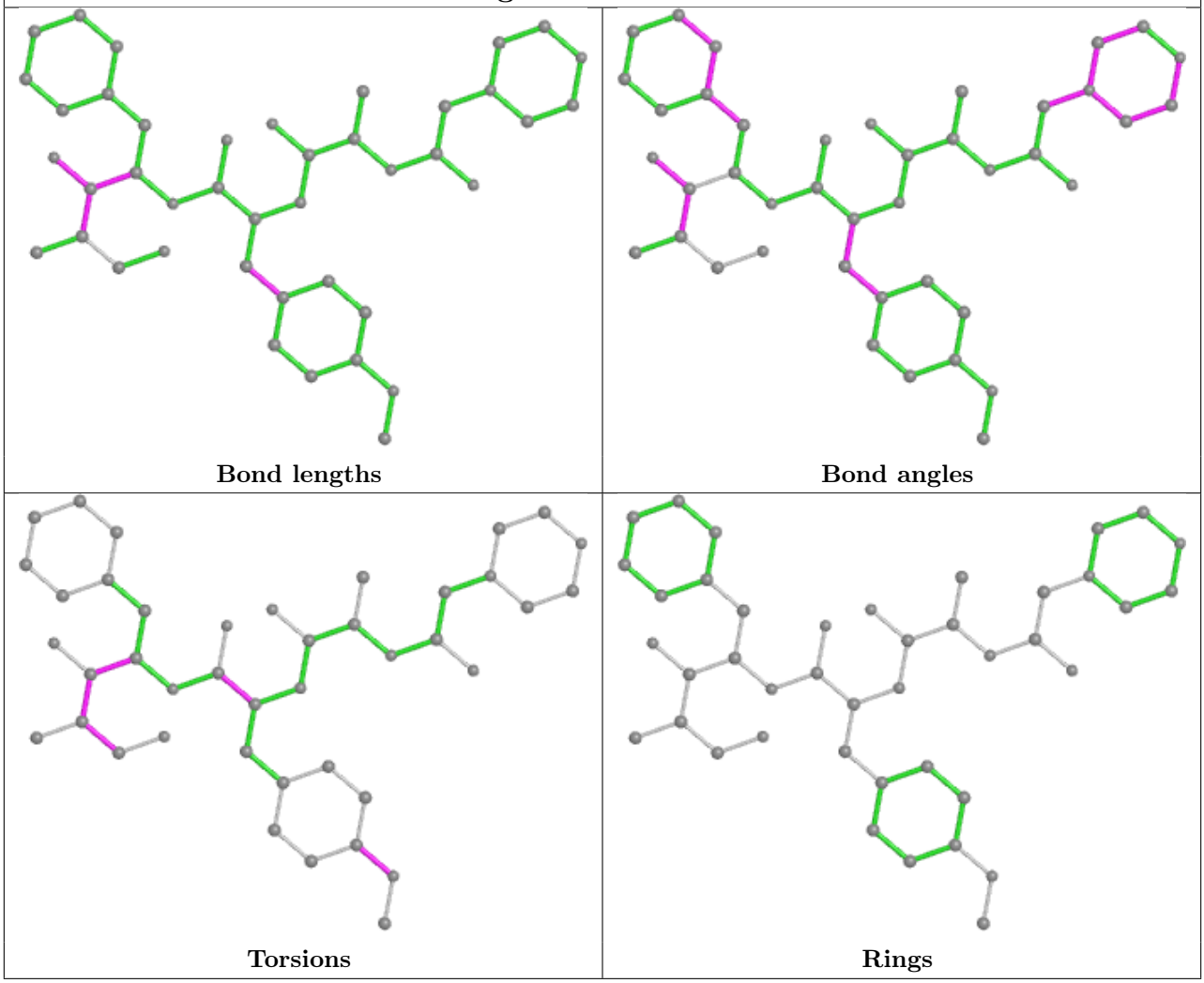


Torsions



Rings

Ligand 37Y K 303



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	250/250 (100%)	-0.58	3 (1%)	79	73	38, 53, 86, 127	0
1	O	250/250 (100%)	-0.56	2 (0%)	86	81	39, 60, 96, 121	0
2	B	244/258 (94%)	-0.44	8 (3%)	46	36	36, 58, 107, 153	0
2	P	244/258 (94%)	-0.37	10 (4%)	37	27	40, 60, 119, 157	0
3	C	240/254 (94%)	-0.36	9 (3%)	40	30	41, 63, 118, 141	0
3	Q	240/254 (94%)	-0.19	13 (5%)	25	17	45, 70, 138, 153	0
4	D	235/260 (90%)	-0.51	2 (0%)	84	80	41, 63, 95, 126	0
4	R	235/260 (90%)	-0.49	3 (1%)	77	72	39, 66, 99, 139	0
5	E	231/234 (98%)	-0.44	2 (0%)	84	80	45, 68, 97, 135	0
5	S	231/234 (98%)	-0.36	2 (0%)	84	80	39, 70, 107, 141	0
6	F	243/288 (84%)	-0.56	3 (1%)	79	73	39, 58, 102, 141	0
6	T	243/288 (84%)	-0.51	1 (0%)	92	91	41, 63, 107, 136	0
7	G	241/252 (95%)	-0.60	1 (0%)	92	91	32, 54, 89, 128	0
7	U	241/252 (95%)	-0.61	0	100	100	37, 55, 85, 122	0
8	H	222/232 (95%)	-0.62	3 (1%)	75	70	33, 53, 77, 126	0
8	V	222/232 (95%)	-0.54	3 (1%)	75	70	42, 56, 83, 138	0
9	I	204/205 (99%)	-0.81	1 (0%)	91	88	35, 50, 77, 107	0
9	W	204/205 (99%)	-0.77	1 (0%)	91	88	35, 52, 80, 118	0
10	J	195/198 (98%)	-0.68	2 (1%)	82	77	35, 51, 82, 136	0
10	X	195/198 (98%)	-0.68	2 (1%)	82	77	38, 53, 78, 145	0
11	K	212/212 (100%)	-0.73	0	100	100	36, 51, 77, 98	0
11	Y	212/212 (100%)	-0.72	1 (0%)	91	88	36, 53, 76, 109	0
12	L	222/222 (100%)	-0.72	0	100	100	36, 54, 79, 95	0
12	Z	222/222 (100%)	-0.72	0	100	100	35, 52, 76, 101	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	M	233/246 (94%)	-0.68	1 (0%) 92 91	37, 53, 79, 106	0
13	a	233/246 (94%)	-0.72	1 (0%) 92 91	36, 50, 72, 108	0
14	N	196/196 (100%)	-0.72	0 100 100	38, 49, 78, 113	0
14	b	196/196 (100%)	-0.73	0 100 100	35, 51, 78, 106	0
All	All	6336/6614 (95%)	-0.58	74 (1%) 79 73	32, 56, 97, 157	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	206	LYS	7.5
3	Q	49	THR	6.9
2	P	219	ALA	6.4
8	V	222	ASP	5.9
2	B	220	ASN	5.2
3	Q	206	LYS	4.9
2	B	219	ALA	4.7
10	X	194	ASP	4.6
5	S	202	ASP	4.6
3	C	49	THR	4.5
5	E	202	ASP	4.3
2	P	218	GLY	4.2
3	C	238	LYS	4.2
3	Q	50	LEU	4.0
2	B	221	ASP	3.8
8	H	222	ASP	3.8
2	P	220	ASN	3.7
1	A	1	MET	3.6
2	P	221	ASP	3.6
8	V	221	CYS	3.5
9	W	1	SER	3.5
8	H	221	CYS	3.4
2	B	218	GLY	3.4
2	B	222	GLY	3.2
2	P	51	VAL	3.1
3	Q	236	GLN	3.1
4	D	242	GLU	3.1
2	P	222	GLY	3.1
2	B	51	VAL	3.0
3	C	202	GLN	3.0
3	Q	48	SER	2.9
10	J	1	MET	2.9

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Mol	Chain	Res	Type	RSRZ
4	R	242	GLU	2.8
6	F	181	GLU	2.8
3	Q	239	GLN	2.8
3	Q	238	LYS	2.7
3	Q	203	THR	2.7
6	T	205	GLU	2.7
2	P	59	ASP	2.7
1	O	249	ALA	2.6
3	Q	180	LYS	2.5
10	J	194	ASP	2.5
3	C	175	LYS	2.5
4	R	125	LEU	2.5
2	B	50	LYS	2.5
4	R	241	ALA	2.5
3	Q	240	GLU	2.5
5	E	123	GLY	2.5
7	G	241	GLU	2.5
13	a	1	THR	2.5
1	O	1	MET	2.4
2	P	60	THR	2.4
11	Y	212	GLY	2.4
3	C	216	ASP	2.4
3	C	240	GLU	2.3
6	F	202	ASP	2.3
8	V	22	GLN	2.3
3	C	239	GLN	2.3
2	P	50	LYS	2.3
9	I	1	SER	2.2
3	Q	55	THR	2.2
3	Q	141	ASP	2.1
1	A	248	GLU	2.1
8	H	198	GLU	2.1
10	X	1	MET	2.1
2	B	242	GLY	2.1
2	P	225	TYR	2.1
13	M	47	ASP	2.1
3	Q	202	GLN	2.1
1	A	2	THR	2.1
3	C	236	GLN	2.1
5	S	165	GLN	2.1
4	D	201	GLU	2.0
6	F	205	GLU	2.0

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)

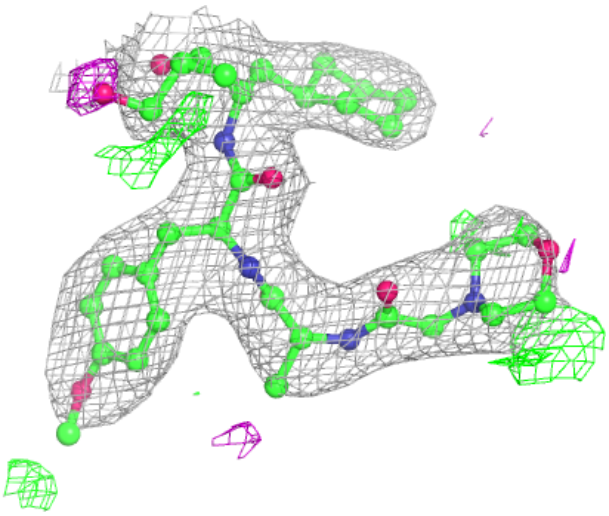
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

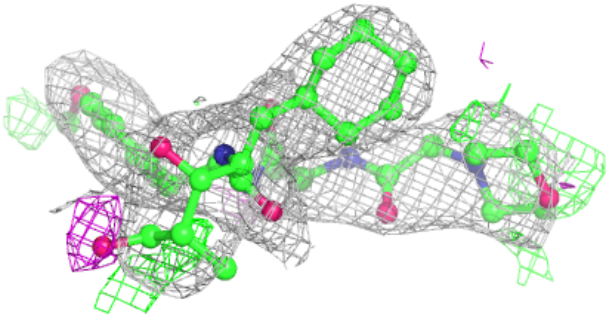
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
15	MG	N	202	1/1	0.90	0.32	78,78,78,78	0
15	MG	G	301	1/1	0.91	0.18	59,59,59,59	0
17	37Y	Y	303	42/42	0.91	0.19	38,50,82,96	0
17	37Y	K	303	42/42	0.92	0.19	37,48,84,96	0
15	MG	Z	301	1/1	0.93	0.34	62,62,62,62	0
15	MG	N	201	1/1	0.94	0.13	53,53,53,53	0
16	MES	Y	302	12/12	0.95	0.19	59,66,72,73	0
16	MES	K	302	12/12	0.96	0.17	59,63,66,66	0
15	MG	Y	301	1/1	0.98	0.10	53,53,53,53	0
15	MG	I	301	1/1	0.98	0.15	56,56,56,56	0
15	MG	V	301	1/1	0.98	0.08	64,64,64,64	0
15	MG	K	301	1/1	0.99	0.05	55,55,55,55	0

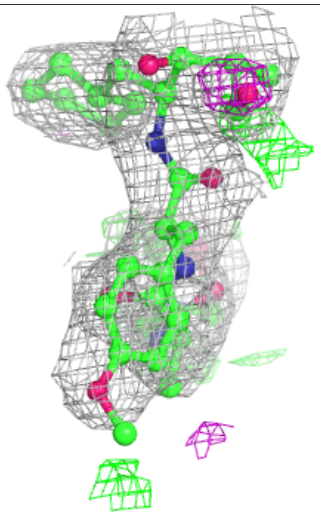
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 37Y Y 303:

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

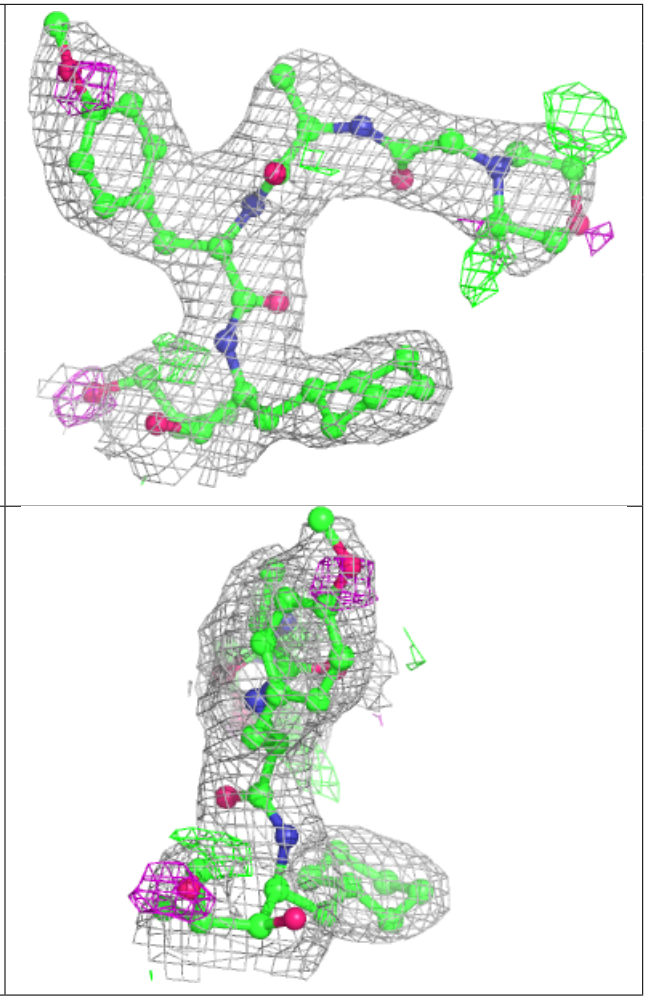






Electron density around 37Y K 303:

$2mF_o$-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.