wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 10:43 AM GMT

PDB ID	:	3MG4
Title	:	Structure of yeast 20S proteasome with Compound 1
Authors	:	Sintchak, M.D.
Deposited on	:	2010-04-05
Resolution	:	3.11 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

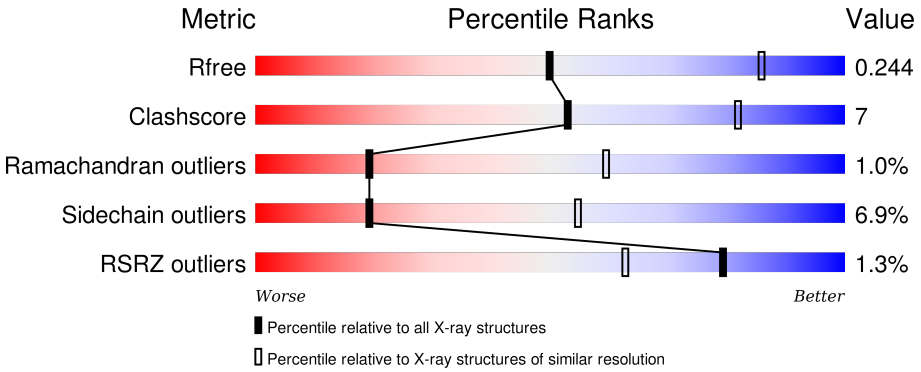
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 3.11 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}	91344	1112 (3.16-3.08)
Clashscore	102246	1218 (3.16-3.08)
Ramachandran outliers	100387	1175 (3.16-3.08)
Sidechain outliers	100360	1175 (3.16-3.08)
RSRZ outliers	91569	1114 (3.16-3.08)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	84% 15%
1	O	250	84% 15%
2	B	244	73% 24%
2	P	244	76% 20%
3	C	241	80% 17%

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Mol	Chain	Length	Quality of chain
3	Q	241	6% 74% 22%
4	D	242	4% 83% 15%
4	R	242	3% 82% 17%
5	E	233	3% 80% 19%
5	S	233	3% 76% 21%
6	F	244	% 77% 20%
6	T	244	% 81% 16%
7	G	243	77% 21%
7	U	243	75% 21%
8	H	222	86% 13%
8	V	222	80% 18%
9	I	204	86% 13%
9	W	204	83% 15%
10	J	198	% 81% 19%
10	X	198	2% 84% 14%
11	K	212	78% 19%
11	Y	212	79% 18%
12	L	222	77% 21%
12	Z	222	77% 18% 5%
13	1	233	80% 17%
13	M	233	83% 16%
14	2	196	% 80% 19%
14	N	196	80% 20%

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
15	MG	G	241	-	-	-	X
15	MG	L	195	-	-	-	X
16	LXT	K	213	-	-	-	X
16	LXT	Y	212	-	-	-	X
17	MES	Y	213	-	-	-	X

2 Entry composition (i)

There are 17 unique types of molecules in this entry. The entry contains 49672 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Proteasome component Y7.

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

- Molecule 2 is a protein called Proteasome component Y13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1905	1201	321	380	3			
2	P	244	Total	C	N	O	S	0	0	0
			1905	1201	321	380	3			

- Molecule 3 is a protein called Proteasome component PRE6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1891	1181	331	375	4			
3	Q	241	Total	C	N	O	S	0	0	0
			1891	1181	331	375	4			

- Molecule 4 is a protein called Proteasome component PUP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	242	Total	C	N	O	S	0	0	0
			1862	1162	314	379	7			
4	R	242	Total	C	N	O	S	0	0	0
			1862	1162	314	379	7			

- Molecule 5 is a protein called Proteasome component PRE5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			
5	S	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			

- Molecule 6 is a protein called Proteasome component C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	244	Total	C	N	O	S	0	0	0
			1897	1205	330	358	4			
6	T	244	Total	C	N	O	S	0	0	0
			1897	1205	330	358	4			

- Molecule 7 is a protein called Proteasome component C7-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			
7	U	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			

- Molecule 8 is a protein called Proteasome component PUP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1685	1061	293	324	7			
8	V	222	Total	C	N	O	S	0	0	0
			1685	1061	293	324	7			

- Molecule 9 is a protein called Proteasome component PUP3.

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

- Molecule 10 is a protein called Proteasome component C11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

- Molecule 11 is a protein called Proteasome component PRE2.

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

- Molecule 12 is a protein called Proteasome component C5.

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

- Molecule 13 is a protein called Proteasome component PRE4.

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

- Molecule 14 is a protein called Proteasome component PRE3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	2	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	2	Total	Mg	0	0
			2	2		
15	D	1	Total	Mg	0	0
			1	1		

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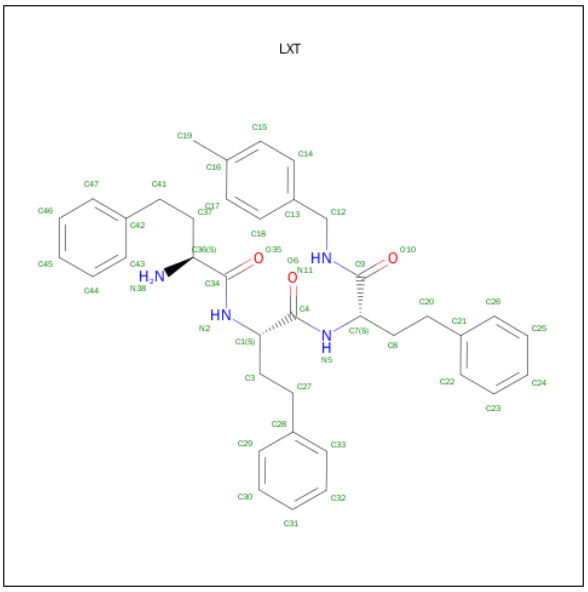
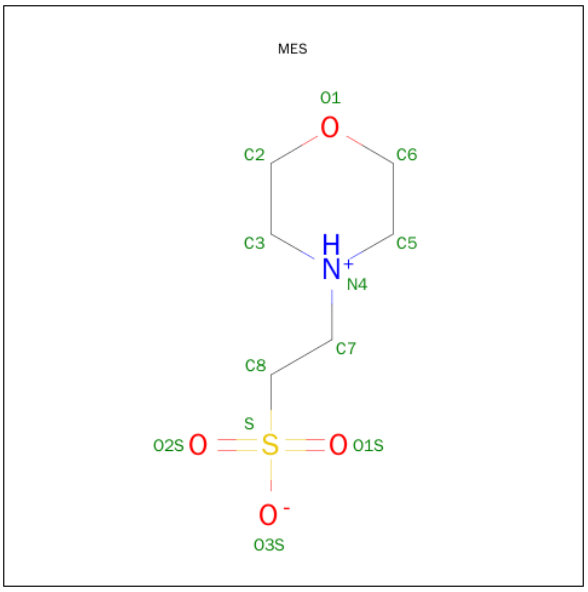
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	K	1	Total Mg 1 1	0	0
15	H	1	Total Mg 1 1	0	0
15	I	2	Total Mg 2 2	0	0
15	N	1	Total Mg 1 1	0	0
15	L	1	Total Mg 1 1	0	0
15	F	1	Total Mg 1 1	0	0

- Molecule 16 is (2S)-2-AMINO-N-[(1S)-1-({(1S)-1-[(4-METHYLBENZYL)CARBAMOYL]-3-PHENYLPROPYL}CARBAMOYL)-3-PHENYLPROPYL]-4-PHENYLBUTANAMIDE (three-letter code: LXT) (formula: $C_{38}H_{44}N_4O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	K	1	Total C N O 45 38 4 3	0	0
16	Y	1	Total C N O 45 38 4 3	0	0

- Molecule 17 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



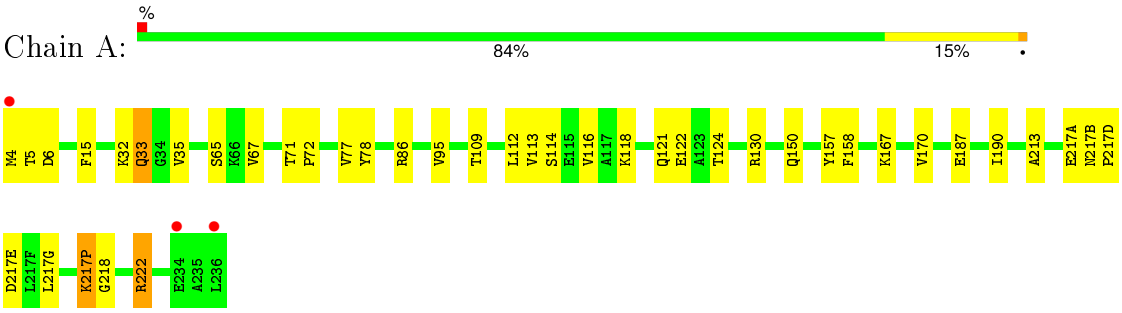
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
17	Y	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

3 Residue-property plots (i)

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

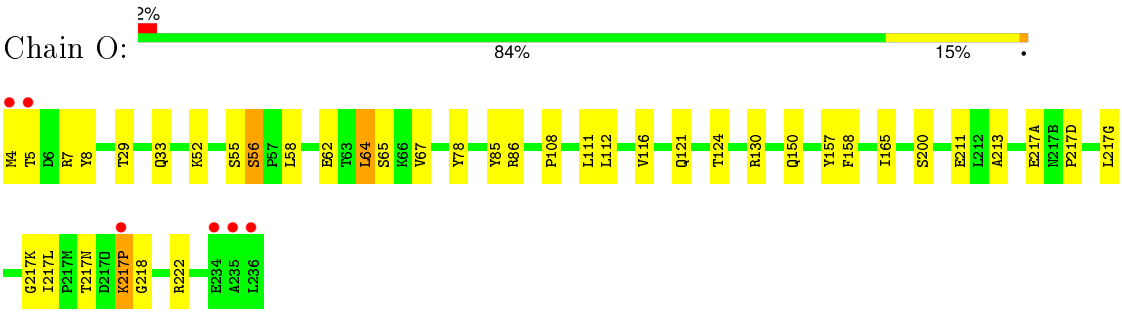
- Molecule 1: Proteasome component Y7

Chain A:



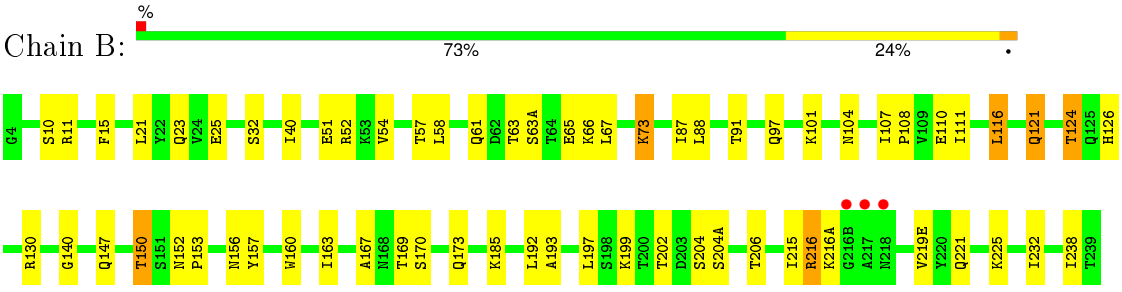
- Molecule 1: Proteasome component Y7

Chain O:



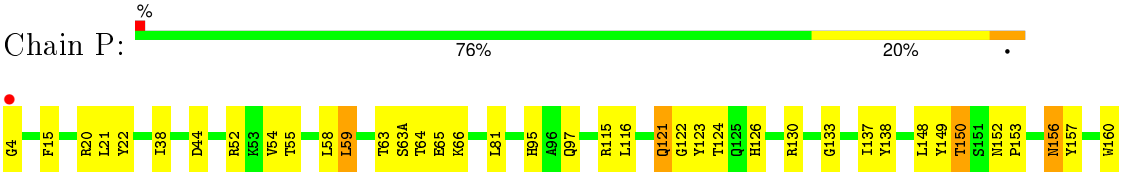
- Molecule 2: Proteasome component Y13

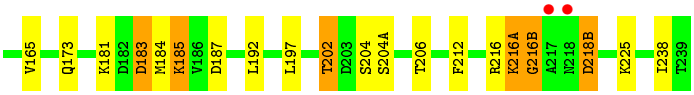
Chain B:



- Molecule 2: Proteasome component Y13

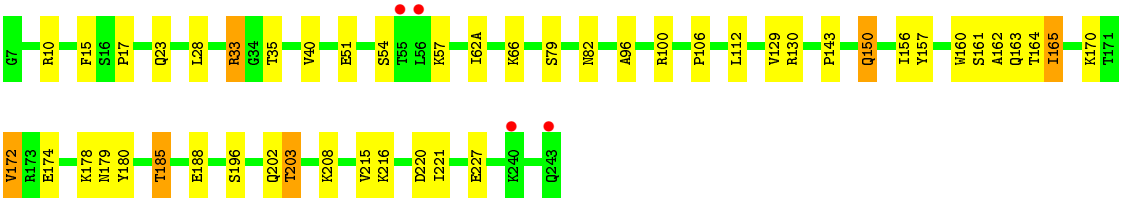
Chain P:





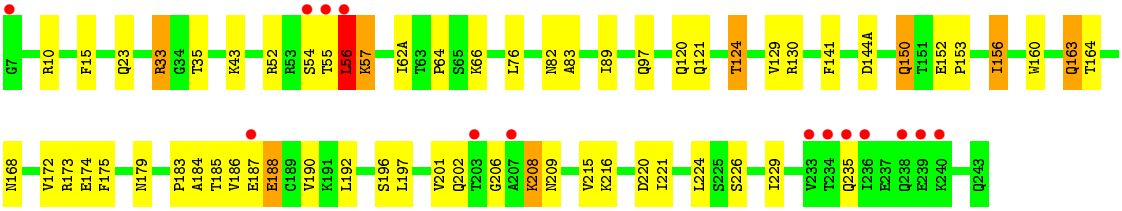
- Molecule 3: Proteasome component PRE6

Chain C:



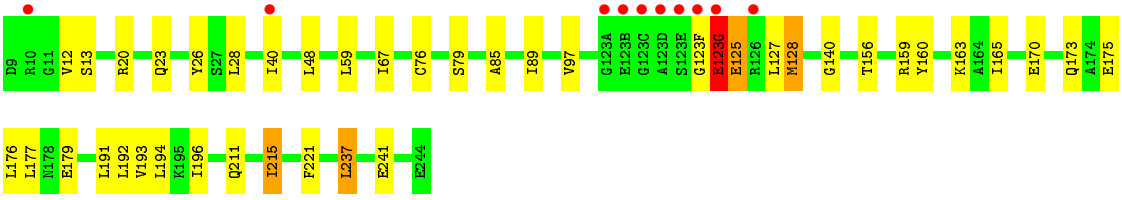
- Molecule 3: Proteasome component PRE6

Chain Q:



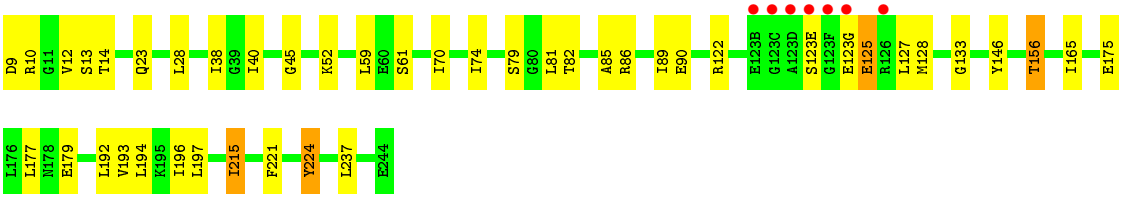
- Molecule 4: Proteasome component PUP2

Chain D:



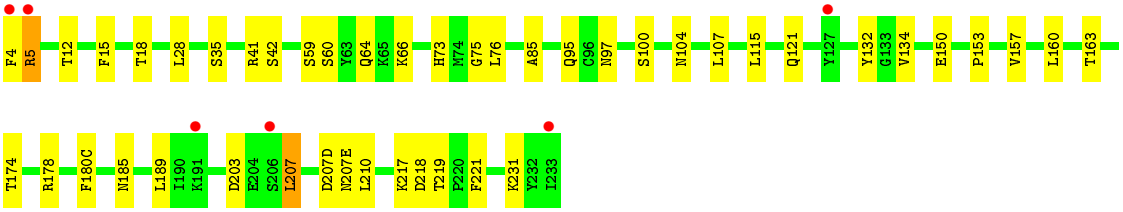
- Molecule 4: Proteasome component PUP2

Chain R:

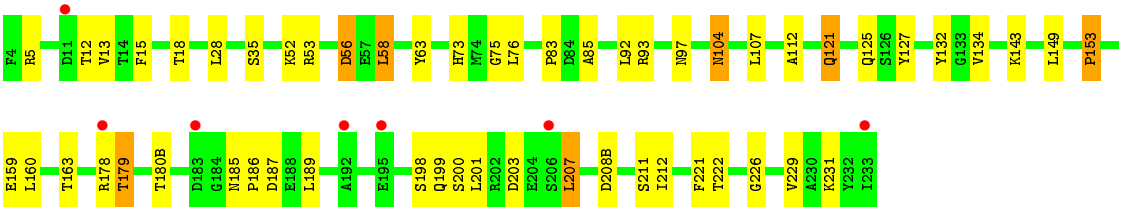


- Molecule 5: Proteasome component PRE5

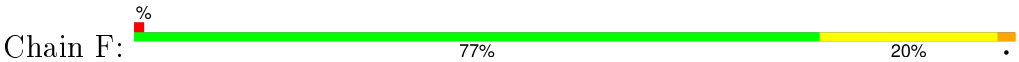
Chain E:

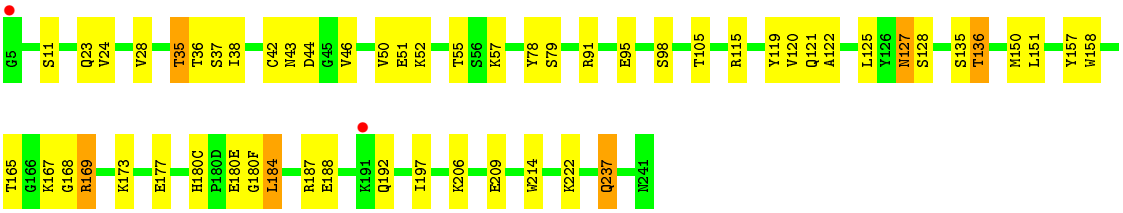


• Molecule 5: Proteasome component PRE5

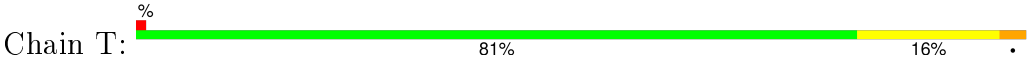


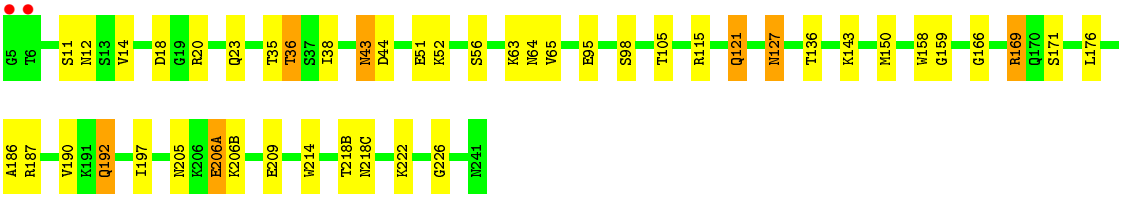
• Molecule 6: Proteasome component C1



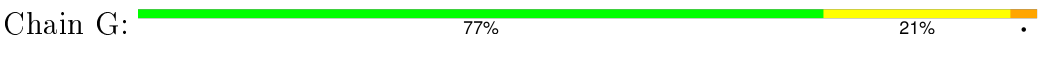


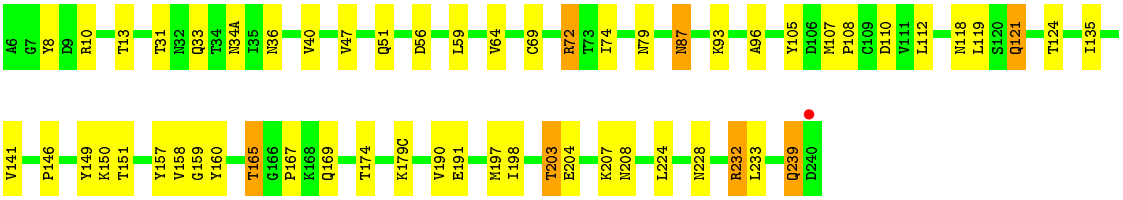
• Molecule 6: Proteasome component C1





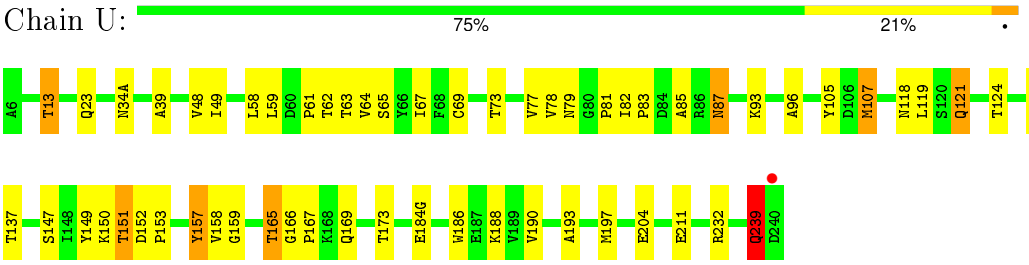
• Molecule 7: Proteasome component C7-alpha





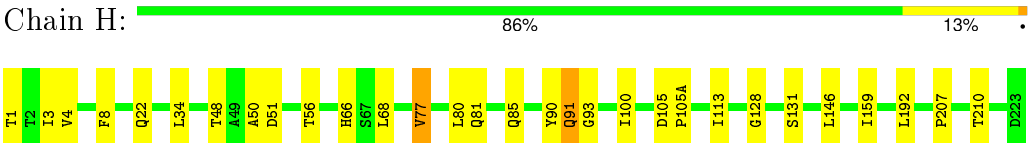
• Molecule 7: Proteasome component C7-alpha

Chain U:



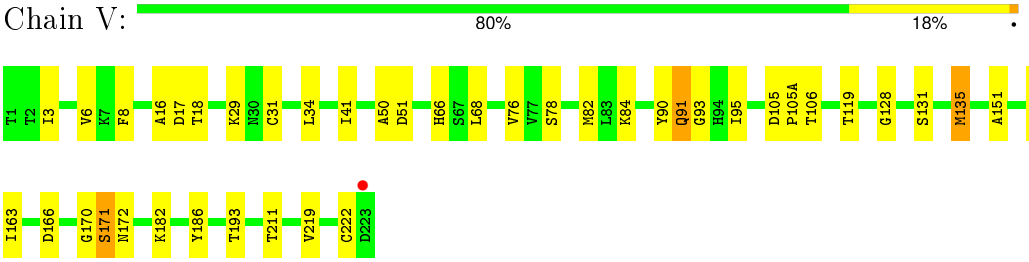
• Molecule 8: Proteasome component PUP1

Chain H:



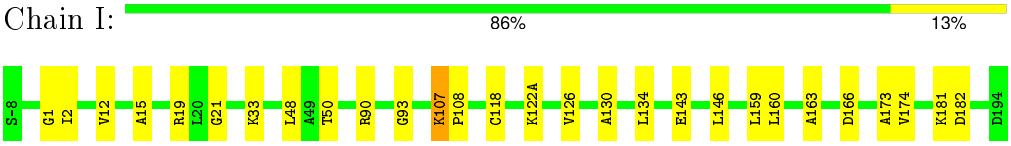
• Molecule 8: Proteasome component PUP1

Chain V:



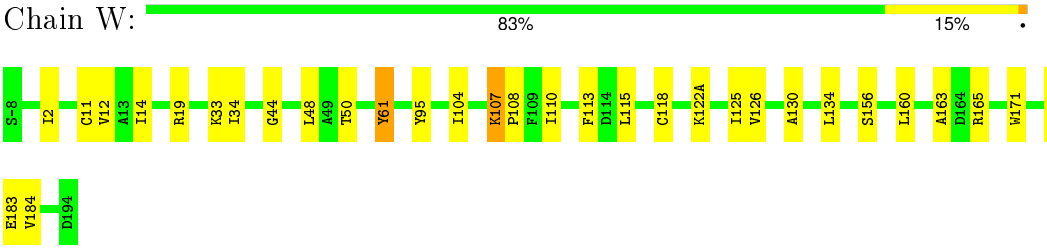
• Molecule 9: Proteasome component PUP3

Chain I:



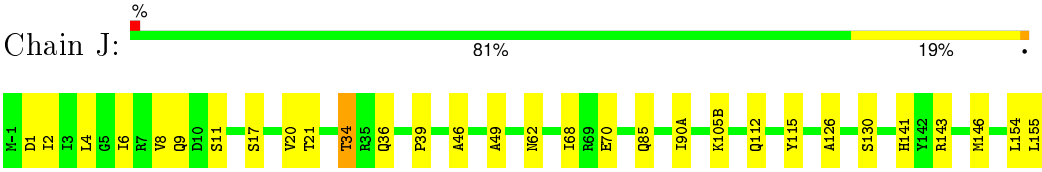
• Molecule 9: Proteasome component PUP3

Chain W:



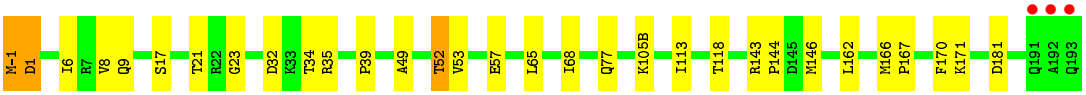
• Molecule 10: Proteasome component C11

Chain J:



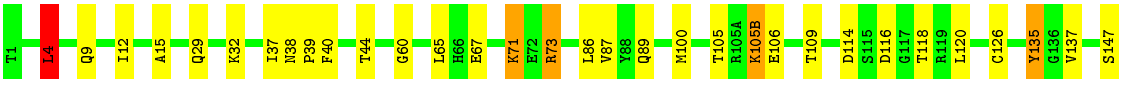
• Molecule 10: Proteasome component C11

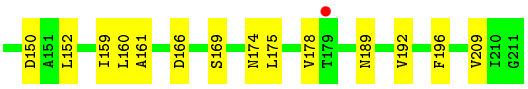
Chain X:



• Molecule 11: Proteasome component PRE2

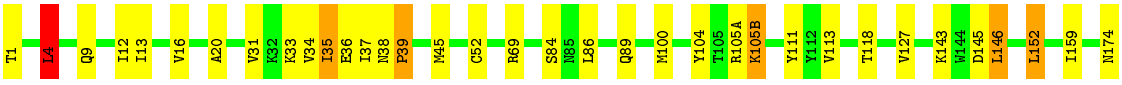
Chain K:

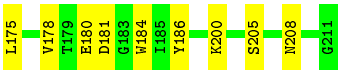




• Molecule 11: Proteasome component PRE2

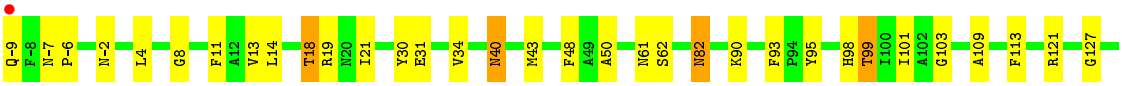
Chain Y:





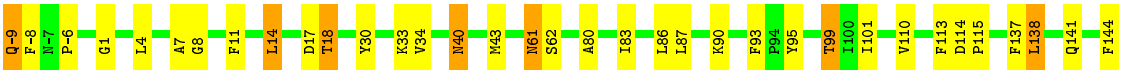
• Molecule 12: Proteasome component C5

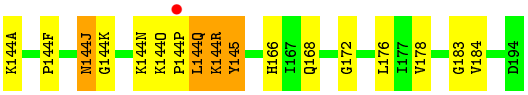
Chain L:



• Molecule 12: Proteasome component C5

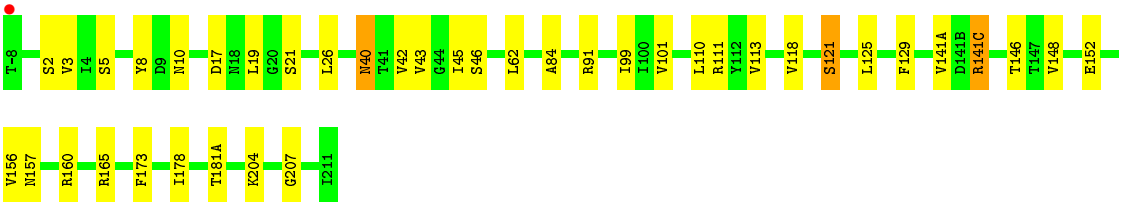
Chain Z:





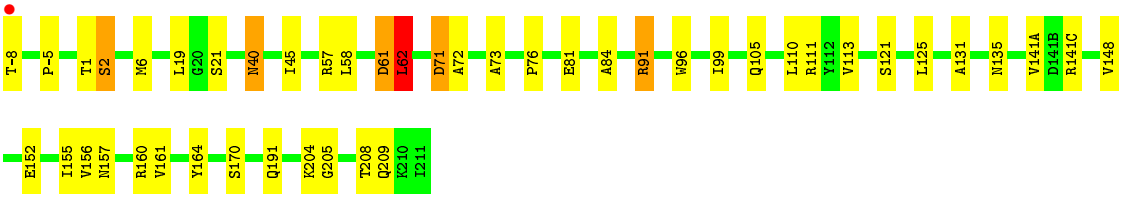
- Molecule 13: Proteasome component PRE4

Chain M:



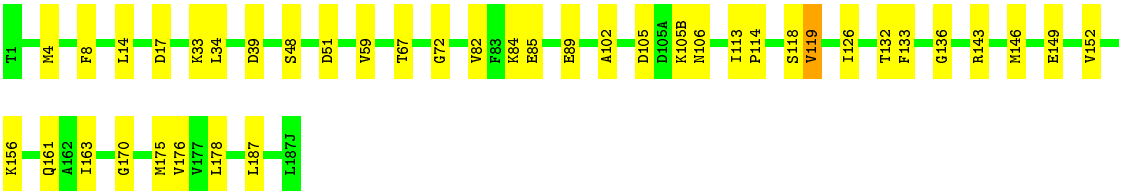
- Molecule 13: Proteasome component PRE4

Chain 1:



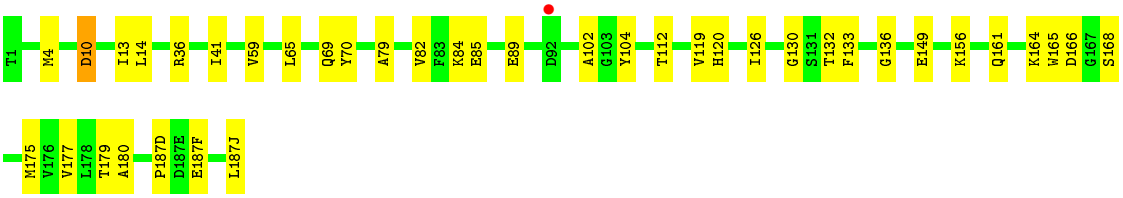
- Molecule 14: Proteasome component PRE3

Chain N:



- Molecule 14: Proteasome component PRE3

Chain 2:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	134.56Å 300.79Å 144.71Å 90.00° 112.73° 90.00°	Depositor
Resolution (Å)	50.00 – 3.11 47.61 – 3.11	Depositor EDS
% Data completeness (in resolution range)	93.9 (50.00-3.11) 93.9 (47.61-3.11)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.74 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.203 , 0.250 0.200 , 0.244	Depositor DCC
R_{free} test set	3565 reflections (2.05%)	DCC
Wilson B-factor (Å^2)	67.9	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 19.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 177367 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	49672	wwPDB-VP
Average B, all atoms (Å^2)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, LXT, 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	0.41	0/1952	0.57	0/2642
1	O	0.44	0/1952	0.59	0/2642
2	B	0.42	0/1935	0.58	0/2618
2	P	0.43	0/1935	0.61	0/2618
3	C	0.45	2/1920 (0.1%)	0.59	0/2598
3	Q	0.45	0/1920	0.60	1/2598 (0.0%)
4	D	0.46	1/1887 (0.1%)	0.60	0/2541
4	R	0.44	0/1887	0.59	0/2541
5	E	0.40	0/1823	0.57	0/2463
5	S	0.42	0/1823	0.57	0/2463
6	F	0.41	0/1937	0.55	0/2614
6	T	0.44	0/1937	0.58	0/2614
7	G	0.43	0/1959	0.57	0/2652
7	U	0.45	0/1959	0.60	0/2652
8	H	0.43	0/1716	0.58	0/2326
8	V	0.42	0/1716	0.59	0/2326
9	I	0.42	0/1611	0.59	0/2174
9	W	0.44	0/1611	0.60	0/2174
10	J	0.42	0/1613	0.58	0/2173
10	X	0.42	0/1613	0.58	0/2173
11	K	0.43	0/1681	0.58	1/2274 (0.0%)
11	Y	0.43	0/1681	0.60	1/2274 (0.0%)
12	L	0.44	0/1795	0.57	0/2420
12	Z	0.47	0/1795	0.60	0/2420
13	1	0.44	0/1855	0.62	1/2514 (0.0%)
13	M	0.44	0/1855	0.61	0/2514
14	2	0.43	0/1541	0.59	0/2087
14	N	0.41	0/1541	0.55	0/2087
All	All	0.43	3/50450 (0.0%)	0.59	4/68192 (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
1	O	0	1
4	D	0	1
12	Z	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	123(G)	GLU	C-O	7.39	1.37	1.23
3	C	57	LYS	CE-NZ	6.06	1.64	1.49
3	C	203	THR	C-O	5.08	1.32	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	Y	4	LEU	CA-CB-CG	5.38	127.68	115.30
11	K	4	LEU	CA-CB-CG	5.25	127.38	115.30
3	Q	56	LEU	CA-CB-CG	5.08	126.98	115.30
13	1	62	LEU	CA-CB-CG	5.07	126.97	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	123(G)	GLU	Mainchain
1	O	217(N)	THR	Peptide
12	Z	145	TYR	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	1926	24	0
1	O	1915	0	1926	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1905	0	1901	32	0
2	P	1905	0	1901	36	0
3	C	1891	0	1900	30	0
3	Q	1891	0	1900	40	0
4	D	1862	0	1836	23	0
4	R	1862	0	1836	21	0
5	E	1795	0	1797	20	0
5	S	1795	0	1797	28	0
6	F	1897	0	1886	28	0
6	T	1897	0	1886	33	0
7	G	1921	0	1909	31	0
7	U	1921	0	1910	44	0
8	H	1685	0	1688	16	0
8	V	1685	0	1688	24	0
9	I	1581	0	1574	16	0
9	W	1581	0	1574	21	0
10	J	1585	0	1590	16	0
10	X	1585	0	1590	15	0
11	K	1644	0	1595	26	0
11	Y	1644	0	1595	29	0
12	L	1757	0	1711	31	0
12	Z	1757	0	1711	44	0
13	1	1824	0	1832	20	0
13	M	1824	0	1832	23	0
14	2	1512	0	1481	21	0
14	N	1512	0	1481	24	0
15	D	1	0	0	0	0
15	F	1	0	0	0	0
15	G	2	0	0	0	0
15	H	1	0	0	0	0
15	I	2	0	0	0	0
15	K	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
16	K	45	0	44	0	0
16	Y	45	0	44	4	0
17	K	12	0	13	0	0
17	Y	12	0	13	1	0
All	All	49672	0	49367	657	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 7.

The worst 5 of 657 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)
12:Z:144(O):LYS:HB3	12:Z:144(R):LYS:HZ3	1.01	1.13
5:E:97:ASN:HD21	12:L:61:ASN:HD21	1.06	0.96
12:Z:144(O):LYS:HB3	12:Z:144(R):LYS:NZ	1.81	0.95
3:C:163:GLN:HE21	3:C:164:THR:H	0.97	0.94
8:H:128:GLY:O	8:H:131:SER:HB2	1.69	0.93

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	233 (94%)	12 (5%)	3 (1%)	16	53
1	O	248/250 (99%)	230 (93%)	15 (6%)	3 (1%)	16	53
2	B	242/244 (99%)	218 (90%)	22 (9%)	2 (1%)	24	64
2	P	242/244 (99%)	217 (90%)	19 (8%)	6 (2%)	7	33
3	C	239/241 (99%)	232 (97%)	5 (2%)	2 (1%)	24	64
3	Q	239/241 (99%)	223 (93%)	11 (5%)	5 (2%)	9	38
4	D	240/242 (99%)	224 (93%)	13 (5%)	3 (1%)	15	51
4	R	240/242 (99%)	220 (92%)	19 (8%)	1 (0%)	39	77
5	E	231/233 (99%)	218 (94%)	10 (4%)	3 (1%)	15	51
5	S	231/233 (99%)	213 (92%)	13 (6%)	5 (2%)	8	37
6	F	242/244 (99%)	229 (95%)	12 (5%)	1 (0%)	39	77
6	T	242/244 (99%)	226 (93%)	14 (6%)	2 (1%)	24	64
7	G	241/243 (99%)	229 (95%)	11 (5%)	1 (0%)	39	77
7	U	241/243 (99%)	227 (94%)	13 (5%)	1 (0%)	39	77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
8	H	220/222 (99%)	206 (94%)	13 (6%)	1 (0%)	34 73
8	V	220/222 (99%)	207 (94%)	11 (5%)	2 (1%)	21 62
9	I	202/204 (99%)	195 (96%)	6 (3%)	1 (0%)	34 73
9	W	202/204 (99%)	191 (95%)	10 (5%)	1 (0%)	34 73
10	J	196/198 (99%)	183 (93%)	10 (5%)	3 (2%)	13 47
10	X	196/198 (99%)	181 (92%)	10 (5%)	5 (3%)	7 32
11	K	210/212 (99%)	199 (95%)	9 (4%)	2 (1%)	19 59
11	Y	210/212 (99%)	199 (95%)	8 (4%)	3 (1%)	14 49
12	L	220/222 (99%)	205 (93%)	14 (6%)	1 (0%)	34 73
12	Z	220/222 (99%)	204 (93%)	14 (6%)	2 (1%)	21 62
13	1	231/233 (99%)	215 (93%)	15 (6%)	1 (0%)	39 77
13	M	231/233 (99%)	218 (94%)	12 (5%)	1 (0%)	39 77
14	2	194/196 (99%)	185 (95%)	8 (4%)	1 (0%)	34 73
14	N	194/196 (99%)	189 (97%)	5 (3%)	0	100 100
All	All	6312/6368 (99%)	5916 (94%)	334 (5%)	62 (1%)	19 59

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	LYS
4	D	123(G)	GLU
5	E	5	ARG
5	E	203	ASP
5	E	217	LYS

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%)	28 65
1	O	209/209 (100%)	199 (95%)	10 (5%)	31 69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	203/203 (100%)	179 (88%)	24 (12%)	6 26
2	P	203/203 (100%)	186 (92%)	17 (8%)	14 46
3	C	213/213 (100%)	200 (94%)	13 (6%)	23 60
3	Q	213/213 (100%)	193 (91%)	20 (9%)	11 39
4	D	198/198 (100%)	185 (93%)	13 (7%)	21 57
4	R	198/198 (100%)	179 (90%)	19 (10%)	10 37
5	E	192/192 (100%)	176 (92%)	16 (8%)	14 47
5	S	192/192 (100%)	171 (89%)	21 (11%)	8 31
6	F	201/201 (100%)	180 (90%)	21 (10%)	9 32
6	T	201/201 (100%)	183 (91%)	18 (9%)	12 41
7	G	207/207 (100%)	188 (91%)	19 (9%)	11 40
7	U	207/207 (100%)	193 (93%)	14 (7%)	20 55
8	H	181/181 (100%)	175 (97%)	6 (3%)	45 79
8	V	181/181 (100%)	170 (94%)	11 (6%)	23 60
9	I	172/172 (100%)	166 (96%)	6 (4%)	43 79
9	W	172/172 (100%)	164 (95%)	8 (5%)	32 70
10	J	175/175 (100%)	163 (93%)	12 (7%)	19 55
10	X	175/175 (100%)	166 (95%)	9 (5%)	29 66
11	K	169/169 (100%)	158 (94%)	11 (6%)	21 57
11	Y	169/169 (100%)	159 (94%)	10 (6%)	24 60
12	L	185/185 (100%)	175 (95%)	10 (5%)	27 64
12	Z	185/185 (100%)	173 (94%)	12 (6%)	21 57
13	1	199/199 (100%)	184 (92%)	15 (8%)	17 51
13	M	199/199 (100%)	187 (94%)	12 (6%)	24 60
14	2	162/162 (100%)	154 (95%)	8 (5%)	31 69
14	N	162/162 (100%)	158 (98%)	4 (2%)	55 84
All	All	5332/5332 (100%)	4962 (93%)	370 (7%)	19 55

5 of 370 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	121	SER
3	Q	35	THR

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Mol	Chain	Res	Type
12	Z	99	THR
13	M	181(A)	THR
1	O	222	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 146 such sidechains are listed below:

Mol	Chain	Res	Type
13	M	89	GLN
3	Q	150	GLN
13	1	18	ASN
13	M	149	GLN
2	P	125	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 10 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	LXT	K	213	-	48,48,48	0.72	0	61,62,62	0.82	2 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
17	MES	K	214	-	11,12,12	0.67	0	14,16,16	1.14	1 (7%)
16	LXT	Y	212	-	48,48,48	0.71	0	61,62,62	0.86	2 (3%)
17	MES	Y	213	-	11,12,12	0.71	0	14,16,16	1.61	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	LXT	K	213	-	-	0/40/40/40	0/4/4/4
17	MES	K	214	-	-	0/6/14/14	0/1/1/1
16	LXT	Y	212	-	-	0/40/40/40	0/4/4/4
17	MES	Y	213	-	-	0/6/14/14	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	Y	212	LXT	C13-C12-N11	-3.11	105.79	112.88
16	K	213	LXT	C13-C12-N11	-2.73	106.64	112.88
17	Y	213	MES	O3S-S-O1S	-2.00	106.94	111.61
16	K	213	LXT	C1-N2-C34	2.04	126.20	121.62
17	K	214	MES	O2S-S-C8	2.17	108.75	106.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	Y	212	LXT	4	0
17	Y	213	MES	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

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%)	-0.29	3 (1%) 81 65	42, 61, 89, 102	0
1	O	250/250 (100%)	-0.24	6 (2%) 62 40	43, 62, 89, 102	0
2	B	244/244 (100%)	-0.15	3 (1%) 81 65	47, 67, 100, 107	0
2	P	244/244 (100%)	-0.16	3 (1%) 81 65	47, 67, 100, 108	0
3	C	241/241 (100%)	-0.02	4 (1%) 73 53	49, 69, 118, 142	0
3	Q	241/241 (100%)	0.12	14 (5%) 26 11	49, 70, 118, 142	0
4	D	242/242 (100%)	-0.05	10 (4%) 41 19	50, 69, 104, 113	0
4	R	242/242 (100%)	-0.08	7 (2%) 55 32	50, 69, 103, 113	0
5	E	233/233 (100%)	-0.04	6 (2%) 59 37	53, 74, 104, 111	0
5	S	233/233 (100%)	0.06	7 (3%) 54 30	53, 75, 104, 111	0
6	F	244/244 (100%)	-0.16	2 (0%) 87 75	46, 66, 97, 109	0
6	T	244/244 (100%)	-0.10	2 (0%) 87 75	46, 66, 97, 109	0
7	G	243/243 (100%)	-0.22	1 (0%) 93 86	44, 61, 84, 105	0
7	U	243/243 (100%)	-0.27	1 (0%) 93 86	45, 61, 83, 105	0
8	H	222/222 (100%)	-0.37	0 100 100	44, 57, 76, 107	0
8	V	222/222 (100%)	-0.41	1 (0%) 91 84	45, 57, 76, 107	0
9	I	204/204 (100%)	-0.41	0 100 100	44, 57, 69, 77	0
9	W	204/204 (100%)	-0.36	0 100 100	43, 56, 69, 77	0
10	J	198/198 (100%)	-0.31	2 (1%) 84 70	43, 59, 72, 115	0
10	X	198/198 (100%)	-0.19	3 (1%) 76 58	43, 59, 73, 115	0
11	K	212/212 (100%)	-0.26	1 (0%) 91 84	45, 60, 78, 89	0
11	Y	212/212 (100%)	-0.35	0 100 100	44, 60, 79, 89	0
12	L	222/222 (100%)	-0.35	1 (0%) 91 84	40, 57, 84, 90	0
12	Z	222/222 (100%)	-0.25	1 (0%) 91 84	41, 57, 84, 90	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1	233/233 (100%)	-0.30	1 (0%) 93 86	42, 55, 72, 83	0
13	M	233/233 (100%)	-0.41	1 (0%) 93 86	42, 55, 73, 83	0
14	2	196/196 (100%)	-0.37	1 (0%) 91 84	45, 53, 72, 79	0
14	N	196/196 (100%)	-0.37	0 100 100	45, 53, 72, 79	0
All	All	6368/6368 (100%)	-0.22	81 (1%) 79 63	40, 61, 97, 142	0

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	123(A)	GLY	7.5
4	D	123(C)	GLY	7.1
13	1	-8	THR	7.0
4	R	123(E)	SER	6.5
4	R	123(F)	GLY	6.4

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
15	MG	G	241	1/1	0.73	0.82	11.63	85,85,85,85	0
16	LXT	Y	212	45/45	0.85	0.31	3.97	78,84,89,90	0
15	MG	L	195	1/1	0.96	0.28	3.51	58,58,58,58	0
16	LXT	K	213	45/45	0.87	0.31	3.44	66,77,88,88	0
17	MES	Y	213	12/12	0.93	0.23	3.05	90,91,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
15	MG	N	188	1/1	0.92	0.23	1.95	49,49,49,49	0
15	MG	I	196	1/1	0.90	0.18	-0.06	57,57,57,57	0
17	MES	K	214	12/12	0.96	0.17	-0.07	84,86,87,87	0
15	MG	K	212	1/1	0.93	0.17	-0.51	56,56,56,56	0
15	MG	D	2	1/1	0.92	0.08	-2.08	55,55,55,55	0
15	MG	H	224	1/1	0.92	0.12	-2.23	56,56,56,56	0
15	MG	G	1	1/1	0.98	0.06	-3.75	54,54,54,54	0
15	MG	I	195	1/1	0.94	0.33	-	53,53,53,53	0
15	MG	F	242	1/1	0.71	0.41	-	60,60,60,60	0

6.5 Other polymers (i)

There are no such residues in this entry.