



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 01:21 AM GMT

PDB ID : 3SDK
Title : Structure of yeast 20S open-gate proteasome with Compound 34
Authors : Sintchak, M.D.
Deposited on : 2011-06-09
Resolution : 2.70 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

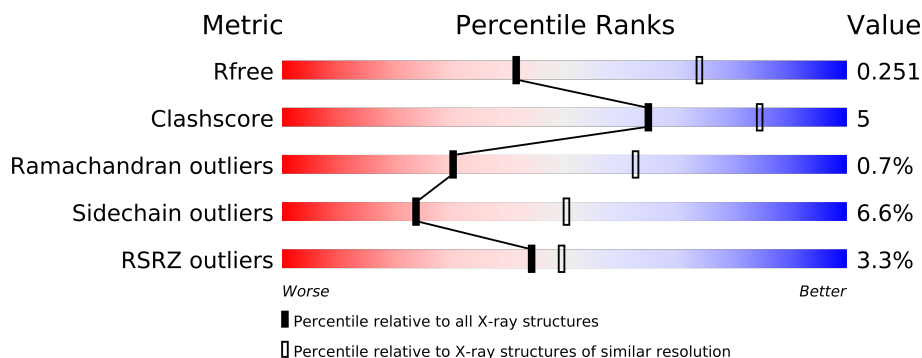
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 Å.

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













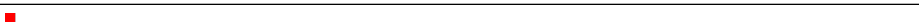

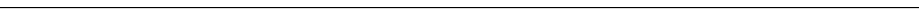

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	250	
1	O	250	
2	B	235	
2	P	235	
3	C	241	
3	Q	241	
4	D	260	
4	R	260	
5	E	233	
5	S	233	
6	F	242	
6	T	242	
7	G	243	
7	U	243	

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Mol	Chain	Length	Quality of chain
8	H	222	
8	V	222	
9	I	204	
9	W	204	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	1	233	
13	M	233	
14	2	196	
14	N	196	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 49255 atoms, of which 0 are hydrogen and 0 are deuterium.

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	235	Total	C	N	O	S	0	0	0
			1829	1158	303	365	3			
2	P	235	Total	C	N	O	S	0	0	0
			1829	1158	303	365	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	233	Total	C	N	O	S	0	0	0
			1794	1123	302	362	7			
4	R	232	Total	C	N	O	S	0	0	0
			1786	1120	298	361	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	236	Total	C	N	O	S	0	0	0
			1840	1171	321	344	4			
6	T	236	Total	C	N	O	S	0	0	0
			1840	1171	321	344	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
			1582	1003	269	305	5			

- 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).

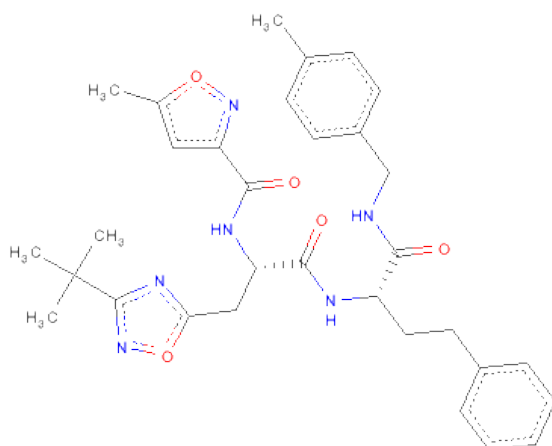
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	K	1	Total	Mg	0	0
			1	1		

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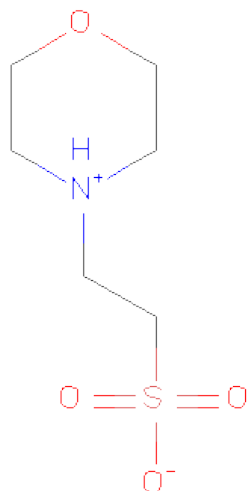
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	H	1	Total	Mg	0	0
			1	1		
15	I	2	Total	Mg	0	0
			2	2		
15	N	1	Total	Mg	0	0
			1	1		
15	L	2	Total	Mg	0	0
			2	2		
15	F	2	Total	Mg	0	0
			2	2		

- Molecule 16 is N-[(2S)-3-(3-TERT-BUTYL-1,2,4-OXADIAZOL-5-YL)-1-({(2S)-1-[(4-METHYLBENZYL)AMINO]-1-OXO-4-PHENYLBUTAN-2-YL}AMINO)-1-OXOPROPAN-2-YL]-5-METHYL-1,2-OXAZOLE-3-CARBOXAMIDE (three-letter code: P3N) (formula: $C_{32}H_{38}N_6O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	K	1	Total	C	N	O	0	0
			43	32	6	5		
16	Y	1	Total	C	N	O	0	0
			43	32	6	5		

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

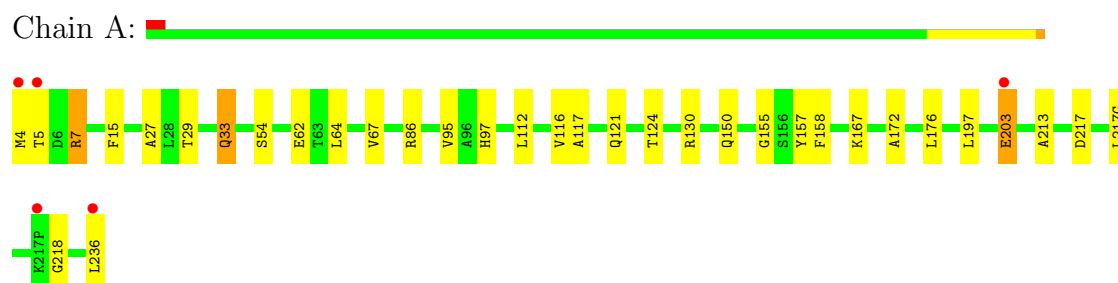


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
17	Y	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

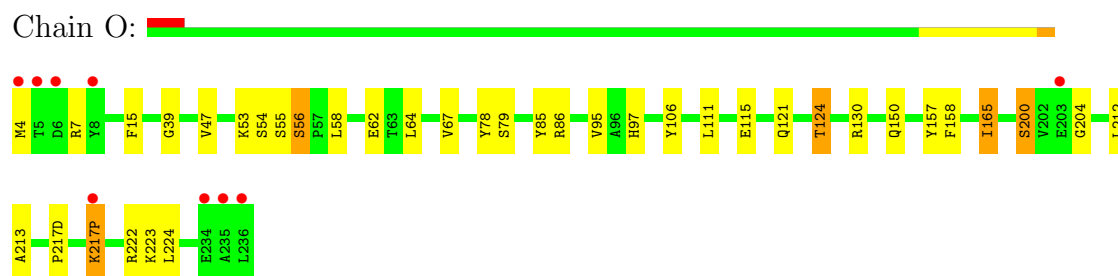
3 Residue-property plots

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.

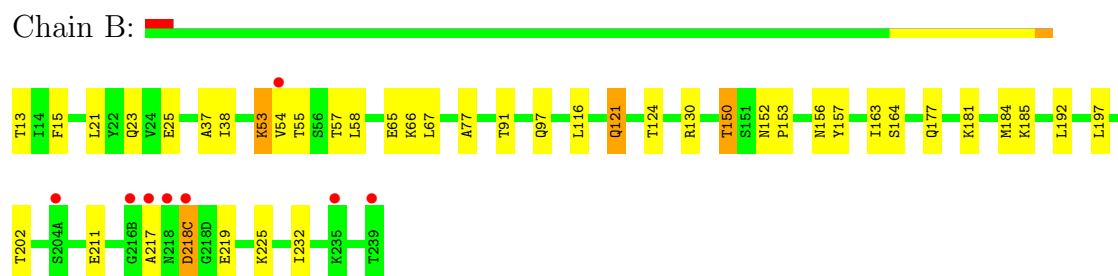
• Molecule 1: Proteasome component Y7



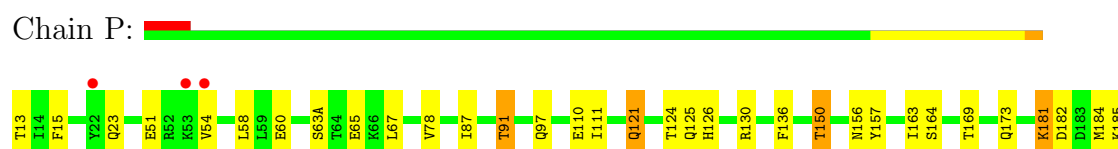
• Molecule 1: Proteasome component Y7

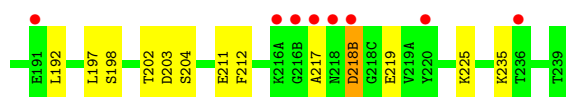


• Molecule 2: Proteasome component Y13



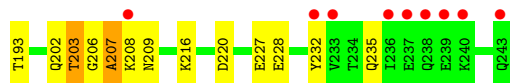
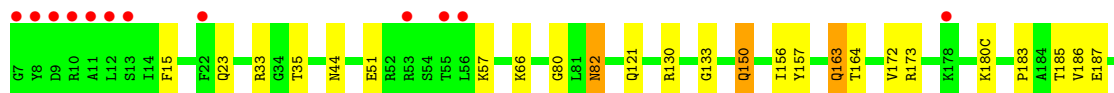
• Molecule 2: Proteasome component Y13





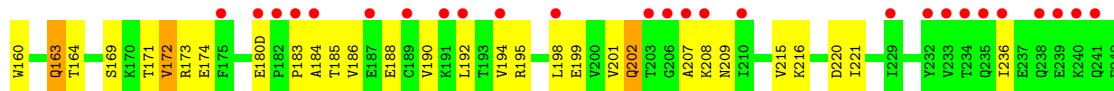
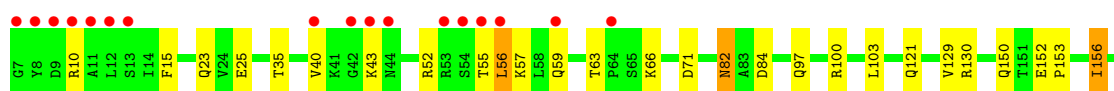
• Molecule 3: Proteasome component PRE6

Chain C:



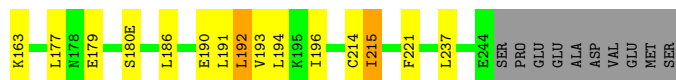
• Molecule 3: Proteasome component PRE6

Chain Q:



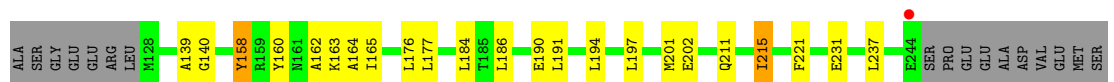
• Molecule 4: Proteasome component PUP2

Chain D:



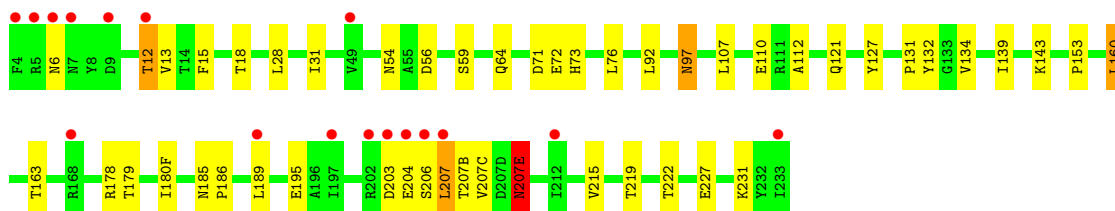
• Molecule 4: Proteasome component PUP2

Chain R:



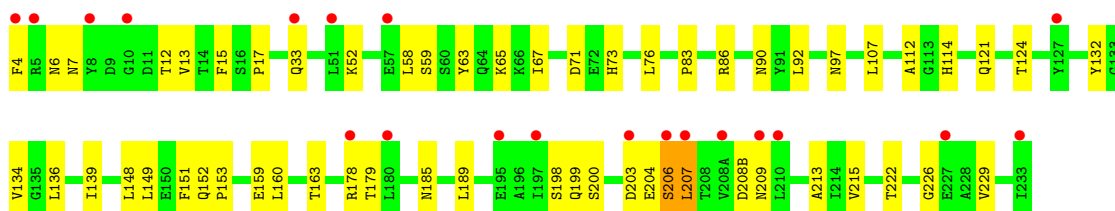
• Molecule 5: Proteasome component PRE5

Chain E:



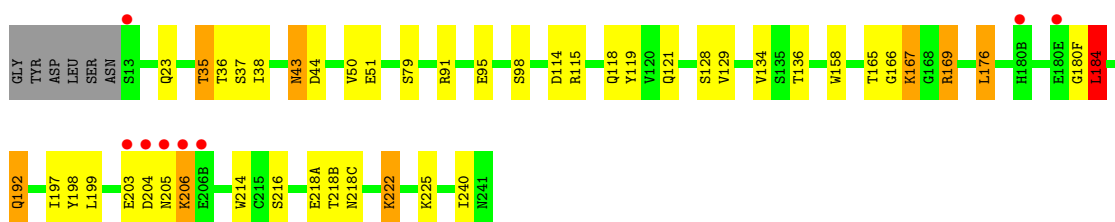
• Molecule 5: Proteasome component PRE5

Chain S:



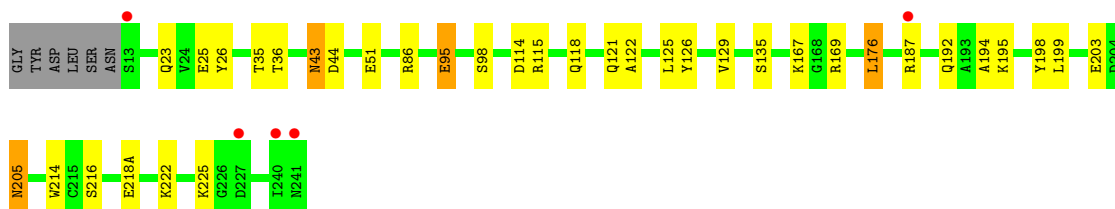
• Molecule 6: Proteasome component C1

Chain F:



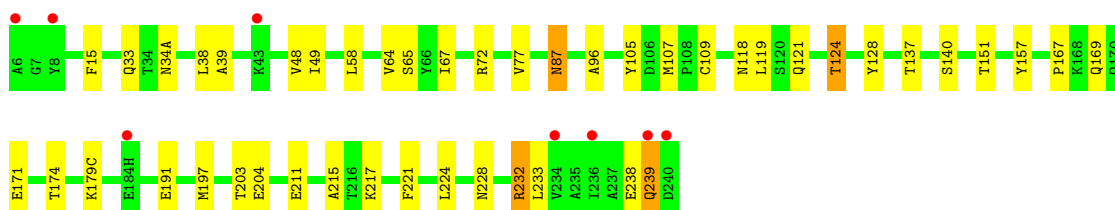
• Molecule 6: Proteasome component C1

Chain T:



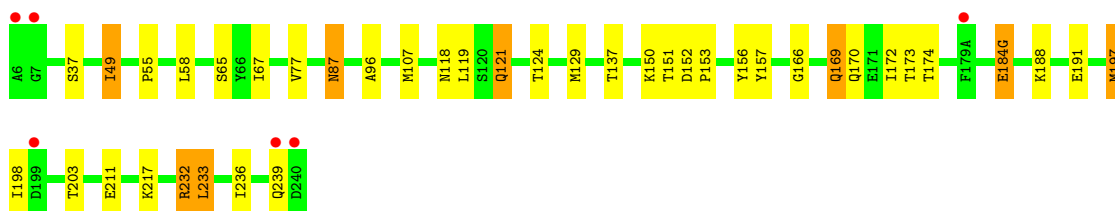
• Molecule 7: Proteasome component C7-alpha

Chain G:



• Molecule 7: Proteasome component C7-alpha

Chain U:



- Molecule 8: Proteasome component PUP1

Chain H:



- Molecule 8: Proteasome component PUP1

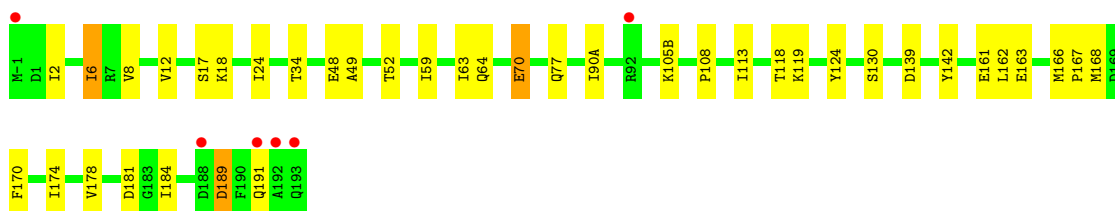
Chain V:



- Molecule 9: Proteasome component PUP3

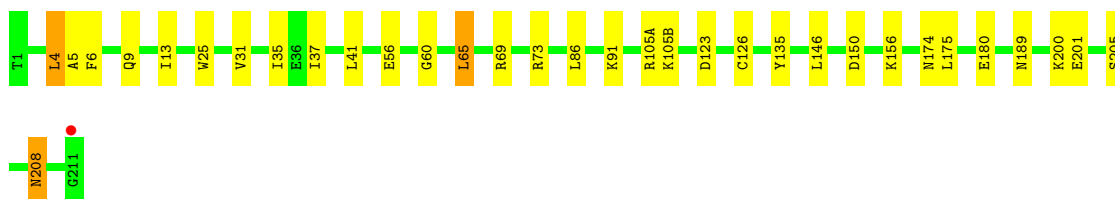
Chain I:





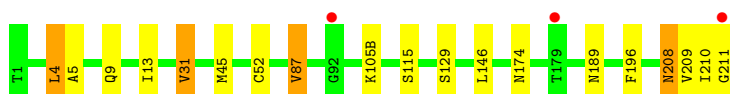
- Molecule 11: Proteasome component PRE2

Chain K:



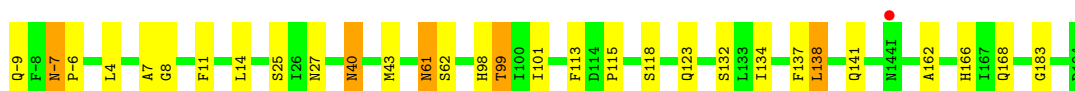
- Molecule 11: Proteasome component PRE2

Chain Y:



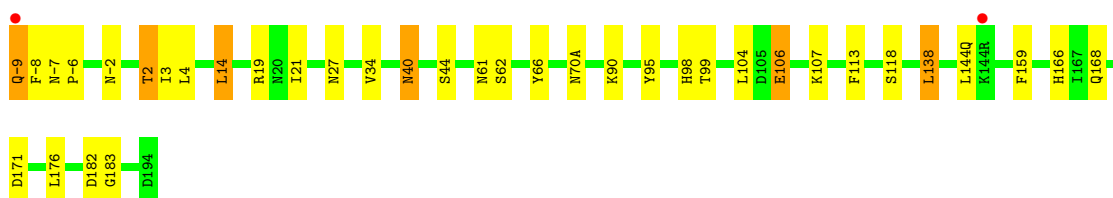
- Molecule 12: Proteasome component C5

Chain L:



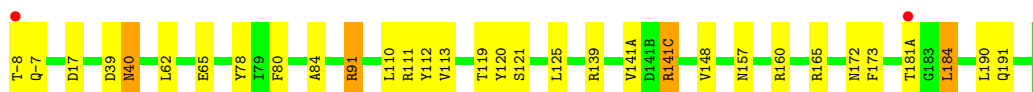
- Molecule 12: Proteasome component C5

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.12Å 299.40Å 146.24Å 90.00° 112.92° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 49.21 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.0 (50.00-2.70) 95.0 (49.21-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.43 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.223 , 0.259 0.218 , 0.251	Depositor DCC
R_{free} test set	5652 reflections (2.06%)	DCC
Wilson B-factor (Å ²)	54.4	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 21.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 279713 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	49255	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, P3N, 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	0.44	0/1952	0.58	0/2642
1	O	0.51	1/1952 (0.1%)	0.58	0/2642
2	B	0.44	0/1858	0.59	0/2516
2	P	0.45	0/1858	0.57	0/2516
3	C	0.45	0/1920	0.59	0/2598
3	Q	0.46	1/1920 (0.1%)	0.59	2/2598 (0.1%)
4	D	0.46	0/1817	0.62	1/2449 (0.0%)
4	R	0.45	0/1810	0.59	0/2440
5	E	0.51	1/1823 (0.1%)	0.60	0/2463
5	S	0.47	0/1823	0.57	0/2463
6	F	0.44	0/1879	0.57	1/2535 (0.0%)
6	T	0.46	0/1879	0.58	0/2535
7	G	0.49	0/1959	0.58	0/2652
7	U	0.46	0/1959	0.58	0/2652
8	H	0.44	0/1716	0.57	0/2326
8	V	0.50	0/1716	0.57	0/2326
9	I	0.55	0/1611	0.60	0/2174
9	W	0.57	1/1611 (0.1%)	0.60	0/2174
10	J	0.50	0/1613	0.61	0/2173
10	X	0.46	0/1610	0.60	0/2170
11	K	0.47	0/1681	0.64	1/2274 (0.0%)
11	Y	0.45	0/1681	0.61	1/2274 (0.0%)
12	L	0.49	0/1795	0.59	0/2420
12	Z	0.50	0/1795	0.59	0/2420
13	1	0.50	0/1855	0.63	0/2514
13	M	0.49	0/1855	0.64	0/2514
14	2	0.57	0/1541	0.59	0/2087
14	N	0.59	1/1541 (0.1%)	0.60	0/2087
All	All	0.48	5/50030 (0.0%)	0.59	6/67634 (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
5	E	0	2
5	S	0	1
14	N	0	1
All	All	0	5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	207(E)	ASN	C-O	8.61	1.39	1.23
1	O	200	SER	C-O	8.24	1.39	1.23
3	Q	180(D)	GLU	C-O	6.81	1.36	1.23
14	N	181	ALA	C-O	5.73	1.34	1.23
9	W	38	TYR	CD1-CE1	-5.10	1.31	1.39

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	4	LEU	CA-CB-CG	5.58	128.15	115.30
6	F	184	LEU	CA-CB-CG	5.22	127.31	115.30
11	Y	4	LEU	CA-CB-CG	5.22	127.31	115.30
3	Q	56	LEU	CA-CB-CG	5.16	127.17	115.30
3	Q	103	LEU	CA-CB-CG	5.12	127.09	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	204	GLU	Peptide
5	E	207(E)	ASN	Mainchain
14	N	181	ALA	Mainchain
1	O	200	SER	Mainchain
5	S	204	GLU	Peptide

5.2 Close contacts ⓘ

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 hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1926	28	0
1	O	1915	0	1926	22	0
2	B	1829	0	1829	25	0
2	P	1829	0	1829	27	0
3	C	1891	0	1900	26	0
3	Q	1891	0	1900	38	0
4	D	1794	0	1778	21	0
4	R	1786	0	1763	19	0
5	E	1795	0	1797	20	0
5	S	1795	0	1797	27	0
6	F	1840	0	1838	30	0
6	T	1840	0	1838	22	0
7	G	1921	0	1910	28	0
7	U	1921	0	1910	33	0
8	H	1685	0	1688	16	0
8	V	1685	0	1688	20	0
9	I	1581	0	1574	15	0
9	W	1581	0	1574	19	0
10	J	1585	0	1590	14	0
10	X	1582	0	1583	20	0
11	K	1644	0	1595	15	0
11	Y	1644	0	1595	10	0
12	L	1757	0	1711	19	0
12	Z	1757	0	1711	24	0
13	1	1824	0	1832	22	0
13	M	1824	0	1832	25	0
14	2	1512	0	1481	13	0
14	N	1512	0	1481	14	0
15	F	2	0	0	0	0
15	G	1	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	2	0	0	0	0
15	N	1	0	0	0	0
16	K	43	0	38	2	0
16	Y	43	0	38	1	0
17	K	12	0	13	1	0
17	Y	12	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	49255	0	48978	519	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 519 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:127:LEU:N	4:D:127:LEU:HD12	1.53	1.02
4:D:127:LEU:H	4:D:127:LEU:CD1	1.70	1.01
1:A:130:ARG:HH21	7:G:124:THR:CG2	1.78	0.97
4:D:127:LEU:H	4:D:127:LEU:HD12	0.81	0.95
1:O:130:ARG:HH21	7:U:124:THR:HG22	1.29	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	239 (96%)	6 (2%)	3 (1%)	19	45
1	O	248/250 (99%)	234 (94%)	12 (5%)	2 (1%)	27	58
2	B	233/235 (99%)	223 (96%)	7 (3%)	3 (1%)	18	43
2	P	233/235 (99%)	218 (94%)	11 (5%)	4 (2%)	14	33
3	C	239/241 (99%)	229 (96%)	6 (2%)	4 (2%)	14	33
3	Q	239/241 (99%)	230 (96%)	6 (2%)	3 (1%)	18	43
4	D	229/260 (88%)	218 (95%)	11 (5%)	0	100	100
4	R	228/260 (88%)	219 (96%)	9 (4%)	0	100	100
5	E	231/233 (99%)	217 (94%)	9 (4%)	5 (2%)	10	25
5	S	231/233 (99%)	216 (94%)	11 (5%)	4 (2%)	14	33
6	F	234/242 (97%)	223 (95%)	10 (4%)	1 (0%)	43	76
6	T	234/242 (97%)	221 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	241/243 (99%)	234 (97%)	6 (2%)	1 (0%)	43	76
7	U	241/243 (99%)	232 (96%)	7 (3%)	2 (1%)	27	58
8	H	220/222 (99%)	211 (96%)	8 (4%)	1 (0%)	38	70
8	V	220/222 (99%)	213 (97%)	6 (3%)	1 (0%)	38	70
9	I	202/204 (99%)	192 (95%)	9 (4%)	1 (0%)	38	70
9	W	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
10	J	196/198 (99%)	188 (96%)	7 (4%)	1 (0%)	38	70
10	X	196/198 (99%)	185 (94%)	8 (4%)	3 (2%)	15	38
11	K	210/212 (99%)	201 (96%)	8 (4%)	1 (0%)	38	70
11	Y	210/212 (99%)	204 (97%)	6 (3%)	0	100	100
12	L	220/222 (99%)	213 (97%)	7 (3%)	0	100	100
12	Z	220/222 (99%)	213 (97%)	7 (3%)	0	100	100
13	1	231/233 (99%)	221 (96%)	9 (4%)	1 (0%)	43	76
13	M	231/233 (99%)	214 (93%)	17 (7%)	0	100	100
14	2	194/196 (99%)	186 (96%)	8 (4%)	0	100	100
14	N	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
All	All	6255/6382 (98%)	5981 (96%)	233 (4%)	41 (1%)	30	62

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	54	VAL
3	C	203	THR
3	C	207	ALA
5	E	6	ASN
6	F	184	LEU

5.3.2 Protein sidechains ⓘ

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%)	32	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	209/209 (100%)	196 (94%)	13 (6%)	26	54
2	B	195/195 (100%)	182 (93%)	13 (7%)	23	49
2	P	195/195 (100%)	180 (92%)	15 (8%)	18	40
3	C	213/213 (100%)	196 (92%)	17 (8%)	17	37
3	Q	213/213 (100%)	200 (94%)	13 (6%)	26	54
4	D	192/215 (89%)	177 (92%)	15 (8%)	18	40
4	R	191/215 (89%)	172 (90%)	19 (10%)	11	26
5	E	192/192 (100%)	171 (89%)	21 (11%)	9	21
5	S	192/192 (100%)	175 (91%)	17 (9%)	14	31
6	F	195/200 (98%)	177 (91%)	18 (9%)	13	29
6	T	195/200 (98%)	180 (92%)	15 (8%)	18	40
7	G	207/207 (100%)	191 (92%)	16 (8%)	18	40
7	U	207/207 (100%)	197 (95%)	10 (5%)	35	68
8	H	181/181 (100%)	174 (96%)	7 (4%)	43	76
8	V	181/181 (100%)	172 (95%)	9 (5%)	34	66
9	I	172/172 (100%)	166 (96%)	6 (4%)	48	80
9	W	172/172 (100%)	164 (95%)	8 (5%)	36	69
10	J	175/175 (100%)	163 (93%)	12 (7%)	22	48
10	X	174/175 (99%)	162 (93%)	12 (7%)	22	48
11	K	169/169 (100%)	156 (92%)	13 (8%)	18	40
11	Y	169/169 (100%)	161 (95%)	8 (5%)	36	69
12	L	185/185 (100%)	175 (95%)	10 (5%)	31	61
12	Z	185/185 (100%)	173 (94%)	12 (6%)	24	51
13	1	199/199 (100%)	187 (94%)	12 (6%)	27	56
13	M	199/199 (100%)	190 (96%)	9 (4%)	38	70
14	2	162/162 (100%)	154 (95%)	8 (5%)	35	67
14	N	162/162 (100%)	154 (95%)	8 (5%)	35	67
All	All	5290/5348 (99%)	4943 (93%)	347 (7%)	24	50

5 of 347 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	L	98	HIS

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Mol	Chain	Res	Type
2	P	121	GLN
12	Z	70(A)	ASN
13	M	65	GLU
1	O	4	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 154 such sidechains are listed below:

Mol	Chain	Res	Type
13	M	157	ASN
4	R	23	GLN
12	Z	166	HIS
14	N	69	GLN
2	P	125	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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	P3N	K	302	-	46,46,46	1.04	4 (8%)	58,64,64	2.55	4 (6%)
17	MES	K	303	-	12,12,12	2.02	1 (8%)	16,16,16	1.17	1 (6%)
16	P3N	Y	301	-	46,46,46	1.09	4 (8%)	58,64,64	2.59	5 (8%)
17	MES	Y	302	-	12,12,12	2.04	1 (8%)	16,16,16	1.34	3 (18%)

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	P3N	K	302	-	-	1/37/40/40	0/3/4/4
17	MES	K	303	-	-	0/6/14/14	0/1/1/1
16	P3N	Y	301	-	-	1/37/40/40	0/3/4/4
17	MES	Y	302	-	-	0/6/14/14	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Y	302	MES	C8-S	-6.48	1.66	1.78
17	K	303	MES	C8-S	-6.39	1.66	1.78
16	K	302	P3N	C35-C28	3.83	1.53	1.48
16	Y	301	P3N	C35-C28	3.34	1.53	1.48
16	K	302	P3N	C2-C1	3.03	1.53	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Y	301	P3N	N36-C37-N38	-14.81	109.56	116.99
16	K	302	P3N	N36-C37-N38	-14.38	109.78	116.99
16	Y	301	P3N	C37-N36-C1	10.40	109.02	101.23
16	K	302	P3N	C37-N36-C1	9.15	108.08	101.23
16	K	302	P3N	C28-O29-N30	-6.51	105.55	107.66

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	K	302	P3N	C32-C31-C33-N4
16	Y	301	P3N	C32-C31-C33-N4

There are no ring outliers.

5.7 Other polymers ⓘ

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, 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%)	0.14	5 (2%) 62 68	35, 50, 71, 89	0
1	O	250/250 (100%)	0.13	9 (3%) 41 46	37, 55, 83, 94	0
2	B	235/235 (100%)	0.18	8 (3%) 43 48	34, 53, 86, 91	0
2	P	235/235 (100%)	0.27	11 (4%) 30 34	33, 55, 85, 94	0
3	C	241/241 (100%)	0.39	21 (8%) 10 10	38, 61, 100, 118	0
3	Q	241/241 (100%)	0.83	44 (18%) 2 2	42, 65, 110, 128	0
4	D	233/260 (89%)	0.15	4 (1%) 67 73	36, 56, 81, 97	0
4	R	232/260 (89%)	0.10	7 (3%) 48 54	35, 57, 80, 94	0
5	E	233/233 (100%)	0.31	17 (7%) 15 16	42, 58, 84, 94	0
5	S	233/233 (100%)	0.46	20 (8%) 11 11	40, 60, 90, 102	0
6	F	236/242 (97%)	0.04	8 (3%) 43 48	33, 51, 80, 88	0
6	T	236/242 (97%)	0.11	5 (2%) 60 67	32, 52, 77, 98	0
7	G	243/243 (100%)	0.00	8 (3%) 44 49	30, 47, 72, 96	0
7	U	243/243 (100%)	0.03	6 (2%) 54 61	31, 47, 70, 86	0
8	H	222/222 (100%)	-0.13	0 100 100	34, 44, 61, 88	0
8	V	222/222 (100%)	-0.03	3 (1%) 72 77	37, 47, 64, 87	0
9	I	204/204 (100%)	-0.23	1 (0%) 88 92	31, 43, 57, 64	0
9	W	204/204 (100%)	0.04	3 (1%) 70 75	31, 44, 61, 66	0
10	J	198/198 (100%)	-0.01	6 (3%) 48 54	33, 45, 58, 110	0
10	X	198/198 (100%)	0.03	6 (3%) 48 54	36, 46, 62, 111	0
11	K	212/212 (100%)	-0.09	1 (0%) 88 92	33, 42, 59, 72	0
11	Y	212/212 (100%)	-0.11	3 (1%) 72 77	32, 44, 60, 65	0
12	L	222/222 (100%)	-0.07	1 (0%) 88 92	32, 44, 65, 72	0
12	Z	222/222 (100%)	-0.11	2 (0%) 81 85	32, 44, 64, 73	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1	233/233 (100%)	-0.05	2 (0%) 81 85	31, 43, 59, 64	0
13	M	233/233 (100%)	-0.08	2 (0%) 81 85	33, 45, 59, 62	0
14	2	196/196 (100%)	-0.14	0 100 100	33, 41, 58, 72	0
14	N	196/196 (100%)	-0.13	0 100 100	32, 41, 57, 71	0
All	All	6315/6382 (98%)	0.08	203 (3%) 44 50	30, 48, 83, 128	0

The worst 5 of 203 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	217	ALA	10.3
3	C	7	GLY	10.2
2	P	218	ASN	8.6
3	Q	55	THR	8.6
13	1	-8	THR	7.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
16	P3N	Y	301	43/43	0.18	-	40,45,58,59	0
15	MG	I	201	1/1	0.44	-	58,58,58,58	0
15	MG	L	202	1/1	0.18	-	54,54,54,54	0
16	P3N	K	302	43/43	0.18	-	38,45,57,58	0
15	MG	G	301	1/1	0.12	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
15	MG	L	201	1/1	0.20	-	56,56,56,56	0
15	MG	I	202	1/1	0.44	-	57,57,57,57	0
15	MG	N	201	1/1	0.17	-	47,47,47,47	0
17	MES	K	303	12/12	0.18	-	62,66,69,69	0
15	MG	F	301	1/1	0.14	-	61,61,61,61	0
15	MG	K	301	1/1	0.17	-	53,53,53,53	0
17	MES	Y	302	12/12	0.15	-	66,69,71,71	0
15	MG	F	302	1/1	1.19	-	107,107,107,107	0
15	MG	H	301	1/1	0.13	-	66,66,66,66	0

6.5 Other polymers ⓘ

There are no such residues in this entry.