



wwPDB X-ray Structure Validation Summary Report

Apr 18, 2014 – 03:12 AM EDT

PDB ID : 4JSU
Title : Yeast 20S proteasome in complex with the dimerized linear mimetic of TMC-95A - yCP:3a
Authors : Desvergne, A.; Genin, E.; Marechal, X.; Gallastegui, N.; Dufau, L.; Richy, N.; Groll, M.; Vidal, J.; Reboud-Ravaux, M.
Deposited on : 2013-03-22
Resolution : 2.90 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>

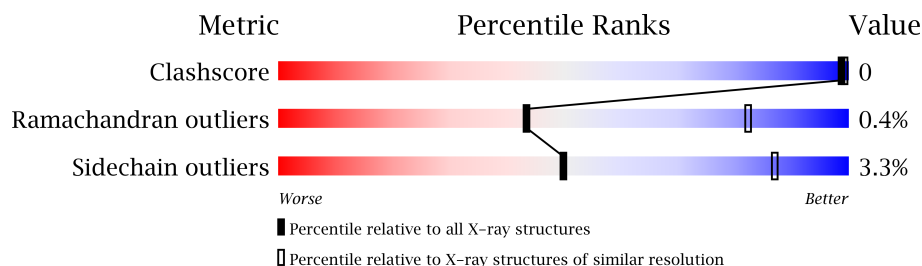
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : **FAILED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)







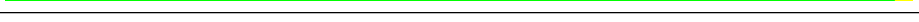

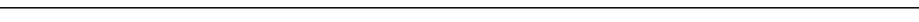







The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The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

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	250	
1	O	250	
2	B	258	
2	P	258	
3	C	254	
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	

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Mol	Chain	Length	Quality of chain
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	233	
13	a	233	
14	N	196	
14	b	196	
15	c	8	
15	d	8	
15	e	8	
15	f	8	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 51118 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 subunit alpha type-2.

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			
3	Q	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			
4	R	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			

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

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 Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			
6	T	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			

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

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 subunit beta type-2.

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	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 subunit beta type-5.

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

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

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

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

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

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

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

- Molecule 15 is a protein called TMC-95A mimic ligand yCP:3a.

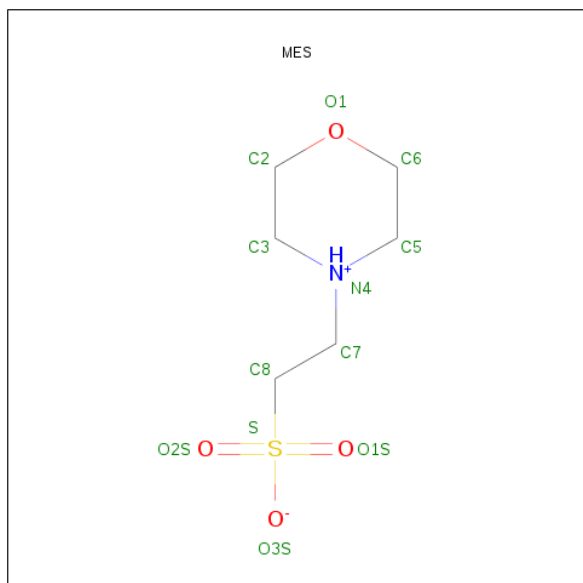
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	c	5	Total	C	N	O	0	0	0
			56	43	6	7			
15	d	5	Total	C	N	O	0	0	0
			56	43	6	7			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	e	5	Total	C	N	O	0	0	0
			56	43	6	7			
15	f	5	Total	C	N	O	0	0	0
			56	43	6	7			

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



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

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	58	Total	O	0	0
			58	58		
17	B	40	Total	O	0	0
			40	40		
17	C	40	Total	O	0	0
			40	40		
17	D	37	Total	O	0	0
			37	37		
17	E	22	Total	O	0	0
			22	22		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	F	47	Total 47	O 47	0	0
17	G	58	Total 58	O 58	0	0
17	H	53	Total 53	O 53	0	0
17	I	62	Total 62	O 62	0	0
17	J	53	Total 53	O 53	0	0
17	K	49	Total 49	O 49	0	0
17	L	58	Total 58	O 58	0	0
17	M	75	Total 75	O 75	0	0
17	N	57	Total 57	O 57	0	0
17	O	33	Total 33	O 33	0	0
17	P	29	Total 29	O 29	0	0
17	Q	29	Total 29	O 29	0	0
17	R	28	Total 28	O 28	0	0
17	S	18	Total 18	O 18	0	0
17	T	44	Total 44	O 44	0	0
17	U	58	Total 58	O 58	0	0
17	V	47	Total 47	O 47	0	0
17	W	58	Total 58	O 58	0	0
17	X	44	Total 44	O 44	0	0
17	Y	46	Total 46	O 46	0	0
17	Z	51	Total 51	O 51	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	a	79	Total 79	O 79	0	0
17	b	57	Total 57	O 57	0	0
17	e	1	Total 1	O 1	0	0
17	f	1	Total 1	O 1	0	0

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.

Note EDS failed to run properly.

- 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: 



- Chain D:



- Chain R:



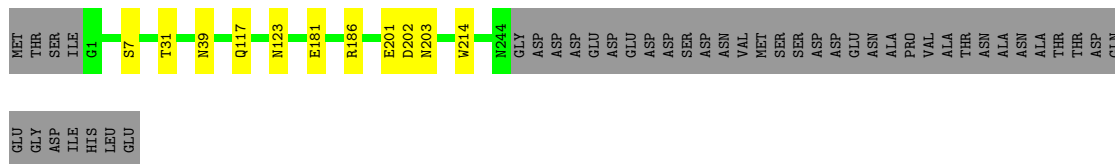
- Chain E:



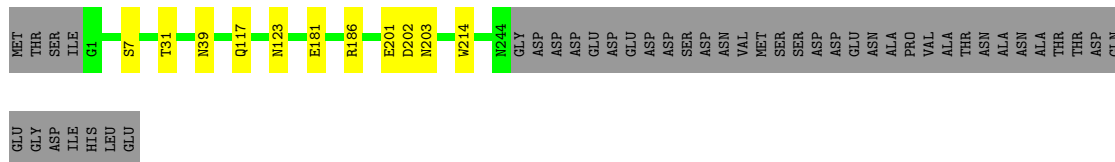
- Chain S:



- Chain F:



- Chain T:



- Chain G:



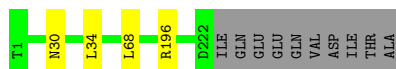
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Chain U:



- 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:



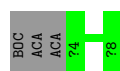
- Molecule 14: Proteasome subunit beta type-1

Chain b:



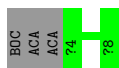
- Molecule 15: TMC-95A mimic ligand yCP:3a

Chain c:



- Molecule 15: TMC-95A mimic ligand yCP:3a

Chain d:



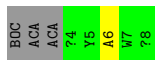
- Molecule 15: TMC-95A mimic ligand yCP:3a

Chain e: 



- Molecule 15: TMC-95A mimic ligand yCP:3a

Chain f: 



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.35Å 299.22Å 144.65Å 90.00° 112.97° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90	Depositor
% Data completeness (in resolution range)	99.1 (15.00-2.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
R, R_{free}	0.221 , 0.227	Depositor
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.159	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 229482 reflections (0.001%)	Xtriage
Total number of atoms	51118	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: TY5, ACA, RE0, ABN, 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	0.37	2/1952 (0.1%)	0.47	0/2642
1	O	0.37	1/1952 (0.1%)	0.48	0/2642
2	B	0.33	0/1934	0.48	0/2618
2	P	0.33	0/1934	0.48	0/2618
3	C	0.34	0/1919	0.49	0/2598
3	Q	0.34	1/1919 (0.1%)	0.49	0/2598
4	D	0.35	0/1886	0.49	0/2541
4	R	0.36	0/1886	0.49	0/2541
5	E	0.31	0/1823	0.47	0/2463
5	S	0.31	0/1823	0.47	0/2463
6	F	0.41	0/1936	0.47	0/2614
6	T	0.41	0/1936	0.47	0/2614
7	G	0.34	0/1959	0.47	0/2652
7	U	0.34	0/1959	0.47	0/2652
8	H	0.44	0/1715	0.48	0/2326
8	V	0.44	2/1715 (0.1%)	0.48	0/2326
9	I	0.34	0/1611	0.49	0/2174
9	W	0.34	0/1611	0.49	0/2174
10	J	0.31	0/1613	0.48	0/2173
10	X	0.31	0/1613	0.48	0/2173
11	K	0.50	2/1681 (0.1%)	0.51	1/2274 (0.0%)
11	Y	0.50	1/1681 (0.1%)	0.51	1/2274 (0.0%)
12	L	0.36	0/1795	0.48	0/2420
12	Z	0.36	0/1795	0.48	0/2420
13	M	0.36	1/1855 (0.1%)	0.49	0/2514
13	a	0.36	1/1855 (0.1%)	0.50	0/2514
14	N	0.39	0/1541	0.45	0/2087
14	b	0.39	0/1541	0.45	0/2087
15	c	0.84	0/4	0.69	0/4
15	d	0.85	0/4	0.70	0/4
15	e	0.83	0/4	0.61	0/4
15	f	0.85	0/4	0.61	0/4

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.37	11/50456 (0.0%)	0.48	2/68208 (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
15	e	0	1
15	f	0	1
All	All	0	2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	K	146	TRP	CD2-CE2	5.05	1.47	1.41
13	M	219	TRP	CD2-CE2	5.04	1.47	1.41
1	A	179	TRP	CD2-CE2	5.04	1.47	1.41
11	Y	146	TRP	CD2-CE2	5.03	1.47	1.41
8	V	42	TRP	CD2-CE2	5.02	1.47	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Y	4	LEU	CA-CB-CG	5.34	127.59	115.30
11	K	4	LEU	CA-CB-CG	5.33	127.55	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	e	6	ALA	Peptide
15	f	6	ALA	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	0	2	0
1	O	1915	0	0	2	0
2	B	1904	0	0	1	0
2	P	1904	0	0	3	0
3	C	1890	0	0	0	0
3	Q	1890	0	0	1	0
4	D	1861	0	0	0	0
4	R	1861	0	0	0	0
5	E	1795	0	0	0	0
5	S	1795	0	0	0	0
6	F	1896	0	0	0	0
6	T	1896	0	0	0	0
7	G	1921	0	0	0	0
7	U	1921	0	0	0	0
8	H	1684	0	0	0	0
8	V	1684	0	0	0	0
9	I	1581	0	0	1	0
9	W	1581	0	0	0	0
10	J	1585	0	0	2	0
10	X	1585	0	0	2	0
11	K	1644	0	0	2	0
11	Y	1644	0	0	2	0
12	L	1757	0	0	0	0
12	Z	1757	0	0	0	0
13	M	1824	0	0	1	0
13	a	1824	0	0	0	0
14	N	1512	0	0	0	0
14	b	1512	0	0	0	0
15	c	56	0	48	0	0
15	d	56	0	48	0	0
15	e	56	0	48	0	0
15	f	56	0	48	0	0
16	K	12	0	13	0	0
16	Y	12	0	13	0	0
17	A	58	0	0	0	0
17	B	40	0	0	0	0
17	C	40	0	0	0	0
17	D	37	0	0	0	0
17	E	22	0	0	0	0
17	F	47	0	0	0	0
17	G	58	0	0	0	0
17	H	53	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	I	62	0	0	0	0
17	J	53	0	0	0	0
17	K	49	0	0	0	0
17	L	58	0	0	0	0
17	M	75	0	0	0	0
17	N	57	0	0	0	0
17	O	33	0	0	0	0
17	P	29	0	0	0	0
17	Q	29	0	0	0	0
17	R	28	0	0	0	0
17	S	18	0	0	0	0
17	T	44	0	0	0	0
17	U	58	0	0	0	0
17	V	47	0	0	0	0
17	W	58	0	0	0	0
17	X	44	0	0	0	0
17	Y	46	0	0	0	0
17	Z	51	0	0	0	0
17	a	79	0	0	0	0
17	b	57	0	0	0	0
17	e	1	0	0	0	0
17	f	1	0	0	0	0
All	All	51118	0	218	14	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 0.

The worst 5 of 14 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:73:ARG:NH2	11:K:104:TYR:O	2.41	0.53
11:Y:73:ARG:NH2	11:Y:104:TYR:O	2.41	0.53
1:O:160:LYS:N	2:P:55:LEU:O	2.47	0.48
2:P:15:GLU:O	3:Q:27:ARG:NH1	2.48	0.47
11:K:38:ASN:O	11:K:40:PHE:N	2.49	0.45

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%)	242 (98%)	4 (2%)	2 (1%)	27	68
1	O	248/250 (99%)	242 (98%)	4 (2%)	2 (1%)	27	68
2	B	242/258 (94%)	230 (95%)	10 (4%)	2 (1%)	27	68
2	P	242/258 (94%)	230 (95%)	10 (4%)	2 (1%)	27	68
3	C	239/254 (94%)	229 (96%)	7 (3%)	3 (1%)	18	54
3	Q	239/254 (94%)	230 (96%)	6 (2%)	3 (1%)	18	54
4	D	240/260 (92%)	231 (96%)	6 (2%)	3 (1%)	18	54
4	R	240/260 (92%)	230 (96%)	7 (3%)	3 (1%)	18	54
5	E	231/234 (99%)	221 (96%)	8 (4%)	2 (1%)	25	66
5	S	231/234 (99%)	221 (96%)	8 (4%)	2 (1%)	25	66
6	F	242/288 (84%)	235 (97%)	7 (3%)	0	100	100
6	T	242/288 (84%)	235 (97%)	7 (3%)	0	100	100
7	G	241/252 (96%)	233 (97%)	8 (3%)	0	100	100
7	U	241/252 (96%)	233 (97%)	8 (3%)	0	100	100
8	H	220/232 (95%)	212 (96%)	8 (4%)	0	100	100
8	V	220/232 (95%)	212 (96%)	8 (4%)	0	100	100
9	I	202/205 (98%)	193 (96%)	9 (4%)	0	100	100
9	W	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	196/198 (99%)	189 (96%)	6 (3%)	1 (0%)	38	79
10	X	196/198 (99%)	189 (96%)	6 (3%)	1 (0%)	38	79
11	K	210/212 (99%)	203 (97%)	6 (3%)	1 (0%)	38	79
11	Y	210/212 (99%)	203 (97%)	6 (3%)	1 (0%)	38	79
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	M	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
13	a	231/233 (99%)	221 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
14	b	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
15	c	1/8 (12%)	1 (100%)	0	0	100	100
15	d	1/8 (12%)	1 (100%)	0	0	100	100
15	e	1/8 (12%)	1 (100%)	0	0	100	100
15	f	1/8 (12%)	1 (100%)	0	0	100	100
All	All	6316/6620 (95%)	6084 (96%)	204 (3%)	28 (0%)	43	82

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	52	LEU
3	Q	52	LEU
1	A	166	LYS
5	E	201	ARG
11	K	39	PRO

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%)	206 (99%)	3 (1%)	78	96
1	O	209/209 (100%)	206 (99%)	3 (1%)	78	96
2	B	203/216 (94%)	192 (95%)	11 (5%)	31	69
2	P	203/216 (94%)	192 (95%)	11 (5%)	31	69
3	C	213/226 (94%)	206 (97%)	7 (3%)	50	87
3	Q	213/226 (94%)	206 (97%)	7 (3%)	50	87
4	D	198/215 (92%)	190 (96%)	8 (4%)	42	81
4	R	198/215 (92%)	190 (96%)	8 (4%)	42	81
5	E	192/193 (100%)	181 (94%)	11 (6%)	29	66
5	S	192/193 (100%)	181 (94%)	11 (6%)	29	66
6	F	201/239 (84%)	190 (94%)	11 (6%)	30	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	T	201/239 (84%)	190 (94%)	11 (6%)	30	68
7	G	207/210 (99%)	199 (96%)	8 (4%)	43	82
7	U	207/210 (99%)	200 (97%)	7 (3%)	49	86
8	H	181/190 (95%)	177 (98%)	4 (2%)	64	92
8	V	181/190 (95%)	177 (98%)	4 (2%)	64	92
9	I	172/173 (99%)	169 (98%)	3 (2%)	73	94
9	W	172/173 (99%)	169 (98%)	3 (2%)	73	94
10	J	175/175 (100%)	173 (99%)	2 (1%)	84	97
10	X	175/175 (100%)	173 (99%)	2 (1%)	84	97
11	K	169/169 (100%)	161 (95%)	8 (5%)	36	75
11	Y	169/169 (100%)	161 (95%)	8 (5%)	36	75
12	L	185/185 (100%)	181 (98%)	4 (2%)	64	92
12	Z	185/185 (100%)	181 (98%)	4 (2%)	64	92
13	M	199/199 (100%)	191 (96%)	8 (4%)	42	81
13	a	199/199 (100%)	192 (96%)	7 (4%)	48	85
14	N	162/162 (100%)	160 (99%)	2 (1%)	82	96
14	b	162/162 (100%)	160 (99%)	2 (1%)	82	96
All	All	5332/5522 (97%)	5154 (97%)	178 (3%)	50	87

5 of 178 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	48	ASN
2	P	184	LYS
11	Y	107	LYS
13	M	70	LEU
1	O	30	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

12 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
15	ACA	c	4	15	7,7,8	6.40	1 (14%)	4,6,8	0.34	0
15	TY5	c	5	15	20,20,21	3.89	1 (5%)	23,25,27	0.96	1 (4%)
15	RE0	c	7	15	17,17,18	4.17	3 (17%)	23,25,27	2.46	6 (26%)
15	ACA	d	4	15	7,7,8	6.34	1 (14%)	4,6,8	0.34	0
15	TY5	d	5	15	20,20,21	3.87	1 (5%)	23,25,27	0.97	1 (4%)
15	RE0	d	7	15	17,17,18	4.17	3 (17%)	23,25,27	2.44	6 (26%)
15	ACA	e	4	15	7,7,8	6.36	1 (14%)	4,6,8	0.37	0
15	TY5	e	5	15	20,20,21	3.86	1 (5%)	23,25,27	0.79	1 (4%)
15	RE0	e	7	15	17,17,18	4.16	3 (17%)	23,25,27	2.31	6 (26%)
15	ACA	f	4	15	7,7,8	6.41	1 (14%)	4,6,8	0.39	0
15	TY5	f	5	15	20,20,21	3.88	1 (5%)	23,25,27	0.83	1 (4%)
15	RE0	f	7	15	17,17,18	4.21	3 (17%)	23,25,27	2.36	7 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	ACA	c	4	15	-	0/4/5/6	0/0/0/0
15	TY5	c	5	15	-	0/9/11/13	0/2/2/2
15	RE0	c	7	15	-	0/5/23/25	0/2/2/2
15	ACA	d	4	15	-	0/4/5/6	0/0/0/0
15	TY5	d	5	15	-	0/9/11/13	0/2/2/2
15	RE0	d	7	15	-	0/5/23/25	0/2/2/2
15	ACA	e	4	15	-	0/4/5/6	0/0/0/0
15	TY5	e	5	15	-	0/9/11/13	0/2/2/2
15	RE0	e	7	15	-	0/5/23/25	0/2/2/2
15	ACA	f	4	15	-	0/4/5/6	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	TY5	f	5	15	-	0/9/11/13	0/2/2/2
15	RE0	f	7	15	-	0/5/23/25	0/2/2/2

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	f	4	ACA	O1-C1	16.86	1.23	1.11
15	c	4	ACA	O1-C1	16.83	1.23	1.11
15	c	5	TY5	O-C	16.74	1.22	1.11
15	e	4	ACA	O1-C1	16.73	1.22	1.11
15	f	5	TY5	O-C	16.70	1.22	1.11

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	c	7	RE0	CG-CD2-CE2	-8.38	106.64	108.85
15	d	7	RE0	CG-CD2-CE2	-8.22	106.69	108.85
15	f	7	RE0	CG-CD2-CE2	-7.52	106.87	108.85
15	e	7	RE0	CG-CD2-CE2	-7.36	106.91	108.85
15	f	7	RE0	C-CA-N	-4.37	109.47	113.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	MES	K	301	-	12,12,12	1.24	3 (25%)	16,16,16	1.32	3 (18%)
16	MES	Y	301	-	12,12,12	1.23	3 (25%)	16,16,16	1.38	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	MES	K	301	-	-	0/6/14/14	0/1/1/1
16	MES	Y	301	-	-	0/6/14/14	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	K	301	MES	O2S-S	2.15	1.51	1.45
16	Y	301	MES	O2S-S	2.12	1.50	1.45
16	Y	301	MES	C5-C6	2.06	1.55	1.51
16	K	301	MES	C3-C2	2.05	1.55	1.51
16	Y	301	MES	C3-C2	2.05	1.55	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Y	301	MES	O3S-S-O1S	2.57	119.21	112.50
16	K	301	MES	C7-N4-C5	2.34	117.52	111.65
16	Y	301	MES	C7-N4-C5	2.29	117.41	111.65
16	K	301	MES	O3S-S-O1S	2.28	118.45	112.50
16	Y	301	MES	O2S-S-O1S	-2.13	107.41	112.39

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.