



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:58 PM GMT

PDB ID : 4YA7
Title : Yeast 20S proteasome beta2-H114D mutant in complex with Ac-LAE-ep
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-02-17
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

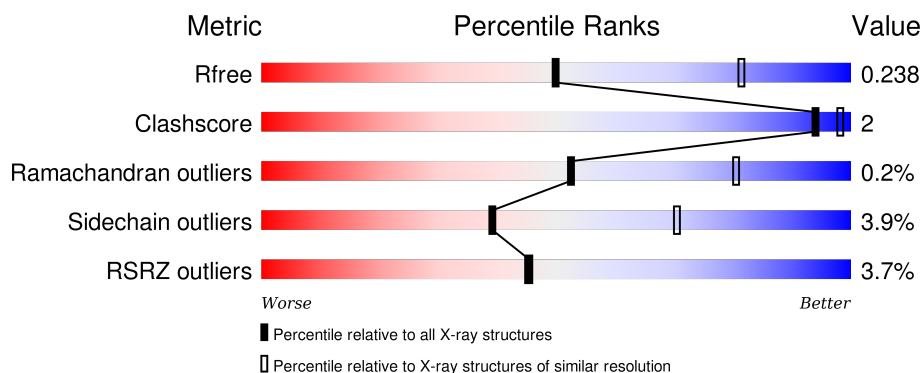
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (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. 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 $\leq 5\%$. 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	<div> <div>3%</div> <div>95%</div> <div>5%</div> </div>
1	O	250	<div> <div>5%</div> <div>95%</div> <div>5%</div> </div>
2	B	258	<div> <div>6%</div> <div>86%</div> <div>8%</div> <div>5%</div> </div>
2	P	258	<div> <div>6%</div> <div>86%</div> <div>8%</div> <div>5%</div> </div>
3	C	254	<div> <div>9%</div> <div>87%</div> <div>7%</div> <div>6%</div> </div>

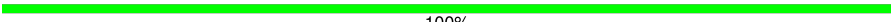
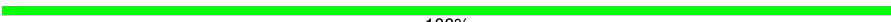


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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	
15	c	5	
15	d	5	

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Mol	Chain	Length	Quality of chain
15	e	5	 100%
15	f	5	 100%
15	g	5	 100%
15	h	5	 100%

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
18	MES	H	302	-	-	-	X
18	MES	K	302	-	-	-	X
18	MES	V	302	-	-	-	X
18	MES	Y	302	-	-	-	X

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 50429 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1682	1059	291	325	7			
8	V	222	Total	C	N	O	S	0	0	0
			1682	1059	291	325	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	114	ASP	HIS	engineered mutation	UNP P25043
V	114	ASP	HIS	engineered mutation	UNP P25043

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	1	0
			1764	1120	305	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 Ac-LAE-ep.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	c	5	Total	C	N	O	0	0	0
			29	19	3	7			
15	d	5	Total	C	N	O	0	0	0
			29	19	3	7			
15	e	5	Total	C	N	O	0	0	0
			29	19	3	7			
15	f	5	Total	C	N	O	0	0	0
			29	19	3	7			
15	g	5	Total	C	N	O	0	0	0
			29	19	3	7			
15	h	5	Total	C	N	O	0	0	0
			29	19	3	7			

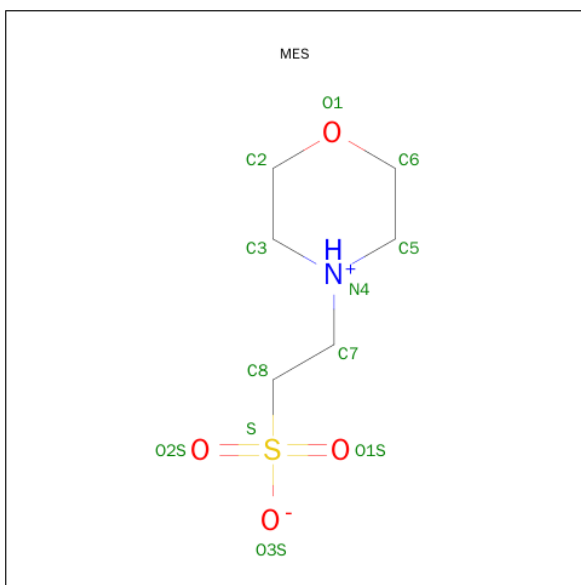
- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	G	1	Total	Mg	0	0
			1	1		
16	K	1	Total	Mg	0	0
			1	1		
16	H	1	Total	Mg	0	0
			1	1		
16	I	1	Total	Mg	0	0
			1	1		
16	V	1	Total	Mg	0	0
			1	1		
16	N	1	Total	Mg	0	0
			1	1		
16	Y	1	Total	Mg	0	0
			1	1		

- Molecule 17 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



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

- Molecule 19 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	44	Total	O	0	0
			44	44		
19	B	34	Total	O	0	0
			34	34		
19	C	22	Total	O	0	0
			22	22		
19	D	19	Total	O	0	0
			19	19		
19	E	21	Total	O	0	0
			21	21		
19	F	26	Total	O	0	0
			26	26		
19	G	36	Total	O	0	0
			36	36		
19	H	50	Total	O	0	0
			50	50		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	I	40	Total O 40 40	0	0
19	J	43	Total O 43 43	0	0
19	K	27	Total O 27 27	0	0
19	L	52	Total O 52 52	0	0
19	M	42	Total O 42 42	0	0
19	N	26	Total O 26 26	0	0
19	O	30	Total O 30 30	0	0
19	P	23	Total O 23 23	0	0
19	Q	18	Total O 18 18	0	0
19	R	18	Total O 18 18	0	0
19	S	11	Total O 11 11	0	0
19	T	27	Total O 27 27	0	0
19	U	31	Total O 31 31	0	0
19	V	43	Total O 43 43	0	0
19	W	35	Total O 35 35	0	0
19	X	29	Total O 29 29	0	0
19	Y	28	Total O 28 28	0	0
19	Z	52	Total O 52 52	0	0
19	a	36	Total O 36 36	0	0
19	b	30	Total O 30 30	0	0
19	d	1	Total O 1 1	0	0

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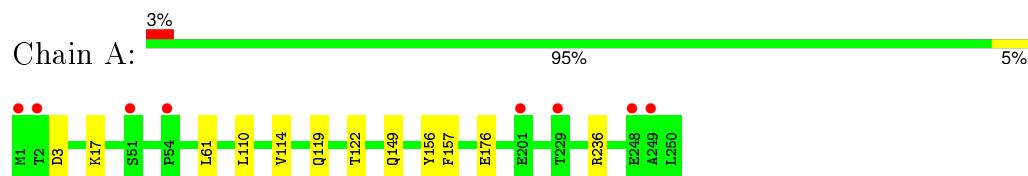
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	e	1	Total 1	O 1	0	0
19	f	1	Total 1	O 1	0	0
19	g	3	Total 3	O 3	0	0

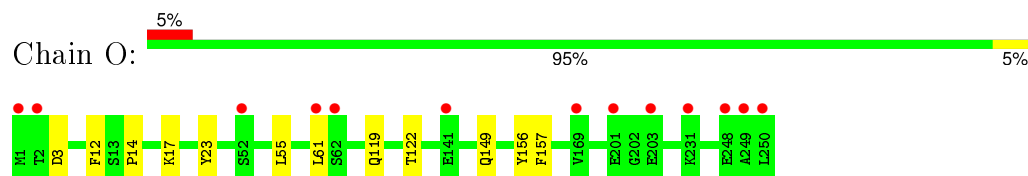
3 Residue-property plots [i](#)

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.

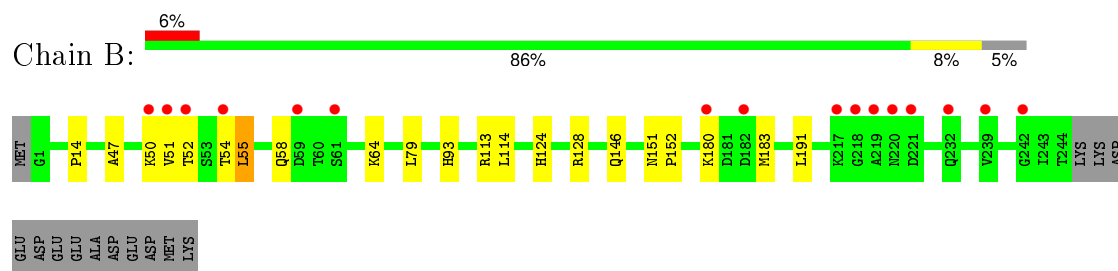
- Molecule 1: Proteasome subunit alpha type-2



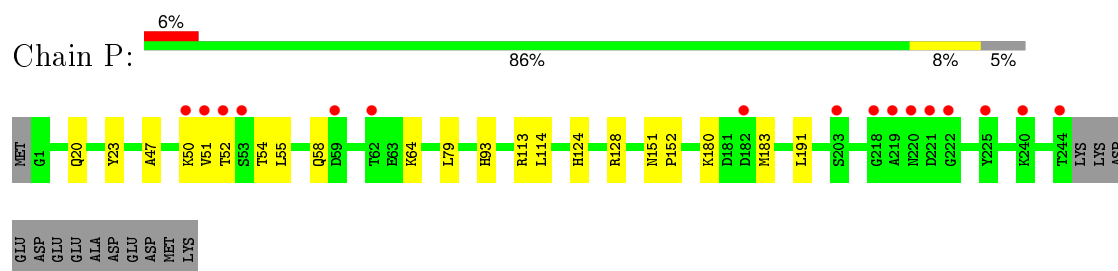
- Molecule 1: Proteasome subunit alpha type-2



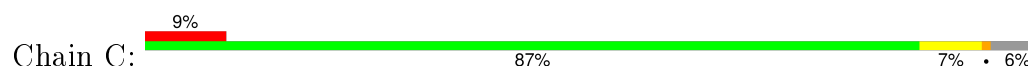
- Molecule 2: Proteasome subunit alpha type-3

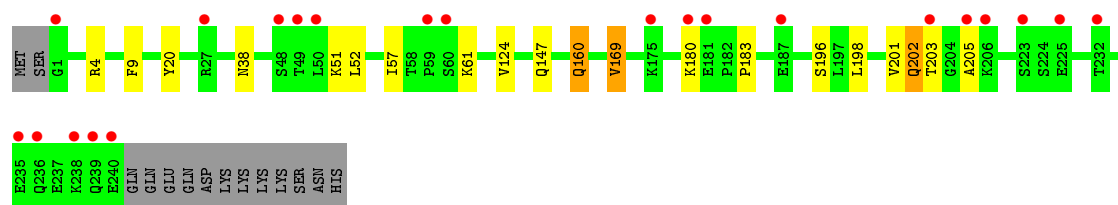


- Molecule 2: Proteasome subunit alpha type-3

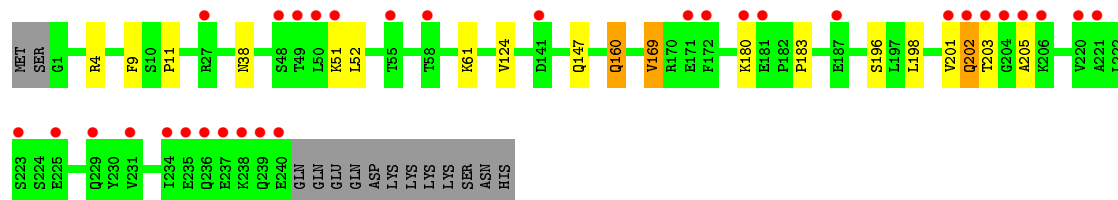
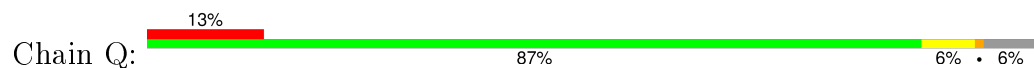


- Molecule 3: Proteasome subunit alpha type-4

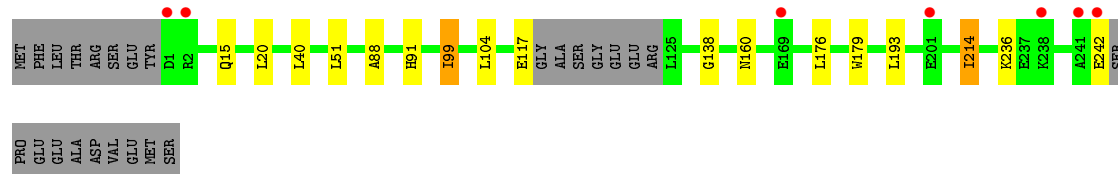
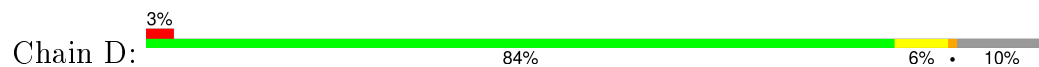




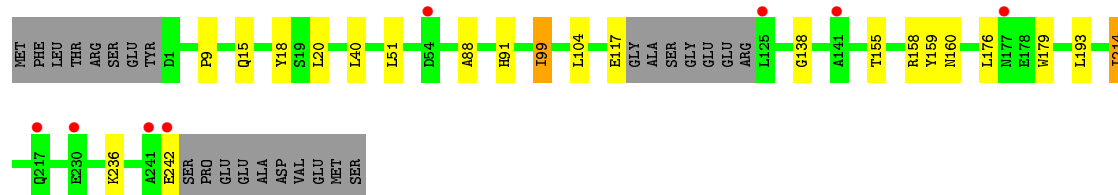
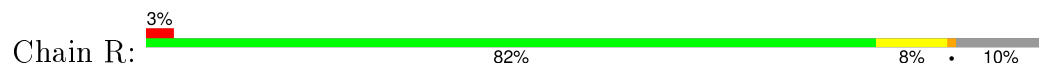
• Molecule 3: Proteasome subunit alpha type-4



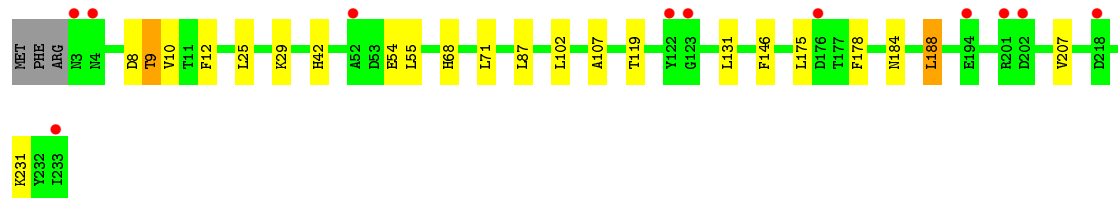
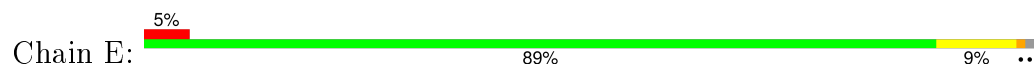
• Molecule 4: Proteasome subunit alpha type-5



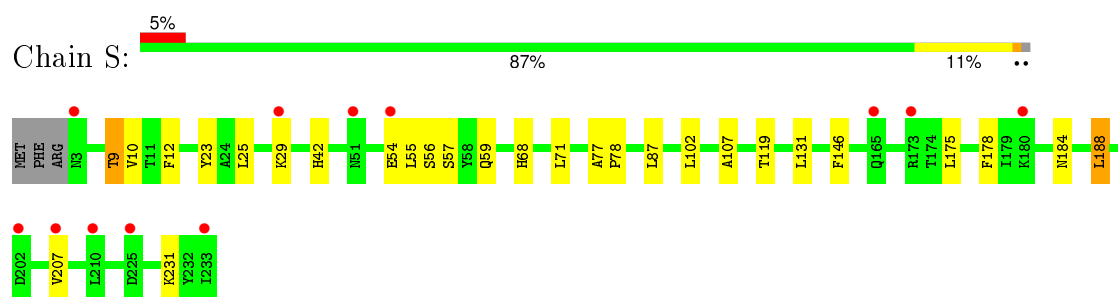
• Molecule 4: Proteasome subunit alpha type-5



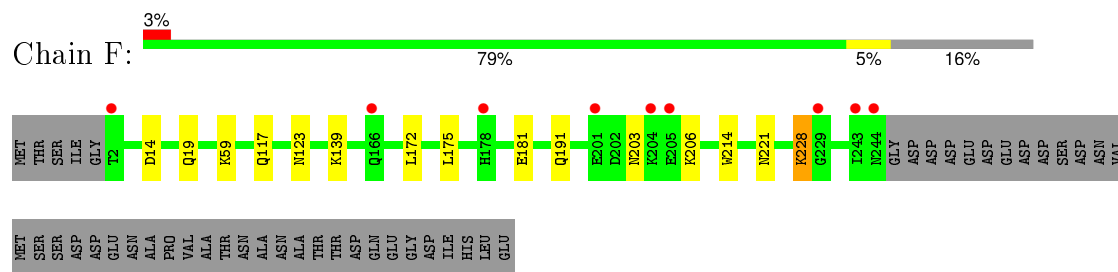
• Molecule 5: Proteasome subunit alpha type-6



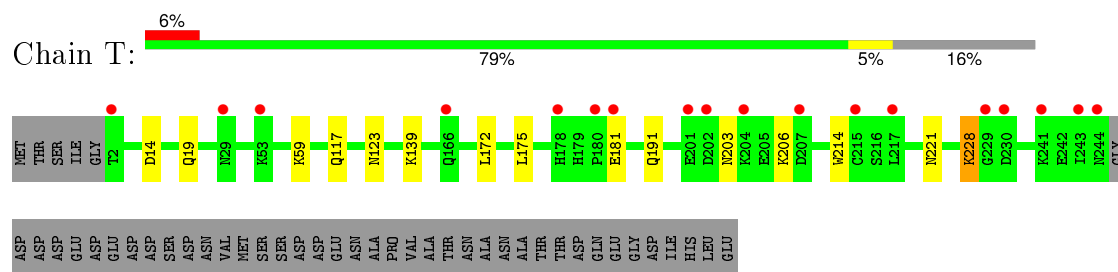
• Molecule 5: Proteasome subunit alpha type-6



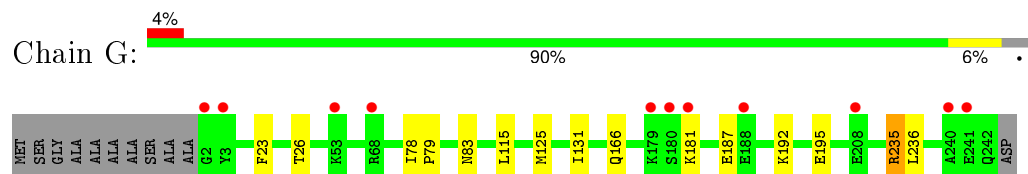
- Molecule 6: Probable proteasome subunit alpha type-7



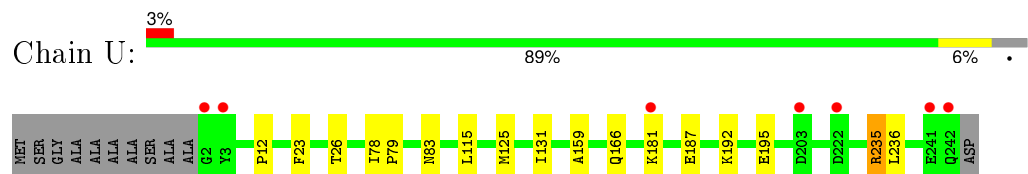
- Molecule 6: Probable proteasome subunit alpha type-7



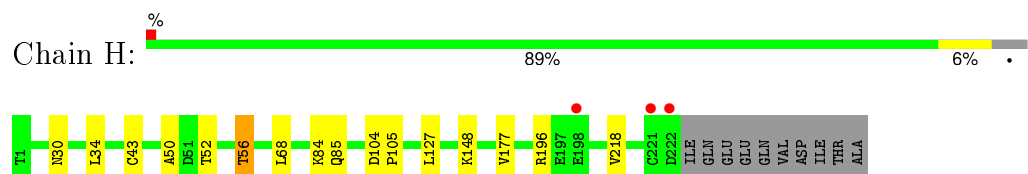
- Molecule 7: Proteasome subunit alpha type-1



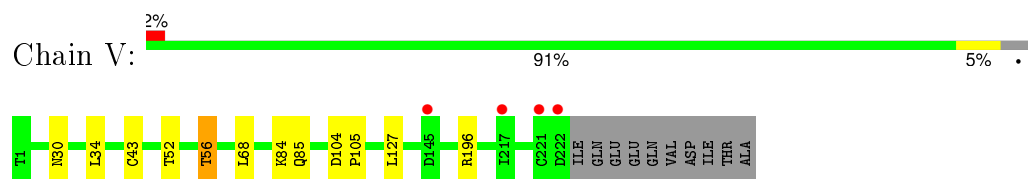
- Molecule 7: Proteasome subunit alpha type-1



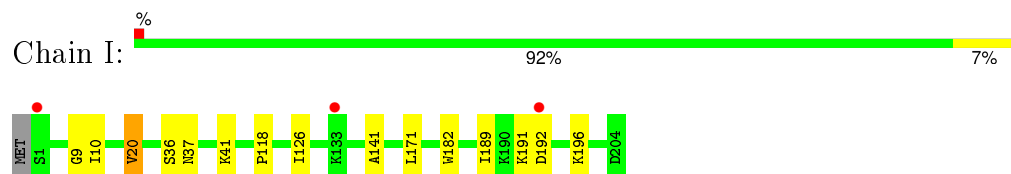
- Molecule 8: Proteasome subunit beta type-2



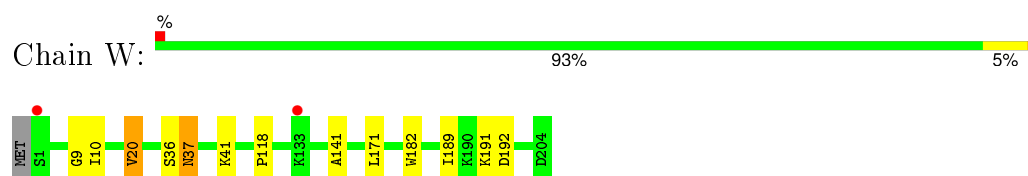
- Molecule 8: Proteasome subunit beta type-2



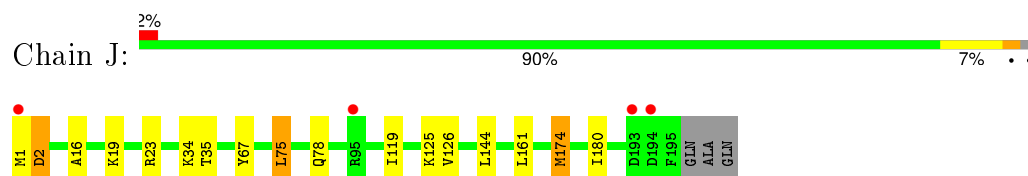
- Molecule 9: Proteasome subunit beta type-3



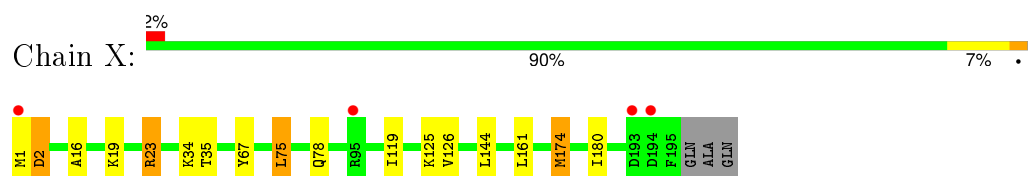
- Molecule 9: Proteasome subunit beta type-3



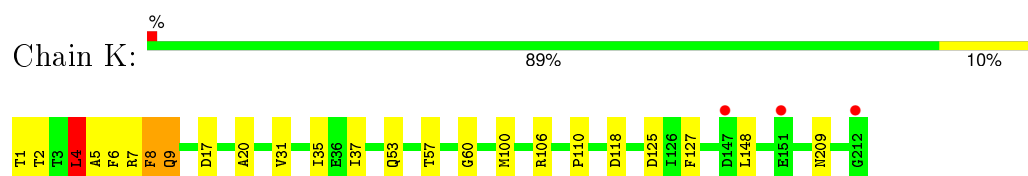
- Molecule 10: Proteasome subunit beta type-4



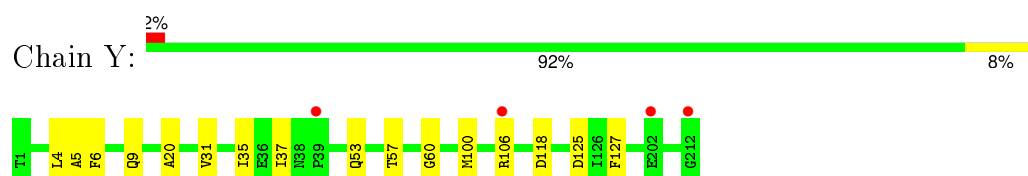
- Molecule 10: Proteasome subunit beta type-4



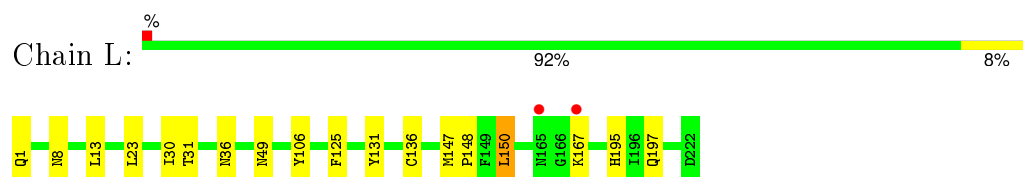
- Molecule 11: Proteasome subunit beta type-5



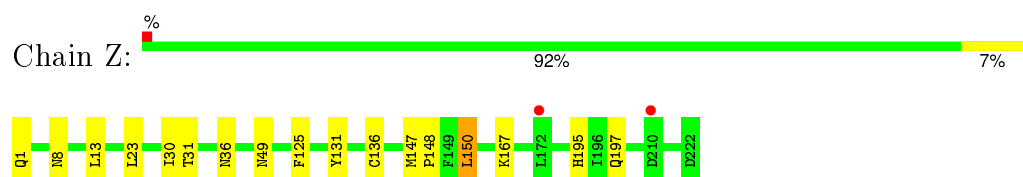
- Molecule 11: Proteasome subunit beta type-5



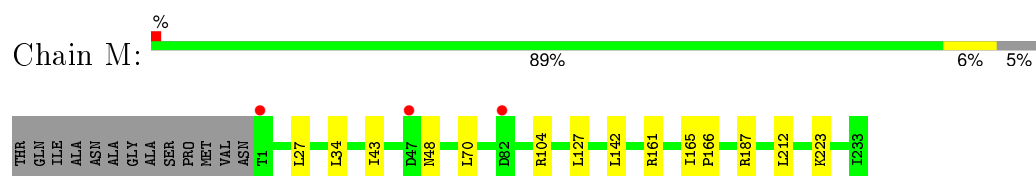
- Molecule 12: Proteasome subunit beta type-6



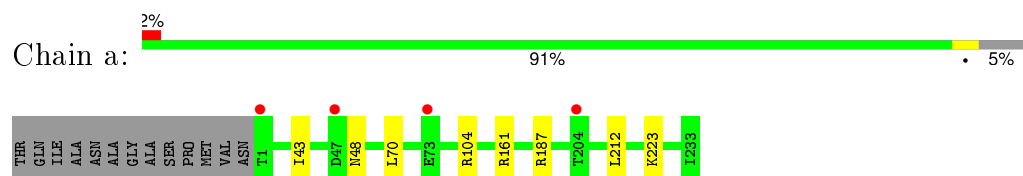
- Molecule 12: Proteasome subunit beta type-6



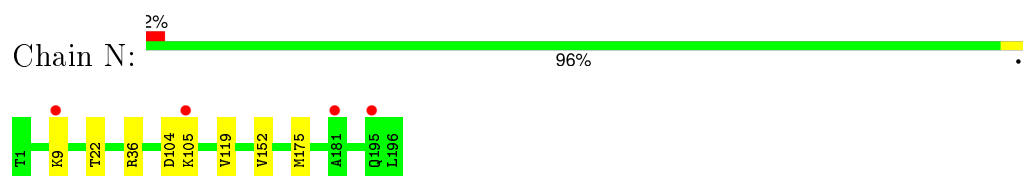
- Molecule 13: Proteasome subunit beta type-7



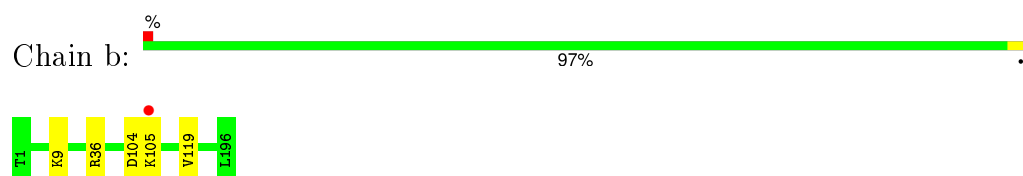
- Molecule 13: Proteasome subunit beta type-7



- Molecule 14: Proteasome subunit beta type-1



- Molecule 14: Proteasome subunit beta type-1




- Molecule 15: Ac-LAE-ep



There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAE-ep

Chain d:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAE-ep

Chain e:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAE-ep

Chain f:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAE-ep

Chain g:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAE-ep

Chain h:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.02Å 299.94Å 144.88Å 90.00° 113.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.0 (15.00-2.70) 96.0 (15.00-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.215 , 0.237 0.217 , 0.238	Depositor DCC
R_{free} test set	13803 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	5 of 276060 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	50429	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ACE, CL, GAU, POL, 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	0.27	0/1952	0.48	0/2642
1	O	0.27	0/1952	0.48	0/2642
2	B	0.27	0/1934	0.51	0/2618
2	P	0.27	0/1934	0.51	0/2618
3	C	0.27	0/1910	0.52	0/2586
3	Q	0.27	0/1910	0.51	0/2586
4	D	0.26	0/1837	0.49	0/2475
4	R	0.26	0/1837	0.49	0/2475
5	E	0.27	0/1800	0.48	0/2433
5	S	0.27	0/1800	0.49	0/2433
6	F	0.27	0/1932	0.47	0/2609
6	T	0.27	0/1932	0.47	0/2609
7	G	0.27	0/1945	0.49	0/2634
7	U	0.27	0/1945	0.48	0/2634
8	H	0.25	0/1712	0.50	0/2322
8	V	0.26	0/1712	0.49	0/2322
9	I	0.28	0/1611	0.50	0/2174
9	W	0.28	0/1611	0.50	0/2174
10	J	0.26	0/1589	0.49	0/2142
10	X	0.26	0/1589	0.49	0/2142
11	K	0.41	0/1681	0.52	1/2274 (0.0%)
11	Y	0.26	0/1681	0.50	0/2274
12	L	0.27	0/1795	0.49	0/2420
12	Z	0.29	0/1806	0.49	0/2435
13	M	0.27	0/1855	0.52	0/2514
13	a	0.27	0/1855	0.52	0/2514
14	N	0.29	0/1541	0.49	0/2087
14	b	0.29	0/1541	0.49	0/2087
15	c	0.34	0/13	1.26	0/17
15	d	1.16	0/13	1.61	0/17
15	e	0.34	0/13	1.20	0/17
15	f	1.09	0/13	1.46	0/17

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	g	0.99	0/13	1.26	0/17
15	h	1.02	0/13	1.10	0/17
All	All	0.28	0/50277	0.50	1/67977 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
11	K	4	LEU	CA-CB-CG	5.30	127.50	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	6	0
1	O	1915	0	1929	7	0
2	B	1904	0	1904	10	0
2	P	1904	0	1904	9	0
3	C	1881	0	1895	11	0
3	Q	1881	0	1895	10	0
4	D	1813	0	1797	6	0
4	R	1813	0	1797	11	0
5	E	1773	0	1775	7	0
5	S	1773	0	1775	12	0
6	F	1892	0	1883	3	0
6	T	1892	0	1883	3	0
7	G	1907	0	1901	5	0
7	U	1907	0	1901	7	0
8	H	1682	0	1682	6	0
8	V	1682	0	1682	3	0
9	I	1581	0	1574	7	0
9	W	1581	0	1574	6	0
10	J	1561	0	1569	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	X	1561	0	1569	11	0
11	K	1644	0	1592	14	0
11	Y	1644	0	1592	8	0
12	L	1757	0	1711	6	0
12	Z	1764	0	1718	6	0
13	M	1824	0	1832	3	0
13	a	1824	0	1832	0	0
14	N	1512	0	1478	1	0
14	b	1512	0	1478	0	0
15	c	29	0	31	0	0
15	d	29	0	30	0	0
15	e	29	0	31	0	0
15	f	29	0	31	0	0
15	g	29	0	30	0	0
15	h	29	0	30	0	0
16	G	1	0	0	0	0
16	H	1	0	0	0	0
16	I	1	0	0	0	0
16	K	1	0	0	0	0
16	N	1	0	0	0	0
16	V	1	0	0	0	0
16	Y	1	0	0	0	0
17	G	1	0	0	0	0
17	U	1	0	0	0	0
18	H	12	0	13	0	0
18	K	12	0	13	0	0
18	V	12	0	13	0	0
18	Y	12	0	13	0	0
19	A	44	0	0	1	0
19	B	34	0	0	0	0
19	C	22	0	0	0	0
19	D	19	0	0	0	0
19	E	21	0	0	0	0
19	F	26	0	0	0	0
19	G	36	0	0	0	0
19	H	50	0	0	0	0
19	I	40	0	0	0	0
19	J	43	0	0	0	0
19	K	27	0	0	0	0
19	L	52	0	0	0	0
19	M	42	0	0	0	0
19	N	26	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	O	30	0	0	0	0
19	P	23	0	0	0	0
19	Q	18	0	0	0	0
19	R	18	0	0	0	0
19	S	11	0	0	0	0
19	T	27	0	0	0	0
19	U	31	0	0	0	0
19	V	43	0	0	0	0
19	W	35	0	0	0	0
19	X	29	0	0	0	0
19	Y	28	0	0	1	0
19	Z	52	0	0	0	0
19	a	36	0	0	0	0
19	b	30	0	0	0	0
19	d	1	0	0	0	0
19	e	1	0	0	0	0
19	f	1	0	0	0	0
19	g	3	0	0	0	0
All	All	50429	0	49286	162	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 2.

All (162) 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)
10:J:1:MET:O	10:J:2:ASP:HB2	1.84	0.77
10:X:1:MET:O	10:X:2:ASP:HB2	1.84	0.75
11:K:9:GLN:NE2	11:K:148:LEU:O	2.20	0.75
4:D:99:ILE:HD11	4:D:104:LEU:HB2	1.70	0.73
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.71	0.73
4:R:99:ILE:HD11	4:R:104:LEU:HB2	1.70	0.72
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.70	0.71
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.72	0.70
11:Y:5:ALA:HB3	11:Y:100:MET:HE2	1.77	0.67
11:K:5:ALA:HB3	11:K:100:MET:HE2	1.75	0.67
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.80	0.64
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.01	0.61
3:C:51:LYS:O	3:C:52:LEU:HB2	2.01	0.61
11:K:100:MET:CE	11:K:127:PHE:HB2	2.32	0.59
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:12:PHE:H	6:T:19:GLN:HE22	1.51	0.58
11:K:5:ALA:HB3	11:K:100:MET:CE	2.34	0.57
11:Y:100:MET:CE	11:Y:127:PHE:HB2	2.32	0.57
7:U:23:PHE:O	7:U:26:THR:HB	2.04	0.57
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.69	0.57
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.70	0.56
7:G:23:PHE:O	7:G:26:THR:HB	2.05	0.56
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.86	0.56
14:N:152:VAL:HA	14:N:175:MET:HE1	1.87	0.56
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.40	0.56
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.89	0.55
8:H:52:THR:O	8:H:56:THR:HB	2.07	0.55
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.90	0.54
8:V:52:THR:O	8:V:56:THR:HB	2.07	0.54
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.73	0.54
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.91	0.53
4:R:88:ALA:HA	4:R:99:ILE:HG21	1.91	0.53
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.91	0.53
5:E:12:PHE:H	6:F:19:GLN:HE22	1.55	0.52
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.74	0.52
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.92	0.51
5:S:9:THR:HG21	5:S:119:THR:HA	1.92	0.51
5:E:9:THR:HG21	5:E:119:THR:HA	1.93	0.51
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.92	0.51
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.74	0.51
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.93	0.51
3:C:201:VAL:O	3:C:202:GLN:CB	2.59	0.51
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.93	0.51
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.92	0.51
11:K:6:PHE:HA	11:K:125:ASP:O	2.11	0.51
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.92	0.50
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.59	0.50
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.94	0.50
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.93	0.50
10:J:1:MET:O	10:J:2:ASP:CB	2.59	0.50
12:L:8:ASN:HA	12:L:30:ILE:O	2.13	0.49
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.93	0.49
3:C:201:VAL:HG13	3:C:202:GLN:N	2.28	0.49
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.94	0.49
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.12	0.49
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.28	0.48
8:H:50:ALA:HB3	9:I:126:ILE:HD12	1.95	0.48
11:Y:53:GLN:O	11:Y:57:THR:HG23	2.13	0.48
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.94	0.48
3:C:201:VAL:O	3:C:202:GLN:HB2	2.13	0.48
10:J:174:MET:HA	10:X:174:MET:HA	1.95	0.48
7:U:26:THR:HG21	7:U:131:ILE:HD12	1.97	0.47
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.80	0.47
11:K:53:GLN:O	11:K:57:THR:HG23	2.14	0.47
10:J:1:MET:HA	10:J:34:LYS:HE3	1.96	0.47
10:X:1:MET:O	10:X:2:ASP:CB	2.58	0.47
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.95	0.47
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.13	0.47
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.79	0.47
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.98	0.47
7:G:26:THR:HG21	7:G:131:ILE:HD12	1.96	0.46
10:X:1:MET:HA	10:X:34:LYS:HE3	1.96	0.46
4:R:158:ARG:HB3	5:S:57:SER:HB3	1.97	0.46
1:O:149:GLN:O	1:O:156:TYR:HA	2.16	0.46
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.51	0.46
7:G:187:GLU:HG2	7:G:192:LYS:HB2	1.97	0.46
13:M:127:LEU:HG	13:M:142:LEU:HD12	1.98	0.46
2:B:146:GLN:HG2	3:C:57:ILE:HG21	1.98	0.46
10:J:119:ILE:HG12	10:J:125:LYS:HG3	1.97	0.46
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.51	0.46
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.98	0.45
6:T:228:LYS:HB2	6:T:228:LYS:HE3	1.72	0.45
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.31	0.45
4:R:155:THR:HG23	5:S:59:GLN:HE22	1.82	0.45
10:X:119:ILE:HG12	10:X:125:LYS:HG3	1.97	0.45
7:U:187:GLU:HG2	7:U:192:LYS:HB2	1.97	0.45
1:A:149:GLN:O	1:A:156:TYR:HA	2.15	0.45
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	1.99	0.45
11:K:7:ARG:NH1	11:K:110:PRO:O	2.47	0.45
3:C:198:LEU:HA	3:C:201:VAL:HG12	1.99	0.45
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.98	0.45
11:K:4:LEU:C	11:K:4:LEU:CD2	2.85	0.45
4:R:9:PRO:HA	5:S:23:TYR:CD1	2.52	0.45
12:L:147:MET:N	12:L:148:PRO:HD2	2.31	0.45
5:S:68:HIS:HE1	5:S:102:LEU:O	2.00	0.45
5:S:131:LEU:HB2	5:S:146:PHE:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.98	0.45
2:P:180:LYS:O	2:P:183:MET:HB2	2.17	0.45
11:Y:5:ALA:HB3	11:Y:100:MET:CE	2.45	0.44
9:W:20:VAL:HG23	9:W:189:ILE:HB	1.99	0.44
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.53	0.44
1:A:236:ARG:NH2	19:A:301:HOH:O	2.49	0.44
10:J:1:MET:HA	10:J:34:LYS:CE	2.47	0.44
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	1.98	0.44
2:B:180:LYS:O	2:B:183:MET:HB2	2.17	0.44
5:E:68:HIS:HE1	5:E:102:LEU:O	2.00	0.44
10:X:1:MET:HA	10:X:34:LYS:CE	2.47	0.44
9:I:20:VAL:HG23	9:I:189:ILE:HB	1.99	0.44
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.53	0.44
8:H:84:LYS:HG3	8:H:85:GLN:N	2.33	0.44
11:K:37:ILE:HG23	11:K:60:GLY:HA2	1.99	0.44
3:C:9:PHE:H	4:D:15:GLN:HE22	1.65	0.44
2:B:14:PRO:HA	3:C:20:TYR:CD1	2.53	0.44
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.48	0.43
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.66	0.43
5:E:131:LEU:HB2	5:E:146:PHE:HB3	1.99	0.43
1:O:55:LEU:HB3	7:U:159:ALA:O	2.18	0.43
11:K:1:THR:HG22	11:K:2:THR:N	2.33	0.43
12:L:195:HIS:HD2	12:L:197:GLN:H	1.66	0.43
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.49	0.43
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.48	0.43
2:B:47:ALA:HB1	2:B:64:LYS:HD2	2.00	0.43
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.53	0.43
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.48	0.43
7:U:78:ILE:N	7:U:79:PRO:CD	2.82	0.43
2:P:47:ALA:HB1	2:P:64:LYS:HD2	2.00	0.43
8:V:84:LYS:HG3	8:V:85:GLN:N	2.33	0.43
1:O:12:PHE:H	2:P:20:GLN:HE22	1.67	0.43
3:Q:11:PRO:HA	4:R:18:TYR:CD1	2.54	0.43
1:O:119:GLN:O	1:O:122:THR:HB	2.19	0.42
7:G:195:GLU:HG3	7:G:235:ARG:HG3	2.00	0.42
4:R:138:GLY:HA2	4:R:214:ILE:HG12	2.01	0.42
7:U:195:GLU:HG3	7:U:235:ARG:HG3	2.00	0.42
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.42
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.54	0.42
10:X:19:LYS:HD3	10:X:180:ILE:HG13	2.01	0.42
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:138:GLY:HA2	4:D:214:ILE:HG12	2.00	0.42
11:Y:6:PHE:HA	11:Y:125:ASP:O	2.19	0.42
5:E:42:HIS:HB2	5:E:188:LEU:HD12	2.02	0.42
8:H:218:VAL:CG2	9:I:196:LYS:HB2	2.50	0.42
10:X:23:ARG:HG2	19:Y:420:HOH:O	2.20	0.42
11:K:209:ASN:O	9:W:37:ASN:ND2	2.52	0.42
1:A:119:GLN:O	1:A:122:THR:HB	2.20	0.42
10:J:19:LYS:HD3	10:J:180:ILE:HG13	2.00	0.42
1:A:176:GLU:HG2	2:B:55:LEU:HD13	2.02	0.42
5:S:42:HIS:HB2	5:S:188:LEU:HD12	2.02	0.41
11:K:20:ALA:HB2	11:K:31:VAL:HG21	2.01	0.41
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.55	0.41
13:M:27:LEU:HD21	13:M:34:LEU:HD22	2.01	0.41
11:K:8:PHE:N	11:K:8:PHE:CD1	2.88	0.41
13:M:165:ILE:HB	13:M:166:PRO:HD3	2.02	0.41
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.56	0.41
1:A:110:LEU:O	1:A:114:VAL:HG23	2.20	0.41
6:F:228:LYS:HB2	6:F:228:LYS:HE3	1.72	0.41
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.56	0.41
6:T:175:LEU:HD21	6:T:191:GLN:NE2	2.36	0.41
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.56	0.40
6:F:175:LEU:HD21	6:F:191:GLN:NE2	2.35	0.40
8:H:148:LYS:HE3	8:H:177:VAL:HG11	2.03	0.40
5:S:77:ALA:N	5:S:78:PRO:CD	2.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	248/250 (99%)	242 (98%)	5 (2%)	1 (0%)	39 69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	248/250 (99%)	242 (98%)	5 (2%)	1 (0%)	39	69
2	B	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	39	69
2	P	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	39	69
3	C	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	15	37
3	Q	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	15	37
4	D	231/260 (89%)	227 (98%)	4 (2%)	0	100	100
4	R	231/260 (89%)	227 (98%)	4 (2%)	0	100	100
5	E	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
5	S	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
6	F	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
6	T	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
7	G	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
7	U	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
8	H	220/232 (95%)	213 (97%)	7 (3%)	0	100	100
8	V	220/232 (95%)	213 (97%)	7 (3%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	34	63
10	X	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	34	63
11	K	210/212 (99%)	205 (98%)	5 (2%)	0	100	100
11	Y	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
12	L	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
12	Z	221/222 (100%)	217 (98%)	4 (2%)	0	100	100
13	M	231/246 (94%)	225 (97%)	6 (3%)	0	100	100
13	a	231/246 (94%)	225 (97%)	6 (3%)	0	100	100
14	N	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
14	b	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
15	c	2/5 (40%)	2 (100%)	0	0	100	100
15	d	2/5 (40%)	2 (100%)	0	0	100	100
15	e	2/5 (40%)	2 (100%)	0	0	100	100
15	f	2/5 (40%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	g	2/5 (40%)	2 (100%)	0	0	100	100
15	h	2/5 (40%)	2 (100%)	0	0	100	100
All	All	6289/6644 (95%)	6123 (97%)	154 (2%)	12 (0%)	52	80

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
10	J	2	ASP
2	P	51	VAL
3	Q	202	GLN
10	X	2	ASP
3	C	205	ALA
3	Q	205	ALA
1	A	3	ASP
1	O	3	ASP
3	C	183	PRO
3	Q	183	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%)	74	92
1	O	209/209 (100%)	206 (99%)	3 (1%)	74	92
2	B	203/216 (94%)	195 (96%)	8 (4%)	39	70
2	P	203/216 (94%)	195 (96%)	8 (4%)	39	70
3	C	212/226 (94%)	204 (96%)	8 (4%)	40	71
3	Q	212/226 (94%)	204 (96%)	8 (4%)	40	71
4	D	194/215 (90%)	184 (95%)	10 (5%)	29	58
4	R	194/215 (90%)	184 (95%)	10 (5%)	29	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	190/193 (98%)	178 (94%)	12 (6%)	22	48
5	S	190/193 (98%)	179 (94%)	11 (6%)	25	52
6	F	201/239 (84%)	189 (94%)	12 (6%)	24	50
6	T	201/239 (84%)	189 (94%)	12 (6%)	24	50
7	G	206/210 (98%)	199 (97%)	7 (3%)	44	75
7	U	206/210 (98%)	199 (97%)	7 (3%)	44	75
8	H	181/190 (95%)	174 (96%)	7 (4%)	39	70
8	V	181/190 (95%)	174 (96%)	7 (4%)	39	70
9	I	172/173 (99%)	166 (96%)	6 (4%)	43	74
9	W	172/173 (99%)	166 (96%)	6 (4%)	43	74
10	J	173/175 (99%)	167 (96%)	6 (4%)	43	74
10	X	173/175 (99%)	167 (96%)	6 (4%)	43	74
11	K	169/169 (100%)	162 (96%)	7 (4%)	37	69
11	Y	169/169 (100%)	164 (97%)	5 (3%)	48	79
12	L	185/185 (100%)	178 (96%)	7 (4%)	40	71
12	Z	186/185 (100%)	180 (97%)	6 (3%)	46	77
13	M	199/208 (96%)	191 (96%)	8 (4%)	38	69
13	a	199/208 (96%)	191 (96%)	8 (4%)	38	69
14	N	162/162 (100%)	156 (96%)	6 (4%)	41	72
14	b	162/162 (100%)	157 (97%)	5 (3%)	47	78
15	c	1/1 (100%)	1 (100%)	0	100	100
15	d	1/1 (100%)	1 (100%)	0	100	100
15	e	1/1 (100%)	1 (100%)	0	100	100
15	f	1/1 (100%)	1 (100%)	0	100	100
15	g	1/1 (100%)	1 (100%)	0	100	100
15	h	1/1 (100%)	1 (100%)	0	100	100
All	All	5319/5546 (96%)	5110 (96%)	209 (4%)	39	70

All (209) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	61	LEU

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Mol	Chain	Res	Type
1	A	157	PHE
2	B	50	LYS
2	B	52	THR
2	B	54	THR
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	114	LEU
2	B	191	LEU
3	C	4	ARG
3	C	38	ASN
3	C	61	LYS
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	203	THR
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	99	ILE
4	D	117	GLU
4	D	176	LEU
4	D	193	LEU
4	D	214	ILE
4	D	236	LYS
4	D	242	GLU
5	E	8	ASP
5	E	9	THR
5	E	10	VAL
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	55	LEU
5	E	71	LEU
5	E	184	ASN
5	E	188	LEU
5	E	207	VAL
5	E	231	LYS
6	F	14	ASP
6	F	59	LYS
6	F	117	GLN

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Mol	Chain	Res	Type
6	F	123	ASN
6	F	139	LYS
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN
6	F	206	LYS
6	F	214	TRP
6	F	221	ASN
6	F	228	LYS
7	G	83	ASN
7	G	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	30	ASN
8	H	34	LEU
8	H	43	CYS
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	196	ARG
9	I	20	VAL
9	I	37	ASN
9	I	171	LEU
9	I	182	TRP
9	I	191	LYS
9	I	192	ASP
10	J	23	ARG
10	J	35	THR
10	J	75	LEU
10	J	78	GLN
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	8	PHE
11	K	9	GLN
11	K	17	ASP
11	K	35	ILE
11	K	106	ARG
11	K	118	ASP

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Mol	Chain	Res	Type
12	L	1	GLN
12	L	23	LEU
12	L	49	ASN
12	L	106	TYR
12	L	136	CYS
12	L	150	LEU
12	L	167	LYS
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	161	ARG
13	M	187	ARG
13	M	212	LEU
13	M	223	LYS
14	N	9	LYS
14	N	22	THR
14	N	36	ARG
14	N	104	ASP
14	N	105	LYS
14	N	119	VAL
1	O	17	LYS
1	O	61	LEU
1	O	157	PHE
2	P	50	LYS
2	P	52	THR
2	P	54	THR
2	P	55	LEU
2	P	58	GLN
2	P	79	LEU
2	P	114	LEU
2	P	191	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	61	LYS
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	203	THR
4	R	20	LEU
4	R	40	LEU

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Mol	Chain	Res	Type
4	R	51	LEU
4	R	99	ILE
4	R	117	GLU
4	R	176	LEU
4	R	193	LEU
4	R	214	ILE
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	10	VAL
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU
5	S	55	LEU
5	S	71	LEU
5	S	184	ASN
5	S	188	LEU
5	S	207	VAL
5	S	231	LYS
6	T	14	ASP
6	T	59	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	214	TRP
6	T	221	ASN
6	T	228	LYS
7	U	83	ASN
7	U	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	30	ASN
8	V	34	LEU
8	V	43	CYS
8	V	56	THR

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Mol	Chain	Res	Type
8	V	68	LEU
8	V	127	LEU
8	V	196	ARG
9	W	20	VAL
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
9	W	191	LYS
9	W	192	ASP
10	X	23	ARG
10	X	35	THR
10	X	75	LEU
10	X	78	GLN
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	9	GLN
11	Y	35	ILE
11	Y	106	ARG
11	Y	118	ASP
12	Z	1	GLN
12	Z	23	LEU
12	Z	49	ASN
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
13	a	212	LEU
13	a	223	LYS
14	b	9	LYS
14	b	36	ARG
14	b	104	ASP
14	b	105	LYS
14	b	119	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN
3	C	38	ASN
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	146	GLN
4	D	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	120	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	191	GLN
6	F	240	GLN
7	G	6	HIS
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN
8	H	57	GLN
8	H	66	HIS
9	I	37	ASN
10	J	55	GLN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
11	K	190	ASN
12	L	3	ASN
12	L	49	ASN
12	L	70	ASN

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Mol	Chain	Res	Type
12	L	95	HIS
12	L	158	ASN
12	L	165	ASN
13	M	2	GLN
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	161	GLN
1	O	94	HIS
2	P	20	GLN
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	176	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	146	GLN
4	R	198	GLN
4	R	225	ASN
5	S	59	GLN
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	191	GLN
6	T	240	GLN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	167	GLN

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Mol	Chain	Res	Type
7	U	175	ASN
8	V	57	GLN
8	V	66	HIS
8	V	165	ASN
10	X	37	GLN
10	X	55	GLN
10	X	86	GLN
10	X	118	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	158	ASN
12	Z	165	ASN
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	179	ASN
13	a	194	ASN
13	a	213	GLN
14	b	161	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	GAU	c	4	8,15	5,8,8	0.78	0	4,9,9	1.98	1 (25%)
15	GAU	d	4	11,15	5,8,8	1.39	0	4,9,9	1.54	1 (25%)
15	GAU	e	4	11,15	5,8,8	0.73	0	4,9,9	1.79	1 (25%)
15	GAU	f	4	15,14	5,8,8	1.33	1 (20%)	4,9,9	2.14	2 (50%)
15	GAU	g	4	15,14	5,8,8	1.85	1 (20%)	4,9,9	2.32	2 (50%)
15	GAU	h	4	8,15	5,8,8	1.32	1 (20%)	4,9,9	1.89	2 (50%)

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	GAU	c	4	8,15	-	0/5/7/7	0/0/0/0
15	GAU	d	4	11,15	-	0/5/7/7	0/0/0/0
15	GAU	e	4	11,15	-	0/5/7/7	0/0/0/0
15	GAU	f	4	15,14	-	0/5/7/7	0/0/0/0
15	GAU	g	4	15,14	-	0/5/7/7	0/0/0/0
15	GAU	h	4	8,15	-	0/5/7/7	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	g	4	GAU	CB-CA	-3.27	1.48	1.53
15	h	4	GAU	OXT-C	-2.64	1.31	1.42
15	f	4	GAU	C-CA	2.08	1.55	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	c	4	GAU	CG-CB-CA	-3.42	105.27	113.80
15	g	4	GAU	CB-CA-N	-3.23	99.91	108.92
15	f	4	GAU	CG-CB-CA	-3.09	106.10	113.80
15	g	4	GAU	CG-CB-CA	-3.01	106.28	113.80
15	e	4	GAU	CG-CB-CA	-2.98	106.37	113.80
15	h	4	GAU	OXT-C-CA	-2.65	104.76	111.77
15	d	4	GAU	OXT-C-CA	-2.56	105.00	111.77
15	h	4	GAU	CB-CA-N	-2.48	102.01	108.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	f	4	GAU	CB-CA-N	-2.26	102.62	108.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 9 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
18	MES	H	302	-	12,12,12	2.14	1 (8%)	15,16,16	1.88	3 (20%)
18	MES	K	302	-	12,12,12	2.10	1 (8%)	15,16,16	1.66	3 (20%)
18	MES	V	302	-	12,12,12	2.19	1 (8%)	15,16,16	1.66	3 (20%)
18	MES	Y	302	-	12,12,12	2.14	1 (8%)	15,16,16	1.71	3 (20%)

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
18	MES	H	302	-	-	0/6/14/14	0/1/1/1
18	MES	K	302	-	-	0/6/14/14	0/1/1/1
18	MES	V	302	-	-	0/6/14/14	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	MES	Y	302	-	-	0/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	V	302	MES	C8-S	-7.29	1.66	1.77
18	H	302	MES	C8-S	-7.12	1.66	1.77
18	Y	302	MES	C8-S	-7.11	1.66	1.77
18	K	302	MES	C8-S	-6.98	1.67	1.77

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	Y	302	MES	O1S-S-C8	2.07	108.33	106.87
18	H	302	MES	O3S-S-C8	2.16	109.48	104.99
18	V	302	MES	O3S-S-C8	2.26	109.69	104.99
18	V	302	MES	O1S-S-C8	2.32	108.51	106.87
18	Y	302	MES	O3S-S-C8	2.40	109.97	104.99
18	K	302	MES	O3S-S-C8	2.69	110.58	104.99
18	K	302	MES	O1S-S-C8	3.14	109.09	106.87
18	H	302	MES	O1S-S-C8	3.25	109.16	106.87
18	K	302	MES	O2S-S-C8	3.71	109.49	106.87
18	Y	302	MES	O2S-S-C8	4.70	110.19	106.87
18	V	302	MES	O2S-S-C8	4.71	110.20	106.87
18	H	302	MES	O2S-S-C8	5.35	110.65	106.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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%)	-0.11	8 (3%)	51	51	32, 45, 81, 121	0
1	O	250/250 (100%)	0.02	13 (5%)	31	30	37, 53, 97, 126	0
2	B	244/258 (94%)	0.08	16 (6%)	22	20	33, 50, 100, 154	0
2	P	244/258 (94%)	0.15	16 (6%)	22	20	37, 54, 106, 155	0
3	C	240/254 (94%)	0.19	22 (9%)	11	9	32, 54, 117, 155	0
3	Q	240/254 (94%)	0.47	32 (13%)	4	3	43, 70, 151, 195	0
4	D	235/260 (90%)	-0.05	7 (2%)	54	54	38, 57, 89, 136	0
4	R	235/260 (90%)	0.10	8 (3%)	49	49	43, 61, 99, 145	0
5	E	231/234 (98%)	0.11	11 (4%)	34	33	40, 60, 95, 137	0
5	S	231/234 (98%)	0.33	12 (5%)	31	30	42, 69, 113, 152	0
6	F	243/288 (84%)	-0.06	9 (3%)	45	45	38, 56, 104, 138	0
6	T	243/288 (84%)	0.16	18 (7%)	17	15	38, 63, 114, 152	0
7	G	241/252 (95%)	-0.11	11 (4%)	36	35	32, 47, 88, 139	0
7	U	241/252 (95%)	-0.12	7 (2%)	55	55	35, 49, 84, 128	0
8	H	222/232 (95%)	-0.27	3 (1%)	78	77	30, 41, 69, 107	0
8	V	222/232 (95%)	-0.24	4 (1%)	71	72	31, 45, 69, 112	0
9	I	204/205 (99%)	-0.46	3 (1%)	76	76	28, 42, 68, 93	0
9	W	204/205 (99%)	-0.43	2 (0%)	84	85	29, 42, 72, 99	0
10	J	195/198 (98%)	-0.34	4 (2%)	67	68	29, 42, 68, 118	0
10	X	195/198 (98%)	-0.27	4 (2%)	67	68	33, 45, 69, 122	0
11	K	212/212 (100%)	-0.27	3 (1%)	78	77	33, 46, 73, 87	0
11	Y	212/212 (100%)	-0.17	4 (1%)	70	70	35, 48, 79, 105	0
12	L	222/222 (100%)	-0.36	2 (0%)	85	86	29, 45, 72, 98	0
12	Z	222/222 (100%)	-0.30	2 (0%)	85	86	31, 45, 74, 102	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.35	3 (1%)	79	79	27, 43, 63, 75	0
13	a	233/246 (94%)	-0.34	4 (1%)	73	74	30, 41, 63, 73	0
14	N	196/196 (100%)	-0.37	4 (2%)	68	69	28, 39, 65, 92	0
14	b	196/196 (100%)	-0.38	1 (0%)	91	93	30, 40, 68, 90	0
15	c	2/5 (40%)	-0.48	0	100	100	45, 45, 45, 48	0
15	d	2/5 (40%)	-0.51	0	100	100	63, 63, 63, 67	0
15	e	2/5 (40%)	-0.37	0	100	100	67, 67, 67, 73	0
15	f	2/5 (40%)	-0.60	0	100	100	48, 48, 48, 57	0
15	g	2/5 (40%)	-0.45	0	100	100	44, 44, 44, 51	0
15	h	2/5 (40%)	-0.73	0	100	100	47, 47, 47, 54	0
All	All	6348/6644 (95%)	-0.11	233 (3%)	45	45	27, 49, 95, 195	0

All (233) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	9.2
2	P	222	GLY	8.5
2	B	218	GLY	8.3
3	Q	50	LEU	7.8
5	S	202	ASP	7.7
2	B	219	ALA	7.4
2	P	219	ALA	6.9
2	P	51	VAL	5.9
4	R	241	ALA	5.5
3	C	205	ALA	5.4
3	Q	206	LYS	5.4
3	Q	49	THR	5.3
6	F	244	ASN	5.3
3	Q	239	GLN	5.2
7	U	2	GLY	5.1
3	C	206	LYS	5.1
2	B	51	VAL	5.0
9	W	1	SER	5.0
1	O	1	MET	5.0
3	C	240	GLU	5.0
6	T	243	ILE	4.9
10	X	1	MET	4.9
2	B	242	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
2	B	220	ASN	4.8
2	P	221	ASP	4.8
2	B	221	ASP	4.7
1	O	201	GLU	4.5
5	E	201	ARG	4.5
13	M	47	ASP	4.5
3	Q	236	GLN	4.5
7	G	240	ALA	4.4
14	N	105	LYS	4.3
3	Q	240	GLU	4.3
10	X	194	ASP	4.3
6	T	244	ASN	4.3
7	U	242	GLN	4.2
3	C	49	THR	4.2
1	O	249	ALA	4.2
3	Q	229	GLN	4.2
3	Q	203	THR	4.0
2	P	52	THR	3.9
5	S	180	LYS	3.9
8	V	221	CYS	3.9
4	D	1	ASP	3.8
8	H	222	ASP	3.8
5	S	233	ILE	3.8
3	C	238	LYS	3.8
6	T	178	HIS	3.7
7	U	241	GLU	3.7
2	B	59	ASP	3.7
10	J	194	ASP	3.7
6	T	201	GLU	3.6
2	B	217	LYS	3.6
5	E	202	ASP	3.6
2	P	220	ASN	3.6
3	Q	48	SER	3.6
3	C	180	LYS	3.6
3	C	203	THR	3.6
6	T	241	LYS	3.6
9	I	1	SER	3.6
3	Q	204	GLY	3.5
5	S	3	ASN	3.5
6	T	180	PRO	3.4
3	Q	205	ALA	3.4
6	T	181	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	O	248	GLU	3.4
2	P	59	ASP	3.4
8	V	222	ASP	3.4
3	Q	55	THR	3.4
3	Q	180	LYS	3.4
4	R	177	ASN	3.4
6	F	205	GLU	3.4
5	S	54	GLU	3.4
7	G	188	GLU	3.4
4	R	242	GLU	3.3
3	C	1	GLY	3.3
2	P	218	GLY	3.3
7	G	3	TYR	3.3
1	O	203	GLU	3.3
5	S	173	ARG	3.2
3	Q	220	VAL	3.2
6	F	178	HIS	3.2
2	P	203	SER	3.2
10	J	193	ASP	3.2
6	F	201	GLU	3.1
8	H	221	CYS	3.1
5	E	233	ILE	3.1
3	C	225	GLU	3.1
2	P	240	LYS	3.1
5	S	51	ASN	3.1
10	X	193	ASP	3.1
1	O	2	THR	3.1
3	Q	225	GLU	3.1
6	T	29	ASN	3.1
4	D	242	GLU	3.1
7	G	179	LYS	3.1
9	W	133	LYS	3.0
3	Q	202	GLN	3.0
5	S	207	VAL	3.0
6	T	2	THR	3.0
11	K	151	GLU	3.0
9	I	192	ASP	3.0
2	B	180	LYS	3.0
13	a	1	THR	3.0
13	M	1	THR	3.0
4	R	230	GLU	3.0
7	G	241	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
4	R	125	LEU	2.9
11	K	147	ASP	2.9
1	A	201	GLU	2.9
2	P	50	LYS	2.9
3	C	236	GLN	2.9
5	E	122	TYR	2.9
6	F	243	ILE	2.9
1	A	54	PRO	2.8
3	C	223	SER	2.8
3	C	239	GLN	2.8
12	Z	172	LEU	2.8
3	Q	171	GLU	2.8
1	O	250	LEU	2.8
6	F	229	GLY	2.8
1	O	169	VAL	2.7
3	Q	58	THR	2.7
5	E	4	ASN	2.7
11	Y	212	GLY	2.7
7	U	3	TYR	2.7
3	Q	201	VAL	2.7
4	R	141	ALA	2.7
10	J	1	MET	2.7
1	A	2	THR	2.7
3	C	181	GLU	2.7
6	T	230	ASP	2.7
6	T	215	CYS	2.7
11	Y	106	ARG	2.7
7	U	222	ASP	2.6
6	F	2	THR	2.6
4	D	241	ALA	2.6
2	B	182	ASP	2.6
12	Z	210	ASP	2.6
1	O	52	SER	2.6
6	T	229	GLY	2.6
1	O	141	GLU	2.6
6	T	207	ASP	2.6
5	E	176	ASP	2.6
1	A	51	SER	2.6
14	N	195	GLN	2.6
3	C	59	PRO	2.6
3	Q	223	SER	2.5
1	O	231	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
6	T	202	ASP	2.5
7	G	208	GLU	2.5
1	A	229	THR	2.5
4	D	238	LYS	2.5
5	E	52	ALA	2.5
11	Y	202	GLU	2.5
2	B	232	GLN	2.5
3	Q	172	PHE	2.5
4	R	54	ASP	2.5
6	T	204	LYS	2.4
2	P	182	ASP	2.4
7	G	2	GLY	2.4
11	K	212	GLY	2.4
6	T	166	GLN	2.4
3	C	187	GLU	2.4
5	E	3	ASN	2.4
3	Q	221	ALA	2.4
3	Q	234	ILE	2.4
12	L	165	ASN	2.4
3	Q	51	LYS	2.4
6	T	53	LYS	2.4
3	Q	181	GLU	2.4
5	E	218	ASP	2.4
13	M	82	ASP	2.4
5	S	29	LYS	2.4
3	Q	187	GLU	2.4
4	D	169	GLU	2.4
3	C	50	LEU	2.3
3	Q	141	ASP	2.3
7	G	53	LYS	2.3
2	P	244	THR	2.3
7	G	180	SER	2.3
1	A	249	ALA	2.3
2	B	239	VAL	2.3
6	F	204	LYS	2.3
12	L	167	LYS	2.3
14	b	105	LYS	2.3
3	C	27	ARG	2.3
5	E	123	GLY	2.3
2	P	53	SER	2.3
1	O	61	LEU	2.3
3	C	60	SER	2.2

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Mol	Chain	Res	Type	RSRZ
3	Q	235	GLU	2.2
3	Q	237	GLU	2.2
8	V	217	ILE	2.2
6	F	166	GLN	2.2
3	Q	238	LYS	2.2
3	Q	231	VAL	2.2
2	B	52	THR	2.2
3	C	175	LYS	2.2
2	B	61	SER	2.2
3	Q	27	ARG	2.2
5	E	194	GLU	2.2
5	S	225	ASP	2.2
13	a	204	THR	2.2
7	G	68	ARG	2.2
4	R	217	GLN	2.2
9	I	133	LYS	2.2
7	G	181	LYS	2.1
5	S	165	GLN	2.1
13	a	73	GLU	2.1
7	U	203	ASP	2.1
14	N	181	ALA	2.1
3	C	232	THR	2.1
4	D	2	ARG	2.1
8	H	198	GLU	2.1
1	O	62	SER	2.1
2	P	225	TYR	2.1
7	U	181	LYS	2.1
8	V	145	ASP	2.1
1	A	248	GLU	2.1
2	B	54	THR	2.1
10	X	95	ARG	2.1
2	P	62	THR	2.1
10	J	95	ARG	2.1
13	a	47	ASP	2.1
6	T	217	LEU	2.1
4	D	201	GLU	2.1
2	B	50	LYS	2.0
3	C	235	GLU	2.0
3	C	48	SER	2.0
5	S	210	LEU	2.0
11	Y	39	PRO	2.0
14	N	9	LYS	2.0

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

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	GAU	f	4	9/9	0.96	0.14	-	49,54,55,57	0
15	GAU	d	4	9/9	0.94	0.15	-	53,63,70,70	0
15	GAU	g	4	9/9	0.93	0.16	-	46,49,51,51	0
15	GAU	e	4	9/9	0.88	0.20	-	66,71,76,78	0
15	GAU	c	4	9/9	0.95	0.17	-	50,53,60,60	0
15	GAU	h	4	9/9	0.95	0.13	-	47,54,63,64	0

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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
18	MES	V	302	12/12	0.88	0.30	8.02	72,109,123,125	0
18	MES	H	302	12/12	0.89	0.33	7.55	62,98,113,113	0
18	MES	K	302	12/12	0.91	0.29	5.93	66,83,84,85	0
18	MES	Y	302	12/12	0.90	0.29	4.84	71,81,85,86	0
16	MG	Y	301	1/1	0.96	0.17	0.79	56,56,56,56	0
16	MG	G	301	1/1	0.97	0.09	-0.95	42,42,42,42	0
16	MG	K	301	1/1	0.94	0.10	-1.25	51,51,51,51	0
16	MG	N	201	1/1	0.98	0.08	-1.59	42,42,42,42	0
16	MG	I	301	1/1	0.99	0.09	-1.91	54,54,54,54	0
16	MG	V	301	1/1	0.98	0.05	-4.62	42,42,42,42	0
17	CL	U	301	1/1	0.95	0.12	-	33,33,33,33	0
17	CL	G	302	1/1	0.99	0.04	-	39,39,39,39	0
16	MG	H	301	1/1	0.43	0.24	-	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.