



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:29 PM UTC

PDB ID : 4FZG / pdb_00004fzg
Title : 20S yeast proteasome in complex with glidobactin
Authors : Stein, M.; Beck, P.; Kaiser, M.; Dudler, R.; Becker, C.F.W.; Groll, M.
Deposited on : 2012-07-06
Resolution : 3.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

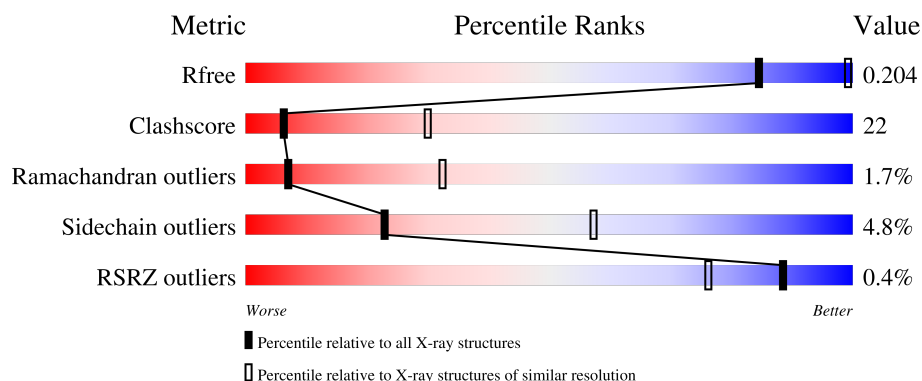
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



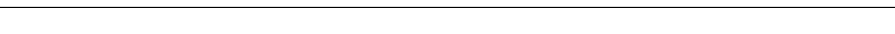
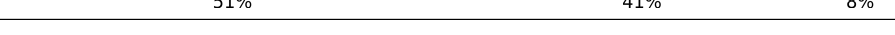
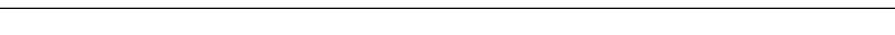
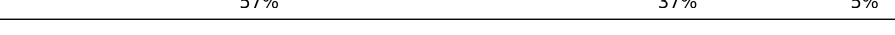
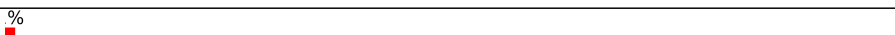
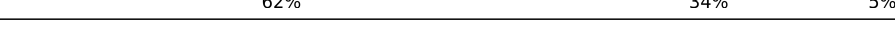
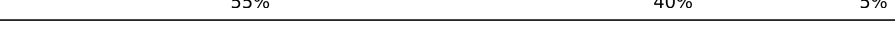
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	62% 34% .
1	O	250	62% 34% .
2	B	244	2% 51% 43% 5%
2	P	244	52% 43% 5%
3	C	241	% 54% 41% .

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Mol	Chain	Length	Quality of chain
3	Q	241	
4	D	242	
4	R	242	
5	E	233	
5	S	233	
6	F	244	
6	T	244	
7	G	243	
7	U	243	
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	M	233	
13	a	233	
14	N	196	
14	b	196	
15	c	4	
15	d	4	

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Mol	Chain	Length	Quality of chain
15	e	4	 25% 75%
15	f	4	 50% 50%

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 50986 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Proteasome component Y7.

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

- Molecule 2 is a protein called Proteasome component Y13.

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

- Molecule 3 is a protein called Proteasome component PRE6.

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

- Molecule 4 is a protein called Proteasome component PUP2.

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

- Molecule 5 is a protein called Proteasome component PRE5.

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

- Molecule 6 is a protein called Proteasome component C1.

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

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

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

- Molecule 8 is a protein called Proteasome component PUP1.

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

- Molecule 9 is a protein called Proteasome component PUP3.

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

- Molecule 10 is a protein called Proteasome component C11.

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

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

- Molecule 11 is a protein called Proteasome component PRE2.

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

- Molecule 12 is a protein called Proteasome component C5.

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

- Molecule 13 is a protein called Proteasome component PRE4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	a	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	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is a protein called Glidobactin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	c	4	Total	C	N	O	0	0	0
			37	27	4	6			
15	d	4	Total	C	N	O	0	0	0
			37	27	4	6			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	e	4	Total	C	N	O	0	0	0
			37	27	4	6			
15	f	4	Total	C	N	O	0	0	0
			37	27	4	6			

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	56	Total	O	0	0
			56	56		
16	B	35	Total	O	0	0
			35	35		
16	C	41	Total	O	0	0
			41	41		
16	D	39	Total	O	0	0
			39	39		
16	E	25	Total	O	0	0
			25	25		
16	F	45	Total	O	0	0
			45	45		
16	G	59	Total	O	0	0
			59	59		
16	H	52	Total	O	0	0
			52	52		
16	I	61	Total	O	0	0
			61	61		
16	J	55	Total	O	0	0
			55	55		
16	K	41	Total	O	0	0
			41	41		
16	L	57	Total	O	0	0
			57	57		
16	M	63	Total	O	0	0
			63	63		
16	N	61	Total	O	0	0
			61	61		
16	O	34	Total	O	0	0
			34	34		
16	P	27	Total	O	0	0
			27	27		
16	Q	29	Total	O	0	0
			29	29		

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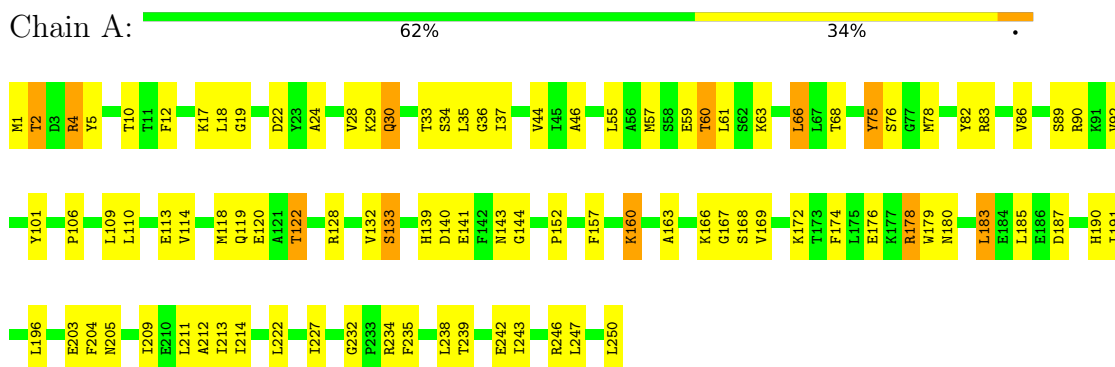
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	R	31	Total 31	O 31	0	0
16	S	21	Total 21	O 21	0	0
16	T	36	Total 36	O 36	0	0
16	U	63	Total 63	O 63	0	0
16	V	46	Total 46	O 46	0	0
16	W	47	Total 47	O 47	0	0
16	X	47	Total 47	O 47	0	0
16	Y	44	Total 44	O 44	0	0
16	Z	49	Total 49	O 49	0	0
16	a	72	Total 72	O 72	0	0
16	b	54	Total 54	O 54	0	0

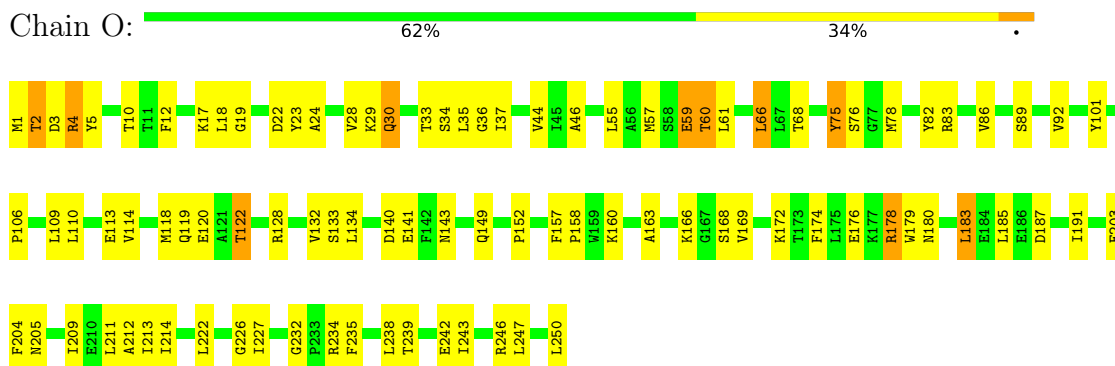
3 Residue-property plots [i](#)

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

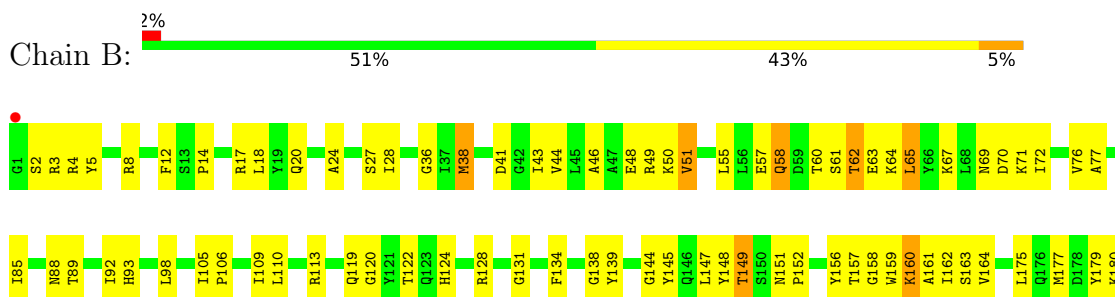
• Molecule 1: Proteasome component Y7

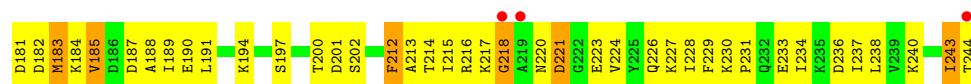


• Molecule 1: Proteasome component Y7



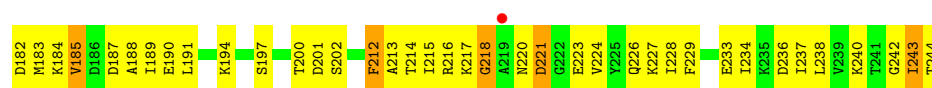
• Molecule 2: Proteasome component Y13





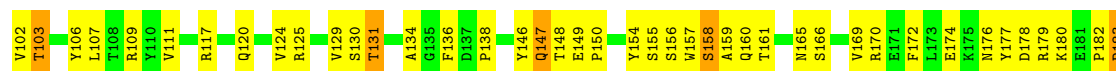
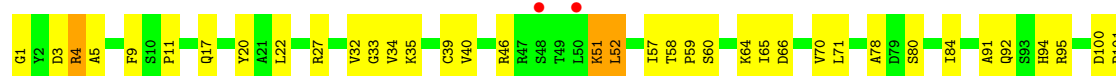
• Molecule 2: Proteasome component Y13

Chain P: 52% 43% 5%



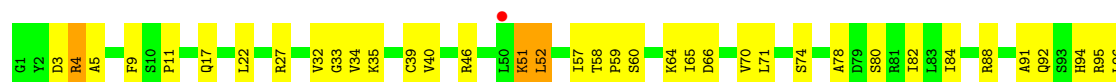
• Molecule 3: Proteasome component PRE6

Chain C: 54% 41% 5%



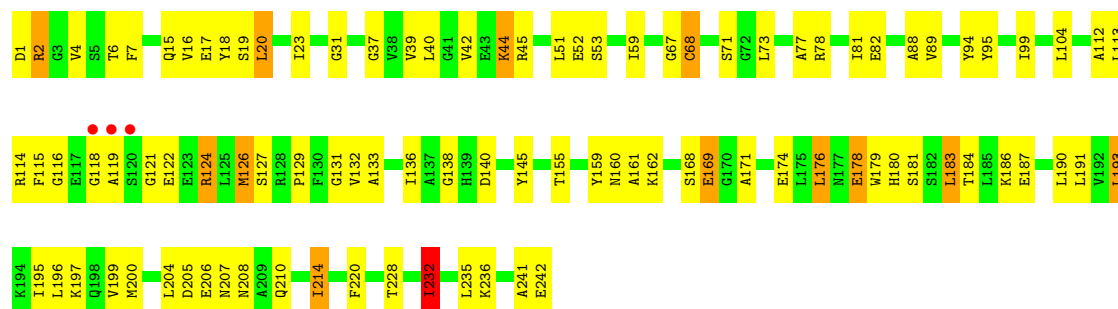
• Molecule 3: Proteasome component PRE6

Chain Q: 53% 43% 5%

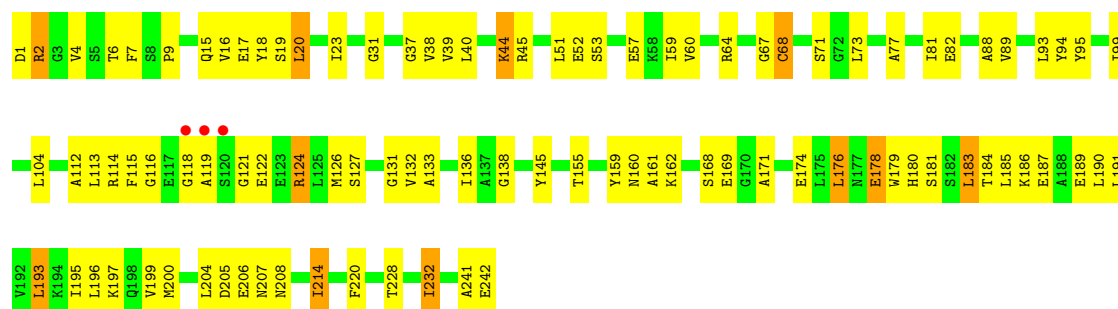


• Molecule 4: Proteasome component PUP2

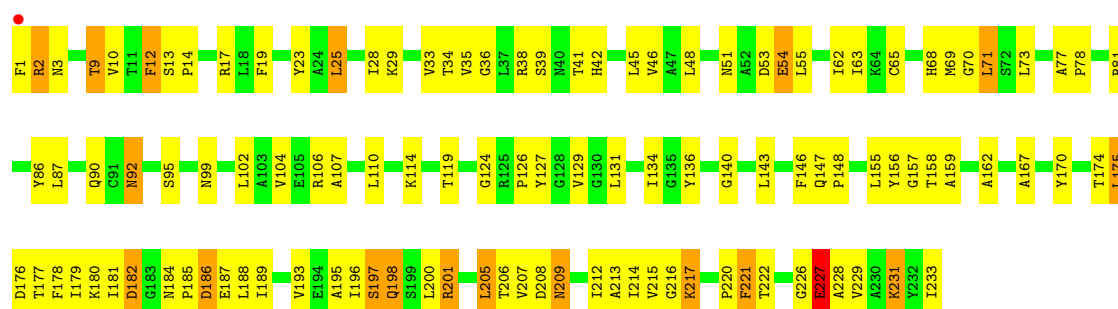
Chain D: 60% 35% 5%



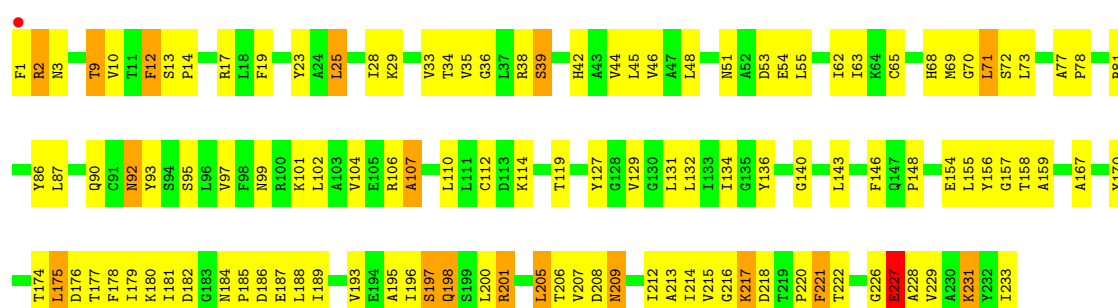
• Molecule 4: Proteasome component PUP2



• Molecule 5: Proteasome component PRE5

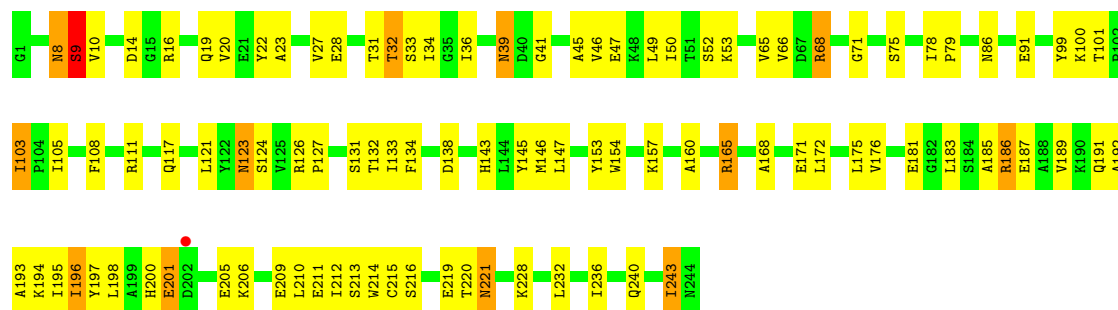


• Molecule 5: Proteasome component PRE5



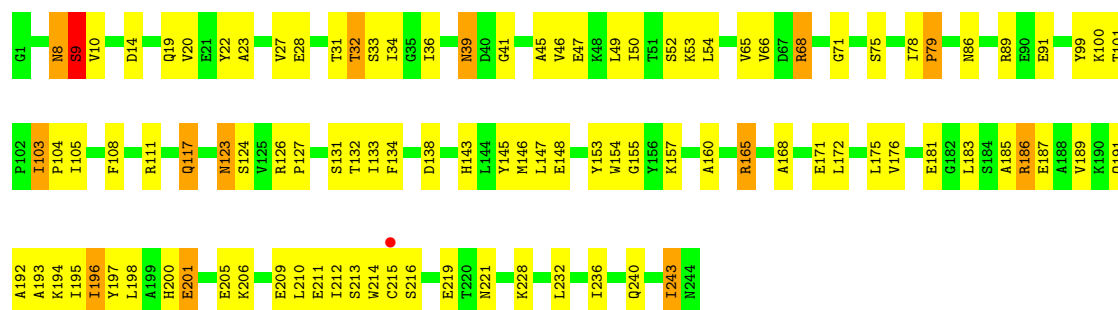
- Molecule 6: Proteasome component C1

Chain F: 



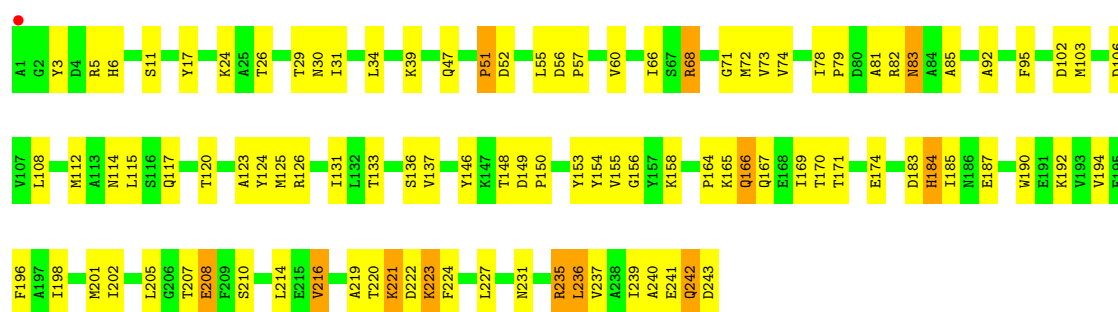
- Molecule 6: Proteasome component C1

Chain T: 



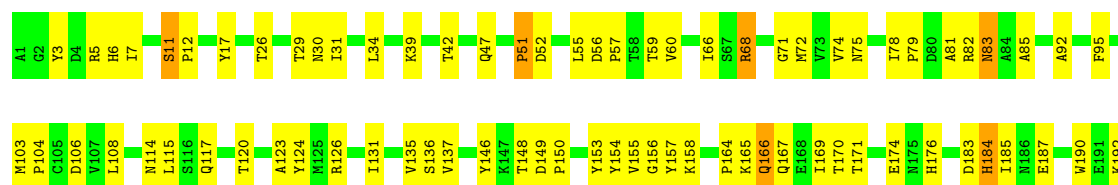
- Molecule 7: Proteasome component C7-alpha

Chain G: 



- Molecule 7: Proteasome component C7-alpha

Chain U: 





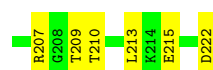
• Molecule 8: Proteasome component PUP1

Chain H: 66% 30% 5%



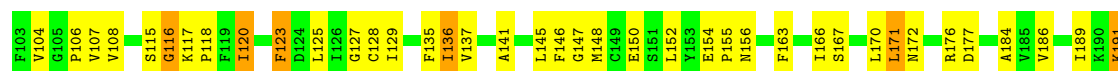
• Molecule 8: Proteasome component PUP1

Chain V: 64% 32% 4%



• Molecule 9: Proteasome component PUP3

Chain I: 61% 35% 4%



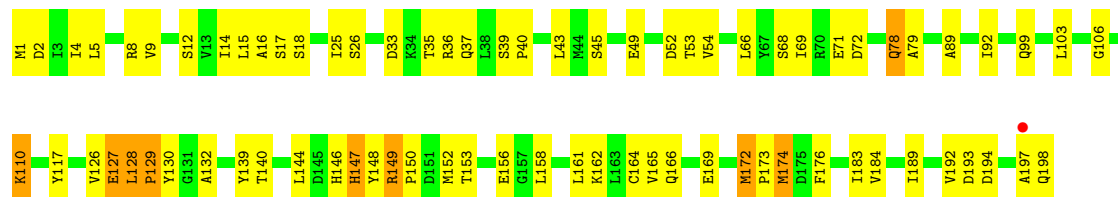
• Molecule 9: Proteasome component PUP3

Chain W: 62% 33% 5%

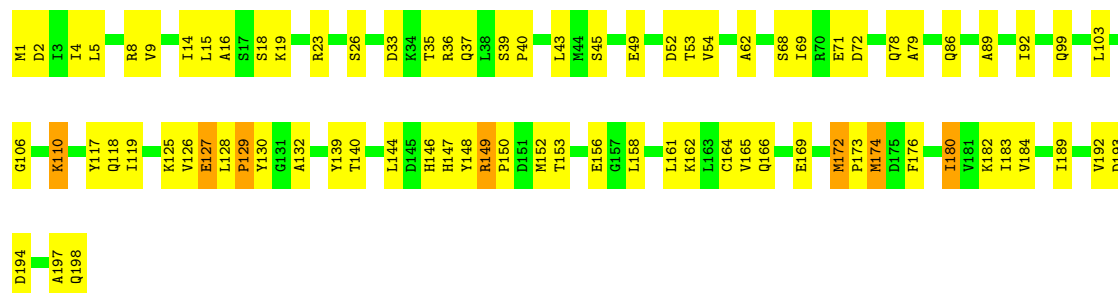




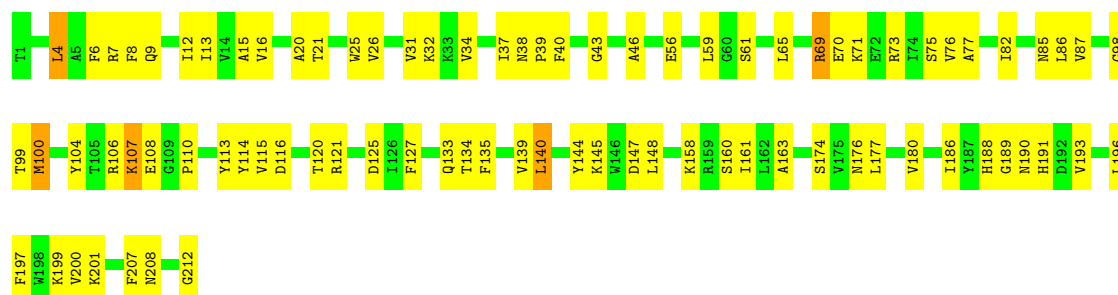
- Molecule 10: Proteasome component C11



- Molecule 10: Proteasome component C11



- Molecule 11: Proteasome component PRE2



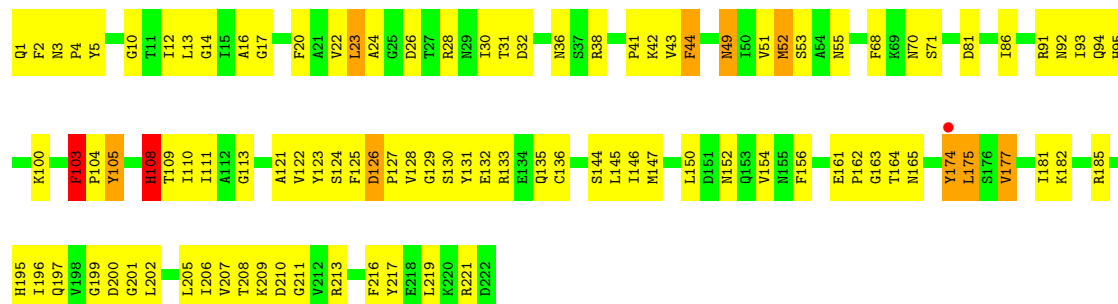
- Molecule 11: Proteasome component PRE2





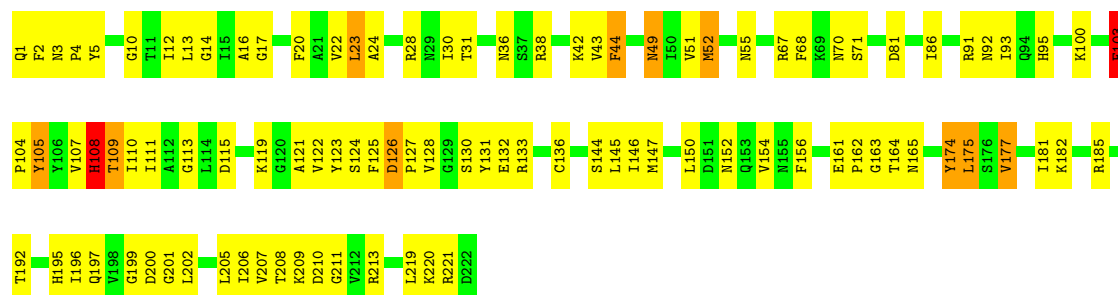
• Molecule 12: Proteasome component C5

Chain L: 54% 41% . .



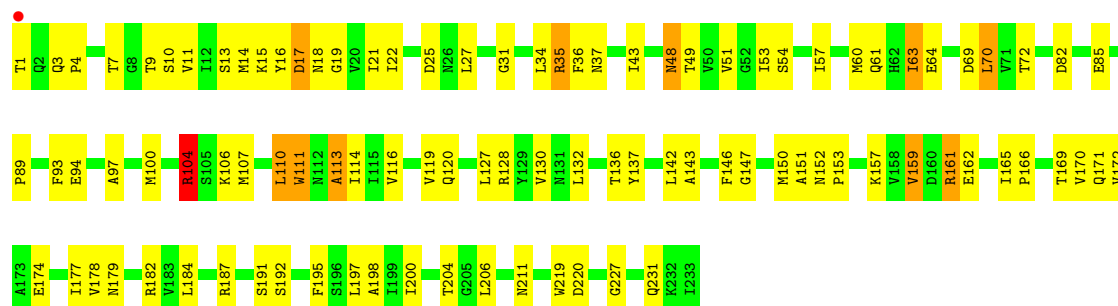
• Molecule 12: Proteasome component C5

Chain Z: 55% 40% 5% .



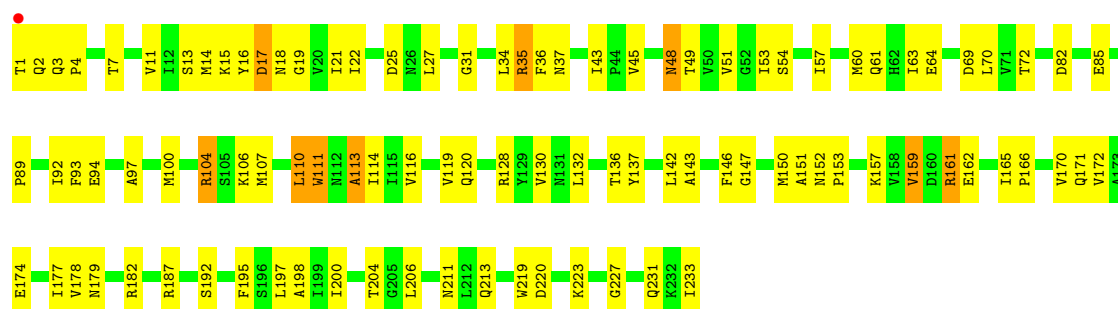
• Molecule 13: Proteasome component PRE4

Chain M: 58% 37% .



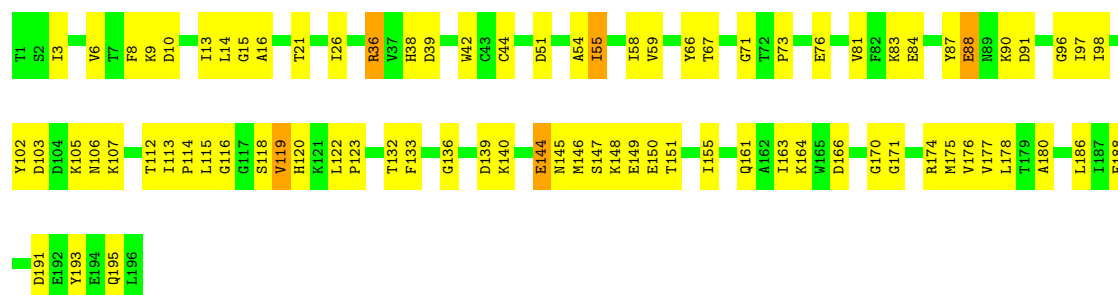
• Molecule 13: Proteasome component PRE4

Chain a: 58% 38% .



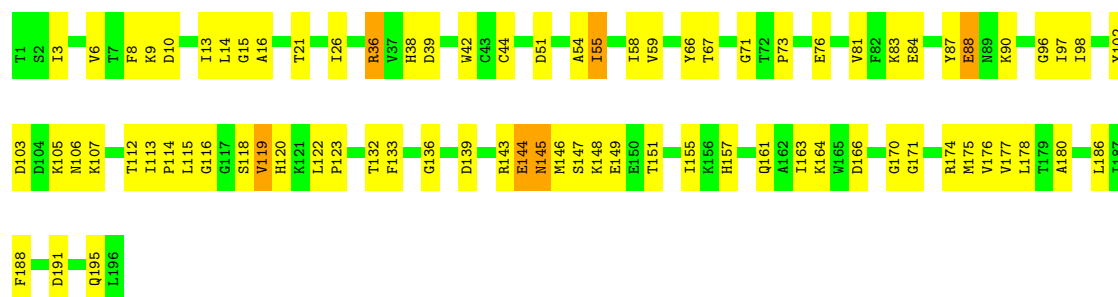
• Molecule 14: Proteasome component PRE3

Chain N: 58% 39%



• Molecule 14: Proteasome component PRE3

Chain b: 59% 38%



• Molecule 15: Glidobactin

Chain c: 100%



• Molecule 15: Glidobactin

Chain d: 50% 50%



• Molecule 15: Glidobactin

Chain e:  25% 75%

KH91	T2	K3	OM64
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● Molecule 15: Glidobactin

Chain f:  50% 50%

KH91	T2	K3	OM64
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	134.77Å 300.35Å 144.49Å 90.00° 112.67° 90.00°	Depositor
Resolution (Å)	15.00 – 3.00 15.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (15.00-3.00) 98.8 (15.00-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.43 (at 2.99Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.197 , 0.226 0.204 , 0.204	Depositor DCC
R_{free} test set	10479 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	66.6	Xtriage
Anisotropy	0.875	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 63.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	50986	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.00% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: LYO, OW6, MH9

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	0.46	0/1952	0.95	5/2642 (0.2%)
1	O	0.44	0/1952	0.95	4/2642 (0.2%)
2	B	0.46	0/1935	0.92	3/2618 (0.1%)
2	P	0.46	0/1935	0.92	3/2618 (0.1%)
3	C	0.44	0/1920	0.91	5/2598 (0.2%)
3	Q	0.42	0/1920	0.91	5/2598 (0.2%)
4	D	0.43	0/1887	0.93	8/2541 (0.3%)
4	R	0.43	0/1887	0.94	7/2541 (0.3%)
5	E	0.42	0/1823	0.89	2/2463 (0.1%)
5	S	0.42	0/1823	0.91	4/2463 (0.2%)
6	F	0.46	0/1937	0.95	6/2614 (0.2%)
6	T	0.45	0/1937	0.96	6/2614 (0.2%)
7	G	0.46	0/1959	0.96	7/2652 (0.3%)
7	U	0.45	0/1959	0.95	7/2652 (0.3%)
8	H	0.48	0/1716	0.94	5/2326 (0.2%)
8	V	0.47	0/1716	0.93	5/2326 (0.2%)
9	I	0.46	0/1611	0.99	8/2174 (0.4%)
9	W	0.47	0/1611	1.00	9/2174 (0.4%)
10	J	0.50	0/1613	1.00	9/2173 (0.4%)
10	X	0.48	0/1613	1.00	7/2173 (0.3%)
11	K	0.47	0/1681	0.92	1/2274 (0.0%)
11	Y	0.47	0/1681	0.92	1/2274 (0.0%)
12	L	0.47	0/1795	1.02	11/2420 (0.5%)
12	Z	0.46	0/1795	1.01	10/2420 (0.4%)
13	M	0.48	0/1855	0.98	13/2514 (0.5%)
13	a	0.48	0/1855	0.98	10/2514 (0.4%)
14	N	0.50	0/1541	0.96	3/2087 (0.1%)
14	b	0.49	0/1541	0.95	3/2087 (0.1%)
15	c	1.05	0/6	0.75	0/7
15	d	1.02	0/6	1.05	0/7
15	e	1.09	0/6	0.74	0/7
15	f	0.75	0/6	1.05	0/7

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.46	0/50474	0.95	167/68220 (0.2%)

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
12	L	0	1
12	Z	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 167 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Y	189	GLY	N-CA-C	9.69	125.24	112.65
11	K	189	GLY	N-CA-C	9.45	124.93	112.65
13	a	35	ARG	N-CA-C	9.26	122.22	111.11
13	M	35	ARG	N-CA-C	9.22	122.18	111.11
10	J	172	MET	CA-C-N	8.98	129.56	119.32

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	L	174	TYR	Sidechain
12	Z	174	TYR	Sidechain

5.2 Too-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 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	86	0
1	O	1915	0	1929	85	0
2	B	1905	0	1904	114	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	1905	0	1904	115	0
3	C	1891	0	1903	99	0
3	Q	1891	0	1903	98	0
4	D	1862	0	1839	71	0
4	R	1862	0	1839	74	0
5	E	1795	0	1800	128	0
5	S	1795	0	1800	140	0
6	F	1897	0	1889	78	0
6	T	1897	0	1889	85	0
7	G	1921	0	1913	90	0
7	U	1921	0	1913	99	0
8	H	1685	0	1687	62	0
8	V	1685	0	1687	63	0
9	I	1581	0	1574	74	0
9	W	1581	0	1574	77	0
10	J	1585	0	1590	71	0
10	X	1585	0	1590	79	0
11	K	1644	0	1594	76	0
11	Y	1644	0	1594	74	0
12	L	1757	0	1711	89	0
12	Z	1757	0	1711	90	0
13	M	1824	0	1832	83	0
13	a	1824	0	1832	85	0
14	N	1512	0	1481	68	0
14	b	1512	0	1481	64	0
15	c	37	0	35	4	0
15	d	37	0	35	1	0
15	e	37	0	35	4	0
15	f	37	0	35	1	0
16	A	56	0	0	2	0
16	B	35	0	0	1	0
16	C	41	0	0	5	0
16	D	39	0	0	3	0
16	E	25	0	0	3	0
16	F	45	0	0	4	0
16	G	59	0	0	7	0
16	H	52	0	0	5	0
16	I	61	0	0	4	0
16	J	55	0	0	3	0
16	K	41	0	0	4	0
16	L	57	0	0	3	0
16	M	63	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	N	61	0	0	5	0
16	O	34	0	0	0	0
16	P	27	0	0	6	0
16	Q	29	0	0	8	0
16	R	31	0	0	4	0
16	S	21	0	0	3	0
16	T	36	0	0	7	0
16	U	63	0	0	6	0
16	V	46	0	0	3	0
16	W	47	0	0	8	0
16	X	47	0	0	4	0
16	Y	44	0	0	4	0
16	Z	49	0	0	6	0
16	a	72	0	0	8	0
16	b	54	0	0	2	0
All	All	50986	0	49432	2205	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 22.

The worst 5 of 2205 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)
1:A:176:GLU:HG2	2:B:55:LEU:HD21	1.30	1.10
2:B:43:ILE:HD11	2:B:145:TYR:HB3	1.36	1.06
2:P:43:ILE:HD11	2:P:145:TYR:HB3	1.37	1.04
1:A:128:ARG:HH21	7:G:120:THR:HG22	1.25	1.01
10:J:174:MET:HE3	10:X:174:MET:HE3	1.39	1.01

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%)	226 (91%)	18 (7%)	4 (2%)	7	34
1	O	248/250 (99%)	224 (90%)	20 (8%)	4 (2%)	7	34
2	B	242/244 (99%)	213 (88%)	21 (9%)	8 (3%)	3	17
2	P	242/244 (99%)	212 (88%)	23 (10%)	7 (3%)	3	20
3	C	239/241 (99%)	214 (90%)	20 (8%)	5 (2%)	5	27
3	Q	239/241 (99%)	215 (90%)	19 (8%)	5 (2%)	5	27
4	D	240/242 (99%)	212 (88%)	19 (8%)	9 (4%)	2	15
4	R	240/242 (99%)	212 (88%)	19 (8%)	9 (4%)	2	15
5	E	231/233 (99%)	202 (87%)	21 (9%)	8 (4%)	3	16
5	S	231/233 (99%)	202 (87%)	22 (10%)	7 (3%)	3	19
6	F	242/244 (99%)	224 (93%)	16 (7%)	2 (1%)	16	50
6	T	242/244 (99%)	223 (92%)	17 (7%)	2 (1%)	16	50
7	G	241/243 (99%)	219 (91%)	19 (8%)	3 (1%)	10	40
7	U	241/243 (99%)	218 (90%)	20 (8%)	3 (1%)	10	40
8	H	220/222 (99%)	197 (90%)	20 (9%)	3 (1%)	9	36
8	V	220/222 (99%)	195 (89%)	22 (10%)	3 (1%)	9	36
9	I	202/204 (99%)	185 (92%)	14 (7%)	3 (2%)	8	35
9	W	202/204 (99%)	185 (92%)	15 (7%)	2 (1%)	12	45
10	J	196/198 (99%)	183 (93%)	10 (5%)	3 (2%)	8	35
10	X	196/198 (99%)	182 (93%)	11 (6%)	3 (2%)	8	35
11	K	210/212 (99%)	199 (95%)	11 (5%)	0	100	100
11	Y	210/212 (99%)	199 (95%)	11 (5%)	0	100	100
12	L	220/222 (99%)	199 (90%)	16 (7%)	5 (2%)	5	25
12	Z	220/222 (99%)	202 (92%)	14 (6%)	4 (2%)	6	31
13	M	231/233 (99%)	206 (89%)	24 (10%)	1 (0%)	30	65
13	a	231/233 (99%)	206 (89%)	24 (10%)	1 (0%)	30	65
14	N	194/196 (99%)	183 (94%)	10 (5%)	1 (0%)	24	60
14	b	194/196 (99%)	183 (94%)	9 (5%)	2 (1%)	12	45
15	c	1/4 (25%)	1 (100%)	0	0	100	100
15	d	1/4 (25%)	1 (100%)	0	0	100	100
15	e	1/4 (25%)	1 (100%)	0	0	100	100
15	f	1/4 (25%)	1 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	6316/6384 (99%)	5724 (91%)	485 (8%)	107 (2%)	7	32

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
2	B	62	THR
2	B	221	ASP
3	C	52	LEU
4	D	122	GLU

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%)	200 (96%)	9 (4%)	26	60
1	O	209/209 (100%)	200 (96%)	9 (4%)	26	60
2	B	203/203 (100%)	195 (96%)	8 (4%)	28	62
2	P	203/203 (100%)	195 (96%)	8 (4%)	28	62
3	C	213/213 (100%)	208 (98%)	5 (2%)	44	74
3	Q	213/213 (100%)	208 (98%)	5 (2%)	44	74
4	D	198/198 (100%)	187 (94%)	11 (6%)	19	52
4	R	198/198 (100%)	188 (95%)	10 (5%)	21	55
5	E	192/192 (100%)	176 (92%)	16 (8%)	10	37
5	S	192/192 (100%)	176 (92%)	16 (8%)	10	37
6	F	201/201 (100%)	188 (94%)	13 (6%)	15	47
6	T	201/201 (100%)	187 (93%)	14 (7%)	14	44
7	G	207/207 (100%)	198 (96%)	9 (4%)	26	60
7	U	207/207 (100%)	198 (96%)	9 (4%)	26	60
8	H	181/181 (100%)	172 (95%)	9 (5%)	22	56
8	V	181/181 (100%)	172 (95%)	9 (5%)	22	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	172/172 (100%)	167 (97%)	5 (3%)	37	70
9	W	172/172 (100%)	166 (96%)	6 (4%)	32	65
10	J	175/175 (100%)	169 (97%)	6 (3%)	32	66
10	X	175/175 (100%)	170 (97%)	5 (3%)	37	70
11	K	169/169 (100%)	161 (95%)	8 (5%)	23	58
11	Y	169/169 (100%)	161 (95%)	8 (5%)	23	58
12	L	185/185 (100%)	176 (95%)	9 (5%)	22	56
12	Z	185/185 (100%)	176 (95%)	9 (5%)	22	56
13	M	199/199 (100%)	187 (94%)	12 (6%)	17	50
13	a	199/199 (100%)	187 (94%)	12 (6%)	17	50
14	N	162/162 (100%)	155 (96%)	7 (4%)	26	60
14	b	162/162 (100%)	155 (96%)	7 (4%)	26	60
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
All	All	5336/5336 (100%)	5082 (95%)	254 (5%)	23	57

5 of 254 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	159	VAL
11	Y	87	VAL
2	P	212	PHE
11	Y	9	GLN
13	a	48	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 217 such sidechains are listed below:

Mol	Chain	Res	Type
2	P	93	HIS
5	S	59	GLN
12	Z	165	ASN
2	P	155	ASN
3	Q	165	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	LYO	f	3	15	7,9,10	1.03	0	7,10,12	1.26	1 (14%)
15	OW6	e	4	15,8	5,6,7	1.17	0	5,6,8	0.84	0
15	OW6	f	4	15,11	5,6,7	1.19	0	5,6,8	0.52	0
15	OW6	d	4	15,11	5,6,7	1.17	0	5,6,8	0.55	0
15	LYO	d	3	15	7,9,10	0.95	0	7,10,12	1.35	1 (14%)
15	LYO	e	3	15	7,9,10	1.01	0	7,10,12	1.18	1 (14%)
15	LYO	c	3	15	7,9,10	1.06	0	7,10,12	1.18	1 (14%)
15	OW6	c	4	15,8	5,6,7	1.57	1 (20%)	5,6,8	0.79	0

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	LYO	f	3	15	-	3/8/9/11	-
15	OW6	e	4	15,8	-	2/4/4/5	-
15	OW6	f	4	15,11	-	1/4/4/5	-
15	OW6	d	4	15,11	-	1/4/4/5	-
15	LYO	d	3	15	-	3/8/9/11	-
15	LYO	e	3	15	-	4/8/9/11	-
15	LYO	c	3	15	-	4/8/9/11	-
15	OW6	c	4	15,8	-	2/4/4/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	c	4	0W6	C17-CA	3.00	1.57	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	d	3	LYO	CB-CA-C	-3.32	105.88	110.99
15	f	3	LYO	CB-CA-C	-3.08	106.25	110.99
15	e	3	LYO	CB-CA-C	-2.92	106.50	110.99
15	c	3	LYO	CB-CA-C	-2.79	106.70	110.99

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	c	3	LYO	N-CA-CB-CG
15	c	3	LYO	C-CA-CB-CG
15	c	3	LYO	CG-CD-CE-NZ
15	d	3	LYO	N-CA-CB-CG
15	d	3	LYO	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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%)	-0.45	0 100 100	61, 83, 116, 141	0
1	O	250/250 (100%)	-0.51	0 100 100	61, 83, 117, 141	0
2	B	244/244 (100%)	-0.30	4 (1%) 70 47	61, 83, 131, 151	0
2	P	244/244 (100%)	-0.35	1 (0%) 88 76	61, 83, 131, 151	0
3	C	241/241 (100%)	-0.33	2 (0%) 82 64	63, 89, 135, 162	0
3	Q	241/241 (100%)	-0.34	1 (0%) 88 76	65, 91, 136, 162	0
4	D	242/242 (100%)	-0.29	3 (1%) 76 55	61, 90, 125, 155	0
4	R	242/242 (100%)	-0.29	3 (1%) 76 55	63, 91, 126, 155	0
5	E	233/233 (100%)	-0.18	1 (0%) 88 76	67, 95, 125, 145	0
5	S	233/233 (100%)	-0.18	1 (0%) 88 76	68, 95, 125, 145	0
6	F	244/244 (100%)	-0.27	1 (0%) 88 76	64, 87, 124, 141	0
6	T	244/244 (100%)	-0.31	1 (0%) 88 76	65, 87, 125, 140	0
7	G	243/243 (100%)	-0.38	1 (0%) 88 76	62, 84, 116, 152	0
7	U	243/243 (100%)	-0.45	1 (0%) 88 76	63, 83, 115, 153	0
8	H	222/222 (100%)	-0.56	0 100 100	59, 75, 98, 140	0
8	V	222/222 (100%)	-0.58	0 100 100	61, 74, 98, 142	0
9	I	204/204 (100%)	-0.63	0 100 100	57, 75, 99, 117	0
9	W	204/204 (100%)	-0.59	0 100 100	58, 75, 99, 116	0
10	J	198/198 (100%)	-0.53	1 (0%) 87 72	56, 76, 99, 161	0
10	X	198/198 (100%)	-0.59	0 100 100	57, 77, 98, 162	0
11	K	212/212 (100%)	-0.62	0 100 100	55, 75, 99, 115	0
11	Y	212/212 (100%)	-0.61	0 100 100	56, 75, 101, 117	0
12	L	222/222 (100%)	-0.54	1 (0%) 87 72	59, 77, 105, 129	0
12	Z	222/222 (100%)	-0.55	0 100 100	59, 77, 104, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/233 (100%)	-0.53	1 (0%) 88 76	59, 77, 99, 110	0
13	a	233/233 (100%)	-0.56	1 (0%) 88 76	58, 77, 99, 110	0
14	N	196/196 (100%)	-0.55	0 100 100	58, 74, 100, 115	0
14	b	196/196 (100%)	-0.58	0 100 100	58, 74, 101, 114	0
15	c	1/4 (25%)	0.01	0 100 100	75, 75, 75, 75	0
15	d	1/4 (25%)	-0.75	0 100 100	63, 63, 63, 63	0
15	e	1/4 (25%)	0.63	0 100 100	75, 75, 75, 75	0
15	f	1/4 (25%)	-1.06	0 100 100	66, 66, 66, 66	0
All	All	6372/6384 (99%)	-0.44	24 (0%) 88 76	55, 81, 120, 162	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	119	ALA	4.1
7	U	243	ASP	3.9
4	R	119	ALA	3.9
2	P	219	ALA	3.8
3	Q	50	LEU	3.8

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	LYO	e	3	10/11	0.91	0.11	73,75,78,79	0
15	LYO	c	3	10/11	0.92	0.10	72,74,78,78	0
15	LYO	d	3	10/11	0.93	0.09	64,68,71,71	0
15	LYO	f	3	10/11	0.93	0.08	64,67,71,72	0
15	OW6	e	4	7/8	0.93	0.12	71,73,77,77	0
15	OW6	d	4	7/8	0.95	0.09	67,67,72,72	0
15	OW6	f	4	7/8	0.96	0.08	67,68,72,73	0
15	OW6	c	4	7/8	0.97	0.08	70,72,76,77	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.