



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:51 AM UTC

PDB ID : 4R02 / pdb_00004r02
Title : yCP in complex with BSc4999 (alpha-Keto Phenylamide)
Authors : Voss, C.; Scholz, C.; Knorr, S.; Beck, P.; Stein, M.; Zall, A.; Kuckelkorn, U.;
Kloetzel, P.-M.; Groll, M.; Hamacher, K.; Schmidt, B.
Deposited on : 2014-07-29
Resolution : 2.50 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

<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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

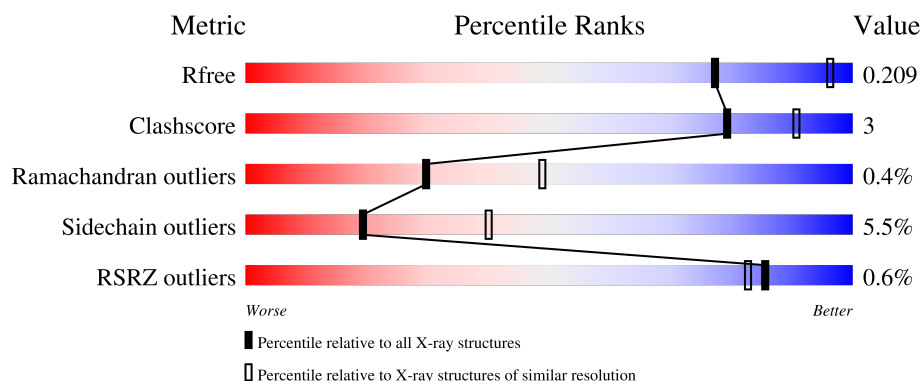
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

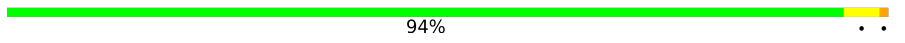
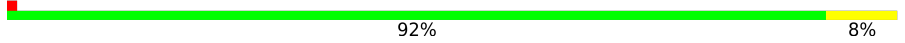
The reported resolution of this entry is 2.50 Å.

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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	 94%
1	O	250	 92% 8%
2	B	258	 83% 10% 5% 2%
2	P	258	 83% 9% 5%
3	C	254	 81% 12% 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	 2% 84% 9% • 6%
4	D	260	 79% 10% • 10%
4	R	260	 78% 10% • 10%
5	E	234	 89% 8% ••
5	S	234	 88% 10% ••
6	F	288	 2% 78% •• 16%
6	T	288	 2% 76% 7% • 16%
7	G	252	 87% 8% ••
7	U	252	 88% 6% ••
8	H	232	 2% 88% 9% •
8	V	232	 2% 89% 7% ••
9	I	205	 91% 8% •
9	W	205	 91% 8%
10	J	198	 2% 90% 7% ••
10	X	198	 2% 89% 8% ••
11	K	212	 2% 92% 6% •
11	Y	212	 91% 8% •
12	L	222	 92% 5% •
12	Z	222	 92% 7% •
13	M	246	 86% 7% • 5%
13	a	246	 84% 9% • 5%
14	N	196	 2% 89% 9% •
14	b	196	 88% 10% •

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 52173 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	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			
8	V	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	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	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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	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 MAGNESIUM ION (CCD ID: MG) (formula: Mg).

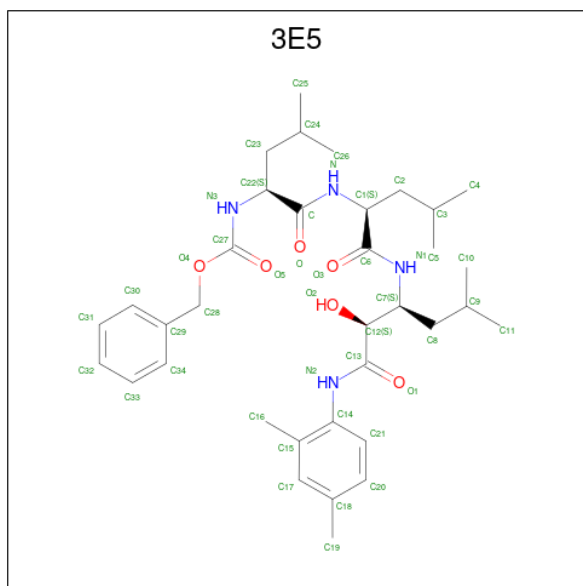
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	I	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	J	1	Total	Mg	0	0
			1	1		
15	K	2	Total	Mg	0	0
			2	2		
15	N	2	Total	Mg	0	0
			2	2		
15	V	1	Total	Mg	0	0
			1	1		
15	Y	1	Total	Mg	0	0
			1	1		
15	Z	1	Total	Mg	0	0
			1	1		

- Molecule 16 is N-[(benzyloxy)carbonyl]-L-leucyl-N-{(2S,3S)-1-[(2,4-dimethylphenyl)amino]-2-hydroxy-5-methyl-1-oxohexan-3-yl}-L-leucinamide (CCD ID: 3E5) (formula: $C_{35}H_{52}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	K	1	Total	C	N	O	0	0
			45	35	4	6		
16	Y	1	Total	C	N	O	0	0
			45	35	4	6		

- Molecule 17 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	121	Total O 121 121	0	0
17	B	84	Total O 84 84	0	0
17	C	88	Total O 88 88	0	0
17	D	82	Total O 82 82	0	0
17	E	44	Total O 44 44	0	0
17	F	93	Total O 93 93	0	0
17	G	117	Total O 117 117	0	0
17	H	110	Total O 110 110	0	0
17	I	106	Total O 106 106	0	0
17	J	101	Total O 101 101	0	0
17	K	119	Total O 119 119	0	0
17	L	118	Total O 118 118	0	0
17	M	141	Total O 141 141	0	0
17	N	108	Total O 108 108	0	0
17	O	79	Total O 79 79	0	0
17	P	73	Total O 73 73	0	0
17	Q	61	Total O 61 61	0	0
17	R	74	Total O 74 74	0	0
17	S	38	Total O 38 38	0	0
17	T	82	Total O 82 82	0	0
17	U	109	Total O 109 109	0	0
17	V	89	Total O 89 89	0	0

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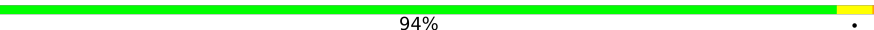
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	W	104	Total 104	O 104	0	0
17	X	92	Total 92	O 92	0	0
17	Y	114	Total 114	O 114	0	0
17	Z	126	Total 126	O 126	0	0
17	a	137	Total 137	O 137	0	0
17	b	96	Total 96	O 96	0	0

3 Residue-property plots [i](#)

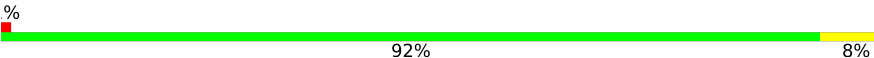
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 subunit alpha type-2

Chain A:  94% . .



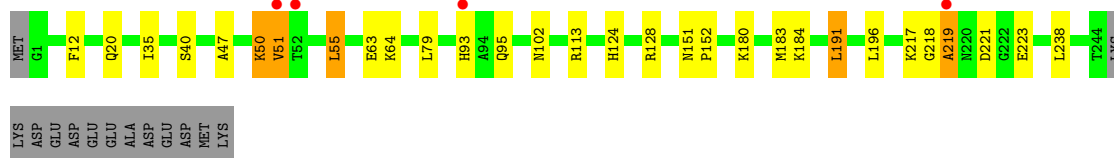
- Molecule 1: Proteasome subunit alpha type-2

Chain O:  92% 8%



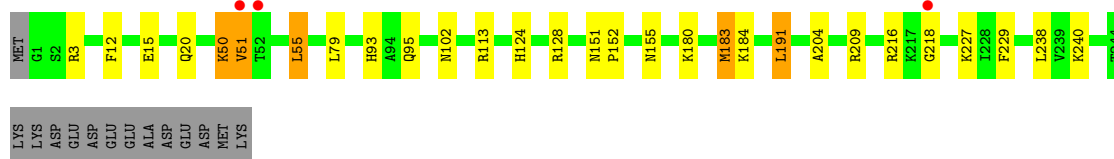
- Molecule 2: Proteasome subunit alpha type-3

Chain B:  83% 10% 5% 2%



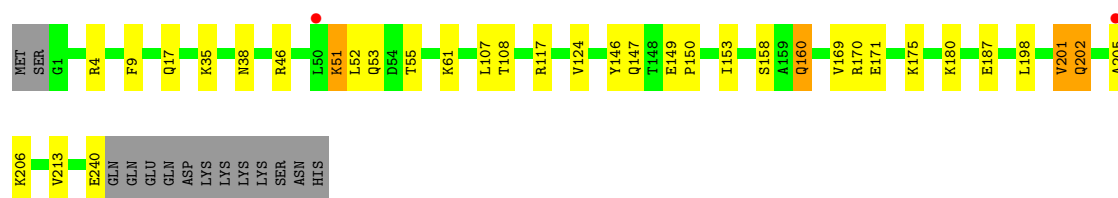
- Molecule 2: Proteasome subunit alpha type-3

Chain P:  83% 9% 5%

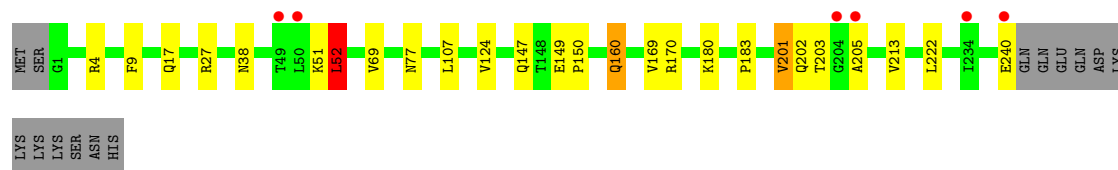
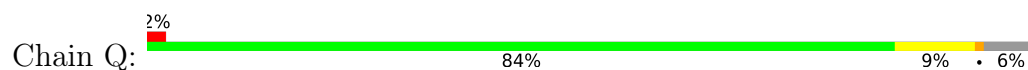


- Molecule 3: Proteasome subunit alpha type-4

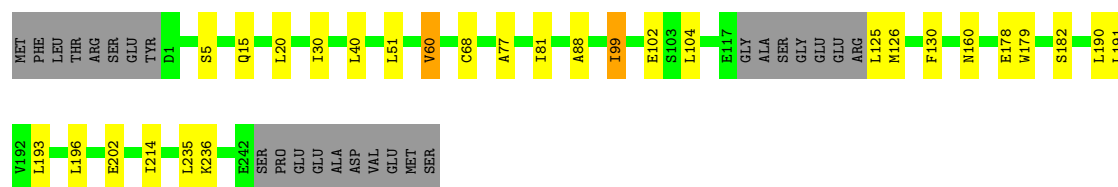
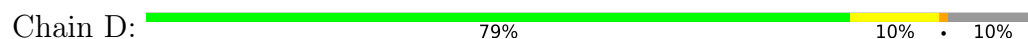
Chain C:  81% 12% 6%



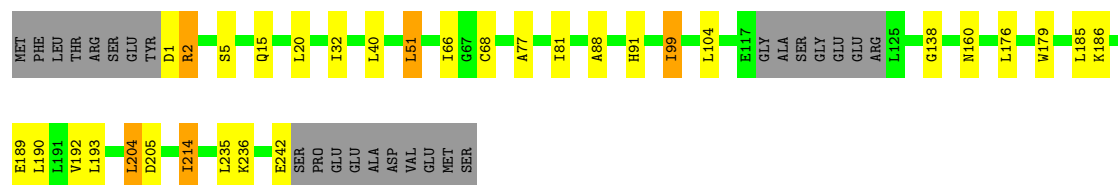
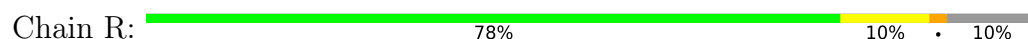
• Molecule 3: Proteasome subunit alpha type-4



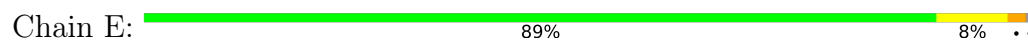
• Molecule 4: Proteasome subunit alpha type-5



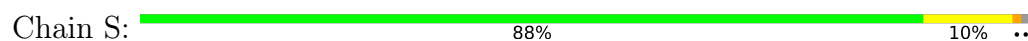
• Molecule 4: Proteasome subunit alpha type-5

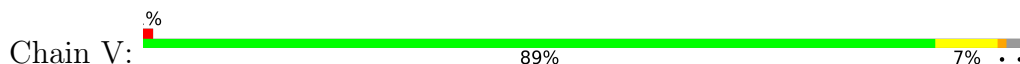


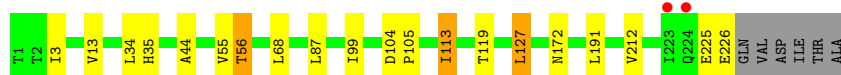
• Molecule 5: Proteasome subunit alpha type-6



• Molecule 5: Proteasome subunit alpha type-6







- Molecule 9: Proteasome subunit beta type-3

Chain I: 91% 8% .



- Molecule 9: Proteasome subunit beta type-3

Chain W: 91% 8%



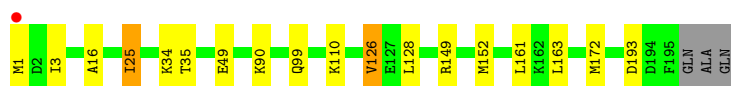
- Molecule 10: Proteasome subunit beta type-4

Chain J: 90% 7% ..



- Molecule 10: Proteasome subunit beta type-4

Chain X: 89% 8% ..



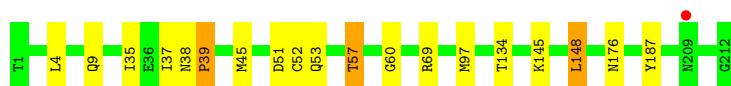
- Molecule 11: Proteasome subunit beta type-5

Chain K: 92% 6% .

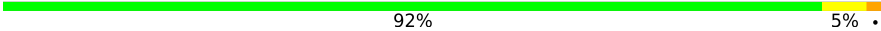


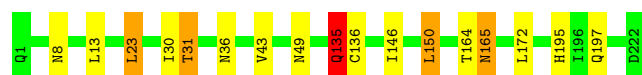
- Molecule 11: Proteasome subunit beta type-5

Chain Y: 91% 8% .

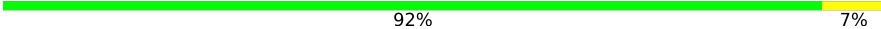


- Molecule 12: Proteasome subunit beta type-6

Chain L:  92% 5% .



- Molecule 12: Proteasome subunit beta type-6

Chain Z:  92% 7% .



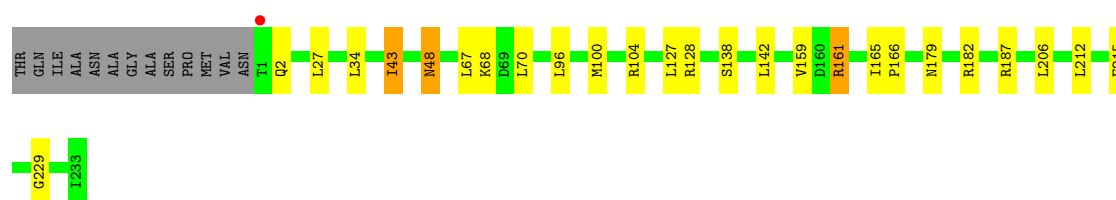
- Molecule 13: Proteasome subunit beta type-7

Chain M:  86% 7% 5% .

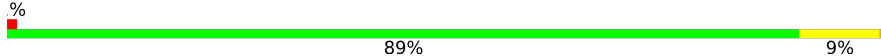


- Molecule 13: Proteasome subunit beta type-7

Chain a:  84% 9% 5% .



- Molecule 14: Proteasome subunit beta type-1

Chain N:  89% 9% .



- Molecule 14: Proteasome subunit beta type-1

Chain b:  88% 10% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	137.24Å 300.87Å 146.29Å 90.00° 113.20° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 15.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.0 (15.00-2.50) 96.5 (15.00-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.51Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.170 , 0.207 0.172 , 0.209	Depositor DCC
R_{free} test set	18074 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.2	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 57.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	52173	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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: MG, 3E5

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	0.40	0/1952	0.68	0/2642
1	O	0.41	0/1952	0.69	0/2642
2	B	0.40	0/1934	0.70	0/2618
2	P	0.40	0/1934	0.69	0/2618
3	C	0.41	0/1910	0.70	0/2586
3	Q	0.42	0/1910	0.73	1/2586 (0.0%)
4	D	0.40	0/1837	0.68	0/2475
4	R	0.40	0/1837	0.68	0/2475
5	E	0.40	0/1800	0.68	0/2433
5	S	0.40	0/1800	0.69	0/2433
6	F	0.42	0/1932	0.71	0/2609
6	T	0.42	0/1932	0.69	0/2609
7	G	0.40	0/1945	0.69	0/2634
7	U	0.38	0/1945	0.69	0/2634
8	H	0.39	0/1750	0.69	0/2373
8	V	0.39	0/1750	0.67	0/2373
9	I	0.39	0/1611	0.69	0/2174
9	W	0.39	0/1611	0.68	0/2174
10	J	0.40	0/1589	0.66	0/2142
10	X	0.40	0/1589	0.67	0/2142
11	K	0.38	0/1681	0.68	0/2274
11	Y	0.40	0/1681	0.68	0/2274
12	L	0.38	0/1795	0.68	0/2420
12	Z	0.39	0/1795	0.68	0/2420
13	M	0.40	0/1855	0.68	0/2514
13	a	0.40	0/1855	0.71	0/2514
14	N	0.38	0/1541	0.68	0/2087
14	b	0.38	0/1541	0.68	1/2087 (0.0%)
All	All	0.40	0/50264	0.69	2/67962 (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
12	L	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	201	VAL	N-CA-C	6.57	118.41	112.17
14	b	115	LEU	N-CA-C	5.02	117.40	111.33

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	L	135	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	8	0
1	O	1915	0	1929	9	0
2	B	1904	0	1904	16	0
2	P	1904	0	1904	20	0
3	C	1881	0	1895	15	0
3	Q	1881	0	1895	11	0
4	D	1813	0	1797	9	0
4	R	1813	0	1797	16	0
5	E	1773	0	1775	8	0
5	S	1773	0	1775	9	0
6	F	1892	0	1883	7	0
6	T	1892	0	1883	7	0
7	G	1907	0	1901	10	0
7	U	1907	0	1901	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1719	0	1719	8	0
8	V	1719	0	1719	11	0
9	I	1581	0	1574	8	0
9	W	1581	0	1574	8	0
10	J	1561	0	1569	10	0
10	X	1561	0	1569	8	0
11	K	1644	0	1594	9	0
11	Y	1644	0	1594	8	0
12	L	1757	0	1711	12	0
12	Z	1757	0	1711	8	0
13	M	1824	0	1832	10	0
13	a	1824	0	1832	10	0
14	N	1512	0	1481	13	0
14	b	1512	0	1481	16	0
15	G	1	0	0	0	0
15	I	2	0	0	0	0
15	J	1	0	0	0	0
15	K	2	0	0	0	0
15	N	2	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	K	45	0	51	1	0
16	Y	45	0	51	0	0
17	A	121	0	0	0	0
17	B	84	0	0	0	0
17	C	88	0	0	0	0
17	D	82	0	0	0	0
17	E	44	0	0	0	0
17	F	93	0	0	0	0
17	G	117	0	0	0	0
17	H	110	0	0	1	0
17	I	106	0	0	0	0
17	J	101	0	0	1	0
17	K	119	0	0	0	0
17	L	118	0	0	1	0
17	M	141	0	0	1	0
17	N	108	0	0	0	0
17	O	79	0	0	0	0
17	P	73	0	0	0	0
17	Q	61	0	0	0	0
17	R	74	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	S	38	0	0	0	0
17	T	82	0	0	0	0
17	U	109	0	0	0	0
17	V	89	0	0	1	0
17	W	104	0	0	0	0
17	X	92	0	0	0	0
17	Y	114	0	0	0	0
17	Z	126	0	0	0	0
17	a	137	0	0	0	0
17	b	96	0	0	1	0
All	All	52173	0	49230	268	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 3.

All (268) 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)
4:D:99:ILE:HD11	4:D:104:LEU:HB2	1.54	0.89
13:a:43:ILE:HD11	13:a:67:LEU:HD12	1.62	0.80
11:Y:53:GLN:O	11:Y:57:THR:HG23	1.81	0.80
4:R:91:HIS:HB3	4:R:99:ILE:HG22	1.71	0.73
5:E:12:PHE:H	6:F:19:GLN:HE22	1.34	0.73
3:Q:51:LYS:O	3:Q:52:LEU:HB2	1.87	0.72
11:K:53:GLN:O	11:K:57:THR:HG23	1.89	0.72
3:C:201:VAL:HG13	3:C:202:GLN:H	1.54	0.71
5:S:12:PHE:H	6:T:19:GLN:HE22	1.40	0.70
4:R:91:HIS:CB	4:R:99:ILE:HG22	2.23	0.68
4:R:91:HIS:CG	4:R:99:ILE:HG22	2.29	0.68
10:J:23:ARG:NH1	11:K:116:ASP:OD1	2.27	0.67
10:J:3:ILE:HD12	10:J:168:LEU:HD13	1.77	0.67
14:N:35:THR:HG21	14:N:45:ARG:HE	1.59	0.67
2:P:12:PHE:H	3:Q:17:GLN:HE22	1.41	0.67
10:X:1:MET:HB2	10:X:34:LYS:HE3	1.79	0.65
2:B:12:PHE:H	3:C:17:GLN:HE22	1.44	0.64
11:K:35:ILE:CG2	11:K:45:MET:HE2	2.28	0.64
11:K:35:ILE:HG22	11:K:45:MET:HE2	1.79	0.63
9:I:26:LEU:HD21	9:I:185:VAL:HG23	1.79	0.63
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.63	0.63
14:b:35:THR:HG21	14:b:45:ARG:HE	1.64	0.62
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:73:ARG:NH2	11:K:104:TYR:O	2.33	0.61
6:F:123:ASN:C	6:F:123:ASN:HD22	2.09	0.61
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.65	0.60
11:K:38:ASN:HB2	11:K:39:PRO:HD2	1.84	0.59
12:Z:172:LEU:HD23	12:Z:172:LEU:H	1.66	0.59
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.68	0.58
9:W:98:ARG:HA	9:W:126:ILE:HD11	1.84	0.58
8:H:3:ILE:HG21	8:H:44:ALA:HB3	1.86	0.58
3:C:9:PHE:H	4:D:15:GLN:HE22	1.52	0.58
11:K:35:ILE:HG22	11:K:45:MET:CE	2.34	0.58
11:Y:51:ASP:HB3	11:Y:97:MET:HE2	1.86	0.57
9:I:26:LEU:HD21	9:I:185:VAL:CG2	2.34	0.57
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.85	0.57
2:B:93:HIS:HB3	2:B:113:ARG:NH2	2.20	0.56
12:L:31:THR:HG22	12:L:36:ASN:HD21	1.70	0.56
4:R:66:ILE:HD12	4:R:99:ILE:HD11	1.87	0.56
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.88	0.56
5:E:9:THR:HG21	5:E:119:THR:HA	1.86	0.56
3:C:201:VAL:HG13	3:C:202:GLN:N	2.20	0.56
10:J:23:ARG:HH21	10:J:50:ALA:CB	2.19	0.55
7:U:34:LEU:C	7:U:34:LEU:HD23	2.31	0.55
12:L:31:THR:CG2	12:L:36:ASN:HD21	2.19	0.55
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.87	0.55
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.54	0.55
3:C:51:LYS:O	3:C:52:LEU:HB2	2.06	0.55
14:N:35:THR:CG2	14:N:45:ARG:HE	2.19	0.55
7:G:83:ASN:C	7:G:83:ASN:HD22	2.16	0.54
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.35	0.54
4:R:185:LEU:O	4:R:189:GLU:HG3	2.08	0.53
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.74	0.53
7:U:23:PHE:O	7:U:26:THR:HB	2.08	0.53
3:C:201:VAL:O	3:C:202:GLN:HB2	2.07	0.53
10:X:25:ILE:HG12	10:X:25:ILE:O	2.07	0.53
5:E:71:LEU:C	5:E:71:LEU:HD23	2.34	0.53
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.56	0.53
8:V:225:GLU:O	8:V:226:GLU:HB2	2.08	0.53
12:Z:13:LEU:HD11	12:Z:150:LEU:HD21	1.90	0.53
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.90	0.53
7:U:26:THR:HG21	7:U:131:ILE:HD12	1.92	0.52
13:M:161:ARG:HG3	13:M:161:ARG:HH11	1.74	0.52
14:b:35:THR:CG2	14:b:45:ARG:HE	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:160:GLN:HE22	3:Q:170:ARG:HE	1.57	0.52
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.91	0.52
1:O:122:THR:CG2	2:P:128:ARG:HH21	2.23	0.52
11:Y:45:MET:HG2	11:Y:52:CYS:HB3	1.92	0.51
9:W:101:PRO:HB3	9:W:126:ILE:CD1	2.41	0.51
13:M:2:GLN:NE2	17:M:422:HOH:O	2.44	0.51
14:N:35:THR:HG21	14:N:45:ARG:NE	2.26	0.51
1:O:12:PHE:H	2:P:20:GLN:HE22	1.58	0.51
2:P:227:LYS:HD3	2:P:229:PHE:CE1	2.46	0.51
5:S:68:HIS:HE1	5:S:102:LEU:O	1.94	0.51
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.40	0.51
14:b:13:ILE:HG21	14:b:175:MET:HE2	1.93	0.51
7:U:63:ILE:HD12	7:U:215:GLU:HB3	1.93	0.51
13:a:179:ASN:HD22	13:a:182:ARG:HH11	1.59	0.51
13:M:27:LEU:HD21	13:M:34:LEU:HD22	1.93	0.50
13:M:48:ASN:H	13:M:48:ASN:HD22	1.59	0.50
11:Y:38:ASN:HB2	11:Y:39:PRO:HD2	1.93	0.50
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.60	0.50
6:T:123:ASN:C	6:T:123:ASN:HD22	2.20	0.50
14:b:83:LYS:HG3	14:b:119:VAL:CG2	2.42	0.50
14:b:152:VAL:HA	14:b:175:MET:HE1	1.94	0.50
7:G:34:LEU:C	7:G:34:LEU:HD23	2.37	0.50
9:I:101:PRO:HB3	9:I:126:ILE:HD12	1.93	0.50
3:C:35:LYS:HG2	3:C:158:SER:O	2.12	0.49
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.94	0.49
2:P:95:GLN:HE22	9:W:71:ASN:HD22	1.60	0.49
13:a:159:VAL:HG23	13:a:159:VAL:O	2.12	0.49
2:P:216:ARG:HB3	2:P:218:GLY:H	1.76	0.49
14:N:20:THR:CG2	14:N:31:THR:OG1	2.60	0.49
6:T:172:LEU:HD13	6:T:195:ILE:HD13	1.94	0.49
10:J:23:ARG:NH2	10:J:50:ALA:CB	2.75	0.49
14:N:161:GLN:HE21	14:b:136:GLY:HA2	1.77	0.49
4:R:51:LEU:C	4:R:51:LEU:HD12	2.38	0.49
7:G:30:ASN:HD22	7:G:164:PRO:HG2	1.77	0.48
10:J:1:MET:HB2	10:J:34:LYS:HE3	1.94	0.48
4:R:1:ASP:O	4:R:2:ARG:HB2	2.12	0.48
11:Y:176:ASN:ND2	11:Y:187:TYR:OH	2.46	0.48
2:B:35:ILE:HD12	2:B:196:LEU:HG	1.95	0.48
8:H:87:LEU:HD12	8:H:113:ILE:HD11	1.95	0.48
10:J:1:MET:SD	10:J:1:MET:N	2.86	0.48
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.94	0.48
8:V:3:ILE:HG21	8:V:44:ALA:HB3	1.95	0.48
10:X:149:ARG:O	10:X:152:MET:HG3	2.13	0.48
3:C:149:GLU:HB2	3:C:150:PRO:HD2	1.96	0.48
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.96	0.48
12:L:23:LEU:HD13	12:L:43:VAL:HG13	1.94	0.48
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.48	0.48
2:P:93:HIS:HB3	2:P:113:ARG:NH2	2.28	0.48
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.96	0.48
2:P:204:ALA:O	2:P:209:ARG:NH2	2.43	0.48
13:a:161:ARG:HG3	13:a:161:ARG:HH11	1.79	0.48
7:G:68:ARG:O	7:G:223:LYS:HA	2.14	0.48
12:L:195:HIS:HD2	12:L:197:GLN:H	1.62	0.47
7:U:167:GLN:HE21	7:U:171:THR:HG23	1.79	0.47
14:b:176:VAL:HG12	14:b:178:LEU:HD13	1.96	0.47
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.49	0.47
13:M:127:LEU:HG	13:M:142:LEU:HD12	1.97	0.47
3:Q:27:ARG:HH11	3:Q:27:ARG:HB2	1.79	0.47
6:T:12:SER:OG	6:T:14:ASP:OD2	2.32	0.47
7:U:83:ASN:C	7:U:83:ASN:HD22	2.22	0.47
8:V:113:ILE:HB	8:V:119:THR:HG22	1.96	0.47
12:L:165:ASN:HD21	8:V:212:VAL:H	1.62	0.47
14:N:13:ILE:HG21	14:N:175:MET:CE	2.45	0.47
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.45	0.46
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.98	0.46
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.51	0.46
6:T:163:LYS:HE2	6:T:203:ASN:ND2	2.29	0.46
5:E:206:THR:OG1	5:E:209:ASN:HB2	2.15	0.46
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.45	0.46
2:P:15:GLU:O	3:Q:27:ARG:NH1	2.48	0.46
9:W:98:ARG:HD2	9:W:126:ILE:HG12	1.97	0.46
6:F:172:LEU:HD13	6:F:195:ILE:HD13	1.97	0.46
10:J:25:ILE:HG12	10:J:25:ILE:O	2.15	0.46
4:D:77:ALA:O	4:D:81:ILE:HG12	2.15	0.46
16:K:301:3E5:O1	16:K:301:3E5:H44	2.14	0.46
5:S:9:THR:HG21	5:S:119:THR:HA	1.98	0.46
7:G:83:ASN:C	7:G:83:ASN:ND2	2.74	0.46
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.45	0.46
14:N:152:VAL:HA	14:N:175:MET:HE1	1.97	0.45
2:P:50:LYS:O	2:P:51:VAL:C	2.58	0.45
1:A:149:GLN:O	1:A:156:TYR:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.97	0.45
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.52	0.45
1:A:83:ARG:HE	7:G:114:ASN:HD21	1.64	0.45
14:b:35:THR:HG22	17:b:201:HOH:O	2.15	0.45
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.97	0.45
1:A:83:ARG:HE	7:G:114:ASN:ND2	2.14	0.45
2:B:183:MET:HE1	2:B:191:LEU:HD12	1.98	0.45
4:D:60:VAL:HG11	4:D:81:ILE:HG21	1.99	0.45
12:L:8:ASN:HA	12:L:30:ILE:O	2.17	0.45
4:R:32:ILE:HD12	4:R:192:VAL:HG23	1.98	0.45
1:A:176:GLU:HG3	2:B:55:LEU:HD22	1.99	0.45
3:C:46:ARG:HH12	3:C:206:LYS:HB3	1.82	0.45
6:T:240:GLN:HE21	6:T:240:GLN:HA	1.81	0.45
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.98	0.45
14:b:35:THR:HG21	14:b:45:ARG:NE	2.30	0.45
6:F:123:ASN:HD22	6:F:124:SER:N	2.15	0.44
14:b:20:THR:CG2	14:b:31:THR:OG1	2.65	0.44
5:E:10:VAL:HG13	5:E:10:VAL:O	2.15	0.44
14:N:20:THR:HG23	14:N:28:ASN:HB3	1.99	0.44
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.98	0.44
7:G:73:VAL:HG12	7:G:133:THR:HB	1.98	0.44
14:b:20:THR:HG23	14:b:28:ASN:HB3	1.99	0.44
13:a:96:LEU:O	13:a:100:MET:HG2	2.17	0.44
14:N:55:ILE:HD11	14:N:93:LEU:HD13	1.99	0.44
13:a:127:LEU:HG	13:a:142:LEU:HD12	1.99	0.44
14:b:14:LEU:HD23	14:b:44:CYS:SG	2.57	0.44
2:P:3:ARG:NH1	5:S:122:TYR:OH	2.51	0.44
1:O:115:ALA:HB1	1:O:154:GLY:O	2.18	0.44
5:E:178:PHE:CD1	5:E:178:PHE:C	2.96	0.44
3:C:108:THR:HG21	3:C:146:TYR:HB3	1.99	0.43
9:I:35:VAL:HG13	17:J:308:HOH:O	2.17	0.43
6:F:228:LYS:H	6:F:228:LYS:HD3	1.81	0.43
4:R:99:ILE:HG13	4:R:104:LEU:HB2	1.99	0.43
1:O:176:GLU:HG3	2:P:55:LEU:HD22	1.99	0.43
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.53	0.43
3:C:198:LEU:HA	3:C:201:VAL:HG12	2.00	0.43
9:W:123:PHE:HA	9:W:128:CYS:O	2.18	0.43
12:L:164:THR:O	12:L:165:ASN:C	2.61	0.43
6:F:198:LEU:HD13	6:F:243:ILE:HG22	2.00	0.43
10:X:1:MET:SD	10:X:1:MET:N	2.86	0.43
13:a:128:ARG:HH11	13:a:138:SER:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:225:GLU:O	8:H:226:GLU:HB2	2.18	0.43
1:A:12:PHE:H	2:B:20:GLN:HE22	1.67	0.43
14:N:136:GLY:HA2	14:b:161:GLN:HE21	1.83	0.43
5:S:49:LYS:HB3	5:S:58:TYR:HB3	2.01	0.43
14:b:20:THR:HG22	14:b:31:THR:OG1	2.19	0.42
14:b:55:ILE:HD11	14:b:93:LEU:HD13	2.01	0.42
10:J:49:GLU:HB2	10:J:99:GLN:HB3	2.00	0.42
7:U:187:GLU:HG2	7:U:192:LYS:HB2	2.01	0.42
5:E:118:ASN:N	5:E:118:ASN:HD22	2.17	0.42
11:K:4:LEU:HD13	11:K:161:ILE:HD11	2.01	0.42
7:U:83:ASN:C	7:U:83:ASN:ND2	2.77	0.42
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.48	0.42
2:P:183:MET:HE1	2:P:191:LEU:HD12	2.00	0.42
3:Q:201:VAL:O	3:Q:201:VAL:HG22	2.19	0.42
8:V:3:ILE:HG22	8:V:99:ILE:HD12	2.01	0.42
13:a:27:LEU:HD21	13:a:34:LEU:HD22	2.01	0.42
2:B:219:ALA:HB3	2:B:223:GLU:HG3	2.02	0.42
6:F:240:GLN:HE21	6:F:240:GLN:HA	1.85	0.42
4:D:30:ILE:HD12	4:D:196:LEU:HG	2.01	0.42
2:P:50:LYS:HE3	2:P:50:LYS:HA	2.02	0.42
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.01	0.42
8:V:87:LEU:HD12	8:V:113:ILE:HD11	2.00	0.42
4:D:126:MET:HE1	4:D:130:PHE:CE2	2.55	0.42
3:C:160:GLN:HE22	3:C:170:ARG:HE	1.68	0.41
13:M:43:ILE:HG12	13:M:43:ILE:O	2.20	0.41
10:X:1:MET:CB	10:X:34:LYS:HE3	2.47	0.41
12:Z:23:LEU:HD13	12:Z:43:VAL:HG13	2.01	0.41
7:G:78:ILE:N	7:G:79:PRO:CD	2.83	0.41
11:K:145:LYS:HB2	11:K:148:LEU:HD13	2.03	0.41
2:B:47:ALA:HB1	2:B:64:LYS:CD	2.51	0.41
8:H:84:LYS:HG3	8:H:85:GLN:N	2.35	0.41
13:M:17:ASP:OD1	13:M:18:ASN:N	2.54	0.41
9:W:20:VAL:HG23	9:W:189:ILE:HB	2.01	0.41
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	2.02	0.41
12:Z:43:VAL:HG12	12:Z:205:LEU:HD22	2.02	0.41
2:B:50:LYS:O	2:B:51:VAL:C	2.64	0.41
8:H:172:ASN:ND2	17:H:401:HOH:O	2.54	0.41
10:J:139:TYR:CZ	11:Y:134:THR:HG22	2.56	0.41
12:L:13:LEU:HD11	12:L:150:LEU:HD21	2.01	0.41
6:T:123:ASN:HD22	6:T:124:SER:N	2.18	0.41
8:V:99:ILE:HG13	8:V:127:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:26:LEU:HD21	9:W:185:VAL:HG23	2.03	0.41
10:X:1:MET:HB2	10:X:34:LYS:CE	2.48	0.41
8:H:98:LEU:HB2	8:H:113:ILE:HG23	2.02	0.41
12:L:135:GLN:NE2	17:L:392:HOH:O	2.52	0.41
12:L:146:ILE:HG22	12:L:150:LEU:HD22	2.01	0.41
1:O:149:GLN:O	1:O:156:TYR:HA	2.21	0.41
3:C:201:VAL:CG1	3:C:202:GLN:H	2.29	0.41
1:O:83:ARG:HE	7:U:114:ASN:ND2	2.19	0.41
5:S:71:LEU:C	5:S:71:LEU:CD2	2.93	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
1:A:1:MET:CG	1:A:2:THR:N	2.84	0.41
4:D:178:GLU:HB3	4:D:191:LEU:HD21	2.03	0.41
9:I:123:PHE:HA	9:I:128:CYS:O	2.20	0.41
4:R:204:LEU:HD23	4:R:205:ASP:N	2.36	0.41
7:U:68:ARG:O	7:U:223:LYS:HA	2.21	0.41
8:V:35:HIS:HB3	8:V:56:THR:HG21	2.03	0.41
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.20	0.41
14:b:13:ILE:HG21	14:b:175:MET:CE	2.51	0.41
13:M:96:LEU:O	13:M:100:MET:HG2	2.21	0.41
2:P:155:ASN:ND2	3:Q:77:ASN:HB2	2.35	0.41
13:a:48:ASN:H	13:a:48:ASN:HD22	1.68	0.41
8:H:114:HIS:CD2	8:H:116:HIS:H	2.39	0.40
13:M:179:ASN:HD22	13:M:182:ARG:HH11	1.69	0.40
1:O:119:GLN:O	1:O:122:THR:HB	2.21	0.40
13:a:165:ILE:HB	13:a:166:PRO:HD3	2.04	0.40
1:A:122:THR:CG2	2:B:128:ARG:HH21	2.35	0.40
9:I:20:VAL:HG23	9:I:189:ILE:HB	2.03	0.40
4:R:77:ALA:O	4:R:81:ILE:HG12	2.21	0.40
10:X:126:VAL:HG13	10:X:128:LEU:HG	2.03	0.40
12:L:136:CYS:SG	12:L:150:LEU:HB3	2.61	0.40
1:O:98:LYS:HE3	1:O:104:TYR:CZ	2.56	0.40
3:Q:149:GLU:HB2	3:Q:150:PRO:HD2	2.02	0.40
4:R:138:GLY:HA2	4:R:214:ILE:HG12	2.04	0.40
8:V:3:ILE:CG2	8:V:44:ALA:HB3	2.51	0.40
1:A:94:HIS:HA	1:A:98:LYS:HB3	2.02	0.40
13:M:159:VAL:O	13:M:159:VAL:CG2	2.68	0.40
14:N:7:THR:HG23	14:N:110:VAL:HG23	2.02	0.40
8:V:172:ASN:ND2	17:V:421:HOH:O	2.53	0.40
7:G:37:ARG:NH2	7:G:183:ASP:HB3	2.36	0.40
7:U:187:GLU:HG2	7:U:192:LYS:CB	2.51	0.40

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%)	241 (97%)	6 (2%)	1 (0%)	30	49
1	O	248/250 (99%)	239 (96%)	7 (3%)	2 (1%)	16	31
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	7	13
2	P	242/258 (94%)	231 (96%)	9 (4%)	2 (1%)	16	31
3	C	238/254 (94%)	231 (97%)	4 (2%)	3 (1%)	9	18
3	Q	238/254 (94%)	232 (98%)	2 (1%)	4 (2%)	7	13
4	D	231/260 (89%)	230 (100%)	1 (0%)	0	100	100
4	R	231/260 (89%)	226 (98%)	4 (2%)	1 (0%)	30	49
5	E	229/234 (98%)	221 (96%)	7 (3%)	1 (0%)	30	49
5	S	229/234 (98%)	219 (96%)	10 (4%)	0	100	100
6	F	241/288 (84%)	235 (98%)	5 (2%)	1 (0%)	30	49
6	T	241/288 (84%)	235 (98%)	5 (2%)	1 (0%)	30	49
7	G	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
7	U	239/252 (95%)	238 (100%)	1 (0%)	0	100	100
8	H	224/232 (97%)	217 (97%)	7 (3%)	0	100	100
8	V	224/232 (97%)	217 (97%)	7 (3%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
10	J	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
10	X	193/198 (98%)	186 (96%)	7 (4%)	0	100	100
11	K	210/212 (99%)	204 (97%)	5 (2%)	1 (0%)	24	43
11	Y	210/212 (99%)	203 (97%)	6 (3%)	1 (0%)	24	43
12	L	220/222 (99%)	214 (97%)	5 (2%)	1 (0%)	24	43
12	Z	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
13	M	231/246 (94%)	222 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	a	231/246 (94%)	223 (96%)	7 (3%)	1 (0%)	30	49
14	N	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
14	b	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
All	All	6284/6614 (95%)	6108 (97%)	152 (2%)	24 (0%)	30	49

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
2	B	51	VAL
3	C	202	GLN
12	L	165	ASN
1	O	2	THR
2	P	51	VAL
2	B	218	GLY
2	B	219	ALA
2	B	221	ASP
3	C	201	VAL
2	P	183	MET
4	R	2	ARG
5	E	231	LYS
6	F	205	GLU
3	Q	52	LEU
3	Q	205	ALA
11	Y	39	PRO
3	C	205	ALA
1	O	3	ASP
3	Q	183	PRO
6	T	180	PRO
11	K	39	PRO
3	Q	202	GLN
13	a	229	GLY

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%)	203 (97%)	6 (3%)	37	65
1	O	209/209 (100%)	201 (96%)	8 (4%)	29	56
2	B	203/216 (94%)	192 (95%)	11 (5%)	20	41
2	P	203/216 (94%)	194 (96%)	9 (4%)	25	50
3	C	212/226 (94%)	194 (92%)	18 (8%)	10	22
3	Q	212/226 (94%)	199 (94%)	13 (6%)	17	35
4	D	194/215 (90%)	178 (92%)	16 (8%)	10	23
4	R	194/215 (90%)	179 (92%)	15 (8%)	12	25
5	E	190/193 (98%)	174 (92%)	16 (8%)	10	22
5	S	190/193 (98%)	177 (93%)	13 (7%)	14	31
6	F	201/239 (84%)	189 (94%)	12 (6%)	17	36
6	T	201/239 (84%)	184 (92%)	17 (8%)	10	22
7	G	206/210 (98%)	196 (95%)	10 (5%)	22	45
7	U	206/210 (98%)	196 (95%)	10 (5%)	22	45
8	H	185/190 (97%)	176 (95%)	9 (5%)	22	45
8	V	185/190 (97%)	177 (96%)	8 (4%)	26	51
9	I	172/173 (99%)	164 (95%)	8 (5%)	23	47
9	W	172/173 (99%)	165 (96%)	7 (4%)	27	53
10	J	173/175 (99%)	164 (95%)	9 (5%)	21	42
10	X	173/175 (99%)	162 (94%)	11 (6%)	16	33
11	K	169/169 (100%)	161 (95%)	8 (5%)	23	47
11	Y	169/169 (100%)	163 (96%)	6 (4%)	31	58
12	L	185/185 (100%)	179 (97%)	6 (3%)	34	62
12	Z	185/185 (100%)	176 (95%)	9 (5%)	22	45
13	M	199/208 (96%)	188 (94%)	11 (6%)	19	40
13	a	199/208 (96%)	188 (94%)	11 (6%)	19	40
14	N	162/162 (100%)	156 (96%)	6 (4%)	30	57
14	b	162/162 (100%)	152 (94%)	10 (6%)	16	34
All	All	5320/5540 (96%)	5027 (94%)	293 (6%)	19	40

All (293) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	59	GLU
1	A	61	LEU
1	A	62	SER
1	A	122	THR
1	A	250	LEU
2	B	40	SER
2	B	50	LYS
2	B	55	LEU
2	B	63	GLU
2	B	79	LEU
2	B	102	ASN
2	B	180	LYS
2	B	184	LYS
2	B	191	LEU
2	B	217	LYS
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	51	LYS
3	C	53	GLN
3	C	55	THR
3	C	61	LYS
3	C	107	LEU
3	C	117	ARG
3	C	147	GLN
3	C	153	ILE
3	C	160	GLN
3	C	169	VAL
3	C	171	GLU
3	C	175	LYS
3	C	180	LYS
3	C	187	GLU
3	C	213	VAL
3	C	240	GLU
4	D	5	SER
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	60	VAL
4	D	68	CYS
4	D	99	ILE
4	D	102	GLU

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Mol	Chain	Res	Type
4	D	125	LEU
4	D	182	SER
4	D	190	LEU
4	D	193	LEU
4	D	202	GLU
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
5	E	4	ASN
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	87	LEU
5	E	106	ARG
5	E	118	ASN
5	E	144	LEU
5	E	180	LYS
5	E	188	LEU
5	E	207	VAL
5	E	208	ASP
6	F	68	ARG
6	F	94	SER
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	198	LEU
6	F	201	GLU
6	F	203	ASN
6	F	221	ASN
6	F	228	LYS
6	F	240	GLN
6	F	241	LYS
7	G	13	GLU
7	G	26	THR
7	G	34	LEU
7	G	83	ASN
7	G	115	LEU
7	G	122	ARG

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Mol	Chain	Res	Type
7	G	125	MET
7	G	166	GLN
7	G	235	ARG
7	G	236	LEU
8	H	13	VAL
8	H	34	LEU
8	H	55	VAL
8	H	68	LEU
8	H	91	GLN
8	H	106	THR
8	H	113	ILE
8	H	127	LEU
8	H	153	LYS
9	I	20	VAL
9	I	31	GLN
9	I	37	ASN
9	I	126	ILE
9	I	131	GLU
9	I	171	LEU
9	I	191	LYS
9	I	193	GLU
10	J	1	MET
10	J	3	ILE
10	J	7	ILE
10	J	35	THR
10	J	49	GLU
10	J	90	LYS
10	J	99	GLN
10	J	163	LEU
10	J	172	MET
11	K	4	LEU
11	K	9	GLN
11	K	35	ILE
11	K	57	THR
11	K	107	LYS
11	K	118	ASP
11	K	148	LEU
11	K	180	VAL
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	135	GLN

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Mol	Chain	Res	Type
12	L	150	LEU
12	L	172	LEU
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	102	GLN
13	M	104	ARG
13	M	129	TYR
13	M	159	VAL
13	M	161	ARG
13	M	187	ARG
13	M	212	LEU
13	M	215	GLU
14	N	9	LYS
14	N	20	THR
14	N	35	THR
14	N	115	LEU
14	N	144	GLU
14	N	178	LEU
1	O	1	MET
1	O	29	LYS
1	O	59	GLU
1	O	61	LEU
1	O	122	THR
1	O	157	PHE
1	O	166	LYS
1	O	250	LEU
2	P	50	LYS
2	P	55	LEU
2	P	79	LEU
2	P	102	ASN
2	P	180	LYS
2	P	184	LYS
2	P	191	LEU
2	P	238	LEU
2	P	240	LYS
3	Q	4	ARG
3	Q	38	ASN
3	Q	52	LEU
3	Q	69	VAL
3	Q	107	LEU
3	Q	147	GLN

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Mol	Chain	Res	Type
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	203	THR
3	Q	213	VAL
3	Q	222	LEU
3	Q	240	GLU
4	R	5	SER
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	68	CYS
4	R	99	ILE
4	R	176	LEU
4	R	186	LYS
4	R	190	LEU
4	R	193	LEU
4	R	204	LEU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	4	ASN
5	S	8	ASP
5	S	9	THR
5	S	25	LEU
5	S	29	LYS
5	S	55	LEU
5	S	71	LEU
5	S	106	ARG
5	S	121	SER
5	S	155	LEU
5	S	180	LYS
5	S	188	LEU
5	S	231	LYS
6	T	29	ASN
6	T	58	GLN
6	T	68	ARG
6	T	117	GLN
6	T	123	ASN
6	T	126	ARG
6	T	148	GLU

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Mol	Chain	Res	Type
6	T	163	LYS
6	T	165	ARG
6	T	171	GLU
6	T	172	LEU
6	T	175	LEU
6	T	181	GLU
6	T	198	LEU
6	T	203	ASN
6	T	215	CYS
6	T	221	ASN
7	U	26	THR
7	U	34	LEU
7	U	68	ARG
7	U	83	ASN
7	U	115	LEU
7	U	122	ARG
7	U	125	MET
7	U	230	GLU
7	U	235	ARG
7	U	236	LEU
8	V	13	VAL
8	V	34	LEU
8	V	55	VAL
8	V	56	THR
8	V	68	LEU
8	V	113	ILE
8	V	127	LEU
8	V	191	LEU
9	W	20	VAL
9	W	30	SER
9	W	31	GLN
9	W	37	ASN
9	W	151	SER
9	W	171	LEU
9	W	192	ASP
10	X	3	ILE
10	X	25	ILE
10	X	35	THR
10	X	49	GLU
10	X	90	LYS
10	X	99	GLN
10	X	110	LYS

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Mol	Chain	Res	Type
10	X	126	VAL
10	X	163	LEU
10	X	172	MET
10	X	193	ASP
11	Y	4	LEU
11	Y	9	GLN
11	Y	35	ILE
11	Y	57	THR
11	Y	69	ARG
11	Y	148	LEU
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	66	LYS
12	Z	132	GLU
12	Z	136	CYS
12	Z	150	LEU
12	Z	172	LEU
12	Z	173	LYS
13	a	2	GLN
13	a	43	ILE
13	a	48	ASN
13	a	68	LYS
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
13	a	206	LEU
13	a	212	LEU
13	a	215	GLU
14	b	9	LYS
14	b	20	THR
14	b	35	THR
14	b	36	ARG
14	b	105	LYS
14	b	107	LYS
14	b	115	LEU
14	b	119	VAL
14	b	144	GLU
14	b	178	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (171) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	58	GLN
2	B	93	HIS
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	176	GLN
3	C	17	GLN
3	C	38	ASN
3	C	53	GLN
3	C	77	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
3	C	233	GLN
4	D	15	GLN
4	D	100	ASN
4	D	106	GLN
4	D	146	GLN
4	D	160	ASN
4	D	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	165	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	191	GLN
6	F	240	GLN
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN

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Mol	Chain	Res	Type
7	G	175	ASN
7	G	212	ASN
8	H	30	ASN
8	H	66	HIS
8	H	86	HIS
8	H	114	HIS
8	H	116	HIS
8	H	165	ASN
8	H	172	ASN
8	H	189	ASN
9	I	63	ASN
9	I	88	GLN
10	J	37	GLN
10	J	63	ASN
10	J	146	HIS
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
11	K	208	ASN
11	K	209	ASN
12	L	3	ASN
12	L	36	ASN
12	L	49	ASN
12	L	70	ASN
12	L	108	HIS
12	L	135	GLN
12	L	158	ASN
12	L	165	ASN
12	L	197	GLN
13	M	2	GLN
13	M	48	ASN
13	M	62	HIS
13	M	102	GLN
13	M	108	ASN
13	M	149	HIS
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
14	N	141	ASN
14	N	161	GLN
1	O	30	GLN

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Mol	Chain	Res	Type
1	O	94	HIS
1	O	149	GLN
2	P	20	GLN
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	146	GLN
2	P	155	ASN
2	P	172	GLN
2	P	176	GLN
3	Q	17	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	115	GLN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	106	GLN
4	R	146	GLN
4	R	149	HIS
4	R	160	ASN
4	R	217	GLN
4	R	225	ASN
5	S	68	HIS
5	S	85	ASN
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	147	GLN
5	S	151	ASN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	178	HIS

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Mol	Chain	Res	Type
6	T	191	GLN
6	T	203	ASN
6	T	240	GLN
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	167	GLN
7	U	175	ASN
7	U	186	ASN
8	V	66	HIS
8	V	165	ASN
8	V	194	ASN
9	W	37	ASN
9	W	63	ASN
9	W	88	GLN
10	X	37	GLN
10	X	55	GLN
10	X	63	ASN
10	X	191	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	143	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	76	HIS
12	Z	79	HIS
12	Z	80	ASN
12	Z	135	GLN
12	Z	158	ASN
12	Z	165	ASN
12	Z	197	GLN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	149	HIS
13	a	179	ASN
14	b	38	HIS

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Mol	Chain	Res	Type
14	b	141	ASN
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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 11 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
16	3E5	Y	301	11	46,46,46	1.25	3 (6%)	60,62,62	1.24	5 (8%)
16	3E5	K	301	11	46,46,46	1.24	3 (6%)	60,62,62	1.17	6 (10%)

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	3E5	Y	301	11	-	8/49/49/49	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	3E5	K	301	11	-	8/49/49/49	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	K	301	3E5	O4-C27	5.52	1.46	1.35
16	Y	301	3E5	O4-C27	5.46	1.46	1.35
16	K	301	3E5	C14-C15	4.93	1.50	1.40
16	Y	301	3E5	C14-C15	4.71	1.50	1.40
16	Y	301	3E5	C14-N2	-2.62	1.36	1.41
16	K	301	3E5	C14-N2	-2.22	1.37	1.41

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Y	301	3E5	C12-C13-N2	-3.93	111.94	115.50
16	Y	301	3E5	O4-C27-N3	3.86	118.71	110.45
16	Y	301	3E5	O4-C27-O5	-3.62	117.32	124.26
16	K	301	3E5	O4-C27-N3	3.53	117.99	110.45
16	K	301	3E5	C21-C14-C15	-3.25	116.99	120.70
16	K	301	3E5	O4-C27-O5	-3.01	118.49	124.26
16	Y	301	3E5	C28-O4-C27	2.95	122.57	115.93
16	Y	301	3E5	C21-C14-C15	-2.62	117.71	120.70
16	K	301	3E5	O2-C12-C13	-2.37	105.67	110.63
16	K	301	3E5	C23-C22-N3	2.37	115.92	110.58
16	K	301	3E5	C28-O4-C27	2.10	120.65	115.93

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	K	301	3E5	N3-C22-C23-C24
16	Y	301	3E5	O5-C27-O4-C28
16	Y	301	3E5	N3-C27-O4-C28
16	K	301	3E5	O5-C27-O4-C28
16	K	301	3E5	C-C22-C23-C24
16	K	301	3E5	N3-C27-O4-C28
16	K	301	3E5	N-C1-C2-C3
16	Y	301	3E5	N3-C22-C23-C24
16	Y	301	3E5	C-C22-C23-C24
16	Y	301	3E5	N-C1-C2-C3

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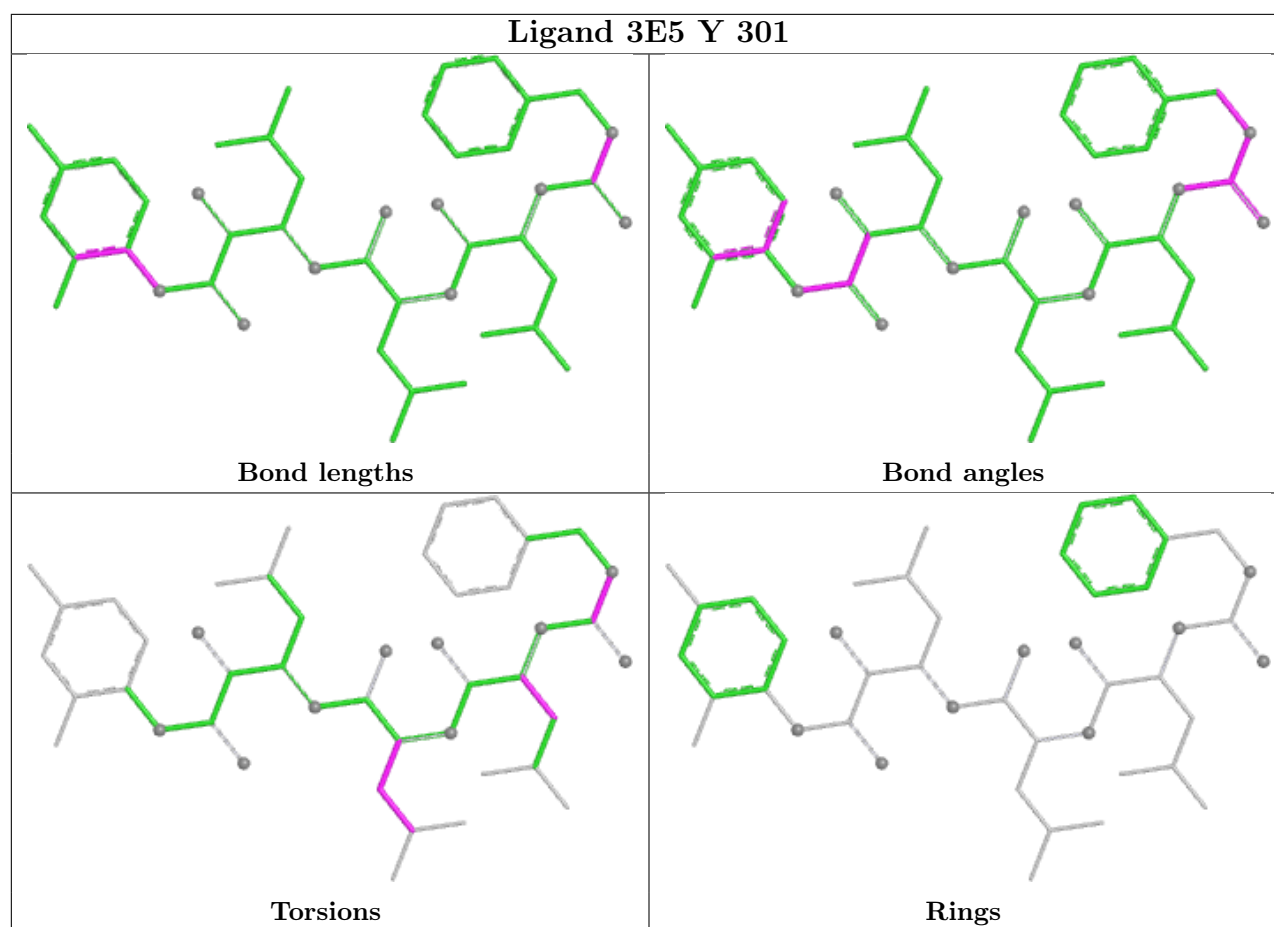
Mol	Chain	Res	Type	Atoms
16	K	301	3E5	C6-C1-C2-C3
16	Y	301	3E5	C6-C1-C2-C3
16	Y	301	3E5	C1-C2-C3-C5
16	Y	301	3E5	C1-C2-C3-C4
16	K	301	3E5	C29-C28-O4-C27
16	K	301	3E5	O2-C12-C7-C8

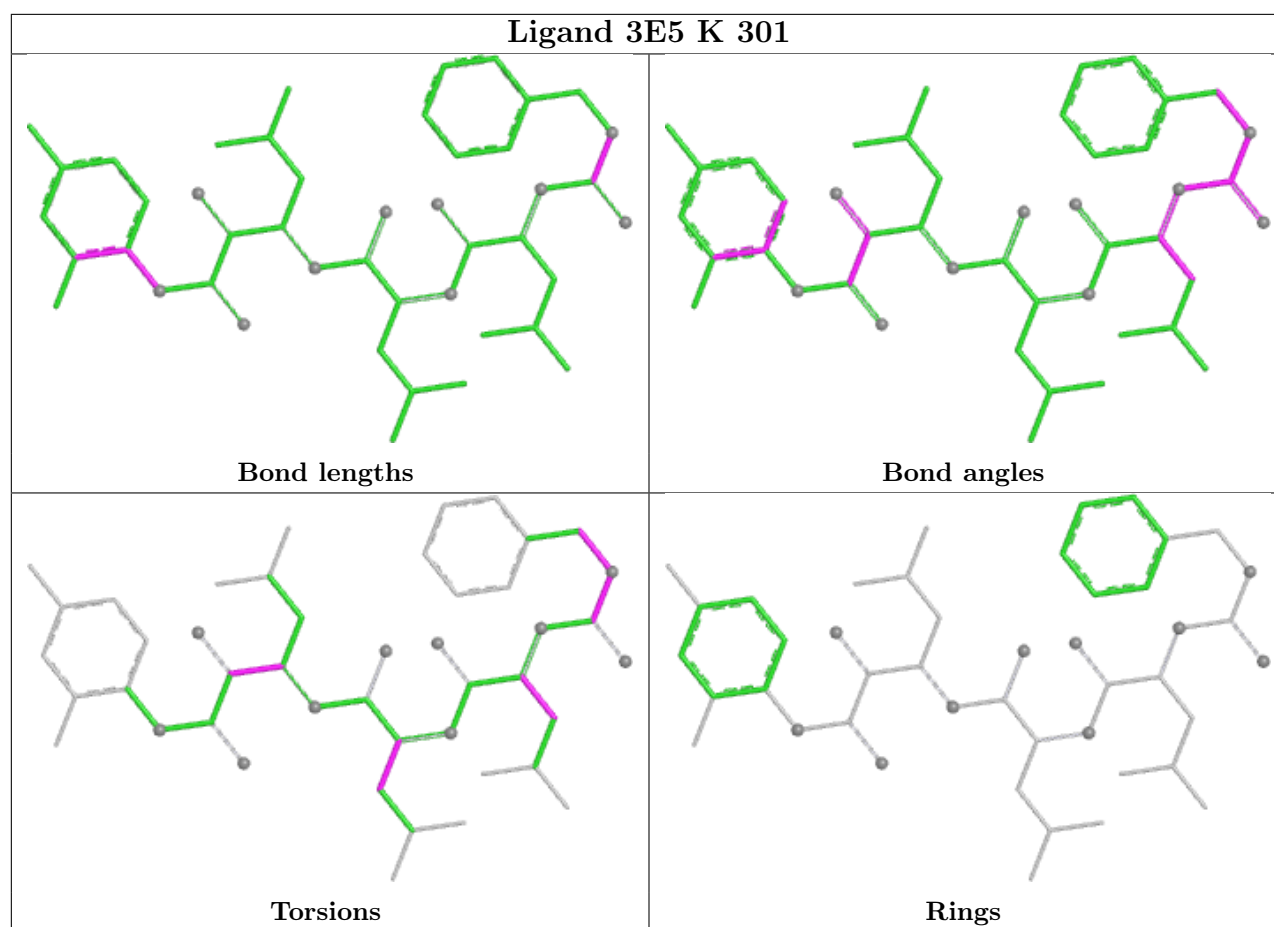
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	K	301	3E5	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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%)	-0.62	0 100 100	33, 45, 74, 117	0
1	O	250/250 (100%)	-0.54	2 (0%) 82 80	36, 51, 88, 125	0
2	B	244/258 (94%)	-0.49	4 (1%) 70 67	33, 50, 90, 144	0
2	P	244/258 (94%)	-0.46	3 (1%) 76 73	37, 53, 102, 153	0
3	C	240/254 (94%)	-0.41	2 (0%) 82 80	34, 55, 115, 143	0
3	Q	240/254 (94%)	-0.26	6 (2%) 58 54	38, 64, 132, 161	0
4	D	235/260 (90%)	-0.54	0 100 100	36, 54, 82, 120	0
4	R	235/260 (90%)	-0.51	0 100 100	36, 56, 85, 136	0
5	E	231/234 (98%)	-0.46	1 (0%) 88 86	39, 57, 86, 120	0
5	S	231/234 (98%)	-0.40	0 100 100	40, 57, 87, 120	0
6	F	243/288 (84%)	-0.55	2 (0%) 82 80	33, 48, 90, 131	0
6	T	243/288 (84%)	-0.46	5 (2%) 63 59	33, 51, 93, 124	0
7	G	241/252 (95%)	-0.68	0 100 100	32, 46, 79, 122	0
7	U	241/252 (95%)	-0.65	0 100 100	33, 47, 78, 106	0
8	H	226/232 (97%)	-0.59	2 (0%) 81 78	34, 44, 73, 133	0
8	V	226/232 (97%)	-0.57	2 (0%) 81 78	34, 47, 78, 159	0
9	I	204/205 (99%)	-0.72	0 100 100	30, 45, 72, 100	0
9	W	204/205 (99%)	-0.65	1 (0%) 87 85	33, 47, 78, 106	0
10	J	195/198 (98%)	-0.63	1 (0%) 87 85	30, 45, 69, 137	0
10	X	195/198 (98%)	-0.60	1 (0%) 87 85	33, 46, 71, 125	0
11	K	212/212 (100%)	-0.56	2 (0%) 81 78	33, 46, 81, 97	0
11	Y	212/212 (100%)	-0.55	1 (0%) 87 85	33, 46, 83, 107	0
12	L	222/222 (100%)	-0.66	0 100 100	32, 46, 75, 100	0
12	Z	222/222 (100%)	-0.65	0 100 100	31, 45, 75, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.72	1 (0%) 88 86	29, 44, 63, 77	0
13	a	233/246 (94%)	-0.75	1 (0%) 88 86	29, 42, 61, 74	0
14	N	196/196 (100%)	-0.77	1 (0%) 87 85	31, 40, 66, 85	0
14	b	196/196 (100%)	-0.77	0 100 100	30, 41, 65, 94	0
All	All	6344/6614 (95%)	-0.57	38 (0%) 85 83	29, 48, 86, 161	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	X	1	MET	7.1
10	J	1	MET	6.0
3	Q	50	LEU	5.1
6	T	178	HIS	4.2
8	H	223	ILE	3.7
1	O	53	SER	3.2
8	V	223	ILE	3.1
13	a	1	THR	3.0
6	T	215	CYS	3.0
3	Q	49	THR	2.8
6	F	215	CYS	2.8
8	V	224	GLN	2.7
2	B	52	THR	2.6
3	Q	205	ALA	2.6
3	Q	204	GLY	2.6
11	K	182	GLU	2.5
2	B	51	VAL	2.5
5	E	122	TYR	2.5
14	N	103	ASP	2.4
8	H	224	GLN	2.4
2	P	52	THR	2.4
6	T	243	ILE	2.4
3	C	205	ALA	2.4
3	Q	240	GLU	2.4
6	T	179	HIS	2.3
2	P	51	VAL	2.3
3	Q	234	ILE	2.3
11	Y	209	ASN	2.2
6	T	204	LYS	2.2
2	P	218	GLY	2.2
2	B	93	HIS	2.1
6	F	178	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	219	ALA	2.1
1	O	249	ALA	2.1
11	K	212	GLY	2.0
13	M	1	THR	2.0
3	C	50	LEU	2.0
9	W	130	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

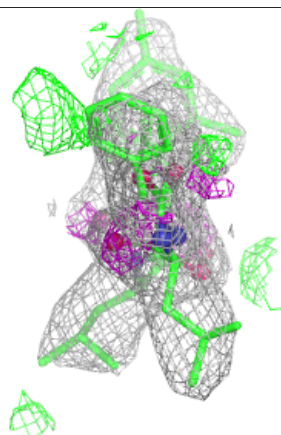
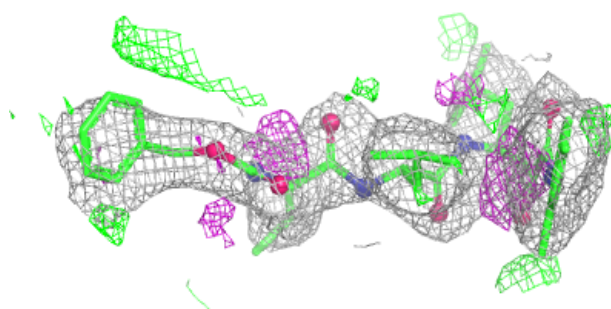
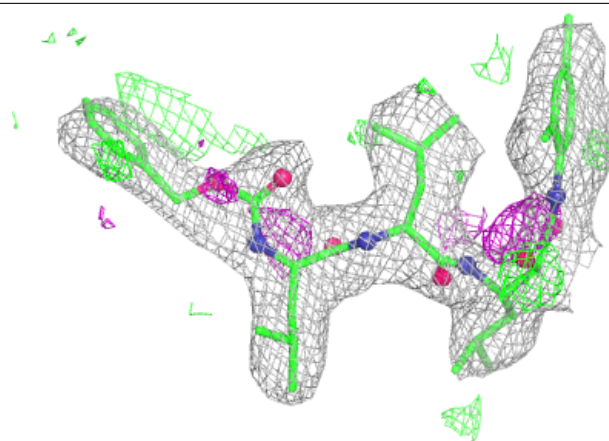
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
16	3E5	Y	301	45/45	0.87	0.14	58,72,101,106	0
16	3E5	K	301	45/45	0.88	0.12	52,69,89,95	0
15	MG	I	302	1/1	0.89	0.30	82,82,82,82	0
15	MG	N	202	1/1	0.91	0.11	82,82,82,82	0
15	MG	K	303	1/1	0.94	0.14	49,49,49,49	0
15	MG	Z	301	1/1	0.95	0.07	54,54,54,54	0
15	MG	J	201	1/1	0.97	0.06	61,61,61,61	0
15	MG	N	201	1/1	0.98	0.12	48,48,48,48	0
15	MG	V	301	1/1	0.98	0.11	42,42,42,42	0
15	MG	Y	302	1/1	0.98	0.10	42,42,42,42	0
15	MG	K	302	1/1	0.99	0.12	47,47,47,47	0
15	MG	G	301	1/1	0.99	0.03	40,40,40,40	0
15	MG	I	301	1/1	0.99	0.04	54,54,54,54	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

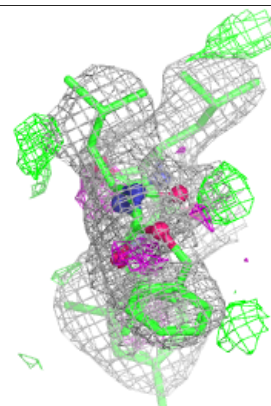
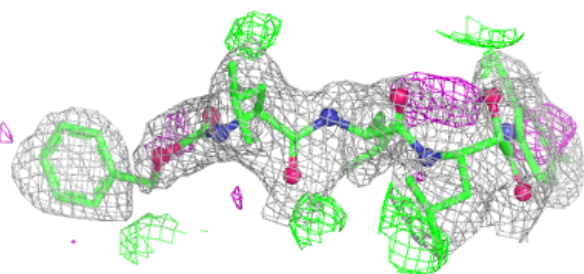
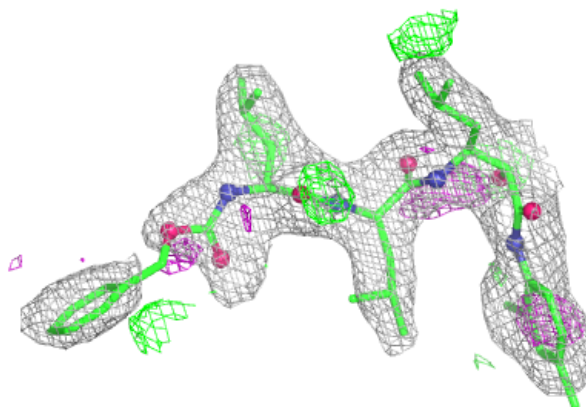
Electron density around 3E5 Y 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 3E5 K 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.