



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:08 PM GMT

PDB ID : 4NNW
Title : yCP in complex with Z-Leu-Leu-Leu-ketoaldehyde
Authors : Stein, M.L.; Cui, H.; Beck, P.; Dubiella, C.; Voss, C.; Krueger, A.; Schmidt, B.; Groll, M.
Deposited on : 2013-11-19
Resolution : 2.60 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

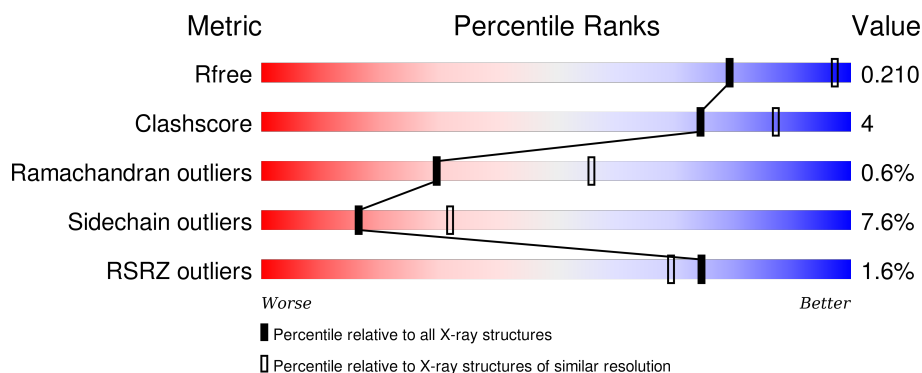
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



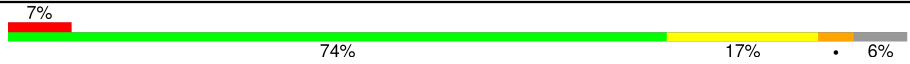

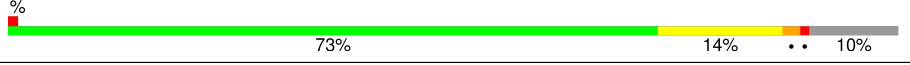



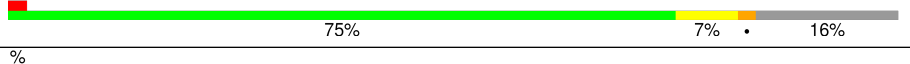

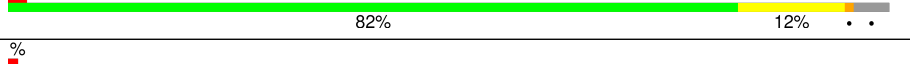


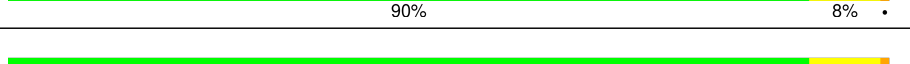

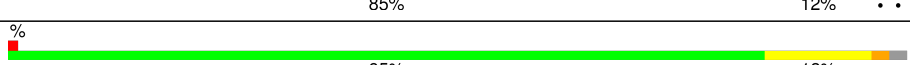

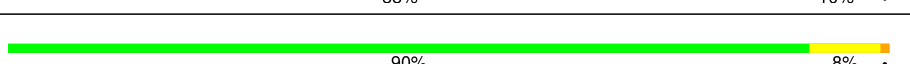
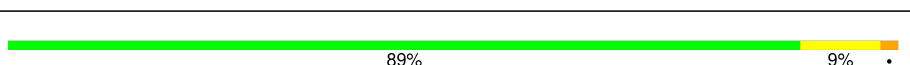
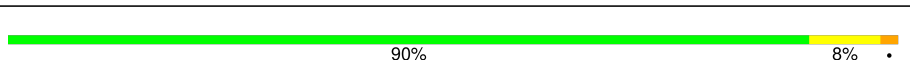
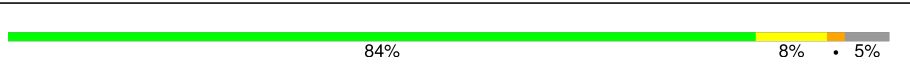

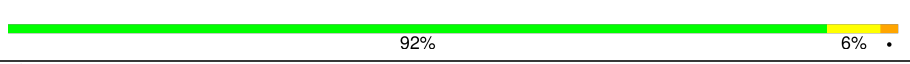
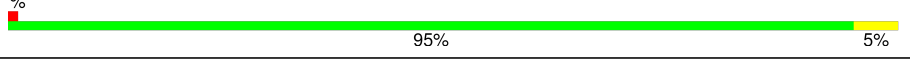
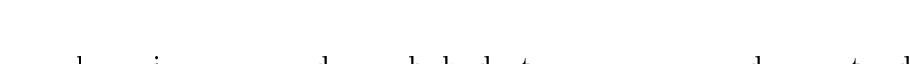
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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>92%</div> <div>7%</div> </div>
1	O	250	<div> <div>2%</div> <div>92%</div> <div>7%</div> </div>
2	B	258	<div> <div>5%</div> <div>73%</div> <div>19%</div> <div>5%</div> </div>
2	P	258	<div> <div>4%</div> <div>75%</div> <div>17%</div> <div>5%</div> </div>
3	C	254	<div> <div>5%</div> <div>74%</div> <div>17%</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	

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
15	MG	Z	301	-	-	-	X
16	2MK	H	301	-	-	-	X
16	2MK	K	301	-	-	-	X
16	2MK	N	201	-	-	-	X
16	2MK	V	301	-	-	-	X
16	2MK	Y	301	-	-	-	X
16	2MK	b	201	-	-	-	X

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 50159 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
			1684	1061	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	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 (three-letter code: MG) (formula: Mg).

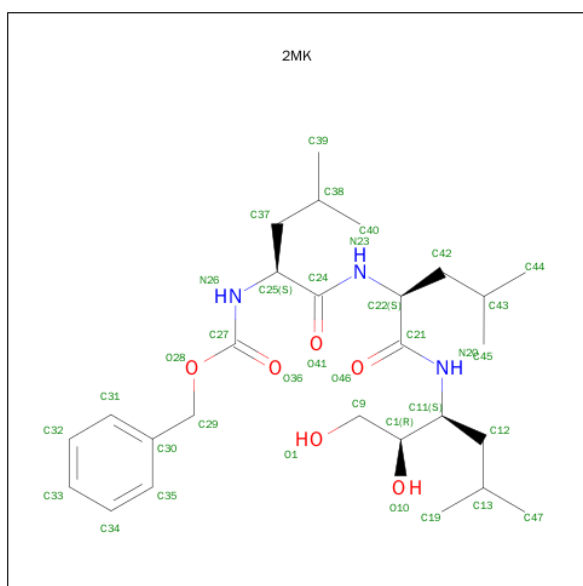
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	K	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	H	1	Total	Mg	0	0
			1	1		
15	I	1	Total	Mg	0	0
			1	1		
15	V	1	Total	Mg	0	0
			1	1		
15	Z	1	Total	Mg	0	0
			1	1		
15	N	1	Total	Mg	0	0
			1	1		
15	Y	1	Total	Mg	0	0
			1	1		

- Molecule 16 is N-[(BENZYLOXY)CARBONYL]-L-LEUCYL-N-[(2R,3S)-1,2-DIHYDROXY-5-METHYLHEXAN-3-YL]-L-LEUCINAMIDE (three-letter code: 2MK) (formula: $C_{27}H_{45}N_3O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	H	1	Total	C	N	O	0	0
			35	27	3	5		
16	K	1	Total	C	N	O	0	0
			35	27	3	5		
16	N	1	Total	C	N	O	0	0
			35	27	3	5		
16	V	1	Total	C	N	O	0	0
			35	27	3	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	Y	1	Total	C	N	O	0	0
			35	27	3	5		
16	b	1	Total	C	N	O	0	0
			35	27	3	5		

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	31	Total	O	0	0
			31	31		
17	B	23	Total	O	0	0
			23	23		
17	C	10	Total	O	0	0
			10	10		
17	D	19	Total	O	0	0
			19	19		
17	E	9	Total	O	0	0
			9	9		
17	F	25	Total	O	0	0
			25	25		
17	G	30	Total	O	0	0
			30	30		
17	H	39	Total	O	0	0
			39	39		
17	I	33	Total	O	0	0
			33	33		
17	J	17	Total	O	0	0
			17	17		
17	K	29	Total	O	0	0
			29	29		
17	L	31	Total	O	0	0
			31	31		
17	M	44	Total	O	0	0
			44	44		
17	N	25	Total	O	0	0
			25	25		
17	O	10	Total	O	0	0
			10	10		
17	P	6	Total	O	0	0
			6	6		
17	Q	7	Total	O	0	0
			7	7		

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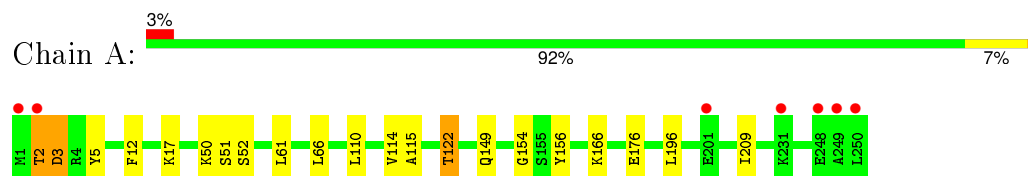
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	R	14	Total 14	O 14	0	0
17	S	8	Total 8	O 8	0	0
17	T	24	Total 24	O 24	0	0
17	U	28	Total 28	O 28	0	0
17	V	31	Total 31	O 31	0	0
17	W	19	Total 19	O 19	0	0
17	X	18	Total 18	O 18	0	0
17	Y	17	Total 17	O 17	0	0
17	Z	34	Total 34	O 34	0	0
17	a	39	Total 39	O 39	0	0
17	b	25	Total 25	O 25	0	0

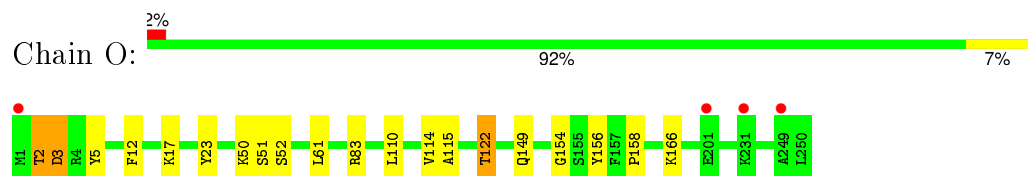
3 Residue-property plots [i](#)

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.

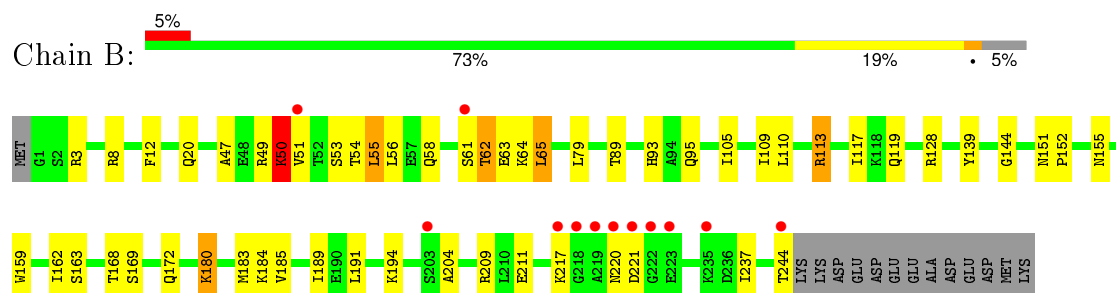
- Molecule 1: Proteasome subunit alpha type-2



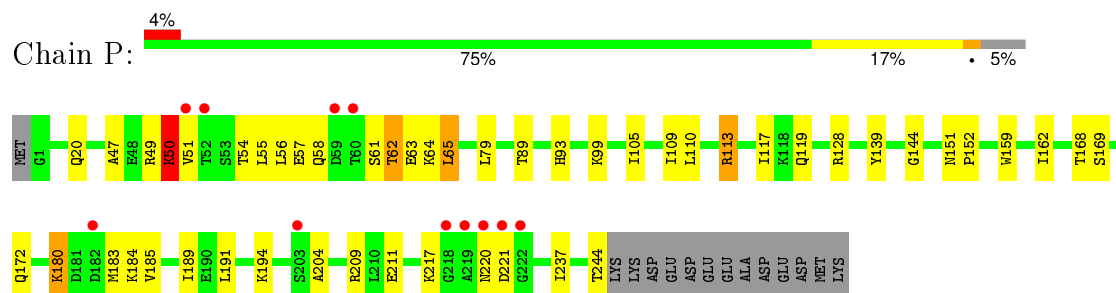
- Molecule 1: Proteasome subunit alpha type-2



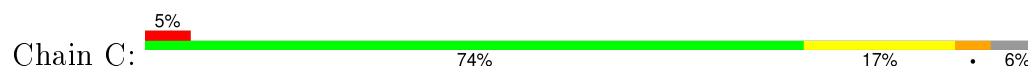
- Molecule 2: Proteasome subunit alpha type-3

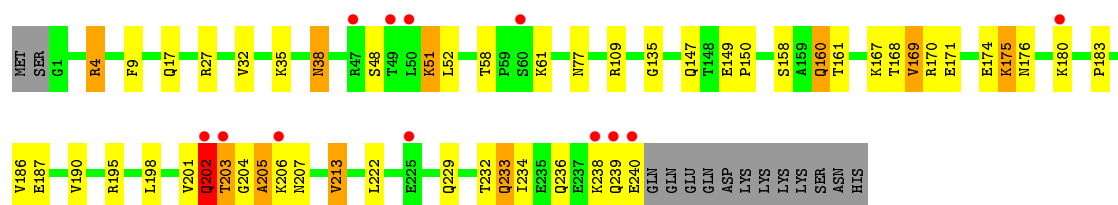


- Molecule 2: Proteasome subunit alpha type-3

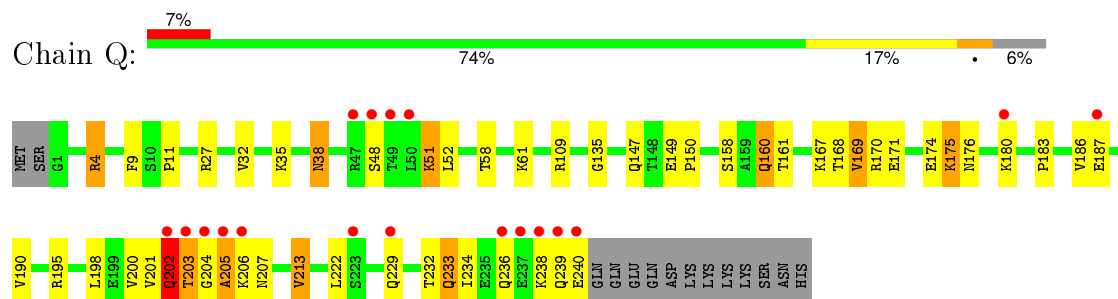


- Molecule 3: Proteasome subunit alpha type-4

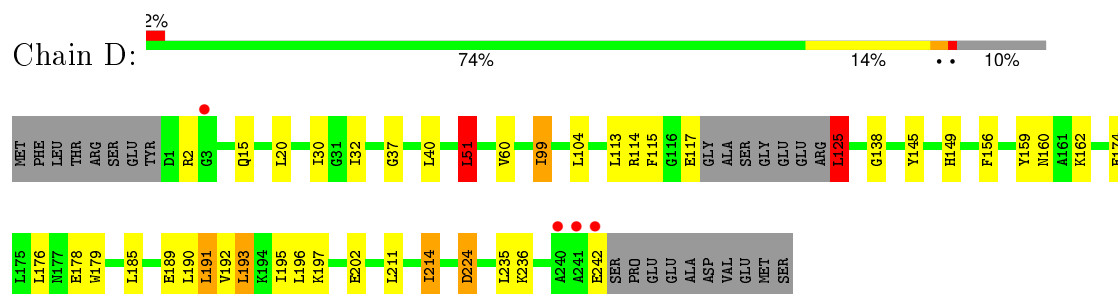




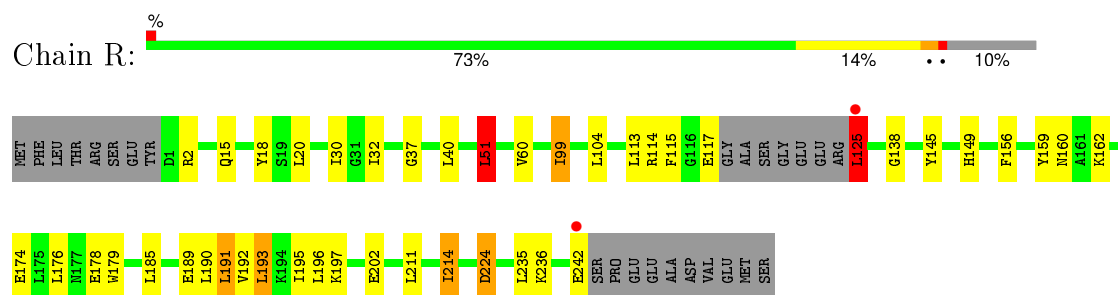
• Molecule 3: Proteasome subunit alpha type-4



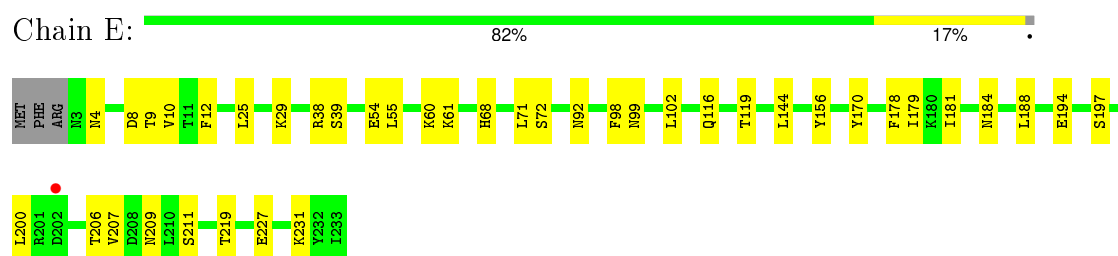
• Molecule 4: Proteasome subunit alpha type-5



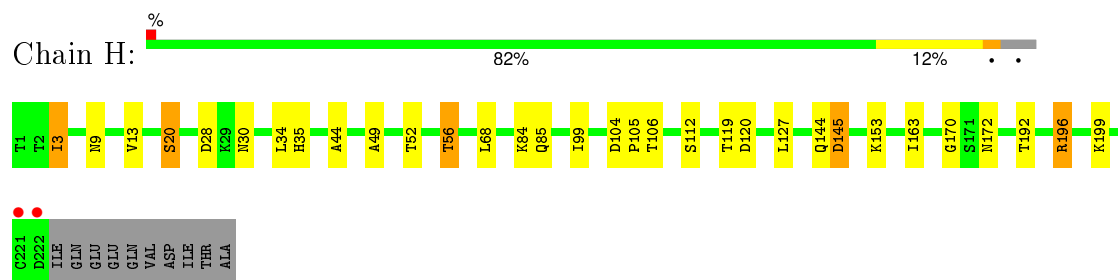
• Molecule 4: Proteasome subunit alpha type-5



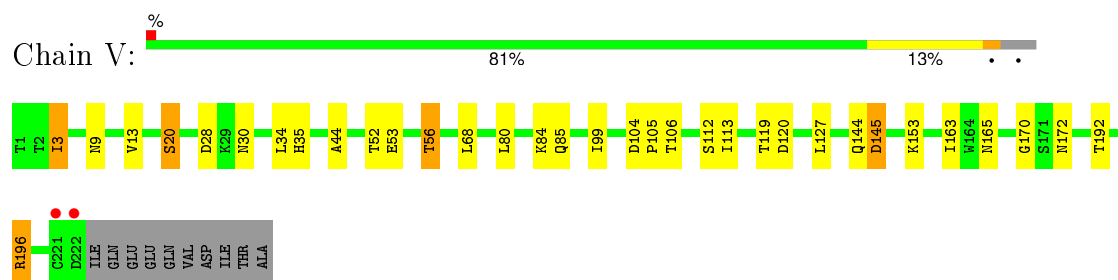
• Molecule 5: Proteasome subunit alpha type-6



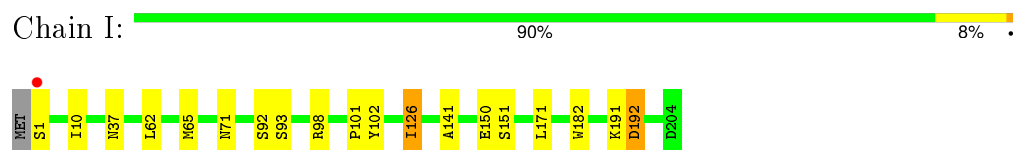
• Molecule 5: Proteasome subunit alpha type-6



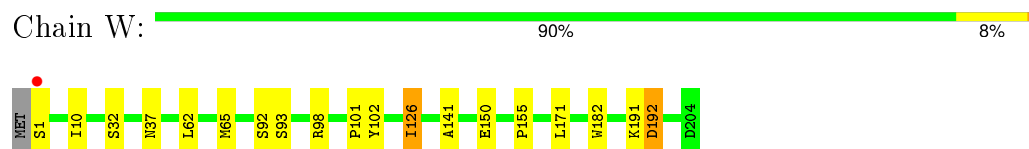
- Molecule 8: Proteasome subunit beta type-2



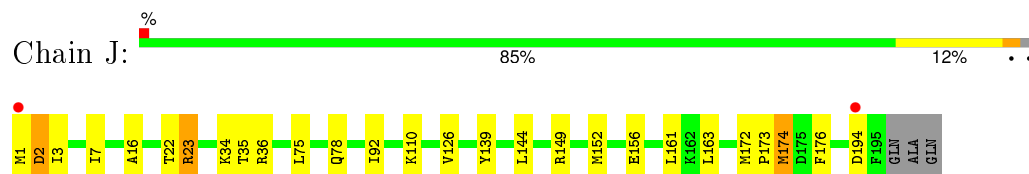
- Molecule 9: Proteasome subunit beta type-3



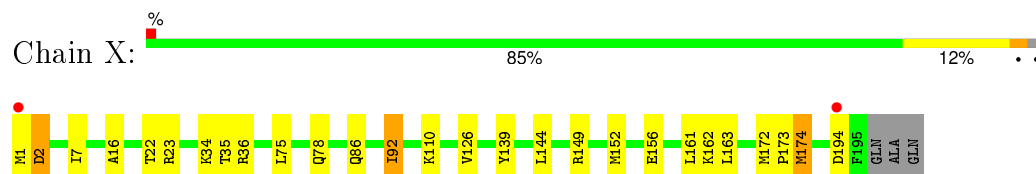
- Molecule 9: Proteasome subunit beta type-3



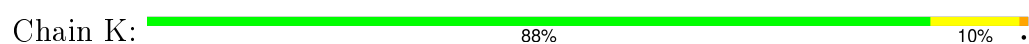
- Molecule 10: Proteasome subunit beta type-4

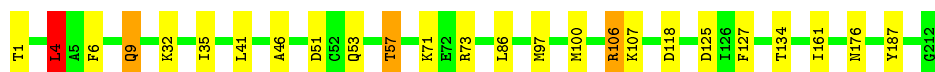


- Molecule 10: Proteasome subunit beta type-4



- Molecule 11: Proteasome subunit beta type-5





- Molecule 11: Proteasome subunit beta type-5

Chain Y: 90% 8%



- Molecule 12: Proteasome subunit beta type-6

Chain L: 89% 9%



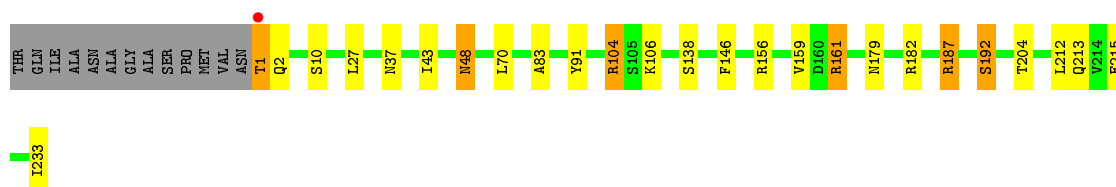
- Molecule 12: Proteasome subunit beta type-6

Chain Z: 90% 8%



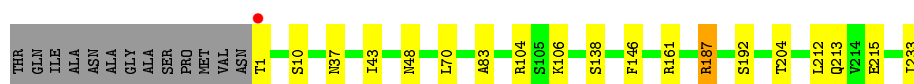
- Molecule 13: Proteasome subunit beta type-7

Chain M: 84% 8% 5%



- Molecule 13: Proteasome subunit beta type-7

Chain a: 87% 7% 5%

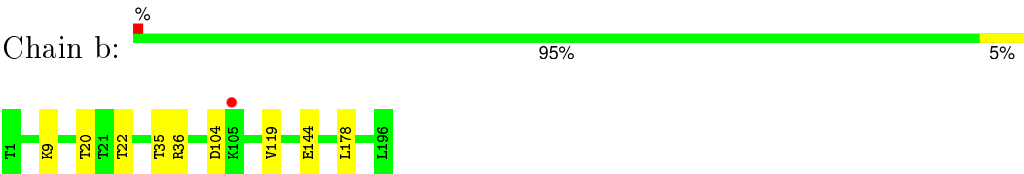


- Molecule 14: Proteasome subunit beta type-1

Chain N: 92% 6% 2%



- Molecule 14: Proteasome subunit beta type-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.64Å 301.29Å 145.12Å 90.00° 113.71° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60 14.99 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.0 (15.00-2.60) 99.0 (14.99-2.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.195 , 0.208 0.197 , 0.210	Depositor DCC
R_{free} test set	16078 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 321558 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	50159	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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: 2MK, MG

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	0.31	0/1952	0.61	0/2642
1	O	0.31	0/1952	0.61	0/2642
2	B	0.30	0/1934	0.63	1/2618 (0.0%)
2	P	0.30	0/1934	0.63	1/2618 (0.0%)
3	C	0.31	0/1910	0.64	0/2586
3	Q	0.31	0/1910	0.64	0/2586
4	D	0.31	0/1837	0.64	2/2475 (0.1%)
4	R	0.31	0/1837	0.64	2/2475 (0.1%)
5	E	0.29	0/1800	0.59	0/2433
5	S	0.29	0/1800	0.59	0/2433
6	F	0.32	0/1932	0.58	0/2609
6	T	0.32	0/1932	0.59	0/2609
7	G	0.30	0/1945	0.59	1/2634 (0.0%)
7	U	0.30	0/1945	0.59	1/2634 (0.0%)
8	H	0.28	0/1715	0.60	0/2326
8	V	0.28	0/1715	0.60	0/2326
9	I	0.30	0/1611	0.60	0/2174
9	W	0.30	0/1611	0.60	0/2174
10	J	0.30	0/1589	0.61	0/2142
10	X	0.29	0/1589	0.61	0/2142
11	K	0.30	0/1681	0.61	1/2274 (0.0%)
11	Y	0.30	0/1681	0.61	1/2274 (0.0%)
12	L	0.29	0/1795	0.57	0/2420
12	Z	0.28	0/1795	0.57	0/2420
13	M	0.32	0/1855	0.65	1/2514 (0.0%)
13	a	0.31	0/1855	0.65	1/2514 (0.0%)
14	N	0.29	0/1541	0.55	0/2087
14	b	0.29	0/1541	0.55	0/2087
All	All	0.30	0/50194	0.61	12/67868 (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
2	B	0	1
2	P	0	1
9	I	0	2
9	W	0	2
12	L	0	1
12	Z	0	1
13	M	0	1
13	a	0	1
All	All	0	10

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	125	LEU	CA-CB-CG	6.62	130.53	115.30
4	D	125	LEU	CA-CB-CG	6.58	130.44	115.30
4	D	51	LEU	CA-CB-CG	5.98	129.05	115.30
4	R	51	LEU	CA-CB-CG	5.96	129.02	115.30
7	U	34	LEU	CA-CB-CG	5.35	127.61	115.30
13	M	187	ARG	NE-CZ-NH1	5.34	122.97	120.30
7	G	34	LEU	CA-CB-CG	5.33	127.56	115.30
11	K	4	LEU	CA-CB-CG	5.14	127.11	115.30
13	a	187	ARG	NE-CZ-NH1	5.10	122.85	120.30
11	Y	4	LEU	CA-CB-CG	5.07	126.96	115.30
2	B	113	ARG	NE-CZ-NH1	5.06	122.83	120.30
2	P	113	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	50	LYS	Peptide
9	I	1	SER	Peptide
9	I	192	ASP	Peptide
12	L	135	GLN	Peptide
13	M	1	THR	Peptide
2	P	50	LYS	Peptide
9	W	1	SER	Peptide

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Mol	Chain	Res	Type	Group
9	W	192	ASP	Peptide
12	Z	135	GLN	Peptide
13	a	1	THR	Peptide

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	12	0
1	O	1915	0	1929	10	0
2	B	1904	0	1904	32	0
2	P	1904	0	1904	25	0
3	C	1881	0	1895	33	0
3	Q	1881	0	1895	33	0
4	D	1813	0	1797	20	0
4	R	1813	0	1797	21	0
5	E	1773	0	1775	14	0
5	S	1773	0	1775	11	0
6	F	1892	0	1883	7	0
6	T	1892	0	1883	8	0
7	G	1907	0	1901	11	0
7	U	1907	0	1901	13	0
8	H	1684	0	1686	19	0
8	V	1684	0	1686	19	0
9	I	1581	0	1574	10	0
9	W	1581	0	1574	9	0
10	J	1561	0	1569	14	0
10	X	1561	0	1569	15	0
11	K	1644	0	1593	13	0
11	Y	1644	0	1593	10	0
12	L	1757	0	1711	12	0
12	Z	1757	0	1711	11	0
13	M	1824	0	1832	11	0
13	a	1824	0	1832	0	0
14	N	1512	0	1479	9	0
14	b	1512	0	1479	0	0
15	G	1	0	0	0	0
15	H	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	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	H	35	0	41	2	0
16	K	35	0	41	0	0
16	N	35	0	41	1	0
16	V	35	0	41	0	0
16	Y	35	0	41	0	0
16	b	35	0	41	0	0
17	A	31	0	0	0	0
17	B	23	0	0	0	0
17	C	10	0	0	0	0
17	D	19	0	0	0	0
17	E	9	0	0	0	0
17	F	25	0	0	0	0
17	G	30	0	0	0	0
17	H	39	0	0	0	0
17	I	33	0	0	0	0
17	J	17	0	0	0	0
17	K	29	0	0	1	0
17	L	31	0	0	0	0
17	M	44	0	0	0	0
17	N	25	0	0	0	0
17	O	10	0	0	0	0
17	P	6	0	0	0	0
17	Q	7	0	0	1	0
17	R	14	0	0	0	0
17	S	8	0	0	0	0
17	T	24	0	0	0	0
17	U	28	0	0	0	0
17	V	31	0	0	0	0
17	W	19	0	0	1	0
17	X	18	0	0	0	0
17	Y	17	0	0	0	0
17	Z	34	0	0	0	0
17	a	39	0	0	0	0
17	b	25	0	0	0	0
All	All	50159	0	49302	367	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 4.

All (367) 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)
3:C:201:VAL:O	3:C:202:GLN:HB3	1.52	1.06
3:Q:201:VAL:O	3:Q:202:GLN:HB3	1.52	1.03
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.24	0.98
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.24	0.97
3:Q:202:GLN:HG3	3:Q:203:THR:H	1.31	0.95
3:C:202:GLN:HG3	3:C:203:THR:H	1.31	0.95
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.54	0.89
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.56	0.88
11:K:100:MET:CE	11:K:127:PHE:HB2	2.07	0.84
11:Y:100:MET:CE	11:Y:127:PHE:HB2	2.06	0.84
3:Q:202:GLN:HG3	3:Q:203:THR:N	1.96	0.81
8:V:3:ILE:HG12	8:V:44:ALA:HB1	1.65	0.78
3:C:202:GLN:HG3	3:C:203:THR:N	1.96	0.78
14:N:20:THR:CG2	14:N:28:ASN:HB3	2.15	0.77
8:H:3:ILE:HG12	8:H:44:ALA:HB1	1.65	0.76
5:S:9:THR:HG21	5:S:119:THR:HA	1.69	0.75
14:N:20:THR:HG23	14:N:28:ASN:HB3	1.67	0.75
14:N:20:THR:HG22	14:N:31:THR:OG1	1.88	0.74
3:C:51:LYS:O	3:C:52:LEU:HB2	1.87	0.74
2:B:50:LYS:HE3	2:B:50:LYS:HA	1.69	0.74
5:E:9:THR:HG21	5:E:119:THR:HA	1.69	0.73
2:P:50:LYS:HA	2:P:50:LYS:HE3	1.69	0.73
4:D:32:ILE:HD12	4:D:192:VAL:HG23	1.69	0.73
4:R:32:ILE:HD12	4:R:192:VAL:HG23	1.69	0.72
3:Q:51:LYS:O	3:Q:52:LEU:HB2	1.87	0.72
3:Q:160:GLN:HE22	3:Q:170:ARG:HE	1.38	0.72
3:C:161:THR:HG21	3:C:169:VAL:HG22	1.71	0.71
11:K:53:GLN:O	11:K:57:THR:HG23	1.90	0.71
3:Q:161:THR:HG21	3:Q:169:VAL:HG22	1.72	0.71
3:C:160:GLN:HE22	3:C:170:ARG:HE	1.38	0.70
7:G:63:ILE:HD12	7:G:215:GLU:HG2	1.73	0.70
7:U:63:ILE:HD12	7:U:215:GLU:HG2	1.74	0.70
11:Y:53:GLN:O	11:Y:57:THR:HG23	1.90	0.70
5:E:12:PHE:H	6:F:19:GLN:HE22	1.40	0.69
3:C:160:GLN:HE21	3:C:161:THR:H	1.41	0.69
3:Q:160:GLN:HE21	3:Q:161:THR:H	1.42	0.68
5:S:12:PHE:H	6:T:19:GLN:HE22	1.43	0.67
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:195:ARG:HG3	3:Q:234:ILE:HD13	1.77	0.67
3:C:195:ARG:HG3	3:C:234:ILE:HD13	1.77	0.66
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.59	0.66
4:R:99:ILE:HD13	4:R:104:LEU:HB2	1.78	0.66
2:B:204:ALA:O	2:B:209:ARG:NH2	2.29	0.66
1:O:122:THR:CG2	2:P:128:ARG:HH21	2.09	0.65
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.42	0.65
2:P:204:ALA:O	2:P:209:ARG:NH2	2.30	0.65
4:R:138:GLY:HA2	4:R:214:ILE:HG12	1.79	0.64
3:C:175:LYS:HD3	3:C:176:ASN:ND2	2.12	0.64
3:Q:175:LYS:HD3	3:Q:176:ASN:ND2	2.13	0.64
4:D:99:ILE:HD13	4:D:104:LEU:HB2	1.78	0.64
2:B:50:LYS:HA	2:B:50:LYS:CE	2.29	0.63
3:Q:175:LYS:HD3	3:Q:176:ASN:HD22	1.64	0.62
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.81	0.62
2:P:50:LYS:HA	2:P:50:LYS:CE	2.29	0.62
4:D:138:GLY:HA2	4:D:214:ILE:HG12	1.80	0.62
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.81	0.62
3:C:175:LYS:HD3	3:C:176:ASN:HD22	1.64	0.61
12:L:17:GLY:HA3	12:L:20:PHE:CE1	2.36	0.61
7:U:23:PHE:O	7:U:26:THR:HB	2.01	0.61
9:I:101:PRO:HB3	9:I:126:ILE:HD12	1.83	0.61
13:M:1:THR:HG22	13:M:2:GLN:H	1.66	0.61
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.64	0.60
9:W:101:PRO:HB3	9:W:126:ILE:HD12	1.83	0.60
12:Z:17:GLY:HA3	12:Z:20:PHE:CE1	2.37	0.60
2:B:180:LYS:O	2:B:183:MET:HB2	2.01	0.60
1:A:122:THR:CG2	2:B:128:ARG:HH21	2.15	0.59
10:J:1:MET:HA	10:J:34:LYS:HE3	1.83	0.59
10:X:1:MET:HA	10:X:34:LYS:HE3	1.83	0.59
2:P:180:LYS:O	2:P:183:MET:HB2	2.01	0.59
3:Q:229:GLN:O	3:Q:233:GLN:HB2	2.02	0.59
7:G:23:PHE:O	7:G:26:THR:HB	2.01	0.59
3:C:229:GLN:O	3:C:233:GLN:HB2	2.02	0.58
4:D:125:LEU:HD12	4:D:125:LEU:O	2.03	0.58
4:R:125:LEU:HD12	4:R:125:LEU:O	2.03	0.58
10:J:23:ARG:HD3	17:K:411:HOH:O	2.02	0.58
3:Q:48:SER:HB2	3:Q:207:ASN:OD1	2.04	0.58
11:Y:106:ARG:HH11	11:Y:106:ARG:HB3	1.68	0.58
11:K:106:ARG:HB3	11:K:106:ARG:HH11	1.68	0.57
3:C:48:SER:HB2	3:C:207:ASN:OD1	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:34:LEU:HD23	7:G:34:LEU:C	2.25	0.57
3:C:9:PHE:H	4:D:15:GLN:HE22	1.52	0.57
10:J:173:PRO:HB3	10:X:22:THR:HG21	1.87	0.57
2:B:12:PHE:H	3:C:17:GLN:HE22	1.51	0.57
1:O:12:PHE:H	2:P:20:GLN:HE22	1.52	0.57
8:H:52:THR:O	8:H:56:THR:HB	2.04	0.57
8:V:52:THR:O	8:V:56:THR:HB	2.05	0.56
10:J:22:THR:HG21	10:X:173:PRO:HB3	1.87	0.56
10:J:7:ILE:HD12	10:J:161:LEU:HD13	1.88	0.56
4:R:193:LEU:HD21	4:R:211:LEU:HD11	1.87	0.56
12:L:49:ASN:HD21	12:L:211:GLY:HA2	1.71	0.56
10:X:7:ILE:HD12	10:X:161:LEU:HD13	1.88	0.56
13:M:161:ARG:HH11	13:M:161:ARG:HG3	1.71	0.55
4:D:113:LEU:HD23	4:D:115:PHE:HE1	1.71	0.55
12:Z:49:ASN:HD21	12:Z:211:GLY:HA2	1.70	0.55
7:U:34:LEU:C	7:U:34:LEU:HD23	2.26	0.55
10:J:152:MET:HE3	10:J:156:GLU:HB3	1.89	0.55
9:I:98:ARG:HD2	9:I:126:ILE:HG12	1.90	0.54
11:Y:100:MET:HE3	11:Y:127:PHE:CB	2.33	0.54
4:R:113:LEU:HD23	4:R:115:PHE:HE1	1.71	0.54
4:R:185:LEU:O	4:R:189:GLU:HG3	2.08	0.54
4:D:185:LEU:O	4:D:189:GLU:HG3	2.07	0.54
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.40	0.54
4:D:30:ILE:HD12	4:D:196:LEU:HG	1.89	0.54
9:W:98:ARG:HD2	9:W:126:ILE:HG12	1.90	0.54
10:J:1:MET:HA	10:J:34:LYS:CE	2.38	0.54
10:X:1:MET:HA	10:X:34:LYS:CE	2.38	0.54
4:D:193:LEU:HD21	4:D:211:LEU:HD11	1.88	0.54
3:C:51:LYS:HA	3:C:51:LYS:HE3	1.89	0.53
6:T:172:LEU:HD13	6:T:195:ILE:HD13	1.90	0.53
6:F:172:LEU:HD13	6:F:195:ILE:HD13	1.90	0.53
4:R:30:ILE:HD12	4:R:196:LEU:HG	1.90	0.53
4:R:193:LEU:CD2	4:R:211:LEU:HD11	2.38	0.53
3:Q:51:LYS:HA	3:Q:51:LYS:HE3	1.89	0.53
14:N:13:ILE:HG21	14:N:175:MET:CE	2.39	0.53
9:W:32:SER:OG	17:W:303:HOH:O	2.18	0.53
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.43	0.53
4:D:193:LEU:CD2	4:D:211:LEU:HD11	2.38	0.53
3:C:35:LYS:HG2	3:C:158:SER:O	2.09	0.53
8:V:144:GLN:O	8:V:145:ASP:HB2	2.09	0.52
3:Q:168:THR:O	3:Q:171:GLU:HB3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:ARG:HD2	3:C:4:ARG:NH2	2.24	0.52
3:C:38:ASN:N	3:C:38:ASN:HD22	2.07	0.52
3:C:168:THR:O	3:C:171:GLU:HB3	2.09	0.52
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.92	0.52
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.91	0.52
3:Q:38:ASN:N	3:Q:38:ASN:HD22	2.07	0.52
11:K:86:LEU:HD13	11:K:86:LEU:C	2.30	0.52
13:M:48:ASN:H	13:M:48:ASN:HD22	1.58	0.52
8:H:144:GLN:O	8:H:145:ASP:HB2	2.09	0.52
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.45	0.52
11:Y:86:LEU:HD13	11:Y:86:LEU:C	2.30	0.52
8:V:163:ILE:HG23	8:V:170:GLY:HA2	1.91	0.52
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.92	0.51
8:H:163:ILE:HG23	8:H:170:GLY:HA2	1.91	0.51
2:B:159:TRP:CD2	2:B:162:ILE:HD13	2.46	0.51
12:L:195:HIS:HD2	12:L:197:GLN:H	1.58	0.51
6:F:123:ASN:HD22	6:F:123:ASN:C	2.14	0.51
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.58	0.51
6:T:123:ASN:HD22	6:T:123:ASN:C	2.14	0.51
12:L:23:LEU:HD13	12:L:43:VAL:HG13	1.93	0.51
14:N:35:THR:CG2	14:N:45:ARG:HE	2.23	0.51
4:R:99:ILE:CD1	4:R:104:LEU:HB2	2.41	0.51
4:D:99:ILE:CD1	4:D:104:LEU:HB2	2.41	0.51
1:A:12:PHE:H	2:B:20:GLN:HE22	1.58	0.51
1:O:115:ALA:HB1	1:O:154:GLY:O	2.11	0.51
9:I:101:PRO:HB3	9:I:126:ILE:CD1	2.41	0.50
7:U:239:ILE:O	7:U:242:GLN:HB3	2.11	0.50
8:V:112:SER:OG	8:V:120:ASP:HB2	2.11	0.50
13:M:156:ARG:HH11	8:V:165:ASN:HD22	1.58	0.50
8:H:49:ALA:HA	16:H:301:2MK:H12	1.93	0.50
3:Q:205:ALA:C	3:Q:207:ASN:H	2.15	0.50
3:C:205:ALA:C	3:C:207:ASN:H	2.14	0.50
1:A:115:ALA:HB1	1:A:154:GLY:O	2.12	0.50
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.92	0.50
7:U:83:ASN:C	7:U:83:ASN:HD22	2.15	0.50
11:K:100:MET:HE3	11:K:127:PHE:CB	2.34	0.50
2:P:89:THR:HG21	2:P:117:ILE:CD1	2.41	0.50
4:R:159:TYR:CZ	4:R:162:LYS:HD3	2.47	0.50
2:B:89:THR:HG21	2:B:117:ILE:CD1	2.41	0.50
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.76	0.50
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.11	0.50
9:W:101:PRO:HB3	9:W:126:ILE:CD1	2.41	0.50
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.93	0.50
8:H:112:SER:OG	8:H:120:ASP:HB2	2.12	0.49
7:G:239:ILE:O	7:G:242:GLN:HB3	2.11	0.49
2:P:159:TRP:CD2	2:P:162:ILE:HD13	2.46	0.49
12:Z:23:LEU:HD13	12:Z:43:VAL:HG13	1.93	0.49
10:X:152:MET:HE3	10:X:156:GLU:HB3	1.94	0.49
4:D:159:TYR:CZ	4:D:162:LYS:HD3	2.47	0.49
7:G:83:ASN:C	7:G:83:ASN:HD22	2.15	0.49
6:T:146:MET:CE	6:T:161:THR:HB	2.42	0.49
11:K:6:PHE:HA	11:K:125:ASP:O	2.13	0.49
8:V:35:HIS:CG	8:V:56:THR:HG21	2.48	0.49
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.95	0.49
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.95	0.49
8:H:35:HIS:CG	8:H:56:THR:HG21	2.48	0.49
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.59	0.49
6:F:146:MET:CE	6:F:161:THR:HB	2.42	0.49
5:S:170:TYR:C	5:S:170:TYR:CD1	2.86	0.49
3:Q:204:GLY:O	3:Q:205:ALA:O	2.32	0.48
3:C:204:GLY:O	3:C:205:ALA:O	2.31	0.48
1:A:149:GLN:O	1:A:156:TYR:HA	2.14	0.48
5:E:68:HIS:HE1	5:E:102:LEU:O	1.97	0.48
5:E:170:TYR:C	5:E:170:TYR:CD1	2.86	0.48
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.44	0.48
14:N:35:THR:HG21	14:N:45:ARG:HE	1.77	0.48
11:Y:6:PHE:HA	11:Y:125:ASP:O	2.14	0.48
6:T:14:ASP:N	6:T:14:ASP:OD2	2.37	0.48
5:S:92:ASN:HD21	12:Z:70:ASN:HD21	1.61	0.48
1:O:149:GLN:O	1:O:156:TYR:HA	2.13	0.48
6:T:228:LYS:HB2	6:T:228:LYS:HE3	1.74	0.48
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.43	0.48
5:S:206:THR:OG1	5:S:209:ASN:HB2	2.14	0.48
12:Z:31:THR:CG2	12:Z:36:ASN:HD21	2.26	0.47
8:H:104:ASP:OD1	8:H:106:THR:HB	2.14	0.47
5:S:68:HIS:HE1	5:S:102:LEU:O	1.97	0.47
3:C:201:VAL:O	3:C:202:GLN:CB	2.40	0.47
2:B:93:HIS:CG	2:B:113:ARG:HE	2.32	0.47
1:A:176:GLU:CG	2:B:55:LEU:HD22	2.44	0.47
5:S:156:TYR:CD1	5:S:179:ILE:HD11	2.49	0.47
5:E:156:TYR:CD1	5:E:179:ILE:HD11	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:104:ASP:OD1	8:V:106:THR:HB	2.15	0.47
3:C:149:GLU:HB2	3:C:150:PRO:HD2	1.96	0.47
2:P:93:HIS:CG	2:P:113:ARG:HE	2.32	0.47
6:T:146:MET:HE1	6:T:161:THR:HB	1.97	0.47
3:Q:149:GLU:HB2	3:Q:150:PRO:HD2	1.96	0.47
3:Q:11:PRO:HA	4:R:18:TYR:CD1	2.50	0.47
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.50	0.47
5:E:206:THR:OG1	5:E:209:ASN:HB2	2.15	0.46
3:Q:236:GLN:C	3:Q:238:LYS:H	2.18	0.46
8:V:84:LYS:HG3	8:V:85:GLN:N	2.30	0.46
8:H:196:ARG:NH2	9:I:150:GLU:O	2.49	0.46
3:Q:160:GLN:NE2	3:Q:170:ARG:HE	2.11	0.46
3:C:236:GLN:C	3:C:238:LYS:H	2.18	0.46
2:B:110:LEU:HD23	2:B:110:LEU:C	2.36	0.45
8:H:84:LYS:HG3	8:H:85:GLN:N	2.31	0.45
10:J:174:MET:HA	10:X:174:MET:HA	1.97	0.45
11:K:51:ASP:HB3	11:K:97:MET:HE2	1.98	0.45
6:F:14:ASP:N	6:F:14:ASP:OD2	2.39	0.45
4:D:37:GLY:HA2	4:D:145:TYR:CE1	2.51	0.45
11:K:176:ASN:ND2	11:K:187:TYR:OH	2.49	0.45
2:B:65:LEU:HD22	2:B:211:GLU:HB3	1.97	0.45
2:P:65:LEU:HD22	2:P:211:GLU:HB3	1.97	0.45
2:B:105:ILE:HD11	2:B:109:ILE:HG22	1.99	0.45
11:Y:176:ASN:ND2	11:Y:187:TYR:OH	2.50	0.45
8:H:199:LYS:HE3	9:I:151:SER:O	2.17	0.45
6:F:228:LYS:HB2	6:F:228:LYS:HE3	1.74	0.45
13:M:179:ASN:HD22	13:M:182:ARG:NH1	2.15	0.45
8:H:84:LYS:HE2	8:H:119:THR:HG23	1.99	0.45
2:P:185:VAL:O	2:P:189:ILE:HG13	2.16	0.45
2:P:105:ILE:HD11	2:P:109:ILE:HG22	1.99	0.45
4:R:149:HIS:O	4:R:156:PHE:HA	2.17	0.45
6:F:146:MET:HE3	6:F:161:THR:HB	1.99	0.45
13:M:179:ASN:HD22	13:M:182:ARG:HH11	1.64	0.45
4:R:37:GLY:HA2	4:R:145:TYR:CE1	2.52	0.45
1:A:176:GLU:HG3	2:B:55:LEU:HD22	1.99	0.45
2:B:168:THR:O	2:B:172:GLN:HB2	2.17	0.45
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.65	0.45
12:L:31:THR:CG2	12:L:36:ASN:HD21	2.26	0.44
2:P:110:LEU:HD23	2:P:110:LEU:C	2.37	0.44
3:C:160:GLN:NE2	3:C:161:THR:H	2.10	0.44
8:V:84:LYS:HE2	8:V:119:THR:HG23	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:LEU:O	1:A:114:VAL:HG23	2.17	0.44
2:P:139:TYR:CE2	2:P:144:GLY:HA2	2.53	0.44
4:D:51:LEU:C	4:D:51:LEU:HD12	2.38	0.44
4:D:149:HIS:O	4:D:156:PHE:HA	2.16	0.44
2:B:185:VAL:O	2:B:189:ILE:HG13	2.17	0.44
5:S:170:TYR:CE2	5:S:194:GLU:HG2	2.53	0.44
4:R:51:LEU:C	4:R:51:LEU:HD12	2.38	0.44
2:B:47:ALA:HB1	2:B:64:LYS:HD2	2.00	0.44
4:D:178:GLU:HB3	4:D:191:LEU:HD21	1.99	0.44
13:M:27:LEU:HB2	13:M:192:SER:HB3	2.00	0.44
1:O:110:LEU:O	1:O:114:VAL:HG23	2.18	0.44
2:P:47:ALA:HB1	2:P:64:LYS:HD2	2.00	0.44
3:Q:27:ARG:NH1	3:Q:27:ARG:HB2	2.33	0.44
5:S:197:SER:HA	5:S:200:LEU:CD1	2.48	0.43
2:P:168:THR:O	2:P:172:GLN:HB2	2.18	0.43
4:R:32:ILE:HD12	4:R:192:VAL:CG2	2.42	0.43
4:R:178:GLU:HB3	4:R:191:LEU:HD21	1.99	0.43
2:P:99:LYS:NZ	10:X:86:GLN:HE21	2.17	0.43
7:U:195:GLU:HG3	7:U:235:ARG:HG3	2.00	0.43
2:B:3:ARG:NH2	5:E:8:ASP:OD2	2.52	0.43
2:P:93:HIS:HB3	2:P:113:ARG:NH2	2.09	0.43
8:V:3:ILE:HG23	8:V:99:ILE:HD12	2.00	0.43
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.49	0.43
2:B:139:TYR:CE2	2:B:144:GLY:HA2	2.53	0.43
10:X:162:LYS:HB3	10:X:162:LYS:HE2	1.89	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.43
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.48	0.43
2:B:49:ARG:HH22	2:B:61:SER:HB3	1.83	0.43
5:E:170:TYR:CE2	5:E:194:GLU:HG2	2.53	0.43
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.48	0.43
7:G:195:GLU:HG3	7:G:235:ARG:HG3	2.00	0.43
7:U:83:ASN:C	7:U:83:ASN:ND2	2.72	0.43
8:H:84:LYS:HE2	8:H:119:THR:CG2	2.48	0.43
11:K:134:THR:HG22	10:X:139:TYR:CZ	2.54	0.43
12:L:161:GLU:HB3	12:L:164:THR:CG2	2.48	0.43
5:E:178:PHE:HA	5:E:181:ILE:HG13	2.01	0.43
11:K:100:MET:HE2	11:K:127:PHE:HB2	1.96	0.43
14:N:20:THR:HB	16:N:201:2MK:H11	2.01	0.43
3:Q:160:GLN:NE2	3:Q:161:THR:H	2.11	0.43
2:B:159:TRP:CE2	2:B:162:ILE:HD13	2.54	0.43
10:X:139:TYR:HD2	10:X:172:MET:HE3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:197:SER:HA	5:E:200:LEU:CD1	2.48	0.43
3:C:27:ARG:NH1	3:C:27:ARG:HB2	2.34	0.43
4:R:224:ASP:OD2	4:R:224:ASP:N	2.51	0.43
2:P:49:ARG:HH22	2:P:61:SER:HB3	1.84	0.43
8:V:84:LYS:HE2	8:V:119:THR:CG2	2.48	0.43
4:D:32:ILE:HD12	4:D:192:VAL:CG2	2.42	0.43
3:Q:149:GLU:HB2	3:Q:150:PRO:CD	2.49	0.42
4:D:224:ASP:N	4:D:224:ASP:OD2	2.52	0.42
2:B:93:HIS:HB3	2:B:113:ARG:NH2	2.09	0.42
12:Z:161:GLU:HB3	12:Z:164:THR:CG2	2.49	0.42
10:X:92:ILE:HD12	10:X:92:ILE:HA	1.85	0.42
9:I:62:LEU:HD21	9:I:102:TYR:CD2	2.54	0.42
3:C:135:GLY:HA2	3:C:213:VAL:HG21	2.01	0.42
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.48	0.42
3:Q:170:ARG:O	3:Q:174:GLU:HG3	2.18	0.42
3:C:170:ARG:O	3:C:174:GLU:HG3	2.19	0.42
5:E:98:PHE:O	13:M:91:TYR:HA	2.19	0.42
7:U:78:ILE:N	7:U:79:PRO:CD	2.82	0.42
8:H:3:ILE:HG23	8:H:99:ILE:HD12	2.00	0.42
12:L:4:PRO:O	13:M:104:ARG:NH1	2.41	0.42
1:O:83:ARG:HE	7:U:114:ASN:ND2	2.17	0.42
9:W:98:ARG:HD2	9:W:126:ILE:CG1	2.50	0.42
3:C:149:GLU:HB2	3:C:150:PRO:CD	2.49	0.42
5:S:38:ARG:HD2	5:S:39:SER:O	2.20	0.42
3:Q:135:GLY:HA2	3:Q:213:VAL:HG21	2.01	0.42
4:R:174:GLU:HB3	4:R:195:ILE:HD13	2.02	0.42
3:Q:4:ARG:NH1	17:Q:302:HOH:O	2.53	0.42
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	2.01	0.42
3:C:160:GLN:NE2	3:C:170:ARG:HE	2.11	0.42
5:S:178:PHE:HA	5:S:181:ILE:HG13	2.01	0.42
3:Q:186:VAL:O	3:Q:190:VAL:HG23	2.20	0.42
3:C:198:LEU:HA	3:C:201:VAL:HG12	2.02	0.42
5:E:61:LYS:O	5:E:72:SER:HA	2.20	0.42
7:G:83:ASN:ND2	7:G:83:ASN:C	2.72	0.42
11:K:1:THR:HG21	11:K:46:ALA:HB2	2.02	0.42
9:I:65:MET:HE1	9:I:93:SER:HB3	2.02	0.42
13:M:159:VAL:HG23	13:M:159:VAL:O	2.19	0.42
1:A:209:ILE:HA	1:A:209:ILE:HD13	1.86	0.41
8:V:172:ASN:HD22	8:V:192:THR:HA	1.86	0.41
9:W:62:LEU:HD21	9:W:102:TYR:CD2	2.55	0.41
8:H:172:ASN:HD22	8:H:192:THR:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:196:PHE:CD1	7:G:196:PHE:C	2.93	0.41
2:B:155:ASN:ND2	3:C:77:ASN:HB2	2.35	0.41
10:X:149:ARG:O	10:X:152:MET:HG3	2.20	0.41
1:O:3:ASP:OD1	1:O:5:TYR:HB2	2.21	0.41
8:H:49:ALA:HB2	16:H:301:2MK:H14	2.03	0.41
2:P:159:TRP:CE2	2:P:162:ILE:HD13	2.55	0.41
8:V:80:LEU:HD12	8:V:113:ILE:HD11	2.02	0.41
3:C:186:VAL:O	3:C:190:VAL:HG23	2.19	0.41
7:U:196:PHE:C	7:U:196:PHE:CD1	2.92	0.41
4:D:174:GLU:HB3	4:D:195:ILE:HD13	2.02	0.41
2:B:180:LYS:HB3	2:B:180:LYS:HE2	1.95	0.41
10:X:152:MET:CE	10:X:156:GLU:HB3	2.51	0.41
1:A:66:LEU:C	1:A:66:LEU:HD23	2.41	0.41
3:Q:169:VAL:HG12	3:Q:200:VAL:HG21	2.03	0.41
14:N:20:THR:CG2	14:N:31:THR:OG1	2.66	0.41
9:W:65:MET:HE1	9:W:93:SER:HB3	2.03	0.41
10:J:139:TYR:HD2	10:J:172:MET:HE3	1.86	0.41
14:N:176:VAL:HG12	14:N:178:LEU:HD13	2.03	0.41
1:A:3:ASP:OD1	1:A:5:TYR:HB2	2.20	0.41
10:J:3:ILE:HD12	10:J:176:PHE:CD2	2.56	0.41
10:J:152:MET:CE	10:J:156:GLU:HB3	2.51	0.41
10:J:139:TYR:CZ	11:Y:134:THR:HG22	2.56	0.41
12:L:8:ASN:HA	12:L:30:ILE:O	2.21	0.40
5:E:38:ARG:HD2	5:E:39:SER:O	2.20	0.40
2:B:162:ILE:HG13	2:B:163:SER:N	2.36	0.40
11:K:4:LEU:HD13	11:K:161:ILE:HD11	2.04	0.40
8:V:196:ARG:NH2	9:W:150:GLU:O	2.54	0.40
7:G:44:VAL:HG21	7:G:73:VAL:CG1	2.51	0.40
1:A:196:LEU:HA	1:A:196:LEU:HD12	1.95	0.40
12:Z:147:MET:N	12:Z:148:PRO:CD	2.84	0.40
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.36	0.40
11:Y:4:LEU:HD13	11:Y:161:ILE:HD11	2.03	0.40
8:V:20:SER:HB3	8:V:28:ASP:HB3	2.03	0.40
6:T:198:LEU:HA	6:T:198:LEU:HD12	1.96	0.40
12:L:125:PHE:N	12:L:125:PHE:CD1	2.90	0.40
9:I:98:ARG:HD2	9:I:126:ILE:CG1	2.50	0.40
13:M:1:THR:HG22	13:M:2:GLN:N	2.35	0.40
10:J:149:ARG:O	10:J:152:MET:HG3	2.21	0.40
1:O:158:PRO:HB2	2:P:57:GLU:HB3	2.03	0.40
8:V:35:HIS:ND1	8:V:53:GLU:OE2	2.55	0.40
8:H:20:SER:HB3	8:H:28:ASP:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:44:VAL:HG21	7:U:73:VAL:CG1	2.51	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%)	241 (97%)	4 (2%)	3 (1%)	16	33
1	O	248/250 (99%)	241 (97%)	4 (2%)	3 (1%)	16	33
2	B	242/258 (94%)	228 (94%)	10 (4%)	4 (2%)	11	22
2	P	242/258 (94%)	228 (94%)	10 (4%)	4 (2%)	11	22
3	C	238/254 (94%)	227 (95%)	7 (3%)	4 (2%)	11	22
3	Q	238/254 (94%)	227 (95%)	7 (3%)	4 (2%)	11	22
4	D	231/260 (89%)	224 (97%)	6 (3%)	1 (0%)	39	65
4	R	231/260 (89%)	224 (97%)	6 (3%)	1 (0%)	39	65
5	E	229/234 (98%)	221 (96%)	7 (3%)	1 (0%)	39	65
5	S	229/234 (98%)	221 (96%)	7 (3%)	1 (0%)	39	65
6	F	241/288 (84%)	229 (95%)	10 (4%)	2 (1%)	24	46
6	T	241/288 (84%)	229 (95%)	10 (4%)	2 (1%)	24	46
7	G	239/252 (95%)	233 (98%)	6 (2%)	0	100	100
7	U	239/252 (95%)	232 (97%)	7 (3%)	0	100	100
8	H	220/232 (95%)	214 (97%)	4 (2%)	2 (1%)	21	42
8	V	220/232 (95%)	214 (97%)	4 (2%)	2 (1%)	21	42
9	I	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
9	W	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
10	J	193/198 (98%)	188 (97%)	4 (2%)	1 (0%)	34	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	X	193/198 (98%)	188 (97%)	4 (2%)	1 (0%)	34	60
11	K	210/212 (99%)	201 (96%)	8 (4%)	1 (0%)	34	60
11	Y	210/212 (99%)	201 (96%)	8 (4%)	1 (0%)	34	60
12	L	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
12	Z	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
13	M	231/246 (94%)	223 (96%)	7 (3%)	1 (0%)	39	65
13	a	231/246 (94%)	223 (96%)	7 (3%)	1 (0%)	39	65
14	N	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
14	b	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
All	All	6276/6614 (95%)	6053 (96%)	183 (3%)	40 (1%)	30	56

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
2	B	51	VAL
3	C	202	GLN
3	C	205	ALA
8	H	9	ASN
11	K	9	GLN
1	O	2	THR
2	P	51	VAL
3	Q	202	GLN
3	Q	205	ALA
8	V	9	ASN
11	Y	9	GLN
1	A	3	ASP
5	E	231	LYS
8	H	145	ASP
1	O	3	ASP
5	S	231	LYS
8	V	145	ASP
2	B	63	GLU
2	B	221	ASP
3	C	183	PRO
3	C	206	LYS
10	J	2	ASP
2	P	63	GLU
2	P	221	ASP

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Mol	Chain	Res	Type
3	Q	183	PRO
3	Q	206	LYS
10	X	2	ASP
1	A	166	LYS
2	B	62	THR
4	D	114	ARG
1	O	166	LYS
2	P	62	THR
4	R	114	ARG
6	F	203	ASN
13	M	83	ALA
6	T	139	LYS
6	T	203	ASN
13	a	83	ALA
6	F	139	LYS

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%)	202 (97%)	7 (3%)	45	73
1	O	209/209 (100%)	202 (97%)	7 (3%)	45	73
2	B	203/216 (94%)	184 (91%)	19 (9%)	11	20
2	P	203/216 (94%)	185 (91%)	18 (9%)	12	23
3	C	212/226 (94%)	190 (90%)	22 (10%)	9	16
3	Q	212/226 (94%)	190 (90%)	22 (10%)	9	16
4	D	194/215 (90%)	175 (90%)	19 (10%)	10	19
4	R	194/215 (90%)	175 (90%)	19 (10%)	10	19
5	E	190/193 (98%)	173 (91%)	17 (9%)	12	23
5	S	190/193 (98%)	173 (91%)	17 (9%)	12	23
6	F	201/239 (84%)	179 (89%)	22 (11%)	8	14
6	T	201/239 (84%)	179 (89%)	22 (11%)	8	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	206/210 (98%)	187 (91%)	19 (9%)	11	21
7	U	206/210 (98%)	187 (91%)	19 (9%)	11	21
8	H	181/190 (95%)	171 (94%)	10 (6%)	27	51
8	V	181/190 (95%)	171 (94%)	10 (6%)	27	51
9	I	172/173 (99%)	165 (96%)	7 (4%)	37	66
9	W	172/173 (99%)	164 (95%)	8 (5%)	32	59
10	J	173/175 (99%)	160 (92%)	13 (8%)	17	33
10	X	173/175 (99%)	160 (92%)	13 (8%)	17	33
11	K	169/169 (100%)	158 (94%)	11 (6%)	21	42
11	Y	169/169 (100%)	158 (94%)	11 (6%)	21	42
12	L	185/185 (100%)	175 (95%)	10 (5%)	27	52
12	Z	185/185 (100%)	175 (95%)	10 (5%)	27	52
13	M	199/208 (96%)	182 (92%)	17 (8%)	13	25
13	a	199/208 (96%)	182 (92%)	17 (8%)	13	25
14	N	162/162 (100%)	153 (94%)	9 (6%)	26	50
14	b	162/162 (100%)	153 (94%)	9 (6%)	26	50
All	All	5312/5540 (96%)	4908 (92%)	404 (8%)	16	32

All (404) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	17	LYS
1	A	50	LYS
1	A	51	SER
1	A	52	SER
1	A	61	LEU
1	A	122	THR
2	B	50	LYS
2	B	53	SER
2	B	54	THR
2	B	55	LEU
2	B	56	LEU
2	B	58	GLN
2	B	62	THR
2	B	65	LEU

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Mol	Chain	Res	Type
2	B	79	LEU
2	B	119	GLN
2	B	169	SER
2	B	180	LYS
2	B	184	LYS
2	B	191	LEU
2	B	194	LYS
2	B	217	LYS
2	B	220	ASN
2	B	237	ILE
2	B	244	THR
3	C	4	ARG
3	C	32	VAL
3	C	38	ASN
3	C	51	LYS
3	C	58	THR
3	C	61	LYS
3	C	109	ARG
3	C	147	GLN
3	C	160	GLN
3	C	167	LYS
3	C	169	VAL
3	C	175	LYS
3	C	180	LYS
3	C	187	GLU
3	C	202	GLN
3	C	203	THR
3	C	213	VAL
3	C	222	LEU
3	C	232	THR
3	C	233	GLN
3	C	239	GLN
3	C	240	GLU
4	D	2	ARG
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	60	VAL
4	D	99	ILE
4	D	117	GLU
4	D	125	LEU
4	D	176	LEU

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Mol	Chain	Res	Type
4	D	190	LEU
4	D	191	LEU
4	D	193	LEU
4	D	197	LYS
4	D	202	GLU
4	D	214	ILE
4	D	224	ASP
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	4	ASN
5	E	10	VAL
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	55	LEU
5	E	60	LYS
5	E	71	LEU
5	E	99	ASN
5	E	116	GLN
5	E	144	LEU
5	E	184	ASN
5	E	188	LEU
5	E	207	VAL
5	E	211	SER
5	E	219	THR
5	E	227	GLU
6	F	14	ASP
6	F	94	SER
6	F	96	LYS
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	148	GLU
6	F	163	LYS
6	F	165	ARG
6	F	167	SER
6	F	172	LEU
6	F	181	GLU
6	F	187	GLU
6	F	198	LEU
6	F	203	ASN

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Mol	Chain	Res	Type
6	F	204	LYS
6	F	205	GLU
6	F	206	LYS
6	F	214	TRP
6	F	221	ASN
6	F	228	LYS
6	F	241	LYS
7	G	24	LYS
7	G	26	THR
7	G	28	GLN
7	G	34	LEU
7	G	40	ASP
7	G	53	LYS
7	G	83	ASN
7	G	115	LEU
7	G	117	GLN
7	G	122	ARG
7	G	125	MET
7	G	165	LYS
7	G	166	GLN
7	G	171	THR
7	G	181	LYS
7	G	221	LYS
7	G	230	GLU
7	G	235	ARG
7	G	236	LEU
8	H	3	ILE
8	H	13	VAL
8	H	20	SER
8	H	30	ASN
8	H	34	LEU
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	153	LYS
8	H	196	ARG
9	I	37	ASN
9	I	92	SER
9	I	126	ILE
9	I	171	LEU
9	I	182	TRP
9	I	191	LYS

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Mol	Chain	Res	Type
9	I	192	ASP
10	J	2	ASP
10	J	23	ARG
10	J	35	THR
10	J	36	ARG
10	J	75	LEU
10	J	78	GLN
10	J	92	ILE
10	J	110	LYS
10	J	126	VAL
10	J	144	LEU
10	J	163	LEU
10	J	174	MET
10	J	194	ASP
11	K	4	LEU
11	K	9	GLN
11	K	32	LYS
11	K	35	ILE
11	K	41	LEU
11	K	57	THR
11	K	71	LYS
11	K	73	ARG
11	K	106	ARG
11	K	107	LYS
11	K	118	ASP
12	L	1	GLN
12	L	3	ASN
12	L	13	LEU
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	80	ASN
12	L	161	GLU
12	L	165	ASN
12	L	167	LYS
13	M	10	SER
13	M	37	ASN
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	106	LYS

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Mol	Chain	Res	Type
13	M	138	SER
13	M	146	PHE
13	M	161	ARG
13	M	187	ARG
13	M	192	SER
13	M	204	THR
13	M	212	LEU
13	M	213	GLN
13	M	215	GLU
13	M	233	ILE
14	N	9	LYS
14	N	20	THR
14	N	22	THR
14	N	35	THR
14	N	36	ARG
14	N	104	ASP
14	N	119	VAL
14	N	144	GLU
14	N	178	LEU
1	O	2	THR
1	O	17	LYS
1	O	50	LYS
1	O	51	SER
1	O	52	SER
1	O	61	LEU
1	O	122	THR
2	P	50	LYS
2	P	54	THR
2	P	55	LEU
2	P	56	LEU
2	P	58	GLN
2	P	62	THR
2	P	65	LEU
2	P	79	LEU
2	P	119	GLN
2	P	169	SER
2	P	180	LYS
2	P	184	LYS
2	P	191	LEU
2	P	194	LYS
2	P	217	LYS
2	P	220	ASN

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Mol	Chain	Res	Type
2	P	237	ILE
2	P	244	THR
3	Q	4	ARG
3	Q	32	VAL
3	Q	38	ASN
3	Q	51	LYS
3	Q	58	THR
3	Q	61	LYS
3	Q	109	ARG
3	Q	147	GLN
3	Q	160	GLN
3	Q	167	LYS
3	Q	169	VAL
3	Q	175	LYS
3	Q	180	LYS
3	Q	187	GLU
3	Q	202	GLN
3	Q	203	THR
3	Q	213	VAL
3	Q	222	LEU
3	Q	232	THR
3	Q	233	GLN
3	Q	239	GLN
3	Q	240	GLU
4	R	2	ARG
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	60	VAL
4	R	99	ILE
4	R	117	GLU
4	R	125	LEU
4	R	176	LEU
4	R	190	LEU
4	R	191	LEU
4	R	193	LEU
4	R	197	LYS
4	R	202	GLU
4	R	214	ILE
4	R	224	ASP
4	R	235	LEU
4	R	236	LYS

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Mol	Chain	Res	Type
4	R	242	GLU
5	S	4	ASN
5	S	10	VAL
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU
5	S	55	LEU
5	S	60	LYS
5	S	71	LEU
5	S	99	ASN
5	S	116	GLN
5	S	144	LEU
5	S	184	ASN
5	S	188	LEU
5	S	207	VAL
5	S	211	SER
5	S	219	THR
5	S	227	GLU
6	T	14	ASP
6	T	94	SER
6	T	96	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	148	GLU
6	T	163	LYS
6	T	165	ARG
6	T	167	SER
6	T	172	LEU
6	T	181	GLU
6	T	187	GLU
6	T	198	LEU
6	T	203	ASN
6	T	204	LYS
6	T	205	GLU
6	T	206	LYS
6	T	214	TRP
6	T	221	ASN
6	T	228	LYS
6	T	241	LYS
7	U	24	LYS
7	U	26	THR

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Mol	Chain	Res	Type
7	U	28	GLN
7	U	34	LEU
7	U	40	ASP
7	U	53	LYS
7	U	83	ASN
7	U	115	LEU
7	U	117	GLN
7	U	122	ARG
7	U	125	MET
7	U	165	LYS
7	U	166	GLN
7	U	171	THR
7	U	181	LYS
7	U	221	LYS
7	U	230	GLU
7	U	235	ARG
7	U	236	LEU
8	V	3	ILE
8	V	13	VAL
8	V	20	SER
8	V	30	ASN
8	V	34	LEU
8	V	56	THR
8	V	68	LEU
8	V	127	LEU
8	V	153	LYS
8	V	196	ARG
9	W	37	ASN
9	W	92	SER
9	W	126	ILE
9	W	155	PRO
9	W	171	LEU
9	W	182	TRP
9	W	191	LYS
9	W	192	ASP
10	X	2	ASP
10	X	23	ARG
10	X	35	THR
10	X	36	ARG
10	X	75	LEU
10	X	78	GLN
10	X	92	ILE

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Mol	Chain	Res	Type
10	X	110	LYS
10	X	126	VAL
10	X	144	LEU
10	X	163	LEU
10	X	174	MET
10	X	194	ASP
11	Y	4	LEU
11	Y	9	GLN
11	Y	32	LYS
11	Y	35	ILE
11	Y	41	LEU
11	Y	57	THR
11	Y	71	LYS
11	Y	73	ARG
11	Y	106	ARG
11	Y	107	LYS
11	Y	118	ASP
12	Z	1	GLN
12	Z	3	ASN
12	Z	13	LEU
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	80	ASN
12	Z	161	GLU
12	Z	165	ASN
12	Z	167	LYS
13	a	10	SER
13	a	37	ASN
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	106	LYS
13	a	138	SER
13	a	146	PHE
13	a	161	ARG
13	a	187	ARG
13	a	192	SER
13	a	204	THR
13	a	212	LEU
13	a	213	GLN

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Mol	Chain	Res	Type
13	a	215	GLU
13	a	233	ILE
14	b	9	LYS
14	b	20	THR
14	b	22	THR
14	b	35	THR
14	b	36	ARG
14	b	104	ASP
14	b	119	VAL
14	b	144	GLU
14	b	178	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (144) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
1	A	241	GLN
2	B	20	GLN
2	B	95	GLN
2	B	102	ASN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN
3	C	17	GLN
3	C	38	ASN
3	C	77	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
3	C	176	ASN
3	C	233	GLN
4	D	15	GLN
4	D	100	ASN
4	D	146	GLN
4	D	198	GLN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN

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Mol	Chain	Res	Type
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	203	ASN
6	F	240	GLN
7	G	6	HIS
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN
7	G	175	ASN
7	G	186	ASN
8	H	66	HIS
8	H	86	HIS
8	H	165	ASN
8	H	172	ASN
8	H	200	GLN
9	I	31	GLN
9	I	37	ASN
10	J	55	GLN
10	J	86	GLN
10	J	118	GLN
10	J	146	HIS
10	J	191	GLN
11	K	85	ASN
11	K	176	ASN
12	L	3	ASN
12	L	49	ASN
12	L	70	ASN
12	L	76	HIS
12	L	80	ASN
12	L	135	GLN
12	L	165	ASN
12	L	195	HIS
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN

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Mol	Chain	Res	Type
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	69	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	155	ASN
2	P	176	GLN
3	Q	17	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
3	Q	176	ASN
3	Q	233	GLN
4	R	15	GLN
4	R	100	ASN
4	R	146	GLN
4	R	198	GLN
4	R	225	ASN
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	165	GLN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
6	T	203	ASN
6	T	240	GLN
7	U	6	HIS
7	U	83	ASN

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Mol	Chain	Res	Type
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	86	HIS
8	V	165	ASN
8	V	172	ASN
10	X	55	GLN
10	X	86	GLN
10	X	118	GLN
10	X	191	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	76	HIS
12	Z	80	ASN
12	Z	135	GLN
12	Z	165	ASN
12	Z	195	HIS
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	179	ASN
13	a	194	ASN
13	a	213	GLN
14	b	69	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 ⓘ

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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	2MK	H	301	8	34,35,36	0.95	1 (2%)	44,46,47	1.19	3 (6%)
16	2MK	K	301	11	34,35,36	1.11	2 (5%)	44,46,47	0.96	1 (2%)
16	2MK	N	201	14	34,35,36	0.96	1 (2%)	44,46,47	0.93	2 (4%)
16	2MK	V	301	8	34,35,36	0.95	1 (2%)	44,46,47	1.17	3 (6%)
16	2MK	Y	301	11	34,35,36	0.91	1 (2%)	44,46,47	1.27	4 (9%)
16	2MK	b	201	14	34,35,36	1.03	1 (2%)	44,46,47	1.01	2 (4%)

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	2MK	H	301	8	-	0/41/41/43	0/1/1/1
16	2MK	K	301	11	-	0/41/41/43	0/1/1/1
16	2MK	N	201	14	-	0/41/41/43	0/1/1/1
16	2MK	V	301	8	-	0/41/41/43	0/1/1/1
16	2MK	Y	301	11	-	0/41/41/43	0/1/1/1
16	2MK	b	201	14	-	0/41/41/43	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	b	201	2MK	C29-C30	-4.05	1.41	1.50
16	K	301	2MK	C29-C30	-4.00	1.41	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	N	201	2MK	C29-C30	-3.92	1.41	1.50
16	V	301	2MK	C29-C30	-3.88	1.41	1.50
16	H	301	2MK	C29-C30	-3.85	1.41	1.50
16	Y	301	2MK	C29-C30	-3.56	1.42	1.50
16	K	301	2MK	C37-C38	2.16	1.62	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	H	301	2MK	C12-C11-N20	-4.89	103.58	110.15
16	V	301	2MK	C12-C11-N20	-4.69	103.84	110.15
16	V	301	2MK	O36-C27-N26	-3.01	119.61	124.86
16	H	301	2MK	O36-C27-N26	-2.90	119.80	124.86
16	Y	301	2MK	O28-C27-O36	-2.89	118.27	124.22
16	Y	301	2MK	O36-C27-N26	-2.79	119.98	124.86
16	N	201	2MK	O36-C27-N26	-2.41	120.66	124.86
16	b	201	2MK	C29-O28-C27	2.07	120.84	115.91
16	Y	301	2MK	C29-O28-C27	2.60	122.11	115.91
16	K	301	2MK	O28-C27-N26	3.21	117.66	110.54
16	b	201	2MK	O28-C27-N26	3.26	117.77	110.54
16	N	201	2MK	O28-C27-N26	3.70	118.75	110.54
16	H	301	2MK	O28-C27-N26	3.78	118.92	110.54
16	V	301	2MK	O28-C27-N26	3.97	119.35	110.54
16	Y	301	2MK	O28-C27-N26	5.02	121.68	110.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	H	301	2MK	2	0
16	N	201	2MK	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.54	7 (2%) 56 49	28, 42, 79, 122	0
1	O	250/250 (100%)	-0.48	4 (1%) 74 69	32, 51, 90, 115	0
2	B	244/258 (94%)	-0.31	12 (4%) 33 26	29, 48, 107, 154	0
2	P	244/258 (94%)	-0.26	11 (4%) 37 29	31, 52, 108, 149	0
3	C	240/254 (94%)	-0.26	12 (5%) 32 26	28, 53, 114, 134	0
3	Q	240/254 (94%)	-0.05	18 (7%) 17 12	34, 62, 136, 150	0
4	D	235/260 (90%)	-0.44	4 (1%) 73 68	32, 52, 83, 105	0
4	R	235/260 (90%)	-0.42	2 (0%) 85 83	32, 53, 84, 121	0
5	E	231/234 (98%)	-0.45	1 (0%) 93 91	35, 53, 82, 112	0
5	S	231/234 (98%)	-0.49	1 (0%) 93 91	33, 51, 83, 119	0
6	F	243/288 (84%)	-0.54	5 (2%) 67 61	29, 46, 87, 131	0
6	T	243/288 (84%)	-0.53	6 (2%) 61 54	30, 46, 84, 120	0
7	G	241/252 (95%)	-0.56	3 (1%) 81 77	27, 43, 76, 127	0
7	U	241/252 (95%)	-0.59	4 (1%) 73 68	27, 43, 74, 103	0
8	H	222/232 (95%)	-0.69	2 (0%) 85 83	24, 38, 62, 116	0
8	V	222/232 (95%)	-0.64	2 (0%) 85 83	27, 41, 66, 133	0
9	I	204/205 (99%)	-0.75	1 (0%) 91 90	28, 39, 68, 95	0
9	W	204/205 (99%)	-0.67	1 (0%) 91 90	27, 43, 72, 108	0
10	J	195/198 (98%)	-0.63	2 (1%) 84 81	27, 43, 64, 127	0
10	X	195/198 (98%)	-0.65	2 (1%) 84 81	31, 45, 71, 134	0
11	K	212/212 (100%)	-0.72	0 100 100	26, 42, 67, 91	0
11	Y	212/212 (100%)	-0.67	1 (0%) 91 90	27, 42, 67, 96	0
12	L	222/222 (100%)	-0.71	0 100 100	26, 42, 65, 86	0
12	Z	222/222 (100%)	-0.76	0 100 100	27, 41, 63, 88	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.75	1 (0%) 93 91	25, 40, 57, 70	0
13	a	233/246 (94%)	-0.79	1 (0%) 93 91	24, 36, 56, 62	0
14	N	196/196 (100%)	-0.80	0 100 100	22, 35, 60, 89	0
14	b	196/196 (100%)	-0.77	1 (0%) 91 90	22, 36, 63, 89	0
All	All	6336/6614 (95%)	-0.56	104 (1%) 74 69	22, 45, 84, 154	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	V	222	ASP	6.4
2	B	219	ALA	5.8
3	C	206	LYS	5.6
2	P	221	ASP	5.6
2	P	51	VAL	5.2
3	Q	239	GLN	4.8
2	P	219	ALA	4.8
3	Q	50	LEU	4.8
2	P	218	GLY	4.7
9	W	1	SER	4.7
8	H	222	ASP	4.6
2	P	222	GLY	4.6
3	Q	48	SER	4.6
3	C	238	LYS	4.4
2	P	59	ASP	4.4
2	B	218	GLY	4.3
3	Q	49	THR	4.3
3	Q	238	LYS	4.2
10	X	194	ASP	4.2
3	Q	206	LYS	4.1
2	B	221	ASP	4.1
2	B	222	GLY	4.0
3	Q	240	GLU	4.0
2	B	51	VAL	3.9
8	V	221	CYS	3.8
3	C	49	THR	3.7
9	I	1	SER	3.5
6	T	244	ASN	3.4
3	C	239	GLN	3.3
1	A	1	MET	3.3
8	H	221	CYS	3.3
13	M	1	THR	3.2

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Mol	Chain	Res	Type	RSRZ
2	P	220	ASN	3.2
2	B	217	LYS	3.2
5	E	202	ASP	3.2
6	T	243	ILE	3.2
1	O	201	GLU	3.1
10	J	194	ASP	3.1
10	J	1	MET	3.0
6	F	202	ASP	3.0
3	Q	236	GLN	3.0
2	B	220	ASN	2.9
3	Q	202	GLN	2.9
7	U	242	GLN	2.9
1	A	201	GLU	2.9
4	R	242	GLU	2.9
4	D	242	GLU	2.9
1	A	249	ALA	2.8
1	O	249	ALA	2.8
3	C	240	GLU	2.8
2	B	203	SER	2.8
2	P	52	THR	2.8
6	F	243	ILE	2.8
3	Q	223	SER	2.7
1	O	1	MET	2.7
2	P	60	THR	2.7
4	D	241	ALA	2.7
2	P	182	ASP	2.7
6	T	205	GLU	2.7
10	X	1	MET	2.6
13	a	1	THR	2.6
2	B	223	GLU	2.6
5	S	202	ASP	2.6
3	C	225	GLU	2.5
7	G	242	GLN	2.5
3	Q	187	GLU	2.5
3	C	50	LEU	2.5
6	F	205	GLU	2.5
3	C	180	LYS	2.4
7	U	2	GLY	2.4
4	D	3	GLY	2.4
3	C	60	SER	2.4
3	C	202	GLN	2.4
1	O	231	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	2	THR	2.3
7	G	2	GLY	2.3
7	U	203	ASP	2.3
6	F	206	LYS	2.3
4	D	240	ALA	2.3
2	B	244	THR	2.3
6	T	178	HIS	2.3
1	A	248	GLU	2.3
1	A	250	LEU	2.3
3	Q	203	THR	2.3
4	R	125	LEU	2.2
1	A	231	LYS	2.2
2	P	203	SER	2.2
3	Q	229	GLN	2.2
6	F	178	HIS	2.2
6	T	2	THR	2.2
7	G	241	GLU	2.2
2	B	235	LYS	2.1
6	T	241	LYS	2.1
3	C	47	ARG	2.1
2	B	61	SER	2.1
3	C	203	THR	2.1
3	Q	47	ARG	2.1
7	U	3	TYR	2.1
3	Q	204	GLY	2.1
3	Q	180	LYS	2.1
11	Y	106	ARG	2.1
14	b	105	LYS	2.0
3	Q	237	GLU	2.0
3	Q	205	ALA	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [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. 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
16	2MK	K	301	35/36	0.81	0.26	5.44	37,54,92,95	0
16	2MK	Y	301	35/36	0.85	0.19	3.43	42,52,84,86	0
16	2MK	N	201	35/36	0.89	0.21	3.37	27,41,88,92	0
16	2MK	b	201	35/36	0.87	0.22	3.25	32,45,94,96	0
16	2MK	V	301	35/36	0.87	0.27	3.04	44,67,121,121	0
16	2MK	H	301	35/36	0.89	0.22	2.68	41,53,117,119	0
15	MG	Z	301	1/1	0.96	0.17	2.41	50,50,50,50	0
15	MG	I	301	1/1	0.98	0.13	0.43	42,42,42,42	0
15	MG	N	202	1/1	0.98	0.10	-0.27	34,34,34,34	0
15	MG	G	301	1/1	0.95	0.07	-0.97	43,43,43,43	0
15	MG	K	302	1/1	0.97	0.09	-1.12	45,45,45,45	0
15	MG	V	302	1/1	0.98	0.05	-2.45	46,46,46,46	0
15	MG	Y	302	1/1	0.99	0.05	-4.11	35,35,35,35	0
15	MG	H	302	1/1	0.94	0.18	-	65,65,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.