



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:03 PM UTC

PDB ID : 3DY3 / pdb_00003dy3
Title : Crystal structure of yeast 20S proteasome in complex with the epimer form of spiro lactacystin
Authors : Groll, M.; Balskus, E.; Jacobsen, E.
Deposited on : 2008-07-25
Resolution : 2.81 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
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

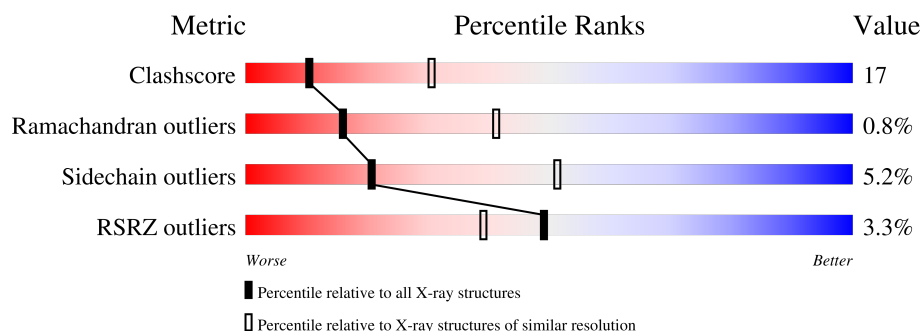
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	2% 77% 21% .
1	O	250	6% 73% 24% .
2	B	244	8% 59% 39% .
2	P	244	7% 58% 39% .
3	C	241	9% 62% 37% .
3	Q	241	9% 60% 37% .

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Mol	Chain	Length	Quality of chain
4	D	242	
4	R	242	
5	E	233	
5	S	233	
6	F	244	
6	T	244	
7	G	243	
7	U	243	
8	H	222	
8	V	222	
9	I	204	
9	W	204	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	1	233	
13	M	233	
14	2	196	
14	N	196	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 50584 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Proteasome component Y7.

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

- Molecule 2 is a protein called Proteasome component Y13.

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

- Molecule 3 is a protein called Proteasome component PRE6.

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

- Molecule 4 is a protein called Proteasome component PUP2.

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

- Molecule 5 is a protein called Proteasome component PRE5.

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

- Molecule 6 is a protein called Proteasome component C1.

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

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

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

- Molecule 8 is a protein called Proteasome component PUP1.

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

- Molecule 9 is a protein called Proteasome component PUP3.

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

- Molecule 10 is a protein called Proteasome component C11.

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

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

- Molecule 11 is a protein called Proteasome component PRE2.

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

- Molecule 12 is a protein called Proteasome component C5.

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

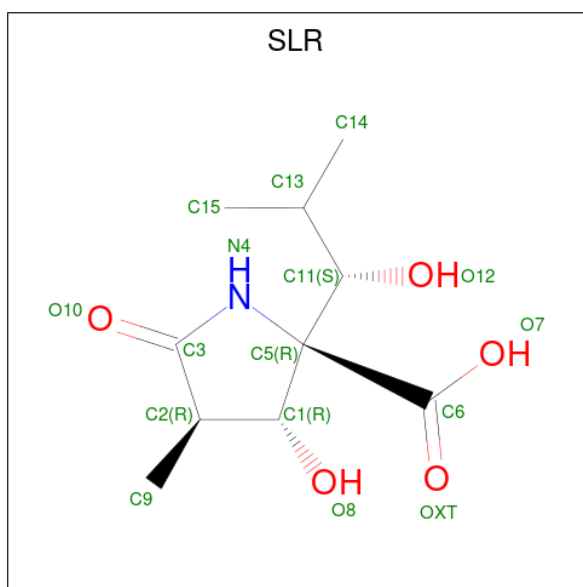
- Molecule 13 is a protein called Proteasome component PRE4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	1	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 14 is a protein called Proteasome component PRE3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	2	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is (3R,4R)-3-hydroxy-2-[(1S)-1-hydroxy-2-methylpropyl]-4-methyl-5-oxo-D-proline (CCD ID: SLR) (formula: C₁₀H₁₇NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
15	K	1	Total	C	N	O	0	0
			15	10	1	4		
15	Y	1	Total	C	N	O	0	0
			15	10	1	4		

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	35	Total	O	0	0
			35	35		
16	B	27	Total	O	0	0
			27	27		
16	C	32	Total	O	0	0
			32	32		
16	D	23	Total	O	0	0
			23	23		
16	E	15	Total	O	0	0
			15	15		
16	F	35	Total	O	0	0
			35	35		
16	G	51	Total	O	0	0
			51	51		
16	H	41	Total	O	0	0
			41	41		
16	I	51	Total	O	0	0
			51	51		
16	J	38	Total	O	0	0
			38	38		

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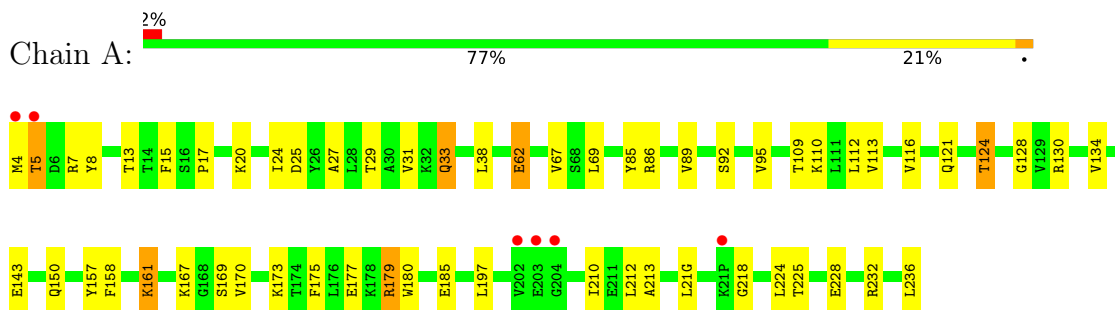
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	K	33	Total 33	O 33	0	0
16	L	43	Total 43	O 43	0	0
16	M	56	Total 56	O 56	0	0
16	N	49	Total 49	O 49	0	0
16	O	28	Total 28	O 28	0	0
16	P	18	Total 18	O 18	0	0
16	Q	19	Total 19	O 19	0	0
16	R	19	Total 19	O 19	0	0
16	S	16	Total 16	O 16	0	0
16	T	30	Total 30	O 30	0	0
16	U	48	Total 48	O 48	0	0
16	V	36	Total 36	O 36	0	0
16	W	40	Total 40	O 40	0	0
16	X	36	Total 36	O 36	0	0
16	Y	36	Total 36	O 36	0	0
16	Z	36	Total 36	O 36	0	0
16	1	64	Total 64	O 64	0	0
16	2	51	Total 51	O 51	0	0

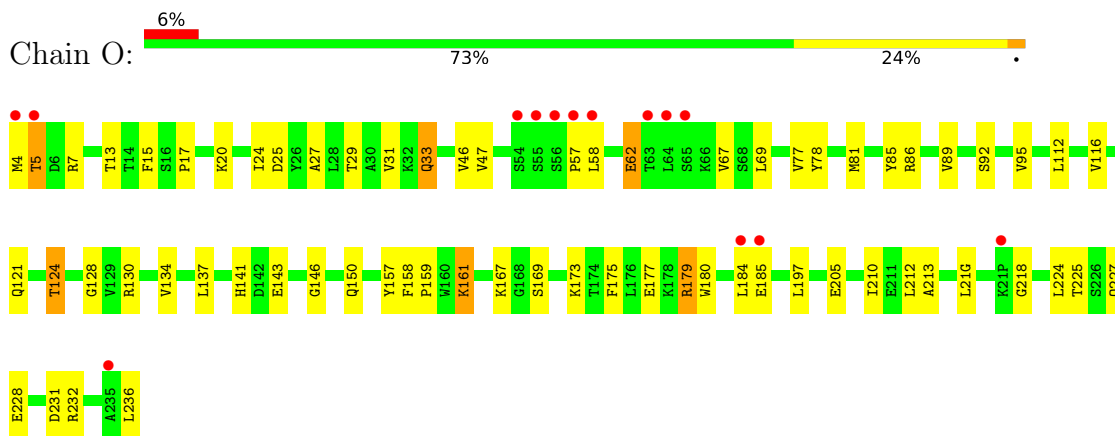
3 Residue-property plots [i](#)

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

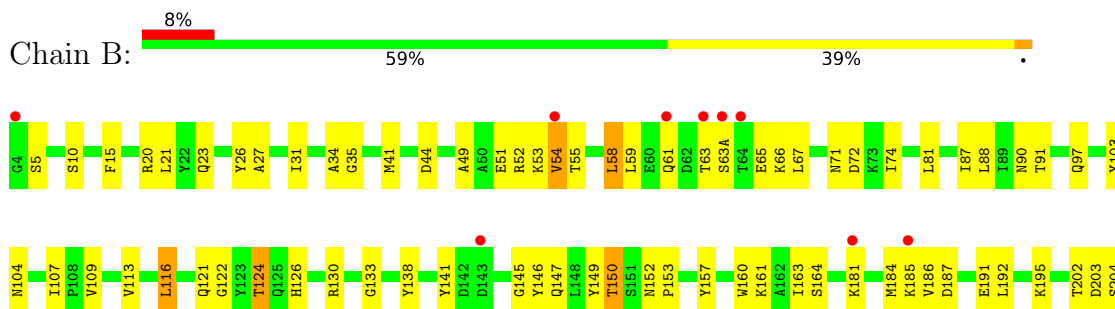
- Molecule 1: Proteasome component Y7



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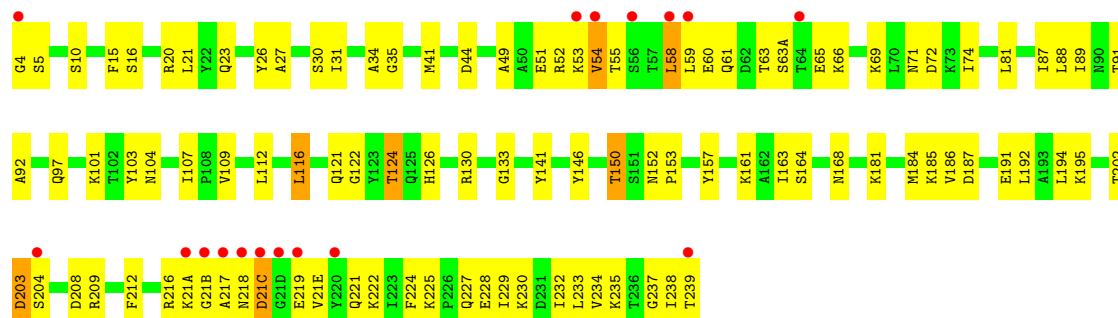


- Molecule 2: Proteasome component Y13

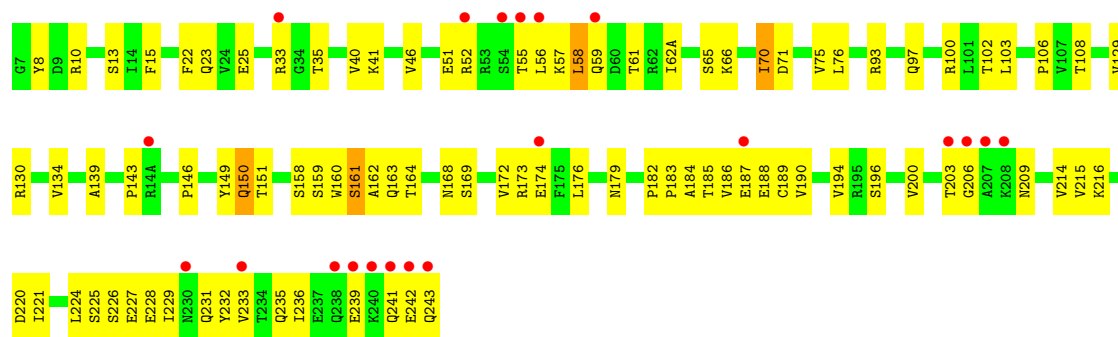




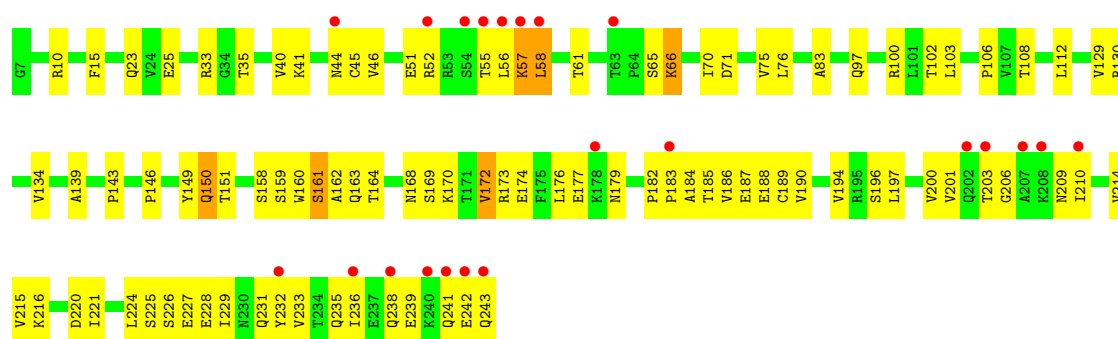
• Molecule 2: Proteasome component Y13



• Molecule 3: Proteasome component PRE6

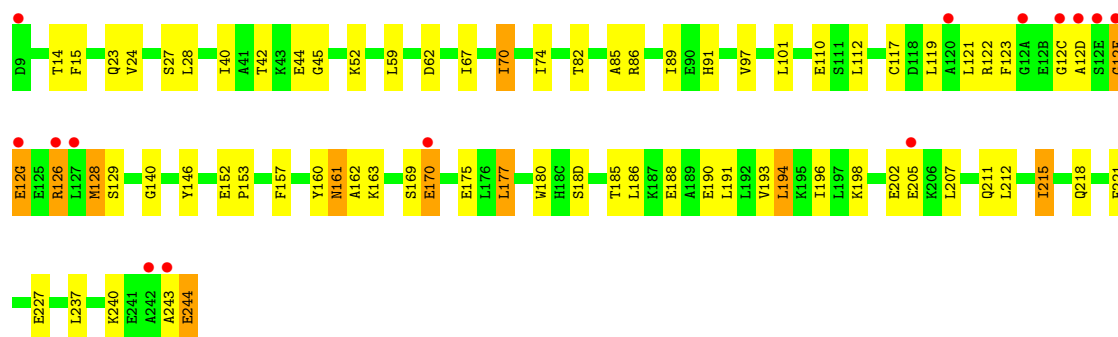


• Molecule 3: Proteasome component PRE6

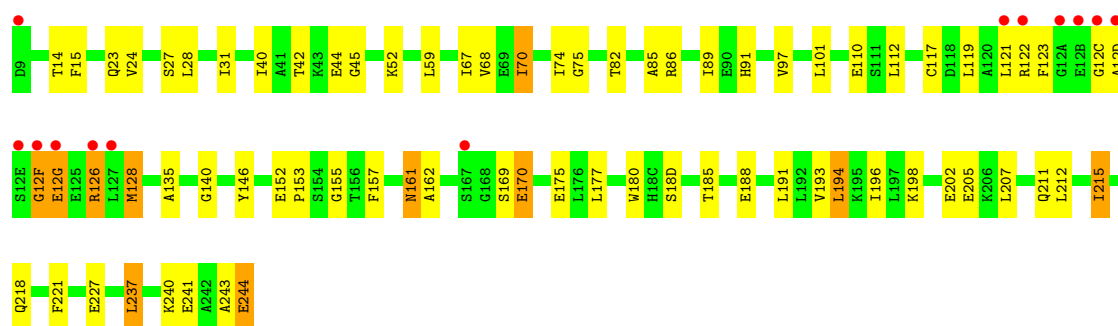


• Molecule 4: Proteasome component PUP2

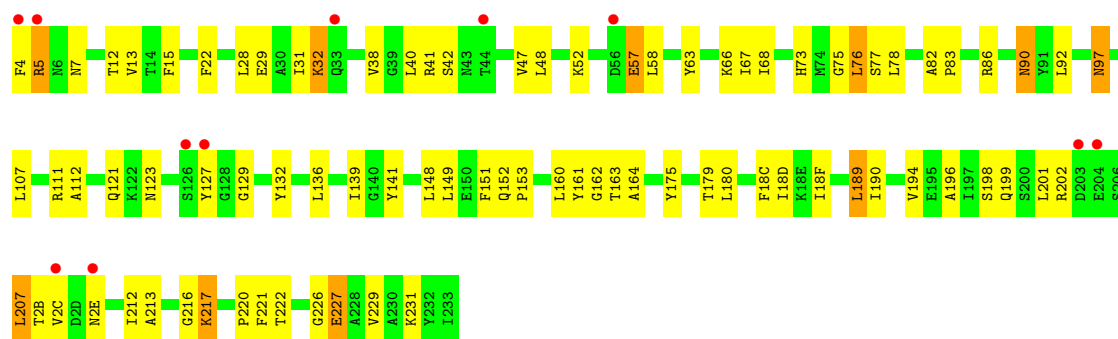




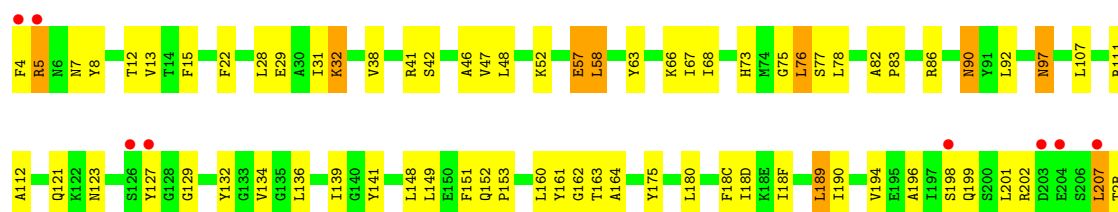
• Molecule 4: Proteasome component PUP2



• Molecule 5: Proteasome component PRE5

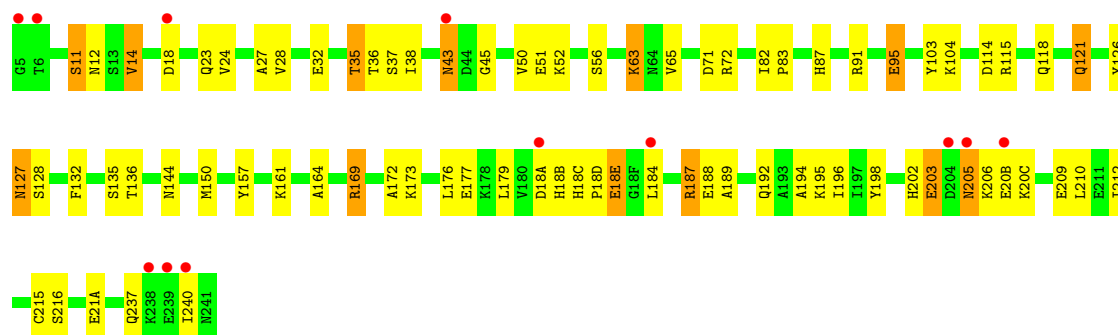


• Molecule 5: Proteasome component PRE5

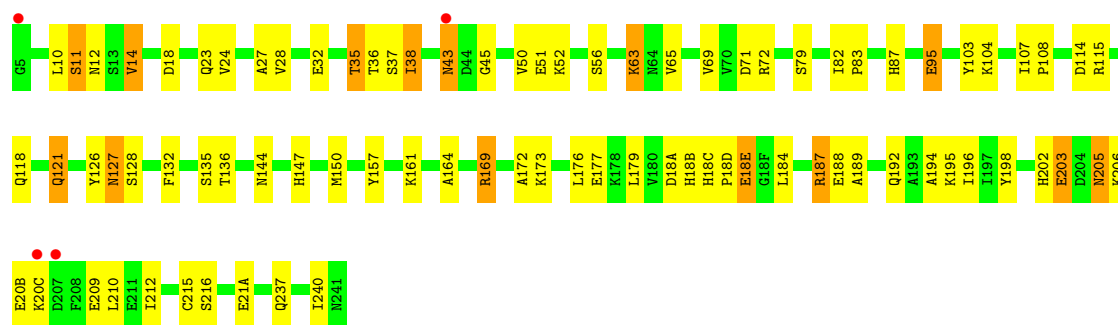




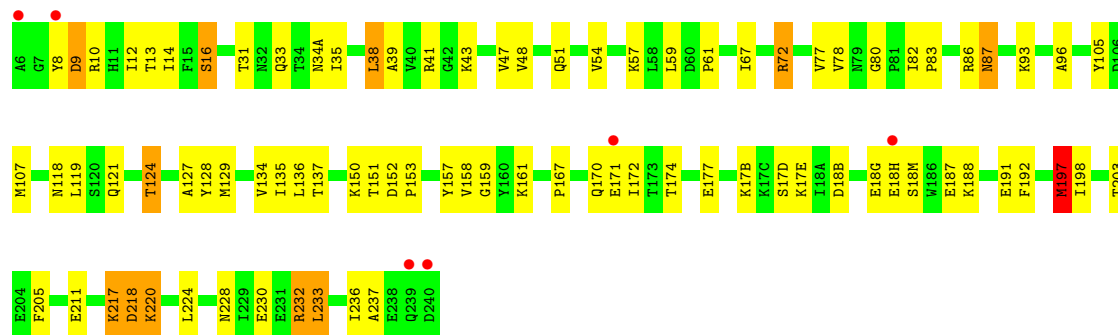
- Molecule 6: Proteasome component C1



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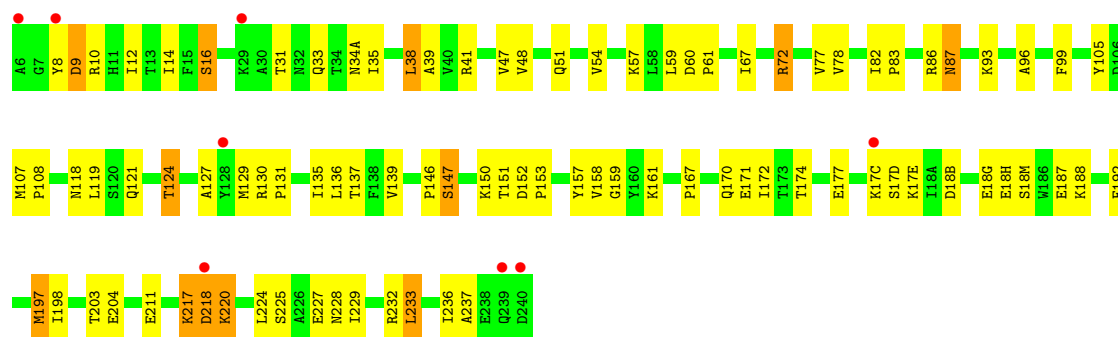


- Molecule 7: Proteasome component C7-alpha



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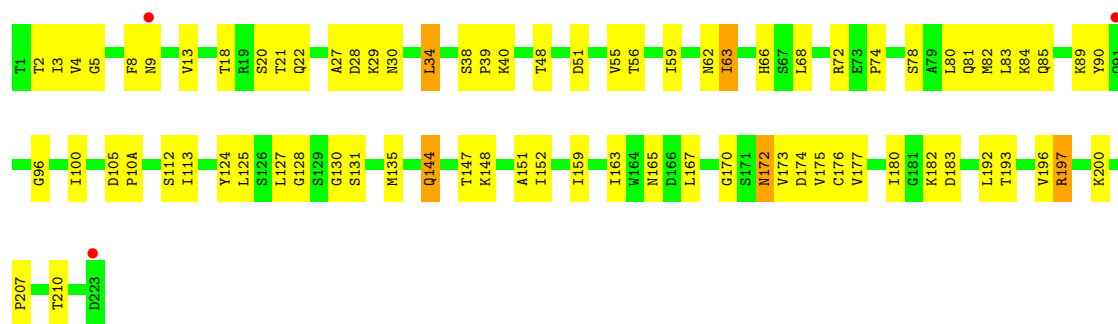




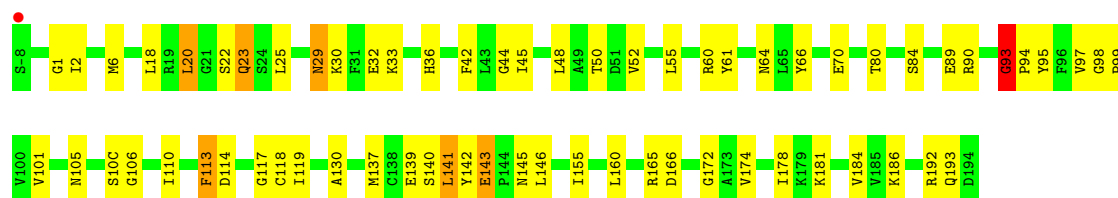
• Molecule 8: Proteasome component PUP1



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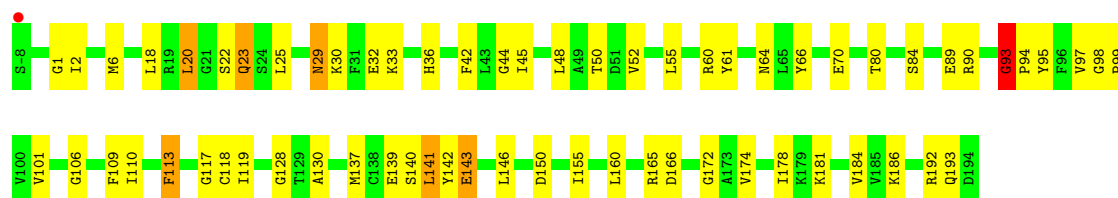


• Molecule 9: Proteasome component PUP3



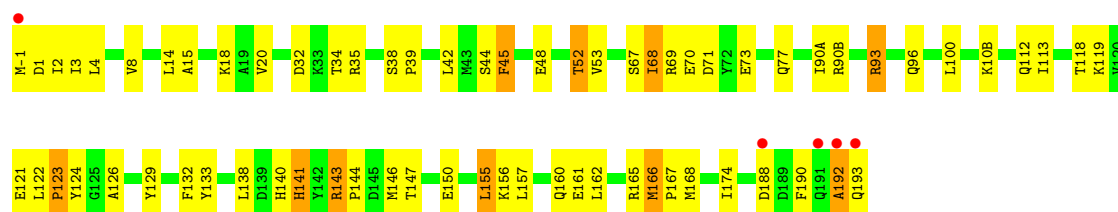
• Molecule 9: Proteasome component PUP3

Chain W:  68% 28% .



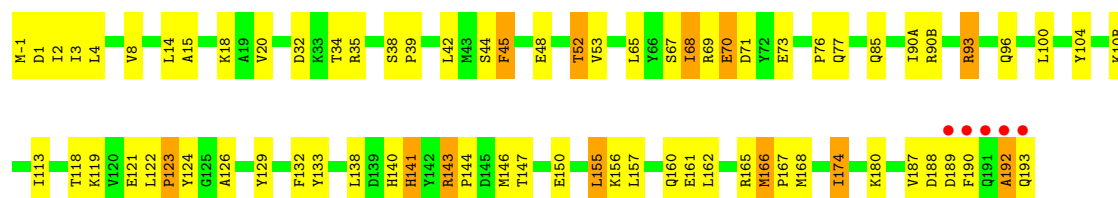
• Molecule 10: Proteasome component C11

Chain J:  3% 65% 30% 5%



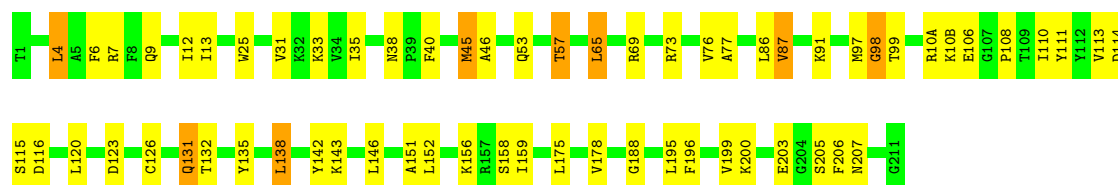
• Molecule 10: Proteasome component C11

Chain X:  3% 62% 32% 6%



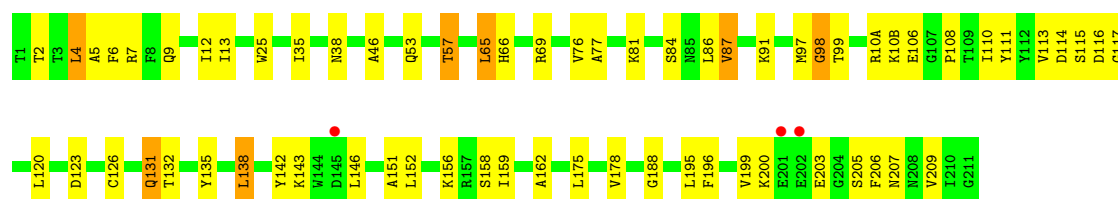
• Molecule 11: Proteasome component PRE2

Chain K:  70% 26% .

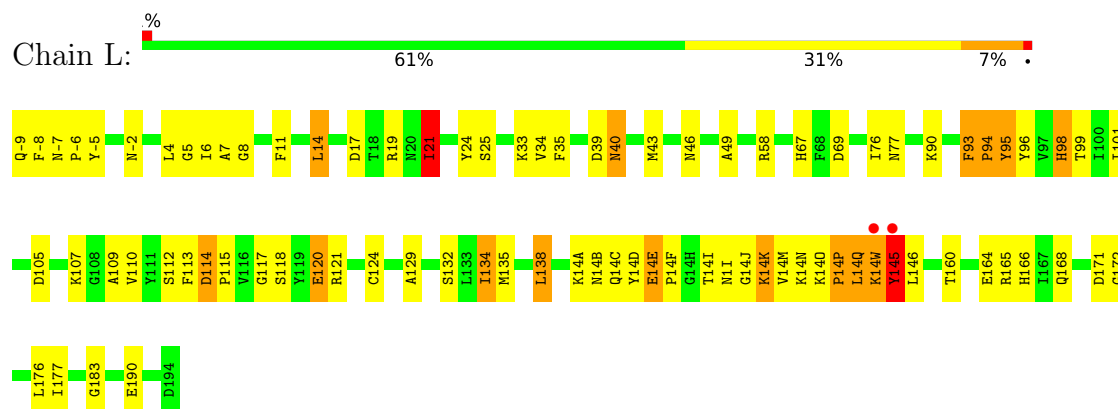


• Molecule 11: Proteasome component PRE2

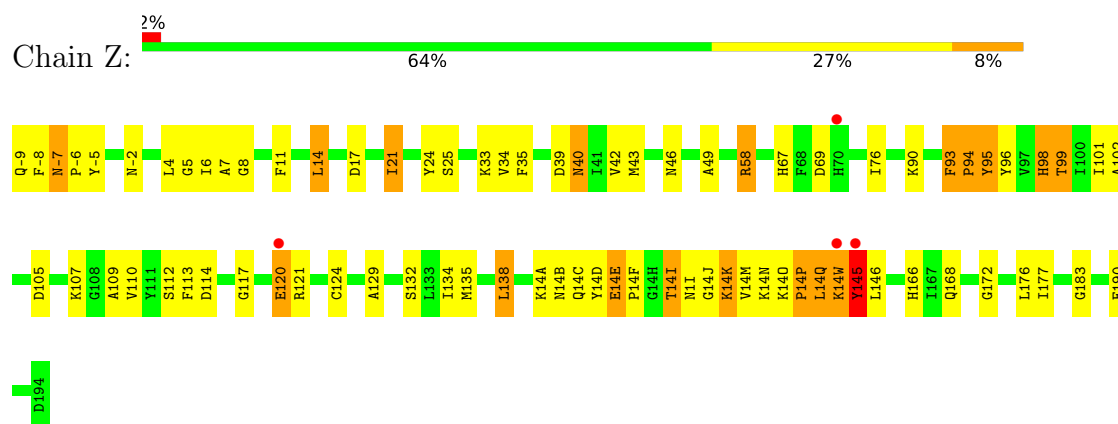
Chain Y:  69% 28% .



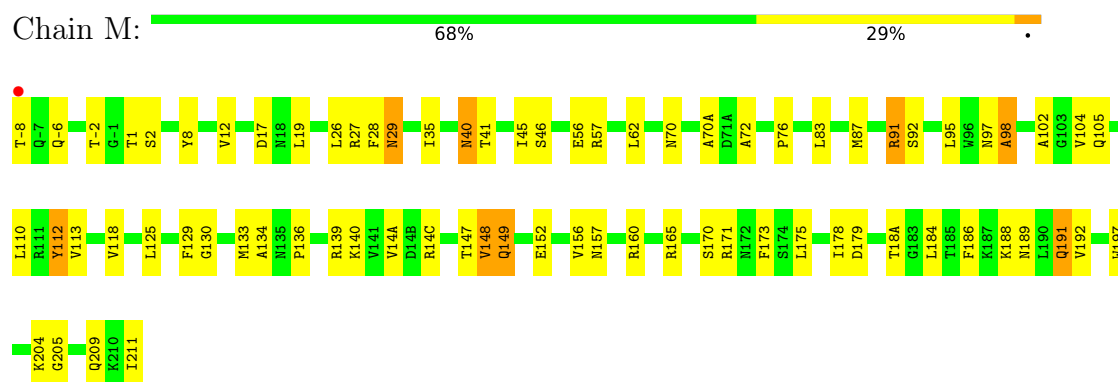
- Molecule 12: Proteasome component C5



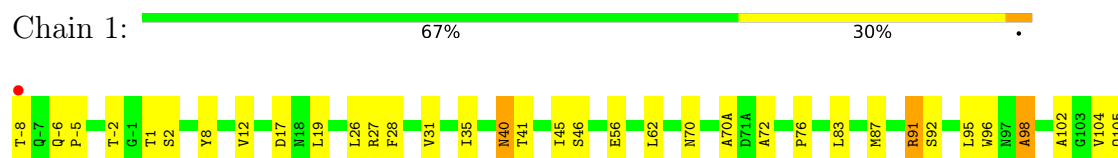
- Molecule 12: Proteasome component C5

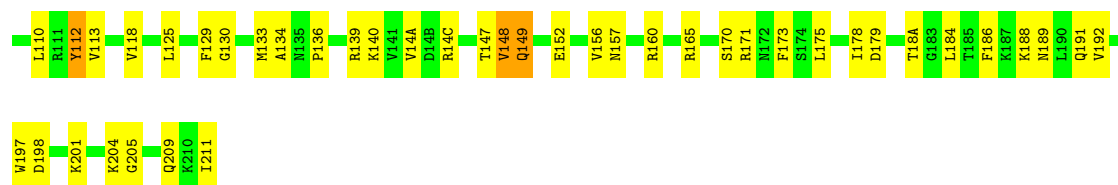


- Molecule 13: Proteasome component PRE4

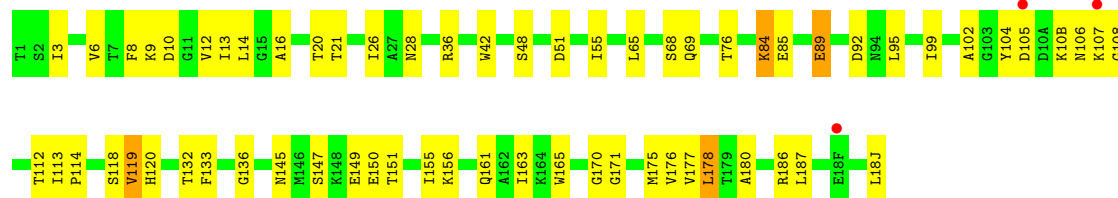


- Molecule 13: Proteasome component PRE4

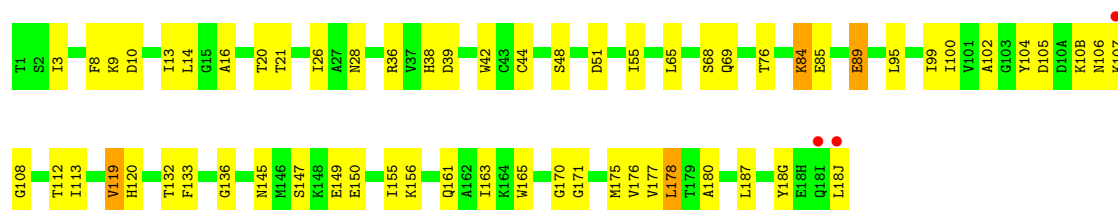




• Molecule 14: Proteasome component PRE3



• Molecule 14: Proteasome component PRE3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.15Å 301.86Å 144.08Å 90.00° 112.81° 90.00°	Depositor
Resolution (Å)	15.00 – 2.81 15.00 – 2.81	Depositor EDS
% Data completeness (in resolution range)	98.6 (15.00-2.81) 98.1 (15.00-2.81)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.83Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.214 , 0.245 0.226 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.834	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	50584	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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: SLR

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	0.45	0/1952	0.90	4/2642 (0.2%)
1	O	0.42	0/1952	0.91	6/2642 (0.2%)
2	B	0.44	0/1935	0.94	5/2618 (0.2%)
2	P	0.45	0/1935	0.94	6/2618 (0.2%)
3	C	0.41	0/1920	0.90	5/2598 (0.2%)
3	Q	0.40	0/1920	0.90	4/2598 (0.2%)
4	D	0.42	0/1887	0.91	8/2541 (0.3%)
4	R	0.40	0/1887	0.90	7/2541 (0.3%)
5	E	0.42	0/1823	0.92	3/2463 (0.1%)
5	S	0.42	0/1823	0.91	4/2463 (0.2%)
6	F	0.43	0/1937	0.94	6/2614 (0.2%)
6	T	0.45	0/1937	0.95	7/2614 (0.3%)
7	G	0.46	0/1959	0.98	10/2652 (0.4%)
7	U	0.46	0/1959	0.98	11/2652 (0.4%)
8	H	0.46	0/1716	0.94	5/2326 (0.2%)
8	V	0.46	0/1716	0.94	6/2326 (0.3%)
9	I	0.44	0/1611	0.99	13/2174 (0.6%)
9	W	0.44	0/1611	0.99	13/2174 (0.6%)
10	J	0.44	0/1613	0.97	13/2173 (0.6%)
10	X	0.45	0/1613	0.97	14/2173 (0.6%)
11	K	0.47	1/1681 (0.1%)	0.95	5/2274 (0.2%)
11	Y	0.42	0/1681	0.93	5/2274 (0.2%)
12	L	0.44	0/1795	1.03	15/2420 (0.6%)
12	Z	0.44	0/1795	1.03	13/2420 (0.5%)
13	1	0.48	0/1855	0.96	6/2514 (0.2%)
13	M	0.45	0/1855	0.96	8/2514 (0.3%)
14	2	0.46	0/1541	0.93	2/2087 (0.1%)
14	N	0.48	0/1541	0.94	2/2087 (0.1%)
All	All	0.44	1/50450 (0.0%)	0.95	206/68192 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
12	L	0	1
12	Z	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	K	45	MET	CA-C	-6.04	1.45	1.52

All (206) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	T	12	ASN	N-CA-C	9.90	121.66	111.07
6	F	12	ASN	N-CA-C	9.75	121.50	111.07
12	Z	93	PHE	CA-C-N	8.97	129.52	119.92
12	Z	93	PHE	C-N-CA	8.97	129.52	119.92
13	M	27	ARG	N-CA-C	8.92	121.91	111.02
12	L	93	PHE	CA-C-N	8.90	129.45	119.92
12	L	93	PHE	C-N-CA	8.90	129.45	119.92
13	1	27	ARG	N-CA-C	8.86	121.83	111.02
2	B	238	ILE	N-CA-C	-8.51	104.88	113.47
2	P	238	ILE	N-CA-C	-8.47	104.92	113.47
2	B	161	LYS	N-CA-C	-8.45	102.56	113.12
2	B	203	ASP	N-CA-C	-7.98	103.56	113.38
2	P	203	ASP	N-CA-C	-7.82	103.76	113.38
11	K	57	THR	N-CA-C	-7.65	103.03	111.36
5	E	57	GLU	N-CA-C	-7.64	103.06	113.30
7	U	127	ALA	N-CA-C	7.64	119.60	111.28
1	O	161	LYS	N-CA-C	-7.63	101.85	112.45
7	G	127	ALA	N-CA-C	7.52	119.47	111.28
3	Q	70	ILE	N-CA-C	-7.46	105.39	111.81
5	S	57	GLU	N-CA-C	-7.36	103.39	112.88
1	A	161	LYS	N-CA-C	-7.31	102.29	112.45
6	T	161	LYS	N-CA-C	-7.30	102.31	112.45
6	F	161	LYS	N-CA-C	-7.28	102.33	112.45
11	Y	57	THR	N-CA-C	-7.28	103.43	111.36
4	D	70	ILE	N-CA-C	-7.22	105.60	111.81
3	C	70	ILE	N-CA-C	-7.19	105.63	111.81
9	W	60	ARG	N-CA-C	-7.10	103.47	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	T	14	VAL	N-CA-C	7.04	118.19	108.89
13	1	95	LEU	N-CA-C	-7.04	97.07	108.41
6	F	14	VAL	N-CA-C	6.99	118.12	108.89
7	U	161	LYS	N-CA-C	-6.94	103.48	112.23
10	J	123	PRO	N-CA-C	-6.93	104.11	113.40
7	G	161	LYS	N-CA-C	-6.92	103.18	111.69
2	P	161	LYS	N-CA-C	-6.88	102.89	112.45
3	Q	161	SER	N-CA-C	-6.86	103.86	111.82
7	G	16	SER	N-CA-C	-6.85	101.19	110.36
4	D	161	ASN	N-CA-C	-6.83	103.95	112.90
13	M	95	LEU	N-CA-C	-6.78	97.49	108.41
13	M	98	ALA	N-CA-C	-6.76	97.40	108.41
4	R	70	ILE	N-CA-C	-6.74	106.01	111.81
8	V	180	ILE	N-CA-C	6.74	118.30	110.62
12	L	95	TYR	N-CA-C	-6.73	98.24	108.67
13	1	98	ALA	N-CA-C	-6.73	97.45	108.41
4	R	161	ASN	N-CA-C	-6.73	104.09	112.90
8	H	180	ILE	N-CA-C	6.70	118.25	110.62
3	Q	108	THR	N-CA-C	-6.66	101.56	110.55
3	C	108	THR	N-CA-C	-6.59	101.65	110.55
7	U	16	SER	N-CA-C	-6.52	101.62	110.36
14	N	99	ILE	N-CA-C	6.48	117.81	108.48
9	I	142	TYR	N-CA-C	6.46	119.14	110.35
3	C	161	SER	N-CA-C	-6.45	104.33	111.82
14	2	99	ILE	N-CA-C	6.40	117.70	108.48
7	G	54	VAL	CA-C-N	6.39	126.15	119.05
7	G	54	VAL	C-N-CA	6.39	126.15	119.05
10	X	123	PRO	N-CA-C	-6.35	104.89	113.40
6	F	135	SER	N-CA-C	-6.31	98.91	109.07
12	L	117	GLY	N-CA-C	6.25	122.24	114.37
12	Z	95	TYR	N-CA-C	-6.25	98.99	108.67
7	U	54	VAL	CA-C-N	6.24	125.98	119.05
7	U	54	VAL	C-N-CA	6.24	125.98	119.05
9	W	142	TYR	N-CA-C	6.22	118.82	110.35
1	O	128	GLY	N-CA-C	6.20	123.84	114.61
8	V	21	THR	N-CA-C	6.17	119.24	109.50
9	W	95	TYR	N-CA-C	-6.15	100.48	110.20
12	L	21	ILE	N-CA-C	6.13	117.75	108.80
2	B	109	VAL	N-CA-C	6.13	116.79	110.36
10	X	165	ARG	N-CA-C	6.08	120.76	113.23
2	P	107	ILE	N-CA-C	6.06	114.89	108.95
4	R	169	SER	N-CA-C	6.02	121.25	111.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	169	SER	N-CA-C	6.01	121.23	111.37
9	I	60	ARG	N-CA-C	-5.99	104.66	111.07
2	P	109	VAL	N-CA-C	5.96	116.62	110.36
6	T	135	SER	N-CA-C	-5.95	99.49	109.07
8	H	21	THR	N-CA-C	5.92	118.86	109.50
9	I	117	GLY	N-CA-C	5.90	122.59	114.92
10	X	166	MET	CA-C-N	5.90	125.77	119.28
10	X	166	MET	C-N-CA	5.90	125.77	119.28
12	Z	21	ILE	N-CA-C	5.89	117.40	108.80
10	J	93	ARG	CA-C-N	5.88	125.82	119.76
10	J	93	ARG	C-N-CA	5.88	125.82	119.76
1	A	128	GLY	N-CA-C	5.85	123.91	114.90
7	G	9	ASP	N-CA-C	-5.85	106.19	113.15
1	A	185	GLU	N-CA-C	-5.85	101.35	110.42
8	H	100	ILE	N-CA-C	-5.83	99.24	107.75
9	W	117	GLY	N-CA-C	5.81	122.47	114.92
1	O	185	GLU	N-CA-C	-5.81	101.42	110.42
9	W	141	LEU	N-CA-C	5.78	117.66	111.36
6	F	71	ASP	CB-CA-C	-5.77	109.94	116.63
10	J	165	ARG	N-CA-C	5.75	120.36	113.23
6	F	63	LYS	N-CA-C	5.75	120.36	111.56
12	Z	49	ALA	N-CA-C	5.73	118.27	111.33
13	M	-2	THR	N-CA-C	5.72	118.39	109.52
10	X	93	ARG	CA-C-N	5.72	125.65	119.76
10	X	93	ARG	C-N-CA	5.72	125.65	119.76
13	1	-2	THR	N-CA-C	5.71	118.37	109.52
4	D	128	MET	N-CA-C	-5.67	98.71	110.80
12	L	69	ASP	N-CA-C	5.66	117.45	111.28
8	V	100	ILE	N-CA-C	-5.66	99.48	107.75
7	U	9	ASP	N-CA-C	-5.61	106.48	113.15
8	H	172	ASN	N-CA-C	5.58	117.99	109.95
9	I	95	TYR	N-CA-C	-5.58	101.38	110.20
13	M	45	ILE	N-CA-C	5.58	116.52	108.48
9	I	141	LEU	N-CA-C	5.57	117.43	111.36
10	J	122	LEU	CA-C-N	5.57	124.92	118.85
10	J	122	LEU	C-N-CA	5.57	124.92	118.85
12	L	114	ASP	CA-C-N	-5.57	113.94	119.56
12	L	114	ASP	C-N-CA	-5.57	113.94	119.56
12	Z	114	ASP	CA-C-N	-5.56	113.95	119.56
12	Z	114	ASP	C-N-CA	-5.56	113.95	119.56
10	X	122	LEU	N-CA-C	5.55	117.21	108.55
2	B	107	ILE	N-CA-C	5.54	114.38	108.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	T	63	LYS	N-CA-C	5.53	120.02	111.56
10	J	166	MET	CA-C-N	5.52	125.87	119.47
10	J	166	MET	C-N-CA	5.52	125.87	119.47
8	V	172	ASN	N-CA-C	5.52	117.89	109.95
4	R	128	MET	N-CA-C	-5.51	99.05	110.80
10	J	122	LEU	N-CA-C	5.50	117.12	108.55
12	L	49	ALA	N-CA-C	5.49	117.97	111.33
8	V	9	ASN	N-CA-C	5.46	119.44	112.34
7	G	218	ASP	N-CA-C	5.46	119.11	111.74
12	L	94	PRO	N-CA-C	5.45	119.79	111.34
8	V	182	LYS	N-CA-C	5.43	118.47	109.94
1	A	143	GLU	N-CA-C	5.43	117.90	111.33
11	Y	98	GLY	N-CA-C	-5.40	100.37	113.18
14	N	76	THR	N-CA-C	-5.39	105.48	111.36
9	I	25	LEU	N-CA-C	5.39	117.51	109.59
11	Y	188	GLY	N-CA-C	5.37	125.91	113.18
11	K	45	MET	N-CA-C	5.37	117.27	108.52
9	I	93	GLY	CA-C-N	5.36	125.36	120.21
9	I	93	GLY	C-N-CA	5.36	125.36	120.21
4	D	202	GLU	N-CA-C	-5.36	105.34	111.07
10	J	141	HIS	N-CA-C	5.36	119.87	113.23
6	T	71	ASP	CB-CA-C	-5.34	110.43	116.63
10	X	45	PHE	N-CA-C	5.34	116.96	108.79
9	W	25	LEU	N-CA-C	5.32	117.41	109.59
12	Z	145	TYR	N-CA-C	5.32	118.78	110.32
4	D	82	THR	N-CA-C	5.31	118.86	112.38
7	U	218	ASP	N-CA-C	5.31	118.91	111.74
12	Z	69	ASP	N-CA-C	5.31	117.06	111.28
11	Y	131	GLN	N-CA-C	5.30	117.49	111.02
9	W	143	GLU	CA-C-N	5.29	125.59	119.92
9	W	143	GLU	C-N-CA	5.29	125.59	119.92
8	H	182	LYS	N-CA-C	5.29	118.25	109.94
13	M	189	ASN	N-CA-C	5.29	119.01	112.24
11	K	188	GLY	N-CA-C	5.29	125.71	113.18
12	L	35	PHE	N-CA-C	5.29	118.02	109.40
11	K	98	GLY	N-CA-C	-5.28	100.66	113.18
13	M	29	ASN	N-CA-C	5.28	120.58	113.72
5	S	58	LEU	N-CA-C	-5.26	106.91	113.38
14	2	76	THR	N-CA-C	-5.26	105.63	111.36
5	E	152	GLN	CA-C-N	5.25	126.40	119.84
5	E	152	GLN	C-N-CA	5.25	126.40	119.84
12	L	145	TYR	N-CA-C	5.25	118.66	110.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	218	GLN	N-CA-C	5.24	116.80	111.14
1	O	143	GLU	N-CA-C	5.24	117.67	111.33
7	U	78	VAL	N-CA-C	5.24	115.44	108.11
12	Z	35	PHE	N-CA-C	5.24	117.93	109.40
9	W	93	GLY	CA-C-N	5.23	125.23	120.21
9	W	93	GLY	C-N-CA	5.23	125.23	120.21
4	D	218	GLN	N-CA-C	5.23	116.79	111.14
3	Q	134	VAL	N-CA-C	5.22	115.24	108.35
5	S	152	GLN	CA-C-N	5.22	126.36	119.84
5	S	152	GLN	C-N-CA	5.22	126.36	119.84
10	X	122	LEU	CA-C-N	5.21	124.53	118.85
10	X	122	LEU	C-N-CA	5.21	124.53	118.85
2	P	16	SER	N-CA-C	-5.21	102.46	110.07
4	R	82	THR	N-CA-C	5.21	118.74	112.38
7	G	78	VAL	N-CA-C	5.20	115.38	108.11
10	J	45	PHE	N-CA-C	5.19	116.73	108.79
6	T	38	ILE	N-CA-C	5.18	116.16	108.65
10	J	143	ARG	CA-C-N	5.18	125.22	119.32
10	J	143	ARG	C-N-CA	5.18	125.22	119.32
3	C	134	VAL	N-CA-C	5.14	115.14	108.35
7	U	147	SER	N-CA-C	5.14	117.80	109.06
10	X	143	ARG	CA-C-N	5.14	125.18	119.32
10	X	143	ARG	C-N-CA	5.14	125.18	119.32
9	W	98	GLY	CA-C-N	5.14	125.04	119.85
9	W	98	GLY	C-N-CA	5.14	125.04	119.85
4	R	202	GLU	N-CA-C	-5.13	105.58	111.07
12	Z	117	GLY	N-CA-C	5.12	120.82	114.37
7	G	43	LYS	N-CA-C	-5.12	105.78	111.36
12	Z	94	PRO	N-CA-C	5.12	119.27	111.34
13	M	97	ASN	N-CA-C	5.12	116.96	109.24
9	I	143	GLU	CA-C-N	5.11	125.39	119.92
9	I	143	GLU	C-N-CA	5.11	125.39	119.92
13	1	45	ILE	N-CA-C	5.10	115.83	108.48
9	W	128	GLY	N-CA-C	5.10	117.97	111.85
11	K	131	GLN	N-CA-C	5.09	117.21	111.11
11	Y	117	GLY	N-CA-C	-5.08	107.69	115.00
13	1	189	ASN	N-CA-C	5.07	118.73	112.24
7	U	60	ASP	CA-C-N	5.07	126.18	119.84
7	U	60	ASP	C-N-CA	5.07	126.18	119.84
12	Z	129	ALA	N-CA-C	5.07	117.21	111.02
4	D	129	SER	N-CA-C	5.07	118.56	112.38
12	L	134	ILE	N-CA-C	5.06	116.94	111.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	X	174	ILE	N-CA-C	-5.04	101.11	108.17
12	L	115	PRO	N-CA-C	-5.04	107.57	113.86
10	X	141	HIS	N-CA-C	5.03	119.47	113.23
9	I	98	GLY	CA-C-N	5.02	124.92	119.85
9	I	98	GLY	C-N-CA	5.02	124.92	119.85
1	O	78	TYR	N-CA-C	5.02	115.94	108.86
3	C	22	PHE	N-CA-C	5.02	117.40	111.33
12	L	129	ALA	N-CA-C	5.01	117.14	111.02
7	G	197	MET	N-CA-C	-5.01	105.90	111.36
1	O	81	MET	N-CA-C	5.00	116.84	108.23
9	I	145	ASN	N-CA-C	5.00	118.10	111.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	L	145	TYR	Sidechain
12	Z	145	TYR	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1926	53	0
1	O	1915	0	1926	65	0
2	B	1905	0	1901	93	0
2	P	1905	0	1901	102	0
3	C	1891	0	1900	96	0
3	Q	1891	0	1900	93	0
4	D	1862	0	1836	55	0
4	R	1862	0	1836	51	0
5	E	1795	0	1797	70	0
5	S	1795	0	1797	73	0
6	F	1897	0	1886	64	0
6	T	1897	0	1886	71	0
7	G	1921	0	1910	66	0
7	U	1921	0	1910	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1685	0	1688	51	0
8	V	1685	0	1688	49	0
9	I	1581	0	1574	53	0
9	W	1581	0	1574	51	0
10	J	1585	0	1590	68	0
10	X	1585	0	1590	72	0
11	K	1644	0	1594	57	0
11	Y	1644	0	1594	55	0
12	L	1757	0	1711	64	0
12	Z	1757	0	1711	66	0
13	1	1824	0	1832	60	0
13	M	1824	0	1832	64	0
14	2	1512	0	1481	51	0
14	N	1512	0	1481	52	0
15	K	15	0	16	2	0
15	Y	15	0	16	0	0
16	1	64	0	0	1	0
16	2	51	0	0	1	0
16	A	35	0	0	2	0
16	B	27	0	0	3	0
16	C	32	0	0	5	0
16	D	23	0	0	1	0
16	E	15	0	0	0	0
16	F	35	0	0	1	0
16	G	51	0	0	2	0
16	H	41	0	0	4	0
16	I	51	0	0	1	0
16	J	38	0	0	1	0
16	K	33	0	0	0	0
16	L	43	0	0	2	0
16	M	56	0	0	4	0
16	N	49	0	0	3	0
16	O	28	0	0	2	0
16	P	18	0	0	2	0
16	Q	19	0	0	4	0
16	R	19	0	0	0	0
16	S	16	0	0	0	0
16	T	30	0	0	5	0
16	U	48	0	0	6	0
16	V	36	0	0	1	0
16	W	40	0	0	1	0
16	X	36	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	Y	36	0	0	2	0
16	Z	36	0	0	7	0
All	All	50584	0	49284	1666	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 17.

All (1666) 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)
7:G:96:ALA:HA	7:G:107:MET:HE2	1.33	1.09
7:U:96:ALA:HA	7:U:107:MET:HE2	1.32	1.07
1:O:130:ARG:HH21	7:U:124:THR:HG22	1.22	1.02
2:B:71:ASN:ND2	2:B:72:ASP:H	1.60	0.99
2:B:202:THR:HG22	2:B:204:SER:H	1.27	0.99
2:P:202:THR:HG22	2:P:204:SER:H	1.26	0.99
1:A:130:ARG:HH21	7:G:124:THR:HG22	1.27	0.99
2:P:71:ASN:ND2	2:P:72:ASP:H	1.60	0.99
1:O:15:PHE:H	2:P:23:GLN:HE22	1.07	0.98
5:S:2(B):THR:H	5:S:2(E):ASN:HD22	0.96	0.96
3:Q:185:THR:HB	3:Q:188:GLU:HG2	1.47	0.95
11:Y:10(B):LYS:H	11:Y:10(B):LYS:HD2	1.30	0.95
3:C:15:PHE:H	4:D:23:GLN:HE22	1.07	0.95
3:C:163:GLN:HE21	3:C:164:THR:H	0.95	0.95
4:D:97:VAL:HG21	11:K:65:LEU:HD13	1.46	0.94
5:E:2(B):THR:H	5:E:2(E):ASN:HD22	0.95	0.94
13:M:157:ASN:HD22	13:M:160:ARG:HH11	1.01	0.94
11:K:10(B):LYS:H	11:K:10(B):LYS:HD2	1.30	0.94
1:O:86:ARG:HE	7:U:118:ASN:HD21	1.16	0.94
6:F:36:THR:HG22	6:F:51:GLU:OE2	1.68	0.93
6:T:36:THR:HG22	6:T:51:GLU:OE2	1.67	0.93
3:C:185:THR:HB	3:C:188:GLU:HG2	1.49	0.93
4:R:97:VAL:HG21	11:Y:65:LEU:HD13	1.48	0.92
1:O:124:THR:HG22	2:P:130:ARG:HH21	1.32	0.92
3:C:100:ARG:NH1	3:C:106:PRO:HB3	1.85	0.91
13:1:157:ASN:HD22	13:1:160:ARG:HH11	1.05	0.91
10:J:168:MET:HE3	10:X:168:MET:HE3	1.53	0.91
3:Q:100:ARG:NH1	3:Q:106:PRO:HB3	1.86	0.90
3:Q:163:GLN:NE2	3:Q:164:THR:H	1.70	0.89
3:Q:163:GLN:HE21	3:Q:164:THR:H	0.93	0.89
1:A:124:THR:HG22	2:B:130:ARG:HH21	1.36	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:2(B):THR:H	5:E:2(E):ASN:ND2	1.69	0.89
3:Q:15:PHE:H	4:R:23:GLN:HE22	1.15	0.88
5:S:2(B):THR:H	5:S:2(E):ASN:ND2	1.71	0.88
11:K:33:LYS:HG2	11:K:45:MET:HE2	1.54	0.88
3:C:163:GLN:NE2	3:C:164:THR:H	1.71	0.88
5:E:207:LEU:HD23	5:E:207:LEU:H	1.39	0.88
12:L:33:LYS:HD2	12:L:46:ASN:HD22	1.40	0.87
9:I:6:MET:HE3	9:I:155:ILE:HG13	1.57	0.87
12:Z:33:LYS:HD2	12:Z:46:ASN:HD22	1.39	0.86
13:M:157:ASN:HD22	13:M:160:ARG:NH1	1.74	0.86
5:S:207:LEU:HD23	5:S:207:LEU:H	1.41	0.86
9:W:6:MET:HE3	9:W:155:ILE:HG13	1.56	0.85
2:P:124:THR:HG22	3:Q:130:ARG:HH21	1.40	0.85
1:A:15:PHE:H	2:B:23:GLN:HE22	1.24	0.84
7:G:87:ASN:C	7:G:87:ASN:HD22	1.84	0.84
5:E:207:LEU:HA	5:E:2(E):ASN:HD21	1.42	0.84
1:A:86:ARG:HE	7:G:118:ASN:HD21	1.26	0.84
2:B:15:PHE:H	3:C:23:GLN:HE22	1.24	0.84
1:O:86:ARG:HE	7:U:118:ASN:ND2	1.76	0.84
13:1:157:ASN:HD22	13:1:160:ARG:NH1	1.77	0.83
5:S:207:LEU:HA	5:S:2(E):ASN:HD21	1.43	0.82
7:U:87:ASN:C	7:U:87:ASN:HD22	1.87	0.82
13:M:35:ILE:HG12	13:M:56:GLU:HG3	1.61	0.82
2:B:61:GLN:OE1	2:B:208:ASP:HA	1.79	0.82
1:A:130:ARG:HH21	7:G:124:THR:CG2	1.93	0.82
2:P:61:GLN:OE1	2:P:208:ASP:HA	1.80	0.82
2:B:124:THR:HG22	3:C:130:ARG:HH21	1.43	0.81
13:M:40:ASN:H	13:M:40:ASN:HD22	1.29	0.81
13:1:35:ILE:HG12	13:1:56:GLU:HG3	1.62	0.81
3:C:163:GLN:HE21	3:C:164:THR:N	1.78	0.81
5:E:201:LEU:HD11	5:E:207:LEU:HD22	1.63	0.81
11:K:31:VAL:HG11	11:K:45:MET:HE1	1.62	0.81
1:O:130:ARG:HH21	7:U:124:THR:CG2	1.93	0.80
2:B:124:THR:CG2	3:C:130:ARG:HH21	1.95	0.80
5:S:201:LEU:HD11	5:S:207:LEU:HD22	1.62	0.80
1:A:33:GLN:HE21	1:A:33:GLN:HA	1.47	0.80
13:M:157:ASN:ND2	13:M:160:ARG:HH11	1.79	0.80
12:L:40:ASN:HD21	12:L:183:GLY:HA2	1.48	0.79
2:P:71:ASN:HD22	2:P:72:ASP:H	1.27	0.79
13:1:40:ASN:H	13:1:40:ASN:HD22	1.28	0.79
2:B:71:ASN:HD22	2:B:72:ASP:H	1.29	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:35:THR:HG21	6:F:51:GLU:O	1.83	0.78
13:1:157:ASN:ND2	13:1:160:ARG:HH11	1.82	0.78
14:N:136:GLY:HA2	14:2:161:GLN:NE2	1.98	0.77
3:Q:163:GLN:HE21	3:Q:164:THR:N	1.77	0.77
2:P:124:THR:CG2	3:Q:130:ARG:HH21	1.98	0.77
1:O:33:GLN:HE21	1:O:33:GLN:HA	1.48	0.77
13:1:104:VAL:HG23	13:1:178:ILE:HG22	1.67	0.77
14:N:136:GLY:HA2	14:2:161:GLN:HE21	1.48	0.76
2:P:71:ASN:ND2	2:P:72:ASP:N	2.34	0.76
3:C:100:ARG:HH11	3:C:106:PRO:HB3	1.49	0.76
13:M:139:ARG:HH11	8:V:165:ASN:HD22	1.32	0.76
14:2:36:ARG:HG3	14:2:42:TRP:CE2	2.21	0.75
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.21	0.75
3:Q:100:ARG:HH11	3:Q:106:PRO:HB3	1.48	0.75
6:T:179:LEU:HD21	6:T:192:GLN:HG2	1.69	0.75
12:Z:-7:ASN:ND2	12:Z:-5:TYR:H	1.85	0.75
4:R:162:ALA:HB3	5:S:58:LEU:HD23	1.66	0.75
8:H:165:ASN:HD22	13:1:139:ARG:HH11	1.32	0.75
13:M:149:GLN:NE2	13:M:149:GLN:H	1.85	0.75
12:Z:40:ASN:HD21	12:Z:183:GLY:HA2	1.52	0.74
2:B:121:GLN:O	2:B:124:THR:HB	1.87	0.74
11:Y:143:LYS:O	11:Y:146:LEU:HD13	1.86	0.74
6:T:35:THR:HG21	6:T:51:GLU:O	1.87	0.74
13:1:14(C):ARG:HG3	13:1:14(C):ARG:HH11	1.52	0.74
10:J:168:MET:HG2	10:X:168:MET:HE3	1.67	0.74
7:U:121:GLN:O	7:U:124:THR:HB	1.87	0.74
14:N:161:GLN:HE21	14:2:136:GLY:HA2	1.52	0.74
2:B:71:ASN:ND2	2:B:72:ASP:N	2.34	0.74
5:E:48:LEU:HG	5:E:139:ILE:HD13	1.70	0.73
10:J:2:ILE:HD13	10:J:162:LEU:HD13	1.70	0.73
11:K:10(B):LYS:H	11:K:10(B):LYS:CD	2.02	0.73
2:P:65:GLU:HG3	2:P:66:LYS:HG3	1.71	0.73
11:K:143:LYS:O	11:K:146:LEU:HD13	1.89	0.73
13:M:57:ARG:NE	16:M:240:HOH:O	2.22	0.73
6:F:179:LEU:HD21	6:F:192:GLN:HG2	1.70	0.73
13:M:14(C):ARG:HG3	13:M:14(C):ARG:HH11	1.54	0.73
2:P:121:GLN:O	2:P:124:THR:HB	1.89	0.73
3:C:172:VAL:HG23	3:C:196:SER:HB2	1.69	0.72
3:Q:41:LYS:HG2	3:Q:161:SER:O	1.89	0.72
13:1:149:GLN:H	13:1:149:GLN:NE2	1.87	0.72
5:S:15:PHE:H	6:T:23:GLN:HE22	1.38	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:161:GLN:NE2	14:2:136:GLY:HA2	2.02	0.72
3:Q:172:VAL:HG23	3:Q:196:SER:HB2	1.70	0.72
10:J:168:MET:HE3	10:X:168:MET:HG2	1.72	0.72
10:X:32:ASP:OD2	10:X:34:THR:HG22	1.89	0.72
2:P:227:GLN:OE1	2:P:230:LYS:HD3	1.89	0.72
7:G:121:GLN:O	7:G:124:THR:HB	1.89	0.72
13:M:76:PRO:HD2	13:M:105:GLN:OE1	1.90	0.72
3:Q:33:ARG:NH1	3:Q:33:ARG:HB2	2.03	0.72
3:Q:106:PRO:HG2	3:Q:143:PRO:CG	2.20	0.72
12:Z:109:ALA:HA	16:Z:204:HOH:O	1.90	0.72
13:1:76:PRO:HD2	13:1:105:GLN:OE1	1.89	0.72
1:A:86:ARG:HE	7:G:118:ASN:ND2	1.88	0.71
7:G:198:ILE:HG23	7:G:203:THR:O	1.90	0.71
7:U:96:ALA:HA	7:U:107:MET:CE	2.15	0.71
3:C:15:PHE:N	4:D:23:GLN:HE22	1.86	0.71
3:C:41:LYS:HG2	3:C:161:SER:O	1.90	0.71
7:G:96:ALA:HA	7:G:107:MET:CE	2.17	0.71
1:O:124:THR:CG2	2:P:130:ARG:HH21	2.02	0.71
3:Q:33:ARG:CB	3:Q:33:ARG:HH11	2.03	0.71
4:R:185:THR:OG1	4:R:188:GLU:HG3	1.91	0.71
1:A:179:ARG:HH11	1:A:179:ARG:HB3	1.54	0.71
2:B:227:GLN:OE1	2:B:230:LYS:HD3	1.90	0.71
1:O:179:ARG:HH11	1:O:179:ARG:HB3	1.54	0.71
3:Q:185:THR:HG22	3:Q:187:GLU:H	1.53	0.71
3:C:185:THR:HG22	3:C:187:GLU:H	1.55	0.71
2:B:65:GLU:HG3	2:B:66:LYS:HG3	1.71	0.71
5:S:48:LEU:HG	5:S:139:ILE:HD13	1.73	0.71
10:X:2:ILE:HD13	10:X:162:LEU:HD13	1.73	0.71
12:L:-9:GLN:NE2	12:L:-8:PHE:H	1.89	0.71
6:T:173:LYS:O	6:T:177:GLU:HG3	1.91	0.71
12:Z:-9:GLN:NE2	12:Z:-8:PHE:H	1.88	0.71
8:H:80:LEU:HD12	8:H:113:ILE:HD11	1.73	0.70
12:L:33:LYS:HD2	12:L:46:ASN:ND2	2.06	0.70
5:S:207:LEU:HA	5:S:2(E):ASN:ND2	2.07	0.70
10:X:156:LYS:O	10:X:160:GLN:HG3	1.90	0.70
5:E:207:LEU:HA	5:E:2(E):ASN:ND2	2.06	0.70
6:F:173:LYS:O	6:F:177:GLU:HG3	1.92	0.70
1:A:20:LYS:HE3	1:A:25:ASP:OD1	1.92	0.70
11:K:142:TYR:O	11:K:143:LYS:HD2	1.91	0.70
8:V:163:ILE:HG23	8:V:170:GLY:HA2	1.74	0.70
5:E:207:LEU:H	5:E:207:LEU:CD2	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:15:PHE:H	4:D:23:GLN:NE2	1.86	0.70
4:D:40:ILE:HD12	4:D:193:VAL:HG23	1.74	0.70
12:L:-7:ASN:ND2	12:L:-5:TYR:H	1.89	0.70
5:S:207:LEU:H	5:S:207:LEU:CD2	2.05	0.70
3:C:186:VAL:HG21	3:C:216:LYS:HE2	1.74	0.69
12:Z:76:ILE:HG22	16:Z:221:HOH:O	1.92	0.69
1:A:124:THR:CG2	2:B:130:ARG:HH21	2.04	0.69
7:U:67:ILE:HD12	7:U:211:GLU:HG2	1.72	0.69
11:Y:142:TYR:O	11:Y:143:LYS:HD2	1.92	0.69
3:C:33:ARG:NH1	3:C:33:ARG:HB2	2.07	0.69
8:H:3:ILE:HD11	8:H:127:LEU:HB2	1.74	0.69
4:R:40:ILE:HD12	4:R:193:VAL:HG23	1.74	0.69
11:K:31:VAL:CG1	11:K:45:MET:HE1	2.21	0.69
12:Z:33:LYS:HD2	12:Z:46:ASN:ND2	2.07	0.69
14:N:84:LYS:HG3	14:N:119:VAL:HG22	1.75	0.69
8:H:163:ILE:HG23	8:H:170:GLY:HA2	1.75	0.69
1:O:20:LYS:HE3	1:O:25:ASP:OD1	1.92	0.69
3:C:106:PRO:HG2	3:C:143:PRO:CG	2.22	0.69
10:J:156:LYS:O	10:J:160:GLN:HG3	1.93	0.69
3:Q:186:VAL:HG21	3:Q:216:LYS:HE2	1.74	0.69
6:T:184:LEU:HD11	6:T:188:GLU:HB3	1.75	0.69
12:Z:-8:PHE:HB2	13:1:-8:THR:HG23	1.75	0.69
8:V:80:LEU:HD12	8:V:113:ILE:HD11	1.74	0.68
3:C:33:ARG:CB	3:C:33:ARG:HH11	2.06	0.68
2:P:15:PHE:H	3:Q:23:GLN:HE22	1.41	0.68
6:T:95:GLU:HG2	6:T:115:ARG:HB3	1.75	0.68
10:X:133:TYR:CE2	10:X:166:MET:HG3	2.27	0.68
4:D:185:THR:OG1	4:D:188:GLU:HG3	1.92	0.68
10:J:32:ASP:OD2	10:J:34:THR:HG22	1.93	0.68
14:N:186:ARG:HD3	16:N:228:HOH:O	1.93	0.68
7:U:96:ALA:CA	7:U:107:MET:HE2	2.20	0.68
3:C:71:ASP:HA	10:J:68:ILE:CD1	2.24	0.68
11:K:7:ARG:HG2	11:K:108:PRO:HB2	1.75	0.68
13:M:104:VAL:HG23	13:M:178:ILE:HG22	1.76	0.68
4:D:162:ALA:HB3	5:E:58:LEU:HD23	1.76	0.67
3:C:41:LYS:HD3	3:C:161:SER:HA	1.75	0.67
7:U:39:ALA:HB2	7:U:48:VAL:HG12	1.76	0.67
11:Y:7:ARG:HG2	11:Y:108:PRO:HB2	1.76	0.67
6:F:184:LEU:HD11	6:F:188:GLU:HB3	1.77	0.67
10:J:133:TYR:CE2	10:J:166:MET:HG3	2.29	0.67
10:J:20:VAL:HG11	11:K:120:LEU:HD11	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:194:LEU:HD22	4:D:212:LEU:HD11	1.77	0.67
8:V:172:ASN:HD22	8:V:193:THR:HA	1.60	0.67
8:V:81:GLN:O	8:V:85:GLN:HG3	1.94	0.67
3:Q:55:THR:HG22	3:Q:56:LEU:HD22	1.77	0.66
13:1:40:ASN:HD22	13:1:40:ASN:N	1.92	0.66
11:K:45:MET:HE3	15:K:301:SLR:H14	1.76	0.66
6:T:35:THR:HG23	6:T:51:GLU:HB3	1.78	0.66
8:V:3:ILE:HD11	8:V:127:LEU:HB2	1.76	0.66
3:Q:41:LYS:HD3	3:Q:161:SER:HA	1.78	0.66
7:U:198:ILE:HG23	7:U:203:THR:O	1.95	0.66
5:E:132:TYR:O	5:E:153:PRO:HB3	1.96	0.66
1:O:159:PRO:O	2:P:59:LEU:HD12	1.96	0.66
2:P:185:LYS:HD3	2:P:186:VAL:N	2.10	0.66
2:B:181:LYS:O	2:B:184:MET:HG3	1.95	0.66
5:S:111:ARG:HH11	5:S:111:ARG:HG2	1.59	0.66
10:J:147:THR:OG1	10:J:150:GLU:HG3	1.96	0.66
6:F:35:THR:HG23	6:F:51:GLU:HB3	1.78	0.66
8:H:173:VAL:HB	8:H:192:LEU:HB2	1.78	0.66
8:V:173:VAL:HB	8:V:192:LEU:HB2	1.76	0.65
7:G:67:ILE:HD12	7:G:211:GLU:HG2	1.77	0.65
1:O:121:GLN:O	1:O:124:THR:HB	1.97	0.65
2:P:71:ASN:HD22	2:P:72:ASP:N	1.93	0.65
4:R:194:LEU:HD22	4:R:212:LEU:HD11	1.78	0.65
3:C:55:THR:HG22	3:C:56:LEU:HD22	1.77	0.65
2:P:146:TYR:OH	2:P:21(A):LYS:HB2	1.97	0.65
10:J:168:MET:HG2	10:X:168:MET:CE	2.26	0.65
3:Q:185:THR:HG22	3:Q:187:GLU:N	2.11	0.65
14:2:84:LYS:HG3	14:2:119:VAL:HG22	1.76	0.65
4:D:12(D):ALA:HB3	4:D:126:ARG:HD3	1.79	0.65
5:E:111:ARG:HG2	5:E:111:ARG:HH11	1.61	0.65
12:L:8:GLY:HA3	12:L:11:PHE:CE2	2.32	0.65
10:J:168:MET:HE3	10:X:168:MET:CE	2.27	0.65
3:Q:216:LYS:HB2	3:Q:220:ASP:HB3	1.79	0.65
5:S:75:GLY:HA3	5:S:221:PHE:CE2	2.31	0.65
2:B:185:LYS:HD3	2:B:186:VAL:N	2.11	0.64
3:C:216:LYS:HB2	3:C:220:ASP:HB3	1.79	0.64
7:G:96:ALA:CA	7:G:107:MET:HE2	2.21	0.64
8:V:62:ASN:HB3	8:V:82:MET:HE1	1.80	0.64
2:P:181:LYS:O	2:P:184:MET:HG3	1.96	0.64
5:S:198:SER:HA	5:S:201:LEU:HG	1.80	0.64
6:T:179:LEU:HD11	6:T:192:GLN:HG3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:168:MET:CE	10:X:168:MET:HG2	2.28	0.64
10:J:168:MET:CE	10:X:168:MET:HE3	2.26	0.64
10:J:52:THR:HG22	10:J:53:VAL:N	2.11	0.64
1:O:33:GLN:HE21	1:O:33:GLN:CA	2.09	0.64
11:Y:10(B):LYS:H	11:Y:10(B):LYS:CD	2.01	0.64
3:Q:33:ARG:HB2	3:Q:33:ARG:HH11	1.60	0.64
10:X:147:THR:HG23	10:X:150:GLU:OE2	1.97	0.64
2:B:88:LEU:HB3	2:B:116:LEU:HD21	1.80	0.64
8:H:81:GLN:O	8:H:85:GLN:HG3	1.97	0.64
8:H:172:ASN:HD22	8:H:193:THR:HA	1.61	0.64
2:B:146:TYR:OH	2:B:21(A):LYS:HB2	1.97	0.64
3:C:35:THR:HB	3:C:51:GLU:HG3	1.78	0.64
8:H:62:ASN:HB3	8:H:82:MET:HE1	1.79	0.64
4:R:12(D):ALA:HB3	4:R:126:ARG:HD3	1.79	0.64
3:C:164:THR:HG21	3:C:172:VAL:HG13	1.81	0.63
7:U:59:LEU:O	7:U:61:PRO:HD3	1.98	0.63
12:Z:8:GLY:HA3	12:Z:11:PHE:CE2	2.33	0.63
12:Z:21:ILE:C	12:Z:21:ILE:HD12	2.23	0.63
3:C:71:ASP:HA	10:J:68:ILE:HD11	1.81	0.63
12:L:21:ILE:C	12:L:21:ILE:HD12	2.23	0.63
3:Q:35:THR:HB	3:Q:51:GLU:HG3	1.80	0.63
4:R:85:ALA:O	4:R:89:ILE:HG12	1.98	0.63
6:T:179:LEU:HD21	6:T:192:GLN:CG	2.28	0.63
2:B:71:ASN:HD22	2:B:72:ASP:N	1.95	0.63
7:U:18(G):GLU:HG2	7:U:188:LYS:HB3	1.81	0.63
10:X:147:THR:OG1	10:X:150:GLU:HG3	1.98	0.63
6:F:95:GLU:HG2	6:F:115:ARG:HB3	1.79	0.63
8:H:18:THR:HB	8:H:30:ASN:HD22	1.64	0.63
5:E:75:GLY:HA3	5:E:221:PHE:CE2	2.34	0.63
12:Z:43:MET:HB2	12:Z:101:ILE:HG22	1.80	0.63
3:C:185:THR:HG22	3:C:187:GLU:N	2.12	0.63
7:G:170:GLN:NE2	7:G:174:THR:HG23	2.14	0.63
4:R:207:LEU:C	4:R:207:LEU:HD23	2.24	0.63
5:E:2(B):THR:N	5:E:2(E):ASN:HD22	1.81	0.63
7:G:18(G):GLU:HG2	7:G:188:LYS:HB3	1.79	0.63
13:M:40:ASN:HD22	13:M:40:ASN:N	1.92	0.63
3:Q:15:PHE:N	4:R:23:GLN:HE22	1.93	0.62
10:X:20:VAL:HG11	11:Y:120:LEU:HD11	1.80	0.62
3:Q:65:SER:HB2	16:Q:247:HOH:O	1.98	0.62
4:R:97:VAL:HG21	11:Y:65:LEU:CD1	2.28	0.62
3:C:46:VAL:O	3:C:215:VAL:HG12	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:106:PRO:HG2	3:Q:143:PRO:HG3	1.81	0.62
11:Y:114:ASP:OD1	11:Y:116:ASP:HB2	2.00	0.62
1:A:121:GLN:O	1:A:124:THR:HB	1.98	0.62
7:G:233:LEU:O	7:G:236:ILE:HG13	2.00	0.62
5:E:198:SER:HA	5:E:201:LEU:HG	1.80	0.62
12:L:-8:PHE:HB2	13:M:-8:THR:HG23	1.81	0.62
1:O:86:ARG:HH21	7:U:118:ASN:HD22	1.48	0.62
10:X:52:THR:HG22	10:X:53:VAL:N	2.14	0.62
11:Y:143:LYS:HB2	11:Y:146:LEU:CD1	2.29	0.62
10:J:147:THR:HG23	10:J:150:GLU:OE2	2.00	0.62
11:K:7:ARG:HD2	11:K:108:PRO:O	2.00	0.62
6:F:179:LEU:HD11	6:F:192:GLN:HG3	1.80	0.62
9:I:29:ASN:ND2	9:I:30:LYS:HG3	2.14	0.62
12:L:90:LYS:HE3	12:L:93:PHE:O	2.00	0.62
7:U:170:GLN:NE2	7:U:174:THR:HG23	2.14	0.62
6:F:179:LEU:HD21	6:F:192:GLN:CG	2.30	0.61
10:J:38:SER:HB2	10:J:39:PRO:HD2	1.80	0.61
3:Q:46:VAL:O	3:Q:215:VAL:HG12	1.99	0.61
1:O:225:THR:OG1	1:O:228:GLU:HG3	1.99	0.61
7:G:39:ALA:HB2	7:G:48:VAL:HG12	1.80	0.61
11:K:143:LYS:HB2	11:K:146:LEU:CD1	2.30	0.61
5:S:38:VAL:HG22	5:S:164:ALA:HB2	1.81	0.61
12:Z:4:LEU:HD11	12:Z:138:LEU:HD21	1.82	0.61
5:S:132:TYR:O	5:S:153:PRO:HB3	1.99	0.61
10:X:38:SER:HB2	10:X:39:PRO:HD2	1.82	0.61
3:C:227:GLU:OE1	3:C:227:GLU:N	2.29	0.61
8:V:18:THR:HB	8:V:30:ASN:HD22	1.66	0.61
8:V:196:VAL:HG23	16:V:242:HOH:O	2.00	0.61
1:A:225:THR:OG1	1:A:228:GLU:HG3	2.00	0.61
4:D:207:LEU:HD23	4:D:207:LEU:C	2.26	0.61
5:S:92:LEU:HD11	5:S:112:ALA:HB1	1.83	0.61
11:Y:7:ARG:HD2	11:Y:108:PRO:O	2.01	0.61
8:H:128:GLY:O	8:H:131:SER:HB2	2.00	0.61
12:Z:90:LYS:HE3	12:Z:93:PHE:O	2.01	0.61
3:C:33:ARG:HB2	3:C:33:ARG:HH11	1.64	0.60
14:N:155:ILE:HG22	14:N:175:MET:HE2	1.83	0.60
3:Q:186:VAL:O	3:Q:190:VAL:HG23	2.01	0.60
8:V:8:PHE:HB3	8:V:151:ALA:HB2	1.83	0.60
7:G:151:THR:HG22	7:G:157:TYR:HB2	1.83	0.60
1:A:177:GLU:HG2	2:B:58:LEU:HD22	1.84	0.60
9:W:150:ASP:HA	16:W:230:HOH:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2:65:LEU:HG	14:2:69:GLN:HE21	1.66	0.60
2:B:97:GLN:HE22	9:I:64:ASN:HD22	1.50	0.60
3:C:227:GLU:H	3:C:227:GLU:CD	2.10	0.60
4:D:122:ARG:HH11	4:D:122:ARG:HG2	1.65	0.60
8:H:8:PHE:HB3	8:H:151:ALA:HB2	1.83	0.60
14:N:92:ASP:HB2	16:N:199:HOH:O	2.01	0.60
8:V:128:GLY:O	8:V:131:SER:HB2	2.00	0.60
9:I:6:MET:HE1	9:I:155:ILE:HA	1.82	0.60
11:K:195:LEU:O	11:K:199:VAL:HG23	2.01	0.60
2:P:101:LYS:HZ2	10:X:85:GLN:NE2	2.00	0.60
3:Q:170:LYS:HB2	16:Q:255:HOH:O	2.01	0.60
7:U:233:LEU:O	7:U:236:ILE:HG13	2.02	0.60
12:Z:-7:ASN:C	12:Z:-7:ASN:HD22	2.07	0.60
3:C:106:PRO:HG2	3:C:143:PRO:HG3	1.83	0.60
2:P:163:ILE:HG13	2:P:164:SER:N	2.16	0.60
8:V:172:ASN:ND2	8:V:193:THR:HA	2.17	0.60
5:E:2(B):THR:OG1	5:E:2(E):ASN:HB3	2.02	0.60
7:G:87:ASN:C	7:G:87:ASN:ND2	2.55	0.60
12:L:135:MET:HE3	9:W:165:ARG:NH2	2.15	0.60
2:P:234:VAL:HA	2:P:239:THR:HA	1.84	0.60
5:E:15:PHE:H	6:F:23:GLN:HE22	1.49	0.60
9:W:6:MET:HE1	9:W:155:ILE:HA	1.83	0.60
3:Q:164:THR:HG21	3:Q:172:VAL:HG13	1.84	0.60
11:Y:195:LEU:O	11:Y:199:VAL:HG23	2.02	0.60
10:X:48:GLU:HB2	10:X:96:GLN:HB2	1.83	0.60
4:D:97:VAL:HG21	11:K:65:LEU:CD1	2.27	0.59
12:L:43:MET:HB2	12:L:101:ILE:HG22	1.84	0.59
4:R:122:ARG:HG2	4:R:122:ARG:HH11	1.67	0.59
6:T:127:ASN:HD22	6:T:128:SER:N	2.00	0.59
10:J:45:PHE:CD1	10:J:52:THR:HG23	2.36	0.59
11:K:114:ASP:OD1	11:K:116:ASP:HB2	2.02	0.59
3:Q:168:ASN:HB2	3:Q:200:VAL:HG11	1.84	0.59
5:S:2(B):THR:N	5:S:2(E):ASN:HD22	1.82	0.59
10:J:18:LYS:HG2	10:J:174:ILE:HG13	1.83	0.59
3:Q:71:ASP:HA	10:X:68:ILE:CD1	2.32	0.59
11:Y:138:LEU:HD13	11:Y:158:SER:OG	2.02	0.59
2:P:88:LEU:HB3	2:P:116:LEU:HD21	1.82	0.59
6:T:37:SER:HB3	6:T:50:VAL:HG23	1.84	0.59
3:C:168:ASN:HB2	3:C:200:VAL:HG11	1.85	0.59
3:C:186:VAL:O	3:C:190:VAL:HG23	2.02	0.59
10:J:10(B):LYS:HB2	10:J:10(B):LYS:NZ	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:15:PHE:N	2:P:23:GLN:HE22	1.91	0.59
3:Q:15:PHE:H	4:R:23:GLN:NE2	1.94	0.59
1:A:173:LYS:O	1:A:177:GLU:HG3	2.03	0.59
11:K:45:MET:HE3	15:K:301:SLR:C14	2.32	0.59
4:D:85:ALA:O	4:D:89:ILE:HG12	2.03	0.59
8:H:172:ASN:ND2	8:H:193:THR:HA	2.18	0.59
11:K:138:LEU:HD13	11:K:158:SER:OG	2.03	0.59
14:N:14:LEU:HD11	14:N:102:ALA:HB3	1.83	0.59
10:X:18:LYS:HG2	10:X:174:ILE:HG13	1.85	0.59
10:X:10(B):LYS:HB2	10:X:10(B):LYS:NZ	2.18	0.59
5:E:38:VAL:HG22	5:E:164:ALA:HB2	1.83	0.59
6:F:127:ASN:HD22	6:F:128:SER:N	2.00	0.59
9:I:29:ASN:C	9:I:29:ASN:HD22	2.11	0.58
1:O:232:ARG:HG3	1:O:232:ARG:HH11	1.67	0.58
10:X:44:SER:OG	10:X:100:LEU:HB2	2.02	0.58
12:Z:-7:ASN:HD22	12:Z:-6:PRO:HD2	1.68	0.58
1:A:232:ARG:HG3	1:A:232:ARG:HH11	1.68	0.58
2:B:225:LYS:HG3	2:B:228:GLU:OE1	2.03	0.58
9:W:29:ASN:ND2	9:W:30:LYS:HG3	2.19	0.58
12:Z:166:HIS:HD2	12:Z:168:GLN:H	1.50	0.58
14:2:14:LEU:HD11	14:2:102:ALA:HB3	1.85	0.58
3:C:232:TYR:O	3:C:236:ILE:HG13	2.03	0.58
4:D:12(D):ALA:HA	5:E:129:GLY:HA2	1.85	0.58
7:G:59:LEU:O	7:G:61:PRO:HD3	2.03	0.58
12:L:-7:ASN:HD22	12:L:-6:PRO:HD2	1.69	0.58
4:R:52:LYS:HE3	4:R:211:GLN:HB2	1.83	0.58
3:Q:227:GLU:H	3:Q:227:GLU:CD	2.11	0.58
1:A:7:ARG:HB2	2:B:5:SER:OG	2.03	0.58
14:N:8:PHE:CE1	14:N:10:ASP:HB2	2.38	0.58
2:P:225:LYS:HG3	2:P:228:GLU:OE1	2.03	0.58
7:U:151:THR:HG22	7:U:157:TYR:HB2	1.86	0.58
7:G:172:ILE:HD13	7:G:197:MET:HE1	1.85	0.58
4:D:52:LYS:HE3	4:D:211:GLN:HB2	1.84	0.58
12:Z:-6:PRO:O	13:1:91:ARG:NH1	2.36	0.58
5:E:180:LEU:O	5:E:18(D):ILE:HG22	2.03	0.58
5:E:190:ILE:O	5:E:194:VAL:HG23	2.04	0.58
5:E:227:GLU:CD	5:E:227:GLU:H	2.12	0.58
10:J:123:PRO:HB2	10:J:124:TYR:CD1	2.39	0.58
1:O:173:LYS:O	1:O:177:GLU:HG3	2.04	0.58
5:S:2(B):THR:OG1	5:S:2(E):ASN:HB3	2.04	0.58
7:G:217:LYS:HE3	7:G:217:LYS:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:3:ILE:HG22	10:J:100:LEU:CD1	2.34	0.58
9:I:1:GLY:HA3	9:I:33:LYS:HE2	1.85	0.57
10:J:48:GLU:HB2	10:J:96:GLN:HB2	1.85	0.57
2:P:126:HIS:HB3	3:Q:129:VAL:HG12	1.86	0.57
3:Q:159:SER:HB2	16:Q:260:HOH:O	2.03	0.57
10:X:113:ILE:HG12	10:X:119:LYS:HG3	1.85	0.57
5:E:86:ARG:O	5:E:90:ASN:HB2	2.04	0.57
6:F:20(B):GLU:CD	6:F:20(C):LYS:HE3	2.29	0.57
1:O:161:LYS:HD2	2:P:58:LEU:HA	1.84	0.57
7:U:236:ILE:HD12	7:U:237:ALA:N	2.19	0.57
10:X:14:LEU:HD12	10:X:42:LEU:HD23	1.86	0.57
10:X:10(B):LYS:HB2	10:X:10(B):LYS:HZ3	1.69	0.57
14:N:65:LEU:HG	14:N:69:GLN:HE21	1.69	0.57
3:Q:232:TYR:O	3:Q:236:ILE:HG13	2.04	0.57
14:2:8:PHE:CE1	14:2:10:ASP:HB2	2.39	0.57
2:B:41:MET:HE3	16:B:240:HOH:O	2.02	0.57
2:B:126:HIS:HB3	3:C:129:VAL:HG12	1.86	0.57
12:L:-7:ASN:HD22	12:L:-7:ASN:C	2.13	0.57
12:L:4:LEU:HD11	12:L:138:LEU:HD21	1.84	0.57
2:P:122:GLY:C	2:P:124:THR:H	2.13	0.57
5:S:86:ARG:O	5:S:90:ASN:HB2	2.04	0.57
6:T:147:HIS:HD2	16:T:242:HOH:O	1.86	0.57
1:A:33:GLN:HE21	1:A:33:GLN:CA	2.09	0.57
5:S:207:LEU:HD23	5:S:207:LEU:N	2.18	0.57
6:T:179:LEU:HD11	6:T:192:GLN:CG	2.33	0.57
5:E:18(C):PHE:HA	5:E:18(F):ILE:HG13	1.86	0.57
11:Y:156:LYS:HB2	11:Y:175:LEU:HD11	1.87	0.57
1:A:86:ARG:HH21	7:G:118:ASN:HD22	1.51	0.57
2:B:53:LYS:HG2	2:B:54:VAL:HG23	1.86	0.57
2:B:234:VAL:HA	2:B:239:THR:HA	1.85	0.57
2:P:53:LYS:HG2	2:P:54:VAL:HG23	1.87	0.57
5:S:180:LEU:O	5:S:18(D):ILE:HG22	2.04	0.57
2:B:49:ALA:HB2	2:B:212:PHE:CE1	2.40	0.57
5:E:207:LEU:HD23	5:E:207:LEU:N	2.16	0.57
12:L:34:VAL:HG12	12:L:176:LEU:HD22	1.87	0.57
1:O:57:PRO:HG3	7:U:177:GLU:CD	2.30	0.57
2:P:152:ASN:HB2	2:P:153:PRO:HD2	1.87	0.57
9:W:97:VAL:HG23	9:W:99:PRO:HD3	1.87	0.57
2:B:152:ASN:HB2	2:B:153:PRO:CD	2.35	0.57
2:P:97:GLN:HE22	9:W:64:ASN:HD22	1.53	0.57
2:P:101:LYS:NZ	10:X:85:GLN:NE2	2.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:126:CYS:HB2	11:K:135:TYR:CE1	2.39	0.57
11:K:156:LYS:HB2	11:K:175:LEU:HD11	1.86	0.57
6:T:95:GLU:CG	6:T:115:ARG:HB3	2.35	0.57
13:1:19:LEU:HB2	13:1:170:SER:HB2	1.86	0.57
3:C:190:VAL:O	3:C:194:VAL:HG23	2.05	0.56
6:T:121:GLN:NE2	16:T:248:HOH:O	2.38	0.56
7:U:217:LYS:HE3	7:U:217:LYS:HA	1.86	0.56
7:U:218:ASP:O	7:U:220:LYS:HB2	2.04	0.56
7:U:87:ASN:C	7:U:87:ASN:ND2	2.57	0.56
8:H:135:MET:HE3	13:1:165:ARG:NH2	2.20	0.56
12:L:98:HIS:HD2	16:L:198:HOH:O	1.88	0.56
13:M:184:LEU:HD23	13:M:184:LEU:C	2.30	0.56
2:P:202:THR:HG21	2:P:204:SER:HB2	1.87	0.56
9:W:1:GLY:HA3	9:W:33:LYS:HE2	1.87	0.56
4:D:227:GLU:OE2	4:D:227:GLU:N	2.33	0.56
6:T:20(B):GLU:CD	6:T:20(C):LYS:HE3	2.31	0.56
2:B:152:ASN:HB2	2:B:153:PRO:HD2	1.87	0.56
4:D:91:HIS:CG	4:D:119:LEU:HD11	2.40	0.56
5:E:123:ASN:N	5:E:123:ASN:HD22	2.03	0.56
14:2:36:ARG:HG3	14:2:42:TRP:CZ2	2.40	0.56
3:C:102:THR:OG1	3:C:103:LEU:HD22	2.05	0.56
5:E:92:LEU:HD11	5:E:112:ALA:HB1	1.87	0.56
10:J:44:SER:OG	10:J:100:LEU:HB2	2.05	0.56
1:O:69:LEU:C	1:O:69:LEU:HD23	2.31	0.56
14:N:147:SER:OG	14:N:150:GLU:HG3	2.06	0.56
12:Z:7:ALA:HB2	12:Z:110:VAL:HG23	1.87	0.56
5:S:18(C):PHE:HA	5:S:18(F):ILE:HG13	1.87	0.56
10:X:3:ILE:HG22	10:X:100:LEU:CD1	2.36	0.56
7:G:218:ASP:O	7:G:220:LYS:HB2	2.06	0.56
14:2:48:SER:HB3	14:2:51:ASP:HB2	1.88	0.56
6:F:179:LEU:HD11	6:F:192:GLN:CG	2.35	0.55
10:J:113:ILE:HG12	10:J:119:LYS:HG3	1.86	0.55
13:M:19:LEU:HB2	13:M:170:SER:HB2	1.88	0.55
3:Q:190:VAL:O	3:Q:194:VAL:HG23	2.05	0.55
7:U:131:PRO:HB3	16:U:259:HOH:O	2.06	0.55
8:V:84:LYS:HG3	8:V:85:GLN:N	2.21	0.55
6:F:82:ILE:HB	6:F:83:PRO:HD3	1.88	0.55
5:S:73:HIS:HE1	5:S:107:LEU:O	1.89	0.55
5:S:107:LEU:HD11	5:S:111:ARG:HG2	1.88	0.55
14:2:161:GLN:HE22	14:2:165:TRP:HE1	1.53	0.55
8:H:105:ASP:HB2	8:H:10(A):PRO:HD2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:152:ASN:HB2	2:P:153:PRO:CD	2.36	0.55
3:C:224:LEU:HD12	3:C:224:LEU:N	2.21	0.55
7:G:77:VAL:CG1	7:G:137:THR:HB	2.36	0.55
5:S:190:ILE:O	5:S:194:VAL:HG23	2.06	0.55
12:Z:-5:TYR:CE2	12:Z:96:TYR:HB2	2.41	0.55
14:2:112:THR:HG22	14:2:120:HIS:HB2	1.89	0.55
7:G:18(G):GLU:HG2	7:G:188:LYS:CB	2.37	0.55
13:1:41:THR:OG1	13:1:76:PRO:HG3	2.06	0.55
1:A:69:LEU:C	1:A:69:LEU:HD23	2.31	0.55
5:S:227:GLU:CD	5:S:227:GLU:H	2.13	0.55
10:X:45:PHE:CD1	10:X:52:THR:HG23	2.41	0.55
12:Z:34:VAL:HG12	12:Z:176:LEU:HD22	1.88	0.55
12:Z:177:ILE:HD12	12:Z:177:ILE:N	2.21	0.55
14:2:155:ILE:HG22	14:2:175:MET:HE2	1.88	0.55
9:I:29:ASN:HD22	9:I:30:LYS:HG3	1.71	0.55
10:J:14:LEU:HD12	10:J:42:LEU:HD23	1.89	0.55
10:J:15:ALA:HB2	10:J:155:LEU:HD11	1.89	0.55
14:N:36:ARG:HG3	14:N:42:TRP:CZ2	2.41	0.55
7:U:8:TYR:C	7:U:10:ARG:H	2.15	0.55
1:A:150:GLN:O	1:A:157:TYR:HA	2.07	0.55
6:F:187:ARG:HG3	6:F:187:ARG:HH11	1.72	0.55
2:P:239:THR:OXT	2:P:239:THR:HG22	2.07	0.55
9:W:29:ASN:C	9:W:29:ASN:HD22	2.13	0.55
2:B:218:ASN:O	2:B:21(C):ASP:HB2	2.07	0.55
6:F:37:SER:HB3	6:F:50:VAL:HG23	1.89	0.55
12:L:90:LYS:HD3	12:L:95:TYR:CE1	2.42	0.55
14:N:156:LYS:HG2	14:N:18(J):LEU:CD1	2.37	0.55
6:T:187:ARG:HH11	6:T:187:ARG:HG3	1.70	0.55
5:E:82:ALA:HB3	5:E:83:PRO:HD3	1.89	0.55
5:E:226:GLY:O	5:E:229:VAL:HG22	2.06	0.55
3:Q:102:THR:OG1	3:Q:103:LEU:HD22	2.06	0.55
4:R:91:HIS:CG	4:R:119:LEU:HD11	2.42	0.55
8:H:172:ASN:HB3	8:H:192:LEU:O	2.07	0.54
2:P:49:ALA:HB2	2:P:212:PHE:CE1	2.40	0.54
6:T:82:ILE:HB	6:T:83:PRO:HD3	1.89	0.54
14:2:156:LYS:HG2	14:2:18(J):LEU:CD1	2.37	0.54
3:C:160:TRP:CE2	4:D:59:LEU:HD23	2.42	0.54
11:K:25:TRP:CH2	12:L:132:SER:HA	2.42	0.54
3:Q:224:LEU:HD12	3:Q:224:LEU:N	2.22	0.54
7:U:77:VAL:CG1	7:U:137:THR:HB	2.38	0.54
2:B:202:THR:HG21	2:B:204:SER:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:179:ARG:HB3	1:O:179:ARG:NH1	2.22	0.54
7:U:18(G):GLU:HG2	7:U:188:LYS:CB	2.38	0.54
3:C:229:ILE:O	3:C:233:VAL:HG23	2.08	0.54
12:L:177:ILE:N	12:L:177:ILE:HD12	2.22	0.54
2:B:141:TYR:CD1	2:B:21(E):VAL:HG21	2.42	0.54
7:G:171:GLU:N	7:G:171:GLU:OE1	2.38	0.54
3:Q:226:SER:HB2	3:Q:227:GLU:OE1	2.07	0.54
7:U:172:ILE:HD13	7:U:197:MET:HE1	1.89	0.54
13:1:184:LEU:C	13:1:184:LEU:HD23	2.33	0.54
2:B:163:ILE:HG13	2:B:164:SER:N	2.22	0.54
13:M:19:LEU:HD21	13:M:26:LEU:HD22	1.90	0.54
7:U:228:ASN:HB3	16:U:242:HOH:O	2.06	0.54
9:I:2:ILE:HG21	9:I:130:ALA:HB3	1.90	0.54
9:I:165:ARG:NH2	12:Z:135:MET:HE3	2.22	0.54
1:O:150:GLN:O	1:O:157:TYR:HA	2.07	0.54
12:L:7:ALA:HB2	12:L:110:VAL:HG23	1.89	0.54
14:N:20:THR:OG1	14:N:28:ASN:HB3	2.07	0.54
4:R:121:LEU:HA	4:R:123:PHE:CE1	2.43	0.54
6:F:95:GLU:CG	6:F:115:ARG:HB3	2.37	0.53
6:T:79:SER:HA	16:T:268:HOH:O	2.06	0.53
8:V:105:ASP:HB2	8:V:10(A):PRO:HD2	1.90	0.53
10:X:15:ALA:HB2	10:X:155:LEU:HD11	1.90	0.53
6:F:28:VAL:O	6:F:32:GLU:HG3	2.07	0.53
8:V:4:VAL:HG22	8:V:159:ILE:HD11	1.90	0.53
8:V:172:ASN:HB3	8:V:192:LEU:O	2.08	0.53
5:E:73:HIS:HE1	5:E:107:LEU:O	1.91	0.53
13:M:12:VAL:HG21	13:M:102:ALA:HB1	1.89	0.53
2:P:103:TYR:O	2:P:104:ASN:HB2	2.08	0.53
4:D:175:GLU:HG2	4:D:196:ILE:HG12	1.90	0.53
11:K:200:LYS:HE3	11:K:206:PHE:O	2.08	0.53
12:L:109:ALA:HA	16:L:225:HOH:O	2.07	0.53
1:O:17:PRO:HA	2:P:26:TYR:CD1	2.43	0.53
5:S:82:ALA:HB3	5:S:83:PRO:HD3	1.90	0.53
9:W:174:VAL:HG21	9:W:186:LYS:HE3	1.90	0.53
14:2:20:THR:OG1	14:2:28:ASN:HB3	2.08	0.53
1:O:7:ARG:HB2	2:P:5:SER:OG	2.08	0.53
8:V:207:PRO:HG2	8:V:210:THR:OG1	2.08	0.53
13:1:12:VAL:HG21	13:1:102:ALA:HB1	1.89	0.53
11:K:46:ALA:HB3	11:K:98:GLY:O	2.09	0.53
2:P:218:ASN:O	2:P:21(C):ASP:HB2	2.08	0.53
11:Y:126:CYS:HB2	11:Y:135:TYR:CE1	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:122:GLY:C	2:B:124:THR:H	2.15	0.53
3:C:163:GLN:HE22	3:C:173:ARG:HE	1.57	0.53
5:E:47:VAL:HG23	5:E:189:LEU:HD13	1.90	0.53
14:N:161:GLN:HE22	14:N:165:TRP:HE1	1.55	0.53
12:Z:-7:ASN:ND2	12:Z:-7:ASN:C	2.66	0.53
14:2:65:LEU:HG	14:2:69:GLN:NE2	2.24	0.53
3:C:13:SER:HA	16:C:251:HOH:O	2.08	0.53
7:G:236:ILE:HD12	7:G:237:ALA:N	2.23	0.53
8:H:4:VAL:HG22	8:H:159:ILE:HD11	1.90	0.53
8:H:105:ASP:HB2	8:H:10(A):PRO:CD	2.39	0.53
12:L:166:HIS:HD2	12:L:168:GLN:H	1.56	0.53
3:Q:71:ASP:HA	10:X:68:ILE:HD11	1.89	0.53
13:1:19:LEU:HD21	13:1:26:LEU:HD22	1.90	0.53
7:G:86:ARG:HD2	16:G:254:HOH:O	2.09	0.53
14:N:112:THR:HG22	14:N:120:HIS:HB2	1.90	0.53
4:R:175:GLU:HG2	4:R:196:ILE:HG12	1.90	0.53
5:S:123:ASN:HD22	5:S:123:ASN:N	2.04	0.53
5:S:136:LEU:HB2	5:S:151:PHE:HB3	1.91	0.53
7:U:105:TYR:OH	8:V:66:HIS:HE1	1.92	0.53
7:U:152:ASP:HB2	7:U:153:PRO:CD	2.38	0.53
9:W:29:ASN:HD22	9:W:30:LYS:HG3	1.73	0.53
4:D:112:LEU:C	4:D:112:LEU:HD13	2.33	0.53
9:I:174:VAL:HG21	9:I:186:LYS:HE3	1.91	0.53
3:Q:163:GLN:HE22	3:Q:173:ARG:HE	1.57	0.53
3:Q:172:VAL:O	3:Q:176:LEU:HG	2.09	0.53
6:T:177:GLU:OE2	7:U:57:LYS:HE2	2.09	0.53
9:W:45:ILE:HB	9:W:52:VAL:HG13	1.91	0.53
3:C:226:SER:HB2	3:C:227:GLU:OE1	2.08	0.52
9:I:55:LEU:CD1	9:I:97:VAL:HG21	2.39	0.52
5:S:148:LEU:CD2	5:S:162:GLY:HA2	2.39	0.52
13:1:149:GLN:H	13:1:149:GLN:HE21	1.57	0.52
8:H:59:ILE:HG12	8:H:83:LEU:HG	1.92	0.52
2:B:239:THR:HG22	2:B:239:THR:OXT	2.09	0.52
7:G:170:GLN:HE21	7:G:174:THR:HG23	1.73	0.52
5:S:226:GLY:O	5:S:229:VAL:HG22	2.09	0.52
10:J:18:LYS:CG	10:J:174:ILE:HG13	2.40	0.52
2:P:168:ASN:HA	16:P:252:HOH:O	2.07	0.52
3:Q:160:TRP:CE2	4:R:59:LEU:HD23	2.45	0.52
10:X:161:GLU:OE2	10:X:161:GLU:HA	2.09	0.52
1:A:21(G):LEU:HD13	1:A:218:GLY:HA2	1.92	0.52
8:H:207:PRO:HG2	8:H:210:THR:OG1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:3:ILE:HG22	10:J:100:LEU:HD12	1.92	0.52
12:L:39:ASP:OD2	12:L:67:HIS:HE1	1.92	0.52
2:P:141:TYR:CD1	2:P:21(E):VAL:HG21	2.44	0.52
7:U:170:GLN:HE21	7:U:174:THR:HG23	1.74	0.52
7:U:171:GLU:N	7:U:171:GLU:OE1	2.37	0.52
10:X:76:PRO:HD2	16:X:206:HOH:O	2.10	0.52
14:2:14:LEU:O	14:2:175:MET:HA	2.10	0.52
3:C:75:VAL:HG13	3:C:221:ILE:HD13	1.91	0.52
12:Z:-7:ASN:HD22	12:Z:-6:PRO:CD	2.22	0.52
14:2:147:SER:OG	14:2:150:GLU:HG3	2.10	0.52
5:S:111:ARG:HG2	5:S:111:ARG:NH1	2.25	0.52
9:I:137:MET:HE3	9:I:141:LEU:HD11	1.92	0.52
11:K:142:TYR:C	11:K:143:LYS:HD2	2.35	0.52
3:Q:229:ILE:O	3:Q:233:VAL:HG23	2.10	0.52
5:S:86:ARG:HG3	5:S:86:ARG:HH11	1.75	0.52
9:W:61:TYR:CD1	9:W:61:TYR:C	2.88	0.52
11:Y:6:PHE:HA	11:Y:123:ASP:O	2.10	0.52
5:E:107:LEU:HD11	5:E:111:ARG:HG2	1.90	0.52
12:Z:39:ASP:OD2	12:Z:67:HIS:HE1	1.92	0.52
2:B:55:THR:HG22	2:B:59:LEU:HD23	1.91	0.52
2:B:147:GLN:HG2	3:C:62(A):ILE:HG21	1.92	0.52
2:B:149:TYR:OH	3:C:62(A):ILE:HB	2.10	0.52
3:C:40:VAL:HG12	3:C:162:ALA:HB1	1.92	0.52
9:I:114:ASP:HB2	16:I:236:HOH:O	2.10	0.52
2:P:228:GLU:O	2:P:232:ILE:HG22	2.10	0.52
3:Q:75:VAL:HG13	3:Q:221:ILE:HD13	1.92	0.52
3:Q:185:THR:CB	3:Q:188:GLU:HG2	2.32	0.52
9:W:89:GLU:O	9:W:90:ARG:NH1	2.42	0.52
7:G:34(A):ASN:HD22	7:G:167:PRO:HG2	1.76	0.51
9:I:97:VAL:HG23	9:I:99:PRO:HD3	1.91	0.51
10:J:161:GLU:HA	10:J:161:GLU:OE2	2.10	0.51
12:L:-5:TYR:CE2	12:L:96:TYR:HB2	2.45	0.51
13:M:179:ASP:HB3	13:M:18(A):THR:OG1	2.10	0.51
2:P:202:THR:HG22	2:P:204:SER:N	2.10	0.51
10:X:123:PRO:HB2	10:X:124:TYR:CD1	2.44	0.51
13:1:104:VAL:CG2	13:1:178:ILE:HG22	2.38	0.51
7:G:105:TYR:OH	8:H:66:HIS:HE1	1.93	0.51
10:X:18:LYS:CG	10:X:174:ILE:HG13	2.39	0.51
10:X:143:ARG:O	10:X:146:MET:HG3	2.10	0.51
7:G:8:TYR:C	7:G:10:ARG:H	2.16	0.51
8:H:84:LYS:HG3	8:H:85:GLN:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:-6:PRO:O	13:M:91:ARG:NH1	2.37	0.51
5:S:141:TYR:CE2	5:S:217:LYS:HA	2.45	0.51
11:Y:12:ILE:HG23	11:Y:110:ILE:HD11	1.92	0.51
13:1:14(A):VAL:HG23	13:1:14(A):VAL:O	2.11	0.51
2:B:219:GLU:HG2	2:B:21(E):VAL:N	2.26	0.51
13:M:211:ILE:HD11	14:2:36:ARG:CD	2.40	0.51
1:O:67:VAL:HG11	1:O:213:ALA:CB	2.41	0.51
3:Q:227:GLU:OE1	3:Q:227:GLU:N	2.31	0.51
6:T:103:TYR:O	6:T:104:LYS:HB3	2.09	0.51
7:U:72:ARG:HB2	7:U:72:ARG:NH1	2.26	0.51
11:Y:35:ILE:CD1	11:Y:53:GLN:HA	2.40	0.51
11:Y:35:ILE:HD13	11:Y:53:GLN:HA	1.92	0.51
2:P:21(C):ASP:OD2	2:P:219:GLU:HB3	2.11	0.51
6:T:127:ASN:HD22	6:T:127:ASN:C	2.19	0.51
13:1:91:ARG:HG3	13:1:92:SER:N	2.25	0.51
4:D:121:LEU:HA	4:D:123:PHE:CE1	2.45	0.51
5:E:67:ILE:HG21	5:E:213:ALA:HB2	1.92	0.51
7:G:38:LEU:C	7:G:38:LEU:HD12	2.35	0.51
14:N:65:LEU:HG	14:N:69:GLN:NE2	2.26	0.51
2:P:219:GLU:HG2	2:P:21(E):VAL:N	2.26	0.51
11:K:6:PHE:HA	11:K:123:ASP:O	2.10	0.51
13:M:165:ARG:NH2	8:V:135:MET:HE3	2.26	0.51
10:X:93:ARG:NH2	11:Y:91:LYS:HD3	2.26	0.51
12:Z:17:ASP:HA	12:Z:172:GLY:O	2.11	0.51
2:B:160:TRP:HA	3:C:59:GLN:HA	1.93	0.51
5:E:148:LEU:CD2	5:E:162:GLY:HA2	2.41	0.51
3:Q:55:THR:C	3:Q:56:LEU:HD22	2.35	0.51
3:Q:158:SER:HB2	4:R:59:LEU:HD21	1.93	0.51
9:W:55:LEU:CD1	9:W:97:VAL:HG21	2.41	0.51
6:F:20(B):GLU:HG3	6:F:20(C):LYS:N	2.26	0.51
2:P:55:THR:HG22	2:P:59:LEU:HD23	1.93	0.51
5:S:227:GLU:CD	5:S:227:GLU:N	2.69	0.51
2:B:186:VAL:HG21	2:B:216:ARG:HD3	1.94	0.50
9:I:106:GLY:HA2	9:I:181:LYS:HD3	1.93	0.50
6:T:172:ALA:O	6:T:176:LEU:HD23	2.11	0.50
8:V:105:ASP:HB2	8:V:10(A):PRO:CD	2.40	0.50
9:W:55:LEU:HD11	9:W:97:VAL:HG21	1.93	0.50
7:G:224:LEU:HB3	7:G:228:ASN:HB2	1.92	0.50
3:Q:46:VAL:HB	3:Q:215:VAL:CG1	2.41	0.50
4:R:24:VAL:O	4:R:27:SER:HB3	2.11	0.50
12:Z:99:THR:HG22	16:Z:201:HOH:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2:10(B):LYS:HD3	14:2:10(B):LYS:C	2.36	0.50
7:G:152:ASP:HB2	7:G:153:PRO:CD	2.40	0.50
12:L:-7:ASN:HD22	12:L:-6:PRO:CD	2.24	0.50
12:L:-2:ASN:HA	12:L:21:ILE:O	2.11	0.50
12:L:17:ASP:HA	12:L:172:GLY:O	2.11	0.50
14:N:10(B):LYS:HD3	14:N:10(B):LYS:C	2.37	0.50
14:N:171:GLY:HA2	13:1:197:TRP:CH2	2.46	0.50
4:R:12(D):ALA:HB3	4:R:126:ARG:CD	2.41	0.50
12:Z:166:HIS:CD2	12:Z:168:GLN:H	2.29	0.50
5:S:4:PHE:CG	5:S:5:ARG:N	2.79	0.50
7:U:9:ASP:OD2	7:U:16:SER:HA	2.12	0.50
11:Y:46:ALA:HB3	11:Y:98:GLY:O	2.12	0.50
11:Y:142:TYR:C	11:Y:143:LYS:HD2	2.36	0.50
13:1:113:VAL:HA	13:1:118:VAL:O	2.12	0.50
1:A:212:LEU:HD22	1:A:224:LEU:HD12	1.94	0.50
9:W:137:MET:HE3	9:W:141:LEU:HD11	1.94	0.50
14:2:175:MET:HB2	14:2:187:LEU:HB2	1.92	0.50
1:A:177:GLU:HG2	2:B:58:LEU:CD2	2.41	0.50
5:E:190:ILE:CG2	5:E:212:ILE:HD13	2.42	0.50
7:G:93:LYS:HD3	14:N:68:SER:HB3	1.94	0.50
13:M:112:TYR:C	13:M:112:TYR:CD2	2.89	0.50
14:N:104:TYR:OH	14:N:180:ALA:HB2	2.12	0.50
9:W:2:ILE:HG21	9:W:130:ALA:HB3	1.92	0.50
9:W:101:VAL:O	9:W:110:ILE:HA	2.12	0.50
12:Z:14(E):GLU:OE2	12:Z:14(P):PRO:HD2	2.11	0.50
2:B:21(C):ASP:OD2	2:B:219:GLU:HB3	2.10	0.50
3:C:224:LEU:N	3:C:224:LEU:CD1	2.74	0.50
6:F:192:GLN:O	6:F:196:ILE:HG13	2.12	0.50
9:I:55:LEU:HD11	9:I:97:VAL:HG21	1.93	0.50
5:S:47:VAL:HG23	5:S:189:LEU:HD13	1.93	0.50
5:S:161:TYR:CD1	5:S:18(D):ILE:HD13	2.47	0.50
11:Y:86:LEU:C	11:Y:86:LEU:HD13	2.37	0.50
12:Z:90:LYS:HE2	16:Z:196:HOH:O	2.12	0.50
2:B:103:TYR:O	2:B:104:ASN:HB2	2.11	0.50
5:E:136:LEU:HB2	5:E:151:PHE:HB3	1.94	0.50
10:J:10(B):LYS:HB2	10:J:10(B):LYS:HZ3	1.75	0.50
4:R:112:LEU:HD13	4:R:112:LEU:C	2.37	0.50
5:S:220:PRO:O	5:S:222:THR:HG23	2.12	0.50
11:Y:25:TRP:CH2	12:Z:132:SER:HA	2.47	0.50
14:2:104:TYR:OH	14:2:180:ALA:HB2	2.12	0.50
1:A:170:VAL:HB	16:A:250:HOH:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:228:GLU:O	2:B:232:ILE:HG22	2.11	0.50
4:D:170:GLU:OE1	4:D:170:GLU:N	2.44	0.50
5:E:227:GLU:CD	5:E:227:GLU:N	2.70	0.50
11:K:4:LEU:HD13	11:K:159:ILE:HD11	1.92	0.50
12:L:1(I):ASN:O	12:L:14(K):LYS:HG2	2.11	0.50
13:M:14(C):ARG:HH11	13:M:14(C):ARG:CG	2.22	0.50
9:W:48:LEU:HG	9:W:50:THR:HG22	1.94	0.50
10:X:4:LEU:HD23	10:X:126:ALA:HB2	1.93	0.50
12:Z:90:LYS:HD3	12:Z:95:TYR:CE1	2.46	0.50
1:A:179:ARG:HB3	1:A:179:ARG:NH1	2.22	0.49
5:E:4:PHE:CG	5:E:5:ARG:N	2.78	0.49
5:E:66:LYS:O	5:E:77:SER:HA	2.12	0.49
8:H:112:SER:HB3	8:H:125:LEU:HD13	1.94	0.49
10:J:133:TYR:HE1	16:X:220:HOH:O	1.94	0.49
12:L:90:LYS:HD3	12:L:95:TYR:CZ	2.47	0.49
2:P:41:MET:HE3	16:Q:246:HOH:O	2.09	0.49
12:Z:-2:ASN:HA	12:Z:21:ILE:O	2.12	0.49
13:1:179:ASP:HB3	13:1:18(A):THR:OG1	2.12	0.49
2:B:191:GLU:O	2:B:195:LYS:HG2	2.12	0.49
13:M:14(A):VAL:HG23	13:M:14(A):VAL:O	2.12	0.49
3:Q:40:VAL:HG12	3:Q:162:ALA:HB1	1.94	0.49
5:S:67:ILE:HG21	5:S:213:ALA:HB2	1.93	0.49
6:T:35:THR:CG2	6:T:36:THR:N	2.75	0.49
8:H:20:SER:HB3	8:H:28:ASP:HB3	1.95	0.49
6:T:28:VAL:O	6:T:32:GLU:HG3	2.12	0.49
3:C:97:GLN:HA	3:C:97:GLN:NE2	2.26	0.49
4:D:59:LEU:HD13	4:D:59:LEU:C	2.37	0.49
4:D:70:ILE:HB	4:D:74:ILE:HG22	1.94	0.49
8:V:59:ILE:HG12	8:V:83:LEU:HG	1.93	0.49
11:Y:200:LYS:NZ	11:Y:209:VAL:O	2.39	0.49
14:N:48:SER:HB3	14:N:51:ASP:HB2	1.95	0.49
5:S:15:PHE:HB2	6:T:23:GLN:HE22	1.77	0.49
10:X:3:ILE:HG22	10:X:100:LEU:HD12	1.95	0.49
12:Z:-8:PHE:CB	13:1:-8:THR:HG23	2.41	0.49
6:F:179:LEU:CD2	6:F:192:GLN:HG2	2.42	0.49
6:T:192:GLN:O	6:T:196:ILE:HG13	2.12	0.49
4:D:12(D):ALA:HB3	4:D:126:ARG:CD	2.42	0.49
7:G:136:LEU:O	7:G:150:LYS:HA	2.12	0.49
8:H:63:ILE:HG23	8:H:74:PRO:HB3	1.95	0.49
10:J:77:GLN:NE2	10:J:77:GLN:C	2.71	0.49
1:O:175:PHE:O	1:O:179:ARG:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:90(B):ARG:NH1	16:X:205:HOH:O	2.43	0.49
14:2:161:GLN:NE2	14:2:165:TRP:HE1	2.11	0.49
5:E:141:TYR:CE2	5:E:217:LYS:HA	2.48	0.49
10:J:133:TYR:HD1	16:Y:322:HOH:O	1.96	0.49
13:M:152:GLU:O	13:M:156:VAL:HG23	2.12	0.49
14:N:36:ARG:CD	13:1:211:ILE:HD11	2.43	0.49
14:N:175:MET:HB2	14:N:187:LEU:HB2	1.94	0.49
6:T:237:GLN:O	6:T:240:ILE:HG22	2.12	0.49
8:V:20:SER:HB3	8:V:28:ASP:HB3	1.95	0.49
10:X:190:PHE:HA	10:X:193:GLN:HB2	1.95	0.49
11:Y:199:VAL:O	11:Y:203:GLU:HB3	2.13	0.49
1:A:67:VAL:HG11	1:A:213:ALA:CB	2.43	0.49
2:B:27:ALA:O	2:B:31:ILE:HG13	2.13	0.49
3:C:55:THR:C	3:C:56:LEU:HD22	2.38	0.49
3:C:172:VAL:O	3:C:176:LEU:HG	2.13	0.49
6:F:103:TYR:O	6:F:104:LYS:HB3	2.13	0.49
6:F:126:TYR:HE1	7:G:129:MET:SD	2.36	0.49
6:F:184:LEU:CD1	6:F:188:GLU:HB3	2.42	0.49
8:H:197:ARG:NH2	9:I:139:GLU:HG3	2.28	0.49
10:J:190:PHE:HA	10:J:193:GLN:HB2	1.94	0.49
11:K:207:ASN:HD21	10:X:144:PRO:CG	2.25	0.49
13:M:19:LEU:HD12	13:M:28:PHE:O	2.13	0.49
13:M:40:ASN:N	13:M:40:ASN:ND2	2.60	0.49
14:N:106:ASN:O	14:N:107:LYS:HB3	2.13	0.49
8:V:63:ILE:HG23	8:V:74:PRO:HB3	1.94	0.49
4:D:205:GLU:OE2	4:D:205:GLU:HA	2.13	0.49
13:M:17:ASP:HA	13:M:173:PHE:CB	2.42	0.49
4:R:45:GLY:HA2	4:R:146:TYR:CE1	2.48	0.49
4:R:170:GLU:N	4:R:170:GLU:OE1	2.46	0.49
2:B:181:LYS:HG3	2:B:184:MET:HG3	1.94	0.48
4:D:45:GLY:HA2	4:D:146:TYR:CE1	2.47	0.48
12:L:-9:GLN:HE21	13:M:-8:THR:HG21	1.78	0.48
12:L:14(E):GLU:OE2	12:L:14(P):PRO:HD2	2.13	0.48
13:M:35:ILE:HD12	13:M:35:ILE:N	2.28	0.48
14:N:14:LEU:O	14:N:175:MET:HA	2.12	0.48
6:T:20(B):GLU:HG3	6:T:20(C):LYS:N	2.28	0.48
7:U:224:LEU:HB3	7:U:228:ASN:HB2	1.93	0.48
4:D:24:VAL:O	4:D:27:SER:HB3	2.12	0.48
9:I:93:GLY:H	9:I:94:PRO:HD3	1.78	0.48
9:I:93:GLY:N	9:I:94:PRO:CD	2.76	0.48
9:I:101:VAL:O	9:I:110:ILE:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:84:LYS:HG3	14:N:119:VAL:CG2	2.41	0.48
2:P:186:VAL:HG21	2:P:216:ARG:HD3	1.95	0.48
11:K:35:ILE:CD1	11:K:53:GLN:HA	2.43	0.48
2:P:186:VAL:HG21	2:P:216:ARG:HG2	1.95	0.48
10:X:190:PHE:C	10:X:192:ALA:H	2.22	0.48
11:K:35:ILE:HD13	11:K:53:GLN:HA	1.95	0.48
13:M:46:SER:OG	13:M:98:ALA:HB3	2.14	0.48
1:O:159:PRO:HB2	2:P:60:GLU:HB3	1.95	0.48
7:U:72:ARG:HG2	16:U:267:HOH:O	2.13	0.48
7:U:152:ASP:HB2	7:U:153:PRO:HD2	1.95	0.48
8:V:112:SER:HB3	8:V:125:LEU:HD13	1.95	0.48
11:Y:4:LEU:HD13	11:Y:159:ILE:HD11	1.96	0.48
12:Z:1(I):ASN:O	12:Z:14(K):LYS:HG2	2.14	0.48
1:A:4:MET:HG2	6:F:126:TYR:CE2	2.49	0.48
1:A:29:THR:O	1:A:33:GLN:HG2	2.13	0.48
2:B:21(A):LYS:O	2:B:217:ALA:N	2.46	0.48
3:C:159:SER:O	4:D:59:LEU:HD22	2.14	0.48
7:G:9:ASP:OD2	7:G:16:SER:HA	2.13	0.48
9:I:48:LEU:HG	9:I:50:THR:HG22	1.95	0.48
10:J:190:PHE:C	10:J:192:ALA:H	2.21	0.48
3:Q:149:TYR:CE1	3:Q:159:SER:HB3	2.48	0.48
13:1:35:ILE:N	13:1:35:ILE:HD12	2.27	0.48
13:1:112:TYR:C	13:1:112:TYR:CD2	2.90	0.48
13:1:205:GLY:HA3	13:1:209:GLN:HB3	1.95	0.48
3:C:100:ARG:HH12	3:C:106:PRO:HB3	1.74	0.48
7:G:192:PHE:CD1	7:G:192:PHE:C	2.92	0.48
12:L:135:MET:CE	9:W:165:ARG:NH2	2.76	0.48
13:M:197:TRP:CH2	14:2:171:GLY:HA2	2.48	0.48
1:O:212:LEU:HD22	1:O:224:LEU:HD12	1.95	0.48
3:Q:97:GLN:HA	3:Q:97:GLN:NE2	2.28	0.48
4:R:227:GLU:OE2	4:R:227:GLU:N	2.35	0.48
7:U:158:VAL:HG22	7:U:159:GLY:N	2.29	0.48
11:Y:10(B):LYS:HD2	11:Y:10(B):LYS:N	2.13	0.48
13:1:19:LEU:HD12	13:1:28:PHE:O	2.13	0.48
6:F:176:LEU:HD22	6:F:196:ILE:HD13	1.95	0.48
7:G:72:ARG:HB2	7:G:72:ARG:NH1	2.28	0.48
11:K:86:LEU:C	11:K:86:LEU:HD13	2.39	0.48
2:P:52:ARG:HH22	2:P:63(A):SER:HB3	1.79	0.48
4:R:59:LEU:C	4:R:59:LEU:HD13	2.39	0.48
6:T:184:LEU:CD1	6:T:188:GLU:HB3	2.41	0.48
8:V:72:ARG:HG3	8:V:72:ARG:HH11	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:113:ILE:HA	10:X:118:THR:O	2.13	0.48
9:I:22:SER:O	9:I:23:GLN:HB2	2.14	0.48
11:K:12:ILE:HG23	11:K:110:ILE:HD11	1.95	0.48
11:K:199:VAL:O	11:K:203:GLU:HB3	2.14	0.48
2:P:21(A):LYS:O	2:P:217:ALA:N	2.47	0.48
4:R:205:GLU:HA	4:R:205:GLU:OE2	2.13	0.48
11:Y:13:ILE:HD12	11:Y:152:LEU:HD23	1.96	0.48
14:2:13:ILE:HG12	14:2:177:VAL:HG13	1.95	0.48
1:A:62:GLU:CD	1:A:62:GLU:H	2.21	0.48
3:C:150:GLN:HG2	3:C:151:THR:N	2.28	0.48
6:F:127:ASN:HD22	6:F:127:ASN:C	2.19	0.48
7:G:77:VAL:HG12	7:G:137:THR:HB	1.95	0.48
9:I:89:GLU:O	9:I:90:ARG:NH1	2.47	0.48
14:N:161:GLN:NE2	14:N:165:TRP:HE1	2.12	0.48
6:T:203:GLU:C	6:T:205:ASN:H	2.22	0.48
7:U:34(A):ASN:HD22	7:U:167:PRO:HG2	1.78	0.48
9:W:106:GLY:HA2	9:W:181:LYS:HD3	1.95	0.48
13:1:1:THR:OG1	13:1:2:SER:N	2.44	0.48
2:B:20:ARG:NH1	2:B:20:ARG:HG2	2.29	0.48
2:B:185:LYS:HD3	2:B:187:ASP:H	1.79	0.48
5:E:86:ARG:HG3	5:E:86:ARG:HH11	1.78	0.48
9:I:29:ASN:HD21	9:I:30:LYS:HZ3	1.61	0.48
13:M:186:PHE:HE1	13:M:188:LYS:HG3	1.79	0.48
14:N:113:ILE:HG12	14:N:119:VAL:HG13	1.94	0.48
1:O:169:SER:O	1:O:173:LYS:HG3	2.14	0.48
3:Q:206:GLY:HA3	3:Q:209:ASN:HB2	1.96	0.48
6:T:176:LEU:HD22	6:T:196:ILE:HD13	1.96	0.48
7:U:192:PHE:CD1	7:U:192:PHE:C	2.91	0.48
8:V:197:ARG:NH2	9:W:139:GLU:HG3	2.29	0.48
9:W:22:SER:O	9:W:23:GLN:HB2	2.14	0.48
3:C:242:GLU:O	3:C:243:GLN:HB2	2.14	0.47
5:E:161:TYR:CD1	5:E:18(D):ILE:HD13	2.49	0.47
1:O:62:GLU:H	1:O:62:GLU:CD	2.22	0.47
4:R:70:ILE:HB	4:R:74:ILE:HG22	1.96	0.47
7:U:136:LEU:O	7:U:150:LYS:HA	2.13	0.47
13:1:14(C):ARG:HH11	13:1:14(C):ARG:CG	2.21	0.47
14:2:84:LYS:HG3	14:2:119:VAL:CG2	2.44	0.47
1:A:13:THR:O	2:B:130:ARG:HD3	2.14	0.47
3:C:241:GLN:C	3:C:243:GLN:H	2.23	0.47
9:I:6:MET:CE	9:I:155:ILE:HA	2.43	0.47
12:L:166:HIS:CD2	12:L:168:GLN:H	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:13:ILE:HG12	14:N:177:VAL:HG13	1.96	0.47
1:O:15:PHE:H	2:P:23:GLN:NE2	1.92	0.47
2:P:20:ARG:NH1	2:P:20:ARG:HG2	2.29	0.47
3:Q:106:PRO:HG2	3:Q:143:PRO:HG2	1.97	0.47
3:Q:241:GLN:C	3:Q:243:GLN:H	2.22	0.47
7:U:38:LEU:C	7:U:38:LEU:HD12	2.39	0.47
9:W:6:MET:CE	9:W:155:ILE:HA	2.44	0.47
14:2:3:ILE:HG22	14:2:16:ALA:HB2	1.96	0.47
1:A:110:LYS:HG2	16:A:245:HOH:O	2.13	0.47
2:B:122:GLY:C	2:B:124:THR:N	2.73	0.47
3:C:46:VAL:HB	3:C:215:VAL:CG1	2.43	0.47
3:C:57:LYS:C	3:C:57:LYS:HD2	2.39	0.47
4:D:122:ARG:HG2	4:D:122:ARG:NH1	2.27	0.47
6:F:20(B):GLU:HG3	6:F:20(C):LYS:H	1.78	0.47
9:I:18:LEU:CD2	9:I:32:GLU:HG2	2.44	0.47
2:P:122:GLY:C	2:P:124:THR:N	2.71	0.47
5:S:190:ILE:CG2	5:S:212:ILE:HD13	2.44	0.47
9:W:80:THR:HG22	9:W:119:ILE:HD13	1.96	0.47
11:Y:66:HIS:HA	16:Y:333:HOH:O	2.14	0.47
12:Z:145:TYR:CD1	12:Z:146:LEU:N	2.82	0.47
13:1:83:LEU:O	13:1:87:MET:HG2	2.14	0.47
14:2:113:ILE:HG12	14:2:119:VAL:HG13	1.95	0.47
9:I:61:TYR:CD1	9:I:61:TYR:C	2.92	0.47
12:L:134:ILE:HG22	12:L:138:LEU:HD22	1.96	0.47
1:O:24:ILE:HD11	1:O:124:THR:HG23	1.95	0.47
2:P:224:PHE:N	2:P:224:PHE:CD2	2.83	0.47
3:Q:224:LEU:N	3:Q:224:LEU:CD1	2.76	0.47
5:S:7:ASN:O	6:T:10:LEU:HD22	2.14	0.47
6:T:136:THR:O	6:T:150:MET:HA	2.14	0.47
1:A:85:TYR:O	1:A:89:VAL:HG23	2.14	0.47
1:A:169:SER:O	1:A:173:LYS:HG3	2.14	0.47
4:D:161:ASN:HB3	4:D:180:TRP:CE2	2.50	0.47
9:I:130:ALA:HB2	9:I:166:ASP:HB2	1.97	0.47
10:J:144:PRO:CG	11:Y:207:ASN:HD21	2.26	0.47
11:K:10(B):LYS:HD2	11:K:10(B):LYS:N	2.14	0.47
12:L:14(Q):LEU:O	12:L:14(W):LYS:C	2.58	0.47
2:P:44:ASP:OD2	2:P:186:VAL:HG23	2.14	0.47
2:P:229:ILE:O	2:P:233:LEU:HB2	2.15	0.47
5:S:66:LYS:O	5:S:77:SER:HA	2.13	0.47
16:T:244:HOH:O	7:U:86:ARG:HD2	2.14	0.47
12:Z:-9:GLN:NE2	12:Z:-8:PHE:N	2.59	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1:186:PHE:CE1	13:1:188:LYS:HG3	2.49	0.47
1:A:5:THR:O	1:A:7:ARG:HG2	2.14	0.47
1:A:24:ILE:HD11	1:A:124:THR:HG23	1.96	0.47
6:F:11:SER:HB3	6:F:14:VAL:HG23	1.96	0.47
12:L:145:TYR:CD1	12:L:146:LEU:N	2.82	0.47
1:O:232:ARG:HG3	1:O:232:ARG:NH1	2.29	0.47
5:S:160:LEU:HD13	5:S:163:THR:HB	1.97	0.47
5:S:18(C):PHE:HA	5:S:18(F):ILE:CD1	2.44	0.47
10:X:52:THR:CG2	10:X:53:VAL:N	2.78	0.47
1:A:232:ARG:HG3	1:A:232:ARG:NH1	2.30	0.47
2:B:235:LYS:C	2:B:237:GLY:H	2.23	0.47
5:E:111:ARG:HG2	5:E:111:ARG:NH1	2.25	0.47
7:G:158:VAL:HG22	7:G:159:GLY:N	2.30	0.47
8:H:3:ILE:CD1	8:H:127:LEU:HB2	2.43	0.47
10:J:140:HIS:HA	11:Y:205:SER:HB2	1.95	0.47
11:K:77:ALA:HA	11:K:111:TYR:CE2	2.49	0.47
13:M:186:PHE:CE1	13:M:188:LYS:HG3	2.49	0.47
14:N:105:ASP:OD2	14:N:106:ASN:N	2.38	0.47
14:N:120:HIS:HA	16:N:234:HOH:O	2.14	0.47
1:O:27:ALA:O	1:O:31:VAL:HG23	2.13	0.47
1:O:21(G):LEU:HD13	1:O:218:GLY:HA2	1.97	0.47
2:P:191:GLU:O	2:P:195:LYS:HG2	2.12	0.47
4:R:122:ARG:HG2	4:R:122:ARG:NH1	2.29	0.47
5:S:123:ASN:N	5:S:123:ASN:ND2	2.63	0.47
8:V:175:VAL:HG12	8:V:176:CYS:N	2.29	0.47
9:W:20:LEU:HD13	9:W:20:LEU:C	2.39	0.47
9:W:66:TYR:CZ	9:W:70:GLU:HG3	2.50	0.47
9:W:93:GLY:H	9:W:94:PRO:HD3	1.78	0.47
12:Z:-9:GLN:HE21	13:1:-8:THR:HG21	1.80	0.47
12:Z:90:LYS:HD3	12:Z:95:TYR:CZ	2.50	0.47
12:Z:134:ILE:HG22	12:Z:138:LEU:HD22	1.97	0.47
13:1:186:PHE:HE1	13:1:188:LYS:HG3	1.79	0.47
14:2:3:ILE:HG22	14:2:16:ALA:CB	2.44	0.47
8:H:5:GLY:O	8:H:124:TYR:HA	2.15	0.47
13:M:205:GLY:HA3	13:M:209:GLN:HB3	1.95	0.47
14:N:9:LYS:HA	14:N:145:ASN:HD22	1.80	0.47
9:W:93:GLY:N	9:W:94:PRO:CD	2.77	0.47
10:X:18:LYS:HD3	10:X:174:ILE:HG13	1.97	0.47
11:Y:200:LYS:HE3	11:Y:206:PHE:O	2.14	0.47
13:1:104:VAL:HG23	13:1:178:ILE:CG2	2.43	0.47
3:C:163:GLN:HG3	3:C:164:THR:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:136:THR:O	6:F:150:MET:HA	2.15	0.47
7:G:18(H):GLU:CD	7:G:18(H):GLU:H	2.23	0.47
8:H:175:VAL:HG12	8:H:176:CYS:N	2.29	0.47
13:M:91:ARG:HG3	13:M:92:SER:N	2.29	0.47
3:Q:242:GLU:O	3:Q:243:GLN:HB2	2.13	0.47
14:2:9:LYS:HA	14:2:145:ASN:HD22	1.80	0.47
14:2:106:ASN:O	14:2:107:LYS:HB3	2.14	0.47
14:2:107:LYS:HG2	14:2:108:GLY:H	1.79	0.47
1:A:175:PHE:O	1:A:179:ARG:HG2	2.15	0.47
10:J:143:ARG:O	10:J:146:MET:HG3	2.15	0.47
14:N:85:GLU:O	14:N:89:GLU:HB2	2.15	0.47
6:T:11:SER:HB3	6:T:14:VAL:HG23	1.96	0.47
6:T:157:TYR:CD1	6:T:157:TYR:C	2.93	0.47
6:T:179:LEU:CD2	6:T:192:GLN:HG2	2.40	0.47
6:T:20(B):GLU:HG3	6:T:20(C):LYS:H	1.79	0.47
2:B:52:ARG:HH22	2:B:63(A):SER:HB3	1.80	0.46
8:H:38:SER:O	8:H:39:PRO:C	2.57	0.46
2:P:20:ARG:HG2	2:P:20:ARG:HH11	1.80	0.46
2:P:185:LYS:HD3	2:P:187:ASP:H	1.79	0.46
7:U:236:ILE:HD12	7:U:236:ILE:C	2.40	0.46
10:X:44:SER:HG	10:X:100:LEU:HB2	1.80	0.46
13:1:133:MET:C	13:1:136:PRO:HD2	2.40	0.46
1:A:92:SER:O	1:A:95:VAL:HG12	2.14	0.46
6:F:203:GLU:C	6:F:205:ASN:H	2.23	0.46
12:L:5:GLY:O	12:L:124:CYS:HA	2.15	0.46
14:N:107:LYS:HG2	14:N:108:GLY:H	1.80	0.46
1:O:29:THR:O	1:O:33:GLN:HG2	2.14	0.46
3:Q:182:PRO:O	3:Q:184:ALA:N	2.49	0.46
9:W:130:ALA:HB2	9:W:166:ASP:HB2	1.96	0.46
13:1:17:ASP:HA	13:1:173:PHE:CB	2.45	0.46
4:D:240:LYS:O	4:D:243:ALA:HB3	2.15	0.46
10:J:113:ILE:HA	10:J:118:THR:O	2.16	0.46
13:M:41:THR:OG1	13:M:76:PRO:HG3	2.16	0.46
2:P:235:LYS:C	2:P:237:GLY:H	2.23	0.46
1:A:4:MET:O	1:A:5:THR:O	2.33	0.46
1:A:112:LEU:O	1:A:116:VAL:HG23	2.16	0.46
2:B:81:LEU:HD23	2:B:133:GLY:HA3	1.98	0.46
6:F:20(B):GLU:OE1	6:F:20(C):LYS:HE3	2.15	0.46
9:I:80:THR:HG22	9:I:119:ILE:HD13	1.97	0.46
1:O:24:ILE:HD11	1:O:124:THR:CG2	2.46	0.46
2:P:224:PHE:N	2:P:224:PHE:HD2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Y:87:VAL:HG11	11:Y:115:SER:HA	1.96	0.46
12:Z:39:ASP:OD2	12:Z:67:HIS:CE1	2.68	0.46
13:1:8:TYR:CZ	13:1:148:VAL:HG13	2.51	0.46
2:B:224:PHE:N	2:B:224:PHE:CD2	2.83	0.46
4:D:91:HIS:CE1	4:D:119:LEU:HD21	2.51	0.46
5:E:18(C):PHE:HA	5:E:18(F):ILE:CD1	2.46	0.46
5:E:220:PRO:O	5:E:222:THR:HG23	2.14	0.46
10:J:39:PRO:HG2	10:J:73:GLU:CD	2.41	0.46
11:K:207:ASN:ND2	10:X:144:PRO:CG	2.79	0.46
13:M:17:ASP:HA	13:M:173:PHE:HA	1.98	0.46
13:M:35:ILE:CG1	13:M:56:GLU:HG3	2.41	0.46
14:N:156:LYS:HG2	14:N:18(J):LEU:HD11	1.98	0.46
10:X:77:GLN:NE2	10:X:77:GLN:C	2.73	0.46
11:Y:87:VAL:CG1	11:Y:115:SER:HA	2.45	0.46
8:H:196:VAL:HG23	16:H:244:HOH:O	2.14	0.46
13:M:83:LEU:O	13:M:87:MET:HG2	2.15	0.46
13:M:113:VAL:HA	13:M:118:VAL:O	2.15	0.46
13:M:133:MET:C	13:M:136:PRO:HD2	2.41	0.46
3:C:8:TYR:HB3	16:C:269:HOH:O	2.15	0.46
3:C:103:LEU:HD13	16:C:270:HOH:O	2.15	0.46
9:I:45:ILE:HB	9:I:52:VAL:HG13	1.98	0.46
2:B:224:PHE:N	2:B:224:PHE:HD2	2.14	0.46
4:D:140:GLY:HA2	4:D:215:ILE:HG12	1.97	0.46
6:F:121:GLN:NE2	16:F:257:HOH:O	2.49	0.46
6:F:20(B):GLU:HG3	6:F:20(C):LYS:HG3	1.98	0.46
3:Q:163:GLN:HG3	3:Q:164:THR:N	2.31	0.46
3:Q:228:GLU:O	3:Q:232:TYR:HD1	1.98	0.46
13:1:198:ASP:OD1	13:1:201:LYS:NZ	2.49	0.46
14:2:85:GLU:O	14:2:89:GLU:HB2	2.16	0.46
10:J:193:GLN:OXT	10:J:193:GLN:HG2	2.16	0.46
1:O:5:THR:O	1:O:7:ARG:HG2	2.15	0.46
6:T:38:ILE:HG22	6:T:164:ALA:CB	2.46	0.46
8:V:5:GLY:O	8:V:124:TYR:HA	2.16	0.46
13:1:133:MET:HE1	13:1:165:ARG:HG3	1.98	0.46
14:2:176:VAL:HG12	14:2:178:LEU:HD13	1.98	0.46
4:D:42:THR:C	4:D:44:GLU:H	2.24	0.46
5:E:5:ARG:HG3	5:E:22:PHE:CZ	2.51	0.46
6:F:172:ALA:O	6:F:176:LEU:HD23	2.16	0.46
8:H:48:THR:HB	8:H:51:ASP:HB2	1.98	0.46
11:K:10(A):ARG:HH11	11:K:10(A):ARG:HG2	1.81	0.46
14:N:3:ILE:HG22	14:N:16:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1:40:ASN:N	13:1:40:ASN:ND2	2.60	0.46
3:C:169:SER:HA	3:C:172:VAL:CG1	2.47	0.45
6:F:18(E):GLU:CD	6:F:18(E):GLU:H	2.24	0.45
6:F:194:ALA:O	6:F:198:TYR:HD1	1.98	0.45
2:P:27:ALA:O	2:P:31:ILE:HG13	2.17	0.45
2:P:81:LEU:HD23	2:P:133:GLY:HA3	1.98	0.45
2:P:97:GLN:NE2	16:P:244:HOH:O	2.46	0.45
10:X:90(A):ILE:HD12	10:X:90(A):ILE:HA	1.75	0.45
13:1:152:GLU:O	13:1:156:VAL:HG23	2.16	0.45
2:B:229:ILE:O	2:B:233:LEU:HB2	2.15	0.45
4:D:86:ARG:HA	4:D:86:ARG:HD3	1.84	0.45
6:F:38:ILE:HG22	6:F:164:ALA:HB2	1.98	0.45
6:F:43:ASN:N	6:F:43:ASN:HD22	2.14	0.45
6:F:210:LEU:HD21	6:F:212:ILE:HD11	1.98	0.45
8:H:72:ARG:HG3	8:H:72:ARG:HH11	1.80	0.45
10:J:93:ARG:NH2	11:K:91:LYS:HD3	2.31	0.45
11:K:13:ILE:HD12	11:K:152:LEU:HD23	1.98	0.45
12:L:105:ASP:OD2	12:L:107:LYS:HB2	2.16	0.45
14:N:3:ILE:HG22	14:N:16:ALA:CB	2.45	0.45
6:T:184:LEU:HD21	6:T:189:ALA:HA	1.97	0.45
6:T:194:ALA:O	6:T:198:TYR:HD1	1.99	0.45
7:U:227:GLU:HG2	16:U:283:HOH:O	2.16	0.45
13:1:31:VAL:HA	16:1:267:HOH:O	2.15	0.45
11:K:4:LEU:C	11:K:4:LEU:CD2	2.89	0.45
11:K:131:GLN:HG3	11:K:132:THR:N	2.31	0.45
12:L:-9:GLN:NE2	12:L:-8:PHE:N	2.61	0.45
3:Q:46:VAL:HG22	3:Q:146:PRO:HB2	1.99	0.45
3:Q:57:LYS:C	3:Q:57:LYS:HD2	2.41	0.45
6:T:38:ILE:HG22	6:T:164:ALA:HB2	1.97	0.45
6:T:43:ASN:N	6:T:43:ASN:HD22	2.14	0.45
7:U:12:ILE:HG13	7:U:14:ILE:HG23	1.98	0.45
12:Z:109:ALA:HB2	12:Z:121:ARG:NH2	2.32	0.45
2:B:21:LEU:HD13	2:B:124:THR:HG23	1.98	0.45
3:C:182:PRO:O	3:C:184:ALA:N	2.49	0.45
5:E:15:PHE:HB2	6:F:23:GLN:HE22	1.81	0.45
13:M:149:GLN:H	13:M:149:GLN:HE21	1.57	0.45
1:O:4:MET:O	1:O:5:THR:O	2.34	0.45
1:O:161:LYS:HD3	1:O:180:TRP:CZ3	2.51	0.45
2:P:194:LEU:HD13	2:P:233:LEU:HD12	1.98	0.45
6:T:20(B):GLU:OE1	6:T:20(C):LYS:HE3	2.16	0.45
8:V:34:LEU:HD22	8:V:174:ASP:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Y:131:GLN:HG3	11:Y:132:THR:N	2.31	0.45
12:Z:4:LEU:CD1	12:Z:138:LEU:HD21	2.46	0.45
12:Z:93:PHE:N	12:Z:94:PRO:HD3	2.31	0.45
1:A:161:LYS:HD3	1:A:180:TRP:CZ3	2.50	0.45
2:B:20:ARG:HG2	2:B:20:ARG:HH11	1.80	0.45
6:F:216:SER:HB3	6:F:21(A):GLU:HB2	1.98	0.45
12:L:-7:ASN:ND2	12:L:-7:ASN:C	2.70	0.45
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.97	0.45
6:T:69:VAL:HG12	16:T:262:HOH:O	2.15	0.45
11:Y:77:ALA:HA	11:Y:111:TYR:CE2	2.52	0.45
1:A:15:PHE:N	2:B:23:GLN:HE22	2.04	0.45
2:B:63:THR:HG22	2:B:63:THR:O	2.17	0.45
2:B:186:VAL:HG21	2:B:216:ARG:HG2	1.97	0.45
5:E:5:ARG:HG3	5:E:22:PHE:CE2	2.51	0.45
11:K:76:VAL:N	11:K:106:GLU:OE2	2.46	0.45
3:Q:57:LYS:O	3:Q:58:LEU:HB2	2.17	0.45
7:U:18(H):GLU:H	7:U:18(H):GLU:CD	2.24	0.45
12:Z:-7:ASN:HD22	12:Z:-6:PRO:N	2.14	0.45
12:Z:43:MET:CB	12:Z:101:ILE:HG22	2.47	0.45
14:2:156:LYS:HG2	14:2:18(J):LEU:HD11	1.98	0.45
3:C:158:SER:HB2	4:D:59:LEU:HD21	1.99	0.45
3:C:235:GLN:O	3:C:239:GLU:HG2	2.16	0.45
5:E:97:ASN:HD22	5:E:97:ASN:HA	1.63	0.45
6:F:237:GLN:O	6:F:240:ILE:HG22	2.16	0.45
11:K:146:LEU:HD23	11:K:151:ALA:HA	1.99	0.45
12:L:165:ARG:NH2	8:V:29:LYS:HE2	2.31	0.45
2:P:4:GLY:HA3	5:S:127:TYR:CZ	2.52	0.45
2:P:150:THR:O	2:P:157:TYR:HA	2.16	0.45
2:P:181:LYS:HG3	2:P:184:MET:HG3	1.98	0.45
3:Q:235:GLN:O	3:Q:239:GLU:HG2	2.16	0.45
4:R:12(D):ALA:HA	5:S:129:GLY:HA2	1.98	0.45
4:R:161:ASN:HB3	4:R:180:TRP:CE2	2.51	0.45
6:T:126:TYR:HE1	7:U:129:MET:SD	2.39	0.45
7:U:130:ARG:HB2	16:U:263:HOH:O	2.17	0.45
11:Y:4:LEU:C	11:Y:4:LEU:CD2	2.90	0.45
12:Z:14(Q):LEU:O	12:Z:14(W):LYS:C	2.59	0.45
3:C:206:GLY:HA3	3:C:209:ASN:HB2	1.97	0.45
5:E:160:LEU:HD13	5:E:163:THR:HB	1.99	0.45
6:F:157:TYR:C	6:F:157:TYR:CD1	2.94	0.45
10:J:52:THR:HG22	10:J:53:VAL:HG23	1.99	0.45
11:K:97:MET:O	11:K:114:ASP:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:166:MET:HA	10:X:167:PRO:HD3	1.80	0.45
11:Y:10(A):ARG:HH11	11:Y:10(A):ARG:HG2	1.81	0.45
13:1:70:ASN:ND2	13:1:70(A):ALA:HA	2.32	0.45
7:G:152:ASP:HB2	7:G:153:PRO:HD2	1.97	0.45
8:H:89:LYS:HE3	8:H:90:TYR:CE2	2.52	0.45
11:K:65:LEU:HD12	11:K:65:LEU:HA	1.84	0.45
12:L:93:PHE:N	12:L:94:PRO:HD3	2.32	0.45
3:Q:168:ASN:CB	3:Q:200:VAL:HG11	2.47	0.45
5:S:48:LEU:HB2	5:S:213:ALA:HB3	1.98	0.45
7:U:39:ALA:HA	7:U:47:VAL:O	2.17	0.45
1:A:17:PRO:HA	2:B:26:TYR:CD1	2.52	0.45
2:B:87:ILE:O	2:B:91:THR:HG23	2.17	0.45
2:B:209:ARG:CZ	2:B:209:ARG:HB3	2.46	0.45
3:C:216:LYS:HD2	3:C:220:ASP:OD1	2.17	0.45
8:H:22:GLN:HG3	8:H:27:ALA:HB2	1.98	0.45
9:I:20:LEU:C	9:I:20:LEU:HD13	2.42	0.45
1:O:67:VAL:HG11	1:O:213:ALA:HB2	1.99	0.45
1:O:85:TYR:O	1:O:89:VAL:HG23	2.17	0.45
8:V:22:GLN:HG3	8:V:27:ALA:HB2	1.98	0.45
2:B:44:ASP:OD2	2:B:186:VAL:HG23	2.17	0.44
4:D:62:ASP:OD2	4:D:62:ASP:N	2.45	0.44
5:E:123:ASN:N	5:E:123:ASN:ND2	2.63	0.44
5:E:2(B):THR:N	5:E:2(E):ASN:ND2	2.50	0.44
9:I:66:TYR:CZ	9:I:70:GLU:HG3	2.52	0.44
1:O:184:LEU:HB2	16:O:247:HOH:O	2.17	0.44
3:Q:52:ARG:HB2	3:Q:209:ASN:HA	1.99	0.44
3:Q:159:SER:O	4:R:59:LEU:HD22	2.17	0.44
4:R:12(F):GLY:O	4:R:12(G):GLU:HB2	2.17	0.44
9:W:93:GLY:H	9:W:94:PRO:CD	2.29	0.44
9:W:178:ILE:HG23	9:W:184:VAL:HG22	1.99	0.44
10:X:140:HIS:CD2	10:X:141:HIS:NE2	2.85	0.44
1:A:24:ILE:HD11	1:A:124:THR:CG2	2.47	0.44
4:D:243:ALA:O	4:D:244:GLU:HB2	2.17	0.44
3:Q:76:LEU:C	3:Q:76:LEU:HD23	2.41	0.44
4:R:240:LYS:O	4:R:243:ALA:HB3	2.17	0.44
6:T:107:ILE:HA	6:T:108:PRO:HD3	1.86	0.44
8:V:3:ILE:CD1	8:V:127:LEU:HB2	2.44	0.44
12:Z:-9:GLN:HE21	12:Z:-8:PHE:H	1.62	0.44
3:C:33:ARG:NH1	3:C:33:ARG:CB	2.71	0.44
6:F:184:LEU:HD21	6:F:189:ALA:HA	1.99	0.44
9:I:93:GLY:H	9:I:94:PRO:CD	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:178:ILE:HG23	9:I:184:VAL:HG22	1.99	0.44
10:J:38:SER:HA	16:J:207:HOH:O	2.16	0.44
13:M:29:ASN:N	16:M:245:HOH:O	2.50	0.44
13:M:104:VAL:CG2	13:M:178:ILE:HG22	2.45	0.44
3:Q:33:ARG:NH1	3:Q:33:ARG:CB	2.68	0.44
6:T:127:ASN:C	6:T:127:ASN:ND2	2.75	0.44
7:U:188:LYS:HD3	7:U:188:LYS:HA	1.84	0.44
10:X:124:TYR:CD2	10:X:138:LEU:HD13	2.52	0.44
4:D:198:LYS:HB2	4:D:207:LEU:HD13	1.99	0.44
4:D:211:GLN:HA	16:D:258:HOH:O	2.17	0.44
7:G:18(M):SER:HB2	7:G:187:GLU:OE2	2.17	0.44
1:O:4:MET:SD	1:O:5:THR:N	2.84	0.44
1:O:92:SER:O	1:O:95:VAL:HG12	2.17	0.44
1:O:236:LEU:HD13	1:O:236:LEU:C	2.42	0.44
2:P:185:LYS:HD3	2:P:185:LYS:C	2.42	0.44
4:R:91:HIS:CE1	4:R:119:LEU:HD21	2.51	0.44
4:R:140:GLY:HA2	4:R:215:ILE:HG12	1.99	0.44
7:U:17(D):SER:O	7:U:17(E):LYS:HB2	2.17	0.44
9:W:18:LEU:CD2	9:W:32:GLU:HG2	2.47	0.44
9:W:36:HIS:HB3	9:W:42:PHE:CD2	2.52	0.44
10:X:193:GLN:OXT	10:X:193:GLN:HG2	2.17	0.44
1:A:27:ALA:O	1:A:31:VAL:HG23	2.16	0.44
2:B:185:LYS:HD3	2:B:185:LYS:C	2.42	0.44
3:C:57:LYS:O	3:C:58:LEU:HB2	2.16	0.44
3:C:185:THR:CB	3:C:188:GLU:HG2	2.34	0.44
5:E:2(C):VAL:HG22	5:E:226:GLY:C	2.43	0.44
11:K:207:ASN:HD21	10:X:144:PRO:HG2	1.83	0.44
12:L:39:ASP:OD2	12:L:67:HIS:CE1	2.69	0.44
14:N:107:LYS:HG2	14:N:108:GLY:N	2.33	0.44
2:P:74:ILE:C	2:P:221:GLN:HE22	2.26	0.44
3:Q:35:THR:OG1	3:Q:66:LYS:NZ	2.49	0.44
3:Q:173:ARG:O	3:Q:177:GLU:HG3	2.18	0.44
5:S:2(C):VAL:HG22	5:S:226:GLY:C	2.42	0.44
6:T:63:LYS:O	6:T:65:VAL:N	2.50	0.44
9:W:113:PHE:CD2	9:W:113:PHE:N	2.85	0.44
14:2:107:LYS:HG2	14:2:108:GLY:N	2.33	0.44
2:B:150:THR:O	2:B:157:TYR:HA	2.17	0.44
3:C:149:TYR:CE1	3:C:159:SER:HB3	2.53	0.44
4:D:12(F):GLY:O	4:D:12(G):GLU:HB2	2.16	0.44
6:F:11:SER:HB3	6:F:14:VAL:CG2	2.47	0.44
6:F:35:THR:CG2	6:F:36:THR:N	2.79	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:38:ILE:HG22	6:F:164:ALA:CB	2.47	0.44
9:I:80:THR:HG23	9:I:113:PHE:CZ	2.53	0.44
2:P:21:LEU:HD13	2:P:124:THR:HG23	2.00	0.44
2:P:87:ILE:O	2:P:91:THR:HG23	2.17	0.44
3:Q:169:SER:HA	3:Q:172:VAL:CG1	2.47	0.44
4:R:101:LEU:CD1	11:Y:57:THR:HG22	2.47	0.44
10:X:52:THR:HG22	10:X:53:VAL:HG23	1.99	0.44
11:Y:97:MET:O	11:Y:114:ASP:HA	2.17	0.44
1:A:8:TYR:HD2	7:G:128:TYR:HB3	1.83	0.44
11:K:87:VAL:CG1	11:K:115:SER:HA	2.48	0.44
13:M:70:ASN:ND2	13:M:70(A):ALA:HA	2.32	0.44
2:P:63:THR:HG22	2:P:63:THR:O	2.17	0.44
3:Q:33:ARG:O	3:Q:33:ARG:HG2	2.17	0.44
5:S:5:ARG:HG3	5:S:22:PHE:CZ	2.52	0.44
7:U:77:VAL:HG12	7:U:137:THR:HB	1.99	0.44
1:A:197:LEU:HD23	1:A:210:ILE:HD12	2.00	0.44
4:D:160:TYR:CZ	4:D:163:LYS:HD3	2.52	0.44
10:J:144:PRO:CG	11:Y:207:ASN:ND2	2.81	0.44
11:K:87:VAL:HG11	11:K:115:SER:HA	2.00	0.44
14:N:13:ILE:HD12	14:N:151:THR:CG2	2.47	0.44
1:O:17:PRO:HA	2:P:26:TYR:CE1	2.53	0.44
4:R:42:THR:C	4:R:44:GLU:H	2.25	0.44
6:T:11:SER:HB3	6:T:14:VAL:CG2	2.47	0.44
8:V:40:LYS:HE2	8:V:183:ASP:HA	2.00	0.44
14:2:105:ASP:OD2	14:2:106:ASN:N	2.37	0.44
1:A:38:LEU:HD12	1:A:38:LEU:C	2.43	0.44
1:A:236:LEU:HD13	1:A:236:LEU:C	2.43	0.44
2:B:145:GLY:O	2:B:147:GLN:HG3	2.18	0.44
3:C:52:ARG:HB2	3:C:209:ASN:HA	2.00	0.44
3:Q:100:ARG:HH12	3:Q:106:PRO:HB3	1.75	0.44
7:U:139:VAL:HA	7:U:147:SER:O	2.18	0.44
1:A:109:THR:O	1:A:113:VAL:HG23	2.18	0.43
2:B:126:HIS:HA	16:B:260:HOH:O	2.18	0.43
8:H:200:LYS:HE3	9:I:140:SER:O	2.18	0.43
11:K:4:LEU:C	11:K:4:LEU:HD22	2.42	0.43
13:M:171:ARG:HG3	13:M:192:VAL:HB	1.98	0.43
2:P:141:TYR:CD1	2:P:141:TYR:C	2.95	0.43
5:S:97:ASN:HD22	5:S:97:ASN:HA	1.61	0.43
8:V:3:ILE:CG1	8:V:127:LEU:HB2	2.47	0.43
9:W:174:VAL:HG21	9:W:186:LYS:CE	2.48	0.43
11:Y:4:LEU:C	11:Y:4:LEU:HD22	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:MET:SD	1:A:5:THR:N	2.83	0.43
7:G:39:ALA:HA	7:G:47:VAL:O	2.18	0.43
10:J:90(A):ILE:HD12	10:J:90(A):ILE:HA	1.77	0.43
10:J:168:MET:CG	10:X:168:MET:HE3	2.41	0.43
12:L:-9:GLN:HE21	12:L:-8:PHE:H	1.66	0.43
13:M:8:TYR:CZ	13:M:148:VAL:HG13	2.52	0.43
3:Q:150:GLN:HG2	3:Q:151:THR:N	2.32	0.43
5:S:31:ILE:HD11	5:S:153:PRO:CG	2.48	0.43
8:V:200:LYS:HE3	9:W:140:SER:O	2.18	0.43
9:W:66:TYR:CE1	9:W:70:GLU:HG3	2.54	0.43
12:Z:120:GLU:OE1	12:Z:120:GLU:HA	2.18	0.43
3:C:106:PRO:HG2	3:C:143:PRO:HG2	1.98	0.43
4:D:101:LEU:CD1	11:K:57:THR:HG22	2.49	0.43
5:E:48:LEU:HB2	5:E:213:ALA:HB3	2.00	0.43
6:F:127:ASN:C	6:F:127:ASN:ND2	2.75	0.43
8:H:3:ILE:CG1	8:H:127:LEU:HB2	2.48	0.43
9:I:165:ARG:NH2	12:Z:135:MET:CE	2.81	0.43
4:R:198:LYS:HB2	4:R:207:LEU:HD13	2.00	0.43
6:T:216:SER:HB3	6:T:21(A):GLU:HB2	1.99	0.43
12:Z:-5:TYR:CD2	12:Z:96:TYR:HB2	2.53	0.43
13:1:-6:GLN:O	13:1:-6:GLN:HG3	2.17	0.43
7:G:197:MET:HG2	7:G:205:PHE:CE1	2.53	0.43
9:I:143:GLU:HG3	9:I:146:LEU:HD21	1.99	0.43
12:L:90:LYS:HE2	16:M:254:HOH:O	2.19	0.43
1:O:57:PRO:HG2	7:U:177:GLU:HG2	2.01	0.43
1:O:112:LEU:O	1:O:116:VAL:HG23	2.18	0.43
1:O:197:LEU:HD23	1:O:210:ILE:HD12	1.99	0.43
2:P:202:THR:CG2	2:P:204:SER:HB2	2.48	0.43
2:P:222:LYS:HZ1	2:P:228:GLU:CD	2.26	0.43
3:Q:46:VAL:HG11	3:Q:139:ALA:HB1	2.00	0.43
6:T:45:GLY:HA3	6:T:215:CYS:O	2.18	0.43
11:Y:38:ASN:OD1	11:Y:38:ASN:C	2.60	0.43
13:1:46:SER:OG	13:1:98:ALA:HB3	2.18	0.43
2:B:185:LYS:HE2	2:B:187:ASP:OD1	2.18	0.43
7:G:236:ILE:HD12	7:G:236:ILE:C	2.44	0.43
12:L:19:ARG:NE	12:L:171:ASP:OD2	2.42	0.43
12:L:109:ALA:HB2	12:L:121:ARG:NH2	2.33	0.43
13:M:-6:GLN:HG3	13:M:-6:GLN:O	2.17	0.43
14:N:163:ILE:HG23	14:N:170:GLY:HA2	2.00	0.43
4:R:68:VAL:HG21	4:R:89:ILE:HD12	2.01	0.43
5:S:31:ILE:HD11	5:S:153:PRO:CD	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:169:ARG:O	6:T:173:LYS:HG3	2.19	0.43
6:T:192:GLN:NE2	6:T:195:LYS:HE3	2.34	0.43
6:T:202:HIS:O	6:T:202:HIS:CG	2.71	0.43
7:U:18(M):SER:HB2	7:U:187:GLU:OE2	2.17	0.43
8:V:48:THR:HB	8:V:51:ASP:HB2	2.00	0.43
2:B:74:ILE:C	2:B:221:GLN:HE22	2.26	0.43
3:C:33:ARG:O	3:C:33:ARG:HG2	2.18	0.43
3:C:228:GLU:O	3:C:232:TYR:HD1	2.01	0.43
6:F:114:ASP:O	6:F:118:GLN:HG2	2.19	0.43
9:I:33:LYS:O	9:I:44:GLY:HA2	2.18	0.43
12:L:24:TYR:HA	8:V:167:LEU:HD12	2.01	0.43
14:N:55:ILE:HD11	14:N:95:LEU:HD13	1.99	0.43
5:S:75:GLY:HA3	5:S:221:PHE:CZ	2.53	0.43
7:U:31:THR:HG21	7:U:135:ILE:HG13	2.01	0.43
12:Z:58:ARG:NH2	16:Z:229:HOH:O	2.51	0.43
6:F:127:ASN:HD22	6:F:127:ASN:N	2.17	0.43
2:P:121:GLN:CG	3:Q:83:ALA:HB1	2.49	0.43
12:Z:98:HIS:ND1	12:Z:98:HIS:C	2.75	0.43
2:B:141:TYR:CD1	2:B:141:TYR:C	2.96	0.43
3:C:70:ILE:O	10:J:68:ILE:HD13	2.19	0.43
4:D:160:TYR:CE2	4:D:163:LYS:HD3	2.53	0.43
5:E:29:GLU:HA	5:E:32:LYS:HE3	2.00	0.43
8:H:147:THR:O	8:H:148:LYS:C	2.62	0.43
10:J:45:PHE:CE1	10:J:52:THR:HG23	2.54	0.43
1:O:7:ARG:HD3	5:S:127:TYR:HD2	1.84	0.43
2:P:97:GLN:NE2	9:W:64:ASN:HD22	2.17	0.43
4:R:243:ALA:O	4:R:244:GLU:HB2	2.19	0.43
6:T:18(E):GLU:H	6:T:18(E):GLU:CD	2.26	0.43
6:T:210:LEU:HD21	6:T:212:ILE:HD11	2.00	0.43
7:U:82:ILE:CG2	7:U:83:PRO:HD3	2.49	0.43
11:Y:76:VAL:N	11:Y:106:GLU:OE2	2.49	0.43
12:Z:6:ILE:HG12	12:Z:124:CYS:HB2	2.01	0.43
12:Z:99:THR:CG2	16:Z:201:HOH:O	2.65	0.43
5:E:52:LYS:HB3	5:E:63:TYR:HB3	2.01	0.43
7:G:82:ILE:CG2	7:G:83:PRO:HD3	2.49	0.43
7:G:177:GLU:O	7:G:17(B):LYS:HG3	2.19	0.43
9:I:36:HIS:HB3	9:I:42:PHE:CD2	2.54	0.43
10:J:18:LYS:HD3	10:J:174:ILE:HG13	2.00	0.43
10:J:124:TYR:CD2	10:J:138:LEU:HD13	2.54	0.43
2:P:27:ALA:O	2:P:30:SER:HB3	2.19	0.43
2:P:209:ARG:HB3	2:P:209:ARG:CZ	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:20(B):GLU:HG3	6:T:20(C):LYS:HG3	2.00	0.43
7:U:99:PHE:CD1	7:U:99:PHE:C	2.97	0.43
7:U:17(C):LYS:HB2	7:U:17(C):LYS:HE3	1.81	0.43
10:X:39:PRO:HG2	10:X:73:GLU:OE2	2.19	0.43
11:Y:146:LEU:HD23	11:Y:151:ALA:HA	2.00	0.43
14:2:112:THR:CG2	14:2:120:HIS:HB2	2.48	0.43
14:2:163:ILE:HG23	14:2:170:GLY:HA2	2.00	0.43
2:B:124:THR:HG22	3:C:130:ARG:NH2	2.23	0.43
7:G:188:LYS:HA	7:G:188:LYS:HD3	1.84	0.43
9:I:29:ASN:ND2	9:I:29:ASN:H	2.16	0.43
11:K:205:SER:HB2	10:X:140:HIS:HA	2.00	0.43
12:L:6:ILE:HG12	12:L:124:CYS:HB2	2.00	0.43
14:N:114:PRO:HD2	14:N:118:SER:O	2.19	0.43
3:Q:216:LYS:HD2	3:Q:220:ASP:OD1	2.18	0.43
13:1:17:ASP:HA	13:1:173:PHE:HA	2.01	0.43
3:C:225:SER:O	3:C:226:SER:C	2.62	0.42
8:H:197:ARG:HH21	9:I:139:GLU:HG3	1.83	0.42
11:K:40:PHE:CD1	11:K:73:ARG:NH1	2.87	0.42
2:P:44:ASP:OD2	2:P:44:ASP:N	2.50	0.42
6:T:24:VAL:O	6:T:27:ALA:HB3	2.19	0.42
8:V:18:THR:HB	8:V:30:ASN:HA	2.01	0.42
9:W:29:ASN:ND2	9:W:29:ASN:H	2.17	0.42
11:Y:65:LEU:HD12	11:Y:65:LEU:HA	1.84	0.42
14:2:55:ILE:HD11	14:2:95:LEU:HD13	2.00	0.42
5:E:4:PHE:CD2	5:E:5:ARG:N	2.86	0.42
6:F:43:ASN:N	6:F:43:ASN:ND2	2.67	0.42
7:G:17(D):SER:O	7:G:17(E):LYS:HB2	2.18	0.42
12:L:-7:ASN:HD22	12:L:-6:PRO:N	2.17	0.42
12:L:98:HIS:C	12:L:98:HIS:ND1	2.77	0.42
4:R:194:LEU:HD12	4:R:194:LEU:HA	1.89	0.42
5:S:8:TYR:CE1	6:T:10:LEU:HD23	2.55	0.42
5:S:68:ILE:HB	5:S:76:LEU:CD2	2.49	0.42
7:U:146:PRO:HD2	16:U:287:HOH:O	2.18	0.42
9:W:18:LEU:HD12	9:W:172:GLY:HA3	2.01	0.42
9:W:143:GLU:HG3	9:W:146:LEU:HD21	2.00	0.42
10:X:157:LEU:HD12	10:X:157:LEU:HA	1.91	0.42
12:Z:5:GLY:O	12:Z:124:CYS:HA	2.18	0.42
2:B:34:ALA:O	2:B:35:GLY:C	2.63	0.42
8:H:90:TYR:O	8:H:91:GLN:C	2.62	0.42
9:I:113:PHE:N	9:I:113:PHE:CD2	2.86	0.42
9:I:193:GLN:HG3	11:Y:196:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:39:PRO:HG2	10:J:73:GLU:OE2	2.18	0.42
13:M:110:LEU:HG	13:M:125:LEU:HD12	2.00	0.42
13:M:147:THR:HB	13:M:149:GLN:NE2	2.34	0.42
13:M:211:ILE:HD11	14:2:36:ARG:HD3	2.01	0.42
14:N:6:VAL:O	14:N:12:VAL:HG23	2.19	0.42
14:N:132:THR:O	14:2:133:PHE:HA	2.19	0.42
1:O:77:VAL:CG1	1:O:137:LEU:HB2	2.49	0.42
2:P:186:VAL:HG11	2:P:216:ARG:CD	2.49	0.42
5:S:29:GLU:HA	5:S:32:LYS:HE3	2.01	0.42
5:S:41:ARG:NH1	5:S:42:SER:O	2.52	0.42
8:V:148:LYS:HE3	8:V:177:VAL:HG11	2.02	0.42
10:X:39:PRO:HG2	10:X:73:GLU:CD	2.44	0.42
2:B:202:THR:HG22	2:B:204:SER:N	2.11	0.42
8:H:18:THR:HB	8:H:30:ASN:HA	2.01	0.42
8:H:148:LYS:HE3	8:H:177:VAL:HG11	2.01	0.42
12:L:4:LEU:CD1	12:L:138:LEU:HD21	2.48	0.42
1:O:58:LEU:HA	1:O:58:LEU:HD23	1.81	0.42
8:V:38:SER:O	8:V:39:PRO:C	2.62	0.42
9:W:80:THR:HG23	9:W:113:PHE:CZ	2.55	0.42
10:X:129:TYR:O	10:X:132:PHE:HB2	2.19	0.42
2:B:222:LYS:HZ1	2:B:228:GLU:CD	2.26	0.42
2:B:235:LYS:C	2:B:237:GLY:N	2.77	0.42
3:C:46:VAL:HG22	3:C:146:PRO:HB2	2.01	0.42
4:D:117:CYS:SG	4:D:157:PHE:HB3	2.59	0.42
5:E:31:ILE:HD11	5:E:153:PRO:CG	2.49	0.42
6:F:91:ARG:O	6:F:95:GLU:HB2	2.20	0.42
9:I:29:ASN:ND2	9:I:29:ASN:C	2.78	0.42
9:I:113:PHE:HA	9:I:118:CYS:O	2.19	0.42
13:M:139:ARG:HH11	8:V:165:ASN:ND2	2.09	0.42
14:N:112:THR:CG2	14:N:120:HIS:HB2	2.49	0.42
1:O:77:VAL:HG12	1:O:137:LEU:HB2	2.00	0.42
5:S:216:GLY:O	5:S:217:LYS:C	2.63	0.42
6:T:52:LYS:HB2	6:T:209:GLU:O	2.19	0.42
8:V:89:LYS:HE3	8:V:90:TYR:CE2	2.55	0.42
13:1:130:GLY:O	13:1:134:ALA:HB3	2.20	0.42
3:C:168:ASN:CB	3:C:200:VAL:HG11	2.48	0.42
4:D:14:THR:HG22	4:D:15:PHE:N	2.35	0.42
7:G:12:ILE:HG13	7:G:14:ILE:HG23	2.01	0.42
8:H:113:ILE:HG12	8:H:119:THR:HG22	2.00	0.42
11:K:99:THR:HG22	11:K:113:VAL:O	2.20	0.42
2:P:112:LEU:C	2:P:112:LEU:HD23	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:185:LYS:HE2	2:P:187:ASP:OD1	2.19	0.42
4:R:117:CYS:SG	4:R:157:PHE:HB3	2.60	0.42
8:V:2:THR:OG1	8:V:130:GLY:HA3	2.20	0.42
12:Z:1(I):ASN:O	12:Z:14(J):GLY:C	2.62	0.42
3:C:33:ARG:HH11	3:C:33:ARG:HB3	1.84	0.42
3:C:71:ASP:HA	10:J:68:ILE:HD13	2.00	0.42
6:F:63:LYS:O	6:F:65:VAL:N	2.52	0.42
6:F:169:ARG:O	6:F:173:LYS:HG3	2.20	0.42
10:J:129:TYR:O	10:J:132:PHE:HB2	2.19	0.42
14:N:36:ARG:HD2	13:1:211:ILE:HD11	2.02	0.42
5:S:52:LYS:HB3	5:S:63:TYR:HB3	2.01	0.42
6:T:87:HIS:HD2	6:T:132:PHE:CE2	2.37	0.42
7:U:41:ARG:NH2	7:U:18(B):ASP:OD2	2.52	0.42
9:W:113:PHE:HA	9:W:118:CYS:O	2.20	0.42
13:1:171:ARG:HG3	13:1:192:VAL:HB	2.00	0.42
2:B:51:GLU:OE2	2:B:202:THR:HG23	2.19	0.42
5:E:31:ILE:HD11	5:E:153:PRO:CD	2.50	0.42
5:E:75:GLY:HA3	5:E:221:PHE:CZ	2.54	0.42
6:F:52:LYS:HB2	6:F:209:GLU:O	2.20	0.42
6:F:87:HIS:HD2	6:F:132:PHE:CE2	2.38	0.42
6:F:177:GLU:OE2	7:G:57:LYS:HE2	2.19	0.42
8:H:167:LEU:HD12	12:Z:24:TYR:HA	2.01	0.42
12:L:-8:PHE:CB	13:M:-8:THR:HG23	2.47	0.42
12:L:14:LEU:HD13	12:L:34:VAL:HG13	2.01	0.42
13:M:133:MET:HE1	13:M:165:ARG:HG3	2.01	0.42
2:P:235:LYS:N	2:P:235:LYS:HD3	2.35	0.42
3:Q:225:SER:O	3:Q:226:SER:C	2.61	0.42
4:R:67:ILE:HG22	4:R:221:PHE:HZ	1.83	0.42
4:R:75:GLY:HA3	4:R:221:PHE:CD2	2.55	0.42
6:T:172:ALA:C	6:T:176:LEU:HD23	2.45	0.42
10:X:-1:MET:HG2	10:X:1:ASP:N	2.34	0.42
12:Z:14:LEU:HD13	12:Z:34:VAL:HG13	2.01	0.42
13:1:110:LEU:HG	13:1:125:LEU:HD12	2.01	0.42
5:E:7:ASN:HD22	5:E:7:ASN:HA	1.72	0.42
5:E:179:THR:HG22	5:E:179:THR:O	2.20	0.42
5:E:18(C):PHE:CD1	5:E:18(C):PHE:C	2.98	0.42
6:F:35:THR:CG2	6:F:51:GLU:O	2.62	0.42
7:G:191:GLU:HG3	7:G:232:ARG:HG3	2.01	0.42
12:L:120:GLU:HA	12:L:120:GLU:OE1	2.19	0.42
12:L:1(I):ASN:O	12:L:14(J):GLY:C	2.62	0.42
13:M:211:ILE:HD11	14:2:36:ARG:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:233:LEU:HD12	2:P:233:LEU:HA	1.92	0.42
2:P:235:LYS:C	2:P:237:GLY:N	2.78	0.42
4:R:14:THR:HG22	4:R:15:PHE:N	2.34	0.42
5:S:5:ARG:HG3	5:S:22:PHE:CE2	2.55	0.42
5:S:2(B):THR:N	5:S:2(E):ASN:ND2	2.51	0.42
14:2:18(G):TYR:C	14:2:18(G):TYR:CD1	2.98	0.42
3:C:93:ARG:NH1	10:J:69:ARG:HA	2.35	0.42
7:G:172:ILE:HD13	7:G:197:MET:CE	2.50	0.42
1:O:205:GLU:OE2	1:O:205:GLU:HA	2.20	0.42
2:P:101:LYS:HZ2	10:X:85:GLN:HE22	1.67	0.42
3:Q:214:VAL:HG23	3:Q:224:LEU:HD11	2.02	0.42
4:R:31:ILE:HD13	4:R:135:ALA:HB2	2.02	0.42
5:S:134:VAL:O	5:S:153:PRO:HG3	2.20	0.42
7:U:121:GLN:NE2	7:U:121:GLN:C	2.78	0.42
8:V:78:SER:O	8:V:82:MET:HG3	2.20	0.42
11:Y:2:THR:HG21	11:Y:162:ALA:CB	2.50	0.42
2:B:202:THR:CG2	2:B:204:SER:HB2	2.50	0.41
6:F:205:ASN:C	6:F:20(B):GLU:H	2.28	0.41
7:G:8:TYR:C	7:G:10:ARG:N	2.78	0.41
7:G:72:ARG:HG2	16:G:246:HOH:O	2.20	0.41
8:H:206:PHE:N	16:H:258:HOH:O	2.45	0.41
10:J:4:LEU:HD23	10:J:126:ALA:HB2	2.01	0.41
12:L:113:PHE:CD1	12:L:113:PHE:N	2.87	0.41
13:M:130:GLY:O	13:M:134:ALA:HB3	2.20	0.41
1:O:33:GLN:CA	1:O:33:GLN:NE2	2.82	0.41
1:O:141:HIS:HA	1:O:146:GLY:O	2.20	0.41
3:Q:224:LEU:CD1	3:Q:224:LEU:H	2.33	0.41
13:1:175:LEU:HD23	13:1:175:LEU:C	2.45	0.41
3:C:76:LEU:HD23	3:C:76:LEU:C	2.44	0.41
3:C:97:GLN:NE2	16:C:244:HOH:O	2.51	0.41
5:E:68:ILE:HB	5:E:76:LEU:CD2	2.50	0.41
7:G:18(H):GLU:CD	7:G:18(H):GLU:N	2.78	0.41
11:K:38:ASN:OD1	11:K:38:ASN:C	2.63	0.41
11:K:196:PHE:CE1	9:W:193:GLN:HG3	2.55	0.41
12:L:43:MET:CB	12:L:101:ILE:HG22	2.48	0.41
1:O:218:GLY:N	16:O:258:HOH:O	2.28	0.41
2:P:69:LYS:HG3	2:P:221:GLN:OE1	2.20	0.41
2:P:89:ILE:O	2:P:92:ALA:HB3	2.21	0.41
5:S:175:TYR:CD2	5:S:196:ALA:HA	2.55	0.41
7:U:93:LYS:HD3	14:2:68:SER:HB3	2.01	0.41
7:U:107:MET:HA	7:U:108:PRO:HD3	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:144:GLN:HE21	8:V:144:GLN:HB2	1.64	0.41
12:Z:4:LEU:HD12	12:Z:5:GLY:N	2.35	0.41
13:1:133:MET:O	13:1:136:PRO:HD2	2.21	0.41
2:B:15:PHE:N	3:C:23:GLN:HE22	2.03	0.41
2:B:97:GLN:NE2	9:I:64:ASN:HD22	2.15	0.41
3:C:224:LEU:CD1	3:C:224:LEU:H	2.32	0.41
4:D:177:LEU:HD22	5:E:58:LEU:HD13	2.01	0.41
8:H:153:LYS:HD2	16:H:247:HOH:O	2.19	0.41
9:I:29:ASN:HD21	9:I:30:LYS:NZ	2.19	0.41
12:L:4:LEU:HD12	12:L:5:GLY:N	2.35	0.41
2:P:44:ASP:CG	2:P:186:VAL:HG23	2.45	0.41
2:P:186:VAL:HG11	2:P:216:ARG:HD3	2.02	0.41
4:R:152:GLU:HB3	4:R:153:PRO:CD	2.50	0.41
6:T:114:ASP:O	6:T:118:GLN:HG2	2.19	0.41
6:T:127:ASN:HD22	6:T:127:ASN:N	2.17	0.41
9:W:84:SER:HB2	9:W:119:ILE:HD11	2.03	0.41
10:X:67:SER:O	10:X:71:ASP:N	2.54	0.41
14:2:156:LYS:HE3	16:2:229:HOH:O	2.19	0.41
5:E:175:TYR:CD2	5:E:196:ALA:HA	2.55	0.41
5:E:216:GLY:O	5:E:217:LYS:C	2.63	0.41
6:F:45:GLY:HA3	6:F:215:CYS:O	2.20	0.41
7:G:13:THR:HB	7:G:124:THR:O	2.20	0.41
11:K:12:ILE:HB	11:K:178:VAL:HB	2.03	0.41
11:K:207:ASN:ND2	10:X:144:PRO:HD3	2.36	0.41
13:M:1:THR:HG22	16:M:214:HOH:O	2.20	0.41
3:Q:241:GLN:C	3:Q:243:GLN:N	2.79	0.41
12:Z:113:PHE:CD1	12:Z:113:PHE:N	2.88	0.41
14:2:44:CYS:HB2	14:2:100:ILE:HB	2.02	0.41
7:G:41:ARG:NH2	7:G:18(B):ASP:OD2	2.53	0.41
7:G:230:GLU:OE2	7:G:230:GLU:HA	2.19	0.41
9:I:18:LEU:HD12	9:I:172:GLY:HA3	2.02	0.41
10:J:67:SER:O	10:J:71:ASP:N	2.53	0.41
14:N:133:PHE:HA	14:2:132:THR:O	2.20	0.41
1:O:227:GLN:NE2	1:O:231:ASP:OD1	2.54	0.41
3:C:40:VAL:HG23	3:C:189:CYS:SG	2.61	0.41
9:I:174:VAL:HG21	9:I:186:LYS:CE	2.50	0.41
10:J:90(B):ARG:HG2	10:J:90(B):ARG:HH11	1.86	0.41
11:K:4:LEU:CD1	11:K:159:ILE:HD11	2.51	0.41
13:M:175:LEU:C	13:M:175:LEU:HD23	2.45	0.41
1:O:86:ARG:NE	7:U:118:ASN:ND2	2.58	0.41
5:S:15:PHE:H	6:T:23:GLN:NE2	2.12	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:35:ILE:HG23	7:U:51:GLN:HB2	2.03	0.41
7:U:18(H):GLU:CD	7:U:18(H):GLU:N	2.79	0.41
11:Y:114:ASP:OD1	11:Y:114:ASP:C	2.63	0.41
3:C:65:SER:HB2	16:C:253:HOH:O	2.20	0.41
4:D:67:ILE:HG22	4:D:221:PHE:HZ	1.86	0.41
4:D:207:LEU:C	4:D:207:LEU:CD2	2.94	0.41
6:T:43:ASN:N	6:T:43:ASN:ND2	2.66	0.41
10:X:187:VAL:O	10:X:189:ASP:N	2.53	0.41
12:Z:-6:PRO:HG2	12:Z:-5:TYR:CD1	2.56	0.41
2:B:220:TYR:CE1	2:B:222:LYS:HB2	2.56	0.41
2:B:235:LYS:N	2:B:235:LYS:HD3	2.34	0.41
6:F:24:VAL:O	6:F:27:ALA:HB3	2.20	0.41
12:L:114:ASP:HB2	12:L:118:SER:HB3	2.03	0.41
14:N:21:THR:HG22	14:N:26:ILE:HA	2.03	0.41
2:P:202:THR:HG22	2:P:203:ASP:N	2.36	0.41
4:R:237:LEU:O	4:R:241:GLU:HG3	2.21	0.41
5:S:15:PHE:HB2	6:T:23:GLN:NE2	2.36	0.41
3:C:214:VAL:HG23	3:C:224:LEU:HD11	2.03	0.41
4:D:67:ILE:HD12	4:D:211:GLN:HE21	1.86	0.41
4:D:170:GLU:CD	4:D:170:GLU:H	2.29	0.41
6:F:202:HIS:O	6:F:202:HIS:CG	2.73	0.41
8:H:34:LEU:HD22	8:H:174:ASP:HB3	2.01	0.41
8:H:165:ASN:ND2	13:1:139:ARG:HH11	2.09	0.41
10:J:93:ARG:HG2	10:J:93:ARG:HH11	1.86	0.41
10:J:157:LEU:HD12	10:J:157:LEU:HA	1.88	0.41
12:L:76:ILE:HG23	12:L:77:ASN:N	2.36	0.41
12:L:160:THR:O	12:L:164:GLU:HG2	2.20	0.41
3:Q:55:THR:O	3:Q:56:LEU:HD22	2.20	0.41
3:Q:197:LEU:O	3:Q:201:VAL:HG23	2.21	0.41
5:S:7:ASN:HD22	5:S:7:ASN:HA	1.73	0.41
8:V:148:LYS:O	8:V:152:ILE:HG13	2.20	0.41
4:D:152:GLU:HB3	4:D:153:PRO:CD	2.51	0.41
6:F:192:GLN:NE2	6:F:195:LYS:HE3	2.36	0.41
7:G:35:ILE:HG23	7:G:51:GLN:HB2	2.02	0.41
9:I:84:SER:HB2	9:I:119:ILE:HD11	2.03	0.41
10:J:166:MET:HA	10:J:167:PRO:HD3	1.82	0.41
12:L:8:GLY:HA3	12:L:11:PHE:CZ	2.56	0.41
1:O:57:PRO:HG3	7:U:177:GLU:OE1	2.21	0.41
2:P:52:ARG:NH2	2:P:63(A):SER:HB3	2.36	0.41
3:Q:40:VAL:HG23	3:Q:189:CYS:SG	2.61	0.41
4:R:117:CYS:HB3	4:R:155:GLY:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:35:THR:HG23	6:T:36:THR:N	2.36	0.41
6:T:205:ASN:C	6:T:20(B):GLU:H	2.28	0.41
8:V:197:ARG:HH21	9:W:139:GLU:HG3	1.86	0.41
9:W:33:LYS:O	9:W:44:GLY:HA2	2.21	0.41
10:X:104:TYR:CD1	10:X:180:LYS:HA	2.56	0.41
12:Z:42:VAL:CG2	12:Z:102:ALA:HB3	2.51	0.41
13:1:-5:PRO:HD3	13:1:96:TRP:CE2	2.56	0.41
14:2:21:THR:HG22	14:2:26:ILE:HA	2.03	0.41
14:2:38:HIS:O	14:2:39:ASP:C	2.64	0.41
3:C:57:LYS:C	3:C:57:LYS:CD	2.94	0.40
3:C:227:GLU:O	3:C:231:GLN:HG3	2.21	0.40
4:D:186:LEU:O	4:D:190:GLU:HG3	2.22	0.40
5:E:180:LEU:HA	5:E:18(C):PHE:CE2	2.57	0.40
10:J:-1:MET:HG2	10:J:1:ASP:N	2.35	0.40
10:J:112:GLN:HE22	10:J:126:ALA:H	1.69	0.40
10:J:140:HIS:CD2	10:J:141:HIS:NE2	2.89	0.40
10:J:144:PRO:HG2	11:Y:207:ASN:HD21	1.86	0.40
2:P:51:GLU:OE2	2:P:202:THR:HG23	2.22	0.40
2:P:121:GLN:NE2	2:P:121:GLN:C	2.80	0.40
3:Q:112:LEU:O	3:Q:112:LEU:HD13	2.21	0.40
3:Q:227:GLU:O	3:Q:231:GLN:HG3	2.21	0.40
10:X:133:TYR:CZ	10:X:166:MET:HG3	2.55	0.40
11:Y:81:LYS:HA	11:Y:84:SER:HB3	2.02	0.40
12:Z:105:ASP:OD2	12:Z:107:LYS:HB2	2.20	0.40
13:1:147:THR:HB	13:1:149:GLN:NE2	2.36	0.40
1:A:7:ARG:NH1	5:E:127:TYR:CD2	2.90	0.40
2:B:44:ASP:OD2	2:B:44:ASP:N	2.52	0.40
2:B:113:VAL:HG22	2:B:138:TYR:CD2	2.57	0.40
2:B:233:LEU:HD12	2:B:233:LEU:HA	1.92	0.40
5:E:41:ARG:NH1	5:E:42:SER:O	2.54	0.40
7:G:31:THR:HG21	7:G:135:ILE:HG13	2.02	0.40
8:H:34:LEU:HB2	16:H:245:HOH:O	2.21	0.40
9:I:105:ASN:HB3	9:I:10(C):SER:OG	2.22	0.40
3:Q:44:ASN:O	3:Q:45:CYS:HB3	2.21	0.40
3:Q:201:VAL:HG21	3:Q:210:ILE:HG12	2.03	0.40
7:U:225:SER:O	7:U:229:ILE:HG13	2.22	0.40
9:W:29:ASN:HD21	9:W:30:LYS:NZ	2.19	0.40
10:X:70:GLU:O	10:X:71:ASP:C	2.65	0.40
1:A:67:VAL:HG11	1:A:213:ALA:HB2	2.02	0.40
2:B:90:ASN:HB2	16:B:262:HOH:O	2.20	0.40
2:B:186:VAL:HG11	2:B:216:ARG:CD	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:241:GLN:C	3:C:243:GLN:N	2.79	0.40
8:H:30:ASN:O	8:H:189:ARG:NH2	2.53	0.40
8:H:32:ALA:HB2	8:H:189:ARG:NH1	2.36	0.40
9:I:93:GLY:N	9:I:94:PRO:HD3	2.36	0.40
13:M:1:THR:OG1	13:M:2:SER:N	2.45	0.40
13:M:12:VAL:CG2	13:M:102:ALA:HB1	2.51	0.40
13:M:191:GLN:HE21	13:M:191:GLN:HB3	1.65	0.40
1:O:13:THR:O	2:P:130:ARG:HD3	2.22	0.40
2:P:34:ALA:O	2:P:35:GLY:C	2.64	0.40
7:U:203:THR:HG22	7:U:204:GLU:O	2.21	0.40
8:V:147:THR:O	8:V:148:LYS:C	2.65	0.40
10:X:65:LEU:HD21	10:X:69:ARG:NH2	2.36	0.40
11:Y:5:ALA:HA	11:Y:13:ILE:O	2.22	0.40
11:Y:12:ILE:HB	11:Y:178:VAL:HB	2.02	0.40
12:Z:90:LYS:CE	16:Z:196:HOH:O	2.70	0.40
7:G:80:GLY:HA3	7:G:134:VAL:HG12	2.03	0.40
5:S:18(C):PHE:HA	5:S:18(F):ILE:CG1	2.52	0.40
5:S:18(C):PHE:CD1	5:S:18(C):PHE:C	2.99	0.40
10:X:143:ARG:HA	10:X:144:PRO:HD3	1.95	0.40
12:Z:14(I):THR:O	12:Z:14(K):LYS:HB2	2.22	0.40
2:B:67:LEU:HD23	2:B:213:ALA:HB2	2.03	0.40
3:C:46:VAL:HG11	3:C:139:ALA:HB1	2.03	0.40
4:D:45:GLY:HA2	4:D:146:TYR:CD1	2.57	0.40
5:E:40:LEU:HD23	5:E:40:LEU:N	2.36	0.40
8:H:17:ASP:HA	8:H:172:ASN:O	2.22	0.40
10:J:133:TYR:CZ	10:J:166:MET:HG3	2.56	0.40
13:M:8:TYR:CE2	13:M:148:VAL:HG22	2.56	0.40
13:M:14(C):ARG:CG	13:M:14(C):ARG:NH1	2.84	0.40
1:O:46:VAL:HG12	1:O:47:VAL:N	2.36	0.40
1:O:67:VAL:HG11	1:O:213:ALA:HB3	2.03	0.40
3:Q:238:GLN:O	3:Q:242:GLU:HG3	2.21	0.40
4:R:86:ARG:HD3	4:R:86:ARG:HA	1.84	0.40
5:S:46:ALA:HB1	5:S:139:ILE:HB	2.04	0.40
9:W:109:PHE:CD2	9:W:109:PHE:C	2.99	0.40
10:X:187:VAL:C	10:X:189:ASP:H	2.30	0.40
11:Y:99:THR:HG22	11:Y:113:VAL:O	2.22	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%)	231 (93%)	15 (6%)	2 (1%)	16	41
1	O	248/250 (99%)	231 (93%)	15 (6%)	2 (1%)	16	41
2	B	242/244 (99%)	221 (91%)	18 (7%)	3 (1%)	10	31
2	P	242/244 (99%)	220 (91%)	19 (8%)	3 (1%)	10	31
3	C	239/241 (99%)	216 (90%)	19 (8%)	4 (2%)	7	23
3	Q	239/241 (99%)	216 (90%)	19 (8%)	4 (2%)	7	23
4	D	240/242 (99%)	219 (91%)	16 (7%)	5 (2%)	5	18
4	R	240/242 (99%)	219 (91%)	16 (7%)	5 (2%)	5	18
5	E	231/233 (99%)	211 (91%)	17 (7%)	3 (1%)	9	29
5	S	231/233 (99%)	211 (91%)	17 (7%)	3 (1%)	9	29
6	F	242/244 (99%)	229 (95%)	11 (4%)	2 (1%)	16	41
6	T	242/244 (99%)	229 (95%)	11 (4%)	2 (1%)	16	41
7	G	241/243 (99%)	231 (96%)	9 (4%)	1 (0%)	30	58
7	U	241/243 (99%)	231 (96%)	9 (4%)	1 (0%)	30	58
8	H	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
8	V	220/222 (99%)	205 (93%)	14 (6%)	1 (0%)	24	53
9	I	202/204 (99%)	193 (96%)	7 (4%)	2 (1%)	12	36
9	W	202/204 (99%)	192 (95%)	8 (4%)	2 (1%)	12	36
10	J	196/198 (99%)	185 (94%)	8 (4%)	3 (2%)	8	26
10	X	196/198 (99%)	183 (93%)	10 (5%)	3 (2%)	8	26
11	K	210/212 (99%)	201 (96%)	9 (4%)	0	100	100
11	Y	210/212 (99%)	201 (96%)	9 (4%)	0	100	100
12	L	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
12	Z	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
13	1	231/233 (99%)	217 (94%)	13 (6%)	1 (0%)	30	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	M	231/233 (99%)	215 (93%)	15 (6%)	1 (0%)	30	58
14	2	194/196 (99%)	182 (94%)	12 (6%)	0	100	100
14	N	194/196 (99%)	184 (95%)	10 (5%)	0	100	100
All	All	6312/6368 (99%)	5895 (93%)	364 (6%)	53 (1%)	16	41

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	THR
3	C	58	LEU
4	D	12(G)	GLU
10	J	192	ALA
1	O	5	THR
3	Q	58	LEU
4	R	12(G)	GLU
10	X	192	ALA
2	B	54	VAL
2	B	21(B)	GLY
2	B	21(C)	ASP
3	C	183	PRO
3	C	203	THR
4	D	128	MET
5	E	202	ARG
6	F	205	ASN
6	F	206	LYS
9	I	93	GLY
10	J	188	ASP
2	P	54	VAL
2	P	21(B)	GLY
2	P	21(C)	ASP
3	Q	183	PRO
3	Q	203	THR
4	R	128	MET
5	S	202	ARG
6	T	205	ASN
6	T	206	LYS
9	W	93	GLY
10	X	188	ASP
3	C	179	ASN
4	D	12(C)	GLY
4	D	18(D)	SER

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Mol	Chain	Res	Type
5	E	5	ARG
5	E	217	LYS
7	G	220	LYS
3	Q	179	ASN
4	R	12(C)	GLY
4	R	18(D)	SER
5	S	217	LYS
7	U	220	LYS
5	S	5	ARG
4	D	12(F)	GLY
9	I	23	GLN
4	R	12(F)	GLY
9	W	23	GLN
1	A	167	LYS
13	M	72	ALA
1	O	167	LYS
10	X	8	VAL
13	1	72	ALA
10	J	8	VAL
8	V	96	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	71
1	O	209/209 (100%)	203 (97%)	6 (3%)	37	71
2	B	203/203 (100%)	197 (97%)	6 (3%)	36	69
2	P	203/203 (100%)	197 (97%)	6 (3%)	36	69
3	C	213/213 (100%)	207 (97%)	6 (3%)	38	71
3	Q	213/213 (100%)	205 (96%)	8 (4%)	29	62
4	D	198/198 (100%)	188 (95%)	10 (5%)	21	52
4	R	198/198 (100%)	188 (95%)	10 (5%)	21	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	192/192 (100%)	176 (92%)	16 (8%)	10	31
5	S	192/192 (100%)	176 (92%)	16 (8%)	10	31
6	F	201/201 (100%)	183 (91%)	18 (9%)	9	27
6	T	201/201 (100%)	183 (91%)	18 (9%)	9	27
7	G	207/207 (100%)	197 (95%)	10 (5%)	23	54
7	U	207/207 (100%)	197 (95%)	10 (5%)	23	54
8	H	181/181 (100%)	173 (96%)	8 (4%)	25	58
8	V	181/181 (100%)	173 (96%)	8 (4%)	25	58
9	I	172/172 (100%)	167 (97%)	5 (3%)	37	71
9	W	172/172 (100%)	167 (97%)	5 (3%)	37	71
10	J	175/175 (100%)	169 (97%)	6 (3%)	32	66
10	X	175/175 (100%)	169 (97%)	6 (3%)	32	66
11	K	169/169 (100%)	163 (96%)	6 (4%)	31	64
11	Y	169/169 (100%)	163 (96%)	6 (4%)	31	64
12	L	185/185 (100%)	160 (86%)	25 (14%)	4	12
12	Z	185/185 (100%)	160 (86%)	25 (14%)	4	12
13	1	199/199 (100%)	189 (95%)	10 (5%)	22	53
13	M	199/199 (100%)	189 (95%)	10 (5%)	22	53
14	2	162/162 (100%)	157 (97%)	5 (3%)	35	69
14	N	162/162 (100%)	157 (97%)	5 (3%)	35	69
All	All	5332/5332 (100%)	5056 (95%)	276 (5%)	21	51

All (276) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	62	GLU
1	A	124	THR
1	A	134	VAL
1	A	158	PHE
1	A	179	ARG
2	B	10	SER
2	B	58	LEU
2	B	116	LEU
2	B	124	THR

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Mol	Chain	Res	Type
2	B	150	THR
2	B	192	LEU
3	C	10	ARG
3	C	25	GLU
3	C	61	THR
3	C	66	LYS
3	C	150	GLN
3	C	174	GLU
4	D	28	LEU
4	D	110	GLU
4	D	126	ARG
4	D	170	GLU
4	D	177	LEU
4	D	191	LEU
4	D	194	LEU
4	D	215	ILE
4	D	237	LEU
4	D	244	GLU
5	E	12	THR
5	E	13	VAL
5	E	28	LEU
5	E	32	LYS
5	E	57	GLU
5	E	76	LEU
5	E	78	LEU
5	E	90	ASN
5	E	97	ASN
5	E	121	GLN
5	E	149	LEU
5	E	189	LEU
5	E	199	GLN
5	E	207	LEU
5	E	227	GLU
5	E	231	LYS
6	F	11	SER
6	F	18	ASP
6	F	35	THR
6	F	43	ASN
6	F	56	SER
6	F	72	ARG
6	F	95	GLU
6	F	121	GLN

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Mol	Chain	Res	Type
6	F	127	ASN
6	F	144	ASN
6	F	169	ARG
6	F	18(A)	ASP
6	F	18(B)	HIS
6	F	18(C)	HIS
6	F	18(D)	PRO
6	F	18(E)	GLU
6	F	187	ARG
6	F	203	GLU
7	G	33	GLN
7	G	38	LEU
7	G	72	ARG
7	G	87	ASN
7	G	119	LEU
7	G	124	THR
7	G	197	MET
7	G	217	LYS
7	G	232	ARG
7	G	233	LEU
8	H	13	VAL
8	H	34	LEU
8	H	55	VAL
8	H	56	THR
8	H	63	ILE
8	H	68	LEU
8	H	144	GLN
8	H	197	ARG
9	I	20	LEU
9	I	29	ASN
9	I	113	PHE
9	I	160	LEU
9	I	192	ARG
10	J	35	ARG
10	J	52	THR
10	J	68	ILE
10	J	70	GLU
10	J	121	GLU
10	J	155	LEU
11	K	4	LEU
11	K	9	GLN
11	K	65	LEU

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Mol	Chain	Res	Type
11	K	69	ARG
11	K	87	VAL
11	K	138	LEU
12	L	14	LEU
12	L	21	ILE
12	L	25	SER
12	L	40	ASN
12	L	58	ARG
12	L	98	HIS
12	L	99	THR
12	L	112	SER
12	L	120	GLU
12	L	138	LEU
12	L	14(A)	LYS
12	L	14(B)	ASN
12	L	14(C)	GLN
12	L	14(D)	TYR
12	L	14(E)	GLU
12	L	14(F)	PRO
12	L	14(I)	THR
12	L	14(K)	LYS
12	L	14(M)	VAL
12	L	14(N)	LYS
12	L	14(O)	LYS
12	L	14(P)	PRO
12	L	14(Q)	LEU
12	L	14(W)	LYS
12	L	190	GLU
13	M	40	ASN
13	M	62	LEU
13	M	91	ARG
13	M	112	TYR
13	M	129	PHE
13	M	140	LYS
13	M	148	VAL
13	M	149	GLN
13	M	191	GLN
13	M	204	LYS
14	N	84	LYS
14	N	89	GLU
14	N	119	VAL
14	N	149	GLU

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Mol	Chain	Res	Type
14	N	178	LEU
1	O	33	GLN
1	O	62	GLU
1	O	124	THR
1	O	134	VAL
1	O	158	PHE
1	O	179	ARG
2	P	10	SER
2	P	58	LEU
2	P	116	LEU
2	P	124	THR
2	P	150	THR
2	P	192	LEU
3	Q	10	ARG
3	Q	25	GLU
3	Q	57	LYS
3	Q	61	THR
3	Q	66	LYS
3	Q	150	GLN
3	Q	172	VAL
3	Q	174	GLU
4	R	28	LEU
4	R	110	GLU
4	R	126	ARG
4	R	170	GLU
4	R	177	LEU
4	R	191	LEU
4	R	194	LEU
4	R	215	ILE
4	R	237	LEU
4	R	244	GLU
5	S	12	THR
5	S	13	VAL
5	S	28	LEU
5	S	32	LYS
5	S	57	GLU
5	S	76	LEU
5	S	78	LEU
5	S	90	ASN
5	S	97	ASN
5	S	121	GLN
5	S	149	LEU

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Mol	Chain	Res	Type
5	S	189	LEU
5	S	199	GLN
5	S	207	LEU
5	S	227	GLU
5	S	231	LYS
6	T	11	SER
6	T	18	ASP
6	T	35	THR
6	T	43	ASN
6	T	56	SER
6	T	72	ARG
6	T	95	GLU
6	T	121	GLN
6	T	127	ASN
6	T	144	ASN
6	T	169	ARG
6	T	18(A)	ASP
6	T	18(B)	HIS
6	T	18(C)	HIS
6	T	18(D)	PRO
6	T	18(E)	GLU
6	T	187	ARG
6	T	203	GLU
7	U	33	GLN
7	U	38	LEU
7	U	72	ARG
7	U	87	ASN
7	U	119	LEU
7	U	124	THR
7	U	197	MET
7	U	217	LYS
7	U	232	ARG
7	U	233	LEU
8	V	13	VAL
8	V	34	LEU
8	V	55	VAL
8	V	56	THR
8	V	63	ILE
8	V	68	LEU
8	V	144	GLN
8	V	197	ARG
9	W	20	LEU

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Mol	Chain	Res	Type
9	W	29	ASN
9	W	113	PHE
9	W	160	LEU
9	W	192	ARG
10	X	35	ARG
10	X	52	THR
10	X	68	ILE
10	X	70	GLU
10	X	121	GLU
10	X	155	LEU
11	Y	4	LEU
11	Y	9	GLN
11	Y	65	LEU
11	Y	69	ARG
11	Y	87	VAL
11	Y	138	LEU
12	Z	-7	ASN
12	Z	14	LEU
12	Z	25	SER
12	Z	40	ASN
12	Z	58	ARG
12	Z	98	HIS
12	Z	99	THR
12	Z	112	SER
12	Z	120	GLU
12	Z	138	LEU
12	Z	14(A)	LYS
12	Z	14(B)	ASN
12	Z	14(C)	GLN
12	Z	14(D)	TYR
12	Z	14(E)	GLU
12	Z	14(F)	PRO
12	Z	14(I)	THR
12	Z	14(K)	LYS
12	Z	14(M)	VAL
12	Z	14(N)	LYS
12	Z	14(O)	LYS
12	Z	14(P)	PRO
12	Z	14(Q)	LEU
12	Z	14(W)	LYS
12	Z	190	GLU
13	1	40	ASN

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Mol	Chain	Res	Type
13	1	62	LEU
13	1	91	ARG
13	1	112	TYR
13	1	129	PHE
13	1	140	LYS
13	1	148	VAL
13	1	149	GLN
13	1	191	GLN
13	1	204	LYS
14	2	84	LYS
14	2	89	GLU
14	2	119	VAL
14	2	149	GLU
14	2	178	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (242) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	97	HIS
1	A	121	GLN
1	A	145	ASN
1	A	227	GLN
2	B	23	GLN
2	B	33	HIS
2	B	71	ASN
2	B	97	GLN
2	B	121	GLN
2	B	125	GLN
2	B	156	ASN
2	B	173	GLN
2	B	177	GLN
2	B	218	ASN
3	C	23	GLN
3	C	82	ASN
3	C	97	GLN
3	C	120	GLN
3	C	121	GLN
3	C	125	GLN
3	C	150	GLN
3	C	163	GLN
3	C	209	ASN

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Mol	Chain	Res	Type
3	C	238	GLN
3	C	243	GLN
4	D	23	GLN
4	D	108	ASN
4	D	161	ASN
4	D	20(A)	ASN
4	D	211	GLN
4	D	218	GLN
4	D	226	ASN
5	E	7	ASN
5	E	33	GLN
5	E	73	HIS
5	E	97	ASN
5	E	104	ASN
5	E	114	HIS
5	E	121	GLN
5	E	123	ASN
5	E	125	GLN
5	E	152	GLN
5	E	156	ASN
5	E	199	GLN
5	E	2(E)	ASN
6	F	23	GLN
6	F	43	ASN
6	F	87	HIS
6	F	90	ASN
6	F	121	GLN
6	F	127	ASN
6	F	192	GLN
7	G	32	ASN
7	G	34(A)	ASN
7	G	87	ASN
7	G	118	ASN
7	G	121	GLN
7	G	125	GLN
7	G	169	GLN
7	G	178	ASN
7	G	18(C)	HIS
7	G	184	ASN
7	G	208	ASN
7	G	228	ASN
8	H	30	ASN

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Mol	Chain	Res	Type
8	H	66	HIS
8	H	144	GLN
8	H	165	ASN
8	H	172	ASN
8	H	190	ASN
9	I	29	ASN
9	I	81	GLN
10	J	36	GLN
10	J	54	GLN
10	J	62	ASN
10	J	64	GLN
10	J	77	GLN
10	J	85	GLN
10	J	112	GLN
10	J	140	HIS
10	J	160	GLN
10	J	186	GLN
11	K	9	GLN
11	K	24	ASN
11	K	85	ASN
11	K	131	GLN
11	K	174	ASN
11	K	207	ASN
12	L	-9	GLN
12	L	-7	ASN
12	L	20	ASN
12	L	27	ASN
12	L	40	ASN
12	L	46	ASN
12	L	61	ASN
12	L	67	HIS
12	L	70(A)	ASN
12	L	85	HIS
12	L	98	HIS
12	L	1(I)	ASN
12	L	166	HIS
12	L	168	GLN
13	M	-7	GLN
13	M	10	ASN
13	M	40	ASN
13	M	54	HIS
13	M	89	GLN

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Mol	Chain	Res	Type
13	M	93	ASN
13	M	132	HIS
13	M	149	GLN
13	M	157	ASN
13	M	191	GLN
14	N	69	GLN
14	N	106	ASN
14	N	145	ASN
14	N	161	GLN
1	O	33	GLN
1	O	97	HIS
1	O	121	GLN
1	O	145	ASN
1	O	227	GLN
2	P	23	GLN
2	P	33	HIS
2	P	71	ASN
2	P	97	GLN
2	P	104	ASN
2	P	121	GLN
2	P	125	GLN
2	P	156	ASN
2	P	173	GLN
2	P	177	GLN
2	P	218	ASN
3	Q	23	GLN
3	Q	82	ASN
3	Q	97	GLN
3	Q	120	GLN
3	Q	121	GLN
3	Q	125	GLN
3	Q	150	GLN
3	Q	163	GLN
3	Q	209	ASN
3	Q	238	GLN
3	Q	243	GLN
4	R	23	GLN
4	R	108	ASN
4	R	114	GLN
4	R	161	ASN
4	R	20(A)	ASN
4	R	211	GLN

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Mol	Chain	Res	Type
4	R	218	GLN
4	R	226	ASN
5	S	7	ASN
5	S	33	GLN
5	S	64	GLN
5	S	73	HIS
5	S	97	ASN
5	S	104	ASN
5	S	114	HIS
5	S	121	GLN
5	S	123	ASN
5	S	125	GLN
5	S	152	GLN
5	S	156	ASN
5	S	199	GLN
5	S	2(E)	ASN
6	T	23	GLN
6	T	43	ASN
6	T	87	HIS
6	T	90	ASN
6	T	121	GLN
6	T	127	ASN
6	T	192	GLN
6	T	241	ASN
7	U	32	ASN
7	U	34(A)	ASN
7	U	87	ASN
7	U	118	ASN
7	U	121	GLN
7	U	125	GLN
7	U	169	GLN
7	U	175	ASN
7	U	178	ASN
7	U	18(C)	HIS
7	U	184	ASN
7	U	208	ASN
7	U	228	ASN
8	V	30	ASN
8	V	66	HIS
8	V	141	HIS
8	V	144	GLN
8	V	165	ASN

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Mol	Chain	Res	Type
8	V	172	ASN
8	V	190	ASN
9	W	29	ASN
9	W	56	ASN
9	W	81	GLN
10	X	36	GLN
10	X	54	GLN
10	X	62	ASN
10	X	64	GLN
10	X	77	GLN
10	X	85	GLN
10	X	112	GLN
10	X	140	HIS
10	X	160	GLN
10	X	186	GLN
11	Y	9	GLN
11	Y	24	ASN
11	Y	62	GLN
11	Y	85	ASN
11	Y	131	GLN
11	Y	174	ASN
11	Y	207	ASN
12	Z	-9	GLN
12	Z	-7	ASN
12	Z	27	ASN
12	Z	40	ASN
12	Z	46	ASN
12	Z	61	ASN
12	Z	67	HIS
12	Z	70(A)	ASN
12	Z	85	HIS
12	Z	14(B)	ASN
12	Z	1(I)	ASN
12	Z	166	HIS
12	Z	168	GLN
13	1	-7	GLN
13	1	10	ASN
13	1	40	ASN
13	1	54	HIS
13	1	89	GLN
13	1	93	ASN
13	1	149	GLN

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Mol	Chain	Res	Type
13	1	157	ASN
13	1	191	GLN
14	2	69	GLN
14	2	106	ASN
14	2	141	ASN
14	2	145	ASN
14	2	157	HIS
14	2	161	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
15	SLR	K	301	11	10,15,16	3.02	2 (20%)	10,23,25	1.90	3 (30%)
15	SLR	Y	301	11	10,15,16	3.04	2 (20%)	10,23,25	1.98	3 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	SLR	K	301	11	-	3/12/32/35	0/1/1/1
15	SLR	Y	301	11	-	3/12/32/35	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	Y	301	SLR	C13-C11	7.19	1.59	1.53
15	K	301	SLR	C13-C11	6.93	1.59	1.53
15	Y	301	SLR	O7-C6	-5.68	1.24	1.42
15	K	301	SLR	O7-C6	-5.63	1.24	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	Y	301	SLR	C9-C2-C1	-3.91	112.51	116.53
15	K	301	SLR	C9-C2-C1	-3.61	112.82	116.53
15	Y	301	SLR	O12-C11-C13	-2.79	103.92	109.90
15	K	301	SLR	O12-C11-C13	-2.75	104.00	109.90
15	K	301	SLR	O10-C3-C2	-2.54	124.16	126.17
15	Y	301	SLR	O10-C3-C2	-2.52	124.17	126.17

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	K	301	SLR	C1-C5-C6-O7
15	K	301	SLR	N4-C5-C6-O7
15	K	301	SLR	C11-C5-C6-O7
15	Y	301	SLR	C1-C5-C6-O7
15	Y	301	SLR	N4-C5-C6-O7
15	Y	301	SLR	C11-C5-C6-O7

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	K	301	SLR	2	0

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%)	-0.05	6 (2%) 59 49	27, 43, 74, 104	0
1	O	250/250 (100%)	0.13	14 (5%) 30 23	31, 52, 78, 101	0
2	B	244/244 (100%)	0.22	19 (7%) 19 13	29, 49, 82, 111	0
2	P	244/244 (100%)	0.30	17 (6%) 22 16	29, 51, 87, 113	0
3	C	241/241 (100%)	0.33	21 (8%) 16 11	31, 54, 102, 119	0
3	Q	241/241 (100%)	0.53	22 (9%) 15 11	37, 57, 105, 120	0
4	D	242/242 (100%)	0.23	14 (5%) 29 21	35, 51, 84, 116	0
4	R	242/242 (100%)	0.31	13 (5%) 31 23	36, 55, 89, 116	0
5	E	233/233 (100%)	0.24	11 (4%) 36 28	34, 51, 77, 103	0
5	S	233/233 (100%)	0.16	9 (3%) 43 34	33, 51, 79, 105	0
6	F	244/244 (100%)	0.06	12 (4%) 35 27	30, 44, 86, 106	0
6	T	244/244 (100%)	-0.11	4 (1%) 70 61	26, 43, 82, 103	0
7	G	243/243 (100%)	-0.16	6 (2%) 58 48	23, 39, 68, 112	0
7	U	243/243 (100%)	-0.06	8 (3%) 49 39	27, 42, 69, 113	0
8	H	222/222 (100%)	-0.21	2 (0%) 81 74	25, 40, 58, 89	0
8	V	222/222 (100%)	-0.12	3 (1%) 73 64	33, 43, 60, 96	0
9	I	204/204 (100%)	-0.31	1 (0%) 87 82	28, 41, 59, 77	0
9	W	204/204 (100%)	-0.38	1 (0%) 87 82	30, 42, 61, 78	0
10	J	198/198 (100%)	-0.13	5 (2%) 58 48	30, 44, 61, 118	0
10	X	198/198 (100%)	-0.11	5 (2%) 58 48	28, 45, 62, 120	0
11	K	212/212 (100%)	-0.23	0 100 100	28, 43, 61, 69	0
11	Y	212/212 (100%)	-0.19	3 (1%) 73 64	27, 44, 63, 72	0
12	L	222/222 (100%)	-0.17	2 (0%) 81 74	26, 43, 65, 86	0
12	Z	222/222 (100%)	-0.17	4 (1%) 67 58	28, 42, 68, 88	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	1	233/233 (100%)	-0.36	1 (0%)	88 84	24, 38, 53, 60	0
13	M	233/233 (100%)	-0.26	1 (0%)	88 84	25, 39, 54, 61	0
14	2	196/196 (100%)	-0.33	3 (1%)	72 63	23, 37, 56, 77	0
14	N	196/196 (100%)	-0.40	3 (1%)	72 63	26, 36, 57, 74	0
All	All	6368/6368 (100%)	-0.03	210 (3%)	49 39	23, 45, 78, 120	0

All (210) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	R	12(D)	ALA	9.8
3	Q	56	LEU	8.3
7	U	240	ASP	8.1
4	R	12(E)	SER	7.9
4	D	12(E)	SER	7.9
4	D	12(D)	ALA	7.1
2	B	21(B)	GLY	6.3
4	D	12(C)	GLY	6.2
13	1	-8	THR	6.1
10	X	192	ALA	5.6
6	F	5	GLY	5.5
3	C	55	THR	5.2
7	G	6	ALA	5.1
3	C	56	LEU	4.9
4	R	12(C)	GLY	4.7
3	Q	55	THR	4.7
5	S	4	PHE	4.6
4	D	126	ARG	4.5
4	R	127	LEU	4.4
1	O	56	SER	4.4
2	B	217	ALA	4.3
12	L	145	TYR	4.2
2	P	21(C)	ASP	4.1
10	X	193	GLN	4.1
2	B	54	VAL	4.1
1	A	203	GLU	4.1
4	R	126	ARG	4.1
2	P	54	VAL	4.1
3	C	208	LYS	4.0
4	D	12(F)	GLY	3.9
3	Q	58	LEU	3.9
3	Q	236	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
2	P	21(D)	GLY	3.9
2	P	4	GLY	3.8
7	U	239	GLN	3.8
10	J	192	ALA	3.8
2	B	21(D)	GLY	3.8
10	J	191	GLN	3.8
4	D	127	LEU	3.8
1	A	5	THR	3.8
5	S	203	ASP	3.7
8	V	91	GLN	3.7
6	F	6	THR	3.7
12	Z	145	TYR	3.7
10	X	191	GLN	3.7
3	C	54	SER	3.6
10	J	193	GLN	3.6
2	B	239	THR	3.6
5	E	127	TYR	3.6
1	O	5	THR	3.6
7	G	8	TYR	3.6
2	P	21(B)	GLY	3.6
5	E	203	ASP	3.6
6	F	204	ASP	3.5
7	G	240	ASP	3.5
2	P	21(A)	LYS	3.5
5	E	4	PHE	3.5
2	B	218	ASN	3.5
3	C	240	LYS	3.4
4	D	242	ALA	3.4
7	G	239	GLN	3.4
1	O	65	SER	3.4
3	Q	208	LYS	3.4
9	W	-8	SER	3.3
6	F	240	ILE	3.3
2	B	21(A)	LYS	3.3
3	C	59	GLN	3.3
13	M	-8	THR	3.3
1	A	204	GLY	3.3
2	B	21(C)	ASP	3.2
3	Q	240	LYS	3.2
2	B	219	GLU	3.2
2	P	217	ALA	3.2
3	Q	54	SER	3.1

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Mol	Chain	Res	Type	RSRZ
2	P	218	ASN	3.1
9	I	-8	SER	3.1
4	R	12(F)	GLY	3.1
3	C	206	GLY	3.1
2	P	219	GLU	3.1
3	Q	183	PRO	3.1
5	S	5	ARG	3.1
3	Q	57	LYS	3.1
3	C	241	GLN	3.1
2	P	239	THR	3.0
1	O	4	MET	3.0
5	S	127	TYR	3.0
1	A	4	MET	2.9
14	2	107	LYS	2.9
12	Z	120	GLU	2.9
14	N	105	ASP	2.9
3	C	33	ARG	2.9
5	S	204	GLU	2.9
2	B	143	ASP	2.9
2	B	63	THR	2.9
4	R	12(B)	GLU	2.8
2	P	220	TYR	2.8
3	Q	241	GLN	2.8
6	F	43	ASN	2.8
1	O	57	PRO	2.8
3	C	238	GLN	2.7
4	R	12(G)	GLU	2.7
6	T	20(C)	LYS	2.7
12	Z	14(W)	LYS	2.7
3	C	242	GLU	2.7
5	S	227	GLU	2.6
7	G	18(H)	GLU	2.6
4	R	167	SER	2.6
2	B	64	THR	2.6
3	Q	238	GLN	2.6
4	R	9	ASP	2.6
2	B	63(A)	SER	2.6
14	N	107	LYS	2.6
4	D	205	GLU	2.6
5	E	33	GLN	2.6
7	U	6	ALA	2.6
1	O	55	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	202	VAL	2.6
1	O	185	GLU	2.6
5	E	5	ARG	2.5
3	C	203	THR	2.5
3	C	52	ARG	2.5
8	V	223	ASP	2.5
1	O	58	LEU	2.5
10	J	188	ASP	2.5
10	X	189	ASP	2.5
6	T	5	GLY	2.5
2	B	216	ARG	2.5
6	F	238	LYS	2.5
6	F	18(A)	ASP	2.5
4	D	12(G)	GLU	2.5
4	D	243	ALA	2.5
5	S	126	SER	2.4
2	B	4	GLY	2.4
6	F	184	LEU	2.4
5	E	2(E)	ASN	2.4
6	F	205	ASN	2.4
4	D	12(A)	GLY	2.4
5	E	56	ASP	2.4
7	U	17(C)	LYS	2.4
5	E	204	GLU	2.4
7	G	171	GLU	2.4
3	Q	202	GLN	2.4
3	Q	232	TYR	2.4
6	T	207	ASP	2.4
10	X	190	PHE	2.4
3	C	174	GLU	2.4
3	Q	242	GLU	2.4
10	J	-1	MET	2.4
1	O	235	ALA	2.3
3	Q	203	THR	2.3
5	E	44	THR	2.3
2	P	53	LYS	2.3
3	Q	178	LYS	2.3
2	P	56	SER	2.3
2	P	58	LEU	2.3
4	R	12(A)	GLY	2.3
3	Q	44	ASN	2.3
6	T	43	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	O	64	LEU	2.3
14	2	18(I)	GLN	2.3
5	E	126	SER	2.3
3	Q	207	ALA	2.2
5	S	207	LEU	2.2
2	B	61	GLN	2.2
3	C	243	GLN	2.2
7	U	29	LYS	2.2
7	U	218	ASP	2.2
1	O	21(P)	LYS	2.2
3	C	233	VAL	2.2
4	R	121	LEU	2.2
11	Y	202	GLU	2.2
4	R	122	ARG	2.2
11	Y	145	ASP	2.2
7	U	128	TYR	2.2
2	P	204	SER	2.2
3	C	187	GLU	2.2
3	C	207	ALA	2.2
3	C	230	ASN	2.1
5	E	2(C)	VAL	2.1
3	C	14(A)	ARG	2.1
1	O	63	THR	2.1
4	D	120	ALA	2.1
8	H	91	GLN	2.1
12	L	14(W)	LYS	2.1
4	D	9	ASP	2.1
3	Q	210	ILE	2.1
14	N	18(F)	GLU	2.1
3	Q	243	GLN	2.1
2	B	185	LYS	2.1
3	Q	63	THR	2.1
6	F	18	ASP	2.1
8	H	221	ILE	2.1
4	D	170	GLU	2.1
1	O	54	SER	2.0
2	B	235	LYS	2.0
2	P	59	LEU	2.0
8	V	9	ASN	2.0
3	Q	52	ARG	2.0
2	P	64	THR	2.0
6	F	20(B)	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	181	LYS	2.0
5	S	198	SER	2.0
12	Z	70	HIS	2.0
1	O	184	LEU	2.0
14	2	18(J)	LEU	2.0
1	A	21(P)	LYS	2.0
3	C	239	GLU	2.0
6	F	239	GLU	2.0
11	Y	201	GLU	2.0
7	U	8	TYR	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($\text{\AA}^2$)	Q<0.9
15	SLR	Y	301	15/16	0.92	0.10	46,48,49,51	0
15	SLR	K	301	15/16	0.95	0.08	42,42,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.